

Genome sequencing of *Xanthomonas axonopodis* pv. *phaseoli* