(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
29 April 2004 (29.04.2004)

PCT

(10) International Publication Number
WO 2004/035760 A2

(51) International Patent Classification[7]: C12N

(21) International Application Number:
PCT/US2003/033142

(22) International Filing Date: 17 October 2003 (17.10.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/419,463 18 October 2002 (18.10.2002) US

(71) Applicants *(for all designated States except US)*: **UNIVERSITY OF FLORIDA** [US/US]; Office of Technology Licensing, P.O.Box 115500, Gainesville, FL 32611-5500 (US). **CENTRE DE COOPERATION INTERNATIONALE EN RECHERCHE AGRONOMIQUE POUR LE DEVELOPPEMENT (CIRAD)** [FR/FR]; 42 rue Scheffer, F-75116 Paris (FR).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **ROYER, Monique** [US/US]; 61, rue de Gascogne, F-34090 Montpellier (FR). **GABRIEL, Dean, W.** [FR/FR]; 5519 N.W.91st Blvd., Gainesville, TX 32653-5117 (US). **FRUTOS, Roger** [FR/FR]; 1, rue des Alicantes, F-34680 Saint Georges d'Orques (FR). **ROTT, Philippe** [FR/FR]; 3 rue Paul Cézanne, F-34830 Clapiers (FR).

(74) Agents: **ELISENSCHENK, Frank, C.** et al.; Saliwanchik, Lloyd & Saliwanchik, 2421 NW 41st Street, Suite A-1, Gainesville, FL 32606-6669 (US).

(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 2004/035760 A2

(54) Title: COMPLETE BIOSYNTHETIC GENE SET FOR SYNTHESIS OF POLYKETIDE ANTIBIOTICS, INCLUDING THE ALBICIDIN FAMILY, RESISTANCE GENES AND USES THEREOF

(57) Abstract: Three gene clusters that together encode albicidin biosynthesis, the complete gene DNA sequences, and the deduced protein sequences for the enzymes and methods for using the DNA sequences are disclosed and discussed as well as methods for plant protection and creating new antibiotics. The novel Albicidin family of antibiotics is disclosed and their structure deduced.

COMPLETE BIOSYNTHETIC GENE SET FOR SYNTHESIS OF POLYKETIDE ANTIBIOTICS, INCLUDING THE ALBICIDIN FAMILY, RESISTANCE GENES, AND USES THEREOF

This application claims the benefit of U.S. Provisional patent application with Serial No. 60/419,463, filed October 18, 2002 the disclosure of which is hereby incorporated by reference in its entirety, including all nucleic acid sequences, amino acid sequences, chemical formulae, tables and figures.

TECHNICAL FIELD

[0001] The invention is in the field of genetic engineering, and in particular the isolation and expression of the biosynthetic genes that produce a family of antibiotics known generically as albicidins.

BACKGROUND OF THE INVENTION

[0002] U.S. Patent No. 4,525,354 to Birch and Patil described a "non-peptide" antibiotic of M.W. "about 842" called "albicidin." Albicidin is described as produced by culturing chlorosis-inducing strains of *Xanthomonas albilineans* isolated from diseased sugarcane, and mutants thereof. The antibiotic was isolated from the culture medium by adsorption on resin and was purified by gel filtration and High Performance Liquid Chromatography (HPLC). The chemical structure of this antibiotic was not determined and remained unknown, although the Birch and Patil patent disclosed spectral data for a fraction having antibiotic activity and the presence of approximately 38 carbon atoms and at least one COOH group.

[0003] *Xanthomonas albilineans* is a systemic, xylem-invading pathogen that causes leaf scald disease of sugarcane (interspecific hybrids of *Saccharum* species) (Ricaud and Ryan, 1989; Rott and Davis, 2000). Leaf scald symptoms include chlorosis, necrosis, rapid wilting, and plant death. Chlorosis-inducing strains of the pathogen produce several toxic compounds. The major toxic component, named albicidin, inhibits chloroplast DNA replication, resulting in blocked chloroplast differentiation and chlorotic leaf streaks that are characteristic of the plant disease (Birch and Patil, 1983, 1985b, 1987a and 1987b). Several studies established that albicidin plays a key role in pathogenesis and especially in the development of disease symptoms (Wall and Birch, 1997; Zhang and Birch, 1997; Zhang *et al.*, 1999; Birch, 2001).

[0004] The prior art indicates that albicidin inhibits prokaryotic DNA replication and is bactericidal to a range of gram-positive and gram-negative bacteria (Birch and Patil, 1985a). Albicidin is therefore of interest as a potential clinical antibiotic (Birch and Patil, 1985a). However, low yield of toxin production in *X. albilineans* has slowed down studies into the chemical structure of albicidin and its therapeutic application (Zhang *et al.*, 1998). The chemical structure of this albicidin remains unknown, however this albicidin has been partially

characterized as a non-peptide antibiotic with a molecular weight of about 842 that contains approximately 38 carbon atoms with three or four aromatic rings, at least one COOH group, two OCH3 groups, a trisubstituted double bond and a CN linkage (Birch and Patil, 1985a; Huang *et al.*, 2001).

[0005] Molecular cloning and characterization of the genes governing the biosynthesis of albicidin is of considerable interest because such information provides approaches to engineer overproduction of albicidin, to characterize its chemical structure, to allow therapeutic applications and to clarify the relationship between toxin production and the ability to colonize sugarcane. Two similar mutagenesis and complementation studies have been conducted to identify the genetic basis of albicidin production in *X. albilineans* strains isolated in two different geographical locations, Australia and Florida.

[0006] One study of *X. albilineans* strain LS155 from Australia revealed that genes for albicidin biosynthesis and resistance span at least 69kb (Wall and Birch, 1997). Subsequently, three genes required for albicidin biosynthesis were identified, cloned and sequenced from two Australian strains of *X. albilineans* (LS155 and Xa13): *xabA*, *xabB* and *xabC* (Huang et al., 2001; Huang et al. 2000a, 2000b). The *xabB* gene encodes a large protein with a predicted size of 525.6 kDa, with a modular architecture indicative of a multi functional polyketide synthase (PKS) linked to a nonribosomal peptide synthetase (NRPS) (Huang *et al.*, 2001). The *xabC* gene, located immediately downstream from *xabB*, encodes an S-adenosyl-L-methionine (SAM)-dependent *O*-methyltransferase (Huang *et al.*, 2000a). The *xabA* gene, located in another region of the genome, encodes a phosphopantetheinyl transferase required for post-translational activation of PKS and NRPS enzymes (Huang *et al.*, 2000b).

[0007] These first results demonstrated that the albicidin biosynthesis apparatus is a PKS and/or NRPS system. Such systems assemble simple acyl-coenzyme A or amino acid monomers to produce polyketides and/or nonribosomal peptides (Marahiel *et al.*, 1997; Cane, 1997; Cane and Walsh, 1999). These metabolites form very large classes of natural products that include numerous important pharmaceuticals, agrochemicals, and veterinary agents such as antibiotics, immunosuppressants, anti-cholesterolemics, as well as antitumor, antifungal and antiparasitic agents. Genetic studies of prokaryotic PKS and NRPS produced detailed information regarding the function and the organization of genes responsible for the biosynthesis of polyketides and nonribosomal peptides. Such knowledge, in turn, made it possible to produce combinations of PKS and NRPS genes from different microorganisms in order to produce novel antibiotics (McDaniel *et al.*, 1999; Rodriguez and McDaniel, 2001; Pfeifer *et al.*, 2001). Investigating the complete albicidin biosynthesis apparatus is therefore of great interest because such results may contribute to the knowledge as to how PKS and NRPS interact and how they might be manipulated to engineer novel molecules.

[0008] A second study with *X. albilineans* strain Xa23R1 from Florida revealed that at least two gene clusters, one spanning more than 48 kb, are involved in albicidin production (Rott *et al.*, 1996). This conclusion was based on the following data: (I) fifty Xa23R1 mutants defective in albicidin production were isolated; (ii) a Xa23R1 genomic library of 845 clones, designated pALB1 to pALB845, was constructed; (iii) two overlapping DNA inserts of approximately 47 kb and 41 kb, from clones pALB540 and pALB571 respectively, complemented forty-five mutants and were supposed to contain a major gene cluster involved in albicidin production; (iv) a DNA insert of approximately 36 kb, from clone pALB639, complemented four of the five remaining mutants not complemented by pALB540 and pALB571, and was supposed to contain a second region involved in albicidin production; and (v) the remaining mutant, AM37, which was not complemented by any of the three cosmids pALB540, pALB571 and pALB639, was supposed to be mutated in a third region of the genome involved in albicidin production.

[0009] The DNA sequences of all of the genes required to produce the albicidin family of polyketide antibiotics, the expressed protein amino acid sequences of all of the genes, and the deduced structure of Albicidin have not been previously reported, although fragmentary sequences that include three of the biosynthetic genes have been reported. Identification of one albicidin gene, *xabC*, as a methyltransferase gene involved in albicidin biosynthesis is reported by Huang, G., Zhang, L. & Birch, R.G. (2000a, Gene **255**, 327-333) and claimed as biologically active in producing a polyketide antibiotic in PCT WO 02/24736 A1. Identification of a second albicidin gene, *xabA*, as a phosphopantetheinyl transferase gene is reported by Huang, G., Zhang, L. and Birch, R.G. (2000b) Gene **258**, 193-199 and claimed as biologically active in producing a polyketide antibiotic in PCT WO 02/24736 A1. Huang, G., Zhang, L. & Birch, R.G. (2001) Microbiology **147**, 631-642, report a DNA sequence of *xabB* (GenBank accession # AF239749), a multi functional polyketide-peptide synthetase that may be essential for albicidin biosynthesis in *Xanthomonas albilineans.* This *xabB* gene is reported as full length by Birch in PCT WO 02/24736 A1 (their seq. ID #1) and claimed by Birch in PCT WO 02/24736 A1 as a biologically active polyketide synthase of 4,801 amino acids in length, enabling production of albicidin. However, the DNA sequence reported by Huang *et al.* (2001) in GenBank AF239749 and by Birch in PCT WO 02/24736 A1 (their seq. ID #1) appears to be incomplete and missing 6,234 bp of DNA sequence encoding 2,078 amino acids. The subject invention provides the complete DNA sequence of *xabB* (*albI*, our seq. 20) as 20,637 bp, encoding a biologically active polyketide synthase of 6,879 amino acids of in this application (our seq ID #26). Factors affecting biosynthesis by *Xanthomonas albilineans* of albicidins antibiotics and phytotoxins are discussed in J. Appl. Microbiol. **85**, 1023-1028. and Wall, M.K. & Birch, R.G. (1997). Genes for albicidin biosynthesis and resistance span at least 69 kb in the genome of *Xanthomonas albilineans*. Lett. Appl. Microbiol. **24**, 256-260. A gene from *X. albilineans* strain Xa13, designed AlbF, which confers high level albicidin resistance in *Escherichia coli* and which encodes a putative albicidin

efflux pump, was directly submitted to Genbank by Bostock and Birch (Accession No. AF403709).

SUMMARY OF THE INVENTION

[0010] The present invention describes and characterizes the family of antibiotics that is produced by culturing chlorosis-inducing strains of *X. albilineans* and mutants thereof, together with the complete set of twenty biosynthetic genes capable of producing the unique and previously uncharacterized family of antibiotics produced by *X. albilineans* and previously lumped together as "albicidins." The set of twenty biosynthetic genes isolated, purified and cloned from a culture of *X. albilineans* revealed that this set of biosynthetic genes is capable of synthesizing products exhibiting a high level of variation among the products, indicating that albicidins comprise a family of polyketide antibiotics. The albicidins described in the present invention are synthesized by twenty genes, including one polyketide-peptide synthase, one polyketide synthase and two peptide synthases, but the substrates of the polyketide-peptide synthase and of one peptide synthase are not α-amino acids. The biosynthetic enzymes represent a previously undescribed and unique polyketide antibiotic biosynthetic system.

BRIEF DESCRIPTION OF THE DRAWINGS

[0011] Figure 1 is a Physical Map and genetic organization of the DNA Region containing the major gene cluster XALB1 involved in the biosynthesis of Albicidins.

[0012] Figure 2 is an illustration of the organization of the four PKS modules and the seven NRPS modules identified in cluster XALB1 and comparison with the organization of the prior art material XabB.

[0013] Figure 3 shows the conserved sequence motifs in O-methyltransferases and C-methyltransferases involved in antibiotic biosynthesis in bacteria and in AlbII.

[0014] Figure 4 shows the conserved sequence motifs in O-methyltransferases and in different tcmP-like hypothetical proteins and AlbVI.

[0015] Figure 5 is an illustration of the alignment of the primary sequences between the conserved motifs A4 and A5 of Alb NPRSs and PKS-4 in *Xanthomonas albilineans* with the corresponding sequences of GrsA (Phe) accession number: P14687 and Blm NRPS-2 (β-Ala) accession number AF210249.

[0016] Figure 6 shows Rho-independent transcription terminators identified in the intergenic regions of XALB1 and XALB3 clusters.

[0017] Figure 7A shows sequences identified as a putative bidirectional promoter between albX and albXVII in XALB1 for transcriptional control of operons 3 and 4.

[0018] Figure 7B shows sequences identified as a putative unidirectional promoter upstream from *albXIX* for transcriptional control of operon 5 if *albXVIII* is not expressed.

[0019] Figure 8 is a physical map and genetic organization of the DNA region containing the gene clusters XALB2 and XALB3 involved in albicidin production.

[0020] Figure 9A is linear model 1 leading to the biosynthesis of only one polyketide-polypeptide albicidin backbone.

[0021] Figure 9B is linear model 2 leading to the biosynthesis of four different polyketide-polypeptide backbone.

[0022] Figure 10A is an alignment of the conserved motifs in AT domains from RifA-1, -2, -3, RifB-1, RifE-1 (Rifamycin PKSs, August *et al.*, 1998) and BlmVIII (Bleomycin PKS; Du *et al.*, 2000).

[0023] Figure 10B is a comparison of AlbXIII, FenF (a malonyl-CoA transacylase located upstream from *mycA*, Duitman *et al.*, 1999) and LipA (a lipase; Valdez *et al.*, 1999).

[0024] Figure 11A is a proposed model for biosynthesis of albicidin, including putative substrates of PKS and NRPS modules.

[0025] Figure 11B shows the proposed compositions and structures of albicidins.

[0026] Figure 12 illustrates subcloning of operons 3 and 4 (from pALB540), XALB2 (from pAC389.1) and XALB3 (from pEV639) into a single plasmid, pOp3-4/XALB2-3. A *Bam*HI–*Pst*I fragment from pALB540, corresponding to a portion of operon 4, was subcloned into pBCKS(+), yielding pBC/Op4D (step 1). A *Xho*I site was introduced into this vector immediately upstream from the *Bfr*I site by directed mutagenesis, yielding pBC/Op4DXhoI (step 2). The *Eco*RI fragment from pAC389.1 (XALB2) was then subcloned into pBC/Op4DXhoI, yielding pBC/Op4D/XALB2 (step 3). A *Bfr*I fragment from pALB540 containing complete operon 3 and the beginning of operon 4 was subcloned into pBC/Op4D/XALB2, yielding pBC/Op3-4/XALB2 (step 4). The *Sal*I fragment from pEV639 (XALB3) was subcloned into pBKS, yielding pBKS/XALB3 (step 5). The *Sal*I site located on the *Kpn*I side of the polylinker was then destroyed and substituted by a *Xho*I restriction site, yielding pBKS/XALB3XhoI (step 6). Finally, the *Xho*I cassette of pBC/Op3-4/XALB2 was subcloned into the *Sal*I restriction site of pBKS/XALB3XhoI, yielding pBKS/Op3-4/XALB2-3 (step 7). An *Xho*I site was added to the BamHI site of pLAFR3, yielding pLAFR3XhoI (step8). The *Xho*I cassette from pBKS/Op3-4/XALB2-3 was then cloned into pLAFR3XhoI, yielding pOp3-4/XALB2-3 (step 9).

DETAILED DESCRIPTION OF THE INVENTION

[0027] The invention results from the DNA sequencing of the complete major gene cluster XALB1, as well as the noncontiguous fragments XALB2 and XALB3. XALB1 is present in the two overlapping DNA inserts of clones pALB540 and pALB571. Reading frame analysis

and homology analyses allow one to predict the genetic organization of XALB1 and to assign a function to the genes potentially required for albicidin production. Based on the alignment of the different PKS and/or NRPS enzymes encoded by XALB1 we proposed a model for the albicidin backbone biosynthesis. However the invention disclosed herein does not depend upon the accuracy of the proposed model. The invention includes the successful cloning and DNA sequencing of the second region of the genome (XALB2) involved in albicidin production and mutated in mutant AM37.

[0028] The invention includes the characterization of the third region of the genome (XALB3) involved in albicidin production present in clone pALB639. These results allowed the possibility to characterize all enzymes of the albicidin biosynthesis pathway including structural, resistance and regulatory elements and to engineer overproduction of albicidin.

[0029] The subject invention provides:

(a) isolated, recombinant, and/or purified polynucleotide sequences comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, and 25;

(b) isolated, recombinant, and/or purified polynucleotide sequences comprising a polynucleotide encoding a polypeptide selected from the group consisting of SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, and 47;

(c) isolated, recombinant, and/or purified polynucleotide sequences comprising a polynucleotide that is complementary to a polynucleotide selected from the group consisting of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, and 25;

(d) isolated, recombinant, and/or purified polynucleotide sequences comprising a polynucleotide that is complementary to a polynucleotide encoding a polypeptide selected from the group consisting of SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, and 47; or

(e) isolated, recombinant, and/or purified polynucleotide sequences comprising a polynucleotide that is at least 70% homologous to: (1) a polynucleotide selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, and 25; (2) a polynucleotide sequence encoding a polypeptide selected from the group consisting of SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, and 47; (3) a polynucleotide that is complementary to a polynucleotide encoding a polypeptide selected from the group consisting of SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, and 47; (3) a polynucleotide that is complementary to a polynucleotide sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, and 25;

(f) isolated, recombinant, and/or purified polynucleotide sequences comprising a polynucleotide sequence encoding variant (e.g., a variant polypeptide) of a polypeptide selected

from the group consisting of SEQ ID NOs: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, and 47, wherein said variant has at least on of the biological activities associated with the polypeptides of SEQ ID NOs: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, and 47;

g) isolated, recombinant, and/or purified polynucleotide sequences comprising polynucleotide sequence encoding a fragment of a polypeptide selected from the group consisting of SEQ ID NOs: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, and 47 or a fragment of a variant polypeptide of SEQ ID NOs: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, and 47;

h) isolated, recombinant, and/or purified polynucleotide sequences comprising a polynucleotide sequence encoding multimeric construct;

j) a genetic construct comprising a polynucleotide sequence as set forth in (a), (b), (c), (d), (e), (f), (g), or (h);

k) a vector comprising a polynucleotide sequence as set forth in (a), (b), (c), (d), (e), (f), (g), or (h);

l) a host cell comprising a vector a polynucleotide sequence as set forth in (a), (b), (c), (d), (e), (f), (g), or (h);

m) a transformed plant cell comprising a vector comprising a polynucleotide sequence as set forth in (a), (b), (c), (d), (e), (f), (g), or (h);

n) a transformed plant comprising a vector comprising a polynucleotide sequence as set forth in (a), (b), (c), (d), (e), (f), (g), or (h); or;

o) a polynucleotide that hybridizes under low, intermediate or high stringency with a polynucleotide sequence as set forth in (a), (b), (c), (d), (e), (f), (g), or (h).

[0030] "Nucleotide sequence", "polynucleotide" or "nucleic acid" can be used interchangeably and are understood to mean, according to the present invention, either a double-stranded DNA, a single-stranded DNA or products of transcription of the said DNAs (e.g., RNA molecules). It should also be understood that the present invention does not relate to genomic polynucleotide sequences in their natural environment or natural state. The nucleic acid, polynucleotide, or nucleotide sequences of the invention can be isolated, purified (or partially purified), by separation methods including, but not limited to, ion-exchange chromatography, molecular size exclusion chromatography, or by genetic engineering methods such as amplification, subtractive hybridization, cloning, subcloning or chemical synthesis, or combinations of these genetic engineering methods.

[0031] A homologous polynucleotide or polypeptide sequence, for the purposes of the present invention, encompasses a sequence having a percentage identity with the polynucleotide or polypeptide sequences, set forth herein, of between at least (or at least about) 70.00% to 99.99% (inclusive). The aforementioned range of percent identity is to be taken as including, and

providing written description and support for, any fractional percentage, in intervals of 0.01%, between 20.00% and, up to, including 99.99%. These percentages are purely statistical and differences between two nucleic acid sequences can be distributed randomly and over the entire sequence length. For example, homologous sequences can exhibit a percent identity of 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 percent with the sequences of the instant invention. Typically, the percent identity is calculated with reference to the polynucleotide of a particular SEQ ID NO.; the full-length of a selected polynucleotide, or the native (naturally occurring) polynucleotide. The terms "identical" or percent "identity", in the context of two or more polynucleotide or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues that are the same, when compared and aligned for maximum correspondence over a comparison window, as measured using a sequence comparison algorithm or by manual alignment and visual inspection.

[0032] A "complementary" polynucleotide sequence, as used herein, generally refers to a sequence arising from the hydrogen bonding between a particular purine and a particular pyrimidine in double-stranded nucleic acid molecules (DNA-DNA, DNA-RNA, or RNA-RNA). The major specific pairings are guanine with cytosine and adenine with thymine or uracil. A "complementary" polynucleotide sequence may also be referred to as an "antisense" polynucleotide sequence or an "antisense" sequence.

[0033] Sequence homology and sequence identity can also be determined by hybridization studies under high stringency, intermediate stringency, and/or low stringency. Various degrees of stringency of hybridization can be employed. The more severe the conditions, the greater the complementarity that is required for duplex formation. Severity of conditions can be controlled by temperature, probe concentration, probe length, ionic strength, time, and the like. Preferably, hybridization is conducted under low, intermediate, or high stringency conditions by techniques well known in the art, as described, for example, in Keller, G.H., M.M. Manak [1987] DNA Probes, Stockton Press, New York, NY, pp. 169-170.

[0034] It is also well known in the art that restriction enzymes can be used to obtain functional fragments of the subject DNA sequences. For example, Bal31 exonuclease can be conveniently used for time-controlled limited digestion of DNA (commonly referred to as "erase-a-base" procedures). See, for example, Maniatis et al. [1982] Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, New York; Wei et al. [1983] J. Biol. Chem. 258:13006-13512.

[0035] The present invention further comprises fragments of the polynucleotide sequences of the instant invention. Representative fragments of the polynucleotide sequences according to the invention will be understood to mean any nucleotide fragment having at least 5

successive nucleotides, preferably at least 12 successive nucleotides, and still more preferably at least 15 or at least 20 successive nucleotides of the sequence from which it is derived. The upper limit for such fragments is the total number of nucleotides found in the full-length sequence encoding a particular polypeptide (e.g., a polypeptide selected from the group consisting of SEQ ID NOs: 26-50). The term "successive" can be interchanged with the term "consecutive". In some embodiments, a polynucleotide fragment may be referred to as "a contiguous span of at least X nucleotides, wherein X is any integer value beginning with 5. The upper limit for polynucleotide fragments of the subject invention is the total number of nucleotides found in the full-length sequence of a particular SEQ ID or the total number of nucleotides encoding a particular polypeptide (e.g., a particular SEQ ID NO).

[0036] In some embodiments, the subject invention includes those fragments capable of hybridizing under various conditions of stringency conditions (e.g., high or intermediate or low stringency) with a nucleotide sequence according to the invention; fragments that hybridize with a nucleotide sequence of the subject invention can be, optionally, labeled as set forth below.

[0037] Thus, the subject invention also provides detection probes (e.g., fragments of the disclosed polynucleotide sequences) for hybridization with a target sequence or the amplicon generated from the target sequence. Such a detection probe will comprise a contiguous/consecutive span of at least 8, 9, 10, 11, 12, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 nucleotides. Labeled probes or primers are labeled with a radioactive compound or with another type of label as set forth above. Alternatively, non-labeled nucleotide sequences may be used directly as probes or primers; however, the sequences are generally labeled with a radioactive element (32P, 35S, 3H, 125I) or with a molecule such as biotin, acetylaminofluorene, digoxigenin, 5-bromo-deoxyuridine, or fluorescein to provide probes that can be used in numerous applications.

[0038] The subject invention also provides for modified nucleotide sequences. Modified nucleic acid sequences will be understood to mean any nucleotide sequence that has been modified, according to techniques well known to persons skilled in the art, and exhibiting modifications in relation to the native, naturally occurring nucleotide sequences.

[0039] The subject invention also provides genetic constructs comprising: a) a polynucleotide sequence encoding a polypeptide sequence selected from the group consisting of SEQ ID NOs: 1-25; b) a polynucleotide sequence having at least about 70% to 99.99% identity to a polynucleotide sequence encoding a polypeptide sequence selected from the group consisting of SEQ ID NO: 26-50, wherein said polynucleotide encodes a polypeptide having at least one of the biological activities of the polypeptides (e.g., a catalytic activity as set forth in Table 4); c) a polynucleotide sequence encoding a biologically active fragment of a polypeptide selected from the group consisting of SEQ ID NO: 26-50, wherein said biologically active fragment has at least

one of the biological activities of the polypeptides (e.g., a catalytic or transport activity as set forth in Table 4); d) a polynucleotide sequence comprising SEQ ID NO: 1, 2, 3, or combinations thereof; e) a polynucleotide sequence encoding variant (e.g., a variant polypeptide) of a polypeptide selected from the group consisting of SEQ ID NOs: 26-48, wherein said variant has at least on of the biological activities associated with the polypeptides (e.g., a catalytic or transport activity as set forth in Table 4); f) a polynucleotide sequence encoding a fragment of a variant polypeptide as set forth in (e); or g) a polynucleotide sequence encoding multimeric construct. Genetic constructs of the subject invention can also contain additional regulatory elements such as promoters and enhancers and, optionally, selectable markers.

[0040] Also within the scope of the subject instant invention are vectors or expression cassettes containing polynucleotides encoding the polypeptides, set forth supra, operably linked to regulatory elements. The vectors and expression cassettes may contain additional transcriptional control sequences as well. The vectors and expression cassettes may further comprise selectable markers. The expression cassette may contain at least one additional gene, operably linked to control elements, to be co-transformed into the organism. Alternatively, the additional gene(s) and control element(s) can be provided on multiple expression cassettes. Such expression cassettes are provided with a plurality of restriction sites for insertion of the sequences of the invention to be under the transcriptional regulation of the regulatory regions. The expression cassette(s) may additionally contain selectable marker genes operably linked to control elements.

[0041] In some embodiments, the expression cassette will include in the 5'-3' direction of transcription, a transcriptional and translational initiation region, a DNA sequence of the invention, and a transcriptional and translational termination region functional in plants. The transcriptional initiation region, the promoter, may be native or analogous, or foreign or heterologous, to the plant host. Additionally, the promoter may be the natural sequence or alternatively a synthetic sequence. By "foreign" is intended that the transcriptional initiation region is not found in the native plant into which the transcriptional initiation region is introduced. As used herein, a chimeric gene comprises a coding sequence operably linked to a transcriptional initiation region that is heterologous to the coding sequence.

[0042] The termination region may be native with the transcriptional initiation region, may be native with the operably linked DNA sequence of interest, or may be derived from another source. Convenient termination regions are available from the Ti-plasmid of A. tumefaciens, such as the octopine synthase and nopaline synthase termination regions. See also Guerineau et al. (1991) Mol. Gen. Genet. 262:141-144; Proudfoot (1991) Cell 64:671-674; Sanfacon et al. (1991) Genes Dev. 5:141-149; Mogen et al. (1990) Plant Cell 2:1261-1272; Munroe et al. (1990) Gene 91:151-158; Ballas et al. (1989) Nucleic Acids Res. 17:7891-7903; and Joshi et al. (1987) Nucleic Acid Res. 15:9627-9639.

[0043] Where appropriate, the polynucleotides encoding the polypeptides set forth supra can be optimized for expression in the transformed plant. That is, the genes can be synthesized using plant-preferred codons corresponding to the plant of interest. Methods are available in the art for synthesizing plant-preferred genes. See, for example, U. S. Patent Nos. 5,380,831 and 5,436,391, and Murray et al. (1989) Nucleic Acids Res. 17:477-498, herein incorporated by reference.

[0044] The expression cassettes may additionally contain 5' leader sequences in the expression cassette construct. Such leader sequences can act to enhance translation. Translation leaders are known in the art and include: picornavirus leaders, for example, EMCV leader (Encephalomyocarditis 5' noncoding region), Elroy-Stein et al. (1989) PNAS USA 86:6126-6130; potyvirus leaders, for example, TEV leader (Tobacco Etch Virus), Allison et al. (1986); MDMV Leader (Maize Dwarf Mosaic Virus), Virology 154:9-20; human immunoglobulin heavy-chain binding protein (BiP), Macejak et al. (1991) Nature 353:90-94; untranslated leader from the coat protein mRNA of alfalfa mosaic virus (AMV RNA 4), Jobling et al. (1987) Nature 325:622-625; tobacco mosaic virus leader (TMV), Gallie et al. (1989) in Molecular Biology of RNA, ed. Cech (Liss, New York), pp. 237-256; and maize chlorotic mottle virus leader (MCMV), Lommel et al. (1991) Virology 81:382-385. See also, Della-Cioppa et al. (1987) Plant Physiol. 84:965-968. Other methods known to enhance translation can also be utilized.

[0045] Also provided are transformed host cells, transformed plant cells and transgenic plants which contain one or more genetic constructs, vectors, or expression cassettes comprising polynucleotides of the subject invention, or biologically active fragments thereof, operably linked to control elements. As used herein, the term "planta" includes algae and higher plants. Thus, algae, monocots, and dicots may be transformed with genetic constructs of the invention, expression cassettes, or vectors according to the invention. In certain embodiments of the subject invention, the transformed cells or transgenic plants comprise at least one polynucleotide seuquence selected from the group consisting of SEQ ID NOs: 1-25. In certain preferred embodiments, transformed cells or transgenic plants comprise at least one polynucleotide sequence comprising SEQ ID NO: 1, 2, or 3. Optionally, the transformed cells or transgenic plants can comprise at least two or all three polynucleotide sequences selected from the group consisting of SEQ ID NOs: 1, 2, and 3.

[0046] Methods of transforming cells with genetic constructs, vectors, or expression cassettes comprising the novel polynucleotides of the invention are also provided. These methods comprise transforming a plant or plant cell with a polynucleotide according to the subject invention. Plants and plant cells may be transformed by electroporation, Agrobacterium transformation (including vacuum infiltration), engineered plant virus replicons, electrophoresis, microinjection, micro-projectile bombardment, vacuum infiltration of Agrobacterium, micro-

LASER beam-induced perforation of cell wall, or simply by incubation with or without polyethylene glycol (PEG). Plants transformed with a genetic construct of the invention may be produced by standard techniques known in the art for the genetic manipulation of plants. DNA can be transformed into plant cells using any suitable technology, such as a disarmed Ti-plasmid vector carried by Agrobacterium exploiting its natural gene transferability. Agrobacterium transformation is used by those skilled in the art to transform algae and dicotyledonous species. Substantial progress has been made towards the routine production of stable, fertile transgenic plants in almost all economically relevant monocot plants. In particular, Agrobacterium mediated transformation has now emerged as a highly efficient transformation method in monocots. Microprojectile bombardment, electroporation, and direct DNA uptake are preferred where Agrobacterium is inefficient or ineffective. Alternatively, a combination of different techniques may be employed to enhance the efficiency of the transformation process, e.g., bombardment with Agrobacterium-coated microparticles (EP-A-486234) or microprojectile bombardment to induce wounding followed by co-cultivation with Agrobacterium (EP-A-486233).

[0047] Following transformation, a plant may be regenerated, e.g., from single cells, callus tissue or leaf discs, as is standard in the art. Almost any plant can be entirely regenerated from cells, tissues, and organs of the plant. Available techniques are reviewed in Vasil et al. (1984) in Cell Culture and Somatic Cell Genetics of Plants, Vols. I, II, and III, Laboratory Procedures and Their Applications (Academic press); and Weissbach et al. (1989) Methods for Plant Mol. Biol.

[0048] The transformed plants may then be grown, and either pollinated with the same transformed strain or different strains, and the resulting hybrid having expression of the desired phenotypic characteristic identified. Two or more generations may be grown to ensure that expression of the desired phenotypic characteristic is stably maintained and inherited, and then seeds harvested to ensure expression of the desired phenotypic characteristic has been achieved.

[0049] The particular choice of a transformation technology will be determined by its efficiency to transform certain plant species as well as the experience and preference of the person practicing the invention with a particular methodology of choice. It will be apparent to the skilled person that the particular choice of a transformation system to introduce nucleic acid into plant cells is not essential to or a limitation of the invention, nor is the choice of technique for plant regeneration.

[0050] Also according to the invention, there is provided a plant cell having the constructs of the invention. A further aspect of the present invention provides a method of making such a plant cell involving introduction of a vector including the construct into a plant cell. For integration of the construct into the plant genome, such introduction will be followed by recombination between the vector and the plant cell genome to introduce the sequence of

nucleotides into the genome. RNA encoded by the introduced nucleic acid construct may then be transcribed in the cell and descendants thereof, including cells in plants regenerated from transformed material. A gene stably incorporated into the genome of a plant is passed from generation to generation to descendants of the plant, so such descendants should show the desired phenotype.

[0051] The present invention also provides a plant comprising a plant cell as disclosed. Transformed seeds and plant parts are also encompassed. As used herein, the expressions "cell," "cell line," and "cell culture" are used interchangeably and all such designations include progeny. Thus, the words "transformants" and "transformed cells" include the primary subject cell and cultures derived therefrom without regard for the number of transfers. It is also understood that all progeny may not be precisely identical in DNA content, due to naturally occurring, deliberate, or inadvertent caused mutations. Mutant progeny that have the same function or biological activity as screened for in the originally transformed cell are included. Where distinct designations are intended, it will be clear from the context.

[0052] In addition to a plant, the present invention provides any clone of such a plant, seed, or hybrid descendants, and any part of any of these, such as cuttings or seed. The invention provides any plant propagule that is any part which may be used in reproduction or propagation, sexual or asexual, including cuttings, seed, and so on. Also encompassed by the invention is a plant which is a sexually or asexually propagated off-spring, clone, or descendant of such a plant; or any part or propagule of said plant, off-spring, clone, or descendant. Plant extracts and derivatives are also provided.

[0053] As is apparent to the routineer in this technology, the disclosed methods allow for the expression of a gene of interest in any plant. The invention thus relates generally to methods for the production of transgenic plants (both monocots and dicots). As used herein, the term "transgenic plants" refers to plants (algae, monocots, or dicots), comprising plant cells in which homologous or heterologous polynucleotides are expressed as the result of manipulation by the hand of man.

[0054] As is apparent to one of ordinary skill in the art, the peptides encoded by the disclosed herein may be encoded by multiple polynucleotide sequences because of the redundancy of the genetic code. It is well within the skill of a person trained in the art to create these alternative DNA sequences encoding the same, or essentially the same, amino acid sequences. These variant DNA sequences are within the scope of the subject invention.

[0055] The terms "purified" and "isolated", when referring to a polynucleotide, nucleotide, or nucleic acid, indicate a nucleic acid the structure of which is not identical to that of any naturally occurring nucleic acid or to that of any fragment of a naturally occurring genomic nucleic acid spanning more than three separate genes. The term therefore covers, for example, (a)

a DNA which has the sequence of part of a naturally occurring genomic DNA molecules but is not flanked by both of the coding or non-coding sequences that flank that part of the molecule in the genome of the organism in which it naturally occurs (e.g., DNA excised with a restriction enzyme); (b) a nucleic acid incorporated into a vector or into the genomic DNA of a prokaryote or eukaryote in a manner such that the resulting molecule is not identical to any naturally occurring vector or genomic DNA; (c) a separate molecule such as a cDNA, a genomic fragment, a fragment produced by polymerase chain reaction (PCR), or a restriction fragment; and (d) a recombinant nucleotide sequence that is part of a hybrid gene, i.e., a gene encoding a fusion protein. Specifically excluded from this definition are nucleic acids present in mixtures of (i) DNA molecules, (ii) transfected cells, and (iii) cell clones, e.g., as these occur in a DNA library such as a cDNA or genomic DNA library.

[0056] The term "polynucleotide" as used herein refers to a polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides. This term refers only to the primary structure of the molecule and thus includes double- and single-stranded DNA and RNA. It also includes known types of modifications, for example, labels which are known in the art, methylation, "caps", substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications, such as those with uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoamidates, carbamates, etc.) and with charged linkages (e.g., phosphorothioates, phosphorodithioates, etc.), those containing pendant moieties, such as proteins (including for e.g., nucleases, toxins, antibodies, signal peptides, poly-L-lysine, etc.), those with intercalators (e.g., acridine, psoralen, etc.), those containing chelators (e.g., metals, radioactive metals, boron, oxidative metals, etc.), those containing alkylators, those with modified linkages (e.g., alpha anomeric nucleic acids, etc.), as well as unmodified forms of the polynucleotide.

[0057] "Control elements" include both "transcriptional control elements" and "translational control elements". "Transcriptional control elements" include "promoter", "enhancer", and "transcription termination" elements. Promoters and enhancers consist of short arrays of DNA sequences that interact specifically with cellular proteins involved in transcription [Maniatis et al. [1987] Science 236:1237). Promoter and enhancer elements have been isolated from a variety of eukaryotic sources including genes in plants, yeast, insect and mammalian cells and viruses (analogous control elements, i.e., promoters, are also found in prokaryotes). The selection of a particular promoter and enhancer depends on what cell type is to be used to express the peptide of interest. Some eukaryotic promoters and enhancers have a broad host range while others are functional in a limited subset of cell types [for review see Voss et al. [1986] Trends Biochem. Sci. 11:287 and Maniatis et al. [1987] supra. Transcriptional control elements suitable for use in plants are well known in the art. "Translational control elements" include translational initiation regions and translational termination regions functional in plants.

[0058] A number of promoters can be used in the practice of the invention. The promoters can be selected based on the desired outcome. Strong promoters may be used to produce high levels of gene transcription. Alternatively, inducible promoters may be used to selectively active gene transcription when the appropriate signal is provided. Constitutive promoters may be utilized to continuously drive gene transcription. Tissue specific promoters may also be used in the practice of the invention in order to provide localized production of gene transcripts in a desired tissue. Developmental promoters may, likewise, be used to drive transcription of a gene during a particular developmental stage of the plant. Thus, a gene of interest can be combined with constitutive, tissue-specific, inducible, developmental, or other promoters for expression in plants depending upon the desired outcome.

[0059] Constitutive promoters include, for example, CaMV 35S promoter (Odell et al. (1985) Nature 313:810-812; rice actin (McElroy et al. (1990) Plant Cell 2:163-171; ubiquitin (Christensen et al. (1989) Plant Mol. Biol. 12:619-632 and Christensen et al. (1992) Plant Mol. Biol. 18:675-689); pEMU (Last et al. (1991) Theor. Appl. Genet. 81:581-588); MAS (Velten et al. (1984) EMBO J. 3:2723-2730); ALS promoter (U. S. Patent No. 5,659,026), and the like. Other constitutive promoters include those in U. S. Patent Nos. 5,608,149; 5,608,144; 5,604,121; 5,569,597; 5,466,785; 5,399,680; 5,268,463; and 5,608,142. Each of the aforementioned patents and references is hereby incorporated by reference in its entirety.

[0060] A number of inducible promoters are known in the art. For example, a pathogen-inducible promoter can be utilized. Such promoters include those from pathogenesis-related proteins (PR proteins), which are induced following infection by a pathogen; e.g., PR proteins, SAR proteins, beta-1,3-glucanase, chitinase, etc. See, for example, Redolfi et al. (1983) Neth. J. Plant Pathol. 89:245-254; Uknes et al. (1992) Plant Cell 4:645-656; and Van Loon (1985) Plant Mol. Virol. 4:111-116; Marineau et al. (1987) Plant Mol. Biol. 9:335-342; Matton et al. (1989) Molecular Plant-Microbe Interactions 2:325-331; Somsisch et al. (1986) Proc. Natl. Acad. Sci. USA 83:2427-2430; Somsisch et al. (1988) Mol. Gen. Genet. 2:93-98; and Yang (1996) Proc. Natl. Acad. Sci. USA 93:14972-14977. See also, Chen et al. (1996) Plant J. 10:955-966; Zhang et al. (1994) Proc. Natl. Acad. Sci. USA 91:2507-2511; Warner et al. (1993) Plant J. 3:191-201; Siebertz et al. (1989) Plant Cell 1:961-968; U. S. Patent No. 5,750,386; Cordero et al. (1992) Physiol. Mol. Plant Path. 41:189-200; each of which is incorporated by reference in its entirety.

[0061] Wound-inducible promoters may be used in the genetic constructs of the invention. Such wound-inducible promoters include potato proteinase inhibitor (pin II) gene (Ryan (1990) Ann. Rev. Phytopath. 28:425-449; Duan et al. (1996) Nature Biotechnology 14:494-498; wun1 and wun2, U. S. Patent No. 5,428,148; win1 and win2 (Stanford et al. (1989) Mol. Gen. Genet. 215:200-208); systemin (McGurl et al. (1992) Science 225:1570-1573); WIP1 (Rohmeier et al. (1993) Plant Mol. Biol. 22:783-792; Eckelkamp et al. (1993) FEBS Letters

323:73-76); MPI gene (Corderok et al. (1994) Plant J. 6(2):141-150; and the like. These references are also incorporated by reference in their entireties.

[0062] Tissue specific promoters can also be used in the practice of the subject invention. For example, leaf-specific promoters can similarly be used if desired, and are taught in references which include Yamamoto et al. (1997) Plant J. 12(2):255-265; Kawamata et al. (1997) Plant Cell Physiol. 38(7):792-803; Hansen et al. (1997) Mol. Gen. Genet. 254(3):337-343; Russel et al. (1997) Transgenic Res. 6(2):157-168; Rinehart et al. (1996) Plant Physiol. 112(3):1331-1341; Van Camp et al. (1996) Plant Physiol. 112(2):525-535; Canevascini et al. (1996) Plant Physiol. 112(2):513-524; Yamamoto et al. (1994) Plant Cell Physiol. 35(5)773-778; Lam (1994) Results Probl. Cell Differ. 20:181-196; Orozco et al. (1993) Plant Mol. Biol. 23(6):1129-1138; Matsuoka et al. (1993) Proc. Natl. Acad. Sci USA:90(20) 9586-9590; and Guevara-Garcia et al. (1993) Plant J. 4(3):495-505. Alternatively, root-specific promoters are known and can be selected from the many available from the literature. See, for example, Hire et al. (1992) Plant Mol. Biol. 20(2):207-218 (soybean root-specific glutamine synthetase gene); Keller and Baumgartner (1991) Plant Cell 3(10):1051-1061 (root-specific control element in the GRP 1.8 gene of French bean); Sanger et al. (1990) Plant Mol. Biol. 14(3):433-443 (root-specific promoter of the mannopine synthase (MAS) gene of Agrobacterium tumefaciens) Miao et al. (1991) Plant Cell 3(1):11-22 (full-length cDNA clone encoding cytosolic glutamine synthetase (GS), which is expressed in roots and root nodules of soybean). Bogusz et al. (1990) Plant Cell 2(7):633-641 (root specific promoters from hemoglobin genes from the nitrogen-fixing nonlegume Parasponia andersonii and the related non-nitrogen-fixing nonlegume Trema tomeniosa; Leach and Aoyagi (1991) Plant Science (Limerick) 79(1):69-76 (rolC and rolD root-including genes of Agrobacterium rhizogenes); Teeri et al. (1989) EMBO J. 8(2):343-350 (octopine synthase and TR2' gene); (VfENOD-GRP3 gene promoter); Kuster et al. (1995) Plant Mol. Biol. 29(4):759-772 and Capana et al. (1994) Plant Mol. Biol. 25(4):681-691 (rolB promoter). See also U. S. Patent Nos. 5,837,876; 5,750,386; 5,633,363; 5,459,252; 5,401,836; 5,110,732; and 5,023,179.

[0063] Other tissue specific promoters can also be used in the practice of the subject invention (see, for example U.S. Patent No. 6,544,783). For example, xylem/vascular/tracheid-specific promoters, such as those disclosed in Milioni et al. (2002) Plant Cell, 14:2813-2824; Zhong et al. (1999) Plant Cell, 11:2139-2152; Ito et al. (2002) Plant Cell, 14:3201-3211; Parker et al. (2003) Development 130:2139-2148; Bourquin et al. (2002) Plant Cell 14:3073-3088 (each of which is hereby incorporated by reference in its entirety) can be used in the practice of the subject invention.

[0064] "Seed-preferred" promoters include both "seed-specific" promoters (those promoters active during seed development such as promoters of seed storage proteins) as well as "seed-germinating" promoters (those promoters active during seed germination). See Thompson

et al. (1989) Bioassays 10:108, herein incorporated by reference. Such seed-preferred promoters include, but are not limited to, Cim1 (cytokinin-induced message); cZ10B1 (Maize 19 kDa zein); celA (cellulose synthase); gama-zein; Glob-1; bean β-phaseolin; napin; β-conglycinin; soybean lectin; cruciferin; maize 15 kDa zein; 22 kDa zein; 27 kDa zein; g-zein; waxy; shrunken 1; shrunken 2; globulin 1; etc.

[0065] "Operably linked" refers to a juxtaposition wherein the components so described are in a relationship permitting them to function in their intended manner. A control sequence "operably linked" to a coding sequence is ligated in such a way that expression of the coding sequence is achieved under conditions compatible with the control sequences.

[0066] As used herein, the term "expression cassette" refers to a molecule comprising at least one coding sequence operably linked to a control sequence which includes all nucleotide sequences required for the transcription of cloned copies of the coding sequence and the translation of the mRNAs in an appropriate host cell. Such expression cassettes can be used to express eukaryotic genes in a variety of hosts such as bacteria, green algae, cyanobacteria, plant cells, fungal cells, yeast cells, insect cells and animal cells. Under the invention, expression cassettes can include, but are not limited to, cloning vectors, specifically designed plasmids, viruses or virus particles. The cassettes may further include an origin of replication for autonomous replication in host cells, selectable markers, various restriction sites, a potential for high copy number and strong promoters.

[0067] By "vector" is meant any genetic element, such as a plasmid, phage, transposon, cosmid, chromosome, virus etc., which is capable of replication when associated with the proper control elements and which can transfer gene sequences between cells. Thus, the term includes cloning and expression vehicles, as well as viral vectors.

[0068] During the preparation of the constructs, the various fragments of DNA will often be cloned in an appropriate cloning vector, which allows for amplification of the DNA, modification of the DNA or manipulation of the DNA by joining or removing sequences, linkers, or the like. Preferably, the vectors will be capable of replication to at least a relatively high copy number in E. coli. A number of vectors are readily available for cloning, including such vectors as pBR322, vectors of the pUC series, the M13 series vectors, and pBluescript vectors (Stratagene; La Jolla, Calif.).

[0069] In order to provide a means of selecting transformed plants or plant cells, the vectors for transformation will typically contain a selectable marker gene. Marker genes are expressible DNA sequences which express a polypeptide which resists a natural inhibition by, attenuates, or inactivates a selective substance. Examples of such substances include antibiotics and, in the case of plant cells, herbicides. Selectable markers for use in animal, bacterial, plant, fungal, yeast, and insect cells are well known in the art. Exemplary selectable markers include

bacterial transposons Tn5 or Tn 601(903) conferring resistance to aminoglycosides (selection for Geneticin-resistance (G418R), mycophenolic acid resistance (MPAR) (utilizing E. coli guanosine phosphoribosyl transferase (gpt) encoding the enzyme XGPRT; selection is performed on medium containing MPA and xanthin), methotrexate resistance (MTXR), or cadmium-resistance which incorporates the mouse metallotheionein gene (as cDNA cassette) on the vector which detoxifies heavy metal ions by chelating them.

[0070] Alternatively, a marker gene may provide some visible indication of cell transformation. For example, it may cause a distinctive appearance or growth pattern relative to plants or plant cells not expressing the selectable marker gene in the presence of some substance, either as applied directly to the plant or plant cells or as present in the plant or plant cell growth media. The use of such a marker for identification of plant cells containing a plastid construct has been described (Svab et al. [1993] supra). Numerous additional promoter regions may also be used to drive expression of the selectable marker gene, including various plant promoters and bacterial promoters which have been shown to function in plants.

[0071] A number of other markers have been developed for use with plant cells, such as resistance to chloramphenicol, the aminoglycoside G418, hygromycin, or the like. Other genes which encode a product involved in chloroplast metabolism may also be used as selectable markers. For example, genes which provide resistance to plant herbicides such as glyphosate, bromoxynil or imidazolinone may find particular use. Such genes have been reported (Stalker et al. [1985] J. Biol. Chem. 260:4724-4728 (glyphosate resistant EPSP); Stalker et al. [1985] J. Biol. Chem. 263:6310-6314 (bromoxynil resistant nitrilase gene); and Sathasivan et al. [1990] Nucl. Acids Res. 18:2188 (AHAS imidazolinone resistance gene)).

[0072] Another aspect of the invention provides vectors for the cloning and/or the expression of a polynucleotide sequences taught herein in procaryotic or animal cells. The subject invention also provides for the expression of a polypeptide, peptide, derivative, or variant encoded by a polynucleotide sequence disclosed herein comprising the culture of a procaryotic or animal cell (a host cell) transformed with a polynucleotide of the subject invention under conditions that allow for the expression of a polypeptide, biologically active fragment, or multimeric construct encoded by said polynucleotide and, optionally, recovering the expressed polypeptide, peptide, derivative, or analog.

[0073] In this aspect of the invention, the polynucleotide sequences can be regulated by a second nucleic acid sequence so that the protein or peptide is expressed in a host cell transformed with the recombinant DNA molecule. For example, expression of a protein or peptide may be controlled by any promoter/enhancer element known in the art. Promoters which may be used to control expression include, but are not limited to, the CMV-IE promoter, the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290:304-310), the promoter contained in the 3' long

terminal repeat of Rous sarcoma virus (Yamamoto, et al., 1980, Cell 22:787-797), the herpes simplex thymidine kinase promoter (Wagner et al., 1981, Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445), the regulatory sequences of the metallothionein gene (Brinster et al., 1982, Nature 296:39-42); prokaryotic vectors containing promoters such as the β-lactamase promoter (Villa-Kamaroff, et al., 1978, Proc. Natl. Acad. Sci. U.S.A. 75:3727-3731), or the tac promoter (DeBoer, et al., 1983, Proc. Natl. Acad. Sci. U.S.A. 80:21-25); see also "Useful proteins from recombinant bacteria" in Scientific American, 1980, 242:74-94; plant expression vectors comprising the nopaline synthetase promoter region (Herrera-Estrella et al., 1983, Nature 303:209-213) or the cauliflower mosaic virus 35S RNA promoter (Gardner, et al., 1981, Nucl. Acids Res. 9:2871), and the promoter of the photosynthetic enzyme ribulose biphosphate carboxylase (Herrera-Estrella et al., 1984, Nature 310:115-120); promoter elements from yeast or fungi such as the Gal 4 promoter, the ADC (alcohol dehydrogenase) promoter, PGK (phosphoglycerol kinase) promoter, and/or the alkaline phosphatase promoter.

[0074] The vectors according to the invention are, for example, vectors of plasmid or viral origin. In a specific embodiment, a vector is used that comprises a promoter operably linked to a nucleic acid sequence encoding a polypeptide as disclosed herein, one or more origins of replication, and, optionally, one or more selectable markers (e.g., an antibiotic resistance gene). Expression vectors comprise regulatory sequences that control gene expression, including gene expression in a desired host cell. Exemplary vectors for the expression of the polypeptides of the invention include the pET-type plasmid vectors (Promega) or pBAD plasmid vectors (Invitrogen) or those provided in the examples below. Furthermore, the vectors according to the invention are useful for transforming host cells so as to clone or express the polynucleotide sequences of the invention.

[0075] The invention also encompasses the host cells transformed by a vector according to the invention. These cells may be obtained by introducing into host cells a nucleotide sequence inserted into a vector as defined above, and then culturing the said cells under conditions allowing the replication and/or the expression of the polynucleotide sequences of the subject invention.

[0076] The host cell may be chosen from eukaryotic or prokaryotic systems, such as for example bacterial cells, (Gram negative or Gram positive), yeast cells (for example, Saccharomyces cereviseae or Pichia pastoris), animal cells (such as Chinese hamster ovary (CHO) cells), plant cells (e.g., algae), and/or insect cells using baculovirus vectors. In some embodiments, the host cells for expression of the polypeptides include, and are not limited to, those taught in U.S. Patent Nos. 6,319,691, 6,277,375, 5,643,570, or 5,565,335, each of which is incorporated by reference in its entirety, including all references cited within each respective patent.

[0077] Furthermore, a host cell strain may be chosen which modulates the expression of

the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Expression from certain promoters can be elevated in the presence of certain inducers; thus, expression of the genetically engineered polypeptide may be controlled. Furthermore, different host cells have characteristic and specific mechanisms for the translational and post-translational processing and modification (e.g., glycosylation, phosphorylation) of proteins. Appropriate cell lines or host systems can be chosen to ensure the desired modification and processing of the foreign protein expressed. For example, expression in a bacterial system can be used to produce an unglycosylated core protein product. Expression in yeast will produce a glycosylated product. Expression in mammalian cells can also to provide glycosylation of a protein.

[0078] The subject invention provides one or more isolated polypeptides comprising:

(a) SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47;

(b) a heterologous polypeptide sequence fused, in frame, to a polypeptide comprising SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47;

(c) a fragment of SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47, wherein said fragment exhibits at least one biological function of the polypeptide of SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47; or

(d) a variant having at least 70% homology to a polypeptide comprising SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47, wherein said variant exhibits at least one biological function of the polypeptide comprising SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47.

[0079] The term "peptide" may be used interchangeably with "oligopeptide" or "polypeptide" in the instant specification to designate a series of residues, typically L-amino acids, connected one to the other, typically by peptide bonds between the α-amino and carboxyl groups of adjacent amino acids. Linker elements can be joined to the polypeptides of the subject invention through peptide bonds or via chemical bonds (e.g., heterobifunctional chemical linker elements).

[0080] The subject invention encompasses polypeptide fragments of the full-length polypeptides disclosed herein. Polypeptide fragments, according to the subject invention, usually comprise a contiguous span of at least 5 consecutive (or contiguous) amino acids. The maximum length for a polypeptide fragment in the context of this invention is an integer that is one amino acid less than the full length of a particular SEQ ID NO: from which the fragment was derived. In certain preferred embodiments, fragments of the polypeptides of the subject invention retain at least one biological activity/function of the full-length polypeptide from which they are derived

(e.g., such similar or identical enzymatic activity or the ability to provide resistance to an antibiotic or transport an antibiotic out of a cell (see, for example, Table 4).

[0081] A "variant" polypeptide (or polypeptide variant) is to be understood to designate polypeptides exhibiting, in relation to the natural polypeptide, certain modifications. These modifications can include a deletion, addition, or substitution of at least one amino acid, a truncation, an extension, a chimeric fusion, a mutation, or polypeptides exhibiting post-translational modifications. Among the homologous polypeptides, those whose amino acid sequences exhibit between at least (or at least about) 70.00% to 99.99% (inclusive) identity to the full length, native, or naturally occurring polypeptide are another aspect of the invention. The aforementioned range of percent identity is to be taken as including, and providing written description and support for, any fractional percentage, in intervals of 0.01%, between 70.00% and, up to, including 99.99%. These percentages are purely statistical and differences between two polypeptide sequences can be distributed randomly and over the entire sequence length. Thus, variant polypeptides can have 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99 percent identity with the polypeptide sequences of the instant invention. In certain preferred embodiments, variants of the polypeptides of the subject invention retain at least one biological activity/function of the full-length polypeptide from which they are derived (e.g., such as similar or identical enzymatic activity or the ability to provide resistance to an antibiotic or transport an antibiotic out of a cell (see, for example, Table 4).

[0082] Variant polypeptides can also comprise one or more heterologous polypeptide sequences (e.g., tags that facilitate purification of the polypeptides of the invention (see, for example, U.S. Patent No. 6,342,362, hereby incorporated by reference in its entirety; Altendorf et al. [1999-WWW, 2000] "Structure and Function of the Fo Complex of the ATP Synthase from Escherichia Coli," J. of Experimental Biology 203:19-28, The Co. of Biologists, Ltd., G.B.; Baneyx [1999] "Recombinant Protein Expression in Escherichia coli," Biotechnology 10:411-21, Elsevier Science Ltd.; Eihauer et al. [2001] "The FLAG™ Peptide, a Versatile Fusion Tag for the Purification of Recombinant Proteins," J. Biochem Biophys Methods 49:455-65; Jones et al. [1995] J. Chromatography 707:3-22; Jones et al. [1995] "Current Trends in Molecular Recognition and Bioseparation," J. of Chromatography A. 707:3-22, Elsevier Science B.V.; Margolin [2000] "Green Fluorescent Protein as a Reporter for Macromolecular Localization in Bacterial Cells," Methods 20:62-72, Academic Press; Puig et al. [2001] "The Tandem Affinity Purification (TAP) Method: A General Procedure of Protein Complex Purification," Methods 24:218-29, Academic Press; Sassenfeld [1990] "Engineering Proteins for Purification," TibTech 8:88-93; Sheibani [1999] "Prokaryotic Gene Fusion Expression Systems and Their Use in Structural and Functional Studies of Proteins," Prep. Biochem. & Biotechnol. 29(1):77-90, Marcel Dekker, Inc.; Skerra et al. [1999] "Applications of a Peptide Ligand for Streptavidin: the Strep-

tag", Biomolecular Engineering 16:79-86, Elsevier Science, B.V.; Smith [1998] "Cookbook for Eukaryotic Protein Expression: Yeast, Insect, and Plant Expression Systems," The Scientist 12(22):20; Smyth et al. [2000] "Eukaryotic Expression and Purification of Recombinant Extracellular Matrix Proteins Carrying the Strep II Tag", Methods in Molecular Biology, 139:49-57; Unger [1997] "Show Me the Money: Prokaryotic Expression Vectors and Purification Systems," The Scientist 11(17):20, each of which is hereby incorporated by reference in their entireties), or commercially available tags from vendors such as such as STRATAGENE (La Jolla, CA), NOVAGEN (Madison, WI), QIAGEN, Inc., (Valencia, CA), or InVitrogen (San Diego, CA). Alternatively, the heterologous sequences may provide for the multimerization of the polypeptides of the subject invention (see, e.g., US Patent Number 5,478,925, WO 98/49305, or U.S. Pat. No. 5,073,627, Landschulz *et al.*, (1988), Science. 240:1759, WO 94/10308, Hoppe *et al.*, (1994), FEBS Letters. 344:191). Other methods of making multimers include the addition of cysteine or biotin to the C-terminus or N-terminus of the polypeptide using techniques known in the art. Where biotin is attached to a polypeptide, avidin can be utilized to create multimers of the polypeptides to which the biotin element is attached (see, e.g., US Patent Number 5,478,925 for numerous methods of multimerization). Multimers of the invention may also be generated using chemical or genetic engineering techniques known in the art.

[0083] The invention, thus, provides a novel antibiotic family, Albicidins, produced by three novel biosynthetic gene clusters (XALB1, XALB2, and XALB3) contained within a host cell DNA in which one strand comprises non-contiguously SEQ. ID No. 1, SEQ. ID No. 2 and SEQ ID No. 3, and the cell expresses the DNA to provide peptides including those named AlbI (SEQ ID No. 26) (encoded by SEQ ID No. 20), AlbII (SEQ ID No. 27) (encoded by SEQ ID No. 21) , AlbIII (SEQ ID No. 28) (encoded by SEQ ID No. 22), AlbIV (SEQ ID No. 29) (encoded by SEQ ID No. 23), AlbVI (SEQ ID No. 31) (encoded by SEQ ID No. 18), AlbVII (SEQ ID No. 32) (encoded by SEQ ID No. 17), AlbVIII (SEQ ID No. 33) (encoded by SEQ ID No. 16), AlbIX (SEQ ID No. 34) (encoded by SEQ ID No. 15), AlbX (SEQ ID No. 35) (encoded by SEQ ID No. 10), AlbXI (SEQ ID No. 36) (encoded by SEQ ID No. 9), AlbXII (SEQ ID No. 37) (encoded by SEQ ID No. 8), AlbXIII (SEQ ID No. 38) (encoded by SEQ ID No. 7), AlbXIV (SEQ ID No. 39) (encoded by SEQ ID No. 6), AlbXV (SEQ ID No. 40) (encoded by SEQ ID No. 5), AlbXVII (SEQ ID No. 42) (encoded by SEQ ID No. 11), AlbXVIII (SEQ ID No. 43) (encoded by SEQ ID No. 12), AlbXIX (SEQ ID No. 44) (encoded by SEQ ID No. 13), AlbXX (SEQ ID No. 45) (encoded by SEQ ID No. 14), AlbXXI (SEQ ID No. 46) (encoded by SEQ ID No. 24), and AlbXXII (SEQ ID No. 47) (encoded by SEQ ID No. 25), that in turn interact within the host cell to produce one or more antibiotics as more fully illustrated in Figure 11.

[0084] In one embodiment, the invention comprises a plurality of isolated and purified DNA strands which comprise nucleotide sequences selected from the group consisting of SEQ ID

No: 1 to SEQ. ID No. 25, each individual sequence, except the transposases AlbV (SEQ ID No. 30) (encoded by SEQ ID No. 19) and AlbXVI (SEQ ID No. 41) (encoded by SEQ ID No. 4) found in the XALB1 cluster, being necessary to the biosynthesis of the novel family of antibiotics, Albicidins.

[0085] The invention also includes the peptides or proteins encoded by the genes of the biosynthetic complex expressed by the combination of DNA with a strand having sequences SEQ ID Nos. 1 to 3. Proteins are named with roman numerals and the prefix Alb from AlbI to Alb XXII have the amino acid sequences of SEQ ID Nos. 26 to 47 (not in Roman numeral order but in the order of placement of the genes within sequences SEQ ID Nos. 1 to 3 that express each protein). Expression of the peptides having the amino acid sequences of SEQ ID Nos. 26 to 29, 31 to 40 and 42 to 47, have been found to be all required for the successful biosynthesis of Albicidins.

[0086] The invention further provides a method for producing Albicidins comprising providing a modified host cell with a heterologous DNA Albicidin Biosynthetic Gene Cluster or set of genes defined as DNA operably comprising DNA sequences substantially similar to SEQ ID Nos. 1 to 3. Substantially the same means DNA having sufficient homology to provide expressed proteins that function to provide an antibiotic material having the structural components identified herein. Preferably a given sequence will have at least 70 percent homology to one of SEQ ID Nos. 1 to 3, preferably 85% homology and most preferably at least 95% homology. The method includes the steps of modifying the DNA of the host cell to comprise an operable expression system for maintaining the modified host cell under conditions supporting biosynthesis of Albicidins and isolation of Albicidins from the host cell or its environment. The invention further provides a method of production of a group of novel antibiotic materials utilizing at least three of the Sequences selected from the group consisting of DNA SEQ ID No. 1 to SEQ ID No. 25 (excluding transposases encoded by SEQ ID Nos. 4 and 19) inclusive in combination with additional sequences to produce a modified Albicidin-like material.

[0087] More specifically, the invention provides DNA Sequences comprising at least about 68,498 base pairs and including an about 55,839 bp region from the genome of *X. albilineans* designated as XALB1 (Albicidin Biosynthetic Gene Cluster 1; SEQ ID. No. 1) an additional non-contiguous region of about 2,986 bp, XALB2 (Albicidin Biosynthetic Gene Cluster 2; SEQ ID. No. 2), and a third region of about 9,673 bp, XALB3 (Albicidin Biosynthetic Gene Cluster 3; SEQ ID. No. 3). Albicidin Biosynthetic Gene Clusters 1-3 may be referred to, collectively, as the Albicidin Biosynthetic Gene Clusters and these sequences were found to be required for biosynthesis of Albicidins. Homology analysis revealed the presence of (i) four large genes with a modular architecture characteristic of polyketide synthases (PKS) and nonribosomal peptide synthetases (NRPS) potentially involved in albicidin precursor biosynthesis; (ii) four

smaller genes potentially involved in albicidin substrate biosynthesis (iii) four modifying genes; (iv) one enzyme activating gene, (v) two regulatory genes, (vi) one chaperone gene, (vii) two genes of unknown function; and (viii) two resistance genes. These are named and discussed more fully below. Together these genes allow the successful operation of the biosynthetic pathway when cloned into suitable host cells.

[0088] Alignment of individual NRPS and PKS domains revealed an extraordinary biosynthetic apparatus believed to involve a *trans*-action of separate PKS and NRPS domains which could contribute to the production of multiple, structurally related albicidins by the same gene cluster. Furthermore, analysis of selectivity-conferring residues indicated that four NRPS modules of XALB1 specify an unusual substrate.

[0089] In an alternate embodiment the invention provides a method of producing a polyketide carrying para-aminobenzoic acid and/or carbamoyl benzoic acid by inserting at least one DNA fragment that encodes a PKS protein into a cell and causing the cell to express the encoded PKS protein under conditions such that the PKS protein functions to produce a polyketide carrying either a para-aminobenzoic acid or a carbamoyl benzoic acid or both. Another embodiment provides a method of producing polyketide/peptides carrying para-aminobenzoic acid and/or carbamoyl benzoic acid by inserting at least one DNA fragment that encodes a PKS protein into a cell and causing the cell to express the encoded PKS protein under conditions such that the PKS protein functions to produce a polyketide carrying either a para-aminobenzoic acid or a carbamoyl benzoic acid or both. In yet another embodiment, the invention provides a method of activating nonproteinogenic amino acids like paraminobenzoic acid and/or carbamoyl benzoic acid for incorporation into peptides or polyketides by inserting at least one DNA fragment that encodes a PKS protein into a cell and causing the cell to express the encoded PKS protein under conditions such that the PKS protein functions to produce a polyketide carrying either a para-aminobenzoic acid or a carbamoyl benzoic acid or both.

[0090] There are three regions of the *X. albilineans* genome specifying albicidin production. XALB2 and XALB3 regions each contain only one gene, both of which are required for post-translational activation and folding of albicidin PKS and NRPS enzymes. The XALB1, XALB2 and XALB3 gene clusters are characterized by an unusual hybrid NRPS-PKS system, indicating that albicidin biosynthesis may provide an excellent model for investigating the biosynthesis of hybrid polyketide-polypeptide metabolites in bacteria. The availability of three genomic regions involved in albicidin production, XALB1 and XALB2 and XALB3, also offers the ability to express individually the enzymes of the albicidin family biosynthetic pathway including structural, resistance, secretory and regulatory elements, and to engineer overproduction of albicidin in mutated or modified host cells of the invention. The invention overcomes prior art limitations in albicidin production due to low yields of toxin production in *X. albilineans* and may

also allow characterization of the chemical structure of albicidin as well as application of this potent inhibitor of prokaryote DNA replication.

[0091] The invention results from a number of unpredictable results namely the number and complexity of the enzymes involved in biosynthesis. The discovery of the complete sequence required for biosynthesis of Albicidins is previously unreported. The invention provides for a novel process for production of molecule having a polyketide-polypeptide backbone and the formula $C_{40}H_{35}O_{15}N_6$, a molecular weight of 839, and the structural elements shown in Figure 11.

[0092] The invention further includes (a) the Albicidin Family Biosynthetic Gene Cluster including (b) the structural and regulatory elements of the operons that encode c) the enzymes PKS-1, PKS-2, PKS-3, PKS-4, NRPS-1, NRPS-2, NRPS-3, NRPS-4, NRPS-5, NRPS-6 and NRPS-7 as well as (d) the proteins AlbI to AlbXXII, (e) the isolated enzymes, proteins, and active forms thereof, as well as mutants, fragments, and fusion proteins comprising any of the forgoing; (f) the uses of the enzymes or proteins encoded by the Albicidins Biosynthesis Gene Cluster or any one of its operons, (g) a host cell expressing one or more enzymes or proteins encoded by the Albicidin Family Biosynthetic Gene Cluster; (h) use of host cells having the Albicidins Biosynthesis Gene Cluster to produce an antibiotic; (i) methods of modifying the DNA sequences to produce members of a series of antibiotic compounds having structures related to Albicidins; (j) DNA sequences that encode the same proteins as any of SEQ. ID. Nos. 1 to 25 but differ in specific codons due to the multiplicity of codons that lead to expression of the same amino acid; (k) antibiotics produced by the process of expression of the Albicidin Family Biosynthetic Genes in a genetically modified host cell sustained in a culture medium and thereafter separation of the antibiotic from the host cell and culture medium; (l) an isolated and purified antibiotic produced by a process that includes at least three proteins coded by DNA sequences selected for the group consisting of SEQ. ID Nos. 1 to 25 in combination with additional enzymes that modify the product to provide a non-naturally occurring Albicidins like product having at least one of the useful properties reported for albicidin; and (m) a process for producing an antibiotic that comprises modifying a host cell to enhance expression of the DNA of the Albicidin Family Biosynthetic Gene Cluster by insertion of expression enhancing DNA into the genome of a *Xanthomonas albilineans* strain in a position operative to enhance expression of the enzymes of the Albicidin Family Biosynthetic Gene Cluster, culturing the modified host cell to produce an antibiotic and isolating the antibiotic. The products and methods described above have utility as proteins or as nucleic acids as the case may be, including such uses sources of pyrimidine or purine bases or amino acids, or as animal food supplements and the like, as well as the more important uses to provide antibiotics, plant disease treatment methods, genetically modified disease resistant plants, phytotoxins and the like.

[0093] The subject invention also provides an isolated and purified antibiotic produced

by a process that includes at least three proteins coded by the nucleic acids of the subject invention in combination with additional enzymes that modify the product to provide a non-naturally occurring Albicidin-like product having at least one of the useful properties reported for albicidin. In certain embodiments, the antibiotic or antibiotics have at least one of the general structures illustrated in Figure 11. In other embodiments, antibiotics of the subject invention have at least 4 of the structural elements illustrated in Figure 11, and an elemental composition of $C_{40}H_{35}N_6O_{15}$.

[0094] The invention further provides a method of protecting a plant against damage from albicidin that comprises applying an agent that blocks expression at least one gene in the Albicidin Biosynthetic Gene Clusters to the plant to be protected. Additional inventions include a method of obtaining agents useful in blocking expression of albicidin by screening materials against a modified host cell line that expresses the Albicidin Biosynthesis Gene Clusters and selecting for materials that stop or decrease albicidin production and a method of protecting a plant against phytotoxic damage from an antibiotic that comprises inserting into the plant and operably expressing at least one resistance gene from the Albicidin Biosynthesis Gene Clusters into the plant to be protected.

EXAMPLE 1 – Materials and Methods

[0095] Bacterial strains and plasmids. The source of bacterial strains and their relevant characteristics are described in Table 1.

[0096] Media, antibiotics, and culture conditions. *X. albilineans* strains were routinely cultured on modified Wilbrink=s (MW) medium at 30□C without benomyl (Rott *et al.*, 1994). For long-term storage, highly turbid distilled water suspensions of *X. albilineans* were supplemented with glycerol to 15% (vol/vol) and frozen at B80□C. For *X. albilineans*, MW medium was supplemented with the following antibiotics as required at the concentrations indicated: kanamycin, 10 or 25 μg/ml; and rifampicin, 50 μg/ml. *E. coli* strains were grown on Luria-Bertani (LB) agar or in LB broth at 37□C and were maintained and stored according to standard protocols (Sambrook *et al.*, 1989). For *E. coli*, LB medium was supplemented with the following antibiotics as required at the concentrations indicated: kanamycin, 50 μg/ml; ampicillin, 50 μg/ml.

[0097] Bacterial conjugation. DNA transfer between *E. coli* donor (DH5_MCR/pAlb389 or pAC389.1, Table 1) and rifampicin-resistant *X. albilineans* recipients (*X.* strains AM10, AM12, AM13, AM36 and AM37, Table 1) was accomplished by triparental conjugation with plasmid pRK2073 as the helper as described previously (Rott *et al.*, 1996).

[0098] Assay of albicidin production. Albicidin production was tested by a microbiological assay as described previously (Rott *et al.*, 1996). Rifampicin and kanamycin exconjugants were spotted with sterile toothpicks (2-mm-diameter spots) onto plates of SPA

medium (2% sucrose, 0.5% peptone, 1.5% agar) and incubated at 28° C for 2-5 days. The plates were then overlaid with a mixture of *E. coli* DH5α (10^7 cells in 2 ml of distilled water) plus 2 ml of molten 1.5% (wt/vol) Noble agar (Difco) at ca. 65° C and examined for inhibition zones after 24 h at 37C.

[0099] Nucleic acid manipulations. Standard molecular techniques were used to manipulate DNA (Sambrook *et al.*, 1989) except for total genomic DNA preparation. Total genomic DNA for southern blot hybridization was prepared as described by Gabriel and De Feyter (1992).

[00100] PCR Conditions. PCR amplifications were performed in an automated thermal cycler PTC-100™ (MJ Research, Inc). The 25 µl PCR reaction mix consisted of 100 ng of genomic DNA or 1 ng of plasmid DNA, 2.5 µl of 10X PCR buffer without MgCl2 (Eurobio), 80 µM dNTP mix, 2.5 units of EUROBIOTAQII®(Eurobio), 25 pmoles of each primer, 2.0 mM $MgCl_2$ (Eurobio) and sterilized distilled water to final volume. The PCR program was 95°C for 2 min, 25 cycles at 94°C for 1 min, Tm for 1 min and 72°C for 1 min, with a final 72°C extension for 5 min. Tm temperature was determined for each couple of primers and varied between 55°C and 60°C. A 5µl aliquot of each amplified product was analyzed by electrophoresis through a 1% agarose gel. For sequencing, PCR products were cloned with the pGEM®-T Easy Vector System (Promega).

[00100] Oligonucleotide synthesis. Oligonucleotides were purchased from Genome Express (Grenoble or Montreuil, France).

[00101] DNA sequencing. Automated DNA sequencing was carried out on double-stranded DNA by the dideoxynucleotide chain termination (Sanger *et al.*, 1977) using a Dye Terminator Cycle Sequencing kit and an ABI Perkin-Elmer sequencer according to the manufacturer's procedure. Both DNA strands were sequenced with universal primers or with internal primers (20mers). This service was provided by Genome Express (Grenoble, France). Computer-aided sequence analyses were carried out using Sequence Navigator™ (Applied Biosystems, Inc) and SeqMan (DNASTAR Inc.) programs.

[00102] Sequence analysis. Nucleotide sequences were translated in all six reading frames using EditSeq (DNASTAR Inc.). Potential products of ORFs longer than 100 b were compared to protein databases by the PSI-BLAST program (Swiss-Prot and Genbank) on the NCBI with site (ncbi.nlm.nih.gov/) using Altschul program (Altschul *et al.*, 1997). The TERMINATOR program of the Genetics Computer Group was used to identify putative Rho-independent transcription terminators.

[00103] **Procedures**

EXAMPLE 2 – Sequencing of the Double Strand Region of 55.839 Bp from *X. albilineans* Containing XALB1 SEQ ID NO. 1

[00104] In Figure 1 is presented a physical map and genetic organization of XALB1. In the figure, E and K are restriction endonuclease sites for *Eco*RI and *Kpn*I, respectively. Rectangular boxes represent DNA fragments labeled A through N. The numbers below each rectangular box are the number of Tn*5-gus* insertion sites previously located in each DNA fragment (Rott *et al.*, 1996). The DNA inserts carried by plasmids pALB571 and pALB540 are represented by bold bars above the physical map. The location and direction of putative orfs identified in the XALB1 gene cluster are shown by arrows. Precise positions and proposed functions for individual orfs are summarized in Tables 2 and 3, respectively. Position of insertional sites of eight albicidin-defective mutants determined by sequencing are indicated by vertical arrows. The location and direction of putative ORFS identified in the XALB1 gene cluster are shown by arrow shapes. These twenty putative ORFs are potentially organized in four or five operons, as indicated at the bottom of the figure. Patterns indicate NRPS and PKS genes (diagonal crosshatch), methyl transferase and esterase genes (hollow rectangles), carbamoyl transferase gene (fine crosshatch), benzoate-derived products biosynthesis genes (white), regulatory genes (vertical lined), resistance genes (diagonal lines) and other genes with function of unknown significance to albicidin production (black), and three insertional sites of eight albicidin-defective mutants determinated by sequencing are indicated by vertical arrows. Dotted regions in the physical map and in ORFs represent the two internal duplicated DNA regions of XALB1.

[00105] The sequence illustrated in Figure 1 was generated as follows. The sources of DNA are set out in Table 1. DNA fragments F, E, B, C, I, and G, generated by the digestion of cosmid pALB571 (Rott *et al.*, 1996) with *Eco*RI and/or *Kpn*I, were subcloned into pBCKS (+) and were sequenced from the resulting subclones, pBC/F, pBC/E, pBC/B, pBC/C, pBC/I and pBC/G. DNA fragment D' which corresponds to the part of fragment D present in cosmid pALB571 was sequenced from plasmid pUFR043/D' obtained following self ligation of the complete *Eco*RI digested cosmid pALB571. DNA fragment H was sequenced from pAM45.1 (Rott *et al.*, 1996), obtained following cloning into vector pBR325 of the 12kb *Eco*RI fragment carrying Tn*5* and flanking sequences from mutant strain XaAM45. DNA fragment A' contains the part of fragment A present in cosmid pALB571 and was subcloned into vector pBCKS (+) and the resulting plasmid pBC/A' was used for sequencing. The presence of a large internal duplication made alignment of sequence data obtained from pBC/A' difficult. This difficulty was

resolved using sequence data obtained from an additional plasmid, pAM4, obtained following cloning into vector pBluescript II KS (+) of the 12kb *Eco*RI fragment carrying Tn*5* and flanking sequences from mutant strain XaAM4, which contains only one copy of the large internal duplication. Sequence data from pBC/A' were used to determine the first 1542 bp of fragment A' between nucleotides C-19001 and G-20543. Sequence data from pAM4 and pBC/A' were used to determine the last 4823bp of fragment A' between nucleotides G-21653 and G-26477. The overlapping region between nucleotides G-20469 and C-22159 was amplified by PCR from cosmid pALB571 using primers contig13-1160 (5'gcgtaccgttgtccagtagg3') SEQ ID NO. 48 and pAM4-14 (5'gctggaaaccgagaatctga3') SEQ ID NO. 49, and was sequenced. Resulting sequence data were used to complete sequencing of DNA fragment A'. The junctions A/F, F/H, H/E, E/B, B/C, C/I, I/G, G/D between corresponding DNA fragments were sequenced directly from cosmid pALB571. EcoRI DNA fragment containing fragments A and F was subcloned from pALB540 into pBCKS (+), and the resulting plasmid pBC/AF was used to determine the part of DNA fragment A which was not present in cosmid pALB571 between nucleotides G-13682 and G-19001. EcoRI DNA fragments J, K, L, N were subcloned from pALB540 into pBCKS (+) and were sequenced from resulting plasmid pBC/J, pBC/K, pBC/L, and pBC/N. The junctions L/K, K/J and J/A between corresponding DNA fragments were sequenced directly from cosmid pALB540. DNA region between nucleotides G-7517 and T-8721 was amplified by PCR from cosmid pALB540 using primers E114 (5'gacacgatcagccgctagga3') SEQ ID NO. 50 and EI4-380 (5'accagcagttgggccagcct3') SEQ ID NO. 51 and was sequenced. Resulting sequence data were used to determine the sequence of fragment M and of junctions N/M and M/L. The nucleotide sequence of 55,839 bp containing the entire major gene cluster involved in Albicidin production was sequenced on both strands.

EXAMPLE 3 – Analysis of the Large Internal Duplications in the DNA Sequence of XALB1

[00106] The sequence of the 55,839 bp genomic region (SEQ ID NO. 1) contains two large internal duplications as shown by the dotted regions in the physical map of Figure 1. A direct duplication of 1736 bp was located in DNA fragment A between nucleotides G-19904 and G-21639 and between nucleotides G-23057 and G-24792. Another direct duplication of a 2727 bp was found in DNA fragments B and C between nucleotides C-40410 and G-43136 and between nucleotides C-46644 and G-49370. Comparison of the two copies of each duplication revealed that the two copies of the 1736 bp duplication are identical except for one nucleotide at position 21058, and that the two copies of the 2727 bp duplication are 98.8% identical and differ by 30 nucleotides.

EXAMPLE 4 – Comparison of XALB1 with the *xabB EcoRI* Fragment

[00107] Comparison of the DNA sequence of the 55,839 bp genomic region described in this study with the partial DNA sequence of 16,511 bp of the same region in Huang et al., 2001 (described by Huang et al. as an *Eco*RI fragment including full length xabB from *X. albilineans* strain Xa13 [GenBank accession No. AF239749]), revealed that the DNA sequence from strain Xa13 over 16,511 bp is identical to the sequence from strain Xa23R1, described herein, with the following exceptions: 1) five nucleotides are different at positions 42963, 42972, 42980, 43014 and 43071 of the XALB1 sequence, and 2) nucleotides from positions 43137 to 49370 are missing (internal to *albI*; refer Fig. 1). Analysis of genomic DNA of seven strains isolated from different countries (Australia, Reunion Island, Kenya, Zimbabwe and USA), digested by *Kpn*I and hybridized with the pBC/C plasmid (Table 1) labeled with ^{32}P, revealed that two DNA fragments corresponding to the XALB1 fragments B and C were present in all strains (data not shown). This result indicated that all studied strains contain *albI* and not *xabB* because in *albI* the pBC/C plasmid probe hybridizes with the large internal duplication present in both DNA fragments B and C (Figure 1). Based on this observation we postulated that the DNA sequence of XabB reported as full length by Birch in PCT WO 02/24736 A1 (Their seq. ID#1) appears to be incomplete and missing 6,234 bp of DNA sequence encoding 2,078 amino acids.

EXAMPLE 5 – Reading Frame Analysis in XALB1

[00108] Analysis of the 55,839 bp double strand region for coding sequences revealed the presence of 20 open reading frames (ORFs) designated *albI* to *albXX* (Table 2 below) which are distributed in four groups of genes according to their position and their orientation in the XALB1 cluster (Figure 1). Genes of each group may form part of the same operon as judged by their overlapping stop and start codons, or by the relatively short intergenic region which varies from 5 to 274 nucleotides. The 20 ORFs appear to be organized in four operons: operon 1 formed by *albI* - *albIV*; operon 2 by *albV* - *albIX*; operon 3 by *albX* - *albXVI*; operon 4 by *albXVII* - *albXX*. The majority of *alb* ORFs are initiated with an ATG codon, except *albI* and *albXVII* which are initiated with a TTG codon, and *albIV* and *albVI* which are initiated with a GTG start codon. In seven ORFs of XALB1, start codons are preceded by the consensus sequence GAGG which may correspond to the ribosome binding site. Other ORFs are preceded by a less conserved sequence which contain at least three nucleotides A or G and which may serve as a weak ribosome binding site.

EXAMPLE 6 – Sequencing of the Tn*5* insertional site of eight tox⁻ mutants previously located in XALB1

[00109] Eight of the 45 *X. albilineans* Tox⁻ mutants complemented by cosmid pALB540 and/or cosmid pALB571 and previously described (Rott *et al.*, 1996) were further analyzed. All eight mutants contain a single Tn*5* insertion and correspond to the following *X. albilineans* strains: XaAM7, XaAM15, XaAM45, and XaAM52 which are complemented by pALB571 but not by pALB540; XaAM4, XaAM29 and XaAM40 which are complemented by both cosmids; and XaAM1 which is complemented by pALB540 but not by pALB571. The Tn*5* insertional site of each Tox⁻ mutant was sequenced from plasmids obtained following cloning in pBR325 or in pBluescript II KS (+) of the EcoRI fragments carrying Tn*5* and flanking sequence using the sequencing primer GUSN (5'tgcccacaggccgtcgagt3') SEQ ID No. 52 that annealed 135 bp downstream from the insertional sequence IS50L of Tn*5*-*gusA*. The sequence of the Tn*5* insertional site was compared with the 55,839 bp sequence containing XALB1 in order to determine the *alb* gene disrupted in each Tox⁻ mutant. *albI* is disrupted by the Tn*5* insertion in XaAM15 and XaAM45 at position 33443 and 34229, respectively (Figure 1). *albIV* is disrupted by the Tn*5* insertion in XaAM7 and XaAM52 at position 53704 and 53915, respectively. *albIX* is disrupted by the Tn*5* insertion in XaAM4, XaAM29 and XaAM40 at position 21653, 23444 and 24376, respectively. *alb XI* is disrupted by the Tn*5* insertion in XaAM1 at position 13301. These results are in accordance with the previous characterization of Tox⁻ mutants using Southern blot hybridization (Rott *et al.*, 1996), except for XaAM1. The Tn*5*-*gusA* insertion site of XaAM1 was previously located in DNA fragment A (Rott *et al.*, 1996) but results of this study showed that this site is located in DNA fragment J (Figure 1).

EXAMPLE 7 – Homology analysis of proteins potentially encoded by XALB1

[00110] Preliminary functional assignments of individual ORFs were made by comparison of the deduced gene products with proteins of known functions in the Genbank database. The results are set out in Table 3 below. Among the ORFs identified from the sequenced XALB1 gene cluster, we found (i) four genes, *albI* SEQ ID No. 20, *albIV* SEQ ID No. 23, *albVII* SEQ ID No. 17 and *albIX* SEQ ID No. 15, encoding PKS and/or NRPS modules; (ii) one carbamoyl transferase gene, *albXV* SEQ ID No. 5; (iii) two esterase genes, *albXI* SEQ ID No. 9 and *albXIII* SEQ ID No. 7; (iv) two methyltransferase genes, *albII* SEQ ID No. 21 and *albVI* SEQ ID No. 18; (v) two benzoate-derived products biosynthesis genes, *albXVII* SEQ ID No. 11 and *albXX* SEQ ID No.14; (vi) two putative albicidin biosynthesis regulatory genes, *albIII* SEQ ID No. 22 and *albVIII* SEQ ID No. 16; (vii) two putative albicidin resistance genes, *albXIV* SEQ ID No. 6 and *albXIX* SEQ ID No. 13; and (viii) two additional ORFs encoding proteins similar to transposition proteins, *albV* SEQ ID No. 19 and *albXVI* SEQ ID No. 4. No known

function was found in the database for *albX* SEQ ID No. 10 and *albXII* SEQ ID No. 8. The potential product of *albXVIII* SEQ ID No. 12 appeared to be a truncation of an enzyme with strong similarity to 4-amino-4-deoxychorismate lyase and branched-chain amino acid aminotransferase. Since the gene encoding the predicted product is roughly half the length of other such lyase or aminotransferase genes, *albXVIII* may be the result of a recombination event and may be non functional.

EXAMPLE 8 – The *alb* PKS and/or NRPS genes

[00111] The potential product of *albI*, designated AlbI SEQ ID No. 20, is a protein of 6879 aa with a predicted size of 755.9 kDa. This protein is very similar to the potential product of the *xabB* gene from *X. albilineans* strain Xa13 from Australia (Huang *et al.*, 2001), but it differs in length and size (See Table 4 below). XabB is a protein of 4801 amino acids with a predicted size of 525.7 kDa. Comparison of AlbI with XabB revealed that the N-terminal regions from Met-1 to Ile-4325 of both proteins are identical except for five amino-acids which are Tyr-3941, Pro-3952, Ala-4054, Ala-4271 and Gln-4284 in AlbI and His-3941, Ala-3952, Val-4054, Val-4271 and Glu-4284 in XabB. The same comparison revealed that the AlbI C-terminal region from Arg-6404 to the stop codon is 100% identical to the XabB C-terminal region from Arg-4326 to the stop codon.

[00112] The N-terminal region (from Met-1 to Asp-3235) of AlbI is 100% identical to the corresponding region in XabB which was previously described as similar to many microbial modular PKS (Huang *et al.*, 2001). This PKS region may be divided into three modules (Figure 2). Abbreviations used in the Figure are: A, adenylation; ACP, acyl carrier protein; AL, acyl-CoA ligase; C, condensation; KR, ß-ketoacyl reductase; KS, ß-ketoacyl synthase; NRPS, nonribosomal peptide synthase; PCP, peptidyl carrier protein; PKS, polyketide synthase; TE, thioesterase; HBCL, 4-hydroxybenzoate-CoA ligase. The question mark in the NRPS-2 domain indicates that this A domain is incomplete. The first module designated PKS-1 contains acyl-CoA ligase (AL) and acyl carrier protein (ACP1) domains. The second module designated PKS-2 contains ß-ketoacyl synthase (KS1) and ß-ketoacyl reductase (KR) domains followed by two consecutive ACP domains (ACP2 and ACP3). The third module designated PKS-3 contains a KS domain (KS2) followed by a PCP domain (PCP1). Apart from their very high similarity with XabB, these three PKS modules exhibited the highest degree of overall similarity with polyketide synthases SafB and PksM from *Myxococcus xanthus* and *Bacillus subtilis*, respectively (Table 4). The motifs characteristic of these domains are 100% identical to those of XabB which were previously aligned with those from other organisms (Huang *et al.*, 2001). The AL domain contains the conserved adenylation core sequence (SGSSG) and the ATPase motif (TGD). The three ACP domains contain a 4'-phosphopantetheinyl-binding cofactor box GxDS(IL), except that

A replaced G in ACP1. Both KS domains contain motif GPxxxxxxxCSxSL around the active site Cys, and two His residues downstream from the active site Cys, in motifs characteristic of these enzymes. The KR domain contains the NAD(P)H-binding site GGxGxLG.

[00113] The PKS part of AlbI is linked by the PCP1 domain to the four apparent nonribosomal peptide synthase modules designated NRPS-1, NRPS-2, NRPS-3 and NRPS-4 (Figure 2). NRPS-1, NRPS-2 and NRPS-3 modules display the ordered condensation, adenylation (A) and PCP domains typical of such enzymes (Marahiel *et al.*, 1997), and NRPS-4 consists of an extra C domain which may correspond to an incomplete NRPS module. Known conserved sequences, characteristic of the domains commonly found in peptide synthases (Marahiel *et al.*, 1997), were compared to those from NRPS-1, NRPS-2, NRPS-3 and NRPS-4 (Tables 5, 6 and 7). Sequences characteristic of C, A, or PCP domains are conserved in these four NRPS, except in A domain of NRPS-2 module, suggesting that this latter A domain may be not functional. Comparison of the four NRPS modules among themselves revealed that NRPS-2, NRPS-3 and NRPS-4 modules were 30.7%, 94.4% and 47.5% similar to NRPS-1 module, respectively. Comparison with XabB revealed NRPS-2 and NRPS-3 modules were not present in XabB which contains only NRPS-1 and NRPS-4 modules (Figure 2). The dotted box in Figure 2 corresponds to the apparent deletion of the NRPS-2 and NRPS-3 modules in XabB as compared to AlbI. Apart their very high similarity with XabB, Alb I NRPS modules exhibited the highest degree of overall similarity with non-ribosomal peptide synthases NosA and NosC from *Nostoc* sp.

[00114] *albIV* potentially encodes a protein of 941 aa (AlbIV) with a predicted size of 104.8 kDa. AlbIV is similar to several non-ribosomal peptide synthases such as the BA3 peptide synthase involved in bacitracin biosynthesis in *Bacillus licheniformis* (Table 4). AlbIV forms one NRPS module designated NRPS-5 that contains only an A domain and a PCP domain (Figure 2). Sequences characteristic of the domains A and PCP commonly found in peptide synthases (Marahiel *et al.*, 1997) are conserved in AlbIV (Tables 6 and 7). However the A domain present in AlbIV differs from A domains commonly found in peptide synthases: conserved sequences corresponding to cores A8 and A9 in AlbIV are separated by a very long peptide sequence of 390 amino-acids. This additional peptide sequence exhibits a significative similarity with the protein WbpG of 377 amino acids involved in the biosynthesis of a lipopolysaccharide in *Pseudomonas aeruginosa* (Table 4).

[00115] *albVII* potentially encodes a protein of 765 aa (AlbVII) with a predicted size of 83.0 kDa similar to the 4-hydroxybenzoate-CoA ligase from several bacteria and the closest protein (HbaA) was from *Rhodopseudomonas palustris* (Table 4). High similarity between AlbVII and HbaA suggests that AlbVII is a 4-hydroxybenzoate-CoA ligase and constitutes a fourth PKS module designed PKS-4. The size of HbaA is smaller (539 aa) and the similarity between the two proteins starts only at the residue 277 of AlbVII and at the residue 28 of HbaA.

Comparison of AlbVII sequence located upstream from residue 277 produced no significant alignment. AlbVII, like 4-hydroxybenzoate-CoA ligases, contains some conserved sequences characteristic of the A domain commonly found in peptide synthases (Table 6).

[00116] *albIX* encodes a protein of 1959 aa (AlbIX) with a predicted size of 218.4 kDa similar to non-ribosomal peptide synthases. Known conserved sequences, characteristic of the domains commonly found in peptide synthases (Marahiel *et al.*, 1997), were compared with those from AlbIX which forms two NRPS modules designated NRPS-6 and NRPS-7 (Tables 5, 6 and 7). NRPS-6 contains only one A and one PCP domain. NRPS-7 contains the three domains characteristic of NRPS modules (A-C-PCP) followed by a TE domain (Figure 2). Apart their very high similarity with XabB, NRPS-6 and NRPS-7 modules exhibited the highest degree of overall similarity and identity with non-ribosomal peptide synthases DhbF from *B. subtilis* and NosA from *Nostoc* sp. (Table 4).

EXAMPLE 9 – The alb carbamoyl transferase gene

[00117] *albXV* potentially encodes a protein of 584 aa with a predicted size of 65.2 kDa. This protein, AlbXV, is similar to BlmD, a carbamoyl transferase involved in bleomycin biosynthesis in *Streptomyces vertillus* (Du *et al.*, 2000), and to a probable carbamoyl transferase potentially expressed in *P. aeruginosa* (Table 4). High similarity of AlbXV with these proteins suggests that AlbXV is a carbamoyl transferase.

EXAMPLE 10 – The alb esterase genes

[00118] *albXI* potentially encodes a protein of 315 aa with a predicted size of 35.9 kDa. This protein, AlbXI, exhibits low similarity to SyrC, a putative thioesterase involved in syringomycin biosynthesis by *Pseudomonas syringae* (Zhang *et al.*, 1995), and to a potential hydrolase encoded by *Streptomyces coelicolor* (Table 4). Precise function of SyrC remains unknown but SyrC is similar to a number of thioesterases, including fatty acid thioesterases, haloperoxidases, and acyltransferases that contain a characteristic GxCxG motif. The corresponding SyrC domain GICAG is conserved in AlbXI which contains the sequence GWCQA, except that A replaces the last G, suggesting that AlbXI may be an esterase despite its low overall similarity with SyrC.

[00119] *albXIII* potentially encodes a protein of 317 aa with a predicted size of 34.5 kDa. This protein, AlbXIII, is similar to hypothetical proteins with unknown function from several bacteria including *Caulobacter crescentus* (Table 4). AlbXIII and these hypothetical proteins contain a GxSxG motif characteristic of serine esterases and thioesterases, the corresponding sequence in AlbXIII being GHSVG. In addition, AlbXIII presents a similarity with

the 2-acetyl-1alkylglycerophosphocholine esterase which hydrolyzes the platelet-activating factor in *Canis familiaris* (Table 4), suggesting that AlbXIII is an esterase.

EXAMPLE 11 – The alb methyltransferase genes

[00120] *albII* potentially encodes a protein of 343 aa (AlbII) with a predicted size of 37.7 kDa. *albII* is 100% identical to the *xabC* cistron, previously described as encoding an *O*-methyltransferase downstream *xabB* (Huang *et al.*, 2000a). This conclusion is based on the similarity of XabC with a family of methyltransferases that utilize S-adenosyl-L-methionine (SAM) as a co-substrate for *O*-methylation including TcmO protein from *Streptomyces glaucescens* (Huang *et al.*, 2000a). AlbII contains three highly conserved motifs of SAM-dependent methyltransferases, including the motif I involved in SAM binding (Figure 3). In the Figure, identical or similar amino acids (A=G; D=E; I=L=V) are shown in bold. Numbers indicate the position of the amino acid from the N-terminus of the protein. Abbreviations used in the Figure are: Sgl-TcmO and Sgl-TcmN, multifunctional cyclase-hydratase-3-*O*-Mtase and tetracenomycin polyketide synthesis 8-*O*-Mtase of *Streptomyces glaucescens*, respectively (accession number: M80674); Smy-MdmC, midecamycin-*O*-Mtase of *Streptomyces mycarofaciens* (accession number: M93958); Mxa-SafC, Saframycin *O*-Mtase of *Myxococcus xanthus* (accession number: U24657); Ser-EryG, erythromycin biosynthesis *O*-Mtase of *Saccharopolyspora erythraea* (accession number: S18533); Spe-DauK, carminomycin 4-O-Mtase of *Streptomyces peucetius* (accession number: L13453); Sal-DmpM, *O*-demethylpuromycin-*O*-Mtase of *Streptomyces alboniger* (accession number: M74560); Shy-RapM, rapamycin *O*-Mtase of *Streptomyces hygroscopicus* (accession number: X86780); Sav-AveD, avermectin B 5-*O*-Mtase of *Streptomyces avermitilis* (accession number: G5921167), Sar-Cmet, mithramycin *C*-methyltransferase of *Streptomyces argillaceus* (accession number: AF077869); AlbII, putative albicidin biosynthesis *C*-Methyltransferase of *Xanthomonas albilineans* (SEQ ID No. 27); identical to XabC, accession number: AF239749).

[00121] Comparison of AlbII with the Genbank database revealed that AlbII, besides 100% identity to XabC, exhibited the highest degree of overall identity with MtmMII, a *C*-methyltransferase from *Streptomyces argillaceus* (Table 4) involved in *C*-methylation of the polyketide chain for mithramycin biosynthesis, suggesting that AlbII is a *C*-methyltransferase. XabC was not compared by Birch and co-workers with MtmMII (Huang *et al.*, 2000a) because the MtmMII sequence was not available until recently in the Genbank database. The three highly conserved motifs in SAM methyltransfererases are also present in MtmMII (Figure 3), suggesting that AlbII is a *C*-methyltransferase SAM-dependent.

[00122] *albVI* potentially encodes a protein of 286 aa (AlbVI) with a predicted size of 32.1 kDa similar to several hypothetical protein from *Mycobacterium tuberculosis*

(Genbank accessions No. AAK46042, AAK48238, AAK44517, AAK46218) and from *S. coelicolor* (Genbank accession No. CAC03631). AlbVI is also similar to the tetracenomycine C synthesis protein (TcmP) of *Pasteurella multocida* (Table 4). Four highly conserved motifs in TcmP and other *O*-methyltransferases are also present in AlbVI (Figure 4), suggesting that AlbVI is an *O*-methyltransferase. In the Figure, identical or similar aa (A=G; D=E; I=L=V; K=R) are shown in bold. Numbers indicate the position of aa from the N-terminus of the protein. Abbreviations used in the Figure are: Sgl-tcmP, tetracenomycin C synthesis protein of *Streptomyces glaucescens* (accession number: C47127); Sme-PKS, putative polyketide synthase of *Sinorhizobium meliloti* (accession number: AAK65734); Pmu-tcmP: tetracenomycin C synthesis protein of *Pasteurella multocida* (accession number: AAK03406); Mtu-Omt: putative *O*-methyltransferase of *Mycobacterium tuberculosis* (accession number: AAK45444); Mlo-Hp: hypothetical protein containing similarity to *O*-methyltransferase of *Mesorhizobium loti* (accession number: BAB50127); Mtu-Hp1: hypothetical protein of *Mycobacterium tuberculosis* (accession number: AAK46042); Mtu-Hp2: hypothetical protein of *Mycobacterium tuberculosis* (accession number: AAK48238); Mtu-Hp3: hypothetical protein of *Mycobacterium tuberculosis* (accession number: AAK44517); AAK46218); Sco-Hp: hypothetical protein of *Streptomyces coelicolor* (accession number: CAC03631); AlbVI, putative albicidin biosynthesis *O*-Methyltransferase of *Xanthomonas albilineans* (this study). The three highly conserved motifs in SAM methyltransfererases are not present in AlbVI, indicating that SAM is not a co-substrate of AlbVI.

EXAMPLE 12 – The alb derived-benzoate products biosynthesis genes

[00123] alb*XVII* potentially encodes a protein of 716 aa with a predicted size of 79.8 kDa. This protein, AlbXVII, is very similar to the para-aminobenzoate (PABA) synthase from *Streptomyces griseus* (Table 4). This enzyme is required for the production of the antibiotic candicidin (Criado *et al.*, 1993).

[00124] *albXVIII* potentially encodes a protein of 137 aa with a predicted size of 15.0 kDa. This protein, AlbXVIII, is similar to the 4-amino-4-deoxychorismate lyase (ADCL) from *P. aeruginosa* (Table 4). The function of ADCL is to convert 4-amino-4-deoxychorismate into PABA and pyruvate. The length of AlbXVIII is smaller (Table 4) than the length of ADCL and the similarity of AlbXVIII with this protein starts only at residue 161. *albXVIII* is preceded by a small ORF encoding a sequence of 59 amino acids similar to the first 42 amino acids of ADCL from *P. aeruginosa*. These data suggest that *albXVIII* is probably a truncated form of *albXVIII* and probably not functional. *albXVIII* may, therefore, not be involved in albicidin biosynthesis. The region between *albXVII* and *albXVIII* was amplified by PCR from total DNA of *X. albilineans* Xa23R1 strain using primers ORFW (5'gcgagaggacaagctgctgc3') SEQ ID No. 53 and ORFY (5'cgttgaggatgcagcgctcg3') SEQ ID No. 54 and was sequenced. Resulting sequence data

showed that the sequence of the PCR fragment was 100% identical to the sequence of pALB540, indicating that the recombination of *albXVIII* did not occur during cloning of the genomic fragment in pALB540.

[00125] *albXX* potentially encodes a protein of 202 aa with a predicted size of 22.6 kDa. This protein AlbXX is similar to the 4-hydroxybenzoate synthase potentially involved in ubiquinone biosynthesis by *Escherichia coli* (Siebert *et al.*, 1992).

EXAMPLE 13 – The alb regulatory genes

[00126] *albIII* potentially encodes a protein of 167 amino acids with a predicted size of 17.8 kDa that is similar to the transcription factors ComA of different bacteria such as *E. coli* and *B. licheniformis* (Table 4). ComA transcription factors appear to be involved in regulation of antibiotic production in bacteria. In *E. coli*, a gene similar to *comA* is present in the enterobactin biosynthesis gene cluster (Liu *et al.*, 1989). In *B. subtilis*, ComAB was described as a probable positive activator of lichenysin synthetase transcription (Yakimov *et al.*, 1998) and a gene similar to *comA* was shown to be essential for bacilysin biosynthesis (Yazgan *et al.*, 2001). These data suggest that AlbIII regulates transcription of genes involved in albicidin biosynthesis.

[00127] *albVIII* potentially encodes a protein of 330 aa with a predicted size of 37.7 kDa. This protein, AlbVIII, is very similar to the SyrP like protein from *S. verticillus* and to SyrP protein from *P. syringae* (Table 4). SyrP participates in a phosphorylation cascade controlling syringomycin synthesis (Zhang *et al.*, 1997) and the *syrP* like gene was described in the *S. verticillus* bleomycin biosynthetic gene cluster (Du *et al.*, 2000). These data suggest that AlbVIII regulates albicidin biosynthesis in *X. albilineans*.

EXAMPLE 14 – The alb resistance genes

[00128] *albXIV* potentially encodes a protein of 496 aa with a predicted size of 52.7 kDa. This protein, AlbXIV, is 100% identical to AlbF isolated from *X. albilineans* strain Xa13 (GenBank Accession AF403709; direct submission by Bostock and Birch and described as "a putative albicidin efflux pump which confers resistance to albicidin in *E. coli*"). AlbXIV and AlbF are closely related to a family of transmembane transporters involved in antibiotic export and antibiotic resistance in many antibiotic-producing organisms. AlbXIV and AlbF exhibited the highest degree of overall identity with the putative transmembrane efflux protein from *S. coelicolor* (Table 4). These data suggest that AlbXIV and AlbF may be involved in albicidin resistance by transporting the toxin out of the bacterial cells that produce it. Alternatively, AlbXIV and AlbF may simply play a role in antibiotic secretion and/or plant pathogenesis to effect the transport of albicidin outside of producing cells.

[00129] *albXIX* potentially encodes a protein of 200 aa with a predicted size of 22.8 kDa. This protein, AlbXIX, is similar to the McbG protein from *E. coli* (Table 4). In *Enterobacteriae,* the McbG protein, together with two other proteins (McbE and McbF), was shown to cause immunity to the peptide antibiotic microcin B17 which inhibits DNA replication by induction of the SOS repair system (Garrido *et al.*, 1988). McbE and McbF proteins serve as a pump for the export of the active antibiotic from the cytoplasm, whereas a McbG alone also provides some protection: a well-characterized deficient-immunity phenotype is exhibited by microcin B17-producing cells in the absence of the immunity gene mcbG (Garrido *et al.*, 1988). The significant similarity between AlbXIX and McbG, together with the fact that albicidin also blocks DNA replication (Birch and Patil, 1985a) suggests that AlbXIX confers immunity against albicidin in *X. albilineans*.

EXAMPLE 15 – Transposition proteins

[00130] *albV* is 100% identical to the *thp* gene described in a divergent position upstream from *xabB* (Huang *et al.*, 2000a). The *thp* gene potentially encodes a protein of 239 aa displaying significant similarity to the IS21-like transposition helper proteins. In *X. albilineans* strain LS155 from Australia, insertional mutagenesis of *thp* blocked albicidin production, but *trans*-complementation failed, indicating the involvement in albicidin production of a downstream gene in the *thp* operon (Huang *et al.*, 2000a).

[00131] *albXVI* potentially encodes a protein of 88 aa with a predicted size of 9.8 kDa similar to the transposases from several bacteria such as *Xanthomonas axonopodis* or *Desulfovibrio vulgaris* (Table 4).

[00132] The presence of transposition proteins in the XALB1 cluster is probably a remnant from a past transposition event that may have contributed to the development of the albicidin XALB1 cluster.

EXAMPLE 16 – Unknown functions

[00133] *AlbX* potentially encodes a protein of 83 aa with a predicted size of 9.4 kDa. This protein, AlbX, is similar to an hypothetical protein from *P. aeruginosa* and to the MbtH protein from *Mycobacterium tuberculosis*. MbtH is a protein with unknown function found in the mycobactin gene cluster (Quadri *et al.*, 1998). A MbtH-like protein with unknown function was also described in the bleomycin biosynthetic gene cluster of *S. verticillus* (Du *et al.*, 2000). These data suggest that AlbX is involved in albicidin biosynthesis but its function remains unknown.

[00134] *albXII* potentially encodes a protein of 451 aa with a predicted size of 51.6 kDa. This protein, AlbXII, is very similar to a protein of 55 kDa encoded by the *boxB* gene in *Azoarcus evansii* (Table 4). This protein is a component of a multicomponent enzyme system

involved in the hydroxylation of benzoyl CoA, a step of aerobic benzoate metabolism in *Azoarcus evansii*, but its function remains unknown (Mohamed *et al.*, 2001).

EXAMPLE 17 – Prediction of amino acid specificity of Alb NRPS modules

[00135] In NRPSs, specificity is mainly controlled by A domains which select and load a particular amino-, hydroxy- or carboxy-acid unit (Marahiel *et al.*, 1997). The substrate-binding pocket of the phenylalanine adenylation (A) domain of the gramicidin S synthetase (GrsA) from *Brevibacillus brevis* was recently identified by crystal structure analysis as a stretch of about 100 amino acid residues between highly conserved motifs A4 and A5 (Conti *et al.*, 1997). Based on sequence analysis of known A domains, in relation to the crystal structure of the GrsA (Phe)substrate binding pocket, similar models have been published to predict the amino acid substrate which is recognized by an unknown NRPS A domain (Challis *et al.*, 2000; Stachelhaus *et al.*, 1999). These models postulate specificity-conferring codes for A domains of NRPS consisting of critical amino acid residues putatively involved in substrate specificity. The model proposed by Marahiel and co-workers (Stachelhaus *et al.*, 1999) defined a signature sequence consisting of ten amino acids lining with the ten residues of the phenylalanine-specific binding pocket located at positions 235, 236, 239, 278, 299, 301, 322, 330, 331 and 517 in the GsrA (Phe) sequence (accession number: P14687). The model proposed by Townsend and co-workers (Challis *et al.*, 2000) uses only the first eight of these critical residues.

[00136] Preliminary specificity assignments of albicidin synthase AlbI, AlbIV, AlbVII and AlbIX NRPS modules were made by comparison of complete sequences between conserved motifs A4 and A5 with sequences in the Genbank database. The corresponding sequence of the AlbIV NRPS-5 module is most related to domain 5 of bacitracin synthase 3 (BA3) from *B. licheniformis* that was suggested to activate Asn (Konz *et al.*, 1997). Corresponding sequences of AlbI and AlbIX NRPS-1, NRPS-3, NRPS-6 and NRPS-7 modules, apart from their very high similarity with XabB, exhibited the highest degree of overall identity (39%) with the Blm NRPS2 module of the biosynthetic gene cluster for bleomycin from *S. verticillus* that specifies for β-Alanine (Du *et al.*, 2000). The corresponding sequence of AlbVII PKS-4 produced the highest significant alignment with acetate-CoA ligase from *Sulfolobus solfataricus* (Genbank accession number: AAK41550), aryl-CoA ligase from *Comamonas testosteroni* (Genbank accession number: AAC38458) and 4-hydroxybenzoate-CoA ligase from *R. palustris*. The sequence between motifs A4 and A5 of the AlbI NRPS-2 could not be significantly aligned with any sequence present in the Genbank database. Comparison of this sequence with the corresponding sequence of GrsA (Phe) revealed that parts of the putative core and structural "anchor" sequences of AlbI NRPS-2 are deleted (Figure 5), suggesting that the AlbI NRPS-2 substrate binding pocket is not functional. In the Figure, amino acids of the six Alb NRPSs and of Alb PKS-4 that are identical or similar to GrsA or Blm sequences (A=G; D=E;

I=L=V; R=K) are shown in bold. Amino acids underlined in the GsrA sequence correspond to the phenylalanine-specific binding pocket. The positions of these amino acids in the GrsA primary sequence are indicated at the top of the figure. Amino acids underlined in the other sequences correspond to putative constituents of binding pockets, aligned with the seven residues of the phenylalanine- specific binding pocket of GrsA. Shaded amino-acids correspond to the putative core sequences and structural "anchors" based on comparison with the GrsA binding-pocket structure.

[00137] Alignment of the primary sequence between conserved motifs A4 and A5 of the AlbI, AlbIV, AlbVII and AlbIX NRPS-1, NRPS-3, NRPS-5, NRPS-6, NRPS-7 and PKS-4 modules with the corresponding sequence of GrsA (Phe) (Figure 5) revealed the putative constituents of binding pockets that constitute the codes as defined by Marahiel and co-workers (Stachelhaus *et al.*, 1999). These codes were compared with those of proteins most related to the sequence between the A4 and A5 motifs (Table 8) and were analyzed with the model proposed by Townsend and co-workers (Challis *et al.*, 2000, jhunix.hcf.jhu.edu/ ~ravel/nrps//). Using these codes, we were able to predict the Asparagine specificity of the AlbIV NRPS-5 module. The AlbIV NRPS-5 signature is 100% identical to BacC-M5 (Asn) and TyrC-M1 (Asn) codes identified in bacitracin synthetase 3 from *B. licheniformis* and in tyrocidine synthetase 3 from *B. brevis* (Table 8). The AlbIV NRPS-5 signature is also identical to the Asn code defined by Marahiel and co-workers (1997), except that I is replaced by L at position 299 (Table 8). The AlbI and AlbIX NRPS-1, 3, 6 and 7 signatures did not match any of those defined by Marahiel and co-workers (1997). Similarly, convincing predictions using the model proposed by Townsend and co-workers were not obtained either (Challis *et al.*, 2000, jhunix.hcf.jhu.edu/~ravel/nrps//). The AlbI and AlbIX NRPS-1, 3, 6 and 7 signatures diverged from all NRPS signatures previously described, except from the XabB signature that is identical to the AlbI NRPS-1 and 3 signatures. The signature most closely related to AlbI NRPS-1 and 3 specify Pro and the signature most closely related to AlbIX NRPS-6 and 7 specify Ser, but the degree of similarity in both cases is very weak (Table 8). The PKS-4 signature is similar to the AlbI NRPS-1 and NRPS-3 signatures at positions 235, 299 and 301.

[00138] Analysis of alignment of the primary sequence between conserved motifs A4 and A5 of the AlbI and AlbIX NRPS-1, NRPS-3, NRPS-6 and NRPS-7 modules with the corresponding sequences of the bleomycin synthase (Blm) NRPS2 (β-Ala) and gramicidin S synthetase (GrsA) modules (Figure 5) revealed that (i) sequences of AlbI NRPS-1 and AlbI NRPS-3 differ only at the level of two residues that are not involved in substrate binding, (ii) sequences of AlbIX NRPS-6 and AlbIX NRPS-7 are 100% identical, (iii) sequences of AlbI NRPS-1 and AlbI NRPS-3 are very similar to sequences of AlbIX NRPS-6 and AlbIX NRPS-7 but differ at the level of five putative constituents of binding pocket, (iv) AlbI and AlbIX NRPS residues, which are similar to residues of Blm NRPS2 (β-Ala) or GrsA (Phe), are essentially

located at the level of the putative core sequences and structural "anchor", and differ at the level of putative constituents of the binding pocket.

[00139] Binding-pocket constituents forming the NRPS signatures have been classified into three subgroups according to their variability among 160 specificity-conferring signature sequences (Stachelhaus *et al.*, 1999): (i) invariant residues Asp235 and Lys517 that mediate key interactions with the α-amino and α-carboxylate group of the substrate, respectively; (ii) moderately variant residues in positions 236, 301 and 330 which correspond to aliphatic amino acids and which may modulate the catalytic activity and fine-tune the specificity of the corresponding domains; (iii) highly variant residues in positions 239, 278, 299, 322 and 331 which may facilitate substrate specificity. AlbI and AlbIX NRPS-1, 3, 6 and 7 signatures are not totally in accordance with this classification. Invariant residue Lys517 is conserved in the four NRPS signatures, indicating the presence of an α-carboxylate group in the corresponding substrates. The Asp235Ala alteration is not consistent with an α-amino acid substrate. Birch and co-workers (Huang *et al.*, 2001) assumed that the initial alanine residue in the XabB signature was consistent with a nonproteinogenic hydroxy acid substrate by analogy with the initial glycine in the signature of the hydroxyisovaleric-acid (HVCL) loading domain of enniatin synthetase. The presence of an initial Alanine in the AlbVII PKS-4 signature (Figure 8) and in several 4-hydroxybenzoate-CoA ligase codes may confirm this hypothesis. However, the HVCL loading domain of enniatin synthetase (Table 8) and AlbVII PKS-4 are not preceded by a C domain and are not followed by a PCP domain, in contrast to the AlbI and AlbIX NRPS-1, 3, 6 and 7 modules. An Asp235Val alteration was recently described in the β-Ala specificity-conferring code (Du *et al.*, 2000, Table 8), suggesting that the substrate of AlbI and AlbIX NRPS-1, 3, 6 and 7 modules may be different from α-amino acids but may contain an amino group. Residue 236 is an aliphatic residue (Val or Ile) in all AlbI and AlbIX NRPS-1, 3, 6 and 7 signatures. Residue 301 is an aliphatic residue (Ala) in the AlbI NRPS-1 and 3 codes, but it is a Ser in the AlbIX NRPS-6 and 7 signatures. Residue 330 is not an aliphatic residue in the four NRPS signatures but an Asp. Similar alterations are present in the β-Ala code: residue 236 is an Asp, residue 301 is a Ser and residue 330 is an aliphatic amino acid. Concerning highly variable residues, AlbI NRPS-1 and 3 signatures differ from AlbIX NRPS-6 and 7 signatures at residue positions 299, 322 and 331, confirming that both types of NRPS modules specify different substrates.

[00140] **Table 8 : Comparison of signature sequences, as defined by Marahiel and co-workers** (Stachelhaus *et al.*, 1999), derived from sequences between the A4 and A5 domains of the AlbI, AlbIV, and AlbIX NRPS modules with those of Tyr-M1 (Pro) (Tyrocidine synthetase 2 module 1, accession number: AAC45929), VirS (Pro) (Virginiamycin S synthetase, accession number : CAA72310), HVCL (hydroxyisovaleric acid-CoA ligase, ACL1 enniatin synthetase, accession number: S39842), EntF-M1 (Ser) (Enterobactin synthase, accession number: AAA92015), β-Ala code (β-Ala selectivity-conferring code defined by Du *et al.* , 2000),

BacC-M5 (Asn) (Bacitracin synthetase 3, accession number: AAC06348), TyrC-M1 (Asn) (Tyrocidine synthetase 3, accession number: AAC45930) and Asn code (Asn selectivity-conferring code defined by Marahiel and co-workers (Stachelhaus *et al.*, 1999). Amino acids of AlbI NRPS-1 and NRPS-3 signatures identical or similar to TyrB-M1 (Pro), VirS (Pro) and HVCL signatures (A=G; D=E; I=L=V; R=K) are shown in bold. Amino acids of AlbIX NRPS-6 and NRPS-7 signatures identical or similar to Vir (Pro) and Blm (ß-Ala) signatures (A=G; D=E; I=L=V; R=K) are shown in bold. Variability: 0 indicates invariant residues, +/- moderately variant residues and ++ highly variant residues.

EXAMPLE 18 – Identification of putative promoters and putative terminators in XALB1

[00141] Putative rho independent terminators were identified downstream from *albIV* and *albXVI* using the Terminator program (Brendel and Trifonov, 1984), run with the Wisconsin Package™ GCG software (Figure 6). In the Figure, dashes indicate palindromic sequences. Symbols used in the Figure are: P, Primary structure value of putative terminator (minimum threshold value of 3.5 represents 95 percent of known, factor-independent, prokaryotic terminators); S, Secondary structure value of putative terminator. The presence of these terminators confirmed the proposed genetic organization of operons 1 and 3. A rho-independent terminator was identified in the intergenic region between *albXVII* and *albXVIII*, suggesting that the group of genes initially supposed to be organized in operon 4 may be in fact organized in two operons, operon 4 formed by *albXVII* and operon 5 by *albXVIII* B *albXX*. No putative rho independent terminator was found downstream from *albIX* and from *albXX*.

[00142] The 236 bp region between *albI* (operon 1) and *albV* (operon 2) is 100% identical to the sequence between *xabB* and *thp* genes that is assumed to contain a bidirectional promoter (Huang *et al.*, 2000a and 2001), suggesting that transcription of operon 1 and 2 is regulated by the same bidirectional promoter region (Huang *et al.*, 2001).

[00143] The 412 bp region comprised between *albX* (operon 3) and *albXVII* (operon 4) also contains a putative bidirectional promoter (Figure 7). In the Figure, the sequence of putative promoters are underlined, and putative ATG or TTG start codons are in bold. The closest matches (TTGACA-18x-TATAGT) to the consensus -35 (TTGACA) and -10 (TATAAT) sequences for *E. coli* σ^{70} promoters occurs 61 bp upstream from *albX* (operon 3). The closest matches (TTCAGA-19x-TATACA) to the consensus sequences for *E. coli* σ^{70} promoters occur 320 bp upstream from *albXVII* (operon 4). The region between *albXVII* and *albXVIII* lacks any apparent *E. coli* σ^{70} promoter. However, the sequence immediately upstream from *albXIX*, corresponding to the coding sequence of *albXVIII*, potentially contains an unidirectional promoter (Figure 7). The closest match (TTGCTC-19x-TATATT) to the consensus sequences for *E. coli* σ

^{70} promoters occurs 33bp upstream from *albXIX*. The presence of a terminator downstream from *albXVII* and of a promoter upstream from *albXIX* suggests that *albXVIII* is not transcribed and that *albXIX* and *albXX* form operon 5.

EXAMPLE 19 – Cloning of the XALB2 gene cluster

[00144] The 6 kb *Eco*R I fragment carrying Tn*5* and flanking sequence from strain AM37 was cloned in pBR325 and the obtained plasmid was designated pAM37 (Table 1). A 1.1 kb *Hind* III-*Hind* III DNA fragment from pAM37, named PR37 (Table 1), was labeled with ^{32}P and used to probe the 845 clones from the genomic library of *X. albilineans* strain Xa23R1, previously described (Rott et al., 1996). Eight new cosmids hybridized to this probe and restored albicidin production in mutant AM37. One of these cosmid, pALB389, carrying an insert of about 37 kb (Table 1), was used for complementation studies of the five mutants not complemented by pALB540 and pALB571. Cosmid pALB389 complemented mutants AM10 and AM37. Mutant AM10 was initially thought to be complemented by pALB639 (Rott et al., 1996). However, further complementation studies showed that mutant AM10 was not complemented by pALB639 and that only three mutants (AM12, AM13 and AM36) were complemented by pALB639 containing the third genomic region XALB3 involved in albicidin production. A 3 kb *Eco*RI- *Eco*RI DNA fragment from pALB389 that hybridized with probe PR37 was sub-cloned in pUFR043 (Table 1). The resulting plasmid pAC389.1 complemented mutants AM10 and AM37, confirming that the second region involved in albicidin production, XALB2, was present in the 3 kb insert of pAC389.1.

EXAMPLE 20 – Cloning of the XALB3 gene cluster

[00145] Cosmid pALB639, carrying an insert of 36 kb (Rott *et al.*, 1996; Table 1) was used as a probe to compare the *Eco*RI restriction profiles of *X. albilineans* strain Xa23R1 with those of mutants AM12, AM13 and AM36 which were supposed to be mutated in the XALB3 gene cluster. An 11 kb band which was found in strain Xa23R1 but not in the three mutants was supposed to contain the XALB3 gene cluster. A 9.7 kb *Eco*RI DNA fragment purified from cosmid pALB639 also used as a probe in Southern blot analyse revealed the same 11 kb band. This 9.7 kb *Eco*RI DNA fragment was sub-cloned in pUFR043 (Table 1) and the resulting plasmid pAlb639A complemented mutants AM12, AM13 and AM36. The third region involved in albicidin production, XALB3, was therefore present in the 9.7 kb insert of pAlb639A.

EXAMPLE 21 – Sequencing of the Tn*5* insertional site of tox^{I} mutants located in XALB2 and XALB3 and sequencing of the genomic regions XALB2 and XALB3

[00146] In Figure 8, E, H, Sa and S indicate restriction endonuclease cut sites for *Eco*RI, *Hin*dIII, *Sal*I and *Sau*3AI, respectively. The DNA inserts carried by plasmids pAC389.1, pALB639A or pEV639 are represented by the bars at the top of the respective figures. Positions of the Tn*5* insertional sites of mutants AM10, AM12, AM36 and AM37 were determined by sequencing and are indicated by vertical arrows. The DNA region corresponding to the Tn*5* flanking regions in pAM10, pAM12.1, pAM36.2 and pAM37 and in the PR37 DNA fragment are represented by the bars at the bottom of the respective figures. The location and direction of *albXXI* and *albXXII* are indicated by thick black arrows. The location of other orfs in XALB2 similar to those described by Huang *et al.* (2000b) are indicated by thick white arrows.

[00147] The 7 kb *Eco*R I fragment carrying Tn*5* and flanking sequence from strain AM10 was cloned in pBluescript II KS (+), and the obtained plasmid was designated pAM10 (Table 1). The sequences between *Eco*RI sites and the Tn*5* insertional site of mutants AM10 and AM37 were sequenced from the resulting plasmids pAM10 and pAM37, respectively. The complete double-strand nucleotide sequence of the 2,986 bp *Eco*R I B *Eco*R I insert of pAC389.1 was determined from sequencing results of plasmids pAC389.1, pAM10 and pAM37 (Figure 8). The Tn*5* *in*sertional sites of mutants AM10 and AM37 were sequenced from plasmids pAM10 and pAM37 (Table 1), respectively, using the sequencing primer GUSN (5'tgcccacaggccgtcgagt3') that annealed 135 bp downstream from the insertional sequence IS50L of Tn*5*-*gusA*. The Tn*5* insertional site of AM10 and AM37 was located at position 2107 and 1882, respectively.

[00148] The *Eco*RI fragments carrying Tn*5* and the flanking sequences from mutants AM12 and AM36 were cloned in pBR325 (Rott *et al.*, 1996; Table1). The sequences between *Eco*RI site and the Tn*5* insertional site of mutants AM12 and AM36 were sequenced from the resulting plasmids pAM12.1 and pAM36.2, respectively. The complete double-strand nucleotide sequence of the 9,673 bp *Eco*R I B *Sau*3A I insert of pALB639A was determined from the sequencing results of plasmids pAM12.1, pAM36.2 and pALB639A (Figure 8). The Tn*5* insertional site of mutants AM12 and AM36 was sequenced from plasmids pAM12.1, pAM36.2 using the sequencing primer GUSN (5'tgcccacaggccgtcgagt3') that annealed 135 bp downstream from the insertional sequence IS50L of Tn*5*-*gus*A. The Tn*5* insertional site of AM12 and AM36 was located at position 6500 and 7232, respectively (Figure 8).

EXAMPLE 22 – Homology analysis and genetic organization of XALB2 (Figure 8).

[00149] The sequence of 2986 bp containing XALB2 is 99.4% identical to the sequence of 2989 bp containing *xabA* described in *X. albilineans* strain LS155 from Australia (Huang et al., 2000b; accession number AF191324). The Tn*5* insertional site of mutant LS156 described in *xabA* is 15 bp upstream from the insertional site of AM37. The orf disrupted in AM37 and AM10, designed albXXI, is identical to *xabA* except a C which replaces a T at position 1642. albXXI potentially encodes a protein of 278 aa with a predicted size of 29.3 kDa which is 100% identical to the potential product of xabA, described as a phosphopantetheinyl transferase (Huang et al., 2000b). Region XALB2 contains three additional orfs (orf1, orf2, and orf3) similar to those described by Huang et al., (2000b; orf, rsp6 and aspT). orf2 and orf3 are 100% identical to rsp6 and aspT respectively, and orf1 is similar to but smaller than orf. There are no close matches to the *E. coli* γ70 promoter B10 (TATAAT) and B35 (TTGACA) consensus sequence, and no putative RBS site upstream from the putative start codon ATG of albXXI. The putative factor-independent transcription site described at 42 bp downstream from the TGA stop codon of xabA (Huang et al., 2000b) is also present at the same position downstream from albXXI.

EXAMPLE 23 – Homology analysis and genetic organization of XALB3 (Figure 8).

[00150] The orf disrupted in mutants AM12 and AM36 was located between nucleotide 6090 (ATG) and 8009 (TAA) and was designed *albXXII*. The first ATG at position 6090 is not preceded by a putative ribosome binding sequence, suggesting that the start codon is the ATG at position 6105 which is preceded at position B9 by the putative ribosome binding site sequence GGAG. A putative rho independent terminator was identified at position 8082, 73 b downstream from *albXXII* (Figure 6). There are no close matches to *E. coli* σ^{70} promoter B10 (TATAAT) and B35 (TTGACA) consensus sequence upstream from the putative start codon. The *Sal*I DNA fragment corresponding to DNA sequence from nucleotide 5510 to nucleotide 8124, which contains the 595 bp upstream from the putative start codon, the orf *albXXII* and the putative rho independent terminator, was sub-cloned in pUFR043 in the opposite direction to LacZ (Table 1). The resulting plasmid pEV639 (Table 1) complemented mutants AM12, AM13 and AM36, confirming that (i) the third region involved in albicidin production, XALB3, was present in the insert of pEV639; (ii) *albXXII* is not transcribed as part of a larger operon; and (iii) the 595 bp upstream the putative start codon contain a promoter.

[00151] The potential product of *albXXII*, designated AlbXXII, is a protein of 634 aa with a predicted size of 71.5 kDa. This protein is very similar to the heat shock protein HtpG from *Pseudomonas aeruginosa* (identities = 82%) and from *Escherichia coli* (identities = 60%) (Table 4). The methionine encoded by the putative start codon at position 6105 was aligned with

the first aminoacid of the heat shock protein HtpG from *Pseudomonas aeruginosa*, confirming that *albXXII* initiates at position 6105.

Complementation of Tox⁻ mutants with the *albXXII* gene in fusion with LacZ

[00152] A 1,948 bp fragment corresponding to the entire 1,903 bp orf of *albXXII* and flanking nucleotides was PCR amplified from cosmid pALB639 with the forward primer 5'tttgaattcgcacctaccgatgagcgtgg3' and the reverse primer 5'tttggatccgtgcgtcactgcttacgccg3'. Convenient in frame-*Eco*RI and *Bam*HI restriction sites for further cloning were simultaneously introduced with forward and reverse PCR primers, respectively. The PCR fragment was cloned into pGEMT vector (Promega) and sequenced. Several clones of the resulting plasmid pGemT/albXXII were sequenced. Because several PCR derived point mutations were observed in all the sequenced clones, a 1,920 bp *Bgl*II – *Sal*I fragment from pEV639 (corresponding to the 1,809 5' terminal nucleotides of *albXXII* orf plus 111 bp downstream the stop codon) was cloned into a pGemT/albXXII clone between the *Bgl*II site located at position 94 of the *albXXII* orf and the *Sal*I site of the vector's multiple cloning site. The resulting plasmid pGemT/albXXIIbis contained an intact *albXXII* orf that was then subcloned as an *Eco*RI – *Sal*I fragment into pUFR043 to generate pEValbXXII. This construct of *albXXII* in fusion with LacZ was transferred by triparental conjugation into Xa23RI insertion mutants. pEValbXXII complemented mutants AM12, AM13 and AM36 (see table 9). These results confirmed that (i) the third region involved in albicidin production, XALB3, was present in the insert of pEValbXXII; and (ii) *albXXII* is not transcribed as a part of a larger operon.

Complementation of Tox⁻ mutants with the *htpG* gene from *E. coli*

[00153] A 2,343bp fragment corresponding to the *htpG* gene of *E. coli* plus 458 bp downstream the stop codon was PCR amplified from purified DH5α genomic DNA with forward primer 5'tttgaattccatgaaaggacaagaaactcgtgg3' and reverse primer 5'gcctgcggaatggtacgcgggaagccgtcc3'. A convenient in frame-*Eco*RI restriction site was introduced with the forward PCR primer. The PCR fragment was cloned using the pGEMT vector system (Promega). Three resulting clones potentially containing plasmid pGemT/HtpG were sequenced, and one clone containing the correct sequence was selected. The 2,343bp PCR insert was then subcloned as an *Eco*RI – *Sal*I fragment into pUFR043 to generate pEVHtpG, the *Sal*I site corresponding to the site of the vector's multiple cloning site. This HtpG gene, in fusion with the LacZ construct, was able to restore albicidin production after transfer by triparental conjugation into AM12, AM13 and AM36 Xa23RI mutants. This result is i/ further evidence of the involvement of a molecular chaperone HtpG in the biosynthesis of albicidin (table 9), ii/ the first report of the requirement of a molecular chaperone HtpG in NRPS and PKS metabolism.

EXAMPLE 24 - Heterologous production of albicidin in fast growing *Xanthomonas axonopodis* pv. Vesicatoria.

[00154] This example illustrates the construction of a heterologous expression system harboring the three XALB regions, its transfer into a fast growing host, *Xanthomonas axonopodis* pv. vesicatoria and the subsequent production of a potent toxin with an antibiotic activity similar to that of albicidin. This work is a milestone in the validation of the albicidin biosynthesis model because it gives experimental evidence that the entire biosynthetic machinery required for albicidin biosynthesis has been identified, cloned, sequenced and transferred into an heterologous host, driving the production of albicidin. Cosmid pALB571 which covers the complete sequences of operons 1 and 2 was used to transfer operons 1 and 2 (Figure 1). Operons 3 and 4 (from pALB540), XALB2 (from pAC389.1) and XALB3 (from pEV639) were subcloned into a single plasmid, pOp3-4/XALB2-3 (see below). Plasmid pOp3-4/XALB2-3 derived from shuttle vector pLAFR3 that carries one selective gene for resistance to tetracyclin and that belongs to incompatibility group IncP (Table 1). Cosmid pALB571 derived from shuttle vector pUFR043 that carries two selective genes for resistance to kanamycine and gentamycine and that belongs to incompatibility group IncW (Table 1).

Sub-cloning of operons 3 and 4 and XALB2 and XALB3 regions into a single plasmid (Figure 12).

[00155] A 2,787 bp *Bam*HI – *Pst*I fragment from pALB540, corresponding to a portion of operon 4, was subcloned into pBCKS(+), yielding pBC/Op4Δ (step 1). A *Xho*I site was introduced into this vector immediately upstream from the *Bfr*I site by directed mutagenesis. Mutagenesis was performed with primers XhoIAlb anticodant 5'cgccttaagcagctcgagtagactgcaatc3' and XhoIAlbcodant 5'gattgcagtctactcgagctgcttaaggcg3' and yielded plasmid pBC/Op4ΔXhoI (step 2). The 2,986 bp *Eco*RI fragment from pAC389.1 (containing XALB2) was then subcloned into pBC/Op4ΔXhoI, yielding pBC/Op4Δ/XALB2 (step 3). A 10,762 bp *Bfr*I fragment from pALB540 and containing complete operon 3 and the beginning of operon 4 was subcloned into pBC/Op4Δ/XALB2 yielding pBC/Op3-4/XALB2 (step 4). The 2,615 bp *Sal*I fragment from pEV639 (containing XALB3) was subcloned into pBKS, yielding pBKS/XALB3 (step 5). The *Sal*I site located on the *Kpn*I side of the polylinker was then destroyed and substituted by a *XhoI* restriction site by directed mutagenesis. This mutagenesis was performed with primers XhoSalXaHTPGR 5'gcttatcgataccctcgaggaaggcgatatcg3' and XhoSalXaHTPGF 5'cgatatcgccttcctcgagggtatcgataagc3', yielding pBKS/XALB3XhoI (step 6). Finally, the *Xho*I cassette of pBC/Op3-4/XALB2 was subcloned into the *Sal*I restriction site of pBKS/XALB3XhoI, yielding pBKS/Op3-4/XALB2-3 (step 7). This construct harbours an *Xho*I cassette containing complete operons 3 and 4 from XALB1, *albXXI* from XALB2 and *albXXII*

from XALB3. An *Xho*I site was added to the *Bam*HI site of the pLAFR3 shuttle vector polylinker using the adaptor AdApTBamHIXhoI 5'gatcgctcgagc3', yielding pLAFR3XhoI (step 8). The *Xho*I cassette from pBKS/Op3-4/XALB2-3 was then cloned into pLAFR3XhoI, yielding pOp3-4/XALB2-3 (step 9). This last construct was used, along with pALB571 (operons 1 and 2), for heterologous expression of albicidin in *X. axonopodis* pv. vesicatoria.

Albicidin production assays

[00156] The four combinations of plasmids (i.e. pUFR043–pLAFR3, pUFR043-pOp3-4/XALB2-3, pAlb571-pLAFR3 and pAlb571-pOp3-4/XALB2-3) were transferred into *X. axonopodis* pv. vesicatoria strain Xcv 91-11BR1 by triparental mating. Exconjugant clones resistant to tetracycline and kanamycin were isolated. Assays for albicidin production were performed with these exconjugants clones using the same method described in Example 1 except that tetracycline (12 mg/ml) and/or kanamycin (50 mg/ml) were added to SPA medium. Tetracycline and kanamycin resistant *E. coli* clones, DH5αKT and DH5αAlb^{r}KT (Table 1), were used as tester strains to evaluate albicidin production to ensure that growth inhibition was not due to the presence of these two antibiotics in SPA medium. Both clones, DH5αKT and DH5αAlb^{r}KT, are tetracycline and kanamycin resistant because they carry plasmids pLAFR3 and pUFR043. The albicidin resistant DH5αAlb^{r}KT clone derived from strain DH5αAlb^r (Table 1) which is a spontaneous albicidin resistant clone isolated in a growth inhibition zone produced by *X. albilineans* strain Xa23R1.

[00157] Without antibiotics in the SPA medium, growth of clones DH5αKT and DH5αAlb^{r}KT was not inhibited in all assays performed with the different *X. axonopodis* pv. vesicatoria exconjugants. Surprisingly, when kanamycin was present in the SPA medium, growth of both DH5αKT and DH5αAlb^{r}KT was inhibited in all assays performed with the *X. axonopodis* pv. vesicatoria exconjugants. These results suggested that, in the presence of kanamycin, all *X. axonopodis* pv. vesicatoria exconjugants produced an antibiotic inhibiting growth of *E. coli*. Because exconjugants containing only empty vectors (pUF043 and pLAFR3) induced inhibition of *E. coli*, this antibiotic did not result from the expression of XALB1, XALB2 and/or XALB3. Additionally, there was no cross resistance between this antibiotic and albicidin. When tetracyclin was present in the bioassay medium, but not kanamycin, growth of the albicidin resistant clone (DH5αAlb^{r}KT) was not inhibited by any of the exconjugants. In contrast, growth of the albicidin susceptible *E. coli* strain (DH5αKT) was inhibited by the exconjugants harbouring pALB571 and pOp3-4/XALB2-3 plasmids, but not by exconjugants harbouring the other three combinations of plasmids (Table 10). This result suggested that expression of the XALB1, XALB2 and XALB3 regions in *X. axonopodis* pv. vesicatoria (harbouring pALB571 and pOp3-4/XALB2-3 plasmids) led to the production of an albicidin-like antibiotic. This product inhibited growth of an albicidin sensitive *E. coli* (DH5αKT) and had no effect on the growth of an albicidin resistant clone

(DH5αAlb^{r}KT).

[00158] Preliminary results indicated that pLAFR3 derived plasmids were relatively unstable in the absence of tetracycline in the culture medium, suggesting that genes carried by pOp3-4/XALB2-3 were not expressed when *X. axonopodis* pv. vesicatoria exconjugants pALB571/pOp3-4/XALB2-3 were grown without tetracycline. Consequently, these exconjugants did not produce the albicidin-like compound in absence of any antibiotic in the culture medium (Table 10). Preliminary results also indicated that pUFR043 derived plasmids are relatively stable in *X. axonopodis* pv. vesicatoria in absence of antibiotic selection, suggesting that genes carried by pALB571 are expressed when *X. axonopodis* pv. vesicatoria exconjugants pALB571/pOp3-4/XALB2-3 were grown on media without kanamycin. Consequently, these exconjugants produced the albicidin-like compound on SPA containing only tetracyclin.

[00159] Two *E. coli* DH5αKT clones, that spontaneously grew within the growth inhibition zone of a *X. axonopodis* pv. vesicatoria pALB571-pOp3-4/XALB2-3 exconjugant on SPA + tetracycline medium, were isolated and tested for resistance to albicidin. No growth inhibition was observed when these clones were used as tester strains in an albicidin production assay performed with *X. albilineans* Xa23R1. These results showed that cross-resistance occurs between the albicidin-like product of *X. axonopodis* pv. vesicatoria and albicidin produced by *X. albilineans*, suggesting that both molecules are similar. Comparison of chemical characteristics of the two molecules will, however, be necessary to confirm that the two molecules are identical.

[00160] The invention includes the isolation and sequencing of a region of 55,839 bp from *X. albilineans* strain Xa23R1 containing the major gene cluster XALB1 involved in albicidin production. Analysis of this region allowed us to predict the genetic organization of the gene cluster XALB1 which contains 20 ORFs grouped in four or five operons (Figure 1). Because *albXVIII* is a truncated gene, XALB1 genes may be organized in five operons. Therefore, we will from now on consider *albXVII* as part of operon 4 and *albXIX* and *albXX* as part of operon 5. Similar operon-type organizations for antibiotic biosynthesis clusters are well known and have been postulated to facilitate cotranslation of genes within the operon to yield equimolar amounts of proteins for optimal interactions to form the biosynthesis complexes (Cane, 1997). Overlapping genes involved in the same process are also quite common in bacteria (Normark *et al.*, 1983).

[00161] Previous results of transposon mutagenesis and complementation studies (Rott *et al.*, 1996; Rott, unpublished results) are in accordance with the predicted genetic organization of XALB1 described in this study, and allowed us to establish that operons 1, 2 and 3 are involved in albicidin biosynthesis: (I) Tox$^-$ mutants with a Tn*5-gusA* insertion site located in DNA fragments B, C, G and D were complemented by cosmid pALB571 and not by cosmid pALB540, confirming that cosmid pALB571 potentially contains the entire operon 1; (ii) Tox$^-$ mutants with a Tn*5-gusA* insertion site located in DNA fragments A and H were complemented

by both cosmids pALB540 and pALB571, confirming that both cosmids potentially contain the entire operon 2; (iii) mutant XaAM1 with a Tn*5-gusA* insertion site located in DNA fragment J is the only Tn*5* Tox$^-$ mutant complemented by cosmid pALB540 and not by cosmid pALB571, confirming that cosmid pALB540 potentially contains the entire operon 3. Our mutagenesis studies did not confirm that operons 4 and 5 are required for biosynthesis of albicidin. The para-aminobenzoate (PABA) is required for the growth of many bacteria probably including *X. albilineans*, suggesting that a mutation in *albXVII* may be lethal and explaining why we did not obtain any mutant disrupted in this gene.

[00162] Putative bidirectional promoters were identified between operons 1 and 2 (Huang et al., 2001) and between 3 and 4 (Figure 7), confirming the prediction of genetic organization of XALB1. The region upstream from operon 1 is 100 % identical to the region upstream from the *xabB* start codon which was described as a functional promoter during the phase of albicidin accumulation in Australian strain Xa13 of *X. albilineans* (Huang *et al.*, 2001). Involvement of several operons in albicidin biosynthesis suppose that they are transcribed during the same time. Promoter activities of regions upstream from putative operons 2, 3, 4 and 5 need to be determined to precise if these promoters are functional during the same growth phase of *X. albilineans* as the promoter upstream from operon 1.

[00163] Potential rho-independent transcription terminators were identified downstream from operons 1, 3 and 4 (Figure 6) confirming prediction of the genetic organization of these three operons. Because operons 2 and 5 are convergent (Figure 1) and separated by a very short region of 22 bp between *albIX* and *albXX*, stop codons may allow transcription termination in the absence of sequences corresponding to potential rho-independent transcription terminators downstream from these operons. It is quite possible that simultaneous transcription of operons 2 and 5 involving the presence of two RNA polymerases (one on each strand of DNA) may cause RNA polymerases to pause at the end of each operon because of steric interference between both polymerase complexes in the same short region.

[00164] The presence of putative RBSs upstream of the ATG start codons of all ORFs, except for *albXVIII*, suggests that these ORFs are translated in *X. albilineans*. The absence of a canonical RBS upstream from *albXVIII* further indicates that this ORF is probably not expressed. GTG and TTG codons (usually valine and leucine codons) generally serve as procaryotic start codons when located near the 5' end of an RNA message, but GTG start codons were also described far from the 5' end of messenger RNA in the bacitracin biosynthesis cluster of *B. lucheniformis* (Genbank Accession No. AF184956) or in the bleomycin biosynthetic gene cluster of *S. verticillus* (Genbank Accession No. AF210249). This is in accordance with the fact that the two potential TTG start codons are the first start codons in operons 1 and 4 of XALB1, and that the two potential GTG start codons initiate internal cistrons. The *albI* and *albXVII* genes,

like *xabB* (Huang *et al.*, 2001), use TTG as a start codon, which may impose post-transcriptional control of the rate of gene product formation (McCarthy and Gualerzi, 1990).

[00165] The predicted genetic organization of operons 1 and 2 presents similarities with the organization of the region involved in albicidin production in strain Xa13 of *X. albilineans* from Australia (Huang *et al.* 2000a, Huang *et al.*, 2001). This latter region also contains two divergent operons involved in albicidin production, one comprising the *xabB* gene (similar to *albI*, but with a large deletion) and the *xabC* gene (100% identical to *albII*) and the other containing *thp* gene (100% identical to *albV*). In addition, the sequence between the two operons in strain Xa13 is 100% identical to the sequence between operons 1 and 2, indicating that both clusters are controlled by the same bidirectional promoter. However, transposon mutagenesis studies of Xa13 showed no evidence of another cistron downstream of *xabC* that may be involved in albicidin production (Huang *et al.*, 2000a), suggesting that the Xa13 *xab* operon differs from the Xa23R1 operon 1, which contains two additional genes downstream from *albII* that are potentially involved in albicidin production (*albIII* and *albIV*; refer Figure 1).

[00166] Homology analysis revealed that four NRPS and/or PKS genes are present in XALB1 (Figure 2), and these genes may be involved in the biosynthesis of the albicidin polyketide-polypeptide backbone (*albI*, *albIV*, *albVII* and *albIX*). NRPS and PKS enzymes are generally organized into repeated functional units known as modules, each of which is responsible for a discrete stage of polyketide or polypeptide chain elongation (Cane and Walsh, 1999). Each PKS or NRPS module is made up of a set of three core domains, two of which are catalytic and one of which acts as a carrier, and together are responsible for the central chain-building reactions of polyketide or polypeptide biosynthesis. Both PKS and NRPS core domains utilize analogous acyl-chain elongation strategies in which the growing chain, tethered as an acyl-S-enzyme to the flexible 20 Å long phosphopantetheinyl arm of an acyl carrier protein (ACP) or peptidyl carrier protein (PCP) domain, acts as the electrophilic partner that undergoes attack by a nucleophilic chain-elongation unit, a malonyl- or aminoacyl-S-enzyme derivative, respectively, itself covalently bound to a downstream ACP/PCP domain. In the case of a PKS, the fundamental chain-elongation reaction, a C-C bond-forming step, is mediated by a ketosynthase (KS) domain that catalyzes the transfer of the polyketide acyl chain to an active-site cysteine of the KS domain, followed by condensation with the methylmalonyl- or malonyl-S-ACP by a decarboxylative acylation of the malonyl donor unit. An additional essential component of the core PKS chain-elongation apparatus is an associated acetyltransferase (AT) domain, which catalyzes the priming of the donor ACP sidearm with the appropriate monomer substrate, usually methylmalonyl- or malonyl-CoA. The comparable core domains of an NRPS biosynthetic module function in a chemically distinct but architecturally and mechanistically analogous fashion. In the latter case, the key chain-building reaction, a C-N bond-forming reaction, involves the generation of the characteristic peptide bond by nucleophilic attack of the amino group of an amino acyl-S-PCP

donor on the acyl group of an upstream electrophilic acyl- or peptidyl acyl-S-PCP chain, catalyzed by a condensation (C) domain. In functional analogy to the PKS AT domain, the core of the NRPS module utilizes an adenylation (A) domain to activate the donor amino-acid monomer as an acyl-AMP intermediate, which is then loaded onto the downstream PCP side chain. Both the AT and A domains of the respective PKS and NRPS modules act as important gatekeepers for polyketide or polypeptide biosynthesis, exhibiting strict or at least high specificity for their cognate malonyl-CoA, methylmalonyl-CoA or amino acid substrates. In addition to the basic subset of core domains, each PKS or NRPS also has a special set of dedicated domains responsible both for the initiation of acyl-chain assembly by loading of a starter unit onto the first, furthest upstream PKS/NRPS module, as well as a chain-terminating thioesterase (TE) domain, most often found fused to the last module, that is responsible for detachment of the most downstream covalent acyl enzyme intermediate and off-loading of the mature polyketide or polypeptide chain (Cane and Walsh, 1999).

[00167] XALB1 potentially encodes four PKS modules and seven NRPS modules. Most of the bacterial NRPS gene clusters described up to now are organized in operon-type structures, encoding multi modular NRPS proteins with individual modules organized along the chromosome in a linear order that parallels the order of amino acids in the resultant peptide, following the "colinearity rule" for the NRPS-template assembly of peptides from amino acids (Cane, 1997; Cane *et al.*, 1998; Cane and Walsh, 1999; von Döhren *et al.*, 1999). PKS and NRPS modules are apparently not organized according to this "colinearity rule" for albicidin biosynthesis because of the following features : (I) NRPS and PKS genes are expressed in two divergent operons; (ii) no AT domain was identified in PKS-2 and PKS-3 domains, suggesting involvement of a separate enzyme ; (iii) the A domain of NRPS-2 is not functional, suggesting the involvement of a *trans*-acting A domain ; (iv) a single chain-terminating TE domain was identified in XALB1 which may be responsible of the release of the full length albicidin polyketide-polypeptide backbone from the enzyme complexes. Exception to the "colinearity rule" has also been shown for the syringomycin synthetase of *P. syringae* (Guenzi *et al.*, 1998), for the exochelin synthetase of *Mycobacterium smegmatis* (Yu *et al.*, 1998) and for the bleomycin synthetases of *S. verticillus* (Du *et al.*, 2000).

[00168] On the basis of the deduced functions of individual NRPS and PKS domains we have aligned the four PKS and the seven NRPS modules to suggest two different putative linear models for the synthesis of the albicidin polyketide-peptide backbone (Figure 9). In the Figure, NRPS and PKS domains are abbreviated as follows: A, adenylation; ACP, acyl carrier protein; AL, acyl-CoA ligase; AT, acyltransferase; C, condensation; HBCL,hydroxybenzoate-CoA ligase; KR, ketoreductase; KS, ketoacyl synthase; PCP, peptidyl carrier protein. Asn designates asparagine. X1 and X2 indicate substrates incorporated by NRPS - 1 and 3 and by NRPS-6 and 7, respectively. The crossed A domain in NRPS-2 indicates that this

deleted domain may be not functional. In model 1, (Figure 9A), (i) the PKS-1 module alone is responsible for the initiation of the acyl-chain assembly, (ii) PKS-4 (HBCL) interacts with PKS-2 and PKS-3 as an AT domain to allow acyl transfer and (iii) NRPS-5 interacts with only NRPS-2. In model 2 (Figure 9B) two different modules, PKS-1 and PKS-4, are responsible for this initiation step. Model 2 leads to the biosynthesis of four different polyketide-polypetide backbones; in this model (i) PKS-1 (AL) and PKS-4 (HBCL) are in competition for initiation of albicidin precursors; (ii) a separate AT enzyme (potentially AlbXIII) interacts with PKS-2 and PKS-3 to allow acyl transfer; (iii) NRPS-5 interacts with NRPS-2; and (iv) NRPS-5 and NRPS-6 are in competition for interaction with NRPS-4.

[00169] Both models are based on the fact that PKS-1 contains the AL and ACP1 domains, and PKS-4 shows homology with the hydroxybenzoate-CoA ligases. In other PKS systems, an N-terminal AL domain is involved in the activation and incorporation of an 3,4-dihydroxycyclo hexane carboxylic acid, a 3-amino-5-hydroxybenzoic acid or a long-chain fatty acid as a starter (Aparicio *et al.*, 1996; Motamedi and Shafiee, 1998; Tang *et al.*, 1998; Duitman *et al.*, 1999). PKS-4 may be also involved in the activation and incorporation of hydroxy-benzoate but this latter domain lacks any ACP or PCP domain, suggesting that PKS-4 is responsible for initiation of the acyl-chain assembly (Figure 9B) onto one of the three ACP domains of AlbI (ACP1, ACP2 or ACP3). The 277 amino-acids preceding the PKS-4 module in AlbVII may be necessary for the intercommunication between AlbVII and AlbI. The presence of two different PKS modules potentially involved in the initiation of the acyl-chain assembly suggests a competition of these two modules for the initiation of two different albicidin polyketide-polypeptide backbones, and this could contribute to the production of multiple, structurally related albicidins by the same cluster XALB1. Production of two different components, one initiated by PKS-4 containing an additional aromatic ring due to incorporation of hydroxybenzoate, may explain why partial characterization of albicidin indicated the presence of a variable number (three or four) of aromatic rings (Huang *et al.*, 2001).

[00170] In AlbI, PKS-1 is followed by the PKS-2 module which contains a KS domain and a KR domain upstream from two ACP domains (ACP2 and ACP3) and it lacks any discernable AT domain. Tandem ACP domains are unusual within PKS modules but have been shown to occur in the biosynthesis of several fungal and bacterial polyketide synthases (Mayorga and Timberlake, 1992; Yu and Leonard, 1995; Takano *et al.*, 1995; Albertini *et al.*, 1995). However, the significance of the tandem ACP domains in these systems has not been solved yet. In our model 2, one of the tandem ACP (ACP2 or ACP3) may interact with PKS-4 for the initiation of an acyl-chain assembly (Figure 9B). The absence of an AT domain in the PKS-2 module suggests that a separate AT domain is indispensable for the elongation of the acyl-chain initiated by this module. Separate AT enzymes encoded elsewhere in the genome were described in other systems for two PKS modules lacking AT domains: malonyl-CoA transacyclase gene

(*fen*F) located immediately upstream from the *B. subtilis* PKS-NRPS *mycA* gene (Duitman *et al.*, 1999) and an AT gene located 20kb upstream from the *M. xanthus* NRPS-PKS *tal* gene (Paitan *et al.*, 1999). We have not identified an AT gene in the gene cluster XALB1 and in the two other genomic regions involved in albicidin production, XALB2 and XALB3, suggesting that the *trans*-acting AT gene may be encoded elsewhere in the genome. However, AlbXIII, which contains the motif GHSxG conserved in AT domains, may be potentially involved in the acyl transfer, but the similarity of AlbXIII with AT domains is not high enough to confirm this potential function of AlbXIII (Figure 10). Figure 10A describes alignment of the conserved motifs in AT domains from RifA-1, -2, -3, RifB-1, RifE-1 (Rifamycin PKSs, August *et al.*, 1998) and BlmVIII (Bleomycin PKS; Du *et al.*, 2000), identical amino acids are shown in bold. Figure 10B describes alignment of AlbXIII (SEQ ID NO. 38), FenF (a malonyl-CoA transacylase located upstream from *mycA*, Duitman *et al.*, 1999) and LipA (a lipase; Valdez *et al.*, 1999); amino acids identical to conserved AT domains motifs are shown in bold.

[00171] AlbXIII contains only four of the eleven amino acids conserved in AT domains of rifamycin PKSs (August *et al.*, 1998) and Bleomycin PKS (Du *et al.*, 2000), and the AlbXIII sequence appears to be more closely related to lipases such as LipA (Valdez *et al.*, 1999) rather than to AT domains (Figure 10). However, FenF, the *trans*-acting AT domain involved in mycosubtilin biosynthesis, contains only seven of the eleven amino acids conserved in AT domains (Duitman *et al.*, 1999; Figure 10). AlbVII, that contains a HBCL domain, may be another candidate for the acyl transfer in PKS-2 (Figure 9A) because HBCL exhibits some similarity with A domains at the level of cores A1, A2, A3, A4, A5 and A6 (Table 6). However, no HBCL involved in such a function has been described in the PKSs characterized so far.

[00172] In AlbI, PKS-2 is followed by the PKS-3 module which contains the KS2 and the PCP1 domains and it lacks any discernable AT or A domain. PKS-3 is located upstream from the NRPS modules and should therefore be involved in the linkage of polyketide and polypeptide moieties. The presence of a PCP domain in the PKS-3 module suggests the involvement of a *trans*-acting A domain rather than an AT domain. A putative candidate for this *trans*-acting A domain is the AlbIV NRPS-5 A domain because of the lack of a C domain in the AlbIV NRPS-5 module. However, by analogy with the BlmVIII PKS module, which is involved in the linkage of polypeptide and polyketide moieties of bleomycin and which contains an AT domain followed by a PCP domain (Du *et al*, 2000), the presence of a PCP is not incompatible with a possible interaction of the AlbI PKS-3 module with a separate AT domain. This latter *trans*-acting AT domain may be the same that interacts with the AlbI PKS-2 module, the AlbVII PKS-4 module, AlbXIII or an unindentified separate AT domain.

[00173] In AlbI, the PKS-3 module is followed by four NRPS modules. The NRPS-1, 2 and 3 modules display the ordered C, A and PCP domains, suggesting that they are

involved in the incorporation of three amino acid residues. The A domain of the NRPS-2 module exhibits poor consensus at A2, A3, A5, A7, A8 A9 and A10 motifs and lacks completely the A6 motif (Table 6). In addition the NRPS-2 substrate binding pocket is partially deleted (Figure 5). These features strongly suggest that the NRPS-2 A domain is inactive and that the loading of an amino-acid on the NRPS-2 PCP domain (PCP3) is possibly catalyzed by a *trans*-acting A domain as in HMWP1 (Gehring *et al.*, 1998) and BlmIII (Du *et al.*, 2000). A putative candidate for this *trans*-acting A domain is the NRPS-5 A domain present in AlbIV because of the lack of a C domain in NRPS-5 (Figure 2). The additional sequence of 300 amino-acids present in the A domain of NRPS-5 may be necessary for the intercommunication between AlbI and AlbIV. As a consequence of the interaction between NRPS-2 and NRPS-5, a competition between PCP-3 and PCP-5 domains must occur to bind the amino acid activated by the NRPS-5 A domain. A similar competition between two PCP domains was described for syringomycin biosynthesis, during the interaction between SyrB, which contains A and PCP domains, and the last module of SyrE which contains C and PCP domains (Guenzi *et al.*, 1998). The NRPS-4 module contains only a C domain which may transfer the intermediate products synthetized by AlbI to a PCP domain present in an other albicidin synthase. Similar transfers were described for mycosubtilin biosynthesis in which the MycA and MycB C-terminal C domains interact with the MycB and MycC N-terminal A domains, respectively (Duitman *et al.*, 1999). Two different PCP domains may be involved in the transfer of the intermediate products synthetized by AlbI: the PCP-5 and PCP-6 domains which are present in the AlbIV NRPS-5 and AlbIX NRPS-6 modules, respectively. This possible competition between the two NRPS modules that contain two different A domains could also contribute to the production of multiple, structurally related albicidins by the gene cluster XALB1 (Figure 9B). Because of the absence of a C-domain in the AlbIX NRPS-6 module, the intermediate product bound on the AlbIV PCP-5 domain would be necessarily transferred to the AlbIX PCP-7 domain, like the intermediate product bound on AlbIX PCP-6. AlbIX NRPS-7, which contains the single chain-terminating TE domain, may then be responsible for detachment of the mature albicidin polyketide-polypeptide backbone from the complex of enzymes.

[00174] The linear model 1 implies that operon 1 and operon 2 in *X. Albilineans* strain Xa23R1 from Florida potentially produce only one albicidin polyketide-polypetide backbone, with a competion at the level of ACP2/ACP3 and PCP3 and PCP5 which could explain the production by *X. albilineans* of compounds structurally related to albicidin (Figure 9A). The linear model 2 implies that operon 1 and operon 2 in *X. albilineans* strain Xa23R1 from Florida potentially produce four different albicidin polyketide-polypetide backbones (Figure 9B) because of (i) the competition of AL and HBCL domains for initation of acyl chain assembly and (ii) the competition of AlbIV NRPS-5 and AlbIX NRPS-6 modules for the incorporation of the next to last amino acid of the albicidin backbone. These four albicidin backbones may lead to the

production of four components structurally very different. The polyketide moieties of the acyl chains initiated by the AlbI AL domain or by the AlbVII HBCL domain may be very different. The polyketide moiety of acyl chains initiated by the AlbVII HBCL domain may be shorter and may contain an additional aromatic ring. The presence of four structuraly different metabolites may explain the difficulty observed by Birch and Patil (1985a) to purify albicidin and to determine its chemical structure.

[00175] Homology analysis also revealed that AlbI NRPS-1 and 3 and AlbIX NRPS-6 and 7 specify unusual substrates which seem to contain an amino group and a carboxylate group but to be different from α-amino acids and β-alanine. Identification of several aromatic rings in albicidin (Huang *et al.*, 2001) suggested that NRPS-1, -3, -6 and -7 are involved in incorporation of aromatic substrates. By analogy with the Asp235Val alteration in the β-Ala specificity-conferring code (Du *et al.* 2000), the Asp235Ala alteration in the NRPS-1, -3, -6 and -7 signatures could be consistent with a large distance between the amino group and the carboxylate group in the substrate specified by these modules. Based on this hypothesis, we suggest that operons 3, 4 and 5 are involved in the biosynthesis of two aromatic substrates: the para-aminobenzoate potentially synthesized by AlbXVII (para-aminobenzoate synthase), and the carbamoyl benzoate potentially synthesized by AlbXX (hydroxybenzoate synthase) and AlbXV (carbamoyl transferase). Incorporation of these nonproteinogenic substrates may explain why albicidin is insensitive to proteases (Birch and Patil, 1985a).

[00176] According to biosynthesis model 1 leading to the biosynthesis of only one polyketide-polypeptide albicidin backbone that may correspond to the major component produced by XAlb1, we propose a model allowing prediction of the composition and the structure of albicidin (Figure 11). In the Figure, NRPS and PKS domains are abbreviated as follows: A, adenylation; ACP, acyl carrier protein; AL, acyl-CoA ligase; C, condensation; KR, ß-ketoreductase; KS, ß-ketoacyl synthase; PCP, peptidyl carrier protein. C atoms of albicidin-backbone are numbered 1 to 38. Bold methyl groups correspond to methylation of the albicidin backbone by AlbII or AlbVI. In this model, albicidin biosynthesis is initiated by loading of an acetyl-CoA by PKS-1 (step 1), and the chain product is elongated by incorporation of (I) malonyl-CoA by PKS-2 and PKS-3 (steps 2 and 3), (ii) para-aminobenzoate or carbamoyl benzoate by NRPS-1 and NRPS-3 (steps 4 and 6), (iii) asparagine by NRPS-2 coupled to NRPS-5 (step 5) and (iv) para-aminobenzoate or carbamoyl benzoate by NRPS-6 and NRPS-7 (steps 7 and 8). The presence of the KR domain in the PKS-2 module may lead to the formation of an hydroxyl group at the C_2 atom of the albicidin backbone. This hydroxyl group might be methylated by AlbVI (*O*-methyltransferase). The acyl chain may also be modified by AlbII (*C*-methyltransferase) at C_{13} or C_{14}.

[00177] The chemical composition ($C_{40}O_{15}N_6H_{35}$), the molecular weight (839), and the structure of the putative XALB1 product are in accordance with the partial characterization of albicidin published by Birch and Patil (1985a) which indicated that albicidin contains approximately 38 carbon atoms and a carboxylate group and that the molecular weight of albicidin was about 842. The presence of two ester linkages in our predicted albicidin structure is also in accordance with the fact that albicidin is detoxified by the AlbD esterase (Zhang and Birch, 1997). However, an unpublished albicidin analysis cited by Huang *et al.* (2001) indicated the presence of (I) two OCH3 groups and not one as in our predictive albicidin structure, (ii) one CN linkage and not eleven as in our predictive albicidin structure and (iii) a trisubstituted double bond that is not present in the putative XALB1 product.

[00178] In conclusion, homology analysis of XALB1 revealed unprecedented features for hybrid polyketide-peptide biosynthesis in bacteria involving a *trans*-action of four PKS and seven NRPS separate modules which could contribute to the production of multiple, structurally related polyketide-peptide compounds by the same gene cluster. Characterization of the full chemical structure of albicidin may be necessary to validate these models. Four NRPS modules seem to activate a very unusual substrate. Over- expression and purification of A domains from these four NRPS modules will be necessary to examine their substrate specificities. Substrate specificity of each A domain will therefore be determinated by analysis of the ATP-PPi exchange reaction with different substrate putatively incorporated into albicidin. Investigating albicidin backbone biosynthesis will be of great interest because such information adds to the limited knowledge as to how PKS and NRPS interact and how they might be manipulated to engineer novel molecules, and may explain how *X. albilineans* produces several structurally related, toxic compounds.

[00179] Cloning and sequencing of XALB2 showed that the same phosphopantetheinyl transferase is required for albicidin production in an *X. albilineans* strain from Florida and in an *X. albilineans* strain from Australia (Huang *et al.*, 2000b), explaining the precedented results showing that strain LS156 mutated in *xabA* (100% identical to *albXXI*) was not complemented by pALB540, pALB571 and pALB639 (Rott *et al.*, 1996). Mutant LS156 was shown to be complemented by a construction containing the coding sequence of *xabA* in fusion with *lacZ*, revealing that *xabA* is required for albicidin production and that no other cistron downstream from *xabA* was involved in albicidin production (Huang *et al.*, 2000b). However, this complementation study did not allow determination of whether *xabA* is transcribed as a part of a larger operon. Here we disclose the complementation of mutant AM37 with a 2986 bp insert from *X. albilineans* containing *albXXI* (100% identical to *xabA*), confirming that *albXXI* is involved in albicidin biosynthesis and indicating that the promoter of *albXXI* is present in the 2986 bp insert and that *albXXI* is not expressed as part of a operon.

[00180] Cloning and sequencing of XALB3 showed that a heat shock protein HtpG was involved in albicidin production in *X. albilineans*. The heat shock protein HtpG is an *Escherichia coli* homologue of eukaryotic HSP90 molecular chaperone. Hsp90 from eukaryotes has been demonstrated to possess chaperone activity (Jakob *et al.*, 1995), acting as a non-ATP dependent "holder," and it also has an important role in signal transduction and the cell cycle. This protein is essential in both drosophila and yeast (Borkovich et al., 1989; Cutforth and Rubin, 1994). In contrast, the HtpG gene can be deleted in *E. coli* with no effect on the viability of the strain with the exception of decreased growth rate at high temperatures (Bardwell and Craig, 1988). The *in vivo* role of the HtpG protein remains unknown. However, preliminary results indicated that HtpG facilitates *de novo* protein folding in stressed *E. coli* cells, presumably by expanding the ability of the DnaK-DnaJ-GrpE molecular chaperone system to interact with newly synthesized polypeptides (Thomas and Baneyx, 2000). Furthermore, HtpG was copurified in *E. coli* with MccB17 synthetase, an enzyme involved in the biosynthesis of the peptide antibiotic microcin B17 which inhibits DNA replication by induction of the SOS repair system, suggesting the requirement of HtpG for production of the antibiotic (Li *et al.*, 1996). However, when microcin B17 production by the *E. coli* strain deleted for HtpG was compared to the one of the parental strain, there was no effect on microcin B17 production *in vivo*. This result implied that the copurification of HtpG with the MccB17 synthetase was potentially an artifact, or that another *E. coli* chaperone could substitute for HtpG (Milne *et al.*, 1999). To examine the effect of HtpG on the reconstitution of MccB17 synthetase *in vitro*, the chaperone was expressed and purified as a fusion to a hexahistidine (His_6) tag. Addition of the His_6-HtpG did not stimulate MccB17 synthetase reconstitution or heterocyclisation activity *in vitro*, suggesting that HtpG mediates complex assembly or stabilizes protein subunits prior to the hetero-oligomerisation (Milne *et al.*, 1999). Based on these results, we suggest that the function of AlbXXII is to mediate complex assembly by facilitating *de novo* protein folding of PKS and NRPS enzymes (AlbI, AlbIV, AlbVII and AlbIX) involved in the albicidin backbone biosynthesis.

[00181] Characterization of the complete sequence of XALB1, XALB2 and XALB3 clusters enables one to characterize all enzymes of the albicidin biosynthesis pathway including structural, resistance, secretory and regulatory elements, and to engineer overproduction of albicidin. For example one may insert expression enhancing DNA into the genome of *X. albilineans* in a position operable to enhance expression of the Albicidins Biosynthesis Gene Clusters. One may also modify naturally occurring Albicidins to obtain additional non-naturally occurring antibiotics by adding DNA encoding additional enzymes selected to produce a modified albicidin like molecule. This approach will allow (I) the purification of albicidin and the other compounds structurally related and potentially produced by the same biosynthesis apparatus; (ii) the characterization of chemical structure of albicidin; (iii) the investigation of mode of action of

albicidin in the pathogenesis of *X. albilineans* in sugarcane; and (iv) the characterization of the bactericidal activity of albicidin. For example one may also increase the resistance of plants to damage from *X. albilineans* infection by inserting one or more of the resistance genes identified herein into the genome of the plant. One may also provide materials to prevent damage by albicidin produced by *X. albilineans* by applying an agent that blocks expression of the Albicidin Biosynthesis Gene Clusters to the plant to be protected. One may also use portions of the DNA of the Albicidin Biosynthesis Gene Clusters to obtain agents useful in blocking expression of albicidin by screening materials against a modified hast cell line that expresses the Albicidin Biosynthesis Gene Clusters and selecting for materials that stop or decrease albicidin production.

Table 1 : Bacterial strains and plasmids used in this study		
	Relevant characteristics[a]	**Reference or source**
Strains		
E. coli		
DH5α	F-/80d*lac*ZΔM15 Δ(*lac*ZYA-*arg*F)U169 *deo*R *recA*1 *endA*1 *hsdR17*(r_k^- m_k^+) supE44 thi-1 *gyrA*96 *relA*1	Gibco-BRL
DH5α MCR	DH5α*mcrA mcrBC mrr*	"
Xcv 91-11B	Wild type strain of *Xanthomonas axonopodis* pv. vesicatoria from tomato (race 3)	Astua-Monge *et al.*, 2000
Xcv 91-11BR1	Spontaneous Rif^r derivative of Xcv 91-11B	This study
DH5αKT	*Escherichia coli* DH5α strain transformed by both pUFR043 and pLAFR3 plasmids	"
DH5αAlb^r	Spontaneous Alb^r derivative of DH5α	"
DH5αAlb^rKT	DH5αAlb^r transformed by both pUFR043 and pLAFR3 plasmids	"
Plasmids		
PBR325	Tc^r, Ap^r, Cm^r	Gibco-BRL
pBCKS (+)	Cm^r	Stratagene
pBluescript II KS (+)	Ap^r	"
PRK2073	PRK2013 derivative, Km^s (*npt*::Tn*7*), Sp^r, Tra^+, helper plasmid	Leong *et al.*, 1982
pUFR043	IncW Mob^+ LacZα Gm^r, Km^r, Cos	De Feyter and Gabriel, 1991
pAlb540	47 kb insert from Xa23R1 in pUFR043, Gm^r, Km^r	Rott *et al.*, 1996
pAlb571	36.8 kb insert from Xa23R1 in pUFR043, Gm^r, Km^r	"
PAlb639	36 kb insert from Xa23R1 in pUFR043, Gm^r, Km^r	"
pAM15.1	24 kb *Eco*R I fragment carrying Tn*5* and flanking sequences of mutant AM15 in pBR325, Km^r, Tc^r, Ap^r, Cm^r	"
pAM40.2	11 kb *Eco*R I fragment carrying Tn*5* and flanking sequences of mutant AM40 in pBR325, Km^r, Tc^r, Ap^r, Cm^r	"
pAM45.1	12 kb *Eco*R I fragment carrying Tn*5* and flanking sequences of mutant AM45 in pBR325, Km^r, Tc^r, Ap^r, Cm^r	"
pAM12.1	13 kb *Eco*R I fragment carrying Tn*5* and flanking sequences of mutant AM12 in pBR325, Km^r, Tc^r, Ap^r, Cm^r	A
PAM36.2	9 kb*Eco*R I fragment carrying Tn*5* and flanking sequences of mutant AM36 in pBR325, Km^r, Tc^r, Ap^r, Cm^r	A
pAlb389	37 kb insert from Xa23R1 in pUFR043, Gm^r, Km^r	This study
pAC389.1	2.9 kb insert from Xa23R1 in pUFR043, Gm^r, Km^r	"
PAlb639A	9.4 kb insert from Xa23R1 in pUFR043, Gm^r, Km^r	"
PEV639	2.6 kb *Sal* I insert from Xa23R1 in pUFR043, Gm^r, Km^r	"
pBC/A'	7.5 kb *Kpn* I fragment carrying a part of fragment A from pAlb571 in pBCKS (+), Cm^r	"
pBC/AF	15.2 kb *Eco*R I fragment carrying fragments A and F from pALB540 in pBCKS (+), Cm^r	"
pBC/B	11.0 kb *Kpn* I fragment B from pAlb571 in pBCKS (+), Cm^r	"
pBC/C	6.0 kb *Kpn* I fragment C from pAlb571 in pBCKS (+), Cm^r	"
pBC/E	2.8 kb *Kpn* I fragment E from pAlb571 in pBCKS (+), Cm^r	"
pBC/F	2.5 kb *Kpn* I-*Eco*R I fragment F from pAlb571 in pBCKS (+), Cm^r	"
pBC/G	1.9 kb *Eco*R I fragment G from pAlb571 in pBCKS (+), Cm^r	"

Table 1 : Bacterial strains and plasmids used in this study		
	Relevant characteristics[a]	**Reference or source**
pBC/I	1.4 kb *Kpn* I-*Eco*R I fragment I from pAlb571 in pBCKS (+), Cm^r	"
pBC/J	0.6 kb *Eco*R I fragment J from pALB540 in pBCKS (+), Cm^r	"
pBC/K	4.7 kb *Eco*R I fragment K from pALB540 in pBCKS (+), Cm^r	"
pBC/L	0.4 kb *Eco*R I fragment L from pALB540 in pBCKS (+), Cm^r	"
pBC/N	7.7 kb *Eco*R I fragment N from pALB540 in pBCKS (+), Cm^r	"
pUFR043/D=	2.2 kb *Eco*R IB*Sau*3A I fragment carrying a part of fragment D from pAlb571 in pUFR043	"
pAM1	5 kb *Eco*R I fragment carrying Tn*5* and flanking sequences of mutant AM1 in pBluescript II KS (+), Km^r, Ap^r	"
pAM4	12 kb *Eco*R I fragment carrying Tn*5* and flanking sequences of mutant AM4 in pBluescript II KS (+), Km^r, Ap^r	"
pAM7	6 kb *Eco*R I fragment carrying Tn*5* and flanking sequences of mutant AM7 in pBluescript II KS (+), Km^r, Ap^r	"
pAM10	7 kb *Eco*R I fragment carrying Tn*5* and flanking sequences of mutant AM10 in pBluescript II KS (+), Km^r, Ap^r	"
pAM29	10 kb *Eco*R I fragment carrying Tn*5* and flanking sequences of mutant AM29 in pBluescript II KS (+), Km^r, Ap^r	"
pAM37	6 kb *Eco*R I fragment carrying Tn*5* and flanking sequences of mutant AM37 in pBR325, Km^r, Tc^r, Ap^r, Cm^r	"
pAM52	5 kb *Eco*R I fragment carrying Tn*5* and flanking sequences of mutant AM52 in pBluescript II KS (+), Km^r, Ap^r	"
PLAFR3	IncP, Mob+, *LacZα*, Tc^r, *cos*	Staskawicz *et al.*, 1987
PLAFR3XhoI	pLAFR3 with a *Xho*I site added to the *Bam*HI site using an adaptator	This study
pBC/Op4Δ	*Bam*HI-*PstI* fragment from pALB540 cloned between *Bam*HI and *Pst*I sites of pBCKS(+)	"
pBC/Op4ΔXhoI	PBC/Op4Δ with a *Xho*I site created by directed mutagenesis upstream from the *Bfr*I site	"
pBC/Op4Δ/XALB2	*Eco*RI DNA fragment from pAC389.1 cloned into the *Eco*RI site of pBC/Op4ΔXhoI	"
pBC/Op3-4/XALB2	*Bfr*I DNA fragment from pALB540 cloned into the *Bfr*I site of pBC/Op4Δ/XALB2	"
pBKS/XALB3	*Sal*I DNA fragment from pEV639 cloned into the *Sal*I site of pBluescript II KS (+)	"
pBKS/XALB3XhoI	pBKS/XALB3 with a *Xho*I site created by directed mutagenesis to substitute the *Sal*I site located on the *Kpn*I side of the polylinker	"
pBKS/Op3-4/XALB2-3	*Xho*I DNA fragment from pBC/Op3-4Δ/XALB2 cloned into the *Sal*I site of pBKS/XALB3XhoI	"
pOp3-4/XALB2-3	*Xho*I DNA fragment from pBKS/Op3-4/XALB2-3 cloned into the *Xho*I site of pLAFR3XhoI	"
pEValbXXII	*albXXII* in fusion with LacZ in pUFR043, Gm^r, Km^r	"
pEVHtpG	*E. coli htpG* in fusion with LacZ in pUFR043, Gm^r, Km^r	"
PGemT	ColE1 replicon, Ap^r, LacZα, single 3'-T overhangs at the insertion site	Promega
PGemT/albXXII	PCR fragment containing *albXXII* cloned into pGemT	This study
PGemT/albXXII bis	*Bgl*II-*Sal*IDNA fragment from pBKS/XALB3 cloned between the *BglII* and *Sal*I sites of pGemT/albXXII	"
PGemT/HtpG	PCR fragment containing the *E. coli htpG* gene cloned into pGemT	"

Table 1 : Bacterial strains and plasmids used in this study		
	Relevant characteristics[a]	**Reference or source**
DNA Fragment		
PR37	1.1 kb *Hin*d III-*Hin*d III from pAM37	"

[a] Ap^r, Cm^r, Gm^r, Km^r, Rif^r, Sp^r, Tc^r: resistant to ampicilin, chloramphenicol, gentamycin, kanamycin, rifampicin, spectinomycin, tetracycline, respectively. Tox-, deficient in albicidin production. Tn*5-gusA*, Tn*5-uidA1* Km^r Tc^r, forms transcriptional fusions. Alb^r, Ap^r, Gm^r, Rif^r and Tc^r: resistant to albicidin, ampicilin, gentamycin, rifampicin and tetracycline, respectively.

Table 2: Analysis of putative translational signals and location of all putative orfs identified in the XALB1 gene cluster

Intergenic spacing between consecutive ORFs in each putative operon	ORF	Potential RBS[a] (distance from start codon)	Start codon (position)	Stop codon (position)
Operon 1 (strand +)				
	albI	GAGGG (5 b)	TTG (30166)	TAG (50805)
45 b	*albII*	GAGGG (5 b)	ATG (50851)	TAA (51882)
ATG overlaps TAA	*albIII*	GAGGG (7 b)	ATG (51882)	TGA (52385)
GTG overlaps TGA	*albIV*	GAGG (7 b)	GTG (52382)	TAA (55207)
Operon 2 (strand -)				
	albV	GGAGG (8 b)	ATG (29929)	TAA (29210)
87 b	*albVI*	AAGG (4 b)	GTG (29122)	TGA (28262)
61 b	*albVII*	GAG (4 b)	ATG (28200)	TAG (25903)
7 b	*albVIII*	AGGTG (4 b)	ATG (25895)	TAA (24903)
20 b	*albIX*	GGTG (3 b)	ATG (24882)	TGA (19003)
Operon 3 (strand -)				
	albX	GGGGG (8 b)	ATG (14497)	TGA (14246)
81 b	*albXI*	AGGAAA (6 b)	ATG (14164)	TGA (13217)
5 b	*albXII*	GGCCTGA (5 b)	ATG (13211)	TAA (11856)
36 b	*albXIII*	GGGG (3 b)	ATG (11819)	TAA (10866)
12 b	*albXIV*	GGAG (8 b)	ATG (10853)	TAG (9363)
41 b	*albXV*	GGAA (6 b)	ATG (9321)	TAG (7567)
208 b	*albXVI*	GGAGG (4 b)	ATG (7358)	TAG (7092)
Operon 4 (strand +)				
	albXVII	GGGAGG (5 b)	TTG (14909)	TGA (17059)
274 b	*albXVIII*	GCTCAG (8 b)	ATG (17334)	TGA (17747)
Overlap (17 b)	*albXIX*	AGG (9 b)	ATG (17728)	TGA (18330)
41 b	*albXX*	GCAA (8 b)	ATG (18372)	TAG 18980)

[a]: Ribosomal Binding Site

Table 3: Deduced functions of the ORFs in the major albicidin biosynthetic cluster X-ALB1

ORF	Number of amino acids	Sequence homolog [a]	Proposed function[b, c]
Operon 1			
AlbI	6879	XabB (AAK15074)	Polyketide- peptide synthase PKS modules PKS domains PKS-1 AL ACP1 PKS-2 KS1 KR ACP2 ACP3 PKS-3 KS2 PCP1 NRPS modules NRPS domains NRPS-1 C A PCP2 NRPS-2 C A PCP3 NRPS-3 C A PCP4 NRPS-4 C
Alibi	343	XabC (AAK15075)	*C*-methyltransferase
AlbIII	167	ComAB (CAA71583)	Activator of *alb* genes transcription
AlbIV	941	MycA (T44806) WbpG (E83253)	Peptide synthase NRPS module NRPS domains NRPS-5 A PCP5
Operon 2			
AlbV	239	Thp (AAK15074)	No function (transposition)
AlbVI	286	TcmP (AAA67510)	*O*-methyltransferase
AlbVII	765	HbaA (A58538)	4-hydroxybenzoate CoA ligase
albVIII	330	SyrP (AAB63253)	Regulation
AlbIX	1959	DhbF (CAB04779)	Peptide synthase NRPS modules NRPS domains NRPS-6 A PCP6 NRPS-7 C A PCP7
Operon 3			
AlbX	83	MbtH (O05821)	Unknown
AlbXI	315	SyrC (U25130)	Thioesterase
AlbXII	451	BoxB (AAK006000.1)	Unknown
albXIII	317	hp[d] (AAK25001)	Esterase
albXIV	496	ActII-2 (p46105)	Albicidin transporter
AlbXV	584	hp[d] (08390)	Carbamoyl transferase
AlbXVI	88	OrfA (AAC03166)	No function (transposition)
Operon 4			
albXVII	716	PabAB (CAC22117)	Para-amino benzoate synthase
Operon 5			
albXVIII	137	ADCL (AAG06352)	No function (not functional)
albXIX	200	McbG (P05530)	Immunity against albicidin
albXX	202	UbiC (S25660)	4-hydroxybenzoate synthetase

[a]Protein accession numbers in Genbank are given in parentheses.
[b]NRPS and PKS domains are abbreviated as follows: A, adenylation; ACP, acyl carrier protein; AL, acyl CoA ligase; C, condensation; KR, ketoreductase; KS, ketoacyl synthase; PCP, peptidyl carrier protein.
[c]Underlined domains are likely inactive due to the lack of highly conserved motifs.
[d]hypothetical protein

Table 4: Summary of results obtained from BLAST analyses.

Putative Alb protein	No. of aa residues	Protein homolog	Origin	Genbank accession #	Score	Expect	Identities	Positives	Gaps
AlbI	6879								
PKS-1		XabB (4801 aa) SafB (1770 aa)	*Xanthomonas albilineans* *Myxococcus xanthus*	AAK15074 AAC44128	1352 bits (3498) 231 bits (589)	0.0 2e-59	730/730 (100%) 175/532 (32%)	730/730 (100%) 269/532 (49%)	- 23/532 (4%)
PKS-2		XabB (4801 aa) PksM (4273 aa)	*X. albilineans* *Bacillus subtilis*	AAK15074 CAB13603	3464 bits (8983) 887 bits (2292)	0.0 0.0	1882/1882 (100%) 626/1896 (33%)	1882/1882 (100%) 938/1896 (49%)	- 140/1896=7%
PKS-3		XabB (4801 aa) PksM (4273 aa)	*X. albilineans* *B. subtilis*	AAK15074 CAB13603	1274 bits (3296) 577 bits (1486)	0.0 e-163	653/653 (100%) 293/584 (50%)	653/653 (100%) 391/584 (66%)	- 17/584 (2%)
NRPS-I		XabB (4801 aa) NosA (4379 aa)	*X. albilineans* *Nostoc* sp.	AAK15074 AF204805	1934 bits (5010) 618 bits (1594)	0.0 e-176	1035/1046 (99%) 398/1104 (36%)	1039/1046 (99%) 586/1104 (53%)	- 86/1104 (7%)
NRPS-2		NosA (4379 aa) Peptide synthase (5060 aa)	*Nostoc sp* *Anabaena* sp.	AF204805 CAC01604	416 bits (1069) 402 bits (1034)	e-115 e-111	337/1127 (29%) 315/1073 (29%)	496/1127 (43%) 479/1073 (44%)	128/1127 (11%) 114/1073 (10%)
NRPS-3		XabB (4801 aa) NosA (4379 aa)	*X. albilineans* *Nostoc* sp.	AAK15074 AF204805	1847 bits (4784) 610 bits (1573)	0.0 e-173	997/1044 (95%) 392/1069 (36%)	1007/1044 (96%) 571/1069 (52%)	- 86/1069 (8%)
NRPS-4		XabB (4801 aa) NosC (3317 aa)	*X. albilineans* *Nostoc sp.*	AAK15074 AAF17280	889 bits (2297) 240 bits (613)	0.0 2e-62	468/468 (100%) 156/438 (35%)	468/468 (100%) 229/438 (51%)	- 20/438 (4%)
AlbII	343	XabC (343 aa) MtmMII (326 aa) TcmO (339 aa)	*X. albilineans* *Streptomyces argillaceus* *S. glaucescens*	AAK15075 AAD55584 P39896	633 bits (1633) 144 bits (361) 81.7 bits (199)	0.0 1e-34 1e-14	343/343 (100%) 98/323 (30%) 79/314 (25%)	343/343 (100%) 154/323 (47%) 140/314 (44%)	- 4/323 (1%) 12/314 (3%)
AlbIII	167	*comA* operon protein 2 (136 aa) ComAB (116 aa)	*E. coli* *Bacillus licheniformis*	AAC74756 CAA71583	133 bits (335) 97.6 bits (242)	1e-30 8e-20	68/135 (50%) 53/111 (47%)	89/135 (65%) 68/111 (60%)	- 1/111 (0%)
AlbIV	941								
PKS-4		BA3 (6359 aa) WbpG (377 aa)	*B. licheniformis* *Pseudomonas aeruginosa*	AAC06348 E83253	361 bits (926) 81.6 bits (200)	2e-98 4e-15	190/441 (43%) 44/119 (36%)	267/441 (60%) 70/119 (57%)	14/441 (3%) 4/119 (3%)
AlbV	239	Thp (240 aa) IS transposase (260 aa)	*X. albilineans* *Yersinia pestis*	nd AAC82714	nd 160 bits (404)	0.0 1e-38	240/240 (100%) 87/183 (47%)	240/240 (100%) 122/183 (66%)	- 2/183 (1%)
AlbVI	286	Hypothetical protein TcmP (276 aa)	*Mycobacterium tuberculosis* *Pasteurella multocida*	AAK46042 AAK03406	138 bits (347) 36.6 bits (83)	6e-32 0.24	92/224 (41%) 32/132 (28%)	125/224 (55%) 65/132 (49%)	18/224 (8%) 29/197 (6%)

Table 4: Summary of results obtained from BLAST analyses.

Putative Alb protein	No. of aa residues	Protein homolog	Origin	Genbank accession #	Score	Expect	Identities	Positives	Gaps
AlbVII	765	4-hydroxybenzoate-CoA ligase (539 aa)	*Rhodopseudomonas palustris*	AAA62604	203 bits (513)	5e-51	156/492 (31%)	242/492 (48%)	31/492 (6%)
AlbVIII	330	SyrP Like (339 aa) SyrP (353 aa)	*S. verticillus* *Pseudomonas syringae*	AF210249 AAB63253	245 bits (619) 182 bits (458)	6e-64 5e-45	130/309 (42%) 106/306 (34%)	182/309 (58%) 155/306 (50%)	2/309 (0%) 4/306 (1%)
AlbIX	1959								
NRPS-6		XabB (4801 aa) DhbF (1278 aa)	*X. albilineans* *B. subtilis*	AAK15074 CAB15186	481 bits (1239) 354 bits (908)	e-135 1e-96	286/608 (47%) 222/608 (36%)	374/608 (61%) 341/608 (55%)	23/208 (3%) 21/608 (3%)
NRPS-7		XabB (4801 aa) NosA (4379 aa)	*X. albilineans* *Nostoc* sp.	AAK15074 AF204805	874 bits (2258) 551 bits (1420)	0.0 e-155	515/1110 (46%) 388/1148 (33%)	682/1110 (61%) 583/1148 (49%)	52/1110 (4%) 84/1148 (7%)
AlbX	83	Hypothetical protein (72 aa) MbtH (71 aa)	*P. aeruginosa* *M. tuberculosis*	AAG05800 CAB08480	75.6 bits (185) 59 bits (142)	1e-13 9e-09	34/61 (55%) 25/55 (45%)	44/61 (71%) 37/55 (66%)	- -
AlbXI	315	SyrC (433 aa) Hydrolase (261 aa)	*P. syringae* *S. coelicolor*	AAA85161 CAA16200	34.4 bits (78) 34 bits (77)	1.9 2.9	23/93 (24%) 19/60 (31%)	40/93 (42%) 30/60 (49%)	- -
AlbXII	451	BoxB (473 aa	*Azoarcus evansii*	AAK00599	293 bits (751)	3e-78	174/448 (38%)	243/448 (53%)	12/448 (2%)
AlbXIII	317	Hypothetical protein (335 aa) Plasma PAF acetylhydrolase (444 aa)	*Caulobacter crescentus* *Canis familiaris*	AAK25001 AAC48484	99.5 bits (247) 37.5 bits (86)	5e-200	88/296 (29%) 43/156	125/296 (41%) 56/156	5/296 (1%) 44/156 (28%)
AlbXIV	496	Putative trans-membrane efflux protein (505 aa) AlbF, putative albicidin efflux pump (496 aa)	*S. coelicolor* *X. albilineans*	CAB90983 AF403709	225 bits (574) 736 bits (1900)	0	154/465 (33%) 496/496 (100%)	240/465 (51%) 496/496 (100%)	8/465 (1%) -
AlbXV	584	Probable carbamoyl transferase (585 aa) BlmD (545 aa)	*P. aeruginosa* *S. verticillus*	AAG08390 AAG02370	201 bits (513) 192 bits (506)	1e-50 1e-47	158/458 (34%) 149/441 (33%)	222/458 (47%) 209/441 (46%)	39/458 (8%) 33/441 (7%)
AlbXVI	88	Transposase (363 aa) Transposase OrfA (88 aa)	*X. axonopodis* *Desulfovibrio vulgaris*	AF263433 AAC03166	64.8 bits (157) 61.0 bits (147)	2e-10 3e-09	27/45 (60%) 29/54 (53%)	40/45 (88%) 38/54 (69%)	- -

Table 4: Summary of results obtained from BLAST analyses.

Putative Alb protein	No. of aa residues	Protein homolog	Origin	Genbank accession #	Score	Expect	Identities	Positives	Gaps
AlbXVII	716	Para-aminobenzoate synthase (723 aa)	*Streptomyces griseus*	CAC22117	503 bits (1295)	e-141	302/699 (43%)	409/699 (58%)	36/699 (5%)
AlbXVII I	137	4-amino-4-deoxychorismate lyase (271 aa)	*P. aeruginosa*	AAG06352	81.4 bits (200)	4e-15	46/105 (43%)	65/105 (61%)	-
AlbXIX	200	McbG (187 aa)	*E. coli*	CAA30724	60.5 bits (145)	9e-09	36/141 (25%)	58/141 (40%)	5/141 (3%)
AlbXX	202	4-hydroxybenzoate synthase (202 aa)	*E. coli*	AAC77009	45.6 bits (107)	5e-04	42/161 (26%)	21/161 (13%)	-
AlbXXI	278	XabA (278aa)	*X. albilineans*	AAG28384	430 bits (1106)	0	278/278 (100%)	278/278 (100%)	-
AlbXXII	634	Heat shock protein HtpG (634)	*P. aeruginosa*	AAG04985	1051 bits (2688)	0	523/634 (82%)	588/634 (92%)	-
		Heat shock protein HtpG (624)	*E. coli*	AAC73575	743 bits (1899)	0	376/624 (60%)	476/624 (76%)	4/624 (0%)

Table 5 : Comparison of conserved sequences in C domains of peptide synthestases and in putative C domains of the Alb modules

Core	Sequences conserved in peptide synthetases*	Sequence	Alb module
C1	SxAQxR(L/M) (W/Y)xL	TYAQERLWLV	NRPS-1
		STAQERMWFL	NRPS-2
		SYAQERLWLV	NRPS-3
		SLFQERLWFV	NRPS-4
		SYQQERLWFV	NRPS-7
C2	*RHExLRTxF*	*RHEVLRTRF*	NRPS-1 and NRPS-3
		RHAVLRTHF	NRPS-2
		RHEILRTRF	NRPS-4
		RHETLRTRI	NRPS-7
C3	*MHHxISDG(W/V)S*	IHHIISDGWS	NRPS-1 and NRPS-3
		IHHIVFDGWS	NRPS-2
		MHHLIYDAWS	NRPS-4
		MHHIICDGWS	NRPS-7
C4	YxD(F/Y)AVW	YADYALW	NRPS-1 and NRPS-3
		YADYARW	NRPS-2
		YADYAIW	NRPS-4
		YADYATW	NRPS-7
C5	(I/V)GxFVNT(Q/L) (C/A)xR	*IGFFINILPLR*	NRPS-1, NRPS-3 and NRPS-4
		IGLFVNTLAVR	NRPS-2
		IGFFVNILAVR	NRPS-7
C6	(H/N)QD(Y/V)PFE	HQSVPFE	NRPS-1 and NRPS-3
		HQDVPFE	NRPS-2
		NQALPFE	NRPS-4
		HRALPFE	NRPS-7
C7	RDxSRNPL	RDSSQIPL	NRPS-1 and NRPS-3
		RDTARNPL	NRPS-2
		RDTSRIPL	NRPS-4
		RDSSQIPL	NRPS-7

*Sourced from Marahiel *et al.*, 1997

Table 6 : Comparison of conserved sequences in A domains of peptide synthestases and in putative A domains of the Alb modules

Core	Sequences conserved in peptide synthetases*	Sequence	Alb module
A1	L(T/S)YxEL	WSYAQL	NRPS-1 and NRPS-3
		LSYAQL	NRPS-2
		MSYGQL	NRPS-5
		FSYRQL	PKS-4
		LSYAQL	NRPS-6 and NRPS-7
A2	LKAGxAYL(V/L)P(L/I)D	FKAGACYVPID	NRPS-1 and NRPS-3
		SLCGAASVLID	NRPS-2
		MKAGAAYVPID	NRPS-5
		LAGGLVFAPIN	PKS-4
		LKAGGCYVPLD	NRPS-6 and NRPS-7
A3	LAYxxYTSG(S/T)TGxPKG	LACVMVTSGSTGRPKG	NRPS-1 and NRPS-3
		?TRTIMVESGSLSSRLL?	NRPS-2
		PVYCIYTSGSTGSPKG	NRPS-5
		PAVMICTSGSTGTPKA	PKS-4
		LAYVMYTSGSTGRPKG	NRPS-6 et NRPS-7
A4	FDxS	FAVS	NRPS-1 and NRPS-3
		FDAA	NRPS-2
		FDLT	NRPS-5
		FAYG	PKS-4
		FAIS	NRPS-6 and NRPS-7
A5	NxYGPTE	NNYGCTE	NRPS-1 and NRPS-3
		?AAYGNAE?	NRPS-2
		NEYGPTE	NRPS-5
		DGIGCTE	PKS-4
		YIYGCTE	NRPS-6 and NRPS-7
A6	GELxIxGxG(V/L)ARGYL	GELHVHSVGMARGYW	NRPS-1 and NRPS-3
		np	NRPS-2
		GQIHIGGAGVAIGYV	NRPS-5
		GSLWVRGNTLTRGYV	PKS-4
		GEVHIESLGITHGYW	NRPS-6 and NRPS-7
A7	Y(R/K)TGDL	*YKTGDM*	NRPS-1 and NRPS-3
		?YKTDAL?	NRPS-2
		YASGDL	NRPS-5
		?FDTRDL?	PKS-4
		YRTGDM	NRPS-6 and NRPS-7
A8	GRxDxQVKIRGxRIELGEIE	GRQDFEVKVRGHRVDTRQVE	NRPS-1 and NRPS-3
		?GSLDVQSRIDDPRIDLCVVE?	NRPS-2
		GRKDSQIKLRGYRIELGEIE	NRPS-5
		?GRMGSAIKINGCWLSPETLE?	PKS-4
		GRRDYEVKVRGYRVDVRQVE	NRPS-6 and NRPS-7
A9	LPxYM(I/V)P	LPTYMLP	NRPS-1 and NRPS-3
		?LPDYLLP?	NRPS-2
		LPEYMLP	NRPS-5
		?LGKHHYP?	PKS-4
		LPTYMLP	NRPS-6 and NRPS-7

Table 6 : Comparison of conserved sequences in A domains of peptide synthestases and in putative A domains of the Alb modules

Core	Sequences conserved in peptide synthetases*	Sequence	Alb module
A10	NGK(V/L)DR	*NGKLDR*	NRPS-1 and NRPS-3
		?HGRVDL?	NRPS-2
		NGKVNR	NRPS-5
		?SGKVIR?	PKS-4
		NGKLDT	NRPS-6 and NRPS-7

*Sourced from Marahiel *et al.*, 1997
?: non conserved sequences
np: not present

Table 7 : Comparison of conserved sequences in PCP and TE domains of peptide synthestases and in putative PCP and TE domains of the Alb modules

Domain	Sequences conserved in peptide synthetases*	Sequence	Alb module (domain)
PCP	DxFFxxLGG(H/D)S(L/I)	D-FFAVGGHSVL	PKS-3 (PCP1)
		DNFFALGGHSL*S*	NRPS-1 and NRPS-3 (PCP2 and PCP4)
		DNFFELGGHSVL	NRPS-2 (PCP3)
		DNFFELGGHSLS	NRPS-5 (PCP5)
		DNFFNLGGHSLL	NRPS-6 and NRPS-7 (PCP6 and PCP7)
TE	G(H/Y)SxG	GWSSG	NRPS-7

*Sourced from Marahiel *et al.*, 1997

Table 8.

Domains	Position in GsrA (Phe) and variability									
	235	236	239	278	299	301	322	330	331	517
	0	+/-	++	++	++	+/-	++	+/-	++	0
Alb NRPS-1	**A**	**V**	K	**Y**	**V**	**A**	**N**	D	A	**K**
Alb NRPS-3	**A**	**V**	K	**Y**	**V**	**A**	**N**	D	A	**K**
TyrB-M1 (Pro)	D	**V**	Q	S	**I**	**A**	**N**	V	V	**K**
VirS (Pro)	D	**V**	Q	**Y**	A	**A**	H	V	M	**K**
HVCL	**G**	A	L	H	**V**	V	G	S	I	**K**
Alb NRPS-6	A	**I**	K	**Y**	**F**	**S**	**I**	D	**M**	**K**
Alb NRPS-7	A	**I**	K	**Y**	**F**	**S**	**I**	D	**M**	**K**
VirS (Pro)	D	**V**	Q	**Y**	A	A	H	V	**M**	**K**
EntF-M1 (Ser)	D	**V**	W	H	**F**	**S**	**L**	V	D	**K**
β-Ala code	V	D	W	V	I	**S**	**L**	A	D	**K**
Alb NRPS-5	D	L	T	K	I	G	E	V	G	K
BacC-M5 (Asn)	D	L	T	K	I	G	E	V	G	K
TyrC-M1 (Asn)	D	L	T	K	I	G	E	V	G	K
Asn code	D	L	T	K	L	G	E	V	G	K

Table 9: Complementation studies of Xa23RI insertion mutants

Donor	Recipient				
	AM12	AM13	AM36	AM10	AM15
pEV639	+	+	+	-	-
pEValbXXII	+	+	+	-	-
pEVHtpG	+	+	+	-	-
pALB639	+	+	+	-	-
pUFR043	-	-	-	-	-
none	-	-	-	-	-

+ : restoration of albicidin production by alb⁻ mutant, - : no complementation. All experiments were performed at least in duplicate with at least 2 exconjugants obtained from two independent triparental conjugations.

Table 10: Albicidin production assays with *X. axonopodis* pv. vesicatoria exconjugants harbouring different plasmids: analysis of growth inhibition of *E. coli* DH5αKT (susceptible to albicidin) and DH5αAlb^{r}KT (resistant to albicidin) in assays performed with different antibiotic combinations (no antibiotic, tetracycline only, kanamycin only and tetracycline+kanamycin).

		Combination of plasmids			
Bioassay medium containing	Tester strain	pUFR043 and pLAFR3	pUFR043 and pOp3-4/XALB2-3	PALB571 and pLAFR3	PALB571 and pOp3-4/XALB2-3
No antibiotic	DH5αKT	-	-	-	-
	DH5αAlb^{r}KT	-	-	-	-
Tetracycline	DH5αKT	-	-	-	+
	DH5αAlb^{r}KT	-	-	-	-
Kanamycin	DH5αKT	+	+	+	+
	DH5αAlb^{r}KT	+	+	+	+
Tetracycline+kanamycin	DH5αKT	+	+	+	+
	DH5αAlb^{r}KT	+	+	+	+

+: presence of a growth inhibition zone

All experiments were performed at least in duplicate with at least 2 exconjugants obtained from two independent triparental conjugations.

REFERENCES

1. Albertini, A.M., Caramori, T., Scoffone, F., Scotti, C. & Galizzi, A. (1995). Sequence around the 159 degree region of the *Bacillus subtilis* genome: the pksX locus spans 33.6 kb. *Microbiology* **141**, 299-309.

2. Altschul, S.F., Madden, T.L., Schäffer, A.A., Zhang, J., Zhang, Z., Miller, W. & Lipman, D.J. (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein data base search programs," *Nucleic Acids Res.* **25**, 3389-3402.

3. Aparicio, J.F., Molnar, I., Schwecke, T., Konig, A., Haydock, S.F., Khaw, L.E., Staunton, J. & Leadlay, P.F. (1996). Organization of the biosynthetic gene cluster for rapamycin in *Streptomyces hygroscopicus*: analysis of the enzymatic domains in the modular polyketide synthase. *Gene* **169**, 9-16.

4. Astua-Monge, G., Minsavage, G.V., Stall, R.E., Davis, M.J., Bonas, U. and Jones, J.B. (2000). Resistance of tomato and pepper to T3 strains of *Xanthomonas campestris* pv. vesicatoria is specified by a plant-inducible avirulence gene. Mol. Plant Microbe Interact. 13:911-21.

5. August, P.R., Tang, L., Yoon, Y.J., Ning, S., Muller, R., Yu, T.W., Taylor, M., Hoffmann, D., Kim, C.G., Zhang, X., Hutchinson, C.R. & Floss, H.G. (1998). Biosynthesis of the ansamycin antibiotic rifamycin: deductions from the molecular analysis of the rif biosynthetic gene cluster of *Amycolatopsis mediterranei* S699. *Chem. Biol.* **5**, 69-79.

6. Bardwell, J.C. & Craig, E.A. (1988). Ancient heat shock gene is dispensable. *J. Bacteriol.* **170**, 2977-83.

7. Birch, R.G. (2001). *Xanthomonas albilineans* and the antipathogenesis approach to disease control. *Mol. Plant Pathol.* **2**, 1-11.

8. Birch, R.G. & Patil, S.S. (1983). The relation of blocked chloroplast differentiation to sugarcane leaf scal disease. *Phytopathology* **73**, 1368-1374.

9. Birch, R.G. & Patil, S.S. (1985a). June 1985. Antibiotic and process for the production thereof. U. S. Patent No. 4,525,354.

10. Birch, R.G. & Patil, S.S. (1985b) Preliminary characterization of an antibiotic produced by *Xanthomonas albilineans* which inhibits DNA synthesis in *Escherichia coli. J. Gen. Microbiol.* **131**, 1069-1075.

11. Birch, R.G. & Patil, S.S. (1987a). Correlation between albicidin production and chlorosis induction by *Xanthomonas albilineans*, the sugarcane leaf scald pathogen. *Physiol. Mol. Plant Pathol.* **30**, 199-206.

12. Birch, R.G. & Patil, S.S. (1987b). Evidence that an albicidin-like phytotoxin induces chlorosis in sugarcane leaf scald disease by blocking plastid DNA replication. *Mol. Plant Pathol.* **30**, 207-214.

13. Borkovich, K.A., Farrelly, F.W., Finkelstein, D.B., Taulien, J. & Lindquist, S. (1989). Hsp82 is an essential protein that is required in higher concentrations for growth of cells at higher temperatures. *Mol. Cell. Biol.* **9**, 3919-30.

14. Brendel, V. & Trifonov, E. N. (1984). A computer algorithm for testing potential prokaryotic terminators. *Nucl. Acids Res.* **12** 4411-4427.

15. Cane, D.E. (1997). A special thematic issue on polyketide and nonribosomal polypeptide biosynthesis. *Chem. Rev.* **97**, 2463-2706.

16. Cane, D.E., Walsh, C.T. & Khosla, C. (1998). Harnessing the biosynthetic code: combinations, permutations, and mutations. *Science* **282**, 63-8.

17. Cane, D.E. & Walsh, C.T. (1999). The parallel and convergent universes of polyketide synthases and nonribosomal peptide synthetases. *Chem. Biol.* **6**, R319-R325.

18. Challis, G.L., Ravel, J. & Townsend, C.A. (2000). Predictive, structure-based model of amino acid recognition by nonribosomal peotide synthetase adenylation domains. *Chem. Biol.* **7**, 211-224.

19. Conti, E., Stachelhaus, T. Marahiel, M.A. & Brick, P. (1997). Structural basis for the activation of phenylalanine in the non-ribosomal biosynthesis of gramicidin S. *EMBO J.* **16**, 4174-4183.

20. Criado, L.M. , Martin, J.F. & Gil, J.A. (1993). The pab gene of *Streptomyces griseus*, encoding p-aminobenzoic acid synthase, is located between genes possibly involved in candicidin biosynthesis. *Gene* **126**, 135-139.

21. Cutforth, T. & Rubin, G.M. (1994). Mutations in Hsp83 and cdc37 impair signaling by the sevenless receptor tyrosine kinase in Drosophila. *Cell.* **77**, 1027-36.

22. De Feyter, R. & Gabriel, D.W. (1991). Use of cloned DNA methylase genes to increase the frequency of transfer of foreign genes into *Xanthomonas campestris pv. malvacearum. J. Bacteriol.* 173, 336-342.

23. von Döhren, H., Dieckmann, R. & Pavela-Vrancic, M. (1999). The nonribosomal code. *Chem. Biol.* **6**, R273-R279.

24. Du, L., Sanchez, C., Chen, M., Edwards, D.J. & Shen, B. (2000). The biosynthetic gene cluster for the antitumor drug bleomycin from *Streptomyces verticillus* ATCC15003 supporting functional interactions between nonrobosomal peptide synthetases and a polyketide synthase. *Chem. Biol.* 7, 623-642.

25. Duitman, E.H., Hamoen, L.W., Rembold, M., Venema, G., Seitz, H., Saenger, W., Bernhard, F., Reinhardt, R., Schmidt, M., Ullrich, C., Stein, T., Leenders, F. & Vater, J. (1999). The mycosubtilin synthetase of *Bacillus subtilis* ATCC6633: a multifunctional hybrid between a peptide synthetase, an amino transferase, and a fatty acid synthase. *Proc. Natl. Acad. Sci. USA* **96**, 13294-13299.

26. Gabriel, D.W & De Feyter, R. (1992). RFLP analyses and gene tagging for bacterial identification and taxonomy. In *Molecular Plant Pathology: A Practical Approach.* (Gurr, S.J., McPherson, M.J. & Bowles, D.J. Ed.), vol 1, pp51-66, IRL Press, Oxford.

27. Garrido, M.C., Herrero, M., Kolter, R. & Moreno, F. (1988). The export of the DNA replication inhibitor Microcin B17 provides immunity for the host cell. *EMBO J.* 7, 1853-1862.

28. Gehring, A.M., DeMoll, E., Fetherston, J.D., Mori, I., Mayhew, G.F., Blattner, F.R., Walsh, C.T. & Perry, R.D. (1998). Iron acquisition in plague: modular logic in enzymatic biogenesis of yersiniabactin by *Yersinia pestis*. *Chem. Biol.* **5**, 573-86.

29. Guenzi, E., Galli, G., Grgurina, I., Gross, D.C. & Grandi, G. (1998). Characterization of the syringomycin synthetase gene cluster. A link between prokaryotic and eukaryotic peptide synthetases. *J. Biol. Chem.* **273**, 32857-32863.

30. Huang, G., Zhang, L. & Birch, R.G. (2000a). Analysis of the genes flanking *xabB*: a methyltransferase gene is involved in albicidin biosynthesis in *Xanthomonas albilineans*. *Gene* **255**, 327-333.

31. Huang, G., Zhang, L. & Birch, R.G. (2000b). Albicidin antibiotic and phytotoxin biosynthesis in *Xanthomonas albilineans* requires a phosphopantetheinyl transferase gene. *Gene* **258**, 193-199.

32. Huang, G., Zhang, L. & Birch, R.G. (2001). A multifunctional polyketide-peptide synthetase essential for albicidin biosynthesis in *Xanthomonas albilineans*. *Microbiology* **147**, 631-642.

33. Jakob, U., Lilie, H., Meyer,I. & Buchner, J. (1995). Transient interaction of Hsp90 with early unfolding intermediates of citrate synthase. Implications for heat shock *in vivo*. *J. Biol. Chem.* **270**, 7288-94.

34. Konz, D., Klens, A., Schorgendorfer, K. & Marahiel, M.A. (1997). The bacitracin biosynthesis operon of *Bacillus licheniformis* ATCC10716 : molecular characterization of three multi-modular peptide synthetase. *Chem. Biol.* **4**, 927-937.

35. Leong, S.A., Ditta, G.S. & Helinski, D.R. (1982). Heme biosynthesis in *Rhizobium*: identification of a cloned gene coding for aminolevulinic acid synthetase from *Rhizobium meliloti*. *J. Biol. Chem.* **257**, 8724-8730.

36. Li, Y.M., Milne, J.C., Madison, L.L., Kolter, R. & Walsh, C.T. (1996). From peptide precursors to oxazole and thiazole-containing peptide antibiotics: microcin B17 synthase. *Science*. **274**, 1188-93.

37. Liu, J., Duncan, K. & Walsh, C.T. (1989). Nucleotide sequence of a cluster of *Escherichia coli* enterobactin biosynthesis genes: identification of ent A and purification of its product 2,3-dihydro-2,3-dihydroxybenzoate deshydrogenase. *J. Bacteriol.* **171**, 791-798.

38. Marahiel, M.A. Stachelhaus, T. & Mootz, H.D. (1997). Modular peptide synthetases involved in nonribosomal peptide synthesis. *Chem. Rev.* **97**, 2651-2673.

39. Mayorga, M.E. & Timberlake, W.E. (1992). The developmentally regulated *Aspergillus nidulans wA* gene encodes a polypeptide homologous to polyketide and fatty acid synthases. *Mol. Gen. Genet.* **235**, 205-212.

40. McCarthy, J.E. & Gualerzi, C. (1990). Translational control of prokaryotic gene expression. *Trends Genet.* **6**,78-85.

41. McDaniel, R., Thamchaipenet, A., Gustafsson, C., Fu, H., Betlach, M. & Ashley, G. (1999). Multiple genetic modifications of the erythromycin polyketide synthase to produce a library of novel "unnatural" natural products. *Proc. Natl. Acad. Sci. USA* **96**, 1846-1851.

42. Milne, J.C., Roy, R.S., Eliot, A.C., Kelleher, N.L., Wokhlu, A., Nickels, B. & Walsh, C.T. (1999). Cofactor requirements and reconstitution of microcin B17 synthetase: a multienzyme complex that catalyzes the formation of oxazoles and thiazoles in the antibiotic microcin B17. *Biochemistry*. **38**, 4768-81.

43. Mohamed, I.S., Rott, P., Davis, M.J. & Chatenet, M. (1996). Differentiation of *Xanthomonas albilineans* strains based on multiplication of the pathogen in sugarcane varieties. In *Proceedings XXII Congress of the International Society of Sugarcane Technologists*. (Cock J.H. and Brekelbaum T. Ed.), vol. 2, pp486-492, Cartagena De Indias, Colombia, 5-14 September 1995.

44. Mohamed, M.E., Zaa, A., Ebenau-Jehle, C. & Fuchs, G. (2001). Reinvestigation of a new type of aerobic benzoate metabolism in the proteobacterium *Azoarcus evansii. J. Bacteriol.* **183**, 1899-1908.

45. Motamedi, H. & Shafiee, A. (1998). The biosynthetic gene cluster for the macrolactone ring of the immunosuppressant FK506. *Eur. J. Biochem.* **256**, 528-534.

46. Normark, S., Bergström, S., Edlund, T., Grundström, T., Jaurin, G., Lindberg, F.P. & Olsson O. (1983). Overlapping genes. *Annu. Rev. Genet.* **17**, 499-525.

47. Paitan, Y., Orr, E., Ron, E.Z. & Rosenberg, E. (1999). Genetic and functional analysis of genes required for the post-modification of the polyketide antibiotic TA of *Myxococcus xanthus*. *Microbiology* **145**, 3059-67.

48. Pfeifer, B.A., Admiraal, S.J., Gramajo, H., Cane, D.E. & Khosla C. (2001). Biosynthesis of complex polyketides in a metabolically engineered strain of *E. coli*. *Science* **291**, 1790-1792.

49. Quadri, L.E., Sello, J., Keating, T.A., Weinreb, P.H. & Walsh, C.T. (1998). Identification of a *Mycobaterium tuberculosis* gene cluster encoding the biosynthetic enzymes for assembly of the virulence-conferring siderophore mycobactin. *Chem. Biol.* **5**, 631-645.

50. Ricaud, C. & Ryan, C.C. (1989). Leaf scald. In *Diseases of sugarcane: major diseases*. (Ricaud, C. Egan, B.T., Gillaspie, Jr., A.G. & Hughes, C.G. ed.), pp. 39-58, Elsevier Science Publishers B.V., Amsterdam.

51. Rodriguez, E. & McDaniel, R. (2001). Combinatorial biosynthesis of antimicrobials and other natural products. *Curr. Opin. Microbiol.* **4**, 526-34.

52. Rott, P.C., Costet, L., Davis, M.J., Frutos, R. & Gabriel D.W. (1996). At least two separate gene clusters are involved in albicidin production by *Xanthomonas albilineans*. *J. Bacteriol.* **178**, 4590-4596.

53. Rott, R. & Davis, M.J. (2000). Leaf scald. In *A guide to sugarcane diseases*. (Rott, P., Bailey, R.A., Comstock, J.C., Croft, B.J. and Saumtally, A.S. ed.), pp. 38, Cirad/Issct, Montpellier.

54. Sambrook, J., Fritsch, E.F. & Maniatis, T. (1989) *Molecular cloning: A laboratory Manual* (2nd edn), Cold Spring Harbor Lab. Press, Plainview, NewYork.

55. Sanger, F., Nicklen, S. & Coulson, A.R. (1977). DNA sequencing with chain-terminating inhibitors. *Proc. Natl. Acad. USA* **74**, 5463-5467

56. Siebert, M., Bechthold, A., Melzer, M., May, U., Berger, U. Schroder, G., Schroder, J., Severin, K. & Heide, L. (1992). Ubiquinone biosynthesis. Cloning of the genes coding for chorismate pyruvate-lyase and 4-hydrobenzoate octaprenyl transferase from *Escherichia coli. FEBS Lett.* **307**, 347-350.

57. Stachelhaus, T., Mootz, H.D. & Marahiel, M.A. (1999). The specificity-conferring code of adenylation domains in nonribosomal peptide synthetases. *Chem. Biol.* **6**, 493-505.

58. Staskawicz, B. Dahlbeck, D., Keen, N. and Napoli, C. (1987). Molecular characterization of cloned avirulence genes from race 0 and race 1 of *Pseudomonas syringae* pv. glycenea. J. Bacteriol. 169: 5789-5794.

59. Takano, Y., Kubo, Y., Shimizu, K., Mise, K., Okuno, T. & Furusawa, I. (1995). Structural analysis of PKS1, a polyketide synthase gene involved in melanin biosynthesis in *Colletotrichum lagenarium. Mol. Gen. Genet.* **249**, 162-167.

60. Tang, L., Yoon, Y.J., Choi, C.Y. & Hutchinson, C.R. (1998). Characterization of the enzymatic domains in the modular polyketide synthase involved in rifamycin B biosynthesis by *Amycolatopsis mediterranei. Gene* **216**, 255-65.

61. Thomas, J.G. & Baneyx, F. (2000). ClpB and HtpG facilitate *de novo* protein folding in stressed *Escherichia coli* cells. *Mol. Microbiol.* **36**, 1360-70.

62. Valdez, F., Gonzalez-Ceron, G., Kieser, H.M., Servin-Gonzalez, L. (1999). The *Streptomyces coelicolor* A3(2) lipAR operon encodes an extracellular lipase and a new type of transcriptional regulator. *Microbiology* **145**, 2365-74.

63. Wall, M.K. & Birch, R.G. (1997). Genes for albicidin biosynthesis and resistance span at least 69 kb in the genome of *Xanthomonas albilineans*. *Lett. Appl. Microbiol.* **24**, 256-260.

64. Yakimov, M.M., Kroger, A., Slepak, T.N., Giuliano, L., Timmis, K.N. & Golyshin, P.N. (1998). A putative lichenysin A synthase operon in *Bacillus licheniformis*: initial characterization. *Biochim. Biophys. Acta.* **1399**, 141-153.

65. Yazgan, A., Ozcengiz, G. & Marahiel M.A. (2001). Tn*10* insertional mutations of *Bacillus subtilis* that block the biosynthesis of bacilysin. *Biochim. Biophys. Acta.* **1518**, 87-94.

66. Yu, J.H. & Leonard, T.J. (1995). Sterigmatocystin biosynthesis in *Aspergillus nidulans* requires a novel type I polyketide synthase. *J. Bacteriol.* **177**, 4792-4800.

67. Yu, S., Fiss, E., & Jacobs, W.R. (1998). Analysis of the exochelin locus in *Mycobacterium smegmatis*: biosynthesis genes have homology with genes of the peptide synthetase family. *J. Bacteriol.* **180**, 4676-4685.

68. Zhang, L. & Birch, R.G. (1997). The gene for albicidin detoxification from *Pantoea dispersa* encodes an esterase and attenuates pathogenicity of *Xanthomonas albilineans* to sugarcane. *Proc. Natl. Acad. Sci. USA* **94**, 9984-9989.

69. Zhang, J. H., Quigley, N.B. & Gross, D.C. (1995). Analysis of the syrB and syrC genes of Pseudomonas syringae pv. syringae indicates that

syringomycin is synthesized by a thiotemplate mechanism. *J. Bacteriol.* **177**, 4009-4020.

70. Zhang, J. H., Quigley, N. B. & Gross, D.C. (1997). Analysis of the syrP gene, which regulates syringomycin synthesis by *Pseudomonas syringae pv. syringae*. *Appl. Environ. Microbiol.* **63**, 2771-2778.

71. Zhang, L., Xu, J. & Birch, R.G. (1998). Factors affecting biosynthesis by *Xanthomonas albilineans* of albicidins antibiotics and phytotoxins. *J. Appl. Microbiol.* **85**, 1023-1028.

72. Zhang L., Xu, J. & Birch, R.G. (1999). Engineered detoxification confers resistance against a pathogenic bacterium. *Nat Biotechnol.* **17**:1021-1024.

CLAIMS

We claim:

1. A transformed host cell that comprises one or more genetic construct that comprises SEQ ID NO: 1, SEQ ID NO: 2, and SEQ ID NO:3.

2. The transformed host cell of claim 1, wherein said transformed host cell has been transformed with multiple genetic constructs.

3. The transformed host cell of claim 2, wherein said multiple genetic constructs contain SEQ ID NO: 1, SEQ ID NO:2, SEQ ID NO: 3, polynucleotide fragments of SEQ ID NOs: 1-3, or combinations of polynucleotide fragments of SEQ ID NOs 1-3.

4. The transformed host cell of claim 1, wherein said host cell has been transformed with one or more genetic constructs that provide a combination of polynucleotide fragments of SEQ ID NOs: 1, 2, and 3, wherein said combination of polynucleotide fragments provide a biosynthetic pathway for the production of albicidin or an albicidin-like antibiotic.

5. A genetic construct comprising at least one polynucleotide sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, and SEQ ID NO: 3.

6. A method of making an antibiotic comprising the culturing of a transformed host cell according to claim 1, 2, 3, or 4 under conditions that allow for the production of said antibiotic.

7. The method according to claim 6, further comprising the isolation of said antibiotic.

8. An isolated or purified polynucleotide comprising:

(a) a polynucleotide sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, and 25;

(b) a polynucleotide encoding a polypeptide selected from the group consisting of SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47;

(c) a polynucleotide that is complementary to a polynucleotide selected from the group consisting of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, and 25;

(d) a polynucleotide that is complementary to a polynucleotide encoding a polypeptide selected from the group consisting of SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47; or

(e) a polynucleotide that is at least 70% homologous to: (1) a polynucleotide

selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, and 25; (2) a polynucleotide sequence encoding a polypeptide selected from the group consisting of SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47; (3) a polynucleotide that is complementary to a polynucleotide encoding a polypeptide selected from the group consisting of SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47; (3) a polynucleotide that is complementary to a polynucleotide sequence selected from the group consisting of SEQ ID NO: 1, 2, 3, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 24, and 25;

(f) a polynucleotide sequence encoding a variant of a polypeptide selected from the group consisting of SEQ ID NOs: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47, wherein said variant has at least one of the biological activities associated with the polypeptides of SEQ ID NOs: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47;

g) a polynucleotide sequence encoding a fragment of a polypeptide selected from the group consisting of SEQ ID NOs: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47 or a fragment of a variant polypeptide of SEQ ID NOs: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47;

h) a polynucleotide sequence encoding multimeric construct comprising a polynucleotide as set forth in (a), (b), (c), (d), (e), (f), or (g);

(i) a polynucleotide that hybridizes under low, intermediate or high stringency with a polynucleotide sequence as set forth in (a), (b), (c), (d), (e), (f), (g), or (h);

j) a genetic construct comprising a polynucleotide sequence as set forth in (a), (b), (c), (d), (e), (f), (g), (h), or (i);

k) a vector comprising a polynucleotide sequence as set forth in (a), (b), (c), (d), (e), (f), (g), (h), or (i); or

(l) a promoter operably linked to a polynucleotide sequence as set forth in (a), (b), (c), (d), (e), (f), (g), (h), or (i).

9. A recombinant cell comprising a polynucleotide sequence according to claim 8.

10. The recombinant cell of claim 9, wherein said cell is a plant cell.

11. The recombinant cell of claim 9, wherein said cell is bacterial.

12. The recombinant cell of claim 9, wherein said cell is eukaryotic.

13. The recombinant cell of claim 10, wherein said plant cell comprises seed

propagative materials, or plant parts.

14. A method of producing a protein comprising the steps of expressing a polynucleotide according to claim 8 in a host cell under conditions that allow for the expression of said polynucleotide.

15. The method according to claim 14, further comprising the isolation of said protein.

16. A method of producing a polyketide carrying para-aminobenzoic acid and/or carbamoyl benzoic acid by inserting at least one DNA Fragment of Claim 8 that encodes a polyketide synthetase (PKS) into a cell and causing the cell to express the encoded PKS protein under conditions such that the PKS functions to produce a polyketide carrying either a para-aminobenzoic acid or a carbamoyl benzoic acid or both.

17. A method of activating non-proteinogenic amino acids for incorporation into peptides or polyketides by inserting at least one DNA Fragment of Claim 8 that encodes a polyketide synthetase (PKS) into a cell and causing the cell to express the encoded PKS under conditions such that the PKS activates said non-proteinogenic amino acids.

18. The method according to claim 17, wherein said non-proteinogenic amino acids are paraminobenzoic acid or carbamoyl benzoic acid.

19. A polypeptide comprising:

(a) SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47;

(b) a heterologous polypeptide sequence fused, in frame, to a polypeptide comprising SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47;

(c) a fragment of SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47, wherein said fragment exhibits at least one biological function of the polypeptide of SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47;

(d) a variant having at least 70% homology to a polypeptide comprising SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47, wherein said variant exhibits at least one biological function of the polypeptide comprising SEQ ID NO: 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, or 47;

20. An isolated and purified antibiotic produced by a process that includes at least three proteins coded by DNA sequences of claim 8 in combination with additional

enzymes that modify the product to provide a non-naturally occurring Albicidin-like product having at least one of the useful properties reported for albicidin.

21. The antibiotic or antibiotics of claim 20 having at least one of the general structures illustrated in Figure 11.

22. An antibiotic produced by the process of expressing the DNA of one or more of the genes included in the Albicidin Biosynthetic Gene Clusters of Claim 8 in a genetically modified host cell sustained in a culture media, and thereafter separating the antibiotic from the host cell and culture media.

23. A process for producing an antibiotic that comprises modifying a host cell to enhance expression of a polynucleotide according to claim 8 comprising the insertion of expression enhancing DNA into the genome of a Xanthomonas albilineans strain, Escherichia coli strain, or other Albicidin producing microbial strain, in a position operative to enhance expression of the enzymes of the Albicidin Biosynthetic Gene Clusters, culturing the modified host cell to produce an antibiotic and isolating the antibiotic.

24. An isolated purified antibiotic having at least 4 of the structural elements illustrated in Figure 11, and an elemental composition of $C_{40}H_{35}N_6O_{15}$.

25. A method of protecting a plant against damage from albicidin that comprises applying an agent that blocks expression at least one gene in the Albicidin Biosynthetic Gene Clusters to the plant to be protected.

26. A method of obtaining agents useful in blocking expression of albicidin by screening materials against a modified host cell line that expresses a polynucleotide according to claim 8 and selecting for materials that stop or decrease albicidin production.

27. A method of protecting a plant against phytotoxic damage from an antibiotic that comprises inserting into the plant and operably expressing at least one resistance gene from the polynucleotides according to claim 8 in the plant to be protected.

28. The recombinant cell of claim 9, wherein said cell has been transformed with at least one polynucleotide sequence comprising SEQ ID NO: 1, 2, or 3.

29. The recombinant cell of claim 28, wherein said cell has been transformed with at least two of said polynucleotide sequences.

30. The recombinant cell of claim 28, wherein said cell has been transformed with SEQ ID NO: 1, SEQ ID NO: 2 and SEQ ID NO: 3.

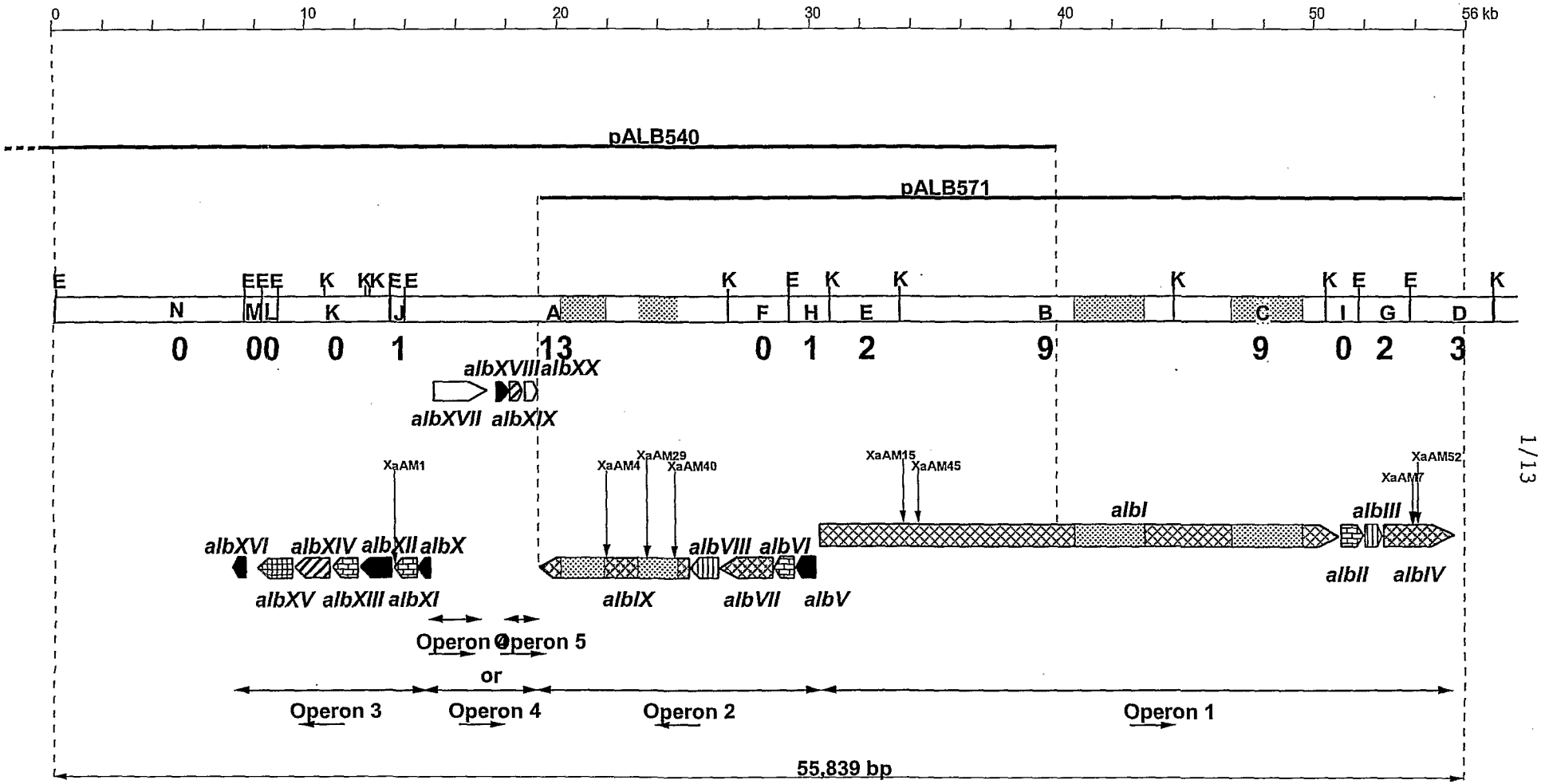

0
10
20
30
40
50
56 kb
pALB540
pALB571
E
E E E
K
K K E E
K
E
K
K
K
K
E
E
K
N
M L
K
J
A
F
H
E
B
C
I
G
D
0
0 0
0
1
13
0
1
2
9
9
0
2
3
albXVIII albXX
albXVII albXIX
XaAM1
XaAM4
XaAM29
XaAM40
XaAM15
XaAM45
XaAM52
XaAM7
albI
albIII
albXVI
albXIV
albXII
albX
albVIII
albVI
albII
albIV
albXV
albXIII
albXI
albIX
albVII
albV
Operon 6
Operon 5
or
Operon 3
Operon 4
Operon 2
Operon 1
55,839 bp

FIG. 1

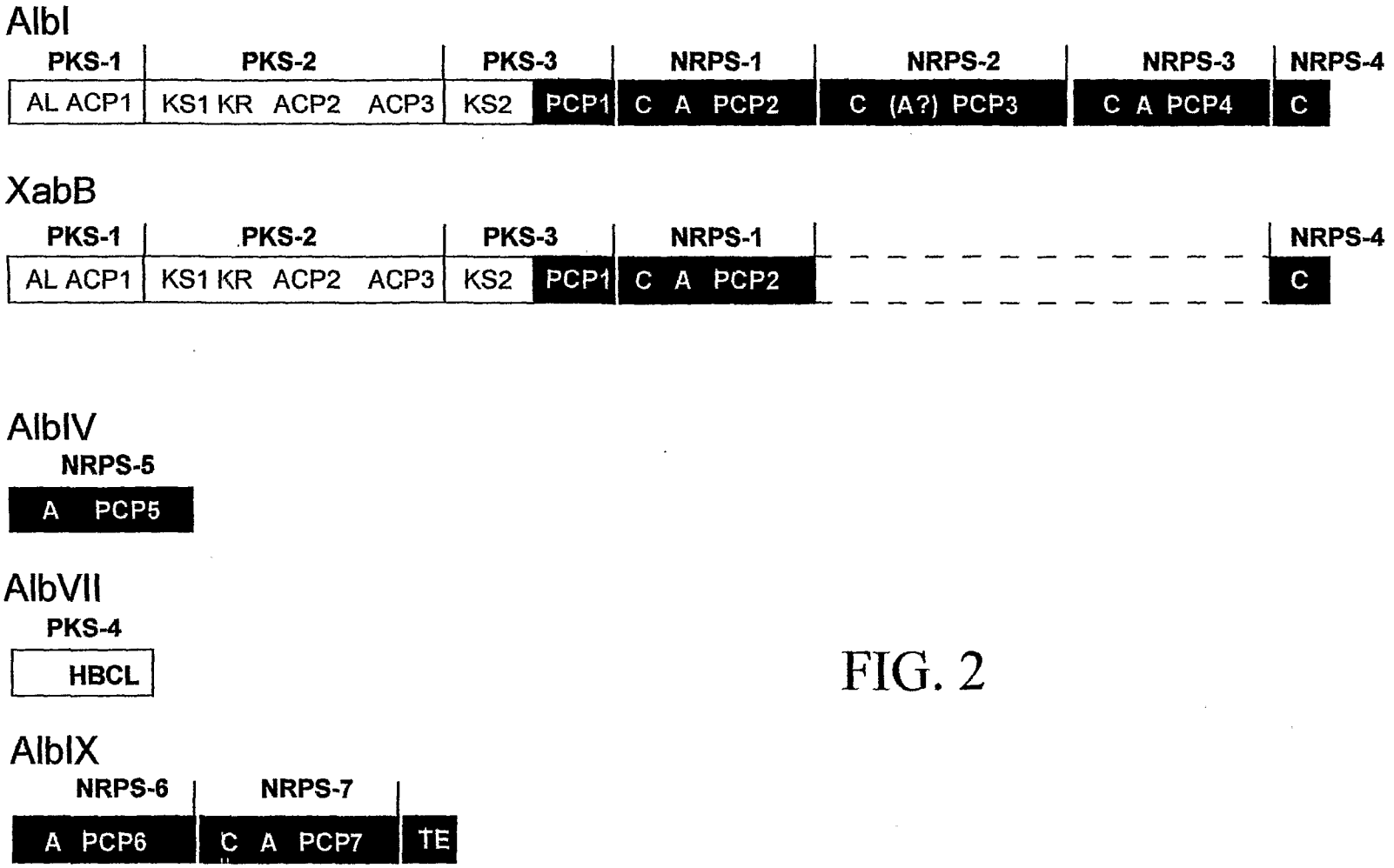

AlbI
PKS-1
PKS-2
PKS-3
NRPS-1
NRPS-2
NRPS-3
NRPS-4
AL ACP1
KS1 KR ACP2 ACP3
KS2
PCP1
C A PCP2
C (A?) PCP3
C A PCP4
C
XabB
PKS-1
PKS-2
PKS-3
NRPS-1
NRPS-4
AL ACP1
KS1 KR ACP2 ACP3
KS2
PCP1
C A PCP2
C
AlbIV
NRPS-5
A PCP5
AlbVII
PKS-4
HBCL
AlbIX
NRPS-6
NRPS-7
A PCP6
C A PCP7
TE

FIG. 2

Sgl-TcmO	173	FV**DLGGA**RG	234	PRA**D**VFIV	263	ALTPG**GAV**LV
Sgl-TcmN	331	IA**DLGGGD**G	393	TGY**D**AYLF	423	IGDDD**ARL**LI
Smy-MdmC	64	VL**EIGTFTG**	135	GAF**D**IVFV	159	LVRPG**GLV**AI
Mxa-SafC	63	TL**EVGVFTG**	134	GTF**D**LAFI	158	LVRPG**GLI**IL
Ser-EryG	85	VL**DVGFGLG**	149	ETF**D**RVTS	178	VLKPG**GVL**AI
Spe-DauK	183	VL**DVGGGKG**	254	RKA**D**AIIL	273	ALEPG**GRI**LI
Sal-DmpM	208	VV**DIGGAD**G	269	GGG**D**LYVL	298	AMPAH**ARL**LV
Shy-RapM	106	VL**EVGCGMG**	155	VQG**D**AEEL	194	ALRRG**GAL**SH
Sav-AveD	71	VL**DVGCGSG**	124	GSF**D**AAWA	151	VLRPG**GRL**AV
Sar-Cmet	158	VL**DVACGHG**	220	GPY**D**LSLI	251	ATRPG**GRI**GI
AlbII	174	VL**DVAAGHG**	236	SGY**D**VILL	267	ALNDD**GMV**IT
		Motif I		Motif II		Motif III

FIG. 3

Sgl-tcmP	84	V**VLHLACGLDSRAFR**MDV**P**D109	**DVDVPDVIELR**	139	E**DWL**DT**V**P	150	**P**ALV**VAEGLTPYL**
Sme-PKS	84	T**VLHLGCGLDSRIFRI**DPGP109	**ELDVPDVISLR**	139	RG**WIERL**P	150	**PTMIVAEGVLPYL**
Pmu-tcmP	86	V**VVQLGAGLDARFERL**GK**P**Q111	**DLDLPEVINIR**	141	T**DWM**KT**V**S	152	**P**VLL**ILEGVLMFF**
Mtu-Omt	85	T**VVALAEGLQTSFWRL**DVAI113	**TVDLPPIVDLR**	144	YS**WM**DS**V**D	155	GVFIT**AEGLLMYL**
Mlo-Hp	84	I**VLHLGCGLDTRVFRV**DP**P**P109	**DADYPQVIELR**	139	PG**WLAEV**P	150	**PAMVVAEGLTPYL**
Mtu-Hp	101	Q**VAILASGLDSRAYRLPWP**T127	**EIDQPKVMEFK**	162	A**DWPTAL**Q	178	**P**TAW**LAEGLLIYL**
Mtu-Hp2	104	Q**VVILASG**DL**SRAWRLPWP**D129	**ELDQPKVLEFK**	162	Q**DWPKAL**Q	178	**P**CAW**LAEGLVRYL**
Mtu-Hp3	98	Q**VVILAAGLDSRAYRLPWP**D123	**ELDRPQVLDFK**	156	D**DWPQAL**R	172	**P**SAW**IAEGLLIYL**
Mtu-Hp4	101	QA**VIVAAGLDCRAYRLDWQ**P126	**EIDVPKVLEFK**	161	T**DWPTPL**T	177	**P**SAWS**VEGLLPYL**
Sco-Hp	93	Q**VVLLGAGMDSRAFRMAWP**E118	**EVDTPAPLEFK**	153	E**DWPSAL**A	169	**P**TAW**IGEGLLIYL**
AlbVI	99	Q**VVILAAGMDARAYRLPWP**S124	**EIDHMDVLSDK**	157	E**DWPQAL**K	173	ATLW**LVEGLLCYL**
		Motif I	Motif II		Motif III		Motif IV

FIG. 4

motif A4
motif A5
pos. 235
pos. 236
pos. 239
pos. 278
pos. 299
pos. 301
pos. 322
pos. 330
pos. 331
GrsA (Phe)
Blm NRPS-2 (β-Ala)
AlbI NRPS-1
AlbI NRPS-3
AlbIX NRPS-6
AlbIX NRPS-7
AlbIV NRPS-5
AlbVII PKS-4
AlbI NRPS-2

FIG. 5

FIG. 6

XALB1 Strand +
29 bp downstream from the TGA stop codon of *albXVII*

```
            -40  -35  -30  -25  -20  -15  -10   -5  -1+  +5          p       s
             .    .    .    .    .    .    .    .   ..   .
17085=>  ACCATTGTGAACGGCCTTCCCGCTTCGTCCATAGCGATTTTCGATCGCGGC        4.30       0
                                 ----      ----
                                   ---     ---
```

XALB1 Strand +
400 bp downstream from the TAA stop codon of *albIV*

```
            -40  -35  -30  -25  -20  -15  -10   -5  -1+  +5          p       s
             .    .    .    .    .    .    .    .   ..   .
55617=> CATGGCTGCAGGCCGAGCTCGCTCAGCTACGGGGTGAGACCGAAGCTGCCC <= 55667  4.13      12
                    ----      ----
                  -- --     -- --
```

XALB1 Strand –
62 bp, 170 bp and 560 bp downstream from the TAG stop codon of *albXVI*

```
           -40  -35  -30  -25  -20  -15  -10   -5  -1+  +5          p       s
            .    .    .    .    .    .    .    .   ..   .
 7030=> GGGGGGCAGTTGCCCGGACCCCGGTTTCTGTAAACGTTTGGCTGTCTGTAG <= 6879   3.95      13
                              ----     ----
                            -- --      -- --
 6922=> AACTCTTAAAAGAGATTGATTTAAATTTCCCTGCGTTTTTGTACGAGAATA <= 6872   4.42       0
 6532=> TACTTAATATAAGATTGCGAAGCTTGCGTTGCGGAATGATTTTTTCAATAT <= 6482   4.27      53
                          -- --    -- --
                    --- -- ---     --- -- ---
```

XALB3 Strand+

```
            -40  -35  -30  -25  -20  -15  -10   -5  -1+  +5          p       s
             .    .    .    .    .    .    .    .   ..   .
  8065=> GCAAAGAAAAGCGGAAACGAAAAAAGGGCCTACGGGCCCTTTTTTCTTCCA        4.78       0
  8072=> AAAGCGGAAACGAAAAAAGGGCCTACGGGCCCTTTTTTCTTCCATCGTCGA        3.94      86
                    ------------     ------------
                     ----- -- --     -- -- -----
```

```
14456 GTCGTTGATCAGCACCAGATAAGCCTGTTCCTCGAACGTCATCCTAAAGATACCCCCGGAAGGCTGCTGCGAAGCACGGAAGTTGCTACATCGCAC
      CAGCAACTAGTCGTGGTCTATTCGGACAAGGAGCTTGCAGTAGGATTTCTATGGGGGCCTTCCGACGACGCTTCGTGCCTTCAACGATGTAGCGTG
       D  N  I  L  V  L  Y  A  Q  E  E  F  T  M          RBS
                  albX
            -35 (PalbX: operon 3)    -10 (PalbX: operon 3)
14552 AATGCGATTCAGATGGACCAAGCAAAGCGACTATACATGACGTCACTTCGAAGATGTCAAGAAAAATAGCGCGTGAAGAGCACGTAAGAGTGATGT
      TTACGCTAAGTCTACCTGGTTCGTTTCGCTGATATGTACTGCAGTGAAGCTTCTACAGTTCTTTTTATCGCGCACTTCTCGTGCATTCTCACTACA
                                  -10 (PalbXVII: operon 4) -35 (PalbXVII: operon4)

14648 GTTTCGCACCGCTGTACGTCCCATCGCCATCGCGGCAAAGCTTACACGAAAAATTCACCAGGGCATGCGTTCAATACGCGGGTCAAAGCAATATCC
      CAAAGCGTGGCGACATGCAGGGTAGCGGTAGCGCCGTTTCGAATGTGCTTTTTAAGTGGTCCCGTACGCAAGTTATGCGCCCAGTTTCGTTATAGG

14744 TTGCGCTTGCAGAGCTATGTTCGTGCGTAAAGCGCCAAGGCAGTGGGGAGCAACACCTTGGGTTTCGGTTGAGGTGCGGGTAGCAATTTCTGCTTA
      AACGCGAACGTCTCGATACAAGCACGCATTTCGCGGTTCCGTCACCCCTCGTTGTGGAACCCAAAGCCAACTCCACGCCCATCGTTAAAGACGAAT

                                                                  RBS
14840 ATATCCACGCGCGGCGGTTTTTGTCTTGCCGGGCGTCAACTGTCTCATCGAGCAGTCTGGGAGGCTATTTTGCGCTGCCTTATCATAAATAATTAC
      TATAGGTGCGCGCCGCCAAAAACAGAACGGCCCGCAGTTGACAGAGTAGCTCGTCAGACCCTCCGATAAAACGCGACGGAATAGTATTTATTAATG
                                                                        M  R  C  L  I  I  N  N  Y
                                                                          albXVII
```

FIG. 7A

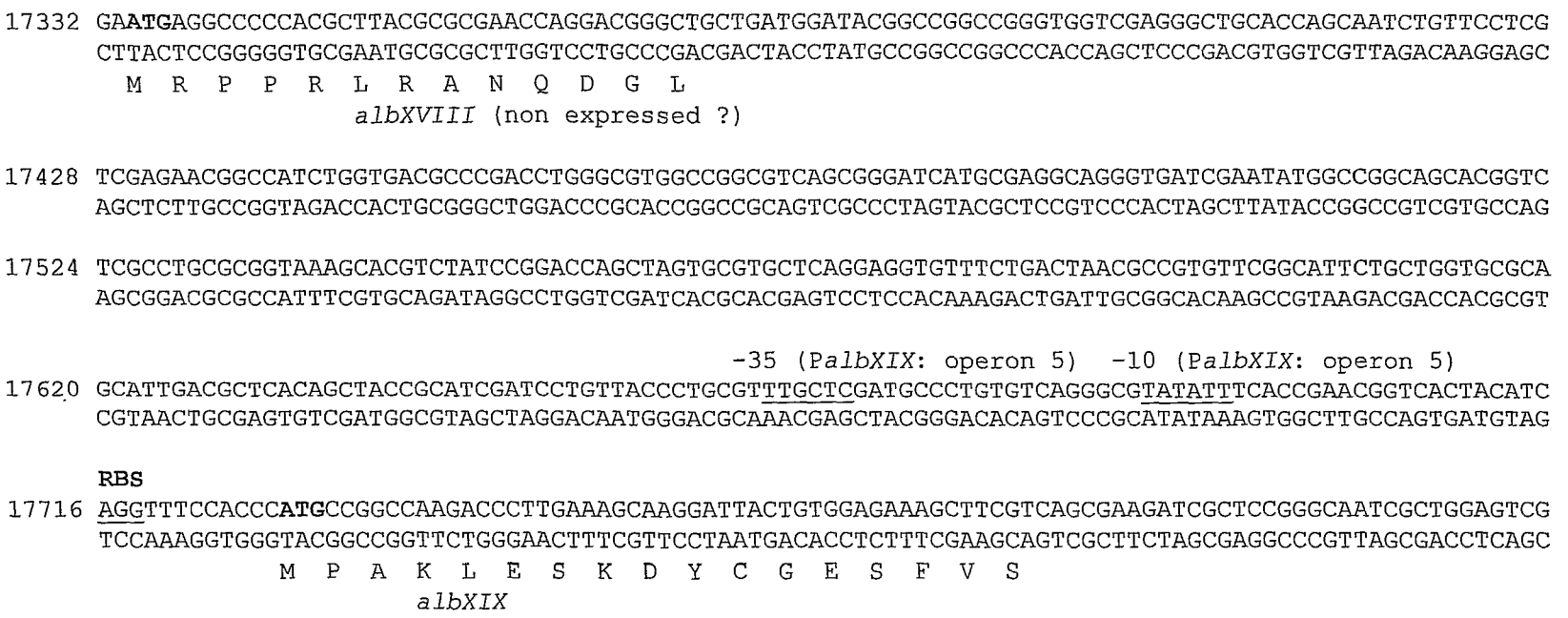
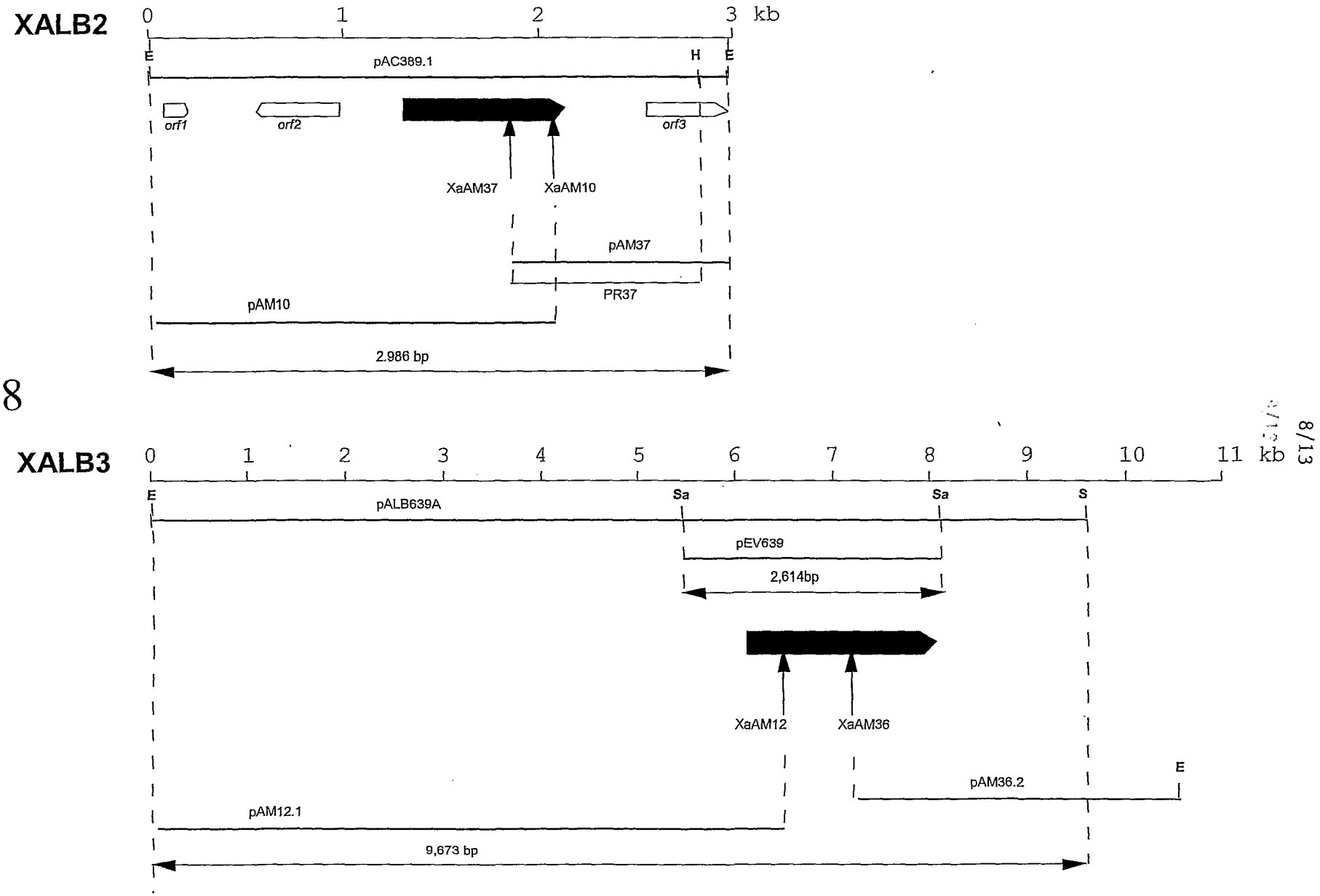

17332 GAATGAGGCCCCCACGCTTACGCGCGAACCAGGACGGGCTGCTGATGGATACGGCCGGCCGGGTGGTCGAGGGCTGCACCAGCAATCTGTTCCTCG
CTTACTCCGGGGGGTGCGAATGCGCGCTTGGTCCTGCCCGACGACTACCTATGCCGGCCGGCCCACCAGCTCCCGACGTGGTCGTTAGACAAGGAGC
M R P P R L R A N Q D G L
albXVIII (non expressed ?)
17428 TCGAGAACGGCCATCTGGTGACGCCCGACCTGGGCGTGGCCGGCGTCAGCGGGATCATGCGAGGCAGGGTGATCGAATATGGCCGGCAGCACGGTC
AGCTCTTGCCGGTAGACCACTGCGGGCTGGACCCGCACCGGCCGCAGTCGCCCTAGTACGCTCCGTCCCACTAGCTTATACCGGCCGTCGTGCCAG
17524 TCGCCTGCGCGGTAAAGCACGTCTATCCGGACCAGCTAGTGCGTGCTCAGGAGGTGTTTCTGACTAACGCCGTGTTCGGCATTCTGCTGGTGCGCA
AGCGGACGCGCCATTTCGTGCAGATAGGCCTGGTCGATCACGCACGAGTCCTCCACAAAGACTGATTGCGGCACAAGCCGTAAGACGACCACGCGT
-35 (PalbXIX: operon 5) -10 (PalbXIX: operon 5)
17620 GCATTGACGCTCACAGCTACCGCATCGATCCTGTTACCCTGCGTTTGCTCGATGCCCTGTGTCAGGGCGTATATTTCACCGAACGGTCACTACATC
CGTAACTGCGAGTGTCGATGGCGTAGCTAGGACAATGGGACGCAAACGAGCTACGGGACACAGTCCCGCATATAAAGTGGCTTGCCAGTGATGTAG
RBS
17716 AGGTTTCCACCCATGCCGGCCAAGACCCTTGAAAGCAAGGATTACTGTGGAGAAAGCTTCGTCAGCGAAGATCGCTCCGGGCAATCGCTGGAGTCG
TCCAAAGGTGGGTACGGCCGGTTCTGGGAACTTTCGTTCCTAATGACACCTCTTTCGAAGCAGTCGCTTCTAGCGAGGCCCGTTAGCGACCTCAGC
M P A K L E S K D Y C G E S F V S
albXIX

FIG. 7B

FIG. 8


XALB2
0
1
2
3 kb
E
pAC389.1
H
E
orf1
orf2
orf3
XaAM37
XaAM10
pAM37
PR37
pAM10
2.986 bp
XALB3
0
1
2
3
4
5
6
7
8
9
10
11 kb
E
pALB639A
Sa
Sa
S
pEV639
2,614bp
XaAM12
XaAM36
E
pAM36.2
pAM12.1
9,673 bp

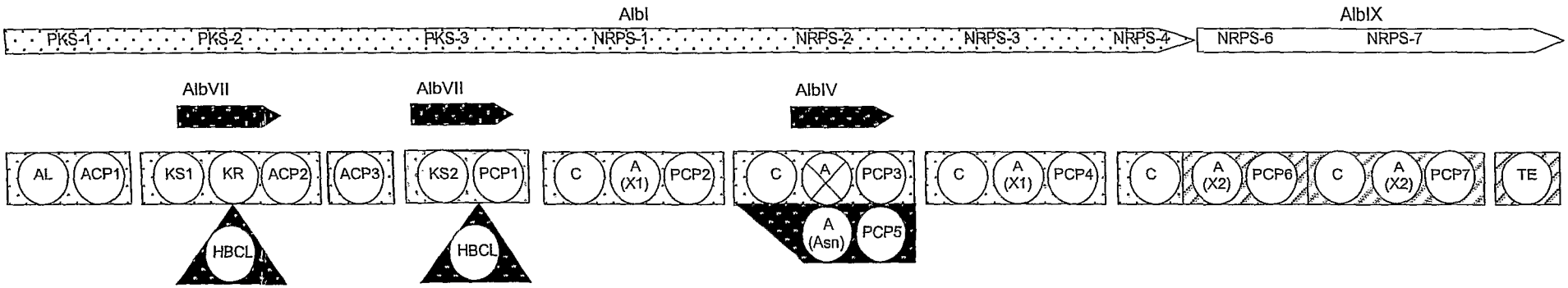

AlbI
AlbIX
PKS-1
PKS-2
PKS-3
NRPS-1
NRPS-2
NRPS-3
NRPS-4
NRPS-6
NRPS-7
AlbVII
AlbVII
AlbIV
AL
ACP1
KS1
KR
ACP2
ACP3
KS2
PCP1
C
A (X1)
PCP2
C
A
PCP3
A (Asn)
PCP5
C
A (X1)
PCP4
C
A (X2)
PCP6
C
A (X2)
PCP7
TE
HBCL
HBCL

FIG. 9A

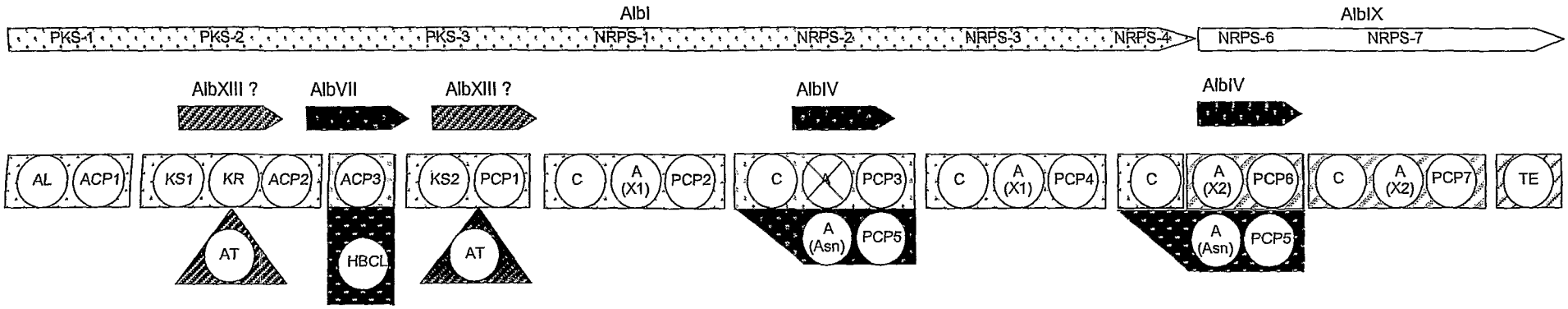

AlbI
AlbIX
PKS-1
PKS-2
PKS-3
NRPS-1
NRPS-2
NRPS-3
NRPS-4
NRPS-6
NRPS-7
AlbXIII ?
AlbVII
AlbXIII ?
AlbIV
AlbIV
AL
ACP1
KS1
KR
ACP2
ACP3
KS2
PCP1
C
A (X1)
PCP2
C
A
PCP3
A (Asn)
PCP5
C
A (X1)
PCP4
C
A (X2)
PCP6
A (Asn)
PCP5
C
A (X2)
PCP7
TE
AT
HBCL
AT

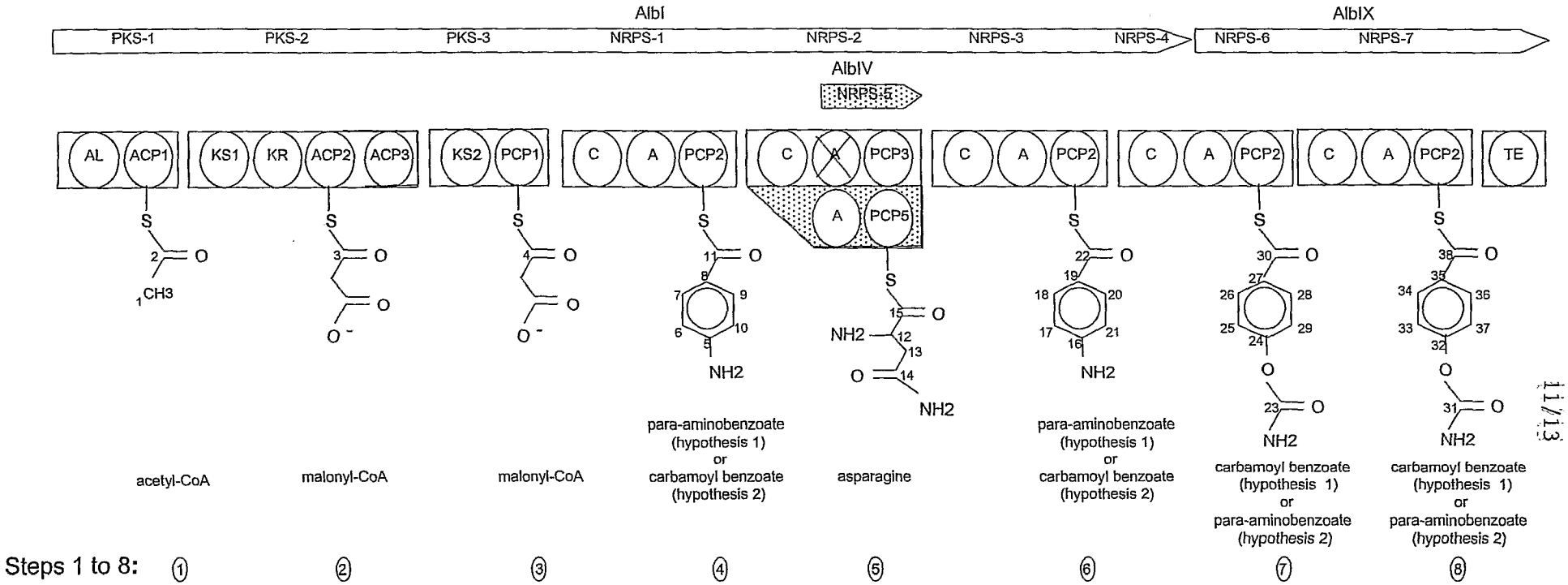
FIG. 9B

RifA-1 LGRVDVLQPAC**FA**VMVG**L**AAVWESV**GV**R**P**DAVV**GHS**Q**GE**I
RifA-2 LDQTMYTQGAL**FA**VETA**L**FRLFESW**GV**R**P**GLLA**GHS**I**GE**L
RifA-3 LDRVDVVQPAS**FA**MMVG**L**AAVWTSL**GV**T**P**DAVL**GHS**Q**GE**I
RifB-1 LDRVDVVQPAS**FA**VMVG**L**AAVWESV**GV**R**P**DAVV**GHS**Q**GE**I
RifE-1 LNQTVFTGAGL**FA**VESA**L**FRLAESW**GV**R**P**DVVL**GHS**I**GE**I
BlmVIII ADDTRAAQPAL**FA**VEYA**L**ARTLMDW**GV**R**P**AAML**GHS**L**GE**V

FIG. 10A

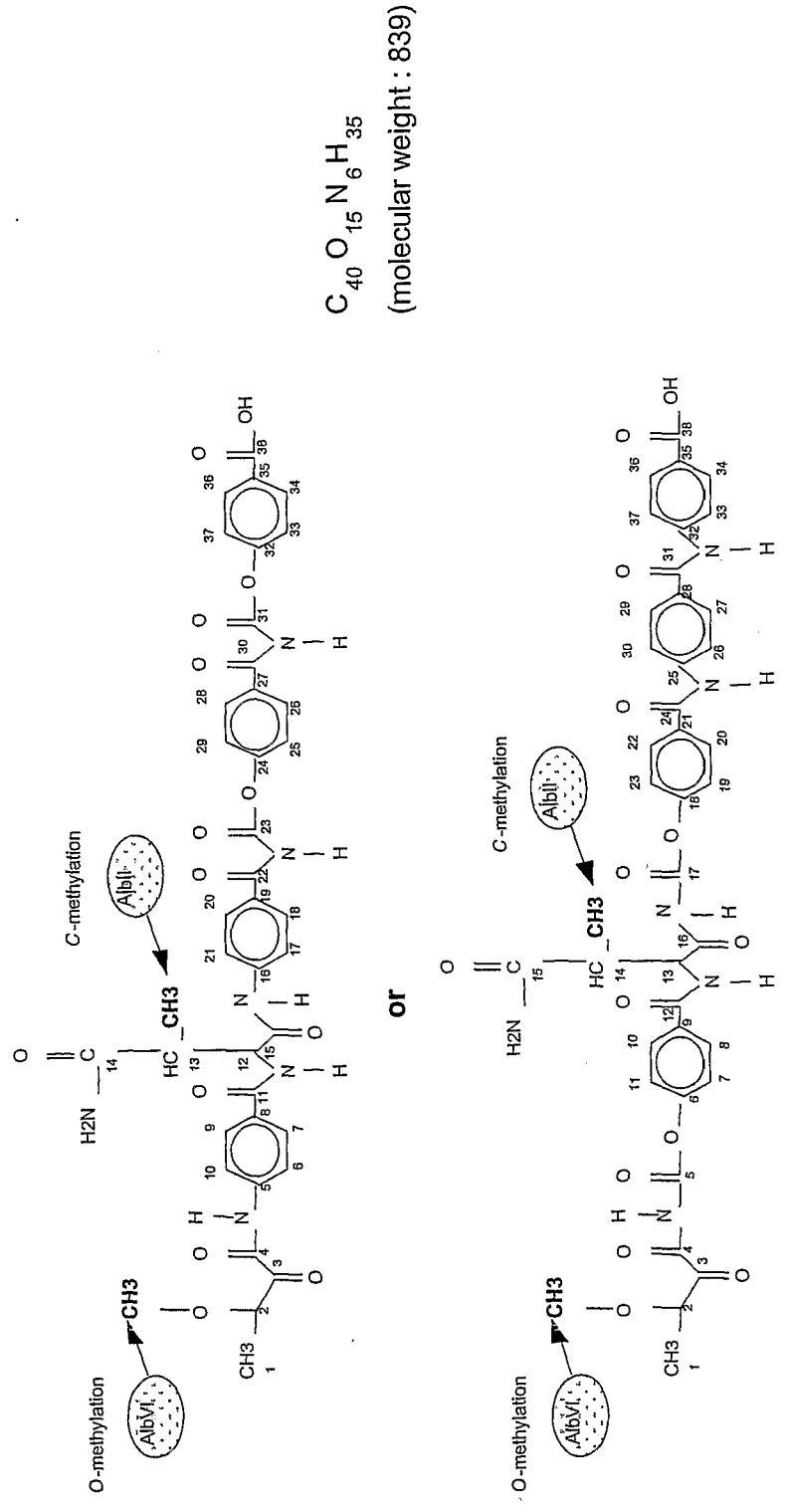
AlbXIII LEDRPRHIRAVIDTLTGHAQFGPAIQAHNVAVI**GHS**V**G**GY
FenF TRTMNAQPAILTVSVIAYQVYMQEI**G**IK**P**HFLA**GHS**L**GE**Y
LipA PDSRGRQLLAALDYLTGRSSVRGRIDSGRLGVM**GHS**M**G**GG

FIG. 10B


AlbI
AlbIX
PKS-1
PKS-2
PKS-3
NRPS-1
NRPS-2
NRPS-3
NRPS-4
NRPS-6
NRPS-7
AlbIV
NRPS-5
AL
ACP1
KS1
KR
ACP2
ACP3
KS2
PCP1
C
A
PCP2
PCP3
PCP5
TE
acetyl-CoA
malonyl-CoA
malonyl-CoA
para-aminobenzoate (hypothesis 1) or carbamoyl benzoate (hypothesis 2)
asparagine
para-aminobenzoate (hypothesis 1) or carbamoyl benzoate (hypothesis 2)
carbamoyl benzoate (hypothesis 1) or para-aminobenzoate (hypothesis 2)
carbamoyl benzoate (hypothesis 1) or para-aminobenzoate (hypothesis 2)
Steps 1 to 8: ① ② ③ ④ ⑤ ⑥ ⑦ ⑧

11/13

FIG. 11A



$C_{40}O_{15}N_6H_{35}$
(molecular weight : 839)

FIG. 11B

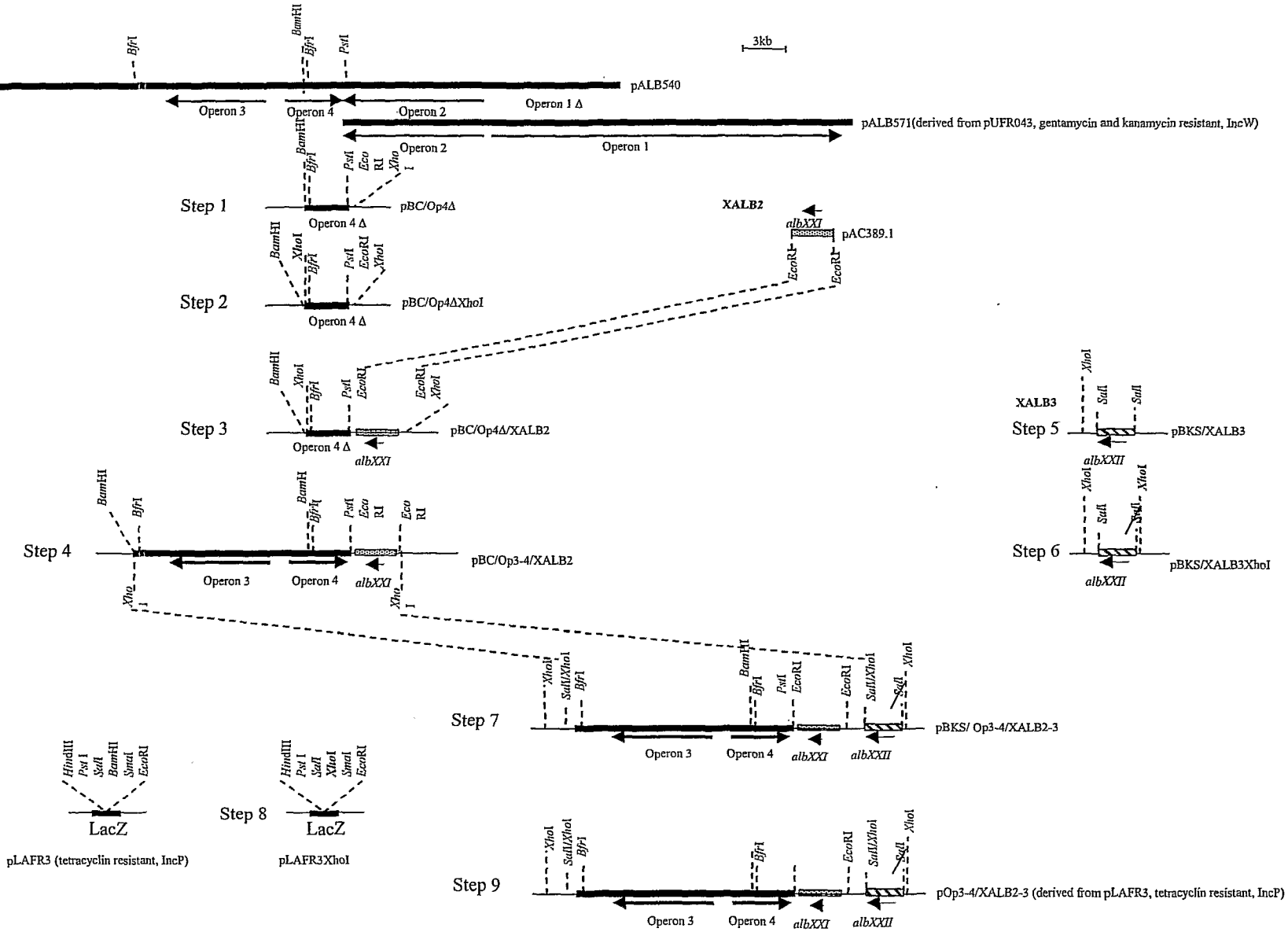

XALB1
BfrI
BamHI
PstI
3kb
pALB540
Operon 3
Operon 4
Operon 2
Operon 1 Δ
pALB571(derived from pUFR043, gentamycin and kanamycin resistant, IncW)
Operon 1
EcoRI
XhoI
Step 1
pBC/Op4Δ
Operon 4 Δ
XALB2
albXXI
pAC389.1
Step 2
pBC/Op4ΔXhoI
Step 3
pBC/Op4Δ/XALB2
Step 4
pBC/Op3-4/XALB2
XALB3
SalI
Step 5
pBKS/XALB3
albXXII
Step 6
pBKS/XALB3XhoI
Step 7
pBKS/ Op3-4/XALB2-3
HindIII
Pst I
SalI
BamHI
SmaI
LacZ
pLAFR3 (tetracyclin resistant, IncP)
Step 8
pLAFR3XhoI
Step 9
pOp3-4/XALB2-3 (derived from pLAFR3, tetracyclin resistant, IncP)

FIG. 12

SEQUENCE LISTING

<110> University of Florida and Centre de Coopération Internationale en Recherche Agronomique pour le Développement (CIRAD)

<120> Complete Biosynthetic Gene Set for Synthesis of Polyketide Antibiotics, Including the Albicidin Family, Resistance Genes, and Uses Thereof

<130> UF-398XC1

<150> US 60/419,463
<151> 2002-10-18

<160> 54

<170> PatentIn version 3.1

<210> 1
<211> 55839
<212> DNA
<213> Xanthomonas albilineans

<400> 1
gaattctttc gccattgccc gggattgatg actggcatcg ggattgtcgg gaccttctct 60
ggcttgttgc tcggtctgca tcagttcgcg gatgctatcg cgccgaaggc caccgcgttg 120
gctactccgg tgcggcagat tggagcgatg ggacatgcac ccgctagcgc ggccagtgcg 180
ccgatgactg gcggggtgtt cgtctctttt tccgcaacgc cggtgcgatt gcccgcggta 240
acaggcatga aggttctcaa tgagggccat gacggcatgg cgggcgcggc tatcactcat 300
gcggcggtaa aaccggtgat ggctccattg acaggggaca tgttgacagg cgcgttgagc 360
tgcctgctgc acagcgtgtc gggcgctttc ctcgtttcgg ccattgcggt gttgtgcgcg 420
cttttgacca cgttcgtcga aaagttacta gtggcgcaat gctttcatca gcttcaggaa 480
ctgtcgtcga cgattgaccg actgttcgca tttaatcctg gcgacgatcc gatgatgcgt 540
ttgacgttga cgtcggaatc gacagagcgg ctaatcaagc ggatcgcgct tgcattagac 600
gacattgcaa tttcgcgaga tcaagttcag tgagatttta tcgatacgga tttcctgtgc 660
ggcgtgacgt cgagcgtggc caggaagaaa gccccttctg gatttcgctg tcagacatga 720
tgaccggcat gaccgcgctt tttctggtgc tggcctgcag catgctgcta atgcgcatca 780
ccgaatcgaa atcgcccagt ggaacgtcgc ccagcgacga gaaagtcgtt gataccgccg 840
cgccgacgca gcgcaacgag cgttccgtgg gtgcggcagt gaacgcttcg catgatgcga 900
accgacttgc tacctacgaa tcggatattt ccaccgtgtt gaaaaatata tcggcgttat 960
cgcagaaata cggattttcg gtcgatgcta ccactaacac gatcgatctc ggccagtcgg 1020
ggctattccc gcttggaagc gaccgcttga gcgcgacaca ggaaaggttg ctgcgcaatt 1080
atgtcgccga tctcatcgca ctgactcaga acgatccggc catggcacca ttgaagagca 1140
tcaccgtggt cggctataca gatccggctg ggtcgtatct gttcaatctc gatctgagtg 1200
cgcgccgcag cgaacgcctg atgtgcgtgc tacttgccac gctggaaaaa cagagtagca 1260
cgacaggtgc accgacgatg accgaggact cgctgcagac catccggcac ctgttcaggg 1320
ttggcggcta ttccgccgac gcacagaagg aaagtgccgc agcaagcagg cgattagcgt 1380
tgaagctgga tttttacaag atcgacgagc cccggcggca agccgctgtg cttgcgatgc 1440
cggtcgggtc gtgcgcgctt ggatcgcgtt agggaaggtc tgaataaccc cctccccagt 1500
aatgcaattt attgatttta taggtgtgaa taagagcgga taacaaaaca tagcgagcga 1560
ctctcaggcg taccgcgcag cacgcaggaa ccggtgtgta cgagtggtac ataaggaatc 1620
cgagcacagc acgcgcccgt ctggcggaca cgcagtagtt ttgttagctg ctctaagcgc 1680
aggatgaggt taatcagagc atcactaaca ggaatgatag tttggaaacg ataacaagta 1740
ttgcgccgtg cgcgctgccg gatgtctggc gtcatgccgc cgaaggcaag accgtcgcct 1800
cgttcgactg cttcgatacg ctgctgtggc gtggcgtgag cgcgccgagc caagtttttt 1860
gtgagttggc cggcaagccg ccgttttcga cgcaaggcta taccgcctac catcgcgtga 1920
tggccgaatc gttggcgcgt cgtgtccggt ttgaacagaa agaggttcca gaagtcacgc 1980
tgcgcgaggt gtatcagcag ttattcccgg agcctgacga tgcaacccgg ataacggcat 2040
gcatggcgtg cgaacaggaa gctgaggcat cgatctgctt cgtcgtgcca gctgtgattg 2100
cctgcatgcg cgaagccagg cgcttgggga tgaccattat cgtcgtcagc gatacctatt 2160
ttaacgctgg ccagctgcgt gcactcattg cgtcagtgtc gcccgaagcc gacgagctgg 2220

tcgaccggat cttctgctct tccgactatc ggaccatgaa gaagtaccag ctatggcacc 2280
gcgtgctcga cgaactgtac gcagcacctg aaacaatcgt gcatttaggc gacaatcgcg 2340
tcgccgacat actaatgccg tcgaagctgg gcatcgcgtg cctgtggcta gatcggtatg 2400
ccggtgcagc catgaccgtg ttgcgccgac gcgaatgcgc gacccgattg atattcagcg 2460
gcgttgaaga gactcggtcc gtgtggacac tttacgacgg cctcgactgt cgaacgcaag 2520
ccgagcgttc gaactggcat gatgaactcg gctggcactt tcttggaccg gtggtctttg 2580
cttttgcgaa aacgctggcc gacgaatttg ccggccaaac acacggaatt gatcagccga 2640
cggttcgctt cgggtttctg atgcgcgatg ctcatctgtt acgcgaagct gcggatatcg 2700
tcgcacctca tgagccgcat ccgtcattgc acatcagtcg aaagaccgcg ttctctgcgt 2760
ccttcgatag tgacgatgcc attctgcatt tcgtcaagtt gggcaggctc gaatatcggt 2820
tgagtgccgc gcaatgtggc gtctgtctac ttctgaacga ggtagagaaa gcgcgtctgg 2880
cggaagcgtt catggcaaaa gaagacacag caggtgcaat gcgggaattt ttttctccgc 2940
agatgttgga cgctatcaag acgcgttcga aagcgttccg tgccaggctc atcaggcaca 3000
tcgtcgcgca gacaggactc aagcgcggcg acacattatg tctcgtcgat acaggttata 3060
atggaacgat tcaatacttg ctgcatgatg tattgcgtaa ggaaatgaac gtcaccgtca 3120
tcggacggta tctaatctac cggcagaacc tcagactgca cggaagggca tcgggcctca 3180
tcgacgaatc gtggctcgac cacggactga ttcatacgct ctcgcagtcg ggtctgtcgt 3240
atctagaggc gctatgcgcc ggtgctggcg gctgcgttgt cgactatgcg cagaatgggc 3300
gctccgtctg caatgcggag atggtctgcc gctcgccatg gatagacgca tgccagcgta 3360
tggcgctgat gttcgtcaat caggtttgcg cctcatccgc gtccgagctg ccgaagctga 3420
cgcgtagccg tttacgcgag tccgcattga cgaacatcag cgccatgctg tttttcccca 3480
gcgagtgcga attgtccgag atcagtcaga tgcaggggga agtgaatctc ggcgccgata 3540
tctgccacag cctgtgcgat ccagaaaaag gcctgagtgg attgcggcgg cgggggctgc 3600
tttatatgac tggcggtggc gagtttcgga gcaattggcc ttttgagctg cgttatgcgg 3660
gcgcagatca gctggccctt tacatggcgt gctttcgcaa cggtttgcgg atgaccgagc 3720
ctgcgttttc ttaccgccac attacattgc cgctgacatt cgcatttgaa gcagacgtcg 3780
cgcgtcgatg cgtgcccgca catgcgacat atgatggata ttacactgcc gtttttccac 3840
ttagccaagg taaggtgtac gttgaaatcg gcgctgtcgc acagtggttg caaatcgaat 3900
cggtgaccag ctttccagct gaggcgtacg gctatatatc tgagtccagt gggccacaac 3960
tgcgcttcga gtcaaccgat tatatatttg atgacgtgac gcgccatggt aacggactgc 4020
tggagtgcga tcatgccgcc gtaatgacgt ttgcgccgat tccggaagga acgtcggatt 4080
acatccggct ggtattccgc cctataaccc ttcgcgacga cccacagcta actgcgtggc 4140
ccgccgacca gcaactcgtt gccgtcaacg gtgtggatag ccactgcggc ggcaaagaca 4200
agtcagcgcc gatacccagc tatgcggcgc ttatcgacgc aaaactggct gcgatcggat 4260
cggttctgaa caccgcggtc tataccggat tgtaatgagc aagggaaaat acttttgag 4320
gatttaatat ggatggtgca gtatttcacg gctaccacac cggaggtatc tacaatgcag 4380
gcaagtttga ggagcggcgt tatacgacca taggtattga tggatacaat aggaggctcg 4440
cgggtgagtt ggagtggacc aacaacgttt atccgcgtcc ctatggccct tccgttgacg 4500
attgggtgga tgaacgcgat agggtgccaa aagagcggcg tgtcaaagac gattatcgcc 4560
atccccggtt ttttgccaaa cccaccacga gcgcggcagt ggaggagtgc aggccggctt 4620
cgggcgtcgt gcagcaggcg cggcggctgg acaatgcgag cgcgagccct cttttcgctg 4680
caagcgcggt gcgacgagga atccggtcgt gtgtcccgtc gaatctgcca ccgagtgtcg 4740
ccgtgggcca taggctagca ggaccattgg catctgagta tattcaaaac tcatgcttgc 4800
tcgtcaatcg gcctgcaagt acgtttgtaa cgttagggag tcgtgttacg gcagggcatg 4860
ccctatcgga catcgccagc ggtgcagacg cgaccaaccg cccgcgcaac gtgaaaggca 4920
aacatgaaaa agacgacatg acccaacggg gccaacataa tgcaggcggt cttgtggcga 4980
gaatcaaggc gaatattcgg aattatatcg atgcaaagtt acgccggtat cctgcaagtc 5040
ggacttgagc tgataaatga tgaacgcggt gattcctgta attaaaattc ttaccactga 5100
tgtcactggg ataaattttt cccatcctcc cactttcgca cagaacggga agactttgaa 5160
tagactctta gaactcctgc gcctaccact tcaaacggag ttttcgactg cgcgagatgc 5220
taccgcgtct ggctcgcgcc atgatgctgc accaagctca tgcgcagccg gtcttgcgga 5280
tggccagtaa ttttcatagc cgagaatatt tactaataaa taacataata gcactatctc 5340
atcgccatca tcagaataga tgatcgattt tatttattaa caaggtaatt atatatgttg 5400
caatacgttg gagaaatttg tgccccacat aatttaagtt atggaaaaaa tatagattcc 5460
tcaagaaata gaatagagat tgaaggtaat gtaaaaattc ccaggcctaa attatgcaat 5520
gaaattgcag ccgttttcag cgcagatcag gccataaatg caaatatgaa aattttgcaa 5580
aaatgcgatt ttggacaatc tacgtctgat acttttagaa aaaaatcttt ttttaaccat 5640
gctagtaatc tagtggggaa aacaatacat ccccaagttg cagatcgctt tcgctcggaa 5700
gtttcctttg atggaacggg taaaataatt ggattcaaaa aggaaatttc aaataataaa 5760
tttgattttc taataaaaaa ttgcattcat tctattaatg agactccgca tttaatagaa 5820
aataagatta gaacccctgg ggagtgctta ataaatattg ccatctctct tgacagtgtc 5880

atgccaccaa tcccgcttaa ggatgaaatt caagcgacta taagatatac ttggcttgat 5940
ggtggcttgt cgcgtcaagc ccttgtaaat ttaatcgagc ttatcaagtt gagaaccagg 6000
tttaatgcgc ctgaattata tccaaaaata agaaggaaaa ttgacgatat tgctggaact 6060
ttggagaaag aaaccttcca gacgaaacgg aatgacaatt tctatggtcg ccttttgaa 6120
acgcatttat cagaatattt aataaaaaat cctgattatg cgatgatgga ggtccgtgat 6180
gcagtggctg catttatttt gcaagacttc atatctccac ttttaacgtg caaagggaat 6240
gaagaatcgc aatctgcaat ttgtgaaagg ctagcttctc ttatggaaga tgaccctcct 6300
tcttggcggt gcaatattga atcagttaag aaatttcttg cctctaagag tcaagctgac 6360
tttatagaaa tgatgaaata tcatggcgaa ttttctgtgc cattgattct ttcgatagca 6420
gtgaaatata ttactatcgc gccaggattg caagagctta aaaataaagc gagtgaattt 6480
tatattgaaa aaatcattcc gcaacgcaag cttcgcaatc ttatattaag taataatgct 6540
cataataaaa aatccaacct ttatggtttg atgcttccat atcaacgtgg agcaaatgca 6600
ggctattcca tgagtggcgg gatcggcatc aggcctattg atcgttatgc actccctggc 6660
gtggaagatg gtatgcatga ggatgatctg gtagcgtcat ccaatgagat aaccattgcg 6720
actggagttt ctggctcatc aaatattctt aattttcttt tcaataaaat tcgaaaaaca 6780
tcaacgaatt ttcctatgga tgccgggaga ttggccgtgg cctcttggct tgcttatagt 6840
ggagggcact cttttaatga agcttattct gtattctcgt acaaaaacgc agggaaattt 6900
aaatcaatct cttttaagag tttagctgaa gactatgatt tgatgaataa aggtgtggag 6960
catgcataca atcaagtact acagacagcc aaacgtttac agaaaccggg gtccgggcaa 7020
ctgccccccc atgtcagagt gtcagcctcc cgtaaaattg atccagccat agctagaggt 7080
ctccgtgcgc actagccacc gaggcgacca acaatgcgca agagcaagtt caccgagagc 7140
cagatcgtcg ccacgctgaa gcaggtggag ggcggtcgcc aggtcaagga tgtatgccgt 7200
gagctgggca tttccgaggc gacgtacttg ctcttccact ggtaataggt cgccgtgctg 7260
atgccgactt ggcgacagat gtctttgact ggaacgcctg cgtcggcctg cttgagcgtg 7320
gcgatgatct gtgtctcgtt gaacttcgat gtgcgcatgg aacctcctga cttgggaacg 7380
atgccagaaa gatctactta tgcggtgtct gcggatcggg ggagcttacg catccagcct 7440
gggtaagtcg cagcagaaga gaagcctaca tcgagaacag tacgttatgc ctagtggttt 7500
ggttcggccc ttgtttgaca cgatcagccg ctaggaaccg ccgccatctg ggttcgccgc 7560
ataagcctac ttttcgatca gtacgtcatc gatgaacatc gcgtccagac cgctggtgaa 7620
gaagatcgac agcgcatcct ccactgaatg ggcgatcggt ttgcccatga cgttgaagct 7680
ggtgttaagc accaggggaa tacccgtcag gcggtagaat tctttgatca gggcgtgata 7740
gcgcgggttc caatgttgct tcaccgtctg cagacgtccg gtgccgtcgt ggtgcacgac 7800
gcccggcacc ttgcgcgtgg cttccgcacg gaacttcagg gtgcgctcca tgtagggcga 7860
ttcctggtac agctcgaaat actccgcgcc gtgctcatgc aaaatcgacg gtgcgaacgg 7920
gcggaactcc tcgcggaact tcacccgcgc attgatgatg tccttgatcg caggcgaacg 7980
cggatctgca aggatcgagc gattgcctag ggcccgtggc ccgaattccg cgcggccttg 8040
cacccaggcg acgatcttac cctcggtcag cagccgggcc gcgcgttgtg ctgcgtcgtc 8100
gaggcaacga gtgaatttgg atagcgcgcc gaagcgctcc acgttatgca aggtctccgc 8160
actcatgctg ctgcccaggt agggcgattg ttcgcgcgca gccggcggtg tctgctcagg 8220
atggtcctcg gcgtgtgccc ataatgcggc gcccaccgcg ttaccgtcat cgccaggggc 8280
ggcgaatacg tgcagatgac ggaacggagt ttcagccagc acgcggccgt tagccgagga 8340
attgagtgca cagccgccgc ccagcaccaa gtggtcggac aagcccaaag cgtgcaggtt 8400
gtgcaggaat tcgaagagga cgtcgcagaa cacctgctgg ccggcatagg ccaggttggc 8460
caattcgatc gttggctggc ccttgcatcg gcgcattgca tacagcgtgc gctgcaactg 8520
gctgaattgt gctgcgggcg caaacctcag cgttaggccg tcgacgcgta gcatctggcg 8580
caacaactcg tacagttgcc gatcatgttg cccgtaggcg gccaggccca tcaccttcca 8640
ttcttcgccg gacagggtgc cgaagccgca aacctcgcag atcataccgt agaagaagcc 8700
caggctggcc caactgctgg tctcgctttg gtggatcggc gtaagcttgc cctgttggta 8760
gtggtagcag gccaaagcat ttttttcacc catgccgtcc agtactgcgc acaccgcctc 8820
ctcgaacggg ctggtgtagc agccggccac cgcgtgggtt aggtggtgct cgtaatgacg 8880
gtagctgggt ggcttgaagg caggctcggc catgtggctc aagtcatatt cgagcaggtg 8940
tccggggtgc tccaccatcg ccagctgcga acggtagaag aagctctgtg ccacgaattg 9000
cttgttgacg tgccaaggca ggtcgccgaa ggcgctgcgg tattggtcta ccgcttgcgc 9060
ggtcttgccc aggccctccc gcatcagttc aggtgtttgc ccgctccaac tagtagcgac 9120
gaccagttcg gcgccgggat cgccgtattc gtggaccagc ttgatggcgc gctgaaacac 9180
gtccggggca acgccgattg aacgcttgta ctgcaggtag cgctcggtgg cctcggcaaa 9240
gcgcacctga ccatcgtcgc cgacgatagc gatggctgaa tcgtggaagg aattggcgag 9300
tccgatgtaa gtgcgcttca tgtccgattc cagtgaaggg gacgatggat gcttccggat 9360
gcctacggcg atgattgtgg cgcaaattgt gtcagtttga actgcaatcc cagcgtagag 9420
agcgccacga aagcattggc cgcgatgtag tacaccaccg tagccccgaa ggcctgcttg 9480
aaagccagag ctacgcctgc cggcccctgc agatgctggt gcaggccgct aaagaaaatt 9540

tccgagacca gggcgatgcc cagcataccg ccgacctgct ggatgacctg cagcgcgccg 9600
gaacctgcgc cggcatcctt cagaggtacc gtacgcatca ctgtctggaa tagcgaggcg 9660
atggtgatgc cacagcccag tccgccgatc agcaacggca gggtaagcgt ccagggatcc 9720
agcgagcctt cactgcgcgt gatgatgacc cacaaggcca gatagctagc gatcatcaga 9780
caggcgccgc tgaagatttt cgcgcgtagg ctttcgacgt gccgagcgag catagaggca 9840
atcgccacgc cgacagggaa aggagtagtg gcgacgccgg tttccagtgc cgaatacgcc 9900
agtccttgct gcagaaagat cacgaacacc aggaaaaaac cctgcagcgc cgaatagaac 9960
accgacacgg acaaggcgcc caagatgtag tcgcgatggc tcatcaggta gatcggcagc 10020
agggccgggc gcgccaagtg ggcttgccga cgttgccagg cgacgaaggc caccagcagc 10080
ggaataccga gcgcaatggc tgcaaagcac catagcggcc agccgtatgc gcgtccttct 10140
attagtggga acaccaggca caacaaggcg agcgcggcca gggcgatgcc gacccagtcg 10200
ttatggatgc ccgcatgcgc cggcaccttg ggcacccaga tggcggccgc cagcaaggtc 10260
acgaggccga tcggcacgtt gatcaggaag atcgcgcgcc agccgacgcc gaacgcatcg 10320
atgtggatca gcaagccgct gacgaggggg ccggcgaatg aggccaggcc cgcgaccagg 10380
ccgaacaacg agaaggcggc cgcgcgctcc ttcggagcga acatggtttg cgcgatggcc 10440
atcacctgtg gtgccagcat ggctgcggcc aagccctgca aagcgcgcgc gatgatgagc 10500
acgtggatat tgccagcgat ggcgcagaac gcggacatca agataaaacc ggccacgccc 10560
gtgccgaaca tgcgcttgcg gccgagcatg tcacccaacc gccccaacgg cagcaacccc 10620
aacgcaaaca gcagaatgta tatcgctacg atccattcca gctgttgctc gtccgcgccc 10680
aggttcttct ggatactggg cagggcgaca ttgacgatgc ctacgtccag caagttcatg 10740
aaattggcgc tcagcaacac gatcatcgct ggccagcgcc atcggtagtc gaactgcgct 10800
ccgggtggtg ccatgccggg cggcataccc agcgcttcct tgggtttttg catgttgtgt 10860
gctccttatc cgcttatggc cgcttcagcc ggtcgcatgg tgacggtgag aaaatgcaag 10920
atgtcgcgct ccaactcgcg ctggaaggcg ctgcggtcga agccaggcgg atcgatggcc 10980
gcctcgccca cgcgagcttt catcgcctcg gggaatacgc tgatgaaggc gtagtggccg 11040
gcattgggca ccacgcgcgc ttccagtcga ccatcattgc ctagcgccgt gcgtgtcgcc 11100
acaatcgttt cgtgcgccca ttgatccttt tcaccgacga tgagcagcac cggtacctcg 11160
actttcgcca gggcatcctc gtgcatgtac aggctgaaat ccggcgcaag cgccaccacg 11220
gcgcgcacgc gcggatcagc tgtgaccggc acggccctga tcggtacccg attttgtcgc 11280
accagcgcgg tccaggcggg ttgttcggcg tgttccgggc gatgcgcaaa atcgaccatg 11340
aaaccggtat gcggttcgcc cccggcgatc gctaaggcgg tgtagccgcc gacggagtgg 11400
ccgatcaccg ctacgttatg ggcctgaatg gcaggaccga actgcgcatg gccggtgagc 11460
gtatcgatca ccgcgcggat gtgccggggg cggtcttcca gattctgata gctgtattcc 11520
agctgatgct ggaacaggtt gtcgcccgga tgctccggca aggcgacgat aaagccgtgc 11580
cgtgctaggt aatgtgccag cgtgcgaaac actaggccgg cgctgcgcgt gccgtgcgag 11640
atcaccgcta gcggaaacgg gccggcttcg atcggcgcgc ccagggccac gtccagcgta 11700
taaggtccca tcgccgtatc ccgtgaaggc gtggcggtgg gatacatcac ccacatcggc 11760
accaccctgc tggcatcacc atcggtttcc agtttttggc aacccacata gctattcatg 11820
cgtaccccaa cgaaagaata aaaaacgcgt gccgcttacg ccggcatcag cttatccaga 11880
cttgcaccgg cgggcgccag ccaaacagcg gtacgacctt cgcccagctc cctgcccatc 11940
aagcctcgca cgccggccag atcctgcggc gttggcagca acgcggccag ccgttggccg 12000
tcggcatcgt gcacggggtt gccatctaag tcgaaggcaa gccccttgca cgggccgaaa 12060
tcgcggtgga aacgctcgtg cggcagctgt agctcaaaag ccaggccaag gcgcctgagc 12120
tgttgattcc agcggccgat gatagcgccg acttcggcta tgtattgtcg gcgcattacc 12180
gcattgattg ccaactcggc aggtgcggtg gacgagacca gtctgtcttc gcagcgcacg 12240
tcgacggcga cctccgtacc ttcgagcttg tcgaagttgc gtgggctgcg gatgccggcc 12300
tggtacagga cgcgtgaacg ctccgaaacg tcgtggccga acagatcaaa gatcttcggt 12360
agccaatagt taaggtattt ctgaacgact ggcaagggga tcgcaccggc gtcgaagatc 12420
gcgtgcgtat cctcacgcaa ggtaatctcg gcgcttcgat acagcacgcg ctccaggcca 12480
tccacgccga acttaatatg cagaggttcc tcgaacatca tgaagcgggc ggtgcgtgcc 12540
aacggcagga aagctgactg ggtcaccgct tgaatctggt acttgcctac ccggtcggcg 12600
aagaagcacc acatgaaatg cgatagccag tcttcggtgt ggtagttgaa ggcatcgagc 12660
aggcgcgggt tctgcgcatc gccactcatg cgttgcagca ggccctcggc ggcgtcggct 12720
ccgtcgctgc caaagtattc gatcagcaga tgcgacatcg cccaggtgtg ccggccttcc 12780
tctagaaaaa actggaataa gtgctccagg tcgatcgcgc tgggcaccat ttgcgtcagc 12840
tcgtggctct gctcaaccgc ggcgttttct acgtcacctt gcacggtgac atgatccagc 12900
agcaggtcac gatattcttc cggcacgcac gaccatgcca cctgtccctt gcgctcgccg 12960
aacactacgg tgttgcggtc tggcggcatc atgaatacgc cccagcggta gtcgctgggg 13020
cgcatgcggt gatagcgcgt ccactcgctg cccttgacgc caccggtagg catgcgcagg 13080
ttcatctcgc gatcgtggaa ttcgctgggg ccgcggaggc gccaccattg caggaagcga 13140
acttggtagg aagtcagttg cctgaccagc gcgctgtgtg gatcaaggtc gatattgtta 13200

ggaatgtaca tgagggtcag gccgcgctgt gcatcgaggt aggggcgact tcgccgaccg 13260
tgagcccgat gaagtcgatg atccgctgag ccacggcacc cggatcattg aacagttgca 13320
ggtgaccgcc atgatctagc aggtccagac gcaaagacgg gtcgtgccta gccaactgca 13380
ccgaggcgga gtagtggctg aagctgtcgt ccttgcagtg cacgatcagg gtagggtgcc 13440
tgcccagggc ggtgggcagc aaggcttgca cggattgctt gttctcttcg taggcacgca 13500
tgtagcgcga gaacaccaat gtgctcgctg gatcggctag gtgcagcatg gtgagctttt 13560
cggccaagtc gtcgccgcgt aaaggttggc cgcggtactt gtccaggatg gcggcgagct 13620
ttttggcctg ttccagaccg tgccgctcga tctgaaggta gatcggcaag gcgcaacgtt 13680
cgaattcgga ttttacgatg ggcggcagca ggcccgccgg cgccacccaa gccatgctgc 13740
gtggtgcgaa gccatgcagc gcaatggcat gcacggccaa ttgtgcagcc tgacaccaac 13800
cgacaaaatg gcaatcggcg tagtcgtgtt ggtgcaggat gcccagcagg gtcgcggctt 13860
ggcgatccag atcgaagtct tccgcggtta ccgatgtctg ggcattcggg cagccgatgg 13920
attcccagca caacacatgg aaatgcctag ccagtcgttg cgccaaccgg ctcagcagca 13980
ggtaggacat gccatagggc ggtagcagca ccagcttggg cgatgcctga gcgcctagcc 14040
aatacagctc aagctgccgt ccatcggtag tgcagtattg cgacagcctt acccctgcga 14100
gcgcgtcgtc cagggcggac agatcttgct tttccagata gtgcggcaag caagcacagc 14160
ccatgagttt cctaccctcg cttgaccaca tgacaagact gcgccgtcac cggtggctgg 14220
aaagcttgcg ccggggcgga acacctcacg agtaactcga ttcgaaccca cttccgtctg 14280
gagagctcgc gtcccctaaa ttcttgtcat cgagttcgcg cagcgataag gggcgcatgt 14340
cggtccaggt ttcgtcgata tacgccatgc actcgtcctt accgccagca tagccttcct 14400
tgcgccagcc aggcgggacc tcaagatcgg acggccacag tgaatactgc agttcgtcgt 14460
tgatcagcac cagataagcc tgttcctcga acgtcatcct aaagataccc ccggaaggct 14520
gctgcgaagc acggaagttg ctacatcgca caatgcgatt cagatggacc aagcaaagcg 14580
actatacatg acgtcacttc gaagatgtca agaaaaatag cgcgtgaaga gcacgtaaga 14640
gtgatgtgtt tcgcaccgct gtacgtccca tcgccatcgc ggcaaagctt acacgaaaaa 14700
ttcaccaggg catgcgttca atacgcgggt caaagcaata tccttgcgct tgcagagcta 14760
tgttcgtgcg taaagcgcca aggcagtggg gagcaacacc ttgggtttcg gttgaggtgc 14820
gggtagcaat ttctgcttaa tatccacgcg cggcggtttt tgtcttgccg ggcgtcaact 14880
gtctcatcga gcagtctggg aggctatttt gcgctgcctt atcataaata attacgattc 14940
gttcacttgg aatctcgccg actacgtagc gcagatcttc ggcgaagatc ccctggtggt 15000
gcacaacgac gagtactcct ggcacgaact gaaggaccgc gggggatttt cctcgatcat 15060
cgtttcgccc ggtcccggct cggtggttaa tgaagcggat tttcacatct cgctgcaggc 15120
gctggagcag aacgaatttc cggtgttagg cgtatgcctg ggctttcagg gacttgcgca 15180
tgtctatggt ggccgcatcc tgcatgcgcc ggtgcccttt catggccgtc gctccaccgt 15240
catcaacacc ggcgacggtt tgttcgaagg catcccgcag cgtttcgagg cagtgcgcta 15300
tcactcgttg atggtctgcc agcaatcgct gccgcctgtg ctgaaagtga cggcgcgtac 15360
cgattgcggt gtggtgatgg gcttgcagca cgtgcaacac ccgaaatggg gagtacagtt 15420
ccaccccgaa tcgatcctca ccgaacacgg caagcgcatt gttgctaact ttgccaagct 15480
ggctgcgcgc cacagtgcac cgttacttgc cgggtcggag caggccggca aggttttaag 15540
cgtttgcgcg cccgagatgg tgacaccgcg ggtacgtcgc atgctgagcc ggaagatcaa 15600
gtgccgttgg caggcggaag atgtctttct ggccttgttc gctgacgaaa agcattgctt 15660
ctggctggac agccagctgg tctgcagtcc aatggcgcgc tattcgttca tgggagcggt 15720
gaacgagagc gaggtagtgc ggcattgcgt gcggccaggg agcatggtgc aggaggcagg 15780
cgagcggttt cttgctgaga tggatcgggc gttgcaatcg gtgcttactg aggacgtcgc 15840
cgagcggcca ccgttcgcgt ttcgcggcgg ctacgtgggc tacatgagct acgaaatgaa 15900
atcggtgttc ggcgcgccgg cttcacatgc caatgccatc cccgatgcgt tgtggatgcg 15960
cgtggagcgc ttcgttgcct tcgaccacgc cactgaggag gtatggttgc tggcgctcgc 16020
cgatacggag gatctgtcgg cattggcttg gctagacgcc atcgagcaac gtatccatgc 16080
cattggtcaa gcggctccgg cttgcatttc gctaggcctg cgcagcatgg aaatcgagct 16140
caatcatggt cgtcgcggct accttgaggc aatcgagcgt tgcaaacaac gcatcgtcga 16200
tggcgagtcc tatgaaatct gtcttaccga cctgttctcg ttccaggccg agctggatcc 16260
attgatgctc tatcgctaca tgcggcgagg gaacccagcg ccgttcgggg cctatttgcg 16320
taacggtagc gattgtatcc ttagtacttc accagagcgt tttctggaag tggacggcca 16380
cggcacgatt cagaccaagc caatcaaggg cacctgccgc cgtgccgagg atccccaact 16440
ggaccgtaac ttggccatgc gcctggccgc ctcggaaaag gaccgagcgg aaaacttgat 16500
gatcgtcgac ttgatgcgca acgacctaag ccgcgtggcg gtgcccggca gcgtcaccgt 16560
gcccaagctg atggacatcg aaagctacaa gaccgtgcat cagatggtca gcacggtgga 16620
agcgaggctg cgcgccgatt gcagtctagt cgacctgctt aaggcggtgt tccccggcgg 16680
ctcgatcacc ggcgcaccga agttgcgcag tatggagatt attgatggcc tggagaatgc 16740
gccgcgtggc gtgtattgcg gcagcatcgg ctacctgggc tacaactgcg tcgccgacct 16800
aaacattgcg atccgcagtc tttcttatga cgggcaggaa atacgtttcg gcgccggcgg 16860

cgccatcacc ttcctgtccg acccgcagga tgagttcgac gaagtgttgc tgaaggcgga 16920
ggcgatcctc aagccgatct ggcattatct acatgcgccg aacactcccc tgcactacga 16980
gttgcgagag gacaagctgc tgctagccga gcactgcgtt agcgaaatgc cggccaggca 17040
ggccttcatc gaaccatgag ccgcggcgag agaggtccat gcacaccatt gtgaacggcc 17100
ttcccgcttc gtccatagcg attttcgatc gcggcctaca gtacggcgat ggattgttcg 17160
aaaccctacg gctaggcatc gcgctgccgg acatccgtca gcaggtctgc gaggccatcg 17220
cgactggcgc cgcgccgcgt gccgtggcga aaaactgatc gtgacgcgtg gcagcaccga 17280
gcgcggctat cgttgtcctc tggcggtggc gcccaactgg gtgctcagcc tgaatgaggc 17340
ccccacgctt acgcgcgaac caggacgggc tgctgatgga tacggccggc cgggtggtcg 17400
agggctgcac cagcaatctg ttcctcgtcg agaacggcca tctggtgacg cccgacctgg 17460
gcgtggccgg cgtcagcggg atcatgcgag gcagggtgat cgaatatggc cggcagcacg 17520
gtctcgcctg cgcggtaaag cacgtctatc cggaccagct agtgcgtgct caggaggtgt 17580
ttctgactaa cgccgtgttc ggcattctgc tggtgcgcag cattgacgct cacagctacc 17640
gcatcgatcc tgttaccctg cgtttgctcg atgccctgtg tcagggcgta tatttcaccg 17700
aacggtcact acatcaggtt tccacccatg ccggccaaga cccttgaaag caaggattac 17760
tgtggagaaa gcttcgtcag cgaagatcgc tccgggcaat cgctggagtc gatccgattc 17820
gaggattgta cgttccgaca atgcaacttc accgaggctg agctcaatcg ctgcaagttc 17880
cgcgaatgcg agttcgtcga ctgcaacctg agcctcatca gcattccgca aaccagcttc 17940
atggaagtgc gcttcgtcga ctgcaagatg ctcggtgtca actggaccag cgcacaatgg 18000
ccatcggtga agatggaggg ggcgctgtcg ttcgagcgct gcatcctcaa cgacagcttg 18060
ttctacggcc tatacctggc cggggtaaaa atggtggagt gccgtatcca cgatgccaac 18120
ttcaccgaag ccgactgcga ggatgcggac ttcacgcaga gcgacctgaa gggcagcacc 18180
ttccacaaca ccaaactgac cggcgccagc ttcatcgatg cggtgaacta ccacattgac 18240
atcttccaca acgatatcaa gcgggctagg ttcagcctgc cggaagcagc ctcgctgctc 18300
aacagcctgg atatcgagct gtccgattga gcctggccat tcgctaccgt gtgactgatg 18360
caacctggcg gatgcatccg ccgtcgccgt tgaacacgca gcagaaagac tggctgacac 18420
gcggtggttc gttgaccgcg cacctgcgcc tgttggggca ggtacaggtg caagtgcaac 18480
gggagcacaa agccatggcc tggctggatg aatatcgggt gctcggactg tcgcgctgcc 18540
tgcttgtatg ggtgcgtgaa gtggtcctgg tggtggacgc caaaccctat gtctatgcgc 18600
gtagcctgac gccgctgacc gccagttaca acgcctggca ggcagtgcgt agcatcggca 18660
gtcgcccgtt agctgatctg ttgttccgtg atcgcagcgt gctacgttcg gcgttggcga 18720
gtcggcgcat caccgcgcag catccgctgc accggcgcgc atgcaacttc gtggcacagt 18780
cgcatgcgac gcaagccctg ctggcgcgcc gctcggtatt tacgcggcaa ggcgccccgt 18840
tgctgatcac cgaatgcatg ctgccagcgt tgtgggcaac gctggaaccg gtggcagctc 18900
cgcgccaggc gagtctgagt gcggacggcc cttgccggca ttcagcgcag atcgtctcgc 18960
ctgagtcgat gctggaatag ccttggcatc gaagccctcc gatcaggcat cgaggtccgt 19020
caccagcatg cgcgccagct cacgcagcgg gtcgccttgt aacatgctgt agtgattgcc 19080
cgccgcgctc ttgatctgcg aaagtggtac gtaacctgtg atatccggca gtacctcgct 19140
acccccgcgt ggcttggaca tgtcggcata ggacacgtgt accgcagtct gtgcctggta 19200
cagatgagcg ttaggctgca ggcactgcgg ctcgaaaccg gccaacagcc ccaggtgata 19260
gcgcgtaacg cgcaattgct cggccagcgg tggccacatg cggctttcca gagtaaacct 19320
caggtgtgcg agcagtttgt ccagtgatgc ctggtggcgg ctgtagtcga acacgtgctc 19380
gtcgtcaccg tcggcgaaca gcagctgccg ggcttcgtct atttcagcct gctcgaagcc 19440
gcgcttggcc aacgcggcca acgtattgag cgctgccacg aaggtaagct gccggggctc 19500
gcgcgcatgt accggtatca ggctgctatc gagcaggccc acgtaatcga cgcgcaggcc 19560
gcgccgctgc aattgctcag ccacagccag ggctagcacg ccgccggagg accagcccag 19620
caagcggtag ggcgcaccgg tcgggccagc cagcaacgca tcgcagtagt gcgcggccag 19680
gtcggacaaa tgcgcgaagc ggcgcaccgg ttcgcattgc aggccataga ccctggcaga 19740
gtgccctagg gcggcagcca gatcgatgta gcaatgaatc tggccgccga tcgggtggat 19800
ggcatacacc gccgcgcgtt cggtgcgtag gctaagcggt acgataagac ttaccggcat 19860
gctgccggct tggctttggc gcatgccgcg ctcgacgaca gcggcaaaat cttccagcac 19920
aggggattcg aacagcgtgt tgacccgcac ttcgatgtcg aaactctggc ggatacgcga 19980
gaacaactgg gtggcaagca gcgagtgacc gccgaggttg aagaagttgt cgttgaggct 20040
cacgcgtaag ggggcggcct gtgcgggggt cagcagttcg ctccacagct tggccagggt 20100
gatttcgacc tcgctgcgcg gagcgaggta gtcgctgtcg ctgctggcgg cttgcggctc 20160
gggcaggctc aaggtatcga gcttgccatt gggcaagcgc ggaagcgccg gcagcgactg 20220
gaagcgcgtt ggcagcatgt aggtaggcaa gcgttcctgc agcagcttgc gcagctcgtc 20280
gaggttcagg acaccctggc gtggcaccac gtaggccaac agttccggcg tgggcgagcc 20340
ttgcggccaa ccgatcacgg cggcctcggc gacctgcagg tgggccgcca gggctttctc 20400
cacctggcgc acgtccacgc ggtagccgcg gaccttgacc tcgtagtcgc gccggccgag 20460
cagttccagc gtaccgttgt ccagtaggcg ggccatgtcg ccggtcctgt acagacgcga 20520

gccgggggcg ccgtagggat tggcgatgaa gcgcgcggcg gtcaggccgc cctggcgcca 20580
atagccgtgc gtaatgccga ggctttcgat gtgcacttcg cccatgatgc caggcggcaa 20640
cggtcgcagt tgttcgtcga gcacatggac cttggtattg gcgatgggcc gtccgaccgg 20700
gacgaagccg ctgccgctgt gctgctcggc cggatcgcaa taggtcatgt cgttgatttc 20760
ggtacacccg tagatgtacc aggccgtgca ggcaggcagc agcgtcctga gccgttgcag 20820
cagttccgcc gggcagggtt cgatggagac gaagagctgg cgcagtcgcg ccagccgctg 20880
cggtgtctca gcaacgtggt cgagcagcgc gttgagctgg gaaggaaagg tatacaggcg 20940
tgtgatctgc caggtttcca gcgcgcgcac gaaagcgggg atgtcacgca cggtatcctc 21000
gtcgatgaac acctgcggta cgccagcaag taggccggcg agcagttcct tgaccgaaat 21060
ggcaaaggcg atcgaggtct tttgcgccac ccgctccccg gcctcgaaag gcgcacgtgc 21120
ccacagcgca tgcagccagt tgaggatttg ccgatggggc accatcaccc ccttgggacg 21180
accggtggaa ccggaggtat acatcacgta ggccagctgc gccggatgca gggcatgcgg 21240
cagtggcgta tgcggttgac gagcgatggc ggcatcgtcc aggcgcagcc gcggtacttg 21300
gatcagttgc ccgtcgatgt ccttgccgca gagcaacagc cgtggctgcg cgtcgtcgag 21360
gatctgctga atgtaggtgg tggggtaatg cgggtccaac ggcacgtagc agccaccggc 21420
cttgagcacg ccgagtaggg caatgaggaa atcgggcgag cggccgaacc acagggcgac 21480
gcgctcctgc gggcgcaggc cgcgctcgat caggcaatgc gccaggcggt tggcgtgttg 21540
gtccagttgg gcatagctca actgtcggtg ttgatcggca caagccagtt cctcggcgtg 21600
cagtgccact tgcgcatcga acagatccag cacactgcgc gaggtatcca gagtatgagg 21660
ggtgaactcg gtgcgagcga ccggcagcga aaaatccgag aggcggcagc gcggttcttc 21720
cagcatccgc tccagcactc tttggtggtg ggccagcatg cgctgaaccg tagccgccga 21780
aaacagctcc gcggcgtatt cgacagtgac ttccaggtgg cttccgtcgc cgatgaactg 21840
caggtccagc tcgttgggtg tggtgcgttc gccaaattcc atctgagcgc tgaggaagat 21900
ctgggcaaat gcattgacgc cttcggtggc gaaattttgg tgtcggagca tgatcggcac 21960
gagcgggatc tggctgctgt cacgcggttt cttgagagcg cttaagacat gctcgaacgg 22020
cagtgcgcga tgcgcgtagg cgtccagcac ttgctggcgc acgtgctgca gaaaatcctc 22080
ggcaaaggcg tgactgccca agtttaggcg taccgccagg atattgacga aaaagccgat 22140
cagattctcg gtttccagct gatcgcgtcc ggcgctggta gtacctaagc agagttctcg 22200
ccggccggtg tactggtgca agacgatcgc caggctcgcc ataagtgtca tgaacaaggt 22260
gacgcgccgt tcctggctga atgcggcgag acgcgcggcc aaggcgtcgg gataggtcag 22320
gtgtagtatg ccagcacgcc aagctcgatt agccgggcgt ggaaaatcgt agggcaaggc 22380
cagcccttct tcgtaaccat gcaaacgctg tttccaataa tccagatcgg cgctgaaatc 22440
ctgtacgcgc tgccatgtag catagtcggc atattgcagt agcagcggtg gcagtgccgg 22500
tggcgtctgc tgtagcgcgg ctatatagaa agcacgtagg tcgtgaaaga tcaggttaat 22560
cgaccagccg tcgcagatga tgtgatgcat gttcatcagg aacacgtggt aatcgtccga 22620
tacgcgcagc accgatacct tgagcagcgg gccgtgggca agatcgaata cgtgcgcggc 22680
gtgctcggcg actaggcgtg gcacttctgc gggtgtcgct gtgatgcaag gcactgggac 22740
ctgcatggcg tcggcgatgt gctggctggg ataatcgccg ccagcgcaag ttgctatgcg 22800
ggtgcgcaag gtttcatgcc tggccaccag cgcctggatc gcctcgcgca gcgctgacat 22860
cgagaaatcg gcactgcgta aatggcaggc gaaggcgaca ttgtaactgg tacgttgctc 22920
gggcatgtgt tcatgcacga accacaggcg ctcctgctga tagctcagcg gaacgggagc 22980
atcgcgcacg gcacgggaag agatggtgtt gccgccagtc ggagcctgtt gttgccgcgc 23040
ttcgttgacc actcgcgcaa aatcttccag cacaggggat tcgaacagcg tgttgacccg 23100
cacttcgatg tcgaaactct ggcggatacg cgagaacaac tgggtggcaa gcagcgagtg 23160
accgccgagg ttgaagaagt tgtcgttgag gctcacgcgt aaggggggcgg cctgtgcggg 23220
ggtcagcagt tcgctccaca gcttggccag ggtgatttcg acctcgctgc gcggagcgag 23280
gtagtcgctg tcgctgctgg cggcttgcgg ctcgggcagg ctcaaggtat cgagcttgcc 23340
attgggcaag cgcggaagcg ccggcagcga ctggaagcgc gttggcagca tgtaggtagg 23400
caagcgttcc tgcagcagct tgcgcagctc gtcgaggttc aggacaccct ggcgtggcac 23460
cacgtaggcc aacagttccg gcgtgggcga gccttgcggc caaccgatca cggcggcctc 23520
ggcgacctgc aggtgggccg ccagggcttt ctccacctgg cgcacgtcca cgcggtagcc 23580
gcggaccttg acctcgtagt cgcgccggcc gagcagttcc agcgtaccgt tgtccagtag 23640
gcgggccatg tcgccggtcc tgtacagacg cgagccgggg gggccgtagg gattggcgat 23700
gaagcgcgcg gcggtcaggc cgccctggcg ccaatagccg tgcgtaatgc cgaggctttc 23760
gatgtgcact tcgcccatga tgccaggcgg caacggtcgc agttgttcgt cgagcacatg 23820
gaccttggta ttggcgatgg gccgtccgac cgggacgaag ccgctgccgc tgtgctgctc 23880
ggccggatcg caataggtca tgtcgttgat ttcggtacac ccgtagatgt accaggccgt 23940
gcaggcaggc agcagcgtcc tgagccgttg cagcagttcc gccgggcagg gttcgatgga 24000
gacgaagagc tggcgcagtc gcgccagccg ctgcggtgtc tcagcaacgt ggtcgagcag 24060
cgcgttgagc tgggaaggaa aggtatacag gcgtgtgatc tgccaggttt ccagcgcgcg 24120
cacgaaagcg gggatgtcac gcacggtatc ctcgtcgatg aacacctgcg gtacgccagc 24180

aagtaggccg gcgagcagtt ccttgaccga gatggcaaag gcgatcgagg tcttttgcgc 24240
cacccgctcc ccggcctcga aaggcgcacg tgcccacagc gcatgcagcc agttgaggat 24300
ttgccgatgg ggcaccatca ccccccttggg acgaccggtg gaaccggagg tatacatcac 24360
gtaggccagc tgcgccggat gcagggcatg cggcagtggc gtatgcggtt gacgagcgat 24420
ggcggcatcg tccaggcgca gccgcggtac ttggatcagt tgcccgtcga tgtccttgcc 24480
gcagagcaac agccgtggct gcgcgtcgtc gaggatctgc tgaatgtagg tggtggggta 24540
atgcgggtcc aacggcacgt agcagccacc ggccttgagc acgccgagta gggcaatgag 24600
gaaatcgggc gagcggccga accacagggc gacgcgctcc tgcgggcgca ggccgcgctc 24660
gatcaggcaa tgcgccaggc ggttggcgtg ttggtccagt tgggcatagc tcaactgtcg 24720
gtgttgatcg gcacaagcca gttcctcggc gtgcagtgcc acttgcgcat cgaacagatc 24780
cagcacactg cgtgaccaat ccaaggcgag cgcggtatcc ggactggccg cggtcagcgc 24840
gacgtcttcg gcatccagta gcgacatgct tgatagtttc atggggcacc gggtcggcag 24900
ggttaaacgt gcagcttgag catggcttcg ccatcgctgc gcgcagcgat gtcaggggac 24960
gattgttcgg gcgaataagg ttcggccatg cacacgagga tcttgcggct gccctcgtag 25020
ggctcgcgtc cgtgcgaaac cagcatattg tcgatcagca gcacgtcgtc ccgatgccag 25080
tcaaaatgga tcttgtgctg ggcgaaaact gtgcgcacat ggtcgagcat ggcggggtcg 25140
atcggcgtgc catcgccgaa ataggcgttg cgcggcagtc cctgctcgcc gaagaacgac 25200
agcatcatct tctgcgcagc tgcctccagc gcagtgtaat gaaacaggtg tgcttggttg 25260
aaccaaactt catcgccggt cgccggatgg cacgcaaagg cccggcagat ctggctggtg 25320
cgcaggccgt cgccggtcca ttcgcattgc atgtcgttgc gggcgcaata agcttctact 25380
tcctgcttgt tgcgggtgtt aaacacgtcc tcccatggca ggtcgacccc tgcacggtag 25440
ttcctgacgt agcgcacctg tttgcgcgca aagatttcgc gcacttgcgg atcgatagcg 25500
gctgtgacct tgagcatgtc agccaacggc gtgcagccgc cctcgctggc cggctgcacg 25560
caatggaaca gcagtttcat cggccagacg cgctggtagg cgttctcgca atgttgcgct 25620
atggacagct gcctgggata ttcggtggcc gtgtagacat gctggccgac gtcggtgcgc 25680
ggtgtggaac gataggtata ggccagtcgc tcatcgaaga aacagcgtga gatctgctcc 25740
aagccaccag ggtgcgcaaa gccacggaac agtaacgccc tgtgttgcca tagcagggta 25800
ggccacgtcg cgcggtgcgt ggcattccaa tcagtcagcg tggcctcggc cgagtcggcc 25860
ttgatggtca ggggaagatc agcgtttgtg tgcatggggc acctaggttc gagcatggcc 25920
gacgaagaac aggtgggatt gcaggtgctt ggcgctagcc agtgtctcca acagcgcagg 25980
ccggattacc ttgccgctgc aggtacgtgg gatcgtgctc acttcgacga atagatgggg 26040
atagtgatgc ttgcctagcg cgttcttgca caaggcgcgt aaggcggccc atagcgcccc 26100
tgtatcgatg ctggcatcga caggcaccac gaaggcggcg gggcggggca agccgaactc 26160
gtcttcgatc aggcagatcg cgcactcctt cacgcaggcg tgcgtctgga tgacgctctc 26220
cagcgtctca ggcgaaagcc aacaaccgtt gatcttgatg gcggagccca ttctgcccaa 26280
gttatggaag cgccccttgg cgtcggcaaa gaacaggtcg cgtgtatcga accagccgtc 26340
gacgaacaat tgggcactga gtatggggtc gccaacatag cccctcgtca gcgtattgcc 26400
cctcacccac aggctgccga cttcgcctat gcggcagatc tctccctgct tgttcaccag 26460
cttcacaaca aagcctggta ccggcgtgcc agtgcaaccc atgagcgcgt ggcctggccg 26520
attggagatg aaggtggaca gtacctcggt gcagccgata ccgtcgagca cttcgacctg 26580
ccaacgcgtg ctgatcgcat gaccaagcct cgccggcaag ctttcgccgg ccgatatgca 26640
caggcgaagc gccggccaca ccgcatccgg cgcggcctcg gcaagcaaca gcttgaacac 26700
ggcgggcacg gcgagcaata cagtgacgtg gtaagtgtgg atggtttgcg cgatctgcct 26760
gacgctaagc ggcgcggcaa tcacatggct gacaccagcg agcagcgaca gcatcaggtt 26820
gttcaggccg taggcgaaaa acaaccgcga cggtgtatac atcacgtcat cgctgcgcag 26880
cccgagcacg gcctgctggt agttgagatg gcagtgcata aaatcggcat gcgagtgcgt 26940
taccgccttg ggcgtaccag tggagccgga cgtgcatatc atcaccgcgg gtgcatcggc 27000
ggagcagggc gcaaccacca gttcgtcgtt ttcgatcacc ggcatcaggc tcgtcagctc 27060
taaggtcggc aggtggcgca acgcggcatg atgggaaggc ggcagttcgg catcgatcag 27120
cacgaggcga ggcttgatgg tcttgagcgt ggtctcaaag tggacgagcg acacaagctc 27180
gtttatcggc gcaaagacca agccaccggc caagcaggcc agcatcaggg caacgcccgc 27240
taggctgtcg atagcaatca gcgccaccgc atcaccgctt tgcaggccaa gcagactcaa 27300
gtgccgggca taggtcgccg cgcgagagcg caactggcga tagctgaagg cctgctggcg 27360
caacggatcg atcatttgcg ccgtcgaagc cagatgcgct gcggaaaaaa tttgcgcgca 27420
cacgttgacc tggaccgacg ggaggaagcc gataggcgca caggcgaaca ccgccgtgct 27480
tgcgtccgac caggacggca tcggcccatc ggtcgagcgt gcgaaccagc tcgcgggcaa 27540
atgactggca atctgacata gtttgccgtg gtcgcaggcc agcagactgg tatccacctc 27600
gatcaggtct tcgacgcagg aaagcgcagg caaagagatc tgcgccgcgc tgccgcatac 27660
ggcactatcg cgcaagtccg gcaggttcct ttggcggtgg tccgcatgcc atagcagcag 27720
gccatcgctg cgtcgcgtgg ccaaggcttc cagtgccatg cccagggcgc cttgcaaccg 27780
gtccagttgc ttgggttcct cgatacggcc caaatccagt gccagggtgt tggcgccggg 27840

gggcgattcg gacagcacga tttggtgccg atgcttgagg taatcgcaaa tcaggccggc 27900
cagcttgcct aaccgtgcat attcccgtag caggctaccg aagctgccac aggggtaagg 27960
tgcggcatag tcaatggtta tgtgctggcc gatcggcgtg tcgctgacat cgatacgcaa 28020
gccaggataa tcgcgccgcc attgatgcag cagcgtggtc cattgacgag cataggcctc 28080
gttgcgccct ggccgcgtct gacctaccga ccaacgcaaa tctagttcgg tgccagagtg 28140
catcggaaga tttgtcagtg ggctatccat aagcgttctc gggtaaggcg atcgacgcat 28200
cgagctcggc tgtgtgcact ggtttggccg gtacgccagc gcgagagact gttcgcaagc 28260
ttcagcgttt cagcgcgtgg accagataac tttgcggcac gccgtgggtg ccgcgcggtg 28320
cgaccggaaa cggccaacgc cccatttgct ggccagcggc ggcgatggtc aacacccctg 28380
gctcccagcc cagtggttgg atcaggcttt ccggttcgtc agtgccaaac tggcgagcca 28440
tcgcgtgcag cactcgggca ttgggcgagt tgagcataga gaggccgata acatcgaaca 28500
acacgctgct gcccttggca ctcaatgcat cgatgcgcgc gaacagcagc atcactgcct 28560
cggcgctcaa gtagcacagc aagccctcga ccagccacaa ggtggcggcg ctgccgacga 28620
atccactctc cttaagtgcc tggggccagt cttcgcgcaa atcgatcggt agcgcaatgc 28680
gctggcaaac gggctgggcg tcatggagtt tttcgtgctt gtcggagagg acatccatgt 28740
ggtcgatctc gtagacccgg gtatcggacg gccaggggag acgataagcg cgtgcatcca 28800
taccggcggc caggatcacc acctggccaa tgccttcact aaccgcctgc atgatcttgt 28860
cgtcgagcca acgcgtccgt acctcgatcg ccggaggcat cggtacgttc tggttgttgc 28920
gtctgagctc ttcaacgaat tcatcgccgg ccagacgccg tgcgaaaggg tcatggaaca 28980
gcgcctgctc ccgctcgctt tccagcgccc gcatgcctgc cacccataaa gcggttcttt 29040
cgatatctct catgcatacg ctccggttcg tggtcggctt gcgccgatgc atcatagata 29100
tgcatgactc gattcgcggc accgtgcctt gatggtggct gcgaagcgaa aacaataacc 29160
aaagggtggt gctcgacggc tttactgtag cgacaccttg tccatcgcct tacggatggt 29220
ctgatccacg caagcgaaag atgagataaa ccacatcagc tgtcaacgcc gatttaaatt 29280
tgacccactt tcctttgaat cgtcgaagta aatctgaccc acccggggtc ttccatcgtc 29340
gggctgctag gctgcgcagg gcaaagcccg tcgcagccca gcagccctgc gccggctcac 29400
gcccgaaggg caggtagccg atctcgtcga ccaccagcag cttcggccct agtaccgcgc 29460
gattgaagta gtccttcagc cggttctgcg ccttgaccgc tgccagttgc atcatcaggt 29520
cggccgcggt gatgaaacgt gccttgtgcc ccgccatcac cgcacgctgg cacagcgcca 29580
gggcgatgtg ggtcttgccg acaccgctgg ggccaagcat caccacgttc tcggcgcgct 29640
cgacgaaggt caggtggccg agctcgacga tctgcgcctt cgaggcgccg ccggcctggg 29700
cccagtcgaa ctgctccagc gtcttgatgg acggcatcct ggcaagtcgc gtcagcaccg 29760
tgcgcttgcg ctcttcacgc gcgagctgtt cgcttgccag caccttctcc aggaagtagc 29820
tggcatcctc gcacgcggcg gcctgtgcga gtgcttgcca gtccgagctc aggcgtgcca 29880
gcttcaactg ctcgcacagc gcggcgatgc gcgcacactg caggtccatc acgccacctc 29940
cagcagggtg tcatacacgg ccagcggatg ctgcaggttt tccactggca gggccactgg 30000
ctgtcgtaag ggaagcggtg ccttgagcgc cggtgcggac agtataacga cacgttcctt 30060
ggccaagcgc actgtcggca cggccttgct gatgccgccc atgtagccgc gcgcctggat 30120
ctcgcgtagt agcaccacgc tggccgggat ccatcgaggg cgcgcttgcc caatgcgctc 30180
atgcagataa ctcttgtagc cgtccagttt gcaggcgtat tgttaggcgt caccgctcgc 30240
gcggcgatcc ccaataaggc gggtatgaga cgcgcatggc cgcccttccc gcaggcgtgc 30300
tgtcgctcta ttgcttacct catgcagaga tcgccaatgt cgccgttaca gcaaacgctg 30360
ctaacccgcc tcgccagtgc ggccgcctcc cggacaatga tcgagtttcc gcgtccggag 30420
cacgcatcgc cacaatgttg cgacgatgcc gagcttgcgc gactgatcgt gcagttgtcg 30480
gcgggactgc aaccgctggc gatgccgggt acctacgtga tcattgccgc gccacatggt 30540
ggtttgttcg cggcagccct gcttgcctgt ttgcatgcca acctggtggc ggtgccgttt 30600
ccactggatg ttgctcagcc aaatgagcgg gaacaggcca ggctggagac gatccacgca 30660
caattgatgg agcatggcaa tgtagcggtt ctgcttgacg atgtcgccga tcgcagtgcc 30720
ttcgcgcgca tggcgcatgc tgcgggcacc ttcctggcga ccttcgccga tctaaagcgc 30780
gaatcgacca gcgcctcctt gtgcccggcg tcgccttcgg acgccgcctt gctgttgttt 30840
acctctggtt cctcgggtga gtccaagggc atcctgctta gccaccgcaa cctgcatcat 30900
cagatccagg ctggcatccg gcagtggagc ttggacgagc atagccatgt ggtgacctgg 30960
ctttctcccg cgcacaactt cggcctgcat ttcggcttgc tggcaccctg gttcagtggc 31020
gcgacggtca gtttcatcca tccgcacagt tatatgaaac gacccggctt ctggctggag 31080
acggttgcgg ctagagacgc cacgcacatg gccgcgccga acttcgcgtt cgactactgc 31140
tgcgactggg tgatggtcga gcagcttccg ccgtctgcgt tgtctacgct tacgcatatc 31200
gtgtgtggcg gcgagccggt gcgcgcctcg accatgcagc gcttcttcga gaaattcgcc 31260
ggactcggtg cgcgtacgca gactttcatg ccgcacttcg gcttgtctga aaccggtgcg 31320
ctgagtacct tggacgaggc gccccaacag cgcgtcttgg aactagatgc cgacgccttg 31380
aacaaacgca agcgcgtggc ggcaggggcg agccaggcgc gtgtgacagt gctcaattgc 31440
ggcgccgtcg accaagatgt ggagttgcgt atcgtctgtc ctgaaggcga gacgttgtgc 31500

agaccagatg agatcggcga aatatgggta aagtcgcctg cgatcgcccg tggctacctg 31560
tttgcgaagc ccgccgatca gcgacagttc aactgcagca tccgtcatac cgacgatagc 31620
ggttactttc gtaccggcga cctgggtttc attgccgatg gctgtctgta tgtcaccgga 31680
agggtaaagg aggtgctgat catacgcggt aagaatcatt accccgcaca tatcgaagcc 31740
tcgatcgccg ctaccgcatc gcctggcgcg ctgatgccgg tggtgttcag catcgagcgg 31800
caggacgagg agcgcgtagc tgcggtgatc gccgtcaatc acccgtggac gccggcagca 31860
tgcgccgcgc aggcacacaa gatccggcaa caggtagccg accagcatgg agtcgccctg 31920
gcggagctag cctttgccga acaccggcac gtgttcggca cctatccggg caaactgaag 31980
cggcgcctag tcaaggaagc ctatgtcaac ggccagctgc cgttgttatg gcatgagggt 32040
aagaaccggg acgtaccagc ggccgccgcg gacgatcggc aggcgcaaca cgtggcggac 32100
ctgtgtcgga aggtcttttt gccggtgttg ggtgtcgcgc cgccgcatgc ccaatggccg 32160
ctgtgcgaac tggcgctgga ttcgctccaa tgcgtgcgtc ttgccggtgc catcgaagag 32220
tgctacggcg tgcctttcga acccacgttg ctattcaagc ttgagacggt cggggcaatc 32280
gccgaatatg tcctggcgca cggacgtcag gcgcccacgc cgacgcgtgc gccggtggca 32340
agcacaacat gctcagagga accgatcgcc attgtggcga tgcactgtga ggtgcccgga 32400
gcgggcgaga acactgaagc attgtggtcg ttcctgcgga gcgacgtcaa cgcgatccgg 32460
ccgatcgaat caacgcgccc ggacttatgg gcagcgatgc gcgcctatcc cggcctcgcg 32520
ggcgaacagc tgccgcgcta tgcgggtttc ctcgacgacg ttgatgcttt cgatgctgcg 32580
tttttcggta tctcgcgtcg cgaggccgaa tgcatggacc cgcagcagcg caaagtgctg 32640
gagatggtgt ggaagctgat cgagcaagcc ggtcacgatc cgctgtcctg gggcggccag 32700
ccggtcggcc tgttcgtggg tgcgcatacg tccgactatg gcgagctgct ggcgagccag 32760
ccgcaactga tggcccaatg tggcgcttac atcgattcgg gttcgcattt gaccatgatt 32820
ccgaaccggg cttcgcgctg gttcaatttc accggcccca gcgaagtaat caacagcgct 32880
tgctccagct cgctggtggc gctgcatcgg gcggttcaat cgctgcgcca aggcgaaagc 32940
agtgtcgccc tggtactcgg cgtgaacctt atcctggctc ccaaggtgct gttagccagt 33000
gcaagcgcgg gcatgctttc gcccgatggc cgctgcaaga cgcttgacgc cgccgccgat 33060
ggcttcgtgc gttcggaagg gatcgcaggg gtgatattga agccactggc gcaggcgctg 33120
gccgatggtg acagggtcta cggtctagtc cgcggcgtgg cggtcaacca tggcggccgt 33180
tccaattcct tgcgtgctcc caacgtcaac gcgcagcggc aactgctgat ccggacttac 33240
caggaagccg gtgtcgagcc ggccagcgtc ggttatgttg aactacacgg cactggtacc 33300
agcctgggtg atccgatcga aatccaggcg ctgaaggaag ctttcattgc gttgggggca 33360
caggccgccc cgtcaaactg cggcatcggt tcggtgaagt ccgcgctggg ccatctagaa 33420
gccgctgcag gcctgaccgg cctgatcaag gtgctgctga tgctcaagca cggcgagcag 33480
gccggcacgc gccatttcag cacgctcaat ccgctgatcg atttgcgagg tacgtcattc 33540
gaagtggtgg cgcagcatcg cgcatggccg tcgcaggtcg gcattcacgg cacactcttg 33600
ccgcgtcgcg cgggtatcag ctcattcggc ttcggcggcg ccaatgcgca tgcgatcgtg 33660
gaagagcatg tcattgccac gccccctcg acgagctccg ctggcggccc ggtaggtatc 33720
gtgttgtcag ccggtagtga agctgtcttg cggcaacaag tgctggcctt gtcagcctgg 33780
ctaaggcagc aatcgccgac acccgcgcaa atgatcgatg tcgcctacac cttacaggta 33840
ggacgcgcag ccctgtcgca caggttggct tttagcgcga cggacgccga gcaggcattg 33900
gcgaggcttg agggtcgtct ggcgggcgtg atggatgccg aggtccatca cggtgtcgtg 33960
gatgctgccg caacggctcc cgaacatggg cggcagacgc gcgaaggtct tgccggtttg 34020
ctgcgagcct ggactcaggg cgtgcgcgtc gattggtcgg cgctgtacgg catacagcga 34080
ccgcagcgcg ttagcctgcc tgtctacccc ttcgctaggg aacgctattg gctgcccggc 34140
caggctatgc atgccgctgc ggacgctcat ccgatgctgc agctgttgca tgccaatgcc 34200
aaactacatc gctacgcctt gcgtaggtcc ggctgcgcaa gctttcttgt tgatcattgc 34260
gtggatggtc gacaggtact accggcagcc gtgcaactgg aattggtgcg cgccgtggcg 34320
cagcgggtca tggcgcagga tgagggttgt atcgaactgg cgcaggtcgc ctttttgcat 34380
cccctcatga tggaggagac tgagctggag gtcgaaatcg aactgtcgaa gagcgatcaa 34440
gatgagttcg atttccaact tcacgatgct caccgccaac aggtctttag ccaggggcac 34500
gtacgtcgcc gggtctatac ggcgacaccg cgcttggatt tagcccagct gcaaaagctt 34560
tgtgccgagc gcgtgttgtc cggcgaagac tgttatgcgc acttcaccgc ctgcggattg 34620
cagctcggcg accggctcaa atccgtgcaa tcgatcggct gcggacgcaa tggcgagggc 34680
gagccgatcg cattgggtgt cctgcgcctg ccaccatcaa gcgttgaaga cagccatgtg 34740
ctgcctccta gcctgcttga tggtgccttg cagtgtagcc ttggcttgca gcgtgatgtc 34800
gagcacatcg ccatgccata cacgctggag cggatgacgg tgcatgcgcc gattcctccc 34860
gaggcctggg tgctgctgcg tcacggccat gcagccagac agtccctgga catcgatctc 34920
ctggattccg aaggtagggt ctgcgtcagc ctcggcaatt acaccggccg tgcaccgaaa 34980
gccgtttccg ccgtcagggc gcttgtcttg gcaccggtct ggcaagcgtt gaccgaaacg 35040
gcgccggcat ggcccgatcc ggccgaacgc atcgttacgg taggagacga tgcatggcgt 35100
agtcacttcg gtttcgacga gccggccttg tccctggagg acagcgtcga agtcatcgcg 35160

acgcgactgg gccagagcgg caagttcgat catctagtct ggatcgtgcc gatagccgag 35220
agtgaaaccg atattgcagc gcaaggttca gcggcgatcg ccggtttccg gttggtcaag 35280
gcgttgcttg cgttgggcta tgcgcatcgc ccgctgggtc tcaccgtgct gactcgccaa 35340
gcccttacgc ggcagccgtc gcacgcggca gtgcacgggc tgatcgggac gctggccaag 35400
gaatactgca actggaaaat ccgtctgctc gacctgccga gcgtaaaatc ttggccgcaa 35460
tgggagcaat tgcggtcgtt gccttggcat gcgcagggcg aagccctgat cggccgtggg 35520
acttgttggt atcggcggca gttgtgtgaa gtgctgccgc tgccgtcgtt ggaaccgccg 35580
ccgtaccgcg taggcggtgt ctacgtcgtg atcggcggcg ctggcggctt gggtgaagta 35640
ttgagcgaac acttgatccg cacgtacgac gcgcagctga tctggatcgg gcggcgcgtg 35700
ctggacgaag gcattgcgcg caagcagacc cggcttgcgt cgctgggccg cgcaccgcat 35760
tacatctccg cggacgcgag tgacccggct gccctgcagg cggcacataa tgagatcgtt 35820
gcgctgcatg gccagcccca tgggctcatc ctaagcaaca tcgtgctgaa ggatgccagt 35880
ctggctcgta tggaggaagc cgatttccgt gacgtgctgg ccgcgaaact cgacgtcagc 35940
gtgtgtgcgg cacaggtgtt cggcacggcc ccccttgatt tcgtgctgtt tttttcttcc 36000
atccagagca ctaccaaggc ggccgggcaa ggtaactacg ccgccggctg ctgctatgtc 36060
gacgctttcg gcgagctatg ggcgcgccgg ggtttgaggg taaagaccat caactggggc 36120
tactggggca gcgtgggcgt cgtagcgggc gaggactatc gccggcgcat ggcgcaaaaa 36180
cacatggctt cgattgaggg tgccgaagcg atgcaggtgt tgtcgcagtt gttgtgtgcg 36240
ccgttgcaac ggcttgccta cgtcaagatc gacgatgcta acgcaatgcg cgctctgggc 36300
gtagtagagg acgagagcgt gcaaatccct gtgcacgcac cggccgagcc tcccagaggg 36360
cagcctggtc ccgtggtcga gttgtcggtg aatctggatg cccggcgcga acgggaaact 36420
ttgctggcgg cctggctgct tgagttgatc gagcaactcg gtggttttcc gccggcaagt 36480
ttcgacatcg ctacgcttgc gcaacgcctg cacatcgtac ccgcctatcg aagctggctg 36540
gaacacagcg tgcggatgct cggcgtgtat ggttacctca gagcgacggg ggaaagccga 36600
ttcgagctgg ccgacaagcc gcccgatgat gccaggggtg cctggaacgc gcatgtgcac 36660
gaggccagcg tcgaagccgg tgaagaggca cagcggcgtc tgctcgatcg ctgcatgcgg 36720
gcgttgccgg cggtccttcg aggcgaacgc aaggccaccg aattgctgtt tccggaaggt 36780
tcgatggcgt gggtcgaggg tatctaccag aacaacccgc ttgccgatta cttcaacgca 36840
caactagtca cgcgactgat tgcctacttg agacgacgac tagagtcgac gcctacggcg 36900
cgcctgaagc tgtgcgagat cggcgccggc agcggtggta ctactgcaag cgtgctacaa 36960
cagttgcagg catatggtga gcatattgag gaatatctct ataccgacct gtcgcctgtc 37020
ttcctgcatc atgcggaaaa acactatcag ccacgagcgc cttatttgag gaccgcctgt 37080
ttcgacgtag cgcgcgcgcc gacggcgcag gccctggaat ctggcggcta cgacgtggtg 37140
attgccgcca acgtactgca tgctacgcgc gatatcgcca agaccttgcg caatgcgaag 37200
gcactcctca aacctggcgg tctgctcttg ctcaacgaag tgatcgagcg cagcctcgtc 37260
ttgcacctga ctttcggtct gctggagagc tggtggttgc cccaggacaa gatcttgcgc 37320
cttgccggct cgccgttgct ggcttgcgcc acctggcgca gcctgctgga ggctgagggt 37380
tttgcggggc tgagcgtgca cagggcgcaa cccgatgccg ggcaggccat catctgtgcc 37440
tacagcgatg ggatagtgcg gcaagccagt acgatcgagg ttgcgcggaa tgaaaaagta 37500
accgttccgt cgcagccggc ggaagccggg gaatcgccgc tggatctggt caaaaaactg 37560
cttggacgca ttctgaaaat ggatccggcc acactcgata ccagccaccc gctggagtac 37620
tacggtgtcg attcgatcgt ggcgatcgaa ctggctatgg cactgcgcga gacattcccg 37680
ggttttgaag tcagcgagct gtttgaaacg caatccatcg ataccttgtt gggctctctt 37740
gagcaggctc ctctccttgc taccctcaca gctccgccgc aacaagacat gctgcagcag 37800
ctgaaacaac tgctggcgcg tacgctgaag ctggacatta cgcagatcga cacgagcaag 37860
acgctggaga gctatggtgt cgactccatc gtcatcatcg aattagccaa cgccttgcgt 37920
gagcgctatc cgagcttgga cgcgtcacag ctgatggaaa ccttatcgat cgaccggctg 37980
gttgcccaat ggcaggcaac ggagcccgcc gtaccggcag agccaacagc ggaaccgccg 38040
gtagccgacg aagacgccgc tgccatcatc ggactggccg gccgctttcc aggcgcggac 38100
acgttggagg agttctggaa caacctgcgc aacggccaaa gcagtatggg agaggtgcca 38160
ggcgagcgct gggatcacca gcactacttc gacagtgaac gccaggcacc gggcaagacg 38220
tatagccgct ggggtgcgtt tctgagggac atagacggct tcgatgcagc cttctttgaa 38280
tggcccgaca gcgtcgcgct ggaatcggat ccgcaagcgc ggatatttct agagcaggcc 38340
tatgccggga tcgaagatgc cggctacacg cctggctcgc tcagcaagag ccaacgcgta 38400
ggtgtattcg taggtgtgat gaatggttac tacagcggcg gagcgcgctt ctggcaaatc 38460
gccaaccgcg tgtcgtacca gttcgatttt cgcgggccaa gcctggcggt ggataccgcc 38520
tgttcggctt cgctcaccgc gatccacctg gcgctggaaa gcctgcgcag cggcagttgc 38580
gaggtcgcac tggccggtgg cgtgaatctg ctggtcgatc cgcagcaata tcttaatttg 38640
gctggcgccg cgatgctctc cgccggcgcc agctgtcggc cgttcggcga ggccgcggac 38700
ggtttcgtgg ccggcgaagc ctgcggcgtg gtgctgctca agccgctcaa gcaagcgagg 38760
gccgatggcg atgtgatcca tgccgtaatc aggggcagca tgatcaatgc cggtgggcac 38820

accagcgcgt tctcctcgcc taaccctgcc gcccaggccg aagtcgtgcg gcaggccttg 38880
cagcgcgcgg gcgtggcgcc cgattcgatc agctacatcg aggcgcatgg caccggcacc 38940
gtactaggcg atgcagtgga gttgggtgct ttgaataaag tgttcgacaa gcgcgcggcg 39000
ccatgcccga tcggctcgct gaaggcgaac atcggccatg ccgaaagcgc cgcgggcatc 39060
gccggcctgg ccaagctggt attgcagttc aggcatggcg agttggtgcc tagtctgaat 39120
gcgtttccct tgaatcccta tattgagttc ggtcgcttcc aggtacaaca gcagccggca 39180
ccgtggccgc gccgtggcgc ccagccgcgg cgcgccgggt tatctgcctt cggtgctggc 39240
ggatcgaatg cgcacctagt ggtagaggaa gctccggcta tggctcccgg ggtctcgatc 39300
agcgccagct ctccagcctt gatcgtgctt tcggcgcgaa cgctgcctgc cttgcaacag 39360
cgtgctcgcg atctgctcgt ctggatgcaa gcgcggcagg tggatgacgt catgctggcc 39420
gacgttgctt atacgctgca cttgggccgc gtcgcgatgg agcaacgcct ggcttttacc 39480
gctggctcgg ctgccgagtt gagcgagaaa ttacaggctt acctgggcca tgcgattcgg 39540
gccgacatct atctgagcga ggacacgccc ggcaaaccgg caggcgctcc gatcgtggcc 39600
gaggaagatc tgctcacgct gatggatgcc tggatcgaaa agggccagta cggtcgtttg 39660
ctggagtact ggaccaaggg ccaaccgatc gactggaaca aactctattg gcgcaagctg 39720
tatgcggacg gacggccgcg gcggatcagc ctgcccacct atccgttcga gcaccggcgt 39780
tattggcaaa cgccggtgcc gggcgagcga agcctgcacg ccaccgcgcc agctactcgg 39840
gaaacggttg cggttggtgc catgccggat ccggccggcg ctacggtgca agcccggttg 39900
tgcgccttgt gccaagtgtt gttgggcaaa ccggtcacgg cccagatgga tttctttgcc 39960
gtcggcggcc attcggtgct ggcgatccaa ttggtctcgc gcatccgcaa aagcttcggg 40020
gtggagtatc cggtcagcgc tttgttcgaa tcggcgctgt tgtcggacat ggcgcggcag 40080
atcgaacaat tgcgggtgaa cggagtcgcc aagcgcatgc cggcgttgtt gcctgccggg 40140
cgcgtgggcg cgattcctgc gacttatgca caggagcgcc tatggctcgt ccacgaacat 40200
atgagtgagc aacgcagtag ttacaacatc acctttgcca tgcacttcag aggcgtcgac 40260
ttccgtgctg aagcgatgcg tgccgcattg aacgcgctgg tggtgcggca cgaagtgctg 40320
cgcacacgct ttctttcgga ggacgggcag ctgcaacagg tgatcgctgc ctcgttgacg 40380
ttggaggtgc cggtaagaga gatgtcggtc gaggaggtcg acctgctgct ggccgcgagc 40440
acgcgggaga ctttcgatct gcggcagggg cccttgttca aggcacgcat cctgcgcgtg 40500
gcggccgatc accatgtggt gttgagcagc atccaccaca tcatttccga cggctggtcg 40560
ctgggagtgt tcaaccgtga cctgcaccag ctgtacgagg cgtgtttgcg cggcacgccc 40620
cccacactgc cgacgctggc ggtgcagtat gccgactacg cgctgtggca acggcaatgg 40680
gagctggcgg ctccgctgtc gtactggacg cgggcactgg aaggctacga cgacggcctg 40740
gacttgccct acgaccggcc gcgcggcgcc acgcgggcgt ggcgggcagg gctggtcaaa 40800
caccgctatc cgccgcaact ggcccagcag ttggcggcct acagccaaca gtaccaagcg 40860
acgctgttca tgagcctgct ggcaggcctg gcgttggtgc tgggccgtta cgccgatcgc 40920
aaggacgtgt gcatcggcgc gacggtctcc ggccgcgacc agctggagct ggaagagctg 40980
atcggctttt tcatcaatat tttgccgctg cgggtggacc tgtcgggggа tccgtgcctg 41040
gaggaggtgc tgctgcgcac gcgtcaagtg gtactggatg gcttcgcgca ccagtcggtg 41100
ccgttcgagc acgtgttgca ggcgctgcgg cgtcagcgcg acagtagcca gatcccgctg 41160
gtgccggtga tgctgcgaca ccagaacttc ccgacgcagg agattggcga ttggcccgag 41220
ggagtgcggc tgacgcagat ggagctgggg ctggaccgta gcacgccgag cgagctggat 41280
tggcagttct acggcgacgg cagctcgctg gagctgacgc tggaatacgc gcaggacctc 41340
ttcgacgaag cgacggtgcg gcggatgatc gcacaccacc agcaggcgtt ggaggcgatg 41400
gtgagccggc cacagctgcg ggtgggcaag tgggacatgc tgacggccga agagcgccgg 41460
ctgtttgccg cgctaaatgc gacaggtacg ccacgggagt ggcccagtct ggcgcagcag 41520
ttcgaacggc aggcgcaggc gacgccgcag gccatcgcgt gcgtgagcga tgggcagtcg 41580
tggagctatg cgcagttgga ggcgcgcgcc aaccagctgg cacaggcgct gcgggggcag 41640
ggcgcgggcc gggacgtgcg ggtggcggta cagagtgcgc gcacgccgga actgctgatg 41700
gccttgctgg cgatctttaa ggccggtgcg tgctatgtgc cgatcgatcc ggcctacccg 41760
gcggcctacc gcgagcagat cctggccgag gtgcaggtgt cgatcgtgct ggagcaagac 41820
gagctggcgc tggacgagca agggcagttc cacaatccgc gttggcgcga gcaagccccg 41880
acgccgctgg ggctgaggga gcatccgggc gacctggcgt gcgtgatggt gacctccggc 41940
tcgaccggcc ggcccaaggg cgtgatggtg ccgtatgcgc agctgtacaa ctggctgcat 42000
gcaggctggc agcgttctcc gttcgaggcc ggggagcggg tgctgcagaa gacctcgatc 42060
gcctttgcgg tgtcggtaaa ggagttgcta agcgggctgc tggcgggggt ggaacaggtg 42120
atgctgccgg acgagcaggt gaaggacagc ctggcgttgg cgcgggcgat tgagcaatgg 42180
caggtgacgc ggctgtacct agtgccatcg cacctgcagg cgctgctgga cgcgacgcaa 42240
ggacgagacg ggctactgca ctcgctgcgt cacgtggtga cggcgggggа agcgttgccg 42300
tctgcggtgc gcgaaacggt gcgggcgcgt ctgccacagg tgcagctatg gaacaactac 42360
ggctgcacgg aactgaacga cgcgacctac caccggtcgg atacggtggc gccaggaacg 42420
tttgtgccga tcggcgcacc gatcgccaac accgaggtat acgtgctgga ccggcagctg 42480

cggcaggtgc cgatcggggt gatgggcgag ctgcacgtac acagcgtggg gatggcgcgc 42540
ggctactgga accggccggg gctgacggcc tcgcgcttca tcgcgcaccc gtatagcgag 42600
gagccgggca cacggctgta caagaccggt gacatggtac gccggctggc ggacgggacg 42660
ctggaatacc tgggccgaca ggacttcgag gtcaaggtgc gcggccaccg ggtggatacg 42720
cggcaggtgg aggcggcctt gcgggcgcag cccgcggtgg ccgaggcggt ggtgagcggt 42780
caccgggtgg acggggacat gcagttggtg gcctatgtgg tggcgcgtga agggcaggca 42840
ccgagcgcgg gcgagttgaa acaacagctg tcggcgcagt tgccgaccta catgctgccg 42900
accgtgtacc agtggctgga gcagttgccg cggctgtcca acggcaagtt ggaccggttg 42960
gccctgccgg caccgcaggc ggtacacgcg caggagtacg tcgcgccacg caaccaggcc 43020
gagcaacggc tggcggcact gtttgccgag gtgctgcggg tggagcaggt aggcatccac 43080
gacaacttct tcgccttggg tgggcactcg ctgtctgcat cgcaactgat ctcgcgtatt 43140
gccagggata tggcgatcga tctgcccctg gccatgctgt tcgagctgcc cacggtagcg 43200
cagcttagcg aatccctcgc cagccatgca cgcgacagcg attacgatgt catccccgca 43260
agcaccgagg aggcgaccat tccgctttcc actgcgcagg agcgcatgtg gttcctgcac 43320
aagttcgtgc aggagacgcc gtacaacacc ccgggtctcg ccttattgca aggcgaactg 43380
gacatttcgg ccttgcaggt agcatttcgc tgtgtgctag aacggcacgc cgtgctgcgt 43440
acccatttcg tggaaaccga gcagcaatgc gtacaggtca ttggcgcagc agagcagttc 43500
gtgctgcagc ttaggtcgat tcgcgacgag gctgatctgc atggcctatt gcacacagcc 43560
gtcagcgaac ccttcgattt agaacgcgag ctgccattgc gcgccctgct gtatcgcctg 43620
gacgaccggc ggcattacct agcagtggtc atccatcaca tcgtcttcga cggctggtcg 43680
acctcaatcc tgtttcgtga gctggccacg cactatgctg catgccgcca tggccaatcc 43740
gcgcctttgc caccgctgga gcttagctat gccgattacg cacgctggga gcgtgcgagg 43800
ctgaaccagg aagacgcgct gcgcaagctc gaatattgga aaacgcagct tgccgatgca 43860
ccgccgctgg tgttgcccac gacctatgcg cggccggttt tccagaactt caatggcgcg 43920
actgtggcgc ttcagatcga gccgccgctg ctgcaacgcc tgcagcgttt cgccgacgca 43980
cacagcttta cattgtacat gctacttctg gcagcactgg gcgtcgtatt gtcgcgccat 44040
gcccggcaga agcatttctg cattggcagt ccggtcgcca atcgcgcccg agccgagttg 44100
cacggtttga tcggtttgtt cgtcaacacc ctggcggtac ggctcgattt ggacggcaat 44160
cccagcgtgc gcgagctgct cgaacgcatc cactgcacca cgctggccgc ctacgagcac 44220
caggatgtgc cgttcgaaag aatcgtggaa agcctgaagg taccgcgcga taccgcgcgt 44280
aacccgctgg ggcaggtgat gctcaatttc cagaacatgc caatgtcggc gttcgacctg 44340
gatggtgtcc aggtgcaggt gctccccatg cacaacggca cggccaagtg cgagctgacc 44400
ttcgacctgc tgctggatgg ctcacgccta tccggtttcg tcgaatacgc cactgggctg 44460
tttgcgccgg aatgggtcca ggcgctggta cagcaattca agtgtgtgct ggcggcattg 44520
gtggaacggc cggaggcatc gctgaatgat ttgcccatgg cgcccaacga ggcgcaaccg 44580
gcgtcgccgg cattgatgaa gcatgtcgcg ccgagcttgc ccaacttact tgaggctatg 44640
gcggccaatg atgccgcacg cctcgccttg caagcgccgg aaggtgcgct cagttacgct 44700
cagctaatcg aggcagcaaa cgagttcgcc tggcgtttgc ggtgcgagca cgccggtccg 44760
gacaaagtcg ttgccctgtg cctagcgcct tgctccgcct tggtggttgc tttgctggcc 44820
gcttcattat gcggtgcggc gagcgtgctg atcgatccga cgacgactgc cgaggcgcaa 44880
tacgaccagt tgttcgaaac gcgggccggc atcgtggtga cctgttctag cttgctggag 44940
aagttgccgc tcgacgacca ggctgtagtg ctgatcgacg agcaagctgc agaagcgacg 45000
ccgcgtttga tgcatttcac cgacgatcca gctttgcccg caatgctgta ttgtgtgtgt 45060
gacgaaaagg ggcgaacccg cacgatcatg gtcgaaagcg gcagtttgtc gagtcgcctg 45120
ctcgatagcg tgcagcgttt cagtctcgaa cgcaccgatc gcttcctgct gcgcagcccg 45180
ctttctgccg aactggcgaa taccgaagta ctgcaatggt tggcggcagg cggcagcctc 45240
agcatcgcac ccatgcatgg cgatttcgat gccgctgcct ggctggagac cctcgcgacg 45300
tacgcgatca ccgtggccta cctggctcaa gttgaattga ccgagatgct ggcgcatctg 45360
caaaaccatc ctcttgagcg caacaagctg gccggcttac gcgtgctggt ggtgcatggc 45420
gcgcccttgc cgatcgcgcc actgatgcgc ctagacgcgt ggttgcgaga ggtgggcggt 45480
tccgcacgga tcttcgccgc ctacgggaat gccgagttcg gtgccgaaat attgagccag 45540
gatgtcagcg ctgcattgca agcgggtatt ggcgctcaat acaagcatcg ccgtggtctg 45600
ttcccgttgg gtgccaactc gatgtgtcac gtggtgcaga gcaacggccg catcgcgccc 45660
gacggcatgg ttggtgaatt gtggatcaca cagccagcct gcttgtacaa aaccgatgca 45720
ttggtgcgtc gcctggcaaa tgggcaactg gaatggttgg gctccctcga tgtccagtcg 45780
cgtatcgatg atccccgcat cgatctgtgc gtcgtggagg cacaactgcg cttgtgcgaa 45840
gacgtcggcg aagcggtagt gctgtatgag ccgttgaagc gctgcttggt agcctatctc 45900
tcggcccgta gcacagctgc aatcatgacc gacgagacgc tggccaggat ccgccaggcc 45960
ctgagcgaaa ccttgccgga ttatctactg cctgcaatct gggtgccgct cgcgcactgg 46020
ccacgcttac cccatgggcg ggtcgacctc ggcgccttgc ctgcaccgga tttcgatctt 46080
gcgcggcatg agtcgtacat agcgccacgc acagccgtcg aacaggccgt ggccgaaata 46140

```
tggcaacgcg tgttgaagcg tacccaggtc ggcgtgcatg acaatttctt cgagctgggc  46200
ggccattcgg tgctggcgat ccagctggtg tccggcttgc gcaaggcttt ggccatcgaa  46260
gtgccggtca ccctggtgtt cgaggcgccg atactggggg cgctggcgcg gcagatcgcc  46320
cccttgttgg tcagcgaacg gcgtccgcgc ccgcctggcc tgacgcgcct ggagcataca  46380
gggccgattc cggcttcgta tgcacaggag cggttatggc tggtgcacga gcatatggag  46440
gagcagcgaa ccagctacaa catcagtaac gcagcgcatt tcatcggagc agccttcagc  46500
gtcgaagcga tgcgtgccgc attgaacgcg ctggtggcgc ggcacgaagt gctgcgcaca  46560
cgctttcttt cggaggacgg gcagctgcaa caggtgatcg ctgcctcgtt gacgctggag  46620
gtgccggtac gcgaggtgtc ggccgaggag gtcgacctgc tgctggccgc gagcacgcgg  46680
gagactttcg atctgcggca ggggcccttg ttcaaggcac gcatcctgcg cgtggcggcc  46740
gatcaccatg tggtgttgag cagcatccac cacatcattt ccgacggctg gtcgctggga  46800
gtgttcaacc gtgacctgca ccagctgtac gaggcgtgtt tgcgcggcac gccccccaca  46860
ctgccgacgc tggcggtgca gtatgccgac tacgcgctgt ggcaacggca atgggagctg  46920
gcggctccgc tgtcgtactg gacgcgggca ctggaaggct acgacgacgg cctggacttg  46980
ccctacgacc ggccgcgcgg cgccacgcgg gcgtggcggg cagggctggt caaacaccgc  47040
tatccgccgc aactggccca gcagttggcg gcctacagcc aacagtacca agcgacgctg  47100
ttcatgagcc tgctggcagg cctggcgttg gtgctgggcc gttacgccga tcgcaaggac  47160
gtgtgcatcg gcgcgacggt ctccggccgc gaccagctgg agctggaaga gctgatcggc  47220
tttttcatca atattttgcc gctgcgggtg gacctgtcgg gggatccgtg cctggaggag  47280
gtgctgctgc gcacgcgtca agtggtactg gatggcttcg cgcaccagtc ggtgccgttc  47340
gagcacgtgt tgcaggcgct gcggcgtcag cgcgacagta gccagatccc gctggtgccg  47400
gtgatgctgc gacaccagaa cttcccgacg caggagattg gcgattggcc cgagggagtg  47460
cggctgacgc agatggagct ggggctggac cgtagcacgc cgagcgagct ggattggcag  47520
ttctacggcg acggcagctc gctggagctg acgctggaat acgcgcagga cctcttcgac  47580
gaagcgacgg tgcggcggat gatcgcacac caccagcagg cgttggaggc gatggtgagc  47640
cggccacagc tgcgggtggg caagtgggac atgctgacgg ccgaagagcg ccggctgttt  47700
gccgcgctaa atgcgacagg tacgccacgg gagtggccca gtctggcgca gcagttcgaa  47760
cggcaggcgc aggcgacgcc gcaggccata gcatgcgtga gcgatgggca gtcgtggagc  47820
tatgcgcagt tggaggcgcg cgccaaccag ctggcacagg cgctgcgtgg gcagggcgcg  47880
ggccgggacg tgcgggtggc ggtacagagt gcgcgcacgc cggaactgct gatggccttg  47940
ctggcgatct tcaaggccgg tgcatgctat gtgccgatcg atccggccta cccggcggcc  48000
taccgcgagc aaatcctggc cgaggtgcag gtgtcgatcg tgctggagca aggcgagctg  48060
gcgctggacg agcaagggca gttccgcaat cggcgttggc gcgagcaagc cccgacgccg  48120
ctggggctga ggggacatcc gggcgacctg gcgtgcgtga tggtgacctc cggctcgacc  48180
ggccggccca agggcgtgat ggtgccgtat gcgcagctgc acaactggct gcatgcaggc  48240
tggcagcgtt ctgcgttcga ggccggggag cgggtgctgc agaagacctc gatcgccttt  48300
gcggtgtcgg taaaggagtt gctaagcggg ctgctggcgg gggtggggca ggtgatgctg  48360
ccggacgagc aggtgaagga cagcctggcg ttggcgcggg cgatcgagca atggcaggtg  48420
acgcggctgt acctagtgcc gtcgcacctg caggcgctgc tggacgcgac gcaaggacgc  48480
gacgggctac tgcactcgct gcgtcacgtg gtgacggcgg gggaagcgtt gccgtcggcg  48540
gtgggcgaag cggtgcgggt gcgcctgcca caggtgcagc tatggaacaa ctatggctgc  48600
acggaactga acgacgcgac ctaccatcgg tcggatacgg tggcgccagg aacgtttgtg  48660
ccgatcggcg caccgatcgc caacaccgag gtatacgtgc tggaccggca gctgcggcag  48720
gtgccgatcg gggtgatggg cgagctgcac gtacacagcg tggggatggc gcgcggctac  48780
tggaaccggc cggggctgac ggcctcgcgc ttcatcgcgc acccgtatag cgaggagccg  48840
ggcacacggc tgtacaagac cggtgatatg gtacgccggc tggcggacgg gacgctggaa  48900
tacctgggcc gacaggactt cgaggtcaag gtgcgcggcc accgggtgga tacgcggcag  48960
gtggaggcgg ccttgcgggc gcagcccgcg gtggccgagg cggtggtgag cggtcaccgg  49020
gtggacgggg acatgcagtt ggtggcctat gtggtggcgc gtgaagggca ggcaccgagc  49080
gcgggcgagt tgaaacaaca gctgtcggcg cagttgccga cctacatgct gccgaccgtg  49140
taccagtggc tggagcagtt gccgcggctg tccaacggca agttggaccg gttggcgctg  49200
ccggcgccgc aggtggtaca cgcgcaggag tacgtcgcgc cacgcaacga ggccgagcaa  49260
cggctggcgg cactgtttgc cgaggtgctg cgggtggagc aggtgggcat ccacgacaac  49320
ttcttcgcct tgggtgggca ctcgctgtct gcatcgcaac tgatctcgcg catccgccaa  49380
agttttcacg tcgatctgcc gctgagccgg atcttcgagg cacccacgat cgagggcctg  49440
gtcaggcagc tagcgttgcc tagtgaaggc ggcgtggcca gcatcgccag ggtagcgcga  49500
aaccggacga tcccattgtc gctgttccag gaacgcctgt ggttcgtgca ccaacacatg  49560
cctgagcaac gcaccagtta caacggcacg ctcgccttgc gtttgcgtgg tcctttgtcg  49620
gtggaagcga tgcgtgcagc gctgcgtgcg ttagtgctgc gccacgaaat cttgcgtacc  49680
cgcttcgtgt tgccgaccgg tgctagcgag ccggtgcagg tcattgacga gcacagcgat  49740
ttccagctct cagtacagct agtcgaggat actgagatcg cgtcgctgat ggatgaactg  49800
```

gcaagtcata tctacgactt agccaacggc ccgctgttca ttgcatgcct tttgcaactg 49860
gatgagcaag aacatgtgct gctaatcggc atgcatcacc ttatctacga cgcttggtcg 49920
caattcaccg tgatgaaccg cgatctacgc gtgctgtatc accgccacct cggacttgcc 49980
ggcggagatc tgccggaatt accgatccaa tatgccgact atgcgatctg gcaacgcgcc 50040
cagaacctgg acgcgcaact ggcctattgg caggctatgt tgcacgacta cgacgacggc 50100
ctggagctgc cctacgacta tccgcgtccg cgcaatcgca cctggcacgc agcggtctac 50160
acacacacct atccggctga actggtacag cgctttgccg gcttcgtaca ggcgcatcag 50220
tcgaccttgt tcatcgggct gttggccagc ttcgcggtcg tgttgaacaa atacaccggc 50280
cgggacgact tgtgcatcgg taccaccacg gcagggcgca cgcacctgga gctggagaac 50340
ctgatcggtt tcttcatcaa catcttgcct ttgcgcttgc gcttggacgg cgatccggac 50400
gttgccgaaa tcatgcggcg aacacggttg gtggcgatga gcgcgtttga gaaccaggcg 50460
ctaccgttcg agcacctgct caacgccctg cacaagcaac gtgacaccag ccggattccg 50520
ctagttccgg tggtgatgcg tcatcagaac ttcccggaca cgatcggcga ctggagcgat 50580
ggcatccgta ccgaagtgat ccagcgcgat ctgcgtgcca cccccaatga aatggacctg 50640
caattcttcg gcgacggtac ggggctttcg gtcacagtgg aatacgcggc ggagctgttc 50700
tcagaagcga ccattcgccg cctgatccac catcaccaac tcgtcctgga gcagatgttg 50760
gcggcccatg aaagcgccac gtgccccttg gatgttgccg actagcaaaa gccggccgcc 50820
gtcacccgtt catcgatagc gagggcaatc atggattcag cgttacctac atctgcattt 50880
accttcgatc tcttttacac cacggttaac gcctactatc gcactgccgc agtcaaggcg 50940
gcgatcgaac tggggctatt cgatgtggtg gggcagcagg gccgaactcc cgcagccatc 51000
gccgaggcct gccaggcgtc gccgcgcggc attcgcatcc tttgctatta cctagtatcg 51060
atcggttttc tacgccgcaa cggtggcctg ttctacatag atcgcaacat ggccatgtac 51120
ctggatcgta gttcgcccgg ctacctgggt ggcagcatca agttcctgct ctcgccctac 51180
atcatgagcg ccttcaccga tctgaccgcc gtagtcagga ccggcaagat caacctggcg 51240
caggacggcg tggtggcacc ggatcacccg cagtgggtgg aatttgcacg cgcgatggca 51300
ccgatgatgg cgctgccctc ggcgttgatc gccaatatgg tgtcgttgcc cgctgatcgg 51360
ccgattcgtg tgctggacgt ggcagccggc cacggcctgt tcggcatcgc cttcgcgcag 51420
cgcttccgcc aggctgaagt gagcttcctg gactgggaca acgtgctaga cgtagcacgc 51480
gaaaacgccc aggcggccaa agtggccgag cgagcgcgtt tcctgcccgg caacgcattc 51540
gacctcgatt acggcagcgg ctacgacgtg atcttgttga ccaacttcct gcaccatttc 51600
gatgaggtcg atggcgagcg catcttggct aagacgcgcg atgcgctgaa cgacgacggc 51660
atggtgatca ctttcgaatt catcgccgac gaagagcgtt cctcaccgcc gctggccgcc 51720
accttcagca tgatgatgct gggcaccacc ccggcgggcg agtcctacac ctatagcgat 51780
ctggaaagga tgtttcggca tgccggcttc ggccacgtgg aactaaaatc gataccgccg 51840
gccttgctga aagtggtggt ttcccgcaag agggccccat aatgatcgaa tcggcgacat 51900
cccctgtggc gaaaaccgag cgcatctggt gcaccgagct ggacctggat gcactcaacg 51960
ccatgtcggc caacacgatg caggccctgc tcggtatacg catgatcgag atcggctcgg 52020
actatctggt ctcctgcatg tcggtggact ggcgttgcca ccagccctat ggggtattgc 52080
atggcggcgc atcggtcacc ctggccgagg ctaccggcag catggcggcc tccatgtgcg 52140
tgccggccgg ccaacgttgc gttggcctag acatcaatgc caaccacatc gcgagcatct 52200
ccagtggcca agtacagtgc atcgcgcggc cgctgcacat aggggccttg acccaggtat 52260
ggcagatgcg catctatgac gaaggtgacc gcacgatctg cgtgtcgcgc ctgaccatgg 52320
cggtattatc ggtgcacgtc gcgcgcgtat ccccgaatcc agccagcagc ggagtccaga 52380
cgtgaacgaa actgcaactg taaccaaggc taccctcagt tcagcgaagg cgagtataac 52440
gccagcctgc gttcaccaat ggtttgaagc gcaggtgagt tcgacaccgg atgcgcctgc 52500
tgccttctta ggcgagcgtc gaatgagtta tggccagctc aacacccgcg ccaatcggct 52560
tgcacggctg ttgcagtcac agggcgttgg gcctggtgcc cgggtcgcgg tgtggatgaa 52620
tcgcagcccc gaatgcctgg ccgctttgct ggcggtcatg aaggccgggg cagcttatgt 52680
accgatcgac ctgagcctgc cgatccgacg tgtccaatac atcttgcagg acagccaggc 52740
ccggctcgta ctggtcgatg acgaagggca aggccgcctg gacgaacttg agctgggcgc 52800
gatgactgcc gtcgatgtct gcggcactct ggacggcgac gaggcgaatc tggacctgcc 52860
ttgcgatccg gcgcagccgg tttattgcat ctatacctcc ggctccacag gtagccccaa 52920
gggcgtgctg gtacggcaca gcgggttggc taactacgtg gcctgggcta agcggcaata 52980
cgttacggct gacacgacga gtttcgcctt ttactcctcg ctgtcgttcg atctgaccgt 53040
cacctcgatc tacgtgcccc tggtggctgg cctgtgtgtg catgtgtacc cggagcaggg 53100
cgacgacgtg ccggtaatca accgcgtgct ggacgacaac caagtagacg tgatcaagct 53160
gacaccctcg cacatgctga tgctgcgcaa cgcggcactg gcgacgtctc ggctgaagac 53220
gctgatcgtg ggtggcgagg acctgaaagc ggcggtggcg tacgacatcc atcagcggtt 53280
ccgccgcgat gtggcgatct acaacgaata cggtcctacc gaaaccgtag tggggtgcgc 53340
gatccatcgt tacgatccgg cgaccgaacg cgaaggctcg gtgccgattg gtgtgccgat 53400
cgatcacacc agcctccacc tgctcgatga acgtctgcag ccggtcgcac cgggcgaggt 53460

cggccagatc cacatcggtg gcgcgggcgt ggccatcggc tatgtgaaca agccggagat 53520
caccgatgcg caattcattg acaatccctt cgaaggcagc ggccggcttt acgccagtgg 53580
cgacctagga cgcatgcgtg ccgacggtaa gcttgaattc cttggccgca aggattcgca 53640
gatcaagctg cgcggctacc gcatcgaact gggcgagata gagaacgttc tgcttggcca 53700
cgcagccttg cgcgaatgca tcgtggatac caccgtggcg ccgcgccgcg actatgacag 53760
caagagcttg cgctattgcg cgcgttgcgg tatcgcttca aatttcccca ataccagctt 53820
cgacgagcac ggtgtctgca accattgcca cgcctacgac aaataccgga acgtggtcga 53880
ggattatttc cggaccgaag atgagctacg tactatcttc gagcaggtca aggcgcacaa 53940
caggctccgc tacgactgcc tggtggcttt cagcggcggc aaggacagca cctatgcgct 54000
atgccgcgta gtggacatgg gcctgcgcgt gttggcgtac accctggaca atggctacat 54060
ctccgacgag gccaaggcaa acgtcgaccg cgtcgtgcgc gagctggggg tggaccatcg 54120
ctatctgggt actccacaca tgaacgccat cttcgtggac agcctgcatc gccacagcaa 54180
cgtctgcaac ggctgcttca agaccatcta tacgctgggt atcaacctgg cgcacgaagt 54240
gggcgtaagc gacattgtaa tgggcctgtc caaaggacag ctgttcgaga cgcgcctgtc 54300
tgagctgttt cgcgccagca ccttcgacaa ccaggtattt gagaagaacc tgatggaggc 54360
gcgcaagatc taccatcgca tcgacgacgc ggcggcccgc ctgctggaca cctcttgcgt 54420
gcgcaacgat cgcttgctcg aaagtacgcg tttcatcgac ttctaccgct actgcagtgt 54480
cagccgcaag gacatgtatc gctatatcgc cgagcgcgta ggctggagcc gtccggctga 54540
caccggccgc tcgactaact gcctgctcaa cgatgtgggc atctacatgc acaagaagca 54600
acgtggctat cacaactatt cgttgcccta cagttgggac gtgcgggtag gccatatccc 54660
aagggaagac gcgatgcgcg agctggagga caccgacgat atagacgagg ccaaggtact 54720
gggcctgctc aagcagatcg gctatgactc aagcctgatc gatacccagg cgggcgatgc 54780
gcagctgatc gcctactacg tggcggcgga ggaactggat ccggtggcat tgcgcaattt 54840
tgctgctgcg atcttgcccg agtacatgct gccttcgtat ttcgtgcggc tggaccgaat 54900
gccgttgacg ccgaatggca aggtgaaccg ccgagcattg ccgaggccgg agttgaagaa 54960
gaacgccagc gaggcgcata ccgagccgag cagtgcgcta gagcaggaac tggtgcaaat 55020
ctggaaagag gtgctgatgg tcgacaaggt cggcgtcagg gacaactttt tcgagctggg 55080
cggccactcg ctgagcgcgc tgatgttgct ctacagcata gccgagcgct accagaagat 55140
ggtcagcatc caggcattct cggttaatcc gaccatcgaa ggtctgtcgg agcatctggt 55200
cgcataaaag ggcaaggacc tcagcgctgt cctctgcatg gtgcggcgtt ggggttcgca 55260
cgccattcaa tatgattgtc atcacttatc gtgagtacgc taatcatagg gcagggcgcc 55320
gacacaggag gcattcacgg cgctgccgac gcacttgtgc cgccggcgaa cgcccgactg 55380
tggagcgcat ccgtgcccac ctaggcactg ggtctccgaa caccgtggtg cgctggctgg 55440
atacctggtg gcaaggcttg ggagatcgaa tcgccaacgt gcctgaagca gtctccgcac 55500
tggtagggca gtggtggacg ctggctttgg atcatgcgcg aagccatgcc ggtgaggcca 55560
tcgctgctga gcgcacagcc ctccaagatg cacgcagcag cttggagggc gaccgccatg 55620
gctgcaggcc gagctcgctc agctacgggg tgagaccgaa gctgcccact aaacggaaca 55680
gctcgcgacg acccgagcta ttgagctgga gcgcctggtc gagcaactcc aacgccagat 55740
taatgagatg gagcggcagc gtgacacggc ggtgcagcgc atcaccgagg ctgaggaggc 55800
acgggaggtg ctccggaggc agtacgtgaa aatttgatc 55839

<210> 2
<211> 2986
<212> DNA
<213> Xanthomonas albilineans

<400> 2

gaattcagcg atgttggctg cggtggccgg caccgccttg ccctgcggca ccaggtagtt 60
gcggccgtaa cccggcttga cgtcgacctt gtcgccgagg ccgcccaggt tggtgacttt 120
ctgcagaaga atcaattgca tggcgttact ccgttattcg ttagcggcgg catgcggcca 180
ccgcaacgcg tgctgtccga ataggacggg attggattgc gcggagtcgg acatgtaccc 240
aaccgacacc cggcggttgc ttcggtcgcc gcacacggga atgcgcgcgc ttccgaacga 300
ctcggatcaa acgtcgtggt tgtccgtgta cgggatcagc gccaggaaac gcgcacgctt 360
gaccgccgtg gccaactgac gctggtactt ggacttggtg ccggtcacgc ggctcggcac 420
gatcttgccg ttctcggtga ggtactggcg cagggtgttg agatccttgt agtcgatctc 480
tttgacgccc tcggcggtga atttgcagaa cttgcgacga cggaagaact tggacatgga 540
cctgctcctt aggcggcttc gacggcgtcg ccgtcggctt cgttggcggc ggcggacaca 600
tcgccatcgt cgtcgtcgcg acgacgacgc tcaccacggt cgggcttgtc gcccttctcg 660
tccttgctct tcatgatcag cgactgctcg gtgtcggcgc catcgcgctt gatcgccagg 720

tgacgcagca cggcgtcgtt gaagcggaag ctctcgacca actcgctcag cacggcctga 780
tccacttcga tgttgagcat gacgtagtgc gccttcacca gattctggat cgggtaggcc 840
aactgtcggc ggccccagtc ttccaggcgg tggatggtgc cgccgccgtt ctcgaccagc 900
gacttgtagc gctcgatcat ggcggggacc tgctcgctct ggtccggatg gaccaggaac 960
acgatttcgt aatgacgact catgtggttg tacctttcgg atgtggccca agggccagtc 1020
agcccccgc aggtggcggt ggagcaaggg ttcccgcccg aataggcgca ggaagccaat 1080
aagtatggca gcgcccttga ccaatgacaa gctcatgcac ccaggacgcc cgctctgctc 1140
cgcgtcgtcc atcgccattg cgcccctccc cgaccccaag catcgaccaa aggaccgaat 1200
gcggcgggta ggcgcgactc tgcgacacta gcgcaatgtt atcgtcgaca ttgacgccca 1260
cagccctcag cgcaacgcaa tgcccaatgc cgtaccgatg cagggcgcgc ggggactccc 1320
gcagccgcaa gcgatgaacc cagggttgcc gagcgtcggc ggcttgagcg caggccagcc 1380
attgcagttg tcgttagcac cggaactgca ggcagccgcg cgcagtgccc accgccatct 1440
gctcgacgac ggcacggcgc tttacctgct ggcgttcgat accgcgcaat tcgacccggg 1500
ggctttcgcg gcaatggcaa tcgcccgccc ggacagcatc gcccgcagcg tgcgcaagcg 1560
tcaggccgag ttcctgttcg gccgtctggc cgcgcgactg gcgctgcaag aggtgctggg 1620
acctgcgcaa gcgcaggcag acattgcaat cggcgcgacg cgcgcgccct gctggcctgc 1680
cggcagcctg ggcagcattt cccattgcga ggactacgcg gccgccatcg ccatggcggc 1740
cggcacccgc cacggcgtgg gcatcgatct ggaacgacca atcacacccg cggcgcgcgc 1800
ggcgttgctg agcatcgcaa tcgatgccga cgaagccgct cgtctggcaa aggcggcaga 1860
cgcgcagtgg ccgcaagacc tgctgctgac cgcactattt tcggccaagg aaagcctgtt 1920
caaagccgcc tacagcgcgg tcggacgcta cttcgacttc agcgcggcac gcctgtgcgg 1980
catcgacctg gcacggcaat gcctgcatct gcgcctgacc gagacactct gcgcgcaatt 2040
cgtggccggg caagtgtgcg aggtcggctt cgcgcgccta ccaccggacc tggtgctcac 2100
ccactacgcc tggtgagcac gcggacagtc gaacccgcca acgccaacgg cactcaagac 2160
gtggcgtgcg ccgcgtcggt cgtgaagctc tccccgcagc cgcactcggc ggtggcattg 2220
ggattgcgga acacgaaggt ctcacccaag ccctgcttgg cgaagtcgat ttcggtgcca 2280
tcgaccaact gcagactggc ggcatcgaca taaatccgca ctccgtcctg ctcgaacacc 2340
gcatcgtccg cgcgtgcctc gtgcgccaga tcggtgacat ggccccaacc ggaacagcct 2400
gtgcgtacca ccccgaaacg tagacccagc gcaccgggag tctggtcgag gaaacgctgc 2460
acgcgtgcaa acgcggcggg ggtgaggcgg atggccatga cgaacgactc caacgacttg 2520
cgatacgaca ttatacgacc gatgcccgca acgcctcgca agcgctacgc tccagccagt 2580
acacttgttc attccatatc gagccactgc ggcgaggatt caagtcatga cggtggtgag 2640
cgttgaacat gcgctggcag ggaagatccc ggtcggcggc gaagtgaccg tccgcggctg 2700
ggtccgtacc cggcgcgact ccaaagcggg gctgtccttc gtcaatgtca gcgacggttc 2760
ctgcttcgcg ccgatccagg tggtggctcc ggccgcgctg cccaactacg aaccggaagt 2820
gaagcgcctg accgccggct gcgcggtgat cgcgcgcggg cacctggtcg cctcgcaagg 2880
ccagggccaa agcttcgaga tccaggccga gagcatcgag gtactgggct gggtcgagga 2940
cccggagacc tacccgatcc aacccaaagc gcattcgctc gaattc 2986

<210> 3
<211> 9673
<212> DNA
<213> Xanthomonas albilineans

<400> 3

gaattcggac ctggcgagta cttggaccgc gctgtgatgg tcaactgcca gggtggaagc 60
ttcgctcccg gcatcgagat gacgttcgtc gtgcgcgatc cggcgctcta ccgcgccgac 120
tggcaaagca gcggctgcgg accattccga atccgaggac gtgcgttgga ctacgccagc 180
gtgcaatacg gccagccatt tctgagcgtt ggctatctcc cctaccaacc cggtccggat 240
ggcatcgacc ccgcgccgct ggagccaggc gacctctcca agtttatgtc gattccttgg 300
caaaccgact acaacgcctg cgcgacgttc actgccgacc cgaatccgga caacagcacc 360
acactttact gggcctggcc agcacagcgc ccattcaccg tgcatgtagc caccgatgtc 420
agggacggca agccaggccc gcaacgctat tccattcgcg gtgcgggcac cacatccgac 480
gatctgagta acgctggccg tttccaaaac catatcgaca tggtgaacaa ctggcaccgc 540
atcggcttcg tcatccaggg cagcgcgatc gacggcgata ttcgctacag cccggacatg 600
tacctggaag tggccagtca actggacgaa ccggagatcg cgccctggcc gatgaatgcc 660
aacagcgcgg acacttgaag catgaatacc cactgcgacg tggcggtcat cggcgcaggg 720
ccggcgggat gcgcggcagc catcgcattg cgccgtgccg gcgtcggcag cgtggtcctg 780
atcgatgccg gcgacggtca gcgcccgcgt tacggcgaga gcctgcctcc ggcgaccggc 840

ctgctgctgc atgcactggg cgtggccgat accttcgctg cgctggacat gcgcagatgc 900
atcggcaacg cctcgtcatg gggagcgcaa acgttgggct acaacgactt cctgttcgat 960
ccacacgggc ccggttggca ggtggatcgc cgcgatttcg atgcgttcct gctgcaacag 1020
gcgagcagcg gcggtaccgg cgtgcgcttg cacacccgcc tggagagtgc ctccgacgcg 1080
gacccggatg gtctgcgact gcgcttgcgc tcgcacggca cggcactaac cacgctgcat 1140
gcccgtttcg ccgtcgatgc cagcggccaa cgcgcacggc tggcacaggc gctgggcgcc 1200
gaacgcgtca ccggtgatcg cttggtctgc cttgccgcgc tgttgccggt ggacaccacg 1260
agtcggctcg ggcaacgctc gctgctcgaa gcagtcgact atggctggtg gtatgcggca 1320
ccgttgacgt ccggcgaagc catcgtcgtc ctcgccaccg atgcggcggt cctgcgcgaa 1380
cagcgtctgc aagaacccgc gcgatggtcg gtgcggttgg cacaaaccca ccatatcggc 1440
gccaccgtcg gctggatgcg cagggcacca ccatactgcc tgtccacgcg ccaggcgcgc 1500
tctgcacgat tgagccactg ctgtggagcg cgctggctgg caatcggcga tgcagcgtcc 1560
agctacgatc cgctgtcctc acaaggcgtg cataaggcat tggccgatgc gctcgcagcc 1620
gccccgcgca tttgcgccgt gctcgaacga caccaagaca ctgcggtgat ggaacaggca 1680
cagcagatgc tggcgcgttt cgaaggctac cagcgcatgc gcgagcattt ctatcggcag 1740
gaagcacgct ggctggatgc gccattctgg cgccggcgcc gtgccgcgca aatacctgcc 1800
ccgccccaca cggaccattc ccctataaaa acccaccgca tgaacgtatc gccttgagcg 1860
atcatcaata caaccaaata cccacgacat aggttcatgc tgggacgacg acactgcacc 1920
tgaaccacat gccgatgttc ggctagcagg accgcatcct gaacagcgct gccgcccgcg 1980
cagcacgcaa gcccgcccgg atgcacgacg tgcagcgcgg caccaggatc gccgacgcgc 2040
gcatcgcgtg gtcagtgcgc cggcattgcc agttgcacct cggcactacc gaccttgttg 2100
cgcgggtcgc tggcggcacc tagctcatcg cggcgtttgt cccattccac cgtctgcagg 2160
ttgccccaga catggctgga accgcgcccg tccttggcgc tgtcgccagg caacttgagc 2220
ggatggtcca tcgccttcag cccctgcacg gtggctgcat cgaaggtacc ggtctcggcc 2280
tcgatcacgt ccggcaacca ctggtggtgg tagcgcttca gcgcggcgac ctgttgcgga 2340
tccagaccgt cgtcgtagcc gaggatgcca agcagaacca tggtgatgat acgactaccg 2400
cccggagtac cgagcacgat cgccttgtcc gcgttctcca tgaaggtcgg cgtcatcgag 2460
ctgagcgggc gcttgcccgg tttgggtgca ttggccgcat agcccatcac cccgaatacg 2520
ttgggcgtac ccggacgcaa ggcgaagtcg tccatctcat cgttgagcag cacgccggtg 2580
cccttgggga tcagtcccga gccgtacaac agattgaccg tctgggtggc gccgacacga 2640
ttgccttcac ggtcgatgat cgaaaaatgc gtggtctcat cgtcttccag cggggtcggc 2700
tgacccgaca acaggtcgct gggcgtggcc ttgtccgggt tgatggtcga acgcaggccc 2760
accgcatagt ccttgctcaa taaaatgcgc tgcggcacaa cggtgaaatc cgggtcgccc 2820
aggaagaagg tgcggtcacg gtaggcacgg cgcatcgctt ccacggtcag atggatccgg 2880
tgcaccgggt ccatcgcctt gagatcgtag gcttccagga tctgcagcat gctggccagc 2940
gcaatgccgc cggaggatgg tggcggcgcc gtggtgatcg tccagccctt gtagtcgaag 3000
cggatcggcg tgcgctgctt gaccgtgtag ccggccaact cgtcagcggt ccagcggcca 3060
ccggcctgct tgaccccagc cagcagcttc ctggcggtga cgccgcgata aaagccgtcg 3120
aagcccttgt cggccagcaa ctgcagagtg acggccagtt ccggctgctt gaacaggtcg 3180
ccctcggcga tcggccggcc atgacgcaga taaacctcgc gcgtgcccgg ataacgctcc 3240
atcaccttac gccgggcctg atagccctcg gccatgcgcg catacaccgg gaagccgtcg 3300
cgggcgatgc ggatcgccgg cgccagcgac tgccgcagcg gcaaccgacc atgccgggtc 3360
gccaactcca ccagcgccgc aggcagaccg ggaatgccag cggaccatgg gccgttgacc 3420
gagcggtcgt ggtccagtgc gcccttggcg tcgaggaacg tgtcgggcgt cgccgattcc 3480
ggcgccactt cgcgcgcgtc cagcatcgtg tcctggcccg tcctggcatc gtgcaggaga 3540
aagaaaccgc cgccgccgag accggagctg atcggttcga ccaccgacag cgtcgaggac 3600
accgccaccg ccgcatcgaa ggcattgccg ccctcgcgca ggatctgcaa gcccgcctcg 3660
gtggcgaggc ggtggccgct ggcgattgcg tcaccgggcg gatgcgacgt gggcgcagcg 3720
gcgctcgcac cgagcgaggc ctgggcccac gccgatgaca tcagcaccca ggcaagcaac 3780
aggacacagc gaacgctacg cctcatgcgc agcccccgct ccgtgtgggt acaactcggg 3840
gtggtcgcgg cgcaaccgcg ccagcttggc cagcaactgc ggatgggttt ccggaatcgc 3900
cggatccgga tcgatgcact ccacggggca caccaccacg cactacggct catcgaaatg 3960
accgacgcat tcggtgcagc gggccgggtc gatcacgtag atcgtctcgc ccatgaagat 4020
ggcctggttt gggcaggccg gttcgcaaac gtcgcagttg acgcagagcg cgttgatctt 4080
gagggacata gtgcgccatc ggaccctgac cagcgcatct taccggatcg tgatgacacg 4140
accatgcatt gacctgtaca acggcgccac cgcctacgcc tcgccactgc gggcgacgcg 4200
tgcgtgagga cgccggcgcg cgcaacgcgc gccggcgatg cacaacctac ttggcttcga 4260
cgaagatgta atcggcaccg gtcggcttga ccaccgcctc gacacgggca ttgtcggccg 4320
gggcgccgat atagaccacg cgcacgccct tcatgctgtt cggctcgacc ttggcgaagg 4380
ccgctgcgat caggtcggcc atcttggacg atgccgagga gccgaacgcc agcatgttcc 4440
ccggctgaat accacgaccg acggcggtgg tggcgctttc gacctgacgc tcgtacttgg 4500

```
cctggaactc cgcatccgac tccggcggca agtagtacag gaacgggctg ttggtgacat   4560
tgcccatgtt ctggattgcc acttgctgca ggtatttttt ccaaccggca tcgtcgtcct   4620
tggccggggc agtcagcgcc ggttgcgcat cggcgaccgg tttggccgcc tcttcctttt   4680
tgcaggcgct cacgcccagg gccaacgaga caatcaacaa cgcgcgtgcg gtggtcttca   4740
tggaacggtt tcctctgtgt agtcgatgaa tgacgggcgg ctcagccccg cgtcgcggcc   4800
tggcgggcct gaaccagcgc ctgcaacacc gaaggcggaa cgaagccgga cacgtccccg   4860
ccgaggcgcg caatctcgcg caccagcgag gacgagatga aactgtgttg ctcagccggg   4920
gtgaggaaca gcgtctccac ctcggggatc agatgccggt tcatgctcgc catctggaac   4980
tcgtactcga aatcggacac cgcgcgcagg ccgcgcagca gaaccccacc accgaccgaa   5040
cgcacgaaat gcgccaacag cgtgtcgaag ccgatcacct ccacgttgcg gtgtccagcc   5100
agcgcctcgc gggccagggc cacgcgcaat tccagcgaca gggtgggccc cttggacgga   5160
ctctgcgcca cgccgaccac cacctgctcg aacagcggtg cggcccgatt gaccaaatcg   5220
atatgcccat tggtgatcgg atcgaaggtg ccgggataga cggcgatgcg gctattggcc   5280
acggtcatgc gtaggatacc gcgtgaaagt cgccgggcag tttagcagcg gtgcgtcggt   5340
acagggcagc acggacctcg cggctaccgc cctcgcggta caacgcccag ccgaccggca   5400
gcgctggcgc ctgcccggcg ggcgattcca agtacaacca ggcatcgacc gccaggcgtg   5460
ccggcaaacg ctgcaacgcc ttctcccaca gaccggccgt gaaaggcggg tcgacgaagg   5520
cgatatcggc cagcgcggcg ccatcgtgtt cggccagcca gcgcagcgca tcgccctgca   5580
ccacctccac ctgagtctgg gcctgcaatc tggcgacggt ggcgcgcaac tgtgccgcct   5640
gggccgggtc gcgttcgatc agacaagcgc tgtgcgcgcc gcgcgacacc gcctccaacc   5700
ccagcgcacc gctgcctgcg aacaggtcca acacgcgcgc accgggcagt atcggctgca   5760
accaattgaa cagtgtctcg cggacccggt cggacgtcgg gcgcagcccg gccaggtcgg   5820
gcaccggcaa gcgcgtattg cgccaacgcc cgccgatgat gcgtacctgc cccgcaccgg   5880
gacggttcat cggcagcctc gcgcgggtgt gacggcaaca gaaaccaggc gcagggtcgg   5940
catcgacggc aagcgttgcg gaacggaacc cggatgatag accagccccc tctgcggcgt   6000
atgcatcggg cacggcttga agccgacctc tgccgccacc atgtccgctg atagagccgc   6060
gcgccccccgc gcacggccat ccgtcctcca tggagcacct accgatgagc gtggaaaccc   6120
aaaaagaaac cctgggcttt cagaccgagg tcaaacagct gctgcagctg atgatccatt   6180
cgttgtattc caacaaggag atcttcctgc gcgagctgat ctccaatgcc tccgacgcgg   6240
ccgacaaact gcgcttcgag gcactggtca agccggaact tctggacggc gatgcgcaac   6300
tgcgcatccg catcggcttc gacaaggacg ccggcaccgt caccatcgac gacaacggca   6360
tcggcatgag ccgcgaggag atcgtcgcgc acctgggcac catcgccaaa tccggcacct   6420
ccgatttcct caagcatctg tccggcgatc agaagaagga ttcgcacctg atcggccagt   6480
tcggtgtcgg cttctacagt gccttcatcg tcgccgatca agtggacgtg tacagccgtc   6540
gcgccgggct gccggccagc gacggcgtac actggtcctc gcgtggcgaa ggcgagttcg   6600
aggtcgccac catcgacaag cccgagcgcg gcacccgcat cgtgctgcac ttgaaggagg   6660
aagagaaagg cttcgccgac ggttggaagt tgcgcagcat cgtgcgcaag tactccgacc   6720
acatcgcctt gccgatcgag ctaatcaagg aacactacgg cgaggacaag gacaagccgg   6780
aaacccccga gtgggagacc gtcaatcgcg ccagcgcgct gtggacacgg ccgcgcaccg   6840
agatcaagga cgaggaatac caagaactgt acaagcacat tgcccacgac cacgaaaacc   6900
cggtggcgtg gagccataac aaggtcgaag gcaaactgga atacacctcg ctgctgtacc   6960
tgcccggccg cgccccgttc gacctgtacc agcgcgatgc ctcgcgcggg ctcaagctgt   7020
acgtgcagcg cgtcttcatc atggaccagg ccgaccaatt cctgccgctg tacctgcgct   7080
tcatcaaggg catcgtcgat tccagcgacc tgccgctgaa cgtctcgcgc gaaatcctgc   7140
aatctggtcc ggtgatcgac tcgatgaagt cggcgctgac caagcgcgca ctggacatgc   7200
tggaaaagct cgccaaagac gatcccgaac gctacaaggg cgtgtggaag aacttcggcc   7260
aggtgctgaa ggaaggtccg gcccaggact tcggcaaccg cgaaaagatc gccggcctgc   7320
tgcgcttcgc gtccacccac agcggcgacg acgcccagaa cgtgtcgctg gccgactacg   7380
tggcgcggat gaaagacggc caggacaagc tgtactacct gaccggggaa agctacgcgc   7440
aaatcaagga cagcccgcac ctggaggtgt tccgcaagaa gggcatcgag gtgctcctgc   7500
tcaccgaccg catcgacgag tggctgatga gctatctcac cgagttcgac agcaaatcct   7560
tcgtcgatgt ggcgcgcggc gacctggacc tgggcaagct ggacagcgaa gaagaaaagc   7620
aggcgcagga agaagccgcc aaggccaagc aagggctggc cgagcgcatc cagcaggtac   7680
tcaaggacga ggtcgccgag gtgcgggtct cgcaccggct gaccgattcg ccggcgattc   7740
ttgccatcgg ccagggcgac atgggtctgc aaatgcggca gatcctggaa gccagcgggc   7800
agaagctgcc ggagagcaag ccggtgttcg agttcaaccc cgcgcatccg ctgatcgaga   7860
aactggatgc ggaacccgat gtcgatcgtt tcggtgatct ggcgcgggtg ctgttcgatc   7920
aggccgcgct ggccgccggc gacagcctca aggacccggc cgcctacgtg cgtcggctca   7980
acaagctgtt gctggagctg tcggcgtaag cagtgacgca cctgcgcgtc gcaccgcgcg   8040
acgcagtcca cagcgcaccg acattgcaaa gaaaagcgga aacgaaaaaa gggcctacgg   8100
gccctttttt cttccatcgt cgacatcggc ttgcagcgca cgagcaacgc tgtaatgcgc   8160
```

cggtgcatca cgctcccgac gcgaccagca gcactcacgc ctgcattaac ttaaaacctc 8220
accagcttag aacttcaccg tcgcccgcgc ccagtaataa cgcccgagta gatcgtaggt 8280
cgccacatcg gtgttggcat tgacgacgtt gttggcgtag tacagtggcg gctgtcggtc 8340
ggtcaggttg tccacgccca cttcgaagcg ggtgtgccac ggcttgacct gatagccgac 8400
ctgcacgctg tgatagacat aggtaccgat gtcgcgcacc acattggcct gaccgatatc 8460
ggccgacaac ccctgacgcg cgtcggcact gccaatctcg gtgcggccga cataacgcac 8520
gcgccaagac gcactccagt cgcccagatt ccagctcaac gtgccgaggc cacgccagcg 8580
cggaaaattg ccgtaagcgt aggtgtactt gccggcattg tggatggtga cggtgtcggg 8640
atcggcggta ttcggattga tatcgtagcg gatcacatag gtgccgttga ggctggcatt 8700
gaagctaccc caggcggtct gcggcaagcg atagttcagg ctgaaatcgg caccgctggc 8760
ccacaacttg cccagattca cggtcggctc ggcgatatag ttgatcgtgc cattgtcgtt 8820
gcgatggatc agcggacaga acggactcgc gtcgttggcg tagcactggt tcagcacggt 8880
ctgcgccgac acctgggtga tggtgtcctt caagtcgatc ttccacaggt ccgtgctcag 8940
cgacaggccg tccacccaac ccgggtcgta aaccatgccg aaatcgtagg acttgccggt 9000
ttccggtttg agccggtagc cggccaccac cgcgcctgaa gccttggcgg acacctgatt 9060
gttctcctgc tggtagctgc catcggtggg cacgtgggca caggcagccg cgtgtccgcc 9120
gctgtagccg tcgcacggat cgttgaccgc cggggcatca ccgaccacgc cggagtaaag 9180
ctcgctgatg ttgggcgcac ggaacacctg cgagaccgtg ccgcgcagca acaggttctc 9240
gaccggacgg tactccaacg ccagtttgct gttggtcttg ctgccgaccg tgtcgtaatc 9300
ggaaaagcgg ctgccgacgg tcaggtttag cgaatgcacg ccaggcagcc ccgccagcaa 9360
cgggaacaac gcctcggcat aggcttcctt gacgctgaaa ctgccaccga gcacgctggc 9420
gcagtattcg agcaccccgc agatgccgtt ctcgtcgccc gtccacagcg gatcggcggc 9480
ggtcgaggtg cgttccttgc ggtaagccac accggccgcc agactcactg caccggccgg 9540
cagatcgaac aggttgccgt tgacgttggc ttcgaactgt ttgacggtgt acacgttggt 9600
caccatcgga ttgacttgca gcgcccgcaa cgcggcctgg ttccctgggt tgttgaggtt 9660
gaacacgtcg atc 9673

<210> 4
<211> 267
<212> DNA
<213> Xanthomonas albilineans

<400> 4

ctagccaccg aggcgaccaa caatgcgcaa gagcaagttc accgagagcc agatcgtcgc 60
cacgctgaag caggtggagg gcggtcgcca ggtcaaggat gtatgccgtg agctgggcat 120
ttccgaggcg acgtacttgc tcttccactg gtaataggtc gccgtgctga tgccgacttg 180
gcgacagatg tctttgactg gaacgcctgc gtcggcctgc ttgagcgtgg cgatgatctg 240
tgtctcgttg aacttcgatg tgcgcat 267

<210> 5
<211> 1755
<212> DNA
<213> Xanthomonas albilineans

<400> 5

ctacttttcg atcagtacgt catcgatgaa catcgcgtcc agaccgctgg tgaagaagat 60
cgacagcgca tcctccactg aatgggcgat cggtttgccc atgacgttga agctggtgtt 120
aagcaccagg ggaatacccg tcaggcggta gaattctttg atcagggcgt gatagcgcgg 180
gttccaatgt tgcttcaccg tctgcagacg tccggtgccg tcgtggtgca cgacgcccgg 240
caccttgcgc gtggcttccg cacggaactt cagggtgcgc tccatgtagg gcgattcctg 300
gtacagctcg aaatactccg cgccgtgctc atgcaaaatc gacggtgcga acgggcggaa 360
ctcctcgcgg aacttcaccc gcgcattgat gatgtccttg atcgcaggcg aacgcggatc 420
tgcaaggatc gagcgattgc ctagggcccg tggcccgaat tccgcgcggc cttgcaccca 480
ggcgacgatc ttaccctcgg tcagcagccg ggccgcgcgt tgtgctgcgt cgtcgaggca 540
acgagtgaat ttggatagcg cgccgaagcg ctccacgtta tgcaaggtct ccgcactcat 600
gctgctgccc aggtagggcg attgttcgcg cgcagccggc ggtgtctgct caggatggtc 660
ctcggcgtgt gcccataatg cggcgcccac cgcgttaccg tcatcgccag gggcggcgaa 720

tacgtgcaga tgacggaacg gagtttcagc cagcacgcgg ccgttagccg aggaattgag 780
tgcacagccg ccgcccagca ccaagtggtc ggacaagccc aaagcgtgca ggttgtgcag 840
gaattcgaag aggacgtcgc agaacacctg ctggccggca taggccaggt tggccaattc 900
gatcgttggc tggcccttgc atcggcgcat tgcatacagc gtgcgctgca actggctgaa 960
ttgtgctgcg ggcgcaaacc tcagcgttag gccgtcgacg cgtagcatct ggcgcaacaa 1020
ctcgtacagt tgccgatcat gttgcccgta ggcggccagg cccatcacct tccattcttc 1080
gccggacagg gtgccgaagc cgcaaacctc gcagatcata ccgtagaaga agcccaggct 1140
ggcccaactg ctggtctcgc tttggtggat cggcgtaagc ttgccctgtt ggtagtggta 1200
gcaggccaaa gcatttttt cacccatgcc gtccagtact gcgcacaccg cctcctcgaa 1260
cgggctggtg tagcagccgg ccaccgcgtg ggttaggtgg tgctcgtaat gacggtagct 1320
gggtggcttg aaggcaggct cggccatgtg gctcaagtca tattcgagca ggtgtccggg 1380
gtgctccacc atcgccagct gcgaacggta gaagaagctc tgtgccacga attgcttgtt 1440
gacgtgccaa ggcaggtcgc cgaaggcgct gcggtattgg tctaccgctt gcgcggtctt 1500
gcccaggccc tcccgcatca gttcaggtgt ttgcccgctc caactagtag cgacgaccag 1560
ttcggcgccg ggatcgccgt attcgtggac cagcttgatg gcgcgctgaa acacgtccgg 1620
ggcaacgccg attgaacgct tgtactgcag gtagcgctcg gtggcctcgg caaagcgcac 1680
ctgaccatcg tcgccgacga tagcgatggc tgaatcgtgg aaggaattgg cgagtccgat 1740
gtaagtgcgc ttcat 1755

<210> 6
<211> 1491
<212> DNA
<213> Xanthomonas albilineans

<400> 6

ctacggcgat gattgtggcg caaattgtgt cagtttgaac tgcaatccca gcgtagagag 60
cgccacgaaa gcattggccg cgatgtagta caccaccgta gccccgaagg cctgcttgaa 120
agccagagct acgcctgccg gcccctgcag atgctggtgc aggccgctaa agaaaatttc 180
cgagaccagg gcgatgccca gcataccgcc gacctgctgg atgacctgca gcgcgccgga 240
acctgcgccg gcatccttca gaggtaccgt acgcatcact gtctggaata gcgaggcgat 300
ggtgatgcca cagcccagtc cgccgatcag caacggcagg gtaagcgtcc agggatccag 360
cgagccttca ctgcgcgtga tgatgaccca caaggccaga tagctagcga tcatcagaca 420
ggcgccgctg aagattttcg cgcgtaggct ttcgacgtgc cgagcgagca tagaggcaat 480
cgccacgccg acagggaaag gagtagtggc gacgccggtt tccagtgccg aatacgccag 540
tccttgctgc agaaagatca cgaacaccag gaaaaaaccc tgcagcgccg aatagaacac 600
cgacacggac aaggcgccca agatgtagtc gcgatggctc atcaggtaga tcggcagcag 660
ggccgggcgc gccaagtggg cttgccgacg ttgccaggcg acgaaggcca ccagcagcgg 720
aataccgagc gcaatggctg caaagcacca tagcggccag ccgtatgcgc gtccttctat 780
tagtgggaac accaggcaca acaaggcgag cgcggccagg gcgatgccga cccagtcgtt 840
atggatgccc gcatgcgccg gcaccttggg cacccagatg gcggccgcca gcaaggtcac 900
gaggccgatc ggcacgttga tcaggaagat cgcgcgccag ccgacgccga acgcatcgat 960
gtggatcagc aagccgctga cgaggggccc ggcgaatgag gccaggcccg cgaccaggcc 1020
gaacaacgag aaggcggccg cgcgctcctt cggagcgaac atggtttgcg cgatggccat 1080
cacctgtggt gccagcatgg ctgcggccaa gccctgcaaa gcgcgcgcga tgatgagcac 1140
gtggatattg ccagcgatgg cgcagaacgc ggacatcaag ataaaaccgg ccacgcccgt 1200
gccgaacatg cgcttgcggc cgagcatgtc acccaaccgc cccaacggca gcaaccccaa 1260
cgcaaacagc agaatgtata tcgctacgat ccattccagc tgttgctcgt ccgcgcccag 1320
gttcttctgg atactgggca gggcgacatt gacgatgcct acgtccagca agttcatgaa 1380
attggcgctc agcaacacga tcatcgctgg ccagcgccat cggtagtcga actgcgctcc 1440
gggtggtgcc atgccgggcg gcatacccag cgcttccttg ggtttttgca t 1491

<210> 7
<211> 954
<212> DNA
<213> Xanthomonas albilineans

<400> 7

ttatccgctt atggccgctt cagccggtcg catggtgacg gtgagaaaat gcaagatgtc 60
gcgctccaac tcgcgctgga aggcgctgcg gtcgaagcca ggcggatcga tggccgcctc 120
gcccacgcga gctttcatcg cctcggggaa tacgctgatg aaggcgtagt ggccggcatt 180
gggcaccacg cgcgcttcca gtcgaccatc attgcctagc gccgtgcgtg tcgccacaat 240
cgtttcgtgc gcccattgat ccttttcacc gacgatgagc agcaccggta cctcgacttt 300
cgccagggca tcctcgtgca tgtacaggct gaaatccggc gcaagcgcca ccacggcgcg 360
cacgcgcgga tcagctgtga ccggcacggc cctgatcggt acccgatttt gtcgcaccag 420
cgcggtccag gcgggttgtt cggcgtgttc cgggcgatgc gcaaaatcga ccatgaaacc 480
ggtatgcggt tcgccccggg cgatcgctaa ggcggtgtag ccgccgacgg agtggccgat 540
caccgctacg ttatgggcct gaatggcagg accgaactgc gcatggccgg tgagcgtatc 600
gatcaccgcg cggatgtgcc gggggcggtc ttccagattc tgatagctgt attccagctg 660
atgctggaac aggttgtcgc ccggatgctc cggcaaggcg acgataaagc cgtgccgtgc 720
taggtaatgt gccagcgtgc gaaacactag gccggcgctg cgcgtgccgt gcgagatcac 780
cgctagcgga aacgggccgg cttcgatcgg cgcgcccagg gccacgtcca gcgtataagg 840
tcccatcgcc gtatcccgtg aaggcgtggc ggtgggatac atcacccaca tcggcaccac 900
cctgctggca tcaccatcgg tttccagttt ttggcaaccc acatagctat tcat 954

<210> 8
<211> 1356
<212> DNA
<213> Xanthomonas albilineans

<400> 8

ttacgccggc atcagcttat ccagacttgc accggcgggc gccagccaaa cagcggtacg 60
accttcgccc agctccctgc ccatcaagcc tcgcacgccg gccagatcct gcggcgttgg 120
cagcaacgcg gccagccgtt ggccgtcggc atcgtgcacg gggttgccat ctaagtcgaa 180
ggcaagcccc ttgcacgggc cgaaatcgcg gtggaaacgc tcgtgcggca gctgtagctc 240
aaaagccagg ccaaggcgcc tgagctgttg attccagcgg ccgatgatag cgccgacttc 300
ggctatgtat tgtcggcgca ttaccgcatt gattgccaac tcggcaggtg cggtggacga 360
gaccagtctg tcttcgcagc gcacgtcgac ggcgacctcc gtaccttcga gcttgtcgaa 420
gttgcgtggg ctgcggatgc cggcctggta caggacgcgt gaacgctccg aaacgtcgtg 480
gccgaacaga tcaaagatct tcggtagcca atagttaagg tatttctgaa cgactggcaa 540
ggggatcgca ccggcgtcga agatcgcgtg cgtatcctca cgcaaggtaa tctcggcgct 600
tcgatacagc acgcgctcca ggccatccac gccgaactta atatgcagag gttcctcgaa 660
catcatgaag cgggcggtgc gtgccaacgg caggaaagct gactgggtca ccgcttgaat 720
ctggtacttg cctacccggt cggcgaagaa gcaccacatg aaatgcgata gccagtcttc 780
ggtgtggtag ttgaaggcat cgagcaggcg cgggttctgc gcatcgccac tcatgcgttg 840
cagcaggccc tcggcggcgt cggctccgtc gctgccaaag tattcgatca gcagatgcga 900
catcgcccag gtgtgccggc cttcctctag aaaaaactgg aataagtgct ccaggtcgat 960
cgcgctgggc accatttgcg tcagctcgtg gctctgctca accgcggcgt tttctacgtc 1020
accttgcacg gtgacatgat ccagcagcag gtcacgatat tcttccggca cgcacgacca 1080
tgccacctgt cccttgcgct cgccgaacac tacggtgttg cggtctggcg gcatcatgaa 1140
tacgccccag cggtagtcgc tggggcgcat gcggtgatag cgcgtccact cgctgccctt 1200
gacgccaccg gtaggcatgc gcaggttcat ctcgcgatcg tggaattcgc tggggccgcg 1260
gaggcgccac cattgcagga agcgaacttg gtaggaagtc agttgcctga ccagcgcgct 1320
gtgtggatca aggtcgatat tgttaggaat gtacat 1356

<210> 9
<211> 948
<212> DNA
<213> Xanthomonas albilineans

<400> 9

tcaggccgcg ctgtgcatcg aggtaggggc gacttcgccg accgtgagcc cgatgaagtc 60
gatgatccgc tgagccacgg cacccggatc attgaacagt tgcaggtgac cgccatgatc 120
tagcaggtcc agacgcaaag acgggtcgtg cctagccaac tgcaccgagg cggagtagtg 180
gctgaagctg tcgtccttgc agtgcacgat cagggtaggg tgcctgccca gggcggtggg 240

cagcaaggct tgcacggatt gcttgttctc ttcgtaggca cgcatgtagc gcgagaacac 300
caatgtgctc gctggatcgg ctaggtgcag catggtgagc ttttcggcca agtcgtcgcc 360
gcgtaaaggt tggccgcggt acttgtccag gatggcggcg agctttttgg cctgttccag 420
accgtgccgc tcgatctgaa ggtagatcgg caaggcgcaa cgttcgaatt cggattttac 480
gatgggcggc agcaggcccg ccggcgccac ccaagccatg ctgcgtggtg cgaagccatg 540
cagcgcaatg gcatgcacgg ccaattgtgc agcctgacac caaccgacaa aatggcaatc 600
ggcgtagtcg tgttggtgca ggatgcccag cagggtcgcg gcttggcgat ccagatcgaa 660
gtcttccgcg gttaccgatg tctgggcatt cgggcagccg atggattccc agcacaacac 720
atggaaatgc ctagccagtc gttgcgccaa ccggctcagc agcaggtagg acatgccata 780
gggcggtagc agcaccagct tgggcgatgc ctgagcgcct agccaataca gctcaagctg 840
ccgtccatcg gtagtgcagt attgcgacag ccttacccct gcgagcgcgt cgtccagggc 900
ggacagatct tgcttttcca gatagtgcgg caagcaagca cagcccat 948

<210> 10
<211> 252
<212> DNA
<213> Xanthomonas albilineans

<400> 10

tcacgagtaa ctcgattcga acccacttcc gtctggagag ctcgcgtccc ctaaattctt 60
gtcatcgagt tcgcgcagcg ataaggggcg catgtcggtc caggtttcgt cgatatacgc 120
catgcactcg tccttaccgc cagcatagcc ttccttgcgc cagccaggcg ggacctcaag 180
atcggacggc cacagtgaat actgcagttc gtcgttgatc agcaccagat aagcctgttc 240
ctcgaacgtc at 252

<210> 11
<211> 2151
<212> DNA
<213> Xanthomonas albilineans

<400> 11

ttgcgctgcc ttatcataaa taattacgat tcgttcactt ggaatctcgc cgactacgta 60
gcgcagatct tcggcgaaga tcccctggtg gtgcacaacg acgagtactc ctggcacgaa 120
ctgaaggacc gcgggggatt ttcctcgatc atcgtttcgc ccggtcccgg ctcggtggtt 180
aatgaagcgg attttcacat ctcgctgcag gcgctggagc agaacgaatt tccggtgtta 240
ggcgtatgcc tgggctttca gggacttgcg catgtctatg gtggccgcat cctgcatgcg 300
ccggtgccct ttcatggccg tcgctccacc gtcatcaaca ccggcgacgg tttgttcgaa 360
ggcatcccgc agcgtttcga ggcagtgcgc tatcactcgt tgatggtctg ccagcaatcg 420
ctgccgcctg tgctgaaagt gacggcgcgt accgattgcg gtgtggtgat gggcttgcag 480
cacgtgcaac acccgaaatg gggagtacag ttccaccccg aatcgatcct caccgaacac 540
ggcaagcgca ttgttgctaa ctttgccaag ctggctgcgc gccacagtgc accgttactt 600
gccgggtcgg agcaggccgg caaggtttta agcgtttgcg cgcccgagat ggtgacaccg 660
cgggtacgtc gcatgctgag ccggaagatc aagtgccgtt ggcaggcgga agatgtcttt 720
ctggccttgt tcgctgacga aaagcattgc ttctggctgg acagccagct ggtctgcagt 780
ccaatggcgc gctattcgtt catgggagcg gtgaacgaga gcgaggtagt gcggcattgc 840
gtgcggccag ggagcatggt gcaggaggca ggcgagcggt ttcttgctga gatggatcgg 900
gcgttgcaat cggtgcttac tgaggacgtc gccgagcggc caccgttcgc gtttcgcggc 960
ggctacgtgg gctacatgag ctacgaaatg aaatcggtgt tcggcgcgcc ggcttcacat 1020
gccaatgcca tccccgatgc gttgtggatg cgcgtggagc gcttcgttgc cttcgaccac 1080
gccactgagg aggtatggtt gctggcgctc gccgatacgg aggatctgtc ggcattggct 1140
tggctagacg ccatcgagca acgtatccat gccattggtc aagcggctcc ggcttgcatt 1200
tcgctaggcc tgcgcagcat ggaaatcgag ctcaatcatg gtcgtcgcgg ctaccttgag 1260
gcaatcgagc gttgcaaaca acgcatcgtc gatggcgagt cctatgaaat ctgtcttacc 1320
gacctgttct cgttccaggc cgagctggat ccattgatgc tctatcgcta catgcggcga 1380
gggaacccag cgccgttcgg ggcctatttg cgtaacggta gcgattgtat ccttagtact 1440
tcaccagagc gttttctgga agtggacggc cacggcacga ttcagaccaa gccaatcaag 1500
ggcacctgcc gccgtgccga ggatccccaa ctggaccgta acttggccat gcgcctggcc 1560

gcctcggaaa aggaccgagc ggaaaacttg atgatcgtcg acttgatgcg caacgaccta 1620
agccgcgtgg cggtgcccgg cagcgtcacc gtgcccaagc tgatggacat cgaaagctac 1680
aagaccgtgc atcagatggt cagcacggtg gaagcgaggc tgcgcgccga ttgcagtcta 1740
gtcgacctgc ttaaggcggt gttccccggc ggctcgatca ccggcgcacc gaagttgcgc 1800
agtatggaga ttattgatgg cctggagaat gcgccgcgtg gcgtgtattg cggcagcatc 1860
ggctacctgg gctacaactg cgtcgccgac ctaaacattg cgatccgcag tctttcttat 1920
gacgggcagg aaatacgttt cggcgccggc ggcgccatca ccttcctgtc cgacccgcag 1980
gatgagttcg acgaagtgtt gctgaaggcg gaggcgatcc tcaagccgat ctggcattat 2040
ctacatgcgc cgaacactcc cctgcactac gagttgcgag aggacaagct gctgctagcc 2100
gagcactgcg ttagcgaaat gccggccagg caggccttca tcgaaccatg a 2151

<210> 12
<211> 414
<212> DNA
<213> Xanthomonas albilineans

<400> 12

atgaggcccc cacgcttacg cgcgaaccag gacgggctgc tgatggatac ggccggccgg 60
gtggtcgagg gctgcaccag caatctgttc ctcgtcgaga acggccatct ggtgacgccc 120
gacctgggcg tggccggcgt cagcgggatc atgcgaggca gggtgatcga atatggccgg 180
cagcacggtc tcgcctgcgc ggtaaagcac gtctatccgg accagctagt gcgtgctcag 240
gaggtgtttc tgactaacgc cgtgttcggc attctgctgg tgcgcagcat tgacgctcac 300
agctaccgca tcgatcctgt taccctgcgt ttgctcgatg ccctgtgtca gggcgtatat 360
ttcaccgaac ggtcactaca tcaggtttcc acccatgccg gccaagaccc ttga 414

<210> 13
<211> 603
<212> DNA
<213> Xanthomonas albilineans

<400> 13

atgccggcca agacccttga aagcaaggat tactgtggag aaagcttcgt cagcgaagat 60
cgctccgggc aatcgctgga gtcgatccga ttcgaggatt gtacgttccg acaatgcaac 120
ttcaccgagg ctgagctcaa tcgctgcaag ttccgcgaat gcgagttcgt cgactgcaac 180
ctgagcctca tcagcattcc gcaaaccagc ttcatggaag tgcgcttcgt cgactgcaag 240
atgctcggtg tcaactggac cagcgcacaa tggccatcgg tgaagatgga gggggcgctg 300
tcgttcgagc gctgcatcct caacgacagc ttgttctacg gcctatacct ggccggggta 360
aaaatggtgg agtgccgtat ccacgatgcc aacttcaccg aagccgactg cgaggatgcg 420
gacttcacgc agagcgacct gaagggcagc accttccaca acaccaaact gaccggcgcc 480
agcttcatcg atgcggtgaa ctaccacatt gacatcttcc acaacgatat caagcgggct 540
aggttcagcc tgccggaagc agcctcgctg ctcaacagcc tggatatcga gctgtccgat 600
tga 603

<210> 14
<211> 609
<212> DNA
<213> Xanthomonas albilineans

<400> 14

atgcatccgc cgtcgccgtt gaacacgcag cagaaagact ggctgacacg cggtggttcg 60
ttgaccgcgc acctgcgcct gttggggcag gtacaggtgc aagtgcaacg ggagcacaaa 120
gccatggcct ggctggatga atatcgggtg ctcggactgt cgcgctgcct gcttgtatgg 180
gtgcgtgaag tggtcctggt ggtggacgcc aaaccctatg tctatgcgcg tagcctgacg 240
ccgctgaccg ccagttacaa cgcctggcag gcagtgcgta gcatcggcag tcgcccgtta 300
gctgatctgt tgttccgtga tcgcagcgtg ctacgttcgg cgttggcgag tcggcgcatc 360

accgcgcagc atccgctgca ccggcgcgca tgcaacttcg tggcacagtc gcatgcgacg 420
caagccctgc tggcgcgccg ctcggtattt acgcggcaag gcgccccgtt gctgatcacc 480
gaatgcatgc tgccagcgtt gtgggcaacg ctggaaccgg tggcagctcc gcgccaggcg 540
agtctgagtg cggacggccc ttgccggcat tcagcgcaga tcgtctcgcc tgagtcgatg 600
ctggaatag 609

<210> 15
<211> 5880
<212> DNA
<213> Xanthomonas albilineans

<400> 15

tcaggcatcg aggtccgtca ccagcatgcg cgccagctca cgcagcgggt cgccttgtaa 60
catgctgtag tgattgcccg ccgcgctctt gatctgcgaa agtggtacgt aacctgtgat 120
atccggcagt acctcgctac ccccgcgtgg cttggacatg tcggcatagg acacgtgtac 180
cgcagtctgt gcctggtaca gatgagcgtt aggctgcagg cactgcggct cgaaaccggc 240
caacagcccc aggtgatagc gcgtaacgcg caattgctcg gccagcggtg gccacatgcg 300
gctttccaga gtaaacctca ggtgtgcgag cagtttgtcc agtgatgcct ggtggcggct 360
gtagtcgaac acgtgctcgt cgtcaccgtc ggcgaacagc agctgccggg cttcgtctat 420
ttcagcctgc tcgaagccgc gcttggccaa cgcggccaac gtattgagcg ctgccacgaa 480
ggtaagctgc cggggctcgc gcgcatgtac cggtatcagg ctgctatcga gcaggcccac 540
gtaatcgacg cgcaggccgc gccgctgcaa ttgctcagcc acagccaggg ctagcacgcc 600
gccggaggac cagcccagca agcggtaggg cgcaccggtc gggccagcca gcaacgcatc 660
gcagtagtgc gcggccaggt cggacaaatg cgcgaagcgg cgcaccggtt cgcattgcag 720
gccatagacc ctggcagagt gccctagggc ggcagccaga tcgatgtagc aatgaatctg 780
gccgccgatc gggtggatgg catacaccgc cgcgcgttcg gtgcgtaggc taagcggtac 840
gataagactt accggcatgc tgccggcttg gctttggcgc atgccgcgct cgacgacagc 900
ggcaaaatct tccagcacag gggattcgaa cagcgtgttg acccgcactt cgatgtcgaa 960
actctggcgg atacgcgaga acaactgggt ggcaagcagc gagtgaccgc cgaggttgaa 1020
gaagttgtcg ttgaggctca cgcgtaaggg ggcggcctgt gcgggggtca gcagttcgct 1080
ccacagcttg gccagggtga tttcgacctc gctgcgcgga gcgaggtagt cgctgtcgct 1140
gctggcggct tgcggctcgg gcaggctcaa ggtatcgagc ttgccattgg gcaagcgcgg 1200
aagcgccggc agcgactgga agcgcgttgg cagcatgtag gtaggcaagc gttcctgcag 1260
cagcttgcgc agctcgtcga ggttcaggac accctggcgt ggcaccacgt aggccaacag 1320
ttccggcgtg ggcgagcctt gcggccaacc gatcacggcg gcctcggcga cctgcaggtg 1380
ggccgccagg gctttctcca cctggcgcac gtccacgcgg tagccgcgga ccttgacctc 1440
gtagtcgcgc cggccgagca gttccagcgt accgttgtcc agtaggcggg ccatgtcgcc 1500
ggtcctgtac agacgcgagc cgggggggcc gtagggattg gcgatgaagc gcgcggcggt 1560
caggccgccc tggcgccaat agccgtgcgt aatgccgagg ctttcgatgt gcacttcgcc 1620
catgatgcca ggcggcaacg gtcgcagttg ttcgtcgagc acatggacct tggtattggc 1680
gatgggccgt ccgaccggga cgaagccgct gccgctgtgc tgctcggccg gatcgcaata 1740
ggtcatgtcg ttgatttcgg tacacccgta gatgtaccag gccgtgcagg caggcagcag 1800
cgtcctgagc cgttgcagca gttccgccgg gcagggttcg atggagacga agagctggcg 1860
cagtcgcgcc agccgctgcg gtgtctcagc aacgtggtcg agcagcgcgt tgagctggga 1920
aggaaaggta tacaggcgtg tgatctgcca ggtttccagc gcgcgcacga aagcggggat 1980
gtcacgcacg gtatcctcgt cgatgaacac ctgcggtacg ccagcaagta ggccggcgag 2040
cagttccttg accgaaatgg caaaggcgat cgaggtcttt tgcgccaccc gctccccggc 2100
ctcgaaaggc gcacgtgccc acagcgcatg cagccagttg aggatttgcc gatggggcac 2160
catcaccccc ttgggacgac cggtggaacc ggaggtatac atcacgtagg ccagctgcgc 2220
cggatgcagg gcatgcggca gtggcgtatg cggttgacga gcgatggcgg catcgtccag 2280
gcgcagccgc ggtacttgga tcagttgccc gtcgatgtcc ttgccgcaga gcaacagccg 2340
tggctgcgcg tcgtcgagga tctgctgaat gtaggtggtg gggtaatgcg ggtccaacgg 2400
cacgtagcag ccaccggcct tgagcacgcc gagtagggca atgaggaaat cgggcgagcg 2460
gccgaaccac agggcgacgc gctcctgcgg gcgcaggccg cgctcgatca ggcaatgcgc 2520
caggcggttg gcgtgttggt ccagttgggc atagctcaac tgtcggtgtt gatcggcaca 2580
agccagttcc tcggcgtgca gtgccacttg cgcatcgaac agatccagca cactgcgcga 2640
ggtatccaga gtatgagggg tgaactcggt gcgagcgacc ggcagcgaaa aatccgagag 2700
gcggcagcgc ggttcttcca gcatccgctc cagcactctt tggtggtggg ccagcatgcg 2760
ctgaaccgta gccgccgaaa acagctccgc ggcgtattcg acagtgactt ccaggtggct 2820

tccgtcgccg atgaactgca ggtccagctc gttgggtgtg gtgcgttcgc caaattccat 2880
ctgagcgctg aggaagatct gggcaaatgc attgacgcct tcggtggcga aattttggtg 2940
tcggagcatg atcggcacga gcgggatctg gctgctgtca cgcggtttct tgagagcgct 3000
taagacatgc tcgaacggca gtgcgcgatg cgcgtaggcg tccagcactt gctggcgcac 3060
gtgctgcaga aaatcctcgg caaaggcgtg actgcccaag tttaggcgta ccgccaggat 3120
attgacgaaa aagccgatca gattctcggt ttccagctga tcgcgtccgg cgctggtagt 3180
acctaagcag agttctcgcc ggccggtgta ctggtgcaag acgatcgcca ggctcgccat 3240
aagtgtcatg aacaaggtga cgcgccgttc ctggctgaat gcggcgagac gcgcggccaa 3300
ggcgtcggga taggtcaggt gtagtatgcc agcacgccaa gctcgattag ccgggcgtgg 3360
aaaatcgtag ggcaaggcca gcccttcttc gtaaccatgc aaacgctgtt tccaataatc 3420
cagatcggcg ctgaaatcct gtacgcgctg ccatgtagca tagtcggcat attgcagtag 3480
cagcggtggc agtgccggtg gcgtctgctg tagcgcggct atatagaaag cacgtaggtc 3540
gtgaaagatc aggttaatcg accagccgtc gcagatgatg tgatgcatgt tcatcaggaa 3600
cacgtggtaa tcgtccgata cgcgcagcac cgataccttg agcagcgggc cgtgggcaag 3660
atcgaatacg tgcgcggcgt gctcggcgac taggcgtggc acttctgcgg gtgtcgctgt 3720
gatgcaaggc actgggacct gcatggcgtc ggcgatgtgc tggctgggat aatcgccgcc 3780
agcgcaagtt gctatgcggg tgcgcaaggt ttcatgcctg gccaccagcg cctggatcgc 3840
ctcgcgcagc gctgacatcg agaaatcggc actgcgtaaa tggcaggcga aggcgacatt 3900
gtaactggta cgttgctcgg gcatgtgttc atgcacgaac cacaggcgct cctgctgata 3960
gctcagcgga acgggagcat cgcgcacggc acgggaagag atggtgttgc cgccagtcgg 4020
agcctgttgt tgccgcgctt cgttgaccac tcgcgcaaaa tcttccagca caggggattc 4080
gaacagcgtg ttgacccgca cttcgatgtc gaaactctgg cggatacgcg agaacaactg 4140
ggtggcaagc agcgagtgac cgccgaggtt gaagaagttg tcgttgaggc tcacgcgtaa 4200
gggggcggcc tgtgcggggg tcagcagttc gctccacagc ttggccaggg tgatttcgac 4260
ctcgctgcgc ggagcgaggt agtcgctgtc gctgctggcg gcttgcggct cgggcaggct 4320
caaggtatcg agcttgccat tgggcaagcg cggaagcgcc ggcagcgact ggaagcgcgt 4380
tggcagcatg taggtaggca agcgttcctg cagcagcttg cgcagctcgt cgaggttcag 4440
gacaccctgg cgtggcacca cgtaggccaa cagttccggc gtgggcgagc cttgcggcca 4500
accgatcacg gcggcctcgg cgacctgcag gtgggccgcc agggctttct ccacctggcg 4560
cacgtccacg cggtagccgc ggaccttgac ctcgtagtcg cgccggccga gcagttccag 4620
cgtaccgttg tccagtaggc gggccatgtc gccggtcctg tacagacgcg agccgggggg 4680
gccgtaggga ttggcgatga agcgcgcggc ggtcaggccg ccctggcgcc aatagccgtg 4740
cgtaatgccg aggctttcga tgtgcacttc gcccatgatg ccaggcggca acggtcgcag 4800
ttgttcgtcg agcacatgga ccttggtatt ggcgatgggc cgtccgaccg ggacgaagcc 4860
gctgccgctg tgctgctcgg ccggatcgca ataggtcatg tcgttgattt cggtacaccc 4920
gtagatgtac caggccgtgc aggcaggcag cagcgtcctg agccgttgca gcagttccgc 4980
cgggcagggt tcgatggaga cgaagagctg gcgcagtcgc gccagccgct gcggtgtctc 5040
agcaacgtgg tcgagcagcg cgttgagctg ggaaggaaag gtatacaggc gtgtgatctg 5100
ccaggtttcc agcgcgcgca cgaaagcggg gatgtcacgc acggtatcct cgtcgatgaa 5160
cacctgcggt acgccagcaa gtaggccggc gagcagttcc ttgaccgaga tggcaaaggc 5220
gatcgaggtc ttttgcgcca cccgctcccc ggcctcgaaa ggcgcacgtg cccacagcgc 5280
atgcagccag ttgaggattt gccgatgggg caccatcacc cccttgggac gaccggtgga 5340
accggaggta tacatcacgt aggccagctg cgccggatgc agggcatgcg gcagtggcgt 5400
atgcggttga cgagcgatgg cggcatcgtc caggcgcagc cgcggtactt ggatcagttg 5460
cccgtcgatg tccttgccgc agagcaacag ccgtggctgc gcgtcgtcga ggatctgctg 5520
aatgtaggtg gtggggtaat gcgggtccaa cggcacgtag cagccaccgg ccttgagcac 5580
gccgagtagg gcaatgagga aatcgggcga gcggccgaac cacagggcga cgcgctcctg 5640
cgggcgcagg ccgcgctcga tcaggcaatg cgccaggcgg ttggcgtgtt ggtccagttg 5700
ggcatagctc aactgtcggt gttgatcggc acaagccagt tcctcggcgt gcagtgccac 5760
ttgcgcatcg aacagatcca gcacactgcg tgaccaatcc aaggcgagcg cggtatccgg 5820
actggccgcg gtcagcgcga cgtcttcggc atccagtagc gacatgcttg atagtttcat 5880

<210> 16
<211> 993
<212> DNA
<213> Xanthomonas albilineans

<400> 16

ttaaacgtgc agcttgagca tggcttcgcc atcgctgcgc gcagcgatgt caggggacga 60

ttgttcgggc gaataaggtt cggccatgca cacgaggatc ttgcggctgc cctcgtaggg 120
ctcgcgtccg tgcgaaacca gcatattgtc gatcagcagc acgtcgtccc gatgccagtc 180
aaaatggatc ttgtgctggg cgaaaactgt gcgcacatgg tcgagcatgg cggggtcgat 240
cggcgtgcca tcgccgaaat aggcgttgcg cggcagtccc tgctcgccga agaacgacag 300
catcatcttc tgcgcagctg cctccagcgc agtgtaatga aacaggtgtg cttggttgaa 360
ccaaacttca tcgccggtcg ccggatggca cgcaaaggcc cggcagatct ggctggtgcg 420
caggccgtcg ccggtccatt cgcattgcat gtcgttgcgg gcgcaataag cttctacttc 480
ctgcttgttg cgggtgttaa acacgtcctc ccatggcagg tcgacccctg cacggtagtt 540
cctgacgtag cgcacctgtt tgcgcgcaaa gatttcgcgc acttgcggat cgatagcggc 600
tgtgaccttg agcatgtcag ccaacggcgt gcagccgccc tcgctggccg gctgcacgca 660
atggaacagc agtttcatcg gccagacgcg ctggtaggcg ttctcgcaat gttgcgctat 720
ggacagctgc ctgggatatt cggtggccgt gtagacatgc tggccgacgt cggtgcgcgg 780
tgtggaacga taggtatagg ccagtcgctc atcgaagaaa cagcgtgaga tctgctccaa 840
gccaccaggg tgcgcaaagc cacggaacag taacgccctg tgttgccata gcagggtagg 900
ccacgtcgcg cggtgcgtgg cattccaatc agtcagcgtg gcctcggccg agtcggcctt 960
gatggtcagg ggaagatcag cgtttgtgtg cat 993

<210> 17
<211> 2298
<212> DNA
<213> Xanthomonas albilineans

<400> 17

ctaggttcga gcatggccga cgaagaacag gtgggattgc aggtgcttgg cgctagccag 60
tgtctccaac agcgcaggcc ggattacctt gccgctgcag gtacgtggga tcgtgctcac 120
ttcgacgaat agatggggat agtgatgctt gcctagcgcg ttcttgcaca aggcgcgtaa 180
ggcggcccat agcgcccctg tatcgatgct ggcatcgaca ggcaccacga aggcggcggg 240
gcggggcaag ccgaactcgt cttcgatcag gcagatcgcg cactccttca cgcaggcgtg 300
cgtctggatg acgctctcca gcgtctcagg cgaaagccaa caaccgttga tcttgatggc 360
ggagcccatt ctgcccaagt tatggaagcg ccccttggcg tcggcaaaga acaggtcgcg 420
tgtatcgaac cagccgtcga cgaacaattg ggcactgagt atggggtcgc caacatagcc 480
cctcgtcagc gtattgcccc tcacccacag gctgccgact tcgcctatgc ggcagatctc 540
tccctgcttg ttcaccagct tcacaacaaa gcctggtacc ggcgtgccag tgcaacccat 600
gagcgcgtgg cctggccgat tggagatgaa ggtggacagt acctcggtgc agccgatacc 660
gtcgagcact tcgacctgcc aacgcgtgct gatcgcatga ccaagcctcg ccggcaagct 720
ttcgccggcc gatatgcaca ggcgaagcgc cggccacacc gcatccggcg cggcctcggc 780
aagcaacagc ttgaacacgg cgggcacggc gagcaataca gtgacgtggt aagtgtggat 840
ggtttgcgcg atctgcctga cgctaagcgg cgcggcaatc acatggctga caccagcgag 900
cagcgacagc atcaggttgt tcaggccgta ggcgaaaaac aaccgcgacg gtgtatacat 960
cacgtcatcg ctgcgcagcc cgagcacggc ctgctggtag ttgagatggc agtgcataaa 1020
atcggcatgc gagtgcgtta ccgccttggg cgtaccagtg gagccggacg tgcatatcat 1080
caccgcgggt gcatcggcgg agcagggcgc aaccaccagt tcgtcgtttt cgatcaccgg 1140
catcaggctc gtcagctcta aggtcggcag gtggcgcaac gcggcatgat gggaaggcgg 1200
cagttcggca tcgatcagca cgaggcgagg cttgatggtc ttgagcgtgg tctcaaagtg 1260
gacgagcgac acaagctcgt ttatcggcgc aaagaccaag ccaccggcca agcaggccag 1320
catcagggca acgcccgcta ggctgtcgat agcaatcagc gccaccgcat caccgctttg 1380
caggccaagc agactcaagt gccgggcata ggtcgccgcg cgagagcgca actggcgata 1440
gctgaaggcc tgctggcgca acggatcgat catttgcgcc gtcgaagcca gatgcgctgc 1500
ggaaaaaatt tgcgcgcaca cgttgacctg gaccgacggg aggaagccga taggcgcaca 1560
ggcgaacacc gccgtgcttg cgtccgacca ggacggcatc ggcccatcgg tcgagcgtgc 1620
gaaccagctc gcgggcaaat gactggcaat ctgacatagt ttgccgtggt cgcaggccag 1680
cagactggta tccacctcga tcaggtcttc gacgcaggaa agcgcaggca aagagatctg 1740
cgccgcgctg ccgcatacgg cactatcgcg caagtccggc aggttccttt ggcggtggtc 1800
cgcatgccat agcagcaggc catcgctgcg tcgcgtggcc aaggcttcca gtgccatgcc 1860
cagggcgcct tgcaaccggt ccagttgctt gggttcctcg atacggccca aatccagtgc 1920
cagggtgttg gcgccggggg gcgattcgga cagcacgatt tggtgccgat gcttgaggta 1980
atcgcaaatc aggccggcca gcttgcctaa ccgtgcatat tcccgtagca ggctaccgaa 2040
gctgccacag gggtaaggtg cggcatagtc aatggttatg tgctggccga tcggcgtgtc 2100
gctgacatcg atacgcaagc caggataatc gcgccgccat tgatgcagca gcgtggtcca 2160

ttgacgagca taggcctcgt tgcgccctgg ccgcgtctga cctaccgacc aacgcaaatc 2220
tagttcggtg ccagagtgca tcggaagatt tgtcagtggg ctatccataa gcgttctcgg 2280
gtaaggcgat cgacgcat 2298

<210> 18
<211> 861
<212> DNA
<213> Xanthomonas albilineans

<400> 18

tcagcgtttc agcgcgtgga ccagataact ttgcggcacg ccgtgggtgc cgcgcggtgc 60
gaccggaaac ggccaacgcc ccatttgctg gccagcggcg gcgatggtca acacccctgg 120
ctcccagccc agtggttgga tcaggctttc cggttcgtca gtgccaaact ggcgagccat 180
cgcgtgcagc actcgggcat tgggcgagtt gagcatagag aggccgataa catcgaacaa 240
cacgctgctg cccttggcac tcaatgcatc gatgcgcgcg aacagcagca tcactgcctc 300
ggcgctcaag tagcacagca agccctcgac cagccacaag gtggcggcgc tgccgacgaa 360
tccactctcc ttaagtgcct ggggccagtc ttcgcgcaaa tcgatcggta gcgcaatgcg 420
ctggcaaacg ggctgggcgt catggagttt ttcgtgcttg tcggagagga catccatgtg 480
gtcgatctcg tagacccggg tatcggacgg ccaggggaga cgataagcgc gtgcatccat 540
accggcggcc aggatcacca cctggccaat gccttcacta accgcctgca tgatcttgtc 600
gtcgagccaa cgcgtccgta cctcgatcgc cggaggcatc ggtacgttct ggttgttgcg 660
tctgagctct tcaacgaatt catcgccggc cagacgccgt gcgaaagggt catggaacag 720
cgcctgctcc cgctcgcttt ccagcgcccg catgcctgcc acccataaag cggttctttc 780
gatatctctc atgcatacgc tccggttcgt ggtcggcttg cgccgatgca tcatagatat 840
gcatgactcg attcgcggca c 861

<210> 19
<211> 720
<212> DNA
<213> Xanthomonas albilineans

<400> 19

ttacggatgg tctgatccac gcaagcgaaa gatgagataa accacatcag ctgtcaacgc 60
cgatttaaat ttgacccact ttcctttgaa tcgtcgaagt aaatctgacc cacccggggt 120
cttccatcgt cgggctgcta ggctgcgcag ggcaaagccc gtcgcagccc agcagccctg 180
cgccggctca cgcccgaagg gcaggtagcc gatctcgtcg accaccagca gcttcggccc 240
tagtaccgcg cgattgaagt agtccttcag ccggttctgc gccttgaccg ctgccagttg 300
catcatcagg tcggccgcgg tgatgaaacg tgccttgtgc cccgccatca ccgcacgctg 360
gcacagcgcc agggcgatgt gggtcttgcc gacaccgctg gggccaagca tcaccacgtt 420
ctcggcgcgc tcgacgaagg tcaggtggcc gagctcgacg atctgcgcct tcgaggcgcc 480
gccggcctgg gcccagtcga actgctccag cgtcttgatg gacggcatcc tggcaagtcg 540
cgtcagcacc gtgcgcttgc gctcttcacg cgcgagctgt tcgcttgcca gcaccttctc 600
caggaagtag ctggcatcct cgcacgcggc ggcctgtgcg agtgcttgcc agtccgagct 660
caggcgtgcc agcttcaact gctcgcacag cgcggcgatg cgcgcacact gcaggtccat 720

<210> 20
<211> 20640
<212> DNA
<213> Xanthomonas albilineans

<400> 20

ttgcccaatg cgctcatgca gataactctt gtagccgtcc agtttgcagg cgtattgtta 60
ggcgtcaccg ctcgcgcggc gatccccaat aaggcgggta tgagacgcgc atggccgccc 120
ttcccgcagg cgtgctgtcg ctctattgct tacctcatgc agagatcgcc aatgtcgccg 180
ttacagcaaa cgctgctaac ccgcctcgcc agtgcggccg cctcccggac aatgatcgag 240

```
tttccgcgtc cggagcacgc atcgccacaa tgttgcgacg atgccgagct tgcgcgactg    300
atcgtgcagt tgtcggcggg actgcaaccg ctggcgatgc cgggtaccta cgtgatcatt    360
gccgcgccac atggtggttt gttcgcggca gccctgcttg cctgtttgca tgccaacctg    420
gtggcggtgc cgtttccact ggatgttgct cagccaaatg agcgggaaca ggccaggctg    480
gagacgatcc acgcacaatt gatggagcat ggcaatgtag cggttctgct tgacgatgtc    540
gccgatcgca gtgccttcgc gcgcatggcg catgctgcgg gcaccttcct ggcgaccttc    600
gccgatctaa agcgcgaatc gaccagcgcc tccttgtgcc cggcgtcgcc ttcggacgcc    660
gccttgctgt tgtttacctc tggttcctcg ggtgagtcca agggcatcct gcttagccac    720
cgcaacctgc atcatcagat ccaggctggc atccggcagt ggagcttgga cgagcatagc    780
catgtggtga cctggctttc tcccgcgcac aacttcggcc tgcatttcgg cttgctggca    840
ccctggttca gtggcgcgac ggtcagtttc atccatccgc acagttatat gaaacgaccc    900
ggcttctggc tggagacggt tgcggctaga gacgccacgc acatggccgc gccgaacttc    960
gcgttcgact actgctgcga ctgggtgatg gtcgagcagc ttccgccgtc tgcgttgtct   1020
acgcttacgc atatcgtgtg tggcggcgag ccggtgcgcg cctcgaccat gcagcgcttc   1080
ttcgagaaat tcgccggact cggtgcgcgt acgcagactt tcatgccgca cttcggcttg   1140
tctgaaaccg gtgcgctgag taccttggac gaggcgcccc aacagcgcgt cttggaacta   1200
gatgccgacg ccttgaacaa acgcaagcgc gtggcggcag gggcgagcca ggcgcgtgtg   1260
acagtgctca attgcggcgc cgtcgaccaa gatgtggagt tgcgtatcgt ctgtcctgaa   1320
ggcgagacgt tgtgcagacc agatgagatc ggcgaaatat gggtaaagtc gcctgcgatc   1380
gcccgtggct acctgtttgc gaagcccgcc gatcagcgac agttcaactg cagcatccgt   1440
cataccgacg atagcggtta ctttcgtacc ggcgacctgg gtttcattgc cgatggctgt   1500
ctgtatgtca ccggaagggt aaaggaggtg ctgatcatac gcggtaagaa tcattacccc   1560
gcacatatcg aagcctcgat cgccgctacc gcatcgcctg gcgcgctgat gccggtggtg   1620
ttcagcatcg agcggcagga cgaggagcgc gtagctgcgg tgatcgccgt caatcacccg   1680
tggacgccgg cagcatgcgc cgcgcaggca cacaagatcc ggcaacaggt agccgaccag   1740
catggagtcg ccctggcgga gctagccttt gccgaacacc ggcacgtgtt cggcacctat   1800
ccgggcaaac tgaagcggcg cctagtcaag gaagcctatg tcaacggcca gctgccgttg   1860
ttatggcatg agggtaagaa ccgggacgta ccagcggccg ccgcggacga tcggcaggcg   1920
caacacgtgg cggacctgtg tcggaaggtc tttttgccgg tgttgggtgt cgcgccgccg   1980
catgcccaat ggccgctgtg cgaactggcg ctggattcgc tccaatgcgt gcgtcttgcc   2040
ggtgccatcg aagagtgcta cggcgtgcct ttcgaaccca cgttgctatt caagcttgag   2100
acggtcgggg caatcgccga atatgtcctg gcgcacggac gtcaggcgcc cacgccgacg   2160
cgtgcgccgg tggcaagcac aacatgctca gaggaaccga tcgccattgt ggcgatgcac   2220
tgtgaggtgc ccggagcggg cgagaacact gaagcattgt ggtcgttcct gcggagcgac   2280
gtcaacgcga tccggccgat cgaatcaacg cgcccggact tatgggcagc gatgcgcgcc   2340
tatcccggcc tcgcgggcga acagctgccg cgctatgcgg gtttcctcga cgacgttgat   2400
gctttcgatg ctgcgttttt cggtatctcg cgtcgcgagg ccgaatgcat ggacccgcag   2460
cagcgcaaag tgctggagat ggtgtggaag ctgatcgagc aagccggtca cgatccgctg   2520
tcctggggcg gccagccggt cggcctgttc gtgggtgcgc atacgtccga ctatggcgag   2580
ctgctggcga gccagccgca actgatggcc caatgtggcg cttacatcga ttcgggttcg   2640
catttgacca tgattccgaa ccgggcttcg cgctggttca atttcaccgg ccccagcgaa   2700
gtaatcaaca gcgcttgctc cagctcgctg gtggcgctgc atcgggcggt tcaatcgctg   2760
cgccaaggcg aaagcagtgt cgccctggta ctcggcgtga accttatcct ggctcccaag   2820
gtgctgttag ccagtgcaag cgcgggcatg ctttcgcccg atggccgctg caagacgctt   2880
gacgccgccg ccgatggctt cgtgcgttcg gaagggatcg caggggtgat attgaagcca   2940
ctggcgcagg cgctggccga tggtgacagg gtctacggtc tagtccgcgg cgtggcggtc   3000
aaccatggcg gccgttccaa ttccttgcgt gctcccaacg tcaacgcgca gcggcaactg   3060
ctgatccgga cttaccagga agccggtgtc gagccggcca gcgtcggtta tgttgaacta   3120
cacggcactg gtaccagcct gggtgatccg atcgaaatcc aggcgctgaa ggaagctttc   3180
attgcgttgg gggcacaggc cgccccgtca aactgcggca tcggttcggt gaagtccgcg   3240
ctgggccatc tagaagccgc tgcaggcctg accggcctga tcaaggtgct gctgatgctc   3300
aagcacggcg agcaggccgg cacgcgccat ttcagcacgc tcaatccgct gatcgatttg   3360
cgaggtacgt cattcgaagt ggtggcgcag catcgcgcat ggccgtcgca ggtcggcatt   3420
cacggcacac tcttgccgcg tcgcgcgggt atcagctcat tcggcttcgg cggcgccaat   3480
gcgcatgcga tcgtggaaga gcatgtcatt gccacgcccc cctcgacgag ctccgctggc   3540
ggcccggtag gtatcgtgtt gtcagccggt agtgaagctg tcttgcggca acaagtgctg   3600
gccttgtcag cctggctaag gcagcaatcg ccgacacccg cgcaaatgat cgatgtcgcc   3660
tacaccttac aggtaggacg cgcagccctg tcgcacaggt tggcttttag cgcgacggac   3720
gccgagcagg cattggcgag gcttgagggt cgtctggcgg gcgtgatgga tgccgaggtc   3780
catcacggtg tcgtggatgc tgccgcaacg gctcccgaac atgggcggca gacgcgcgaa   3840
ggtcttgccg gtttgctgcg agcctggact cagggcgtgc gcgtcgattg gtcggcgctg   3900
```

```
tacggcatac agcgaccgca gcgcgttagc ctgcctgtct acccccttcgc tagggaacgc   3960
tattggctgc ccggccaggc tatgcatgcc gctgcggacg ctcatccgat gctgcagctg   4020
ttgcatgcca atgccaaact acatcgctac gccttgcgta ggtccggctg cgcaagcttt   4080
cttgttgatc attgcgtgga tggtcgacag gtactaccgg cagccgtgca actggaattg   4140
gtgcgcgccg tggcgcagcg ggtcatggcg caggatgagg gttgtatcga actggcgcag   4200
gtcgcctttt tgcatcccct catgatggag gagactgagc tggaggtcga aatcgaactg   4260
tcgaagagcg atcaagatga gttcgatttc caacttcacg atgctcaccg ccaacaggtc   4320
tttagccagg ggcacgtacg tcgccgggtc tatacggcga caccgcgctt ggatttagcc   4380
cagctgcaaa agctttgtgc cgagcgcgtg ttgtccggcg aagactgtta tgcgcacttc   4440
accgcctgcg gattgcagct cggcgaccgg ctcaaatccg tgcaatcgat cggctgcgga   4500
cgcaatggcg agggcgagcc gatcgcattg ggtgtcctgc gcctgccacc atcaagcgtt   4560
gaagacagcc atgtgctgcc tcctagcctg cttgatggtg ccttgcagtg tagccttggc   4620
ttgcagcgtg atgtcgagca catcgccatg ccatacacgc tggagcggat gacggtgcat   4680
gcgccgattc ctcccgaggc ctgggtgctg ctgcgtcacg gccatgcagc cagacagtcc   4740
ctggacatcg atctcctgga ttccgaaggt agggtctgcg tcagcctcgg caattacacc   4800
ggccgtgcac cgaaagccgt ttccgccgtc agggcgcttg tcttggcacc ggtctggcaa   4860
gcgttgaccg aaacggcgcc ggcatggccc gatccggccg aacgcatcgt tacggtagga   4920
gacgatgcat ggcgtagtca cttcggtttc gacgagccgg ccttgtccct ggaggacagc   4980
gtcgaagtca tcgcgacgcg actgggccag agcggcaagt tcgatcatct agtctggatc   5040
gtgccgatag ccgagagtga aaccgatatt gcagcgcaag gttcagcggc gatcgccggt   5100
ttccggttgg tcaaggcgtt gcttgcgttg ggctatgcgc atcgcccgct gggtctcacc   5160
gtgctgactc gccaagccct tacgcggcag ccgtcgcacg cggcagtgca cgggctgatc   5220
gggacgctgg ccaaggaata ctgcaactgg aaaatccgtc tgctcgacct gccgagcgta   5280
aaatcttggc cgcaatggga gcaattgcgg tcgttgcctt ggcatgcgca gggcgaagcc   5340
ctgatcggcc gtgggacttg ttggtatcgg cggcagttgt gtgaagtgct gccgctgccg   5400
tcgttggaac cgccgccgta ccgcgtaggc ggtgtctacg tcgtgatcgg cggcgctggc   5460
ggcttgggtg aagtattgag cgaacacttg atccgcacgt acgacgcgca gctgatctgg   5520
atcgggcggc gcgtgctgga cgaaggcatt gcgcgcaagc agacccggct tgcgtcgctg   5580
ggccgcgcac cgcattacat ctccgcggac gcgagtgacc cggctgccct gcaggcggca   5640
cataatgaga tcgttgcgct gcatggccag ccccatgggc tcatcctaag caacatcgtg   5700
ctgaaggatg ccagtctggc tcgtatggag gaagccgatt tccgtgacgt gctggccgcg   5760
aaactcgacg tcagcgtgtg tgcggcacag gtgttcggca cggcccccct tgatttcgtg   5820
ctgttttttt cttccatcca gagcactacc aaggcggccg ggcaaggtaa ctacgccgcc   5880
ggctgctgct atgtcgacgc tttcggcgag ctatgggcgc gccggggttt gagggtaaag   5940
accatcaact ggggctactg gggcagcgtg ggcgtcgtag cgggcgagga ctatcgccgg   6000
cgcatggcgc aaaaacacat ggcttcgatt gagggtgccg aagcgatgca ggtgttgtcg   6060
cagttgttgt gtgcgccgtt gcaacggctt gcctacgtca agatcgacga tgctaacgca   6120
atgcgcgctc tgggcgtagt agaggacgag agcgtgcaaa tccctgtgca cgcaccggcc   6180
gagcctccca gagggcagcc tggtcccgtg gtcgagttgt cggtgaatct ggatgcccgg   6240
cgcgaacggg aaactttgct ggcggcctgg ctgcttgagt tgatcgagca actcggtggt   6300
tttccgccgg caagtttcga catcgctacg cttgcgcaac gcctgcacat cgtacccgcc   6360
tatcgaagct ggctggaaca cagcgtgcgg atgctcggcg tgtatggtta cctcagagcg   6420
acgggggaaa gccgattcga gctggccgac aagccgcccg atgatgccag gggtgcctgg   6480
aacgcgcatg tgcacgaggc cagcgtcgaa gccggtgaag aggcacagcg gcgtctgctc   6540
gatcgctgca tgcgggcgtt gccggcggtc cttcgaggcg aacgcaaggc caccgaattg   6600
ctgtttccgg aaggttcgat ggcgtgggtc gagggtatct accagaacaa cccgcttgcc   6660
gattacttca acgcacaact agtcacgcga ctgattgcct acttgagacg acgactagag   6720
tcgacgccta cggcgcgcct gaagctgtgc gagatcggcg ccggcagcgg tggtactact   6780
gcaagcgtgc tacaacagtt gcaggcatat ggtgagcata ttgaggaata tctctatacc   6840
gacctgtcgc ctgtcttcct gcatcatgcg gaaaaacact atcagccacg agcgccttat   6900
ttgaggaccg cctgtttcga cgtagcgcgc gcgccgacgg cgcaggccct ggaatctggc   6960
ggctacgacg tggtgattgc cgccaacgta ctgcatgcta cgcgcgatat cgccaagacc   7020
ttgcgcaatg cgaaggcact cctcaaacct ggcggtctgc tcttgctcaa cgaagtgatc   7080
gagcgcagcc tcgtcttgca cctgactttc ggtctgctgg agagctggtg gttgccccag   7140
gacaagatct tgcgccttgc cggctcgccg ttgctggctt gcgccacctg gcgcagcctg   7200
ctggaggctg agggttttgc ggggctgagc gtgcacaggg cgcaacccga tgccgggcag   7260
gccatcatct gtgcctacag cgatgggata gtgcggcaag ccagtacgat cgaggttgcg   7320
cggaatgaaa aagtaaccgt tccgtcgcag ccggcggaag ccggggaatc gccgctggat   7380
ctggtcaaaa aactgcttgg acgcattctg aaaatggatc cggccacact cgataccagc   7440
cacccgctgg agtactacgg tgtcgattcg atcgtggcga tcgaactggc tatggcactg   7500
cgcgagacat tcccgggttt tgaagtcagc gagctgtttg aaacgcaatc catcgatacc   7560
```

ttgttgggct ctcttgagca ggctcctctc cttgctaccc tcacagctcc gccgcaacaa 7620
gacatgctgc agcagctgaa acaactgctg gcgcgtacgc tgaagctgga cattacgcag 7680
atcgacacga gcaagacgct ggagagctat ggtgtcgact ccatcgtcat catcgaatta 7740
gccaacgcct tgcgtgagcg ctatccgagc ttggacgcgt cacagctgat ggaaacctta 7800
tcgatcgacc ggctggttgc ccaatggcag gcaacggagc ccgccgtacc ggcagagcca 7860
acagcggaac cgccggtagc cgacgaagac gccgctgcca tcatcggact ggccggccgc 7920
tttccaggcg cggacacgtt ggaggagttc tggaacaacc tgcgcaacgg ccaaagcagt 7980
atgggagagg tgccaggcga gcgctgggat caccagcact acttcgacag tgaacgccag 8040
gcaccgggca agacgtatag ccgctggggt gcgtttctga gggacataga cggcttcgat 8100
gcagccttct ttgaatggcc cgacagcgtc gcgctggaat cggatccgca agcgcggata 8160
tttctagagc aggcctatgc cgggatcgaa gatgccggct acacgcctgg ctcgctcagc 8220
aagagccaac gcgtaggtgt attcgtaggt gtgatgaatg gttactacag cggcggagcg 8280
cgcttctggc aaatcgccaa ccgcgtgtcg taccagttcg attttcgcgg gccaagcctg 8340
gcggtggata ccgcctgttc ggcttcgctc accgcgatcc acctggcgct ggaaagcctg 8400
cgcagcggca gttgcgaggt cgcactggcc ggtggcgtga atctgctggt cgatccgcag 8460
caatatctta atttggctgg cgccgcgatg ctctccgccg gcgccagctg tcggccgttc 8520
ggcgaggccg cggacggttt cgtggccggc gaagcctgcg gcgtggtgct gctcaagccg 8580
ctcaagcaag cgagggccga tggcgatgtg atccatgccg taatcagggg cagcatgatc 8640
aatgccggtg ggcacaccag cgcgttctcc tcgcctaacc ctgccgccca ggccgaagtc 8700
gtgcggcagg ccttgcagcg cgcgggcgtg gcgcccgatt cgatcagcta catcgaggcg 8760
catggcaccg gcaccgtact aggcgatgca gtggagttgg gtgctttgaa taaagtgttc 8820
gacaagcgcg cggcgccatg cccgatcggc tcgctgaagg cgaacatcgg ccatgccgaa 8880
agcgccgcgg gcatcgccgg cctggccaag ctggtattgc agttcaggca tggcgagttg 8940
gtgcctagtc tgaatgcgtt tcccttgaat ccctatattg agttcggtcg cttccaggta 9000
caacagcagc cggcaccgtg gccgcgccgt ggcgcccagc cgcggcgcgc cgggttatct 9060
gccttcggtg ctggcggatc gaatgcgcac ctagtggtag aggaagctcc ggctatggct 9120
cccggggtct cgatcagcgc cagctctcca gccttgatcg tgctttcggc gcgaacgctg 9180
cctgccttgc aacagcgtgc tcgcgatctg ctcgtctgga tgcaagcgcg gcaggtggat 9240
gacgtcatgc tggccgacgt tgcttatacg ctgcacttgg gccgcgtcgc gatggagcaa 9300
cgcctggctt ttaccgctgg ctcggctgcc gagttgagcg agaaattaca ggcttacctg 9360
ggccatgcga ttcgggccga catctatctg agcgaggaca cgcccggcaa accggcaggc 9420
gctccgatcg tggccgagga agatctgctc acgctgatgg atgcctggat cgaaaagggc 9480
cagtacggtc gtttgctgga gtactggacc aagggccaac cgatcgactg gaacaaactc 9540
tattggcgca agctgtatgc ggacggacgg ccgcggcgga tcagcctgcc cacctatccg 9600
ttcgagcacc ggcgttattg gcaaacgccg gtgccgggcg agcgaagcct gcacgccacc 9660
gcgccagcta ctcgggaaac ggttgcggtt ggtgccatgc cggatccggc cggcgctacg 9720
gtgcaagccc ggttgtgcgc cttgtgccaa gtgttgttgg gcaaaccggt cacggcccag 9780
atggatttct ttgccgtcgg cggccattcg gtgctggcga tccaattggt ctcgcgcatc 9840
cgcaaaagct tcggggtgga gtatccggtc agcgctttgt tcgaatcggc gctgttgtcg 9900
gacatggcgc ggcagatcga acaattgcgg gtgaacggag tcgccaagcg catgccggcg 9960
ttgttgcctg ccgggcgcgt gggcgcgatt cctgcgactt atgcacagga gcgcctatgg 10020
ctcgtccacg aacatatgag tgagcaacgc agtagttaca acatcacctt tgccatgcac 10080
ttcagaggcg tcgacttccg tgctgaagcg atgcgtgccg cattgaacgc gctggtggtg 10140
cggcacgaag tgctgcgcac acgctttctt tcggaggacg ggcagctgca acaggtgatc 10200
gctgcctcgt tgacgttgga ggtgccggta agagagatgt cggtcgagga ggtcgacctg 10260
ctgctggccg cgagcacgcg ggagactttc gatctgcggc aggggccctt gttcaaggca 10320
cgcatcctgc gcgtggcggc cgatcaccat gtggtgttga gcagcatcca ccacatcatt 10380
tccgacggct ggtcgctggg agtgttcaac cgtgacctgc accagctgta cgaggcgtgt 10440
ttgcgcggca cgccccccac actgccgacg ctggcggtgc agtatgccga ctacgcgctg 10500
tggcaacggc aatgggagct ggcggctccg ctgtcgtact ggacgcgggc actggaaggc 10560
tacgacgacg gcctggactt gccctacgac cggccgcgcg gcgccacgcg ggcgtggcgg 10620
gcagggctgg tcaaacaccg ctatccgccg caactggccc agcagttggc ggcctacagc 10680
caacagtacc aagcgacgct gttcatgagc ctgctggcag gcctggcgtt ggtgctgggc 10740
cgttacgccg atcgcaagga cgtgtgcatc ggcgcgacgg tctccggccg cgaccagctg 10800
gagctggaag agctgatcgg ctttttcatc aatattttgc cgctgcgggt ggacctgtcg 10860
ggggatccgt gcctggagga ggtgctgctg cgcacgcgtc aagtggtact ggatggcttc 10920
gcgcaccagt cggtgccgtt cgagcacgtg ttgcaggcgc tgcggcgtca gcgcgacagt 10980
agccagatcc cgctggtgcc ggtgatgctg cgacaccaga acttcccgac gcaggagatt 11040
ggcgattggc ccgagggagt gcggctgacg cagatggagc tggggctgga ccgtagcacg 11100
ccgagcgagc tggattggca gttctacggc gacggcagct cgctggagct gacgctggaa 11160
tacgcgcagg acctcttcga cgaagcgacg gtgcggcgga tgatcgcaca ccaccagcag 11220

gcgttggagg cgatggtgag ccggccacag ctgcgggtgg gcaagtggga catgctgacg 11280
gccgaagagc gccggctgtt tgccgcgcta aatgcgacag gtacgccacg ggagtggccc 11340
agtctggcgc agcagttcga acggcaggcg caggcgacgc cgcaggccat cgcgtgcgtg 11400
agcgatgggc agtcgtggag ctatgcgcag ttggaggcgc gcgccaacca gctggcacag 11460
gcgctgcggg ggcagggcgc gggccgggac gtgcgggtgg cggtacagag tgcgcgcacg 11520
ccggaactgc tgatggcctt gctggcgatc tttaaggccg gtgcgtgcta tgtgccgatc 11580
gatccggcct acccggcggc ctaccgcgag cagatcctgg ccgaggtgca ggtgtcgatc 11640
gtgctggagc aagacgagct ggcgctggac gagcaagggc agttccacaa tccgcgttgg 11700
cgcgagcaag ccccgacgcc gctggggctg agggagcatc cgggcgacct ggcgtgcgtg 11760
atggtgacct ccggctcgac cggccggccc aagggcgtga tggtgccgta tgcgcagctg 11820
tacaactggc tgcatgcagg ctggcagcgt tctccgttcg aggccgggga gcgggtgctg 11880
cagaagacct cgatcgcctt tgcggtgtcg gtaaaggagt tgctaagcgg gctgctggcg 11940
ggggtggaac aggtgatgct gccggacgag caggtgaagg acagcctggc gttggcgcgg 12000
gcgattgagc aatggcaggt gacgcggctg tacctagtgc catcgcacct gcaggcgctg 12060
ctggacgcga cgcaaggacg agacgggcta ctgcactcgc tgcgtcacgt ggtgacggcg 12120
ggggaagcgt tgccgtctgc ggtgcgcgaa acggtgcggg cgcgtctgcc acaggtgcag 12180
ctatggaaca actacggctg cacggaactg aacgacgcga cctaccaccg gtcggatacg 12240
gtggcgccag gaacgtttgt gccgatcggc gcaccgatcg ccaacaccga ggtatacgtg 12300
ctggaccggc agctgcggca ggtgccgatc ggggtgatgg gcgagctgca cgtacacagc 12360
gtggggatgg cgcgcggcta ctggaaccgg ccggggctga cggcctcgcg cttcatcgcg 12420
cacccgtata gcgaggagcc gggcacacgg ctgtacaaga ccggtgacat ggtacgccgg 12480
ctggcggacg ggacgctgga atacctgggc cgacaggact tcgaggtcaa ggtgcgcggc 12540
caccgggtgg atacgcggca ggtggaggcg gccttgcggg cgcagcccgc ggtggccgag 12600
gcggtggtga gcggtcaccg ggtggacggg gacatgcagt tggtggccta tgtggtggcg 12660
cgtgaagggc aggcaccgag cgcgggcgag ttgaaacaac agctgtcggc gcagttgccg 12720
acctacatgc tgccgaccgt gtaccagtgg ctggagcagt tgccgcggct gtccaacggc 12780
aagttggacc ggttggccct gccggcaccg caggcggtac acgcgcagga gtacgtcgcg 12840
ccacgcaacc aggccgagca acggctggcg gcactgtttg ccgaggtgct gcgggtggag 12900
caggtaggca tccacgacaa cttcttcgcc ttgggtgggc actcgctgtc tgcatcgcaa 12960
ctgatctcgc gtattgccag ggatatggcg atcgatctgc ccctggccat gctgttcgag 13020
ctgcccacgg tagcgcagct tagcgaatcc ctcgccagcc atgcacgcga cagcgattac 13080
gatgtcatcc ccgcaagcac cgaggaggcg accattccgc tttccactgc gcaggagcgc 13140
atgtggttcc tgcacaagtt cgtgcaggag acgccgtaca acaccccggg tctcgcctta 13200
ttgcaaggcg aactggacat ttcggccttg caggtagcat ttcgctgtgt gctagaacgg 13260
cacgccgtgc tgcgtaccca tttcgtggaa accgagcagc aatgcgtaca ggtcattggc 13320
gcagcagagc agttcgtgct gcagcttagg tcgattcgcg acgaggctga tctgcatggc 13380
ctattgcaca cagccgtcag cgaacccttc gatttagaac gcgagctgcc attgcgcgcc 13440
ctgctgtatc gcctggacga ccggcggcat tacctagcag tggtcatcca tcacatcgtc 13500
ttcgacggct ggtcgacctc aatcctgttt cgtgagctgg ccacgcacta tgctgcatgc 13560
cgccatggcc aatccgcgcc tttgccaccg ctggagctta gctatgccga ttacgcacgc 13620
tgggagcgtg cgaggctgaa ccaggaagac gcgctgcgca agctcgaata ttggaaaacg 13680
cagcttgccg atgcaccgcc gctggtgttg cccacgacct atgcgcggcc ggttttccag 13740
aacttcaatg gcgcgactgt ggcgcttcag atcgagccgc cgctgctgca acgcctgcag 13800
cgtttcgccg acgcacacag ctttacattg tacatgctac ttctggcagc actgggcgtc 13860
gtattgtcgc gccatgcccg gcagaagcat ttctgcattg gcagtccggt cgccaatcgc 13920
gcccgagccg agttgcacgg tttgatcggt ttgttcgtca acaccctggc ggtacggctc 13980
gatttggacg gcaatcccag cgtgcgcgag ctgctcgaac gcatccactg caccacgctg 14040
gccgcctacg agcaccagga tgtgccgttc gaaagaatcg tggaaagcct gaaggtaccg 14100
cgcgataccg cgcgtaaccc gctggggcag gtgatgctca atttccagaa catgccaatg 14160
tcggcgttcg acctggatgg tgtccaggtg caggtgctcc ccatgcacaa cggcacggcc 14220
aagtgcgagc tgaccttcga cctgctgctg gatggctcac gcctatccgg tttcgtcgaa 14280
tacgccactg ggctgtttgc gccggaatgg gtccaggcgc tggtacagca attcaagtgt 14340
gtgctggcgg cattggtgga acggccggag gcatcgctga atgatttgcc catggcgccc 14400
aacgaggcgc aaccggcgtc gccggcattg atgaagcatg tcgcgccgag cttgcccaac 14460
ttacttgagg ctatggcggc caatgatgcc gcacgcctcg ccttgcaagc gccggaaggt 14520
gcgctcagtt acgctcagct aatcgaggca gcaaacgagt tcgcctggcg tttgcggtgc 14580
gagcacgccg gtccggacaa agtcgttgcc ctgtgcctag cgccttgctc cgccttggtg 14640
gttgctttgc tggccgcttc attatgcggt gcggcgagcg tgctgatcga tccgacgacg 14700
actgccgagg cgcaatacga ccagttgttc gaaacgcggg ccggcatcgt ggtgacctgt 14760
tctagcttgc tggagaagtt gccgctcgac gaccaggctg tagtgctgat cgacgagcaa 14820
gctgcagaag cgacgccgcg tttgatgcat ttcaccgacg atccagcttt gcccgcaatg 14880

ctgtattgtg tgtgtgacga aaaggggcga acccgcacga tcatggtcga aagcggcagt 14940
ttgtcgagtc gcctgctcga tagcgtgcag cgtttcagtc tcgaacgcac cgatcgcttc 15000
ctgctgcgca gcccgctttc tgccgaactg gcgaataccg aagtactgca atggttggcg 15060
gcaggcggca gcctcagcat cgcacccatg catggcgatt tcgatgccgc tgcctggctg 15120
gagaccctcg cgacgtacgc gatcaccgtg gcctacctgg ctcaagttga attgaccgag 15180
atgctggcgc atctgcaaaa ccatcctctt gagcgcaaca agctggccgg cttacgcgtg 15240
ctggtggtgc atggcgcgcc cttgccgatc gcgccactga tgcgcctaga cgcgtggttg 15300
cgagaggtgg gcggttccgc acggatcttc gccgcctacg ggaatgccga gttcggtgcc 15360
gaaatattga gccaggatgt cagcgctgca ttgcaagcgg gtattggcgc tcaatacaag 15420
catcgccgtg gtctgttccc gttgggtgcc aactcgatgt gtcacgtggt gcagagcaac 15480
ggccgcatcg cgcccgacgg catggttggt gaattgtgga tcacacagcc agcctgcttg 15540
tacaaaaccg atgcattggt gcgtcgcctg gcaaatgggc aactggaatg gttgggctcc 15600
ctcgatgtcc agtcgcgtat cgatgatccc cgcatcgatc tgtgcgtcgt ggaggcacaa 15660
ctgcgcttgt gcgaagacgt cggcgaagcg gtagtgctgt atgagccgtt gaagcgctgc 15720
ttggtagcct atctctcggc ccgtagcaca gctgcaatca tgaccgacga gacgctggcc 15780
aggatccgcc aggccctgag cgaaaccttg ccggattatc tactgcctgc aatctgggtg 15840
ccgctcgcgc actggccacg cttaccccat gggcgggtcg acctcggcgc cttgcctgca 15900
ccggatttcg atcttgcgcg gcatgagtcg tacatagcgc cacgcacagc cgtcgaacag 15960
gccgtggccg aaatatggca acgcgtgttg aagcgtaccc aggtcggcgt gcatgacaat 16020
ttcttcgagc tgggcggcca ttcggtgctg gcgatccagc tggtgtccgg cttgcgcaag 16080
gctttggcca tcgaagtgcc ggtcaccctg gtgttcgagg cgccgatact gggggcgctg 16140
gcgcggcaga tcgccccctt gttggtcagc gaacggcgtc cgcgcccgcc tggcctgacg 16200
cgcctggagc atacagggcc gattccggct tcgtatgcac aggagcggtt atggctggtg 16260
cacgagcata tggaggagca gcgaaccagc tacaacatca gtaacgcagc gcatttcatc 16320
ggagcagcct tcagcgtcga agcgatgcgt gccgcattga acgcgctggt ggcgcggcac 16380
gaagtgctgc gcacacgctt tctttcggag gacgggcagc tgcaacaggt gatcgctgcc 16440
tcgttgacgc tggaggtgcc ggtacgcgag gtgtcggccg aggaggtcga cctgctgctg 16500
gccgcgagca cgcgggagac tttcgatctg cggcaggggc ccttgttcaa ggcacgcatc 16560
ctgcgcgtgg cggccgatca ccatgtggtg ttgagcagca tccaccacat catttccgac 16620
ggctggtcgc tgggagtgtt caaccgtgac ctgcaccagc tgtacgaggc gtgtttgcgc 16680
ggcacgcccc ccacactgcc gacgctggcg gtgcagtatg ccgactacgc gctgtggcaa 16740
cggcaatggg agctggcggc tccgctgtcg tactggacgc gggcactgga aggctacgac 16800
gacggcctgg acttgcccta cgaccggccg cgcggcgcca cgcgggcgtg gcgggcaggg 16860
ctggtcaaac accgctatcc gccgcaactg gcccagcagt tggcggccta cagccaacag 16920
taccaagcga cgctgttcat gagcctgctg gcaggcctgg cgttggtgct gggccgttac 16980
gccgatcgca aggacgtgtg catcggcgcg acggtctccg gccgcgacca gctggagctg 17040
gaagagctga tcggcttttt catcaatatt ttgccgctgc gggtggacct gtcgggggat 17100
ccgtgcctgg aggaggtgct gctgcgcacg cgtcaagtgg tactggatgg cttcgcgcac 17160
cagtcggtgc cgttcgagca cgtgttgcag gcgctgcggc gtcagcgcga cagtagccag 17220
atcccgctgg tgccggtgat gctgcgacac cagaacttcc cgacgcagga gattggcgat 17280
tggcccgagg gagtgcggct gacgcagatg gagctggggc tggaccgtag cacgccgagc 17340
gagctggatt ggcagttcta cggcgacggc agctcgctgg agctgacgct ggaatacgcg 17400
caggacctct tcgacgaagc gacggtgcgg cggatgatcg cacaccacca gcaggcgttg 17460
gaggcgatgg tgagccggcc acagctgcgg gtgggcaagt gggacatgct gacggccgaa 17520
gagcgccggc tgtttgccgc gctaaatgcg acaggtacgc cacgggagtg gcccagtctg 17580
gcgcagcagt tcgaacggca ggcgcaggcg acgccgcagg ccatagcatg cgtgagcgat 17640
gggcagtcgt ggagctatgc gcagttggag gcgcgcgcca accagctggc acaggcgctg 17700
cgtgggcagg gcgcgggccg ggacgtgcgg gtggcggtac agagtgcgcg cacgccggaa 17760
ctgctgatgg ccttgctggc gatcttcaag gccggtgcat gctatgtgcc gatcgatccg 17820
gcctacccgg cggcctaccg cgagcaaatc ctggccgagg tgcaggtgtc gatcgtgctg 17880
gagcaaggcg agctggcgct ggacgagcaa gggcagttcc gcaatcggcg ttggcgcgag 17940
caagccccga cgccgctggg gctgagggga catccgggcg acctggcgtg cgtgatggtg 18000
acctccggct cgaccggccg gcccaagggc gtgatggtgc cgtatgcgca gctgcacaac 18060
tggctgcatg caggctggca gcgttctgcg ttcgaggccg gggagcgggt gctgcagaag 18120
acctcgatcg cctttgcggt gtcggtaaag gagttgctaa gcgggctgct ggcgggggtg 18180
gggcaggtga tgctgccgga cgagcaggtg aaggacagcc tggcgttggc gcgggcgatc 18240
gagcaatggc aggtgacgcg gctgtaccta gtgccgtcgc acctgcaggc gctgctggac 18300
gcgacgcaag gacgcgacgg gctactgcac tcgctgcgtc acgtggtgac ggcgggggaa 18360
gcgttgccgt cggcggtggg cgaagcggtg cgggtgcgcc tgccacaggt gcagctatgg 18420
aacaactatg gctgcacgga actgaacgac gcgacctacc atcggtcgga tacggtggcg 18480
ccaggaacgt ttgtgccgat cggcgcaccg atcgccaaca ccgaggtata cgtgctggac 18540

cggcagctgc ggcaggtgcc gatcggggtg atgggcgagc tgcacgtaca cagcgtgggg 18600
atggcgcgcg gctactggaa ccggccgggg ctgacggcct cgcgcttcat cgcgcacccg 18660
tatagcgagg agccgggcac acggctgtac aagaccggtg atatggtacg ccggctggcg 18720
gacgggacgc tggaatacct gggccgacag gacttcgagg tcaaggtgcg cggccaccgg 18780
gtggatacgc ggcaggtgga ggcggccttg cgggcgcagc ccgcggtggc cgaggcggtg 18840
gtgagcggtc accgggtgga cggggacatg cagttggtgg cctatgtggt ggcgcgtgaa 18900
gggcaggcac cgagcgcggg cgagttgaaa caacagctgt cggcgcagtt gccgacctac 18960
atgctgccga ccgtgtacca gtggctggag cagttgccgc ggctgtccaa cggcaagttg 19020
gaccggttgg cgctgccggc gccgcaggtg gtacacgcgc aggagtacgt cgcgccacgc 19080
aacgaggccg agcaacggct ggcggcactg tttgccgagg tgctgcgggt ggagcaggtg 19140
ggcatccacg acaacttctt cgccttgggt gggcactcgc tgtctgcatc gcaactgatc 19200
tcgcgcatcc gccaaagttt tcacgtcgat ctgccgctga gccggatctt cgaggcaccc 19260
acgatcgagg gcctggtcag gcagctagcg ttgcctagtg aaggcggcgt ggccagcatc 19320
gccagggtag cgcgaaaccg gacgatccca ttgtcgctgt tccaggaacg cctgtggttc 19380
gtgcaccaac acatgcctga gcaacgcacc agttacaacg gcacgctcgc cttgcgtttg 19440
cgtggtcctt tgtcggtgga agcgatgcgt gcagcgctgc gtgcgttagt gctgcgccac 19500
gaaatcttgc gtacccgctt cgtgttgccg accggtgcta gcgagccggt gcaggtcatt 19560
gacgagcaca gcgatttcca gctctcagta cagctagtcg aggatactga gatcgcgtcg 19620
ctgatggatg aactggcaag tcatatctac gacttagcca acggcccgct gttcattgca 19680
tgccttttgc aactggatga gcaagaacat gtgctgctaa tcggcatgca tcaccttatc 19740
tacgacgctt ggtcgcaatt caccgtgatg aaccgcgatc tacgcgtgct gtatcaccgc 19800
cacctcggac ttgccggcgg agatctgccg gaattaccga tccaatatgc cgactatgcg 19860
atctggcaac gcgcccagaa cctggacgcg caactggcct attggcaggc tatgttgcac 19920
gactacgacg acggcctgga gctgccctac gactatccgc gtccgcgcaa tcgcacctgg 19980
cacgcagcgg tctacacaca cacctatccg gctgaactgg tacagcgctt tgccggcttc 20040
gtacaggcgc atcagtcgac cttgttcatc gggctgttgg ccagcttcgc ggtcgtgttg 20100
aacaaataca ccggccggga cgacttgtgc atcggtacca ccacggcagg gcgcacgcac 20160
ctggagctgg agaacctgat cggtttcttc atcaacatct tgcctttgcg cttgcgcttg 20220
gacggcgatc cggacgttgc cgaaatcatg cggcgaacac ggttggtggc gatgagcgcg 20280
tttgagaacc aggcgctacc gttcgagcac ctgctcaacg ccctgcacaa gcaacgtgac 20340
accagccgga ttccgctagt tccggtggtg atgcgtcatc agaacttccc ggacacgatc 20400
ggcgactgga gcgatggcat ccgtaccgaa gtgatccagc gcgatctgcg tgccaccccc 20460
aatgaaatgg acctgcaatt cttcggcgac ggtacggggc tttcggtcac agtggaatac 20520
gcggcggagc tgttctcaga agcgaccatt cgccgcctga tccaccatca ccaactcgtc 20580
ctggagcaga tgttggcggc ccatgaaagc gccacgtgcc ccttggatgt tgccgactag 20640

<210> 21
<211> 1032
<212> DNA
<213> Xanthomonas albilineans

<400> 21

atggattcag cgttacctac atctgcattt accttcgatc tcttttacac cacggttaac 60
gcctactatc gcactgccgc agtcaaggcg gcgatcgaac tggggctatt cgatgtggtg 120
gggcagcagg gccgaactcc cgcagccatc gccgaggcct gccaggcgtc gccgcgcggc 180
attcgcatcc tttgctatta cctagtatcg atcggttttc tacgccgcaa cggtggcctg 240
ttctacatag atcgcaacat ggccatgtac ctggatcgta gttcgcccgg ctacctgggt 300
ggcagcatca agttcctgct ctcgccctac atcatgagcg ccttcaccga tctgaccgcc 360
gtagtcagga ccggcaagat caacctggcg caggacggcg tggtggcacc ggatcacccg 420
cagtgggtgg aatttgcacg cgcgatggca ccgatgatgg cgctgccctc ggcgttgatc 480
gccaatatgg tgtcgttgcc cgctgatcgg ccgattcgtg tgctggacgt ggcagccggc 540
cacggcctgt tcggcatcgc cttcgcgcag cgcttccgcc aggctgaagt gagcttcctg 600
gactgggaca acgtgctaga cgtagcacgc gaaaacgccc aggcggccaa agtggccgag 660
cgagcgcgtt tcctgcccgg caacgcattc gacctcgatt acggcagcgg ctacgacgtg 720
atcttgttga ccaacttcct gcaccatttc gatgaggtcg atggcgagcg catcttggct 780
aagacgcgcg atgcgctgaa cgacgacggc atggtgatca ctttcgaatt catcgccgac 840
gaagagcgtt cctcaccgcc gctggccgcc accttcagca tgatgatgct gggcaccacc 900
ccggcgggcg agtcctacac ctatagcgat ctggaaagga tgtttcggca tgccggcttc 960
ggccacgtgg aactaaaatc gataccgccg gccttgctga aagtggtggt ttcccgcaag 1020

agggccccat aa 1032

<210> 22
<211> 504
<212> DNA
<213> Xanthomonas albilineans

<400> 22

atgatcgaat cggcgacatc ccctgtggcg aaaaccgagc gcatctggtg caccgagctg 60
gacctggatg cactcaacgc catgtcggcc aacacgatgc aggccctgct cggtatacgc 120
atgatcgaga tcggctcgga ctatctggtc tcctgcatgt cggtggactg gcgttgccac 180
cagccctatg gggtattgca tggcggcgca tcggtcaccc tggccgaggc taccggcagc 240
atggcggcct ccatgtgcgt gccggccggc caacgttgcg ttggcctaga catcaatgcc 300
aaccacatcg cgagcatctc cagtggccaa gtacagtgca tcgcgcggcc gctgcacata 360
ggggccttga cccaggtatg gcagatgcgc atctatgacg aaggtgaccg cacgatctgc 420
gtgtcgcgcc tgaccatggc ggtattatcg gtgcacgtcg cgcgcgtatc cccgaatcca 480
gccagcagcg gagtccagac gtga 504

<210> 23
<211> 2826
<212> DNA
<213> Xanthomonas albilineans

<400> 23

gtgaacgaaa ctgcaactgt aaccaaggct accctcagtt cagcgaaggc gagtataacg 60
ccagcctgcg ttcaccaatg gtttgaagcg caggtgagtt cgacaccgga tgcgcctgct 120
gccttcttag gcgagcgtcg aatgagttat ggccagctca acacccgcgc caatcggctt 180
gcacggctgt tgcagtcaca gggcgttggg cctggtgccc gggtcgcggt gtggatgaat 240
cgcagccccg aatgcctggc cgctttgctg gcggtcatga aggccggggc agcttatgta 300
ccgatcgacc tgagcctgcc gatccgacgt gtccaataca tcttgcagga cagccaggcc 360
cggctcgtac tggtcgatga cgaagggcaa ggccgcctgg acgaacttga gctgggcgcg 420
atgactgccg tcgatgtctg cggcactctg gacggcgacg aggcgaatct ggacctgcct 480
tgcgatccgg cgcagccggt ttattgcatc tatacctccg gctccacagg tagccccaag 540
ggcgtgctgg tacggcacag cgggttggct aactacgtgg cctgggctaa gcggcaatac 600
gttacggctg acacgacgag tttcgccttt tactcctcgc tgtcgttcga tctgaccgtc 660
acctcgatct acgtgcccct ggtggctggc ctgtgtgtgc atgtgtaccc ggagcagggc 720
gacgacgtgc cggtaatcaa ccgcgtgctg gacgacaacc aagtagacgt gatcaagctg 780
acaccctcgc acatgctgat gctgcgcaac gcggcactgg cgacgtctcg gctgaagacg 840
ctgatcgtgg gtggcgagga cctgaaagcg gcggtggcgt acgacatcca tcagcggttc 900
cgccgcgatg tggcgatcta caacgaatac ggtcctaccg aaaccgtagt ggggtgcgcg 960
atccatcgtt acgatccggc gaccgaacgc gaaggctcgg tgccgattgg tgtgccgatc 1020
gatcacacca gcctccacct gctcgatgaa cgtctgcagc cggtcgcacc gggcgaggtc 1080
ggccagatcc acatcggtgg cgcgggcgtg gccatcggct atgtgaacaa gccggagatc 1140
accgatgcgc aattcattga caatcccttc gaaggcagcg gccggcttta cgccagtggc 1200
gacctaggac gcatgcgtgc cgacggtaag cttgaattcc ttggccgcaa ggattcgcag 1260
atcaagctgc gcggctaccg catcgaactg ggcgagatag agaacgttct gcttggccac 1320
gcagccttgc gcgaatgcat cgtggatacc accgtggcgc cgcgccgcga ctatgacagc 1380
aagagcttgc gctattgcgc gcgttgcggt atcgcttcaa atttccccaa taccagcttc 1440
gacgagcacg gtgtctgcaa ccattgccac gcctacgaca aataccggaa cgtggtcgag 1500
gattatttcc ggaccgaaga tgagctacgt actatcttcg agcaggtcaa ggcgcacaac 1560
aggctccgct acgactgcct ggtggctttc agcggcggca aggacagcac ctatgcgcta 1620
tgccgcgtag tggacatggg cctgcgcgtg ttggcgtaca ccctggacaa tggctacatc 1680
tccgacgagg ccaaggcaaa cgtcgaccgc gtcgtgcgcg agctgggggt ggaccatcgc 1740
tatctgggta ctccacacat gaacgccatc ttcgtggaca gcctgcatcg ccacagcaac 1800
gtctgcaacg gctgcttcaa gaccatctat acgctgggta tcaacctggc gcacgaagtg 1860
ggcgtaagcg acattgtaat gggcctgtcc aaaggacagc tgttcgagac gcgcctgtct 1920
gagctgtttc gcgccagcac cttcgacaac caggtatttg agaagaacct gatggaggcg 1980

cgcaagatct accatcgcat cgacgacgcg gcggcccgcc tgctggacac ctcttgcgtg 2040
cgcaacgatc gcttgctcga aagtacgcgt ttcatcgact tctaccgcta ctgcagtgtc 2100
agccgcaagg acatgtatcg ctatatcgcc gagcgcgtag gctggagccg tccggctgac 2160
accggccgct cgactaactg cctgctcaac gatgtgggca tctacatgca caagaagcaa 2220
cgtggctatc acaactattc gttgccctac agttgggacg tgcgggtagg ccatatccca 2280
agggaagacg cgatgcgcga gctggaggac accgacgata tagacgaggc caaggtactg 2340
ggcctgctca agcagatcgg ctatgactca agcctgatcg atacccaggc gggcgatgcg 2400
cagctgatcg cctactacgt ggcggcggag gaactggatc cggtggcatt gcgcaatttt 2460
gctgctgcga tcttgcccga gtacatgctg ccttcgtatt tcgtgcggct ggaccgaatg 2520
ccgttgacgc cgaatggcaa ggtgaaccgc cgagcattgc cgaggccgga gttgaagaag 2580
aacgccagcg aggcgcatac cgagccgagc agtgcgctag agcaggaact ggtgcaaatc 2640
tggaaagagg tgctgatggt cgacaaggtc ggcgtcaggg acaacttttt cgagctgggc 2700
ggccactcgc tgagcgcgct gatgttgctc tacagcatag ccgagcgcta ccagaagatg 2760
gtcagcatcc aggcattctc ggttaatccg accatcgaag gtctgtcgga gcatctggtc 2820
gcataa 2826

<210> 24
<211> 837
<212> DNA
<213> Xanthomonas albilineans

<400> 24

atgcccaatg ccgtaccgat gcagggcgcg cggggactcc cgcagccgca agcgatgaac 60
ccagggttgc cgagcgtcgg cggcttgagc gcaggccagc cattgcagtt gtcgttagca 120
ccggaactgc aggcagccgc gcgcagtgcc caccgccatc tgctcgacga cggcacggcg 180
ctttacctgc tggcgttcga taccgcgcaa ttcgacccgg gggctttcgc ggcaatggca 240
atcgcccgcc cggacagcat cgcccgcagc gtgcgcaagc gtcaggccga gttcctgttc 300
ggccgtctgg ccgcgcgact ggcgctgcaa gaggtgctgg gacctgcgca agcgcaggca 360
gacattgcaa tcggcgcgac gcgcgcgccc tgctggcctg ccggcagcct gggcagcatt 420
tcccattgcg aggactacgc ggccgccatc gccatggcgg ccggcacccg ccacggcgtg 480
ggcatcgatc tggaacgacc aatcacaccc gcggcgcgcg cggcgttgct gagcatcgca 540
atcgatgccg acgaagccgc tcgtctggca aaggcggcag acgcgcagtg gccgcaagac 600
ctgctgctga ccgcactatt ttcggccaag gaaagcctgt tcaaagccgc ctacagcgcg 660
gtcggacgct acttcgactt cagcgcggca cgcctgtgcg gcatcgacct ggcacggcaa 720
tgcctgcatc tgcgcctgac cgagacactc tgcgcgcaat tcgtggccgg gcaagtgtgc 780
gaggtcggct tcgcgcgcct accaccggac ctggtgctca cccactacgc ctggtga 837

<210> 25
<211> 1905
<212> DNA
<213> Xanthomonas albilineans

<400> 25

atgagcgtgg aaacccaaaa agaaaccctg ggctttcaga ccgaggtcaa acagctgctg 60
cagctgatga tccattcgtt gtattccaac aaggagatct tcctgcgcga gctgatctcc 120
aatgcctccg acgcggccga caaactgcgc ttcgaggcac tggtcaagcc ggaacttctg 180
gacggcgatg cgcaactgcg catccgcatc ggcttcgaca aggacgccgg caccgtcacc 240
atcgacgaca acggcatcgg catgagccgc gaggagatcg tcgcgcacct gggcaccatc 300
gccaaatccg gcacctccga tttcctcaag catctgtccg gcgatcagaa gaaggattcg 360
cacctgatcg gccagttcgg tgtcggcttc tacagtgcct tcatcgtcgc cgatcaagtg 420
gacgtgtaca gccgtcgcgc cgggctgccg gccagcgacg gcgtacactg gtcctcgcgt 480
ggcgaaggcg agttcgaggt cgccaccatc gacaagcccg agcgcggcac ccgcatcgtg 540
ctgcacttga aggaggaaga gaaaggcttc gccgacggtt ggaagttgcg cagcatcgtg 600
cgcaagtact ccgaccacat cgccttgccg atcgagctaa tcaaggaaca ctacggcgag 660
gacaaggaca agccggaaac ccccgagtgg gagaccgtca atcgcgccag cgcgctgtgg 720
acacggccgc gcaccgagat caaggacgag gaataccaag aactgtacaa gcacattgcc 780
cacgaccacg aaaacccggt ggcgtggagc cataacaagg tcgaaggcaa actggaatac 840

```
acctcgctgc tgtacctgcc cggccgcgcc ccgttcgacc tgtaccagcg cgatgcctcg    900
cgcgggctca agctgtacgt gcagcgcgtc ttcatcatgg accaggccga ccaattcctg    960
ccgctgtacc tgcgcttcat caagggcatc gtcgattcca gcgacctgcc gctgaacgtc   1020
tcgcgcgaaa tcctgcaatc tggtccggtg atcgactcga tgaagtcggc gctgaccaag   1080
cgcgcactgg acatgctgga aaagctcgcc aaagacgatc ccgaacgcta caagggcgtg   1140
tggaagaact tcggccaggt gctgaaggaa ggtccggccc aggacttcgg caaccgcgaa   1200
aagatcgccg gcctgctgcg cttcgcgtcc acccacagcg gcgacgacgc ccagaacgtg   1260
tcgctggccg actacgtggc gcggatgaaa gacggccagg acaagctgta ctacctgacc   1320
ggggaaagct acgcgcaaat caaggacagc ccgcacctgg aggtgttccg caagaagggc   1380
atcgaggtgc tcctgctcac cgaccgcatc gacgagtggc tgatgagcta tctcaccgag   1440
ttcgacagca aatccttcgt cgatgtggcg cgcggcgacc tggacctggg caagctggac   1500
agcgaagaag aaaagcaggc gcaggaagaa gccgccaagg ccaagcaagg gctggccgag   1560
cgcatccagc aggtactcaa ggacgaggtc gccgaggtgc gggtctcgca ccggctgacc   1620
gattcgccgg cgattcttgc catcggccag ggcgacatgg gtctgcaaat gcggcagatc   1680
ctggaagcca gcgggcagaa gctgccggag agcaagccgg tgttcgagtt caaccccgcg   1740
catccgctga tcgagaaact ggatgcggaa cccgatgtcg atcgtttcgg tgatctggcg   1800
cgggtgctgt tcgatcaggc cgcgctggcc gccggcgaca gcctcaagga cccggccgcc   1860
tacgtgcgtc ggctcaacaa gctgttgctg gagctgtcgg cgtaa                    1905
```

<210> 26
<211> 6879
<212> PRT
<213> Xanthomonas albilineans

<400> 26

```
Met Pro Asn Ala Leu Met Gln Ile Thr Leu Val Ala Val Gln Phe Ala
1               5                  10                  15

Gly Val Leu Leu Gly Val Thr Ala Arg Ala Ala Ile Pro Asn Lys Ala
            20                  25                  30

Gly Met Arg Arg Ala Trp Pro Pro Phe Pro Gln Ala Cys Cys Arg Ser
        35                  40                  45

Ile Ala Tyr Leu Met Gln Arg Ser Pro Met Ser Pro Leu Gln Gln Thr
    50                  55                  60

Leu Leu Thr Arg Leu Ala Ser Ala Ala Ala Ser Arg Thr Met Ile Glu
65                  70                  75                  80

Phe Pro Arg Pro Glu His Ala Ser Pro Gln Cys Cys Asp Asp Ala Glu
                85                  90                  95

Leu Ala Arg Leu Ile Val Gln Leu Ser Ala Gly Leu Gln Pro Leu Ala
            100                 105                 110

Met Pro Gly Thr Tyr Val Ile Ile Ala Ala Pro His Gly Gly Leu Phe
        115                 120                 125

Ala Ala Ala Leu Leu Ala Cys Leu His Ala Asn Leu Val Ala Val Pro
    130                 135                 140

Phe Pro Leu Asp Val Ala Gln Pro Asn Glu Arg Glu Gln Ala Arg Leu
145                 150                 155                 160

Glu Thr Ile His Ala Gln Leu Met Glu His Gly Asn Val Ala Val Leu
                165                 170                 175

Leu Asp Asp Val Ala Asp Arg Ser Ala Phe Ala Arg Met Ala His Ala
```

```
            180                 185                 190

Ala Gly Thr Phe Leu Ala Thr Phe Ala Asp Leu Lys Arg Glu Ser Thr
        195                 200                 205

Ser Ala Ser Leu Cys Pro Ala Ser Pro Ser Asp Ala Ala Leu Leu Leu
    210                 215                 220

Phe Thr Ser Gly Ser Ser Gly Glu Ser Lys Gly Ile Leu Leu Ser His
225                 230                 235                 240

Arg Asn Leu His His Gln Ile Gln Ala Gly Ile Arg Gln Trp Ser Leu
                245                 250                 255

Asp Glu His Ser His Val Val Thr Trp Leu Ser Pro Ala His Asn Phe
            260                 265                 270

Gly Leu His Phe Gly Leu Leu Ala Pro Trp Phe Ser Gly Ala Thr Val
        275                 280                 285

Ser Phe Ile His Pro His Ser Tyr Met Lys Arg Pro Gly Phe Trp Leu
    290                 295                 300

Glu Thr Val Ala Ala Arg Asp Ala Thr His Met Ala Ala Pro Asn Phe
305                 310                 315                 320

Ala Phe Asp Tyr Cys Cys Asp Trp Val Met Val Glu Gln Leu Pro Pro
                325                 330                 335

Ser Ala Leu Ser Thr Leu Thr His Ile Val Cys Gly Gly Glu Pro Val
            340                 345                 350

Arg Ala Ser Thr Met Gln Arg Phe Phe Glu Lys Phe Ala Gly Leu Gly
        355                 360                 365

Ala Arg Thr Gln Thr Phe Met Pro His Phe Gly Leu Ser Glu Thr Gly
    370                 375                 380

Ala Leu Ser Thr Leu Asp Glu Ala Pro Gln Gln Arg Val Leu Glu Leu
385                 390                 395                 400

Asp Ala Asp Ala Leu Asn Lys Arg Lys Arg Val Ala Ala Gly Ala Ser
                405                 410                 415

Gln Ala Arg Val Thr Val Leu Asn Cys Gly Ala Val Asp Gln Asp Val
            420                 425                 430

Glu Leu Arg Ile Val Cys Pro Glu Gly Glu Thr Leu Cys Arg Pro Asp
        435                 440                 445

Glu Ile Gly Glu Ile Trp Val Lys Ser Pro Ala Ile Ala Arg Gly Tyr
    450                 455                 460

Leu Phe Ala Lys Pro Ala Asp Gln Arg Gln Phe Asn Cys Ser Ile Arg
465                 470                 475                 480

His Thr Asp Asp Ser Gly Tyr Phe Arg Thr Gly Asp Leu Gly Phe Ile
                485                 490                 495

Ala Asp Gly Cys Leu Tyr Val Thr Gly Arg Val Lys Glu Val Leu Ile
            500                 505                 510
```

```
Ile Arg Gly Lys Asn His Tyr Pro Ala His Ile Glu Ala Ser Ile Ala
        515                 520                 525

Ala Thr Ala Ser Pro Gly Ala Leu Met Pro Val Val Phe Ser Ile Glu
    530                 535                 540

Arg Gln Asp Glu Glu Arg Val Ala Ala Val Ile Ala Val Asn His Pro
545                 550                 555                 560

Trp Thr Pro Ala Ala Cys Ala Ala Gln Ala His Lys Ile Arg Gln Gln
                565                 570                 575

Val Ala Asp Gln His Gly Val Ala Leu Ala Glu Leu Ala Phe Ala Glu
            580                 585                 590

His Arg His Val Phe Gly Thr Tyr Pro Gly Lys Leu Lys Arg Arg Leu
        595                 600                 605

Val Lys Glu Ala Tyr Val Asn Gly Gln Leu Pro Leu Leu Trp His Glu
    610                 615                 620

Gly Lys Asn Arg Asp Val Pro Ala Ala Ala Ala Asp Asp Arg Gln Ala
625                 630                 635                 640

Gln His Val Ala Asp Leu Cys Arg Lys Val Phe Leu Pro Val Leu Gly
                645                 650                 655

Val Ala Pro Pro His Ala Gln Trp Pro Leu Cys Glu Leu Ala Leu Asp
            660                 665                 670

Ser Leu Gln Cys Val Arg Leu Ala Gly Ala Ile Glu Glu Cys Tyr Gly
        675                 680                 685

Val Pro Phe Glu Pro Thr Leu Leu Phe Lys Leu Glu Thr Val Gly Ala
    690                 695                 700

Ile Ala Glu Tyr Val Leu Ala His Gly Arg Gln Ala Pro Thr Pro Thr
705                 710                 715                 720

Arg Ala Pro Val Ala Ser Thr Thr Cys Ser Glu Glu Pro Ile Ala Ile
                725                 730                 735

Val Ala Met His Cys Glu Val Pro Gly Ala Gly Glu Asn Thr Glu Ala
            740                 745                 750

Leu Trp Ser Phe Leu Arg Ser Asp Val Asn Ala Ile Arg Pro Ile Glu
        755                 760                 765

Ser Thr Arg Pro Asp Leu Trp Ala Ala Met Arg Ala Tyr Pro Gly Leu
    770                 775                 780

Ala Gly Glu Gln Leu Pro Arg Tyr Ala Gly Phe Leu Asp Asp Val Asp
785                 790                 795                 800

Ala Phe Asp Ala Ala Phe Phe Gly Ile Ser Arg Arg Glu Ala Glu Cys
                805                 810                 815

Met Asp Pro Gln Gln Arg Lys Val Leu Glu Met Val Trp Lys Leu Ile
            820                 825                 830
Glu Gln Ala Gly His Asp Pro Leu Ser Trp Gly Gly Gln Pro Val Gly
```

```
        835                 840                 845

Leu Phe Val Gly Ala His Thr Ser Asp Tyr Gly Glu Leu Leu Ala Ser
    850                 855                 860

Gln Pro Gln Leu Met Ala Gln Cys Gly Ala Tyr Ile Asp Ser Gly Ser
865                 870                 875                 880

His Leu Thr Met Ile Pro Asn Arg Ala Ser Arg Trp Phe Asn Phe Thr
                885                 890                 895

Gly Pro Ser Glu Val Ile Asn Ser Ala Cys Ser Ser Ser Leu Val Ala
            900                 905                 910

Leu His Arg Ala Val Gln Ser Leu Arg Gln Gly Glu Ser Ser Val Ala
        915                 920                 925

Leu Val Leu Gly Val Asn Leu Ile Leu Ala Pro Lys Val Leu Leu Ala
    930                 935                 940

Ser Ala Ser Ala Gly Met Leu Ser Pro Asp Gly Arg Cys Lys Thr Leu
945                 950                 955                 960

Asp Ala Ala Ala Asp Gly Phe Val Arg Ser Glu Gly Ile Ala Gly Val
                965                 970                 975

Ile Leu Lys Pro Leu Ala Gln Ala Leu Ala Asp Gly Asp Arg Val Tyr
            980                 985                 990

Gly Leu Val Arg Gly Val Ala Val  Asn His Gly Gly Arg  Ser Asn Ser
        995                 1000                1005

Leu Arg  Ala Pro Asn Val Asn  Ala Gln Arg Gln Leu  Leu Ile Arg
    1010                1015                1020

Thr Tyr  Gln Glu Ala Gly Val  Glu Pro Ala Ser Val  Gly Tyr Val
    1025                1030                1035

Glu Leu  His Gly Thr Gly Thr  Ser Leu Gly Asp Pro  Ile Glu Ile
    1040                1045                1050

Gln Ala  Leu Lys Glu Ala Phe  Ile Ala Leu Gly Ala  Gln Ala Ala
    1055                1060                1065

Pro Ser  Asn Cys Gly Ile Gly  Ser Val Lys Ser Ala  Leu Gly His
    1070                1075                1080

Leu Glu  Ala Ala Ala Gly Leu  Thr Gly Leu Ile Lys  Val Leu Leu
    1085                1090                1095

Met Leu  Lys His Gly Glu Gln  Ala Gly Thr Arg His  Phe Ser Thr
    1100                1105                1110

Leu Asn  Pro Leu Ile Asp Leu  Arg Gly Thr Ser Phe  Glu Val Val
    1115                1120                1125

Ala Gln  His Arg Ala Trp Pro  Ser Gln Val Gly Ile  His Gly Thr
    1130                1135                1140

Leu Leu  Pro Arg Arg Ala Gly  Ile Ser Ser Phe Gly  Phe Gly Gly
    1145                1150                1155
```

```
Ala Asn  Ala His Ala Ile Val  Glu Glu His Val Ile  Ala Thr Pro
    1160                 1165                 1170

Pro Ser  Thr Ser Ser Ala Gly  Gly Pro Val Gly Ile  Val Leu Ser
    1175                 1180                 1185

Ala Gly  Ser Glu Ala Val Leu  Arg Gln Gln Val Leu  Ala Leu Ser
    1190                 1195                 1200

Ala Trp  Leu Arg Gln Gln Ser  Pro Thr Pro Ala Gln  Met Ile Asp
    1205                 1210                 1215

Val Ala  Tyr Thr Leu Gln Val  Gly Arg Ala Ala Leu  Ser His Arg
    1220                 1225                 1230

Leu Ala  Phe Ser Ala Thr Asp  Ala Glu Gln Ala Leu  Ala Arg Leu
    1235                 1240                 1245

Glu Gly  Arg Leu Ala Gly Val  Met Asp Ala Glu Val  His His Gly
    1250                 1255                 1260

Val Val  Asp Ala Ala Ala Thr  Ala Pro Glu His Gly  Arg Gln Thr
    1265                 1270                 1275

Arg Glu  Gly Leu Ala Gly Leu  Leu Arg Ala Trp Thr  Gln Gly Val
    1280                 1285                 1290

Arg Val  Asp Trp Ser Ala Leu  Tyr Gly Ile Gln Arg  Pro Gln Arg
    1295                 1300                 1305
Val Ser  Leu Pro Val Tyr Pro  Phe Ala Arg Glu Arg  Tyr Trp Leu
    1310                 1315                 1320

Pro Gly  Gln Ala Met His Ala  Ala Ala Asp Ala His  Pro Met Leu
    1325                 1330                 1335

Gln Leu  Leu His Ala Asn Ala  Lys Leu His Arg Tyr  Ala Leu Arg
    1340                 1345                 1350

Arg Ser  Gly Cys Ala Ser Phe  Leu Val Asp His Cys  Val Asp Gly
    1355                 1360                 1365

Arg Gln  Val Leu Pro Ala Ala  Val Gln Leu Glu Leu  Val Arg Ala
    1370                 1375                 1380

Val Ala  Gln Arg Val Met Ala  Gln Asp Glu Gly Cys  Ile Glu Leu
    1385                 1390                 1395

Ala Gln  Val Ala Phe Leu His  Pro Leu Met Met Glu  Glu Thr Glu
    1400                 1405                 1410

Leu Glu  Val Glu Ile Glu Leu  Ser Lys Ser Asp Gln  Asp Glu Phe
    1415                 1420                 1425

Asp Phe  Gln Leu His Asp Ala  His Arg Gln Gln Val  Phe Ser Gln
    1430                 1435                 1440

Gly His  Val Arg Arg Arg Val  Tyr Thr Ala Thr Pro  Arg Leu Asp
    1445                 1450                 1455

Leu Ala  Gln Leu Gln Lys Leu  Cys Ala Glu Arg Val  Leu Ser Gly
```

```
    1460                1465                1470

Glu Asp  Cys Tyr Ala His Phe  Thr Ala Cys Gly Leu  Gln Leu Gly
    1475                1480                1485

Asp Arg  Leu Lys Ser Val Gln  Ser Ile Gly Cys Gly  Arg Asn Gly
    1490                1495                1500

Glu Gly  Glu Pro Ile Ala Leu  Gly Val Leu Arg Leu  Pro Pro Ser
    1505                1510                1515

Ser Val  Glu Asp Ser His Val  Leu Pro Pro Ser Leu  Leu Asp Gly
    1520                1525                1530

Ala Leu  Gln Cys Ser Leu Gly  Leu Gln Arg Asp Val  Glu His Ile
    1535                1540                1545

Ala Met  Pro Tyr Thr Leu Glu  Arg Met Thr Val His  Ala Pro Ile
    1550                1555                1560

Pro Pro  Glu Ala Trp Val Leu  Leu Arg His Gly His  Ala Ala Arg
    1565                1570                1575

Gln Ser  Leu Asp Ile Asp Leu  Leu Asp Ser Glu Gly  Arg Val Cys
    1580                1585                1590

Val Ser  Leu Gly Asn Tyr Thr  Gly Arg Ala Pro Lys  Ala Val Ser
    1595                1600                1605

Ala Val  Arg Ala Leu Val Leu  Ala Pro Val Trp Gln  Ala Leu Thr
    1610                1615                1620

Glu Thr  Ala Pro Ala Trp Pro  Asp Pro Ala Glu Arg  Ile Val Thr
    1625                1630                1635

Val Gly  Asp Asp Ala Trp Arg  Ser His Phe Gly Phe  Asp Glu Pro
    1640                1645                1650

Ala Leu  Ser Leu Glu Asp Ser  Val Glu Val Ile Ala  Thr Arg Leu
    1655                1660                1665

Gly Gln  Ser Gly Lys Phe Asp  His Leu Val Trp Ile  Val Pro Ile
    1670                1675                1680

Ala Glu  Ser Glu Thr Asp Ile  Ala Ala Gln Gly Ser  Ala Ala Ile
    1685                1690                1695

Ala Gly  Phe Arg Leu Val Lys  Ala Leu Leu Ala Leu  Gly Tyr Ala
    1700                1705                1710

His Arg  Pro Leu Gly Leu Thr  Val Leu Thr Arg Gln  Ala Leu Thr
    1715                1720                1725

Arg Gln  Pro Ser His Ala Ala  Val His Gly Leu Ile  Gly Thr Leu
    1730                1735                1740

Ala Lys  Glu Tyr Cys Asn Trp  Lys Ile Arg Leu Leu  Asp Leu Pro
    1745                1750                1755

Ser Val  Lys Ser Trp Pro Gln  Trp Glu Gln Leu Arg  Ser Leu Pro
    1760                1765                1770
```

```
Trp His  Ala Gln Gly Glu Ala  Leu Ile Gly Arg Gly  Thr Cys Trp
    1775                 1780                 1785

Tyr Arg  Arg Gln Leu Cys Glu  Val Leu Pro Leu Pro  Ser Leu Glu
    1790                 1795                 1800

Pro Pro  Pro Tyr Arg Val Gly  Gly Val Tyr Val Val  Ile Gly Gly
    1805                 1810                 1815

Ala Gly  Gly Leu Gly Glu Val  Leu Ser Glu His Leu  Ile Arg Thr
    1820                 1825                 1830

Tyr Asp  Ala Gln Leu Ile Trp  Ile Gly Arg Arg Val  Leu Asp Glu
    1835                 1840                 1845

Gly Ile  Ala Arg Lys Gln Thr  Arg Leu Ala Ser Leu  Gly Arg Ala
    1850                 1855                 1860

Pro His  Tyr Ile Ser Ala Asp  Ala Ser Asp Pro Ala  Ala Leu Gln
    1865                 1870                 1875

Ala Ala  His Asn Glu Ile Val  Ala Leu His Gly Gln  Pro His Gly
    1880                 1885                 1890

Leu Ile  Leu Ser Asn Ile Val  Leu Lys Asp Ala Ser  Leu Ala Arg
    1895                 1900                 1905

Met Glu  Glu Ala Asp Phe Arg  Asp Val Leu Ala Ala  Lys Leu Asp
    1910                 1915                 1920

Val Ser  Val Cys Ala Ala Gln  Val Phe Gly Thr Ala  Pro Leu Asp
    1925                 1930                 1935

Phe Val  Leu Phe Phe Ser Ser  Ile Gln Ser Thr Thr  Lys Ala Ala
    1940                 1945                 1950

Gly Gln  Gly Asn Tyr Ala Ala  Gly Cys Cys Tyr Val  Asp Ala Phe
    1955                 1960                 1965

Gly Glu  Leu Trp Ala Arg Arg  Gly Leu Arg Val Lys  Thr Ile Asn
    1970                 1975                 1980

Trp Gly  Tyr Trp Gly Ser Val  Gly Val Val Ala Gly  Glu Asp Tyr
    1985                 1990                 1995

Arg Arg  Arg Met Ala Gln Lys  His Met Ala Ser Ile  Glu Gly Ala
    2000                 2005                 2010

Glu Ala  Met Gln Val Leu Ser  Gln Leu Leu Cys Ala  Pro Leu Gln
    2015                 2020                 2025

Arg Leu  Ala Tyr Val Lys Ile  Asp Asp Ala Asn Ala  Met Arg Ala
    2030                 2035                 2040

Leu Gly  Val Val Glu Asp Glu  Ser Val Gln Ile Pro  Val His Ala
    2045                 2050                 2055

Pro Ala  Glu Pro Pro Arg Gly  Gln Pro Gly Pro Val  Val Glu Leu
    2060                 2065                 2070
```

```
Ser Val  Asn Leu Asp Ala Arg  Arg Glu Arg Glu Thr  Leu Leu Ala
    2075                 2080                 2085

Ala Trp  Leu Leu Glu Leu Ile  Glu Gln Leu Gly Gly  Phe Pro Pro
    2090                 2095                 2100

Ala Ser  Phe Asp Ile Ala Thr  Leu Ala Gln Arg Leu  His Ile Val
    2105                 2110                 2115

Pro Ala  Tyr Arg Ser Trp Leu  Glu His Ser Val Arg  Met Leu Gly
    2120                 2125                 2130

Val Tyr  Gly Tyr Leu Arg Ala  Thr Gly Glu Ser Arg  Phe Glu Leu
    2135                 2140                 2145

Ala Asp  Lys Pro Pro Asp Asp  Ala Arg Gly Ala Trp  Asn Ala His
    2150                 2155                 2160

Val His  Glu Ala Ser Val Glu  Ala Gly Glu Glu Ala  Gln Arg Arg
    2165                 2170                 2175

Leu Leu  Asp Arg Cys Met Arg  Ala Leu Pro Ala Val  Leu Arg Gly
    2180                 2185                 2190

Glu Arg  Lys Ala Thr Glu Leu  Leu Phe Pro Glu Gly  Ser Met Ala
    2195                 2200                 2205

Trp Val  Glu Gly Ile Tyr Gln  Asn Asn Pro Leu Ala  Asp Tyr Phe
    2210                 2215                 2220

Asn Ala  Gln Leu Val Thr Arg  Leu Ile Ala Tyr Leu  Arg Arg Arg
    2225                 2230                 2235

Leu Glu  Ser Thr Pro Thr Ala  Arg Leu Lys Leu Cys  Glu Ile Gly
    2240                 2245                 2250

Ala Gly  Ser Gly Gly Thr Thr  Ala Ser Val Leu Gln  Gln Leu Gln
    2255                 2260                 2265

Ala Tyr  Gly Glu His Ile Glu  Glu Tyr Leu Tyr Thr  Asp Leu Ser
    2270                 2275                 2280

Pro Val  Phe Leu His His Ala  Glu Lys His Tyr Gln  Pro Arg Ala
    2285                 2290                 2295

Pro Tyr  Leu Arg Thr Ala Cys  Phe Asp Val Ala Arg  Ala Pro Thr
    2300                 2305                 2310

Ala Gln  Ala Leu Glu Ser Gly  Gly Tyr Asp Val Val  Ile Ala Ala
    2315                 2320                 2325

Asn Val  Leu His Ala Thr Arg  Asp Ile Ala Lys Thr  Leu Arg Asn
    2330                 2335                 2340

Ala Lys  Ala Leu Leu Lys Pro  Gly Gly Leu Leu Leu  Leu Asn Glu
    2345                 2350                 2355

Val Ile  Glu Arg Ser Leu Val  Leu His Leu Thr Phe  Gly Leu Leu
    2360                 2365                 2370

Glu Ser  Trp Trp Leu Pro Gln  Asp Lys Ile Leu Arg  Leu Ala Gly
```

2375 2380 2385

Ser Pro Leu Leu Ala Cys Ala Thr Trp Arg Ser Leu Leu Glu Ala
2390 2395 2400

Glu Gly Phe Ala Gly Leu Ser Val His Arg Ala Gln Pro Asp Ala
2405 2410 2415

Gly Gln Ala Ile Ile Cys Ala Tyr Ser Asp Gly Ile Val Arg Gln
2420 2425 2430

Ala Ser Thr Ile Glu Val Ala Arg Asn Glu Lys Val Thr Val Pro
2435 2440 2445

Ser Gln Pro Ala Glu Ala Gly Glu Ser Pro Leu Asp Leu Val Lys
2450 2455 2460

Lys Leu Leu Gly Arg Ile Leu Lys Met Asp Pro Ala Thr Leu Asp
2465 2470 2475

Thr Ser His Pro Leu Glu Tyr Tyr Gly Val Asp Ser Ile Val Ala
2480 2485 2490

Ile Glu Leu Ala Met Ala Leu Arg Glu Thr Phe Pro Gly Phe Glu
2495 2500 2505

Val Ser Glu Leu Phe Glu Thr Gln Ser Ile Asp Thr Leu Leu Gly
2510 2515 2520

Ser Leu Glu Gln Ala Pro Leu Leu Ala Thr Leu Thr Ala Pro Pro
2525 2530 2535

Gln Gln Asp Met Leu Gln Gln Leu Lys Gln Leu Leu Ala Arg Thr
2540 2545 2550

Leu Lys Leu Asp Ile Thr Gln Ile Asp Thr Ser Lys Thr Leu Glu
2555 2560 2565

Ser Tyr Gly Val Asp Ser Ile Val Ile Ile Glu Leu Ala Asn Ala
2570 2575 2580

Leu Arg Glu Arg Tyr Pro Ser Leu Asp Ala Ser Gln Leu Met Glu
2585 2590 2595

Thr Leu Ser Ile Asp Arg Leu Val Ala Gln Trp Gln Ala Thr Glu
2600 2605 2610

Pro Ala Val Pro Ala Glu Pro Thr Ala Glu Pro Pro Val Ala Asp
2615 2620 2625

Glu Asp Ala Ala Ala Ile Ile Gly Leu Ala Gly Arg Phe Pro Gly
2630 2635 2640

Ala Asp Thr Leu Glu Glu Phe Trp Asn Asn Leu Arg Asn Gly Gln
2645 2650 2655

Ser Ser Met Gly Glu Val Pro Gly Glu Arg Trp Asp His Gln His
2660 2665 2670

Tyr Phe Asp Ser Glu Arg Gln Ala Pro Gly Lys Thr Tyr Ser Arg
2675 2680 2685

```
Trp Gly  Ala Phe Leu Arg Asp  Ile Asp Gly Phe Asp  Ala Ala Phe
    2690                 2695                 2700

Phe Glu  Trp Pro Asp Ser Val  Ala Leu Glu Ser Asp  Pro Gln Ala
    2705                 2710                 2715

Arg Ile  Phe Leu Glu Gln Ala  Tyr Ala Gly Ile Glu  Asp Ala Gly
    2720                 2725                 2730

Tyr Thr  Pro Gly Ser Leu Ser  Lys Ser Gln Arg Val  Gly Val Phe
    2735                 2740                 2745

Val Gly  Val Met Asn Gly Tyr  Tyr Ser Gly Gly Ala  Arg Phe Trp
    2750                 2755                 2760

Gln Ile  Ala Asn Arg Val Ser  Tyr Gln Phe Asp Phe  Arg Gly Pro
    2765                 2770                 2775

Ser Leu  Ala Val Asp Thr Ala  Cys Ser Ala Ser Leu  Thr Ala Ile
    2780                 2785                 2790

His Leu  Ala Leu Glu Ser Leu  Arg Ser Gly Ser Cys  Glu Val Ala
    2795                 2800                 2805

Leu Ala  Gly Gly Val Asn Leu  Leu Val Asp Pro Gln  Gln Tyr Leu
    2810                 2815                 2820

Asn Leu  Ala Gly Ala Ala Met  Leu Ser Ala Gly Ala  Ser Cys Arg
    2825                 2830                 2835

Pro Phe  Gly Glu Ala Ala Asp  Gly Phe Val Ala Gly  Glu Ala Cys
    2840                 2845                 2850

Gly Val  Val Leu Leu Lys Pro  Leu Lys Gln Ala Arg  Ala Asp Gly
    2855                 2860                 2865

Asp Val  Ile His Ala Val Ile  Arg Gly Ser Met Ile  Asn Ala Gly
    2870                 2875                 2880

Gly His  Thr Ser Ala Phe Ser  Ser Pro Asn Pro Ala  Ala Gln Ala
    2885                 2890                 2895

Glu Val  Val Arg Gln Ala Leu  Gln Arg Ala Gly Val  Ala Pro Asp
    2900                 2905                 2910

Ser Ile  Ser Tyr Ile Glu Ala  His Gly Thr Gly Thr  Val Leu Gly
    2915                 2920                 2925

Asp Ala  Val Glu Leu Gly Ala  Leu Asn Lys Val Phe  Asp Lys Arg
    2930                 2935                 2940

Ala Ala  Pro Cys Pro Ile Gly  Ser Leu Lys Ala Asn  Ile Gly His
    2945                 2950                 2955

Ala Glu  Ser Ala Ala Gly Ile  Ala Gly Leu Ala Lys  Leu Val Leu
    2960                 2965                 2970

Gln Phe  Arg His Gly Glu Leu  Val Pro Ser Leu Asn  Ala Phe Pro
    2975                 2980                 2985
```

```
Leu Asn  Pro Tyr Ile Glu Phe  Gly Arg Phe Gln Val  Gln Gln Gln
    2990                 2995                 3000

Pro Ala  Pro Trp Pro Arg Arg  Gly Ala Gln Pro Arg  Arg Ala Gly
    3005                 3010                 3015

Leu Ser  Ala Phe Gly Ala Gly  Gly Ser Asn Ala His  Leu Val Val
    3020                 3025                 3030

Glu Glu  Ala Pro Ala Met Ala  Pro Gly Val Ser Ile  Ser Ala Ser
    3035                 3040                 3045

Ser Pro  Ala Leu Ile Val Leu  Ser Ala Arg Thr Leu  Pro Ala Leu
    3050                 3055                 3060

Gln Gln  Arg Ala Arg Asp Leu  Leu Val Trp Met Gln  Ala Arg Gln
    3065                 3070                 3075

Val Asp  Asp Val Met Leu Ala  Asp Val Ala Tyr Thr  Leu His Leu
    3080                 3085                 3090

Gly Arg  Val Ala Met Glu Gln  Arg Leu Ala Phe Thr  Ala Gly Ser
    3095                 3100                 3105

Ala Ala  Glu Leu Ser Glu Lys  Leu Gln Ala Tyr Leu  Gly His Ala
    3110                 3115                 3120

Ile Arg  Ala Asp Ile Tyr Leu  Ser Glu Asp Thr Pro  Gly Lys Pro
    3125                 3130                 3135

Ala Gly  Ala Pro Ile Val Ala  Glu Glu Asp Leu Leu  Thr Leu Met
    3140                 3145                 3150

Asp Ala  Trp Ile Glu Lys Gly  Gln Tyr Gly Arg Leu  Leu Glu Tyr
    3155                 3160                 3165

Trp Thr  Lys Gly Gln Pro Ile  Asp Trp Asn Lys Leu  Tyr Trp Arg
    3170                 3175                 3180

Lys Leu  Tyr Ala Asp Gly Arg  Pro Arg Arg Ile Ser  Leu Pro Thr
    3185                 3190                 3195

Tyr Pro  Phe Glu His Arg Arg  Tyr Trp Gln Thr Pro  Val Pro Gly
    3200                 3205                 3210

Glu Arg  Ser Leu His Ala Thr  Ala Pro Ala Thr Arg  Glu Thr Val
    3215                 3220                 3225

Ala Val  Gly Ala Met Pro Asp  Pro Ala Gly Ala Thr  Val Gln Ala
    3230                 3235                 3240

Arg Leu  Cys Ala Leu Cys Gln  Val Leu Leu Gly Lys  Pro Val Thr
    3245                 3250                 3255

Ala Gln  Met Asp Phe Phe Ala  Val Gly Gly His Ser  Val Leu Ala
    3260                 3265                 3270

Ile Gln  Leu Val Ser Arg Ile  Arg Lys Ser Phe Gly  Val Glu Tyr
    3275                 3280                 3285

Pro Val  Ser Ala Leu Phe Glu  Ser Ala Leu Leu Ser  Asp Met Ala
```

```
    3290                3295                3300

Arg Gln  Ile Glu Gln Leu Arg  Val Asn Gly Val Ala  Lys Arg Met
    3305                3310                3315

Pro Ala  Leu Leu Pro Ala Gly  Arg Val Gly Ala Ile  Pro Ala Thr
    3320                3325                3330

Tyr Ala  Gln Glu Arg Leu Trp  Leu Val His Glu His  Met Ser Glu
    3335                3340                3345

Gln Arg  Ser Ser Tyr Asn Ile  Thr Phe Ala Met His  Phe Arg Gly
    3350                3355                3360

Val Asp  Phe Arg Ala Glu Ala  Met Arg Ala Ala Leu  Asn Ala Leu
    3365                3370                3375

Val Val  Arg His Glu Val Leu  Arg Thr Arg Phe Leu  Ser Glu Asp
    3380                3385                3390

Gly Gln  Leu Gln Gln Val Ile  Ala Ala Ser Leu Thr  Leu Glu Val
    3395                3400                3405

Pro Val  Arg Glu Met Ser Val  Glu Glu Val Asp Leu  Leu Leu Ala
    3410                3415                3420

Ala Ser  Thr Arg Glu Thr Phe  Asp Leu Arg Gln Gly  Pro Leu Phe
    3425                3430                3435

Lys Ala  Arg Ile Leu Arg Val  Ala Ala Asp His His  Val Val Leu
    3440                3445                3450

Ser Ser  Ile His His Ile Ile  Ser Asp Gly Trp Ser  Leu Gly Val
    3455                3460                3465

Phe Asn  Arg Asp Leu His Gln  Leu Tyr Glu Ala Cys  Leu Arg Gly
    3470                3475                3480

Thr Pro  Pro Thr Leu Pro Thr  Leu Ala Val Gln Tyr  Ala Asp Tyr
    3485                3490                3495

Ala Leu  Trp Gln Arg Gln Trp  Glu Leu Ala Ala Pro  Leu Ser Tyr
    3500                3505                3510

Trp Thr  Arg Ala Leu Glu Gly  Tyr Asp Asp Gly Leu  Asp Leu Pro
    3515                3520                3525

Tyr Asp  Arg Pro Arg Gly Ala  Thr Arg Ala Trp Arg  Ala Gly Leu
    3530                3535                3540

Val Lys  His Arg Tyr Pro Pro  Gln Leu Ala Gln Gln  Leu Ala Ala
    3545                3550                3555

Tyr Ser  Gln Gln Tyr Gln Ala  Thr Leu Phe Met Ser  Leu Leu Ala
    3560                3565                3570

Gly Leu  Ala Leu Val Leu Gly  Arg Tyr Ala Asp Arg  Lys Asp Val
    3575                3580                3585

Cys Ile  Gly Ala Thr Val Ser  Gly Arg Asp Gln Leu  Glu Leu Glu
    3590                3595                3600
```

```
Glu Leu  Ile Gly Phe Phe Ile  Asn Ile Leu Pro Leu  Arg Val Asp
    3605                 3610                 3615

Leu Ser  Gly Asp Pro Cys Leu  Glu Glu Val Leu Leu  Arg Thr Arg
    3620                 3625                 3630

Gln Val  Val Leu Asp Gly Phe  Ala His Gln Ser Val  Pro Phe Glu
    3635                 3640                 3645

His Val  Leu Gln Ala Leu Arg  Arg Gln Arg Asp Ser  Ser Gln Ile
    3650                 3655                 3660

Pro Leu  Val Pro Val Met Leu  Arg His Gln Asn Phe  Pro Thr Gln
    3665                 3670                 3675

Glu Ile  Gly Asp Trp Pro Glu  Gly Val Arg Leu Thr  Gln Met Glu
    3680                 3685                 3690

Leu Gly  Leu Asp Arg Ser Thr  Pro Ser Glu Leu Asp  Trp Gln Phe
    3695                 3700                 3705

Tyr Gly  Asp Gly Ser Ser Leu  Glu Leu Thr Leu Glu  Tyr Ala Gln
    3710                 3715                 3720

Asp Leu  Phe Asp Glu Ala Thr  Val Arg Arg Met Ile  Ala His His
    3725                 3730                 3735

Gln Gln  Ala Leu Glu Ala Met  Val Ser Arg Pro Gln  Leu Arg Val
    3740                 3745                 3750

Gly Lys  Trp Asp Met Leu Thr  Ala Glu Glu Arg Arg  Leu Phe Ala
    3755                 3760                 3765

Ala Leu  Asn Ala Thr Gly Thr  Pro Arg Glu Trp Pro  Ser Leu Ala
    3770                 3775                 3780

Gln Gln  Phe Glu Arg Gln Ala  Gln Ala Thr Pro Gln  Ala Ile Ala
    3785                 3790                 3795

Cys Val  Ser Asp Gly Gln Ser  Trp Ser Tyr Ala Gln  Leu Glu Ala
    3800                 3805                 3810

Arg Ala  Asn Gln Leu Ala Gln  Ala Leu Arg Gly Gln  Gly Ala Gly
    3815                 3820                 3825

Arg Asp  Val Arg Val Ala Val  Gln Ser Ala Arg Thr  Pro Glu Leu
    3830                 3835                 3840

Leu Met  Ala Leu Leu Ala Ile  Phe Lys Ala Gly Ala  Cys Tyr Val
    3845                 3850                 3855

Pro Ile  Asp Pro Ala Tyr Pro  Ala Ala Tyr Arg Glu  Gln Ile Leu
    3860                 3865                 3870

Ala Glu  Val Gln Val Ser Ile  Val Leu Glu Gln Asp  Glu Leu Ala
    3875                 3880                 3885

Leu Asp  Glu Gln Gly Gln Phe  His Asn Pro Arg Trp  Arg Glu Gln
    3890                 3895                 3900
```

```
Ala Pro  Thr Pro Leu Gly Leu  Arg Glu His Pro Gly  Asp Leu Ala
    3905                 3910                 3915

Cys Val  Met Val Thr Ser Gly  Ser Thr Gly Arg Pro  Lys Gly Val
    3920                 3925                 3930

Met Val  Pro Tyr Ala Gln Leu  Tyr Asn Trp Leu His  Ala Gly Trp
    3935                 3940                 3945

Gln Arg  Ser Pro Phe Glu Ala  Gly Glu Arg Val Leu  Gln Lys Thr
    3950                 3955                 3960

Ser Ile  Ala Phe Ala Val Ser  Val Lys Glu Leu Leu  Ser Gly Leu
    3965                 3970                 3975

Leu Ala  Gly Val Glu Gln Val  Met Leu Pro Asp Glu  Gln Val Lys
    3980                 3985                 3990

Asp Ser  Leu Ala Leu Ala Arg  Ala Ile Glu Gln Trp  Gln Val Thr
    3995                 4000                 4005

Arg Leu  Tyr Leu Val Pro Ser  His Leu Gln Ala Leu  Leu Asp Ala
    4010                 4015                 4020

Thr Gln  Gly Arg Asp Gly Leu  Leu His Ser Leu Arg  His Val Val
    4025                 4030                 4035

Thr Ala  Gly Glu Ala Leu Pro  Ser Ala Val Arg Glu  Thr Val Arg
    4040                 4045                 4050

Ala Arg  Leu Pro Gln Val Gln  Leu Trp Asn Asn Tyr  Gly Cys Thr
    4055                 4060                 4065

Glu Leu  Asn Asp Ala Thr Tyr  His Arg Ser Asp Thr  Val Ala Pro
    4070                 4075                 4080

Gly Thr  Phe Val Pro Ile Gly  Ala Pro Ile Ala Asn  Thr Glu Val
    4085                 4090                 4095

Tyr Val  Leu Asp Arg Gln Leu  Arg Gln Val Pro Ile  Gly Val Met
    4100                 4105                 4110

Gly Glu  Leu His Val His Ser  Val Gly Met Ala Arg  Gly Tyr Trp
    4115                 4120                 4125

Asn Arg  Pro Gly Leu Thr Ala  Ser Arg Phe Ile Ala  His Pro Tyr
    4130                 4135                 4140

Ser Glu  Glu Pro Gly Thr Arg  Leu Tyr Lys Thr Gly  Asp Met Val
    4145                 4150                 4155

Arg Arg  Leu Ala Asp Gly Thr  Leu Glu Tyr Leu Gly  Arg Gln Asp
    4160                 4165                 4170

Phe Glu  Val Lys Val Arg Gly  His Arg Val Asp Thr  Arg Gln Val
    4175                 4180                 4185

Glu Ala  Ala Leu Arg Ala Gln  Pro Ala Val Ala Glu  Ala Val Val
    4190                 4195                 4200

Ser Gly  His Arg Val Asp Gly  Asp Met Gln Leu Val  Ala Tyr Val
```

```
    4205                4210                4215

Val Ala  Arg Glu Gly Gln Ala  Pro Ser Ala Gly Glu  Leu Lys Gln
    4220                4225                4230

Gln Leu  Ser Ala Gln Leu Pro  Thr Tyr Met Leu Pro  Thr Val Tyr
    4235                4240                4245

Gln Trp  Leu Glu Gln Leu Pro  Arg Leu Ser Asn Gly  Lys Leu Asp
    4250                4255                4260

Arg Leu  Ala Leu Pro Ala Pro  Gln Ala Val His Ala  Gln Glu Tyr
    4265                4270                4275

Val Ala  Pro Arg Asn Gln Ala  Glu Gln Arg Leu Ala  Ala Leu Phe
    4280                4285                4290

Ala Glu  Val Leu Arg Val Glu  Gln Val Gly Ile His  Asp Asn Phe
    4295                4300                4305

Phe Ala  Leu Gly Gly His Ser  Leu Ser Ala Ser Gln  Leu Ile Ser
    4310                4315                4320

Arg Ile  Ala Arg Asp Met Ala  Ile Asp Leu Pro Leu  Ala Met Leu
    4325                4330                4335

Phe Glu  Leu Pro Thr Val Ala  Gln Leu Ser Glu Ser  Leu Ala Ser
    4340                4345                4350

His Ala  Arg Asp Ser Asp Tyr  Asp Val Ile Pro Ala  Ser Thr Glu
    4355                4360                4365

Glu Ala  Thr Ile Pro Leu Ser  Thr Ala Gln Glu Arg  Met Trp Phe
    4370                4375                4380

Leu His  Lys Phe Val Gln Glu  Thr Pro Tyr Asn Thr  Pro Gly Leu
    4385                4390                4395

Ala Leu  Leu Gln Gly Glu Leu  Asp Ile Ser Ala Leu  Gln Val Ala
    4400                4405                4410

Phe Arg  Cys Val Leu Glu Arg  His Ala Val Leu Arg  Thr His Phe
    4415                4420                4425

Val Glu  Thr Glu Gln Gln Cys  Val Gln Val Ile Gly  Ala Ala Glu
    4430                4435                4440

Gln Phe  Val Leu Gln Leu Arg  Ser Ile Arg Asp Glu  Ala Asp Leu
    4445                4450                4455

His Gly  Leu Leu His Thr Ala  Val Ser Glu Pro Phe  Asp Leu Glu
    4460                4465                4470

Arg Glu  Leu Pro Leu Arg Ala  Leu Leu Tyr Arg Leu  Asp Asp Arg
    4475                4480                4485

Arg His  Tyr Leu Ala Val Val  Ile His His Ile Val  Phe Asp Gly
    4490                4495                4500

Trp Ser  Thr Ser Ile Leu Phe  Arg Glu Leu Ala Thr  His Tyr Ala
    4505                4510                4515
```

```
Ala Cys  Arg His Gly Gln Ser  Ala Pro Leu Pro Pro  Leu Glu Leu
    4520                 4525                 4530

Ser Tyr  Ala Asp Tyr Ala Arg  Trp Glu Arg Ala Arg  Leu Asn Gln
    4535                 4540                 4545

Glu Asp  Ala Leu Arg Lys Leu  Glu Tyr Trp Lys Thr  Gln Leu Ala
    4550                 4555                 4560
Asp Ala  Pro Pro Leu Val Leu  Pro Thr Thr Tyr Ala  Arg Pro Val
    4565                 4570                 4575

Phe Gln  Asn Phe Asn Gly Ala  Thr Val Ala Leu Gln  Ile Glu Pro
    4580                 4585                 4590

Pro Leu  Leu Gln Arg Leu Gln  Arg Phe Ala Asp Ala  His Ser Phe
    4595                 4600                 4605

Thr Leu  Tyr Met Leu Leu Leu  Ala Ala Leu Gly Val  Val Leu Ser
    4610                 4615                 4620

Arg His  Ala Arg Gln Lys His  Phe Cys Ile Gly Ser  Pro Val Ala
    4625                 4630                 4635

Asn Arg  Ala Arg Ala Glu Leu  His Gly Leu Ile Gly  Leu Phe Val
    4640                 4645                 4650

Asn Thr  Leu Ala Val Arg Leu  Asp Leu Asp Gly Asn  Pro Ser Val
    4655                 4660                 4665

Arg Glu  Leu Leu Glu Arg Ile  His Cys Thr Thr Leu  Ala Ala Tyr
    4670                 4675                 4680

Glu His  Gln Asp Val Pro Phe  Glu Arg Ile Val Glu  Ser Leu Lys
    4685                 4690                 4695

Val Pro  Arg Asp Thr Ala Arg  Asn Pro Leu Gly Gln  Val Met Leu
    4700                 4705                 4710

Asn Phe  Gln Asn Met Pro Met  Ser Ala Phe Asp Leu  Asp Gly Val
    4715                 4720                 4725

Gln Val  Gln Val Leu Pro Met  His Asn Gly Thr Ala  Lys Cys Glu
    4730                 4735                 4740

Leu Thr  Phe Asp Leu Leu Leu  Asp Gly Ser Arg Leu  Ser Gly Phe
    4745                 4750                 4755

Val Glu  Tyr Ala Thr Gly Leu  Phe Ala Pro Glu Trp  Val Gln Ala
    4760                 4765                 4770

Leu Val  Gln Gln Phe Lys Cys  Val Leu Ala Ala Leu  Val Glu Arg
    4775                 4780                 4785

Pro Glu  Ala Ser Leu Asn Asp  Leu Pro Met Ala Pro  Asn Glu Ala
    4790                 4795                 4800

Gln Pro  Ala Ser Pro Ala Leu  Met Lys His Val Ala  Pro Ser Leu
    4805                 4810                 4815

Pro Asn  Leu Leu Glu Ala Met  Ala Ala Asn Asp Ala  Ala Arg Leu
```

```
    4820                4825                4830

Ala Leu  Gln Ala Pro Glu Gly  Ala Leu Ser Tyr Ala  Gln Leu Ile
    4835                4840                4845

Glu Ala  Ala Asn Glu Phe Ala  Trp Arg Leu Arg Cys  Glu His Ala
    4850                4855                4860

Gly Pro  Asp Lys Val Val Ala  Leu Cys Leu Ala Pro  Cys Ser Ala
    4865                4870                4875

Leu Val  Val Ala Leu Leu Ala  Ala Ser Leu Cys Gly  Ala Ala Ser
    4880                4885                4890

Val Leu  Ile Asp Pro Thr Thr  Thr Ala Glu Ala Gln  Tyr Asp Gln
    4895                4900                4905

Leu Phe  Glu Thr Arg Ala Gly  Ile Val Val Thr Cys  Ser Ser Leu
    4910                4915                4920

Leu Glu  Lys Leu Pro Leu Asp  Asp Gln Ala Val Val  Leu Ile Asp
    4925                4930                4935

Glu Gln  Ala Ala Glu Ala Thr  Pro Arg Leu Met His  Phe Thr Asp
    4940                4945                4950

Asp Pro  Ala Leu Pro Ala Met  Leu Tyr Cys Val Cys  Asp Glu Lys
    4955                4960                4965

Gly Arg  Thr Arg Thr Ile Met  Val Glu Ser Gly Ser  Leu Ser Ser
    4970                4975                4980

Arg Leu  Leu Asp Ser Val Gln  Arg Phe Ser Leu Glu  Arg Thr Asp
    4985                4990                4995

Arg Phe  Leu Leu Arg Ser Pro  Leu Ser Ala Glu Leu  Ala Asn Thr
    5000                5005                5010

Glu Val  Leu Gln Trp Leu Ala  Ala Gly Gly Ser Leu  Ser Ile Ala
    5015                5020                5025

Pro Met  His Gly Asp Phe Asp  Ala Ala Ala Trp Leu  Glu Thr Leu
    5030                5035                5040

Ala Thr  Tyr Ala Ile Thr Val  Ala Tyr Leu Ala Gln  Val Glu Leu
    5045                5050                5055

Thr Glu  Met Leu Ala His Leu  Gln Asn His Pro Leu  Glu Arg Asn
    5060                5065                5070

Lys Leu  Ala Gly Leu Arg Val  Leu Val Val His Gly  Ala Pro Leu
    5075                5080                5085

Pro Ile  Ala Pro Leu Met Arg  Leu Asp Ala Trp Leu  Arg Glu Val
    5090                5095                5100

Gly Gly  Ser Ala Arg Ile Phe  Ala Ala Tyr Gly Asn  Ala Glu Phe
    5105                5110                5115

Gly Ala  Glu Ile Leu Ser Gln  Asp Val Ser Ala Ala  Leu Gln Ala
    5120                5125                5130
```

Gly Ile Gly Ala Gln Tyr Lys His Arg Arg Gly Leu Phe Pro Leu
5135 5140 5145

Gly Ala Asn Ser Met Cys His Val Val Gln Ser Asn Gly Arg Ile
5150 5155 5160

Ala Pro Asp Gly Met Val Gly Glu Leu Trp Ile Thr Gln Pro Ala
5165 5170 5175

Cys Leu Tyr Lys Thr Asp Ala Leu Val Arg Arg Leu Ala Asn Gly
5180 5185 5190

Gln Leu Glu Trp Leu Gly Ser Leu Asp Val Gln Ser Arg Ile Asp
5195 5200 5205

Asp Pro Arg Ile Asp Leu Cys Val Val Glu Ala Gln Leu Arg Leu
5210 5215 5220

Cys Glu Asp Val Gly Glu Ala Val Val Leu Tyr Glu Pro Leu Lys
5225 5230 5235

Arg Cys Leu Val Ala Tyr Leu Ser Ala Arg Ser Thr Ala Ala Ile
5240 5245 5250

Met Thr Asp Glu Thr Leu Ala Arg Ile Arg Gln Ala Leu Ser Glu
5255 5260 5265

Thr Leu Pro Asp Tyr Leu Leu Pro Ala Ile Trp Val Pro Leu Ala
5270 5275 5280

His Trp Pro Arg Leu Pro His Gly Arg Val Asp Leu Gly Ala Leu
5285 5290 5295

Pro Ala Pro Asp Phe Asp Leu Ala Arg His Glu Ser Tyr Ile Ala
5300 5305 5310

Pro Arg Thr Ala Val Glu Gln Ala Val Ala Glu Ile Trp Gln Arg
5315 5320 5325

Val Leu Lys Arg Thr Gln Val Gly Val His Asp Asn Phe Phe Glu
5330 5335 5340

Leu Gly Gly His Ser Val Leu Ala Ile Gln Leu Val Ser Gly Leu
5345 5350 5355

Arg Lys Ala Leu Ala Ile Glu Val Pro Val Thr Leu Val Phe Glu
5360 5365 5370

Ala Pro Ile Leu Gly Ala Leu Ala Arg Gln Ile Ala Pro Leu Leu
5375 5380 5385

Val Ser Glu Arg Arg Pro Arg Pro Pro Gly Leu Thr Arg Leu Glu
5390 5395 5400

His Thr Gly Pro Ile Pro Ala Ser Tyr Ala Gln Glu Arg Leu Trp
5405 5410 5415

Leu Val His Glu His Met Glu Glu Gln Arg Thr Ser Tyr Asn Ile
5420 5425 5430

```
Ser Asn  Ala Ala His Phe Ile  Gly Ala Ala Phe Ser  Val Glu Ala
    5435                 5440                 5445

Met Arg  Ala Ala Leu Asn Ala  Leu Val Ala Arg His  Glu Val Leu
    5450                 5455                 5460

Arg Thr  Arg Phe Leu Ser Glu  Asp Gly Gln Leu Gln  Gln Val Ile
    5465                 5470                 5475

Ala Ala  Ser Leu Thr Leu Glu  Val Pro Val Arg Glu  Val Ser Ala
    5480                 5485                 5490

Glu Glu  Val Asp Leu Leu Leu  Ala Ala Ser Thr Arg  Glu Thr Phe
    5495                 5500                 5505

Asp Leu  Arg Gln Gly Pro Leu  Phe Lys Ala Arg Ile  Leu Arg Val
    5510                 5515                 5520

Ala Ala  Asp His His Val Val  Leu Ser Ser Ile His  His Ile Ile
    5525                 5530                 5535

Ser Asp  Gly Trp Ser Leu Gly  Val Phe Asn Arg Asp  Leu His Gln
    5540                 5545                 5550

Leu Tyr  Glu Ala Cys Leu Arg  Gly Thr Pro Pro Thr  Leu Pro Thr
    5555                 5560                 5565

Leu Ala  Val Gln Tyr Ala Asp  Tyr Ala Leu Trp Gln  Arg Gln Trp
    5570                 5575                 5580

Glu Leu  Ala Ala Pro Leu Ser  Tyr Trp Thr Arg Ala  Leu Glu Gly
    5585                 5590                 5595

Tyr Asp  Asp Gly Leu Asp Leu  Pro Tyr Asp Arg Pro  Arg Gly Ala
    5600                 5605                 5610

Thr Arg  Ala Trp Arg Ala Gly  Leu Val Lys His Arg  Tyr Pro Pro
    5615                 5620                 5625

Gln Leu  Ala Gln Gln Leu Ala  Ala Tyr Ser Gln Gln  Tyr Gln Ala
    5630                 5635                 5640

Thr Leu  Phe Met Ser Leu Leu  Ala Gly Leu Ala Leu  Val Leu Gly
    5645                 5650                 5655

Arg Tyr  Ala Asp Arg Lys Asp  Val Cys Ile Gly Ala  Thr Val Ser
    5660                 5665                 5670

Gly Arg  Asp Gln Leu Glu Leu  Glu Glu Leu Ile Gly  Phe Phe Ile
    5675                 5680                 5685

Asn Ile  Leu Pro Leu Arg Val  Asp Leu Ser Gly Asp  Pro Cys Leu
    5690                 5695                 5700

Glu Glu  Val Leu Leu Arg Thr  Arg Gln Val Val Leu  Asp Gly Phe
    5705                 5710                 5715

Ala His  Gln Ser Val Pro Phe  Glu His Val Leu Gln  Ala Leu Arg
    5720                 5725                 5730

Arg Gln  Arg Asp Ser Ser Gln  Ile Pro Leu Val Pro  Val Met Leu
```

```
    5735                5740                5745

Arg His  Gln Asn Phe Pro Thr  Gln Glu Ile Gly Asp  Trp Pro Glu
    5750                5755                5760

Gly Val  Arg Leu Thr Gln Met  Glu Leu Gly Leu Asp  Arg Ser Thr
    5765                5770                5775

Pro Ser  Glu Leu Asp Trp Gln  Phe Tyr Gly Asp Gly  Ser Ser Leu
    5780                5785                5790

Glu Leu  Thr Leu Glu Tyr Ala  Gln Asp Leu Phe Asp  Glu Ala Thr
    5795                5800                5805

Val Arg  Arg Met Ile Ala His  His Gln Gln Ala Leu  Glu Ala Met
    5810                5815                5820

Val Ser  Arg Pro Gln Leu Arg  Val Gly Lys Trp Asp  Met Leu Thr
    5825                5830                5835

Ala Glu  Glu Arg Arg Leu Phe  Ala Ala Leu Asn Ala  Thr Gly Thr
    5840                5845                5850

Pro Arg  Glu Trp Pro Ser Leu  Ala Gln Gln Phe Glu  Arg Gln Ala
    5855                5860                5865

Gln Ala  Thr Pro Gln Ala Ile  Ala Cys Val Ser Asp  Gly Gln Ser
    5870                5875                5880

Trp Ser  Tyr Ala Gln Leu Glu  Ala Arg Ala Asn Gln  Leu Ala Gln
    5885                5890                5895

Ala Leu  Arg Gly Gln Gly Ala  Gly Arg Asp Val Arg  Val Ala Val
    5900                5905                5910

Gln Ser  Ala Arg Thr Pro Glu  Leu Leu Met Ala Leu  Leu Ala Ile
    5915                5920                5925

Phe Lys  Ala Gly Ala Cys Tyr  Val Pro Ile Asp Pro  Ala Tyr Pro
    5930                5935                5940

Ala Ala  Tyr Arg Glu Gln Ile  Leu Ala Glu Val Gln  Val Ser Ile
    5945                5950                5955
Val Leu  Glu Gln Gly Glu Leu  Ala Leu Asp Glu Gln  Gly Gln Phe
    5960                5965                5970

Arg Asn  Arg Arg Trp Arg Glu  Gln Ala Pro Thr Pro  Leu Gly Leu
    5975                5980                5985

Arg Gly  His Pro Gly Asp Leu  Ala Cys Val Met Val  Thr Ser Gly
    5990                5995                6000

Ser Thr  Gly Arg Pro Lys Gly  Val Met Val Pro Tyr  Ala Gln Leu
    6005                6010                6015

His Asn  Trp Leu His Ala Gly  Trp Gln Arg Ser Ala  Phe Glu Ala
    6020                6025                6030

Gly Glu  Arg Val Leu Gln Lys  Thr Ser Ile Ala Phe  Ala Val Ser
    6035                6040                6045
```

Val Lys Glu Leu Leu Ser Gly Leu Leu Ala Gly Val Gly Gln Val
6050 6055 6060

Met Leu Pro Asp Glu Gln Val Lys Asp Ser Leu Ala Leu Ala Arg
6065 6070 6075

Ala Ile Glu Gln Trp Gln Val Thr Arg Leu Tyr Leu Val Pro Ser
6080 6085 6090

His Leu Gln Ala Leu Leu Asp Ala Thr Gln Gly Arg Asp Gly Leu
6095 6100 6105

Leu His Ser Leu Arg His Val Val Thr Ala Gly Glu Ala Leu Pro
6110 6115 6120

Ser Ala Val Gly Glu Ala Val Arg Val Arg Leu Pro Gln Val Gln
6125 6130 6135

Leu Trp Asn Asn Tyr Gly Cys Thr Glu Leu Asn Asp Ala Thr Tyr
6140 6145 6150

His Arg Ser Asp Thr Val Ala Pro Gly Thr Phe Val Pro Ile Gly
6155 6160 6165

Ala Pro Ile Ala Asn Thr Glu Val Tyr Val Leu Asp Arg Gln Leu
6170 6175 6180

Arg Gln Val Pro Ile Gly Val Met Gly Glu Leu His Val His Ser
6185 6190 6195

Val Gly Met Ala Arg Gly Tyr Trp Asn Arg Pro Gly Leu Thr Ala
6200 6205 6210

Ser Arg Phe Ile Ala His Pro Tyr Ser Glu Glu Pro Gly Thr Arg
6215 6220 6225

Leu Tyr Lys Thr Gly Asp Met Val Arg Arg Leu Ala Asp Gly Thr
6230 6235 6240

Leu Glu Tyr Leu Gly Arg Gln Asp Phe Glu Val Lys Val Arg Gly
6245 6250 6255

His Arg Val Asp Thr Arg Gln Val Glu Ala Ala Leu Arg Ala Gln
6260 6265 6270

Pro Ala Val Ala Glu Ala Val Val Ser Gly His Arg Val Asp Gly
6275 6280 6285

Asp Met Gln Leu Val Ala Tyr Val Val Ala Arg Glu Gly Gln Ala
6290 6295 6300

Pro Ser Ala Gly Glu Leu Lys Gln Gln Leu Ser Ala Gln Leu Pro
6305 6310 6315

Thr Tyr Met Leu Pro Thr Val Tyr Gln Trp Leu Glu Gln Leu Pro
6320 6325 6330

Arg Leu Ser Asn Gly Lys Leu Asp Arg Leu Ala Leu Pro Ala Pro
6335 6340 6345

Gln Val Val His Ala Gln Glu Tyr Val Ala Pro Arg Asn Glu Ala

6350 6355 6360

Glu Gln Arg Leu Ala Ala Leu Phe Ala Glu Val Leu Arg Val Glu
6365 6370 6375

Gln Val Gly Ile His Asp Asn Phe Phe Ala Leu Gly Gly His Ser
6380 6385 6390

Leu Ser Ala Ser Gln Leu Ile Ser Arg Ile Arg Gln Ser Phe His
6395 6400 6405

Val Asp Leu Pro Leu Ser Arg Ile Phe Glu Ala Pro Thr Ile Glu
6410 6415 6420

Gly Leu Val Arg Gln Leu Ala Leu Pro Ser Glu Gly Gly Val Ala
6425 6430 6435

Ser Ile Ala Arg Val Ala Arg Asn Arg Thr Ile Pro Leu Ser Leu
6440 6445 6450

Phe Gln Glu Arg Leu Trp Phe Val His Gln His Met Pro Glu Gln
6455 6460 6465

Arg Thr Ser Tyr Asn Gly Thr Leu Ala Leu Arg Leu Arg Gly Pro
6470 6475 6480

Leu Ser Val Glu Ala Met Arg Ala Ala Leu Arg Ala Leu Val Leu
6485 6490 6495

Arg His Glu Ile Leu Arg Thr Arg Phe Val Leu Pro Thr Gly Ala
6500 6505 6510

Ser Glu Pro Val Gln Val Ile Asp Glu His Ser Asp Phe Gln Leu
6515 6520 6525

Ser Val Gln Leu Val Glu Asp Thr Glu Ile Ala Ser Leu Met Asp
6530 6535 6540

Glu Leu Ala Ser His Ile Tyr Asp Leu Ala Asn Gly Pro Leu Phe
6545 6550 6555

Ile Ala Cys Leu Leu Gln Leu Asp Glu Gln Glu His Val Leu Leu
6560 6565 6570

Ile Gly Met His His Leu Ile Tyr Asp Ala Trp Ser Gln Phe Thr
6575 6580 6585

Val Met Asn Arg Asp Leu Arg Val Leu Tyr His Arg His Leu Gly
6590 6595 6600

Leu Ala Gly Gly Asp Leu Pro Glu Leu Pro Ile Gln Tyr Ala Asp
6605 6610 6615

Tyr Ala Ile Trp Gln Arg Ala Gln Asn Leu Asp Ala Gln Leu Ala
6620 6625 6630

Tyr Trp Gln Ala Met Leu His Asp Tyr Asp Asp Gly Leu Glu Leu
6635 6640 6645

Pro Tyr Asp Tyr Pro Arg Pro Arg Asn Arg Thr Trp His Ala Ala
6650 6655 6660

```
Val Tyr  Thr His Thr Tyr Pro  Ala Glu Leu Val Gln  Arg Phe Ala
    6665                 6670                 6675

Gly Phe  Val Gln Ala His Gln  Ser Thr Leu Phe Ile  Gly Leu Leu
    6680                 6685                 6690

Ala Ser  Phe Ala Val Val Leu  Asn Lys Tyr Thr Gly  Arg Asp Asp
    6695                 6700                 6705

Leu Cys  Ile Gly Thr Thr Thr  Ala Gly Arg Thr His  Leu Glu Leu
    6710                 6715                 6720

Glu Asn  Leu Ile Gly Phe Phe  Ile Asn Ile Leu Pro  Leu Arg Leu
    6725                 6730                 6735

Arg Leu  Asp Gly Asp Pro Asp  Val Ala Glu Ile Met  Arg Arg Thr
    6740                 6745                 6750

Arg Leu  Val Ala Met Ser Ala  Phe Glu Asn Gln Ala  Leu Pro Phe
    6755                 6760                 6765

Glu His  Leu Leu Asn Ala Leu  His Lys Gln Arg Asp  Thr Ser Arg
    6770                 6775                 6780

Ile Pro  Leu Val Pro Val Val  Met Arg His Gln Asn  Phe Pro Asp
    6785                 6790                 6795

Thr Ile  Gly Asp Trp Ser Asp  Gly Ile Arg Thr Glu  Val Ile Gln
    6800                 6805                 6810

Arg Asp  Leu Arg Ala Thr Pro  Asn Glu Met Asp Leu  Gln Phe Phe
    6815                 6820                 6825

Gly Asp  Gly Thr Gly Leu Ser  Val Thr Val Glu Tyr  Ala Ala Glu
    6830                 6835                 6840

Leu Phe  Ser Glu Ala Thr Ile  Arg Arg Leu Ile His  His His Gln
    6845                 6850                 6855

Leu Val  Leu Glu Gln Met Leu  Ala Ala His Glu Ser  Ala Thr Cys
    6860                 6865                 6870

Pro Leu  Asp Val Ala Asp
    6875

<210>  27
<211>  343
<212>  PRT
<213>  Xanthomonas albilineans

<400>  27

Met Asp Ser Ala Leu Pro Thr Ser Ala Phe Thr Phe Asp Leu Phe Tyr
1               5                  10                  15

Thr Thr Val Asn Ala Tyr Tyr Arg Thr Ala Ala Val Lys Ala Ala Ile
            20                  25                  30

Glu Leu Gly Leu Phe Asp Val Val Gly Gln Gln Gly Arg Thr Pro Ala
        35                  40                  45
```

```
Ala Ile Ala Glu Ala Cys Gln Ala Ser Pro Arg Gly Ile Arg Ile Leu
    50                  55                  60

Cys Tyr Tyr Leu Val Ser Ile Gly Phe Leu Arg Arg Asn Gly Gly Leu
65                  70                  75                  80

Phe Tyr Ile Asp Arg Asn Met Ala Met Tyr Leu Asp Arg Ser Ser Pro
                85                  90                  95

Gly Tyr Leu Gly Gly Ser Ile Lys Phe Leu Leu Ser Pro Tyr Ile Met
            100                 105                 110

Ser Ala Phe Thr Asp Leu Thr Ala Val Val Arg Thr Gly Lys Ile Asn
        115                 120                 125

Leu Ala Gln Asp Gly Val Val Ala Pro Asp His Pro Gln Trp Val Glu
    130                 135                 140

Phe Ala Arg Ala Met Ala Pro Met Met Ala Leu Pro Ser Ala Leu Ile
145                 150                 155                 160

Ala Asn Met Val Ser Leu Pro Ala Asp Arg Pro Ile Arg Val Leu Asp
                165                 170                 175

Val Ala Ala Gly His Gly Leu Phe Gly Ile Ala Phe Ala Gln Arg Phe
            180                 185                 190

Arg Gln Ala Glu Val Ser Phe Leu Asp Trp Asp Asn Val Leu Asp Val
        195                 200                 205

Ala Arg Glu Asn Ala Gln Ala Ala Lys Val Ala Glu Arg Ala Arg Phe
    210                 215                 220

Leu Pro Gly Asn Ala Phe Asp Leu Asp Tyr Gly Ser Gly Tyr Asp Val
225                 230                 235                 240

Ile Leu Leu Thr Asn Phe Leu His His Phe Asp Glu Val Asp Gly Glu
                245                 250                 255

Arg Ile Leu Ala Lys Thr Arg Asp Ala Leu Asn Asp Asp Gly Met Val
            260                 265                 270

Ile Thr Phe Glu Phe Ile Ala Asp Glu Glu Arg Ser Ser Pro Pro Leu
        275                 280                 285

Ala Ala Thr Phe Ser Met Met Met Leu Gly Thr Thr Pro Ala Gly Glu
    290                 295                 300

Ser Tyr Thr Tyr Ser Asp Leu Glu Arg Met Phe Arg His Ala Gly Phe
305                 310                 315                 320

Gly His Val Glu Leu Lys Ser Ile Pro Pro Ala Leu Leu Lys Val Val
                325                 330                 335

Val Ser Arg Lys Arg Ala Pro
            340
```

<210> 28
<211> 167

<212> PRT
<213> Xanthomonas albilineans

<400> 28

Met Ile Glu Ser Ala Thr Ser Pro Val Ala Lys Thr Glu Arg Ile Trp
1 5 10 15

Cys Thr Glu Leu Asp Leu Asp Ala Leu Asn Ala Met Ser Ala Asn Thr
20 25 30

Met Gln Ala Leu Leu Gly Ile Arg Met Ile Glu Ile Gly Ser Asp Tyr
35 40 45

Leu Val Ser Cys Met Ser Val Asp Trp Arg Cys His Gln Pro Tyr Gly
50 55 60

Val Leu His Gly Gly Ala Ser Val Thr Leu Ala Glu Ala Thr Gly Ser
65 70 75 80

Met Ala Ala Ser Met Cys Val Pro Ala Gly Gln Arg Cys Val Gly Leu
85 90 95

Asp Ile Asn Ala Asn His Ile Ala Ser Ile Ser Ser Gly Gln Val Gln
100 105 110

Cys Ile Ala Arg Pro Leu His Ile Gly Ala Leu Thr Gln Val Trp Gln
115 120 125

Met Arg Ile Tyr Asp Glu Gly Asp Arg Thr Ile Cys Val Ser Arg Leu
130 135 140

Thr Met Ala Val Leu Ser Val His Val Ala Arg Val Ser Pro Asn Pro
145 150 155 160

Ala Ser Ser Gly Val Gln Thr
165

<210> 29
<211> 941
<212> PRT
<213> Xanthomonas albilineans

<400> 29

Met Asn Glu Thr Ala Thr Val Thr Lys Ala Thr Leu Ser Ser Ala Lys
1 5 10 15

Ala Ser Ile Thr Pro Ala Cys Val His Gln Trp Phe Glu Ala Gln Val
20 25 30

Ser Ser Thr Pro Asp Ala Pro Ala Ala Phe Leu Gly Glu Arg Arg Met
35 40 45

Ser Tyr Gly Gln Leu Asn Thr Arg Ala Asn Arg Leu Ala Arg Leu Leu
50 55 60

Gln Ser Gln Gly Val Gly Pro Gly Ala Arg Val Ala Val Trp Met Asn
65 70 75 80

```
Arg Ser Pro Glu Cys Leu Ala Ala Leu Leu Ala Val Met Lys Ala Gly
                85                  90                  95

Ala Ala Tyr Val Pro Ile Asp Leu Ser Leu Pro Ile Arg Arg Val Gln
            100                 105                 110

Tyr Ile Leu Gln Asp Ser Gln Ala Arg Leu Val Leu Val Asp Asp Glu
        115                 120                 125

Gly Gln Gly Arg Leu Asp Glu Leu Glu Leu Gly Ala Met Thr Ala Val
    130                 135                 140

Asp Val Cys Gly Thr Leu Asp Gly Asp Glu Ala Asn Leu Asp Leu Pro
145                 150                 155                 160

Cys Asp Pro Ala Gln Pro Val Tyr Cys Ile Tyr Thr Ser Gly Ser Thr
                165                 170                 175

Gly Ser Pro Lys Gly Val Leu Val Arg His Ser Gly Leu Ala Asn Tyr
            180                 185                 190

Val Ala Trp Ala Lys Arg Gln Tyr Val Thr Ala Asp Thr Thr Ser Phe
        195                 200                 205

Ala Phe Tyr Ser Ser Leu Ser Phe Asp Leu Thr Val Thr Ser Ile Tyr
    210                 215                 220

Val Pro Leu Val Ala Gly Leu Cys Val His Val Tyr Pro Glu Gln Gly
225                 230                 235                 240

Asp Asp Val Pro Val Ile Asn Arg Val Leu Asp Asp Asn Gln Val Asp
                245                 250                 255

Val Ile Lys Leu Thr Pro Ser His Met Leu Met Leu Arg Asn Ala Ala
            260                 265                 270

Leu Ala Thr Ser Arg Leu Lys Thr Leu Ile Val Gly Gly Glu Asp Leu
        275                 280                 285

Lys Ala Ala Val Ala Tyr Asp Ile His Gln Arg Phe Arg Arg Asp Val
    290                 295                 300

Ala Ile Tyr Asn Glu Tyr Gly Pro Thr Glu Thr Val Val Gly Cys Ala
305                 310                 315                 320

Ile His Arg Tyr Asp Pro Ala Thr Glu Arg Glu Gly Ser Val Pro Ile
                325                 330                 335

Gly Val Pro Ile Asp His Thr Ser Leu His Leu Leu Asp Glu Arg Leu
            340                 345                 350

Gln Pro Val Ala Pro Gly Glu Val Gly Gln Ile His Ile Gly Gly Ala
        355                 360                 365

Gly Val Ala Ile Gly Tyr Val Asn Lys Pro Glu Ile Thr Asp Ala Gln
    370                 375                 380

Phe Ile Asp Asn Pro Phe Glu Gly Ser Gly Arg Leu Tyr Ala Ser Gly
385                 390                 395                 400

Asp Leu Gly Arg Met Arg Ala Asp Gly Lys Leu Glu Phe Leu Gly Arg
```

```
                405                 410                 415

Lys Asp Ser Gln Ile Lys Leu Arg Gly Tyr Arg Ile Glu Leu Gly Glu
            420                 425                 430

Ile Glu Asn Val Leu Leu Gly His Ala Ala Leu Arg Glu Cys Ile Val
        435                 440                 445

Asp Thr Thr Val Ala Pro Arg Arg Asp Tyr Asp Ser Lys Ser Leu Arg
    450                 455                 460

Tyr Cys Ala Arg Cys Gly Ile Ala Ser Asn Phe Pro Asn Thr Ser Phe
465                 470                 475                 480

Asp Glu His Gly Val Cys Asn His Cys His Ala Tyr Asp Lys Tyr Arg
                485                 490                 495

Asn Val Val Glu Asp Tyr Phe Arg Thr Glu Asp Glu Leu Arg Thr Ile
            500                 505                 510

Phe Glu Gln Val Lys Ala His Asn Arg Leu Arg Tyr Asp Cys Leu Val
        515                 520                 525

Ala Phe Ser Gly Gly Lys Asp Ser Thr Tyr Ala Leu Cys Arg Val Val
    530                 535                 540

Asp Met Gly Leu Arg Val Leu Ala Tyr Thr Leu Asp Asn Gly Tyr Ile
545                 550                 555                 560

Ser Asp Glu Ala Lys Ala Asn Val Asp Arg Val Val Arg Glu Leu Gly
                565                 570                 575

Val Asp His Arg Tyr Leu Gly Thr Pro His Met Asn Ala Ile Phe Val
            580                 585                 590

Asp Ser Leu His Arg His Ser Asn Val Cys Asn Gly Cys Phe Lys Thr
        595                 600                 605

Ile Tyr Thr Leu Gly Ile Asn Leu Ala His Glu Val Gly Val Ser Asp
    610                 615                 620

Ile Val Met Gly Leu Ser Lys Gly Gln Leu Phe Glu Thr Arg Leu Ser
625                 630                 635                 640

Glu Leu Phe Arg Ala Ser Thr Phe Asp Asn Gln Val Phe Glu Lys Asn
                645                 650                 655

Leu Met Glu Ala Arg Lys Ile Tyr His Arg Ile Asp Asp Ala Ala Ala
            660                 665                 670

Arg Leu Leu Asp Thr Ser Cys Val Arg Asn Asp Arg Leu Leu Glu Ser
        675                 680                 685

Thr Arg Phe Ile Asp Phe Tyr Arg Tyr Cys Ser Val Ser Arg Lys Asp
    690                 695                 700

Met Tyr Arg Tyr Ile Ala Glu Arg Val Gly Trp Ser Arg Pro Ala Asp
705                 710                 715                 720

Thr Gly Arg Ser Thr Asn Cys Leu Leu Asn Asp Val Gly Ile Tyr Met
                725                 730                 735
```

```
His Lys Lys Gln Arg Gly Tyr His Asn Tyr Ser Leu Pro Tyr Ser Trp
            740                 745                 750

Asp Val Arg Val Gly His Ile Pro Arg Glu Asp Ala Met Arg Glu Leu
        755                 760                 765

Glu Asp Thr Asp Asp Ile Asp Glu Ala Lys Val Leu Gly Leu Leu Lys
    770                 775                 780

Gln Ile Gly Tyr Asp Ser Ser Leu Ile Asp Thr Gln Ala Gly Asp Ala
785                 790                 795                 800

Gln Leu Ile Ala Tyr Tyr Val Ala Ala Glu Glu Leu Asp Pro Val Ala
                805                 810                 815

Leu Arg Asn Phe Ala Ala Ala Ile Leu Pro Glu Tyr Met Leu Pro Ser
            820                 825                 830

Tyr Phe Val Arg Leu Asp Arg Met Pro Leu Thr Pro Asn Gly Lys Val
        835                 840                 845

Asn Arg Arg Ala Leu Pro Arg Pro Glu Leu Lys Lys Asn Ala Ser Glu
    850                 855                 860

Ala His Thr Glu Pro Ser Ser Ala Leu Glu Gln Glu Leu Val Gln Ile
865                 870                 875                 880

Trp Lys Glu Val Leu Met Val Asp Lys Val Gly Val Arg Asp Asn Phe
                885                 890                 895

Phe Glu Leu Gly Gly His Ser Leu Ser Ala Leu Met Leu Leu Tyr Ser
            900                 905                 910

Ile Ala Glu Arg Tyr Gln Lys Met Val Ser Ile Gln Ala Phe Ser Val
        915                 920                 925

Asn Pro Thr Ile Glu Gly Leu Ser Glu His Leu Val Ala
    930                 935                 940
```

<210> 30
<211> 239
<212> PRT
<213> Xanthomonas albilineans

<400> 30

```
Met Asp Leu Gln Cys Ala Arg Ile Ala Ala Leu Cys Glu Gln Leu Lys
1               5                   10                  15

Leu Ala Arg Leu Ser Ser Asp Trp Gln Ala Leu Ala Gln Ala Ala Ala
            20                  25                  30

Cys Glu Asp Ala Ser Tyr Phe Leu Glu Lys Val Leu Ala Ser Glu Gln
        35                  40                  45

Leu Ala Arg Glu Glu Arg Lys Arg Thr Val Leu Thr Arg Leu Ala Arg
    50                  55                  60

Met Pro Ser Ile Lys Thr Leu Glu Gln Phe Asp Trp Ala Gln Ala Gly
```

65 70 75 80

Gly Ala Ser Lys Ala Gln Ile Val Glu Leu Gly His Leu Thr Phe Val
85 90 95

Glu Arg Ala Glu Asn Val Val Met Leu Gly Pro Ser Gly Val Gly Lys
100 105 110

Thr His Ile Ala Leu Ala Leu Cys Gln Arg Ala Val Met Ala Gly His
115 120 125

Lys Ala Arg Phe Ile Thr Ala Ala Asp Leu Met Met Gln Leu Ala Ala
130 135 140

Val Lys Ala Gln Asn Arg Leu Lys Asp Tyr Phe Asn Arg Ala Val Leu
145 150 155 160

Gly Pro Lys Leu Leu Val Val Asp Glu Ile Gly Tyr Leu Pro Phe Gly
165 170 175

Arg Glu Pro Ala Gln Gly Cys Trp Ala Ala Thr Gly Phe Ala Leu Arg
180 185 190

Ser Leu Ala Ala Arg Arg Trp Lys Thr Pro Gly Gly Ser Asp Leu Leu
195 200 205

Arg Arg Phe Lys Gly Lys Trp Val Lys Phe Lys Ser Ala Leu Thr Ala
210 215 220

Asp Val Val Tyr Leu Ile Phe Arg Leu Arg Gly Ser Asp His Pro
225 230 235

<210> 31
<211> 286
<212> PRT
<213> Xanthomonas albilineans

<400> 31

Met Pro Arg Ile Glu Tyr Cys Ile Ser Met Met His Arg Arg Lys Pro
1 5 10 15

Thr Thr Asn Arg Ser Val Cys Met Arg Asp Ile Glu Arg Thr Ala Leu
20 25 30

Trp Val Ala Gly Met Arg Ala Leu Glu Ser Glu Arg Glu Gln Ala Leu
35 40 45

Phe His Asp Pro Phe Ala Arg Arg Leu Ala Gly Asp Glu Phe Val Glu
50 55 60

Glu Leu Arg Arg Asn Asn Gln Asn Val Pro Met Pro Pro Ala Ile Glu
65 70 75 80

Val Arg Thr Arg Trp Leu Asp Asp Lys Ile Met Gln Ala Val Ser Glu
85 90 95

Gly Ile Gly Gln Val Val Ile Leu Ala Ala Gly Met Asp Ala Arg Ala
100 105 110

```
Tyr Arg Leu Pro Trp Pro Ser Asp Thr Arg Val Tyr Glu Ile Asp His
        115                 120                 125

Met Asp Val Leu Ser Asp Lys His Glu Lys Leu His Asp Ala Gln Pro
    130                 135                 140

Val Cys Gln Arg Ile Ala Leu Pro Ile Asp Leu Arg Glu Asp Trp Pro
145                 150                 155                 160

Gln Ala Leu Lys Glu Ser Gly Phe Val Gly Ser Ala Ala Thr Leu Trp
                165                 170                 175

Leu Val Glu Gly Leu Leu Cys Tyr Leu Ser Ala Glu Ala Val Met Leu
            180                 185                 190

Leu Phe Ala Arg Ile Asp Ala Leu Ser Ala Lys Gly Ser Ser Val Leu
        195                 200                 205

Phe Asp Val Ile Gly Leu Ser Met Leu Asn Ser Pro Asn Ala Arg Val
    210                 215                 220

Leu His Ala Met Ala Arg Gln Phe Gly Thr Asp Glu Pro Glu Ser Leu
225                 230                 235                 240

Ile Gln Pro Leu Gly Trp Glu Pro Gly Val Leu Thr Ile Ala Ala Ala
                245                 250                 255

Gly Gln Gln Met Gly Arg Trp Pro Phe Pro Val Ala Pro Arg Gly Thr
            260                 265                 270

His Gly Val Pro Gln Ser Tyr Leu Val His Ala Leu Lys Arg
        275                 280                 285


<210>  32
<211>  765
<212>  PRT
<213>  Xanthomonas albilineans

<400>  32

Met Arg Arg Ser Pro Tyr Pro Arg Thr Leu Met Asp Ser Pro Leu Thr
1               5                   10                  15

Asn Leu Pro Met His Ser Gly Thr Glu Leu Asp Leu Arg Trp Ser Val
            20                  25                  30

Gly Gln Thr Arg Pro Gly Arg Asn Glu Ala Tyr Ala Arg Gln Trp Thr
        35                  40                  45

Thr Leu Leu His Gln Trp Arg Arg Asp Tyr Pro Gly Leu Arg Ile Asp
    50                  55                  60

Val Ser Asp Thr Pro Ile Gly Gln His Ile Thr Ile Asp Tyr Ala Ala
65                  70                  75                  80

Pro Tyr Pro Cys Gly Ser Phe Gly Ser Leu Leu Arg Glu Tyr Ala Arg
                85                  90                  95

Leu Gly Lys Leu Ala Gly Leu Ile Cys Asp Tyr Leu Lys His Arg His
            100                 105                 110
```

```
Gln Ile Val Leu Ser Glu Ser Pro Pro Gly Ala Asn Thr Leu Ala Leu
        115                 120                 125

Asp Leu Gly Arg Ile Glu Glu Pro Lys Gln Leu Asp Arg Leu Gln Gly
    130                 135                 140

Ala Leu Gly Met Ala Leu Glu Ala Leu Ala Thr Arg Arg Ser Asp Gly
145                 150                 155                 160

Leu Leu Leu Trp His Ala Asp His Arg Gln Arg Asn Leu Pro Asp Leu
                165                 170                 175

Arg Asp Ser Ala Val Cys Gly Ser Ala Ala Gln Ile Ser Leu Pro Ala
            180                 185                 190

Leu Ser Cys Val Glu Asp Leu Ile Glu Val Asp Thr Ser Leu Leu Ala
        195                 200                 205

Cys Asp His Gly Lys Leu Cys Gln Ile Ala Ser His Leu Pro Ala Ser
    210                 215                 220

Trp Phe Ala Arg Ser Thr Asp Gly Pro Met Pro Ser Trp Ser Asp Ala
225                 230                 235                 240

Ser Thr Ala Val Phe Ala Cys Ala Pro Ile Gly Phe Leu Pro Ser Val
                245                 250                 255

Gln Val Asn Val Cys Ala Gln Ile Phe Ser Ala Ala His Leu Ala Ser
            260                 265                 270

Thr Ala Gln Met Ile Asp Pro Leu Arg Gln Gln Ala Phe Ser Tyr Arg
        275                 280                 285

Gln Leu Arg Ser Arg Ala Ala Thr Tyr Ala Arg His Leu Ser Leu Leu
    290                 295                 300

Gly Leu Gln Ser Gly Asp Ala Val Ala Leu Ile Ala Ile Asp Ser Leu
305                 310                 315                 320

Ala Gly Val Ala Leu Met Leu Ala Cys Leu Ala Gly Gly Leu Val Phe
                325                 330                 335

Ala Pro Ile Asn Glu Leu Val Ser Leu Val His Phe Glu Thr Thr Leu
            340                 345                 350

Lys Thr Ile Lys Pro Arg Leu Val Leu Ile Asp Ala Glu Leu Pro Pro
        355                 360                 365

Ser His His Ala Ala Leu Arg His Leu Pro Thr Leu Glu Leu Thr Ser
    370                 375                 380

Leu Met Pro Val Ile Glu Asn Asp Glu Leu Val Val Ala Pro Cys Ser
385                 390                 395                 400

Ala Asp Ala Pro Ala Val Met Ile Cys Thr Ser Gly Ser Thr Gly Thr
                405                 410                 415

Pro Lys Ala Val Thr His Ser His Ala Asp Phe Met His Cys His Leu
            420                 425                 430
```

```
Asn Tyr Gln Gln Ala Val Leu Gly Leu Arg Ser Asp Asp Val Met Tyr
        435                 440                 445

Thr Pro Ser Arg Leu Phe Phe Ala Tyr Gly Leu Asn Asn Leu Met Leu
    450                 455                 460

Ser Leu Leu Ala Gly Val Ser His Val Ile Ala Ala Pro Leu Ser Val
465                 470                 475                 480

Arg Gln Ile Ala Gln Thr Ile His Thr Tyr His Val Thr Val Leu Leu
                485                 490                 495

Ala Val Pro Ala Val Phe Lys Leu Leu Leu Ala Glu Ala Ala Pro Asp
            500                 505                 510

Ala Val Trp Pro Ala Leu Arg Leu Cys Ile Ser Ala Gly Glu Ser Leu
        515                 520                 525

Pro Ala Arg Leu Gly His Ala Ile Ser Thr Arg Trp Gln Val Glu Val
    530                 535                 540

Leu Asp Gly Ile Gly Cys Thr Glu Val Leu Ser Thr Phe Ile Ser Asn
545                 550                 555                 560

Arg Pro Gly His Ala Leu Met Gly Cys Thr Gly Thr Pro Val Pro Gly
                565                 570                 575

Phe Val Val Lys Leu Val Asn Lys Gln Gly Glu Ile Cys Arg Ile Gly
            580                 585                 590

Glu Val Gly Ser Leu Trp Val Arg Gly Asn Thr Leu Thr Arg Gly Tyr
        595                 600                 605

Val Gly Asp Pro Ile Leu Ser Ala Gln Leu Phe Val Asp Gly Trp Phe
    610                 615                 620

Asp Thr Arg Asp Leu Phe Phe Ala Asp Ala Lys Gly Arg Phe His Asn
625                 630                 635                 640

Leu Gly Arg Met Gly Ser Ala Ile Lys Ile Asn Gly Cys Trp Leu Ser
                645                 650                 655

Pro Glu Thr Leu Glu Ser Val Ile Gln Thr His Ala Cys Val Lys Glu
            660                 665                 670

Cys Ala Ile Cys Leu Ile Glu Asp Glu Phe Gly Leu Pro Arg Pro Ala
        675                 680                 685

Ala Phe Val Val Pro Val Asp Ala Ser Ile Asp Thr Gly Ala Leu Trp
    690                 695                 700

Ala Ala Leu Arg Ala Leu Cys Lys Asn Ala Leu Gly Lys His His Tyr
705                 710                 715                 720

Pro His Leu Phe Val Glu Val Ser Thr Ile Pro Arg Thr Cys Ser Gly
                725                 730                 735

Lys Val Ile Arg Pro Ala Leu Leu Glu Thr Leu Ala Ser Ala Lys His
            740                 745                 750

Leu Gln Ser His Leu Phe Phe Val Gly His Ala Arg Thr
```

755 760 765

<210> 33
<211> 330
<212> PRT
<213> Xanthomonas albilineans

<400> 33

Met His Thr Asn Ala Asp Leu Pro Leu Thr Ile Lys Ala Asp Ser Ala
1 5 10 15
Glu Ala Thr Leu Thr Asp Trp Asn Ala Thr His Arg Ala Thr Trp Pro
20 25 30

Thr Leu Leu Trp Gln His Arg Ala Leu Leu Phe Arg Gly Phe Ala His
35 40 45

Pro Gly Gly Leu Glu Gln Ile Ser Arg Cys Phe Phe Asp Glu Arg Leu
50 55 60

Ala Tyr Thr Tyr Arg Ser Thr Pro Arg Thr Asp Val Gly Gln His Val
65 70 75 80

Tyr Thr Ala Thr Glu Tyr Pro Arg Gln Leu Ser Ile Ala Gln His Cys
85 90 95

Glu Asn Ala Tyr Gln Arg Val Trp Pro Met Lys Leu Leu Phe His Cys
100 105 110

Val Gln Pro Ala Ser Glu Gly Gly Cys Thr Pro Leu Ala Asp Met Leu
115 120 125

Lys Val Thr Ala Ala Ile Asp Pro Gln Val Arg Glu Ile Phe Ala Arg
130 135 140

Lys Gln Val Arg Tyr Val Arg Asn Tyr Arg Ala Gly Val Asp Leu Pro
145 150 155 160

Trp Glu Asp Val Phe Asn Thr Arg Asn Lys Gln Glu Val Glu Ala Tyr
165 170 175

Cys Ala Arg Asn Asp Met Gln Cys Glu Trp Thr Gly Asp Gly Leu Arg
180 185 190

Thr Ser Gln Ile Cys Arg Ala Phe Ala Cys His Pro Ala Thr Gly Asp
195 200 205

Glu Val Trp Phe Asn Gln Ala His Leu Phe His Tyr Thr Ala Leu Glu
210 215 220

Ala Ala Ala Gln Lys Met Met Leu Ser Phe Phe Gly Glu Gln Gly Leu
225 230 235 240

Pro Arg Asn Ala Tyr Phe Gly Asp Gly Thr Pro Ile Asp Pro Ala Met
245 250 255

Leu Asp His Val Arg Thr Val Phe Ala Gln His Lys Ile His Phe Asp
260 265 270

Trp His Arg Asp Asp Val Leu Leu Ile Asp Asn Met Leu Val Ser His

275 280 285

Gly Arg Glu Pro Tyr Glu Gly Ser Arg Lys Ile Leu Val Cys Met Ala
290 295 300

Glu Pro Tyr Ser Pro Glu Gln Ser Ser Pro Asp Ile Ala Ala Arg Ser
305 310 315 320

Asp Gly Glu Ala Met Leu Lys Leu His Val
325 330

<210> 34
<211> 1959
<212> PRT
<213> Xanthomonas albilineans

<400> 34

Met Lys Leu Ser Ser Met Ser Leu Leu Asp Ala Glu Asp Val Ala Leu
1 5 10 15

Thr Ala Ala Ser Pro Asp Thr Ala Leu Ala Leu Asp Trp Ser Arg Ser
20 25 30

Val Leu Asp Leu Phe Asp Ala Gln Val Ala Leu His Ala Glu Glu Leu
35 40 45

Ala Cys Ala Asp Gln His Arg Gln Leu Ser Tyr Ala Gln Leu Asp Gln
50 55 60

His Ala Asn Arg Leu Ala His Cys Leu Ile Glu Arg Gly Leu Arg Pro
65 70 75 80

Gln Glu Arg Val Ala Leu Trp Phe Gly Arg Ser Pro Asp Phe Leu Ile
85 90 95

Ala Leu Leu Gly Val Leu Lys Ala Gly Gly Cys Tyr Val Pro Leu Asp
100 105 110

Pro His Tyr Pro Thr Thr Tyr Ile Gln Gln Ile Leu Asp Asp Ala Gln
115 120 125

Pro Arg Leu Leu Leu Cys Gly Lys Asp Ile Asp Gly Gln Leu Ile Gln
130 135 140

Val Pro Arg Leu Arg Leu Asp Asp Ala Ala Ile Ala Arg Gln Pro His
145 150 155 160

Thr Pro Leu Pro His Ala Leu His Pro Ala Gln Leu Ala Tyr Val Met
165 170 175

Tyr Thr Ser Gly Ser Thr Gly Arg Pro Lys Gly Val Met Val Pro His
180 185 190

Arg Gln Ile Leu Asn Trp Leu His Ala Leu Trp Ala Arg Ala Pro Phe
195 200 205

Glu Ala Gly Glu Arg Val Ala Gln Lys Thr Ser Ile Ala Phe Ala Ile
210 215 220

```
Ser Val Lys Glu Leu Leu Ala Gly Leu Leu Ala Gly Val Pro Gln Val
225                 230                 235                 240

Phe Ile Asp Glu Asp Thr Val Arg Asp Ile Pro Ala Phe Val Arg Ala
                245                 250                 255

Leu Glu Thr Trp Gln Ile Thr Arg Leu Tyr Thr Phe Pro Ser Gln Leu
            260                 265                 270

Asn Ala Leu Leu Asp His Val Ala Glu Thr Pro Gln Arg Leu Ala Arg
        275                 280                 285

Leu Arg Gln Leu Phe Val Ser Ile Glu Pro Cys Pro Ala Glu Leu Leu
    290                 295                 300

Gln Arg Leu Arg Thr Leu Leu Pro Ala Cys Thr Ala Trp Tyr Ile Tyr
305                 310                 315                 320

Gly Cys Thr Glu Ile Asn Asp Met Thr Tyr Cys Asp Pro Ala Glu Gln
                325                 330                 335

His Ser Gly Ser Gly Phe Val Pro Val Gly Arg Pro Ile Ala Asn Thr
            340                 345                 350

Lys Val His Val Leu Asp Glu Gln Leu Arg Pro Leu Pro Pro Gly Ile
        355                 360                 365

Met Gly Glu Val His Ile Glu Ser Leu Gly Ile Thr His Gly Tyr Trp
    370                 375                 380

Arg Gln Gly Gly Leu Thr Ala Ala Arg Phe Ile Ala Asn Pro Tyr Gly
385                 390                 395                 400

Pro Pro Gly Ser Arg Leu Tyr Arg Thr Gly Asp Met Ala Arg Leu Leu
                405                 410                 415

Asp Asn Gly Thr Leu Glu Leu Leu Gly Arg Arg Asp Tyr Glu Val Lys
            420                 425                 430

Val Arg Gly Tyr Arg Val Asp Val Arg Gln Val Glu Lys Ala Leu Ala
        435                 440                 445

Ala His Leu Gln Val Ala Glu Ala Ala Val Ile Gly Trp Pro Gln Gly
    450                 455                 460

Ser Pro Thr Pro Glu Leu Leu Ala Tyr Val Val Pro Arg Gln Gly Val
465                 470                 475                 480

Leu Asn Leu Asp Glu Leu Arg Lys Leu Leu Gln Glu Arg Leu Pro Thr
                485                 490                 495

Tyr Met Leu Pro Thr Arg Phe Gln Ser Leu Pro Ala Leu Pro Arg Leu
            500                 505                 510

Pro Asn Gly Lys Leu Asp Thr Leu Ser Leu Pro Glu Pro Gln Ala Ala
        515                 520                 525

Ser Ser Asp Ser Asp Tyr Leu Ala Pro Arg Ser Glu Val Glu Ile Thr
    530                 535                 540

Leu Ala Lys Leu Trp Ser Glu Leu Leu Thr Pro Ala Gln Ala Ala Pro
```

545 550 555 560

Leu Arg Val Ser Leu Asn Asp Asn Phe Phe Asn Leu Gly Gly His Ser
565 570 575

Leu Leu Ala Thr Gln Leu Phe Ser Arg Ile Arg Gln Ser Phe Asp Ile
580 585 590

Glu Val Arg Val Asn Thr Leu Phe Glu Ser Pro Val Leu Glu Asp Phe
595 600 605

Ala Arg Val Val Asn Glu Ala Arg Gln Gln Gln Ala Pro Thr Gly Gly
610 615 620

Asn Thr Ile Ser Ser Arg Ala Val Arg Asp Ala Pro Val Pro Leu Ser
625 630 635 640

Tyr Gln Gln Glu Arg Leu Trp Phe Val His Glu His Met Pro Glu Gln
645 650 655

Arg Thr Ser Tyr Asn Val Ala Phe Ala Cys His Leu Arg Ser Ala Asp
660 665 670

Phe Ser Met Ser Ala Leu Arg Glu Ala Ile Gln Ala Leu Val Ala Arg
675 680 685

His Glu Thr Leu Arg Thr Arg Ile Ala Thr Cys Ala Gly Gly Asp Tyr
690 695 700

Pro Ser Gln His Ile Ala Asp Ala Met Gln Val Pro Val Pro Cys Ile
705 710 715 720

Thr Ala Thr Pro Ala Glu Val Pro Arg Leu Val Ala Glu His Ala Ala
725 730 735

His Val Phe Asp Leu Ala His Gly Pro Leu Leu Lys Val Ser Val Leu
740 745 750

Arg Val Ser Asp Asp Tyr His Val Phe Leu Met Asn Met His His Ile
755 760 765

Ile Cys Asp Gly Trp Ser Ile Asn Leu Ile Phe His Asp Leu Arg Ala
770 775 780

Phe Tyr Ile Ala Ala Leu Gln Gln Thr Pro Pro Ala Leu Pro Pro Leu
785 790 795 800

Leu Leu Gln Tyr Ala Asp Tyr Ala Thr Trp Gln Arg Val Gln Asp Phe
805 810 815

Ser Ala Asp Leu Asp Tyr Trp Lys Gln Arg Leu His Gly Tyr Glu Glu
820 825 830

Gly Leu Ala Leu Pro Tyr Asp Phe Pro Arg Pro Ala Asn Arg Ala Trp
835 840 845

Arg Ala Gly Ile Leu His Leu Thr Tyr Pro Asp Ala Leu Ala Ala Arg
850 855 860

Leu Ala Ala Phe Ser Gln Glu Arg Arg Val Thr Leu Phe Met Thr Leu
865 870 875 880

```
Met Ala Ser Leu Ala Ile Val Leu His Gln Tyr Thr Gly Arg Arg Glu
                885                 890                 895

Leu Cys Leu Gly Thr Thr Ser Ala Gly Arg Asp Gln Leu Glu Thr Glu
            900                 905                 910

Asn Leu Ile Gly Phe Phe Val Asn Ile Leu Ala Val Arg Leu Asn Leu
        915                 920                 925

Gly Ser His Ala Phe Ala Glu Asp Phe Leu Gln His Val Arg Gln Gln
    930                 935                 940

Val Leu Asp Ala Tyr Ala His Arg Ala Leu Pro Phe Glu His Val Leu
945                 950                 955                 960

Ser Ala Leu Lys Lys Pro Arg Asp Ser Ser Gln Ile Pro Leu Val Pro
                965                 970                 975

Ile Met Leu Arg His Gln Asn Phe Ala Thr Glu Gly Val Asn Ala Phe
            980                 985                 990

Ala Gln Ile Phe Leu Ser Ala Gln  Met Glu Phe Gly Glu  Arg Thr Thr
        995                 1000                1005

Pro Asn  Glu Leu Asp Leu Gln  Phe Ile Gly Asp Gly  Ser His Leu
    1010                1015                1020

Glu Val  Thr Val Glu Tyr Ala  Ala Glu Leu Phe Ser  Ala Ala Thr
    1025                1030                1035

Val Gln  Arg Met Leu Ala His  His Gln Arg Val Leu  Glu Arg Met
    1040                1045                1050

Leu Glu  Glu Pro Arg Cys Arg  Leu Ser Asp Phe Ser  Leu Pro Val
    1055                1060                1065

Ala Arg  Thr Glu Phe Thr Pro  His Thr Leu Asp Thr  Ser Arg Ser
    1070                1075                1080

Val Leu  Asp Leu Phe Asp Ala  Gln Val Ala Leu His  Ala Glu Glu
    1085                1090                1095

Leu Ala  Cys Ala Asp Gln His  Arg Gln Leu Ser Tyr  Ala Gln Leu
    1100                1105                1110

Asp Gln  His Ala Asn Arg Leu  Ala His Cys Leu Ile  Glu Arg Gly
    1115                1120                1125

Leu Arg  Pro Gln Glu Arg Val  Ala Leu Trp Phe Gly  Arg Ser Pro
    1130                1135                1140

Asp Phe  Leu Ile Ala Leu Leu  Gly Val Leu Lys Ala  Gly Gly Cys
    1145                1150                1155

Tyr Val  Pro Leu Asp Pro His  Tyr Pro Thr Thr Tyr  Ile Gln Gln
    1160                1165                1170

Ile Leu  Asp Asp Ala Gln Pro  Arg Leu Leu Leu Cys  Gly Lys Asp
    1175                1180                1185
```

```
Ile Asp  Gly Gln Leu Ile Gln  Val Pro Arg Leu Arg  Leu Asp Asp
    1190                 1195                 1200

Ala Ala  Ile Ala Arg Gln Pro  His Thr Pro Leu Pro  His Ala Leu
    1205                 1210                 1215

His Pro  Ala Gln Leu Ala Tyr  Val Met Tyr Thr Ser  Gly Ser Thr
    1220                 1225                 1230

Gly Arg  Pro Lys Gly Val Met  Val Pro His Arg Gln  Ile Leu Asn
    1235                 1240                 1245

Trp Leu  His Ala Leu Trp Ala  Arg Ala Pro Phe Glu  Ala Gly Lys
    1250                 1255                 1260

Arg Val  Ala Gln Lys Thr Ser  Ile Ala Phe Ala Ile  Ser Val Lys
    1265                 1270                 1275

Glu Leu  Leu Ala Gly Leu Leu  Ala Gly Val Pro Gln  Val Phe Ile
    1280                 1285                 1290

Asp Glu  Asp Thr Val Arg Asp  Ile Pro Ala Phe Val  Arg Ala Leu
    1295                 1300                 1305

Glu Thr  Trp Gln Ile Thr Arg  Leu Tyr Thr Phe Pro  Ser Gln Leu
    1310                 1315                 1320

Asn Ala  Leu Leu Asp His Val  Ala Glu Thr Pro Gln  Arg Leu Ala
    1325                 1330                 1335

Arg Leu  Arg Gln Leu Phe Val  Ser Ile Glu Pro Cys  Pro Ala Glu
    1340                 1345                 1350

Leu Leu  Gln Arg Leu Arg Thr  Leu Leu Pro Ala Cys  Thr Ala Trp
    1355                 1360                 1365

Tyr Ile  Tyr Gly Cys Thr Glu  Ile Asn Asp Met Thr  Tyr Cys Asp
    1370                 1375                 1380

Pro Ala  Glu Gln His Ser Gly  Ser Gly Phe Val Pro  Val Gly Arg
    1385                 1390                 1395

Pro Ile  Ala Asn Thr Lys Val  His Val Leu Asp Glu  Gln Leu Arg
    1400                 1405                 1410

Pro Leu  Pro Pro Gly Ile Met  Gly Glu Val His Ile  Glu Ser Leu
    1415                 1420                 1425

Gly Ile  Thr His Gly Tyr Trp  Arg Gln Gly Gly Leu  Thr Ala Ala
    1430                 1435                 1440
Arg Phe  Ile Ala Asn Pro Tyr  Gly Pro Pro Gly Ser  Arg Leu Tyr
    1445                 1450                 1455

Arg Thr  Gly Asp Met Ala Arg  Leu Leu Asp Asn Gly  Thr Leu Glu
    1460                 1465                 1470

Leu Leu  Gly Arg Arg Asp Tyr  Glu Val Lys Val Arg  Gly Tyr Arg
    1475                 1480                 1485

Val Asp  Val Arg Gln Val Glu  Lys Ala Leu Ala Ala  His Leu Gln
    1490                 1495                 1500
```

```
Val Ala  Glu Ala Ala Val Ile  Gly Trp Pro Gln Gly  Ser Pro Thr
    1505                 1510                 1515

Pro Glu  Leu Leu Ala Tyr Val  Val Pro Arg Gln Gly  Val Leu Asn
    1520                 1525                 1530

Leu Asp  Glu Leu Arg Lys Leu  Leu Gln Glu Arg Leu  Pro Thr Tyr
    1535                 1540                 1545

Met Leu  Pro Thr Arg Phe Gln  Ser Leu Pro Ala Leu  Pro Arg Leu
    1550                 1555                 1560

Pro Asn  Gly Lys Leu Asp Thr  Leu Ser Leu Pro Glu  Pro Gln Ala
    1565                 1570                 1575

Ala Ser  Ser Asp Ser Asp Tyr  Leu Ala Pro Arg Ser  Glu Val Glu
    1580                 1585                 1590

Ile Thr  Leu Ala Lys Leu Trp  Ser Glu Leu Leu Thr  Pro Ala Gln
    1595                 1600                 1605

Ala Ala  Pro Leu Arg Val Ser  Leu Asn Asp Asn Phe  Phe Asn Leu
    1610                 1615                 1620

Gly Gly  His Ser Leu Leu Ala  Thr Gln Leu Phe Ser  Arg Ile Arg
    1625                 1630                 1635

Gln Ser  Phe Asp Ile Glu Val  Arg Val Asn Thr Leu  Phe Glu Ser
    1640                 1645                 1650

Pro Val  Leu Glu Asp Phe Ala  Ala Val Val Glu Arg  Gly Met Arg
    1655                 1660                 1665

Gln Ser  Gln Ala Gly Ser Met  Pro Val Ser Leu Ile  Val Pro Leu
    1670                 1675                 1680

Ser Leu  Arg Thr Glu Arg Ala  Ala Val Tyr Ala Ile  His Pro Ile
    1685                 1690                 1695

Gly Gly  Gln Ile His Cys Tyr  Ile Asp Leu Ala Ala  Ala Leu Gly
    1700                 1705                 1710

His Ser  Ala Arg Val Tyr Gly  Leu Gln Cys Glu Pro  Val Arg Arg
    1715                 1720                 1725

Phe Ala  His Leu Ser Asp Leu  Ala Ala His Tyr Cys  Asp Ala Leu
    1730                 1735                 1740

Leu Ala  Gly Pro Thr Gly Ala  Pro Tyr Arg Leu Leu  Gly Trp Ser
    1745                 1750                 1755

Ser Gly  Gly Val Leu Ala Leu  Ala Val Ala Glu Gln  Leu Gln Arg
    1760                 1765                 1770

Arg Gly  Leu Arg Val Asp Tyr  Val Gly Leu Leu Asp  Ser Ser Leu
    1775                 1780                 1785

Ile Pro  Val His Ala Arg Glu  Pro Arg Gln Leu Thr  Phe Val Ala
    1790                 1795                 1800
```

```
Ala Leu  Asn Thr Leu Ala Ala  Leu Ala Lys Arg Gly  Phe Glu Gln
    1805                 1810                 1815

Ala Glu  Ile Asp Glu Ala Arg  Gln Leu Leu Phe Ala  Asp Gly Asp
    1820                 1825                 1830

Asp Glu  His Val Phe Asp Tyr  Ser Arg His Gln Ala  Ser Leu Asp
    1835                 1840                 1845

Lys Leu  Leu Ala His Leu Arg  Phe Thr Leu Glu Ser  Arg Met Trp
    1850                 1855                 1860

Pro Pro  Leu Ala Glu Gln Leu  Arg Val Thr Arg Tyr  His Leu Gly
    1865                 1870                 1875

Leu Leu  Ala Gly Phe Glu Pro  Gln Cys Leu Gln Pro  Asn Ala His
    1880                 1885                 1890

Leu Tyr  Gln Ala Gln Thr Ala  Val His Val Ser Tyr  Ala Asp Met
    1895                 1900                 1905

Ser Lys  Pro Arg Gly Gly Ser  Glu Val Leu Pro Asp  Ile Thr Gly
    1910                 1915                 1920

Tyr Val  Pro Leu Ser Gln Ile  Lys Ser Ala Ala Gly  Asn His Tyr
    1925                 1930                 1935

Ser Met  Leu Gln Gly Asp Pro  Leu Arg Glu Leu Ala  Arg Met Leu
    1940                 1945                 1950

Val Thr  Asp Leu Asp Ala
    1955
```

<210> 35
<211> 83
<212> PRT
<213> Xanthomonas albilineans

<400> 35

```
Met Thr Phe Glu Glu Gln Ala Tyr Leu Val Leu Ile Asn Asp Glu Leu
1               5                  10                  15

Gln Tyr Ser Leu Trp Pro Ser Asp Leu Glu Val Pro Pro Gly Trp Arg
            20                  25                  30

Lys Glu Gly Tyr Ala Gly Gly Lys Asp Glu Cys Met Ala Tyr Ile Asp
        35                  40                  45

Glu Thr Trp Thr Asp Met Arg Pro Leu Ser Leu Arg Glu Leu Asp Asp
    50                  55                  60

Lys Asn Leu Gly Asp Ala Ser Ser Pro Asp Gly Ser Gly Phe Glu Ser
65                  70                  75                  80

Ser Tyr Ser
```

<210> 36

<211> 315
<212> PRT
<213> Xanthomonas albilineans

<400> 36

Met Gly Cys Ala Cys Leu Pro His Tyr Leu Glu Lys Gln Asp Leu Ser
1 5 10 15

Ala Leu Asp Asp Ala Leu Ala Gly Val Arg Leu Ser Gln Tyr Cys Thr
20 25 30

Thr Asp Gly Arg Gln Leu Glu Leu Tyr Trp Leu Gly Ala Gln Ala Ser
35 40 45

Pro Lys Leu Val Leu Leu Pro Pro Tyr Gly Met Ser Tyr Leu Leu Leu
50 55 60

Ser Arg Leu Ala Gln Arg Leu Ala Arg His Phe His Val Leu Cys Trp
65 70 75 80

Glu Ser Ile Gly Cys Pro Asn Ala Gln Thr Ser Val Thr Ala Glu Asp
85 90 95

Phe Asp Leu Asp Arg Gln Ala Ala Thr Leu Leu Gly Ile Leu His Gln
100 105 110

His Asp Tyr Ala Asp Cys His Phe Val Gly Trp Cys Gln Ala Ala Gln
115 120 125

Leu Ala Val His Ala Ile Ala Leu His Gly Phe Ala Pro Arg Ser Met
130 135 140

Ala Trp Val Ala Pro Ala Gly Leu Leu Pro Pro Ile Val Lys Ser Glu
145 150 155 160

Phe Glu Arg Cys Ala Leu Pro Ile Tyr Leu Gln Ile Glu Arg His Gly
165 170 175

Leu Glu Gln Ala Lys Lys Leu Ala Ala Ile Leu Asp Lys Tyr Arg Gly
180 185 190

Gln Pro Leu Arg Gly Asp Asp Leu Ala Glu Lys Leu Thr Met Leu His
195 200 205

Leu Ala Asp Pro Ala Ser Thr Leu Val Phe Ser Arg Tyr Met Arg Ala
210 215 220

Tyr Glu Glu Asn Lys Gln Ser Val Gln Ala Leu Leu Pro Thr Ala Leu
225 230 235 240

Gly Arg His Pro Thr Leu Ile Val His Cys Lys Asp Asp Ser Phe Ser
245 250 255

His Tyr Ser Ala Ser Val Gln Leu Ala Arg His Asp Pro Ser Leu Arg
260 265 270

Leu Asp Leu Leu Asp His Gly Gly His Leu Gln Leu Phe Asn Asp Pro
275 280 285

Gly Ala Val Ala Gln Arg Ile Ile Asp Phe Ile Gly Leu Thr Val Gly

290 295 300

Glu Val Ala Pro Thr Ser Met His Ser Ala Ala
305 310 315

<210> 37
<211> 451
<212> PRT
<213> Xanthomonas albilineans

<400> 37

Met Tyr Ile Pro Asn Asn Ile Asp Leu Asp Pro His Ser Ala Leu Val
1 5 10 15

Arg Gln Leu Thr Ser Tyr Gln Val Arg Phe Leu Gln Trp Trp Arg Leu
20 25 30

Arg Gly Pro Ser Glu Phe His Asp Arg Glu Met Asn Leu Arg Met Pro
35 40 45

Thr Gly Gly Val Lys Gly Ser Glu Trp Thr Arg Tyr His Arg Met Arg
50 55 60

Pro Ser Asp Tyr Arg Trp Gly Val Phe Met Met Pro Pro Asp Arg Asn
65 70 75 80

Thr Val Val Phe Gly Glu Arg Lys Gly Gln Val Ala Trp Ser Cys Val
85 90 95

Pro Glu Glu Tyr Arg Asp Leu Leu Leu Asp His Val Thr Val Gln Gly
100 105 110

Asp Val Glu Asn Ala Ala Val Glu Gln Ser His Glu Leu Thr Gln Met
115 120 125

Val Pro Ser Ala Ile Asp Leu Glu His Leu Phe Gln Phe Phe Leu Glu
130 135 140

Glu Gly Arg His Thr Trp Ala Met Ser His Leu Leu Ile Glu Tyr Phe
145 150 155 160

Gly Ser Asp Gly Ala Asp Ala Ala Glu Gly Leu Leu Gln Arg Met Ser
165 170 175

Gly Asp Ala Gln Asn Pro Arg Leu Leu Asp Ala Phe Asn Tyr His Thr
180 185 190

Glu Asp Trp Leu Ser His Phe Met Trp Cys Phe Phe Ala Asp Arg Val
195 200 205

Gly Lys Tyr Gln Ile Gln Ala Val Thr Gln Ser Ala Phe Leu Pro Leu
210 215 220

Ala Arg Thr Ala Arg Phe Met Met Phe Glu Glu Pro Leu His Ile Lys
225 230 235 240

Phe Gly Val Asp Gly Leu Glu Arg Val Leu Tyr Arg Ser Ala Glu Ile
245 250 255

```
Thr Leu Arg Glu Asp Thr His Ala Ile Phe Asp Ala Gly Ala Ile Pro
            260                 265                 270

Leu Pro Val Val Gln Lys Tyr Leu Asn Tyr Trp Leu Pro Lys Ile Phe
        275                 280                 285

Asp Leu Phe Gly His Asp Val Ser Glu Arg Ser Arg Val Leu Tyr Gln
    290                 295                 300

Ala Gly Ile Arg Ser Pro Arg Asn Phe Asp Lys Leu Glu Gly Thr Glu
305                 310                 315                 320

Val Ala Val Asp Val Arg Cys Glu Asp Arg Leu Val Ser Ser Thr Ala
                325                 330                 335

Pro Ala Glu Leu Ala Ile Asn Ala Val Met Arg Arg Gln Tyr Ile Ala
            340                 345                 350

Glu Val Gly Ala Ile Ile Gly Arg Trp Asn Gln Gln Leu Arg Arg Leu
        355                 360                 365

Gly Leu Ala Phe Glu Leu Gln Leu Pro His Glu Arg Phe His Arg Asp
    370                 375                 380

Phe Gly Pro Cys Lys Gly Leu Ala Phe Asp Leu Asp Gly Asn Pro Val
385                 390                 395                 400

His Asp Ala Asp Gly Gln Arg Leu Ala Ala Leu Leu Pro Thr Pro Gln
                405                 410                 415

Asp Leu Ala Gly Val Arg Gly Leu Met Gly Arg Glu Leu Gly Glu Gly
            420                 425                 430

Arg Thr Ala Val Trp Leu Ala Pro Ala Gly Ala Ser Leu Asp Lys Leu
        435                 440                 445

Met Pro Ala
    450
```

<210> 38
<211> 317
<212> PRT
<213> Xanthomonas albilineans

<400> 38

```
Met Asn Ser Tyr Val Gly Cys Gln Lys Leu Glu Thr Asp Gly Asp Ala
1               5                   10                  15

Ser Arg Val Val Pro Met Trp Val Met Tyr Pro Thr Ala Thr Pro Ser
            20                  25                  30

Arg Asp Thr Ala Met Gly Pro Tyr Thr Leu Asp Val Ala Leu Gly Ala
        35                  40                  45

Pro Ile Glu Ala Gly Pro Phe Pro Leu Ala Val Ile Ser His Gly Thr
    50                  55                  60

Arg Ser Ala Gly Leu Val Phe Arg Thr Leu Ala His Tyr Leu Ala Arg
65                  70                  75                  80
```

```
His Gly Phe Ile Val Ala Leu Pro Glu His Pro Gly Asp Asn Leu Phe
                85                  90                  95

Gln His Gln Leu Glu Tyr Ser Tyr Gln Asn Leu Glu Asp Arg Pro Arg
            100                 105                 110

His Ile Arg Ala Val Ile Asp Thr Leu Thr Gly His Ala Gln Phe Gly
        115                 120                 125

Pro Ala Ile Gln Ala His Asn Val Ala Val Ile Gly His Ser Val Gly
    130                 135                 140

Gly Tyr Thr Ala Leu Ala Ile Ala Gly Gly Glu Pro His Thr Gly Phe
145                 150                 155                 160

Met Val Asp Phe Ala His Arg Pro Glu His Ala Glu Gln Pro Ala Trp
                165                 170                 175

Thr Ala Leu Val Arg Gln Asn Arg Val Pro Ile Arg Ala Val Pro Val
            180                 185                 190

Thr Ala Asp Pro Arg Val Arg Ala Val Val Ala Leu Ala Pro Asp Phe
        195                 200                 205

Ser Leu Tyr Met His Glu Asp Ala Leu Ala Lys Val Glu Val Pro Val
    210                 215                 220

Leu Leu Ile Val Gly Glu Lys Asp Gln Trp Ala His Glu Thr Ile Val
225                 230                 235                 240

Ala Thr Arg Thr Ala Leu Gly Asn Asp Gly Arg Leu Glu Ala Arg Val
                245                 250                 255

Val Pro Asn Ala Gly His Tyr Ala Phe Ile Ser Val Phe Pro Glu Ala
            260                 265                 270
Met Lys Ala Arg Val Gly Glu Ala Ala Ile Asp Pro Pro Gly Phe Asp
        275                 280                 285

Arg Ser Ala Phe Gln Arg Glu Leu Glu Arg Asp Ile Leu His Phe Leu
    290                 295                 300

Thr Val Thr Met Arg Pro Ala Glu Ala Ala Ile Ser Gly
305                 310                 315
```

<210> 39
<211> 496
<212> PRT
<213> Xanthomonas albilineans

<400> 39

```
Met Gln Lys Pro Lys Glu Ala Leu Gly Met Pro Pro Gly Met Ala Pro
1               5                   10                  15

Pro Gly Ala Gln Phe Asp Tyr Arg Trp Arg Trp Pro Ala Met Ile Val
            20                  25                  30

Leu Leu Ser Ala Asn Phe Met Asn Leu Leu Asp Val Gly Ile Val Asn
        35                  40                  45
```

```
Val Ala Leu Pro Ser Ile Gln Lys Asn Leu Gly Ala Asp Glu Gln Gln
    50                  55                  60

Leu Glu Trp Ile Val Ala Ile Tyr Ile Leu Leu Phe Ala Leu Gly Leu
65                  70                  75                  80

Leu Pro Leu Gly Arg Leu Gly Asp Met Leu Gly Arg Lys Arg Met Phe
                85                  90                  95

Gly Thr Gly Val Ala Gly Phe Ile Leu Met Ser Ala Phe Cys Ala Ile
            100                 105                 110

Ala Gly Asn Ile His Val Leu Ile Ile Ala Arg Ala Leu Gln Gly Leu
        115                 120                 125

Ala Ala Ala Met Leu Ala Pro Gln Val Met Ala Ile Ala Gln Thr Met
    130                 135                 140

Phe Ala Pro Lys Glu Arg Ala Ala Ala Phe Ser Leu Phe Gly Leu Val
145                 150                 155                 160

Ala Gly Leu Ala Ser Phe Ala Gly Pro Leu Val Ser Gly Leu Leu Ile
                165                 170                 175

His Ile Asp Ala Phe Gly Val Gly Trp Arg Ala Ile Phe Leu Ile Asn
            180                 185                 190

Val Pro Ile Gly Leu Val Thr Leu Leu Ala Ala Ala Ile Trp Val Pro
        195                 200                 205

Lys Val Pro Ala His Ala Gly Ile His Asn Asp Trp Val Gly Ile Ala
    210                 215                 220

Leu Ala Ala Leu Ala Leu Leu Cys Leu Val Phe Pro Leu Ile Glu Gly
225                 230                 235                 240

Arg Ala Tyr Gly Trp Pro Leu Trp Cys Phe Ala Ala Ile Ala Leu Gly
                245                 250                 255

Ile Pro Leu Leu Val Ala Phe Val Ala Trp Gln Arg Arg Gln Ala His
            260                 265                 270

Leu Ala Arg Pro Ala Leu Leu Pro Ile Tyr Leu Met Ser His Arg Asp
        275                 280                 285

Tyr Ile Leu Gly Ala Leu Ser Val Ser Val Phe Tyr Ser Ala Leu Gln
    290                 295                 300

Gly Phe Phe Leu Val Phe Val Ile Phe Leu Gln Gln Gly Leu Ala Tyr
305                 310                 315                 320

Ser Ala Leu Glu Thr Gly Val Ala Thr Thr Pro Phe Pro Val Gly Val
                325                 330                 335

Ala Ile Ala Ser Met Leu Ala Arg His Val Glu Ser Leu Arg Ala Lys
            340                 345                 350

Ile Phe Ser Gly Ala Cys Leu Met Ile Ala Ser Tyr Leu Ala Leu Trp
        355                 360                 365
```

```
Val Ile Ile Thr Arg Ser Glu Gly Ser Leu Asp Pro Trp Thr Leu Thr
    370                 375                 380

Leu Pro Leu Leu Ile Gly Gly Leu Gly Cys Gly Ile Thr Ile Ala Ser
385                 390                 395                 400

Leu Phe Gln Thr Val Met Arg Thr Val Pro Leu Lys Asp Ala Gly Ala
                405                 410                 415

Gly Ser Gly Ala Leu Gln Val Ile Gln Gln Val Gly Gly Met Leu Gly
            420                 425                 430

Ile Ala Leu Val Ser Glu Ile Phe Phe Ser Gly Leu His Gln His Leu
        435                 440                 445

Gln Gly Pro Ala Gly Val Ala Leu Ala Phe Lys Gln Ala Phe Gly Ala
    450                 455                 460

Thr Val Val Tyr Tyr Ile Ala Ala Asn Ala Phe Val Ala Leu Ser Thr
465                 470                 475                 480

Leu Gly Leu Gln Phe Lys Leu Thr Gln Phe Ala Pro Gln Ser Ser Pro
                485                 490                 495
```

<210> 40
<211> 584
<212> PRT
<213> Xanthomonas albilineans

<400> 40

```
Met Lys Arg Thr Tyr Ile Gly Leu Ala Asn Ser Phe His Asp Ser Ala
1               5                   10                  15

Ile Ala Ile Val Gly Asp Asp Gly Gln Val Arg Phe Ala Glu Ala Thr
            20                  25                  30

Glu Arg Tyr Leu Gln Tyr Lys Arg Ser Ile Gly Val Ala Pro Asp Val
        35                  40                  45

Phe Gln Arg Ala Ile Lys Leu Val His Glu Tyr Gly Asp Pro Gly Ala
    50                  55                  60

Glu Leu Val Val Ala Thr Ser Trp Ser Gly Gln Thr Pro Glu Leu Met
65                  70                  75                  80

Arg Glu Gly Leu Gly Lys Thr Ala Gln Ala Val Asp Gln Tyr Arg Ser
                85                  90                  95

Ala Phe Gly Asp Leu Pro Trp His Val Asn Lys Gln Phe Val Ala Gln
            100                 105                 110

Ser Phe Phe Tyr Arg Ser Gln Leu Ala Met Val Glu His Pro Gly His
        115                 120                 125

Leu Leu Glu Tyr Asp Leu Ser His Met Ala Glu Pro Ala Phe Lys Pro
    130                 135                 140

Pro Ser Tyr Arg His Tyr Glu His His Leu Thr His Ala Val Ala Gly
145                 150                 155                 160
```

```
Cys Tyr Thr Ser Pro Phe Glu Glu Ala Val Cys Ala Val Leu Asp Gly
                165                 170                 175

Met Gly Glu Lys Asn Ala Leu Ala Cys Tyr His Tyr Gln Gln Gly Lys
            180                 185                 190

Leu Thr Pro Ile His Gln Ser Glu Thr Ser Ser Trp Ala Ser Leu Gly
        195                 200                 205

Phe Phe Tyr Gly Met Ile Cys Glu Val Cys Gly Phe Gly Thr Leu Ser
    210                 215                 220

Gly Glu Glu Trp Lys Val Met Gly Leu Ala Ala Tyr Gly Gln His Asp
225                 230                 235                 240

Arg Gln Leu Tyr Glu Leu Leu Arg Gln Met Leu Arg Val Asp Gly Leu
                245                 250                 255

Thr Leu Arg Phe Ala Pro Ala Ala Gln Phe Ser Gln Leu Gln Arg Thr
            260                 265                 270

Leu Tyr Ala Met Arg Arg Cys Lys Gly Gln Pro Thr Ile Glu Leu Ala
        275                 280                 285

Asn Leu Ala Tyr Ala Gly Gln Gln Val Phe Cys Asp Val Leu Phe Glu
    290                 295                 300

Phe Leu His Asn Leu His Ala Leu Gly Leu Ser Asp His Leu Val Leu
305                 310                 315                 320

Gly Gly Gly Cys Ala Leu Asn Ser Ser Ala Asn Gly Arg Val Leu Ala
                325                 330                 335

Glu Thr Pro Phe Arg His Leu His Val Phe Ala Ala Pro Gly Asp Asp
            340                 345                 350

Gly Asn Ala Val Gly Ala Ala Leu Trp Ala His Ala Glu Asp His Pro
        355                 360                 365

Glu Gln Thr Pro Pro Ala Ala Arg Glu Gln Ser Pro Tyr Leu Gly Ser
    370                 375                 380

Ser Met Ser Ala Glu Thr Leu His Asn Val Glu Arg Phe Gly Ala Leu
385                 390                 395                 400

Ser Lys Phe Thr Arg Cys Leu Asp Asp Ala Ala Gln Arg Ala Ala Arg
                405                 410                 415

Leu Leu Thr Glu Gly Lys Ile Val Ala Trp Val Gln Gly Arg Ala Glu
            420                 425                 430

Phe Gly Pro Arg Ala Leu Gly Asn Arg Ser Ile Leu Ala Asp Pro Arg
        435                 440                 445

Ser Pro Ala Ile Lys Asp Ile Ile Asn Ala Arg Val Lys Phe Arg Glu
    450                 455                 460

Glu Phe Arg Pro Phe Ala Pro Ser Ile Leu His Glu His Gly Ala Glu
465                 470                 475                 480
```

```
Tyr Phe Glu Leu Tyr Gln Glu Ser Pro Tyr Met Glu Arg Thr Leu Lys
                485                 490                 495

Phe Arg Ala Glu Ala Thr Arg Lys Val Pro Gly Val Val His His Asp
            500                 505                 510

Gly Thr Gly Arg Leu Gln Thr Val Lys Gln His Trp Asn Pro Arg Tyr
        515                 520                 525

His Ala Leu Ile Lys Glu Phe Tyr Arg Leu Thr Gly Ile Pro Leu Val
    530                 535                 540

Leu Asn Thr Ser Phe Asn Val Met Gly Lys Pro Ile Ala His Ser Val
545                 550                 555                 560

Glu Asp Ala Leu Ser Ile Phe Phe Thr Ser Gly Leu Asp Ala Met Phe
                565                 570                 575

Ile Asp Asp Val Leu Ile Glu Lys
            580
```

<210> 41
<211> 88
<212> PRT
<213> Xanthomonas albilineans

<400> 41

```
Met Arg Thr Ser Lys Phe Asn Glu Thr Gln Ile Ile Ala Thr Leu Lys
1               5                   10                  15

Gln Ala Asp Ala Gly Val Pro Val Lys Asp Ile Cys Arg Gln Val Gly
            20                  25                  30

Ile Ser Thr Ala Thr Tyr Tyr Gln Trp Lys Ser Lys Tyr Val Ala Ser
        35                  40                  45

Glu Met Pro Ser Ser Arg His Thr Ser Leu Thr Trp Arg Pro Pro Ser
    50                  55                  60

Thr Cys Phe Ser Val Ala Thr Ile Trp Leu Ser Val Asn Leu Leu Leu
65                  70                  75                  80

Arg Ile Val Gly Arg Leu Gly Gly
                85
```

<210> 42
<211> 716
<212> PRT
<213> Xanthomonas albilineans

<400> 42

```
Met Arg Cys Leu Ile Ile Asn Asn Tyr Asp Ser Phe Thr Trp Asn Leu
1               5                   10                  15

Ala Asp Tyr Val Ala Gln Ile Phe Gly Glu Asp Pro Leu Val Val His
            20                  25                  30
```

```
Asn Asp Glu Tyr Ser Trp His Glu Leu Lys Asp Arg Gly Gly Phe Ser
        35                  40                  45

Ser Ile Ile Val Ser Pro Gly Pro Gly Ser Val Val Asn Glu Ala Asp
    50                  55                  60

Phe His Ile Ser Leu Gln Ala Leu Glu Gln Asn Glu Phe Pro Val Leu
65                  70                  75                  80

Gly Val Cys Leu Gly Phe Gln Gly Leu Ala His Val Tyr Gly Gly Arg
                85                  90                  95

Ile Leu His Ala Pro Val Pro Phe His Gly Arg Arg Ser Thr Val Ile
            100                 105                 110

Asn Thr Gly Asp Gly Leu Phe Glu Gly Ile Pro Gln Arg Phe Glu Ala
        115                 120                 125

Val Arg Tyr His Ser Leu Met Val Cys Gln Gln Ser Leu Pro Pro Val
    130                 135                 140

Leu Lys Val Thr Ala Arg Thr Asp Cys Gly Val Val Met Gly Leu Gln
145                 150                 155                 160

His Val Gln His Pro Lys Trp Gly Val Gln Phe His Pro Glu Ser Ile
                165                 170                 175

Leu Thr Glu His Gly Lys Arg Ile Val Ala Asn Phe Ala Lys Leu Ala
            180                 185                 190

Ala Arg His Ser Ala Pro Leu Leu Ala Gly Ser Glu Gln Ala Gly Lys
        195                 200                 205

Val Leu Ser Val Cys Ala Pro Glu Met Val Thr Pro Arg Val Arg Arg
    210                 215                 220

Met Leu Ser Arg Lys Ile Lys Cys Arg Trp Gln Ala Glu Asp Val Phe
225                 230                 235                 240

Leu Ala Leu Phe Ala Asp Glu Lys His Cys Phe Trp Leu Asp Ser Gln
                245                 250                 255

Leu Val Cys Ser Pro Met Ala Arg Tyr Ser Phe Met Gly Ala Val Asn
            260                 265                 270

Glu Ser Glu Val Val Arg His Cys Val Arg Pro Gly Ser Met Val Gln
        275                 280                 285

Glu Ala Gly Glu Arg Phe Leu Ala Glu Met Asp Arg Ala Leu Gln Ser
    290                 295                 300

Val Leu Thr Glu Asp Val Ala Glu Arg Pro Pro Phe Ala Phe Arg Gly
305                 310                 315                 320

Gly Tyr Val Gly Tyr Met Ser Tyr Glu Met Lys Ser Val Phe Gly Ala
                325                 330                 335

Pro Ala Ser His Ala Asn Ala Ile Pro Asp Ala Leu Trp Met Arg Val
            340                 345                 350

Glu Arg Phe Val Ala Phe Asp His Ala Thr Glu Glu Val Trp Leu Leu
```

```
        355                 360                 365

Ala Leu Ala Asp Thr Glu Asp Leu Ser Ala Leu Ala Trp Leu Asp Ala
    370                 375                 380

Ile Glu Gln Arg Ile His Ala Ile Gly Gln Ala Ala Pro Ala Cys Ile
385                 390                 395                 400

Ser Leu Gly Leu Arg Ser Met Glu Ile Glu Leu Asn His Gly Arg Arg
                405                 410                 415

Gly Tyr Leu Glu Ala Ile Glu Arg Cys Lys Gln Arg Ile Val Asp Gly
            420                 425                 430

Glu Ser Tyr Glu Ile Cys Leu Thr Asp Leu Phe Ser Phe Gln Ala Glu
        435                 440                 445

Leu Asp Pro Leu Met Leu Tyr Arg Tyr Met Arg Arg Gly Asn Pro Ala
    450                 455                 460

Pro Phe Gly Ala Tyr Leu Arg Asn Gly Ser Asp Cys Ile Leu Ser Thr
465                 470                 475                 480
Ser Pro Glu Arg Phe Leu Glu Val Asp Gly His Gly Thr Ile Gln Thr
                485                 490                 495

Lys Pro Ile Lys Gly Thr Cys Arg Arg Ala Glu Asp Pro Gln Leu Asp
            500                 505                 510

Arg Asn Leu Ala Met Arg Leu Ala Ala Ser Glu Lys Asp Arg Ala Glu
        515                 520                 525

Asn Leu Met Ile Val Asp Leu Met Arg Asn Asp Leu Ser Arg Val Ala
    530                 535                 540

Val Pro Gly Ser Val Thr Val Pro Lys Leu Met Asp Ile Glu Ser Tyr
545                 550                 555                 560

Lys Thr Val His Gln Met Val Ser Thr Val Glu Ala Arg Leu Arg Ala
                565                 570                 575

Asp Cys Ser Leu Val Asp Leu Leu Lys Ala Val Phe Pro Gly Gly Ser
            580                 585                 590

Ile Thr Gly Ala Pro Lys Leu Arg Ser Met Glu Ile Ile Asp Gly Leu
        595                 600                 605

Glu Asn Ala Pro Arg Gly Val Tyr Cys Gly Ser Ile Gly Tyr Leu Gly
    610                 615                 620

Tyr Asn Cys Val Ala Asp Leu Asn Ile Ala Ile Arg Ser Leu Ser Tyr
625                 630                 635                 640

Asp Gly Gln Glu Ile Arg Phe Gly Ala Gly Gly Ala Ile Thr Phe Leu
                645                 650                 655

Ser Asp Pro Gln Asp Glu Phe Asp Glu Val Leu Leu Lys Ala Glu Ala
            660                 665                 670

Ile Leu Lys Pro Ile Trp His Tyr Leu His Ala Pro Asn Thr Pro Leu
        675                 680                 685
```

```
His Tyr Glu Leu Arg Glu Asp Lys Leu Leu Leu Ala Glu His Cys Val
    690                 695                 700

Ser Glu Met Pro Ala Arg Gln Ala Phe Ile Glu Pro
705                 710                 715


<210>  43
<211>  137
<212>  PRT
<213>  Xanthomonas albilineans

<400>  43

Met Arg Pro Pro Arg Leu Arg Ala Asn Gln Asp Gly Leu Leu Met Asp
1               5                   10                  15

Thr Ala Gly Arg Val Val Glu Gly Cys Thr Ser Asn Leu Phe Leu Val
            20                  25                  30

Glu Asn Gly His Leu Val Thr Pro Asp Leu Gly Val Ala Gly Val Ser
        35                  40                  45

Gly Ile Met Arg Gly Arg Val Ile Glu Tyr Gly Arg Gln His Gly Leu
    50                  55                  60
Ala Cys Ala Val Lys His Val Tyr Pro Asp Gln Leu Val Arg Ala Gln
65                  70                  75                  80

Glu Val Phe Leu Thr Asn Ala Val Phe Gly Ile Leu Leu Val Arg Ser
                85                  90                  95

Ile Asp Ala His Ser Tyr Arg Ile Asp Pro Val Thr Leu Arg Leu Leu
            100                 105                 110

Asp Ala Leu Cys Gln Gly Val Tyr Phe Thr Glu Arg Ser Leu His Gln
        115                 120                 125

Val Ser Thr His Ala Gly Gln Asp Pro
    130                 135


<210>  44
<211>  200
<212>  PRT
<213>  Xanthomonas albilineans

<400>  44

Met Pro Ala Lys Thr Leu Glu Ser Lys Asp Tyr Cys Gly Glu Ser Phe
1               5                   10                  15

Val Ser Glu Asp Arg Ser Gly Gln Ser Leu Glu Ser Ile Arg Phe Glu
            20                  25                  30

Asp Cys Thr Phe Arg Gln Cys Asn Phe Thr Glu Ala Glu Leu Asn Arg
        35                  40                  45

Cys Lys Phe Arg Glu Cys Glu Phe Val Asp Cys Asn Leu Ser Leu Ile
    50                  55                  60

Ser Ile Pro Gln Thr Ser Phe Met Glu Val Arg Phe Val Asp Cys Lys
```

65 70 75 80

Met Leu Gly Val Asn Trp Thr Ser Ala Gln Trp Pro Ser Val Lys Met
85 90 95

Glu Gly Ala Leu Ser Phe Glu Arg Cys Ile Leu Asn Asp Ser Leu Phe
100 105 110

Tyr Gly Leu Tyr Leu Ala Gly Val Lys Met Val Glu Cys Arg Ile His
115 120 125

Asp Ala Asn Phe Thr Glu Ala Asp Cys Glu Asp Ala Asp Phe Thr Gln
130 135 140

Ser Asp Leu Lys Gly Ser Thr Phe His Asn Thr Lys Leu Thr Gly Ala
145 150 155 160

Ser Phe Ile Asp Ala Val Asn Tyr His Ile Asp Ile Phe His Asn Asp
165 170 175

Ile Lys Arg Ala Arg Phe Ser Leu Pro Glu Ala Ala Ser Leu Leu Asn
180 185 190

Ser Leu Asp Ile Glu Leu Ser Asp
195 200

<210> 45
<211> 202
<212> PRT
<213> Xanthomonas albilineans

<400> 45

Met His Pro Pro Ser Pro Leu Asn Thr Gln Gln Lys Asp Trp Leu Thr
1 5 10 15

Arg Gly Gly Ser Leu Thr Ala His Leu Arg Leu Leu Gly Gln Val Gln
20 25 30

Val Gln Val Gln Arg Glu His Lys Ser Met Ala Trp Leu Asp Glu Tyr
35 40 45

Arg Val Leu Gly Leu Ser Arg Cys Leu Leu Val Trp Val Arg Glu Val
50 55 60

Val Leu Val Val Asp Ala Lys Pro Tyr Val Tyr Ala Arg Ser Leu Thr
65 70 75 80

Pro Leu Thr Ala Ser Tyr Asn Ala Trp Gln Ala Val Arg Ser Ile Gly
85 90 95

Ser Arg Pro Leu Ala Asp Leu Leu Phe Arg Asp Arg Ser Val Leu Arg
100 105 110

Ser Ala Leu Ala Ser Arg Arg Ile Thr Ala Gln His Pro Leu His Arg
115 120 125

Arg Ala Cys Asn Phe Val Ala Gln Ser His Ala Thr Gln Ala Leu Leu
130 135 140

```
Ala Arg Arg Ser Val Phe Thr Arg Gln Gly Ala Pro Leu Leu Ile Thr
145                 150                 155                 160

Glu Cys Met Leu Pro Ala Leu Trp Ala Thr Leu Glu Pro Val Ala Ala
                165                 170                 175

Pro Arg Gln Ala Ser Leu Ser Ala Asp Gly Pro Cys Arg His Ser Ala
            180                 185                 190

Gln Ile Val Ser Pro Glu Ser Met Leu Glu
        195                 200


<210>  46
<211>  278
<212>  PRT
<213>  Xanthomonas albilineans

<400>  46

Met Pro Asn Ala Val Pro Met Gln Gly Ala Arg Gly Leu Pro Gln Pro
1               5                   10                  15

Gln Ala Met Asn Pro Gly Leu Pro Ser Val Gly Gly Leu Ser Ala Gly
            20                  25                  30

Gln Pro Leu Gln Leu Ser Leu Ala Pro Glu Leu Gln Ala Ala Ala Arg
        35                  40                  45

Ser Ala His Arg His Leu Leu Asp Asp Gly Thr Ala Leu Tyr Leu Leu
    50                  55                  60

Ala Phe Asp Thr Ala Gln Phe Asp Pro Gly Ala Phe Ala Ala Met Ala
65                  70                  75                  80

Ile Ala Arg Pro Asp Ser Ile Ala Arg Ser Val Arg Lys Arg Gln Ala
                85                  90                  95

Glu Phe Leu Phe Gly Arg Leu Ala Ala Arg Leu Ala Leu Gln Glu Val
            100                 105                 110

Leu Gly Pro Ala Gln Ala Gln Ala Asp Ile Ala Ile Gly Ala Thr Arg
        115                 120                 125

Ala Pro Cys Trp Pro Ala Gly Ser Leu Gly Ser Ile Ser His Cys Glu
    130                 135                 140

Asp Tyr Ala Ala Ala Ile Ala Met Ala Ala Gly Thr Arg His Gly Val
145                 150                 155                 160

Gly Ile Asp Leu Glu Arg Pro Ile Thr Pro Ala Ala Arg Ala Ala Leu
                165                 170                 175

Leu Ser Ile Ala Ile Asp Ala Asp Glu Ala Ala Arg Leu Ala Lys Ala
            180                 185                 190

Ala Asp Ala Gln Trp Pro Gln Asp Leu Leu Leu Thr Ala Leu Phe Ser
        195                 200                 205

Ala Lys Glu Ser Leu Phe Lys Ala Ala Tyr Ser Ala Val Gly Arg Tyr
    210                 215                 220
```

```
Phe Asp Phe Ser Ala Ala Arg Leu Cys Gly Ile Asp Leu Ala Arg Gln
225                 230                 235                 240

Cys Leu His Leu Arg Leu Thr Glu Thr Leu Cys Ala Gln Phe Val Ala
                245                 250                 255

Gly Gln Val Cys Glu Val Gly Phe Ala Arg Leu Pro Pro Asp Leu Val
            260                 265                 270

Leu Thr His Tyr Ala Trp
        275
```

<210> 47
<211> 634
<212> PRT
<213> Xanthomonas albilineans

<400> 47

```
Met Ser Val Glu Thr Gln Lys Glu Thr Leu Gly Phe Gln Thr Glu Val
1               5                   10                  15

Lys Gln Leu Leu Gln Leu Met Ile His Ser Leu Tyr Ser Asn Lys Glu
            20                  25                  30

Ile Phe Leu Arg Glu Leu Ile Ser Asn Ala Ser Asp Ala Ala Asp Lys
        35                  40                  45

Leu Arg Phe Glu Ala Leu Val Lys Pro Glu Leu Leu Asp Gly Asp Ala
    50                  55                  60

Gln Leu Arg Ile Arg Ile Gly Phe Asp Lys Asp Ala Gly Thr Val Thr
65                  70                  75                  80

Ile Asp Asp Asn Gly Ile Gly Met Ser Arg Glu Glu Ile Val Ala His
                85                  90                  95

Leu Gly Thr Ile Ala Lys Ser Gly Thr Ser Asp Phe Leu Lys His Leu
            100                 105                 110

Ser Gly Asp Gln Lys Lys Asp Ser His Leu Ile Gly Gln Phe Gly Val
        115                 120                 125

Gly Phe Tyr Ser Ala Phe Ile Val Ala Asp Gln Val Asp Val Tyr Ser
    130                 135                 140

Arg Arg Ala Gly Leu Pro Ala Ser Asp Gly Val His Trp Ser Ser Arg
145                 150                 155                 160

Gly Glu Gly Glu Phe Glu Val Ala Thr Ile Asp Lys Pro Glu Arg Gly
                165                 170                 175

Thr Arg Ile Val Leu His Leu Lys Glu Glu Glu Lys Gly Phe Ala Asp
            180                 185                 190

Gly Trp Lys Leu Arg Ser Ile Val Arg Lys Tyr Ser Asp His Ile Ala
        195                 200                 205

Leu Pro Ile Glu Leu Ile Lys Glu His Tyr Gly Glu Asp Lys Asp Lys
```

```
    210                 215                 220

Pro Glu Thr Pro Glu Trp Glu Thr Val Asn Arg Ala Ser Ala Leu Trp
225                 230                 235                 240

Thr Arg Pro Arg Thr Glu Ile Lys Asp Glu Glu Tyr Gln Glu Leu Tyr
                245                 250                 255

Lys His Ile Ala His Asp His Glu Asn Pro Val Ala Trp Ser His Asn
            260                 265                 270

Lys Val Glu Gly Lys Leu Glu Tyr Thr Ser Leu Leu Tyr Leu Pro Gly
        275                 280                 285

Arg Ala Pro Phe Asp Leu Tyr Gln Arg Asp Ala Ser Arg Gly Leu Lys
    290                 295                 300

Leu Tyr Val Gln Arg Val Phe Ile Met Asp Gln Ala Asp Gln Phe Leu
305                 310                 315                 320

Pro Leu Tyr Leu Arg Phe Ile Lys Gly Ile Val Asp Ser Ser Asp Leu
                325                 330                 335

Pro Leu Asn Val Ser Arg Glu Ile Leu Gln Ser Gly Pro Val Ile Asp
            340                 345                 350

Ser Met Lys Ser Ala Leu Thr Lys Arg Ala Leu Asp Met Leu Glu Lys
        355                 360                 365

Leu Ala Lys Asp Asp Pro Glu Arg Tyr Lys Gly Val Trp Lys Asn Phe
    370                 375                 380

Gly Gln Val Leu Lys Glu Gly Pro Ala Gln Asp Phe Gly Asn Arg Glu
385                 390                 395                 400

Lys Ile Ala Gly Leu Leu Arg Phe Ala Ser Thr His Ser Gly Asp Asp
                405                 410                 415

Ala Gln Asn Val Ser Leu Ala Asp Tyr Val Ala Arg Met Lys Asp Gly
            420                 425                 430

Gln Asp Lys Leu Tyr Tyr Leu Thr Gly Glu Ser Tyr Ala Gln Ile Lys
        435                 440                 445

Asp Ser Pro His Leu Glu Val Phe Arg Lys Lys Gly Ile Glu Val Leu
    450                 455                 460

Leu Leu Thr Asp Arg Ile Asp Glu Trp Leu Met Ser Tyr Leu Thr Glu
465                 470                 475                 480

Phe Asp Ser Lys Ser Phe Val Asp Val Ala Arg Gly Asp Leu Asp Leu
                485                 490                 495

Gly Lys Leu Asp Ser Glu Glu Glu Lys Gln Ala Gln Glu Glu Ala Ala
            500                 505                 510

Lys Ala Lys Gln Gly Leu Ala Glu Arg Ile Gln Gln Val Leu Lys Asp
        515                 520                 525

Glu Val Ala Glu Val Arg Val Ser His Arg Leu Thr Asp Ser Pro Ala
    530                 535                 540
```

Ile Leu Ala Ile Gly Gln Gly Asp Met Gly Leu Gln Met Arg Gln Ile
545 550 555 560

Leu Glu Ala Ser Gly Gln Lys Leu Pro Glu Ser Lys Pro Val Phe Glu
565 570 575

Phe Asn Pro Ala His Pro Leu Ile Glu Lys Leu Asp Ala Glu Pro Asp
580 585 590

Val Asp Arg Phe Gly Asp Leu Ala Arg Val Leu Phe Asp Gln Ala Ala
595 600 605

Leu Ala Ala Gly Asp Ser Leu Lys Asp Pro Ala Ala Tyr Val Arg Arg
610 615 620

Leu Asn Lys Leu Leu Leu Glu Leu Ser Ala
625 630

<210> 48
<211> 20
<212> DNA
<213> Xanthomonas albilineans

<400> 48

gcgtaccgtt gtccagtagg 20

<210> 49
<211> 20
<212> DNA
<213> Xanthomonas albilineans

<400> 49

gctggaaacc gagaatctga 20

<210> 50
<211> 20
<212> DNA
<213> Xanthomonas albilineans

<400> 50

gacacgatca gccgctagga 20

<210> 51
<211> 20
<212> DNA
<213> Xanthomonas albilineans

<400> 51

accagcagtt gggccagcct 20

<210> 52

<211> 19
<212> DNA
<213> Xanthomonas albilineans

<400> 52

tgcccacagg ccgtcgagt 19

<210> 53
<211> 20
<212> DNA
<213> Xanthomonas albilineans

<400> 53

gcgagaggac aagctgctgc 20

<210> 54
<211> 20
<212> DNA
<213> Xanthomonas albilineans

<400> 54

cgttgaggat gcagcgctcg 20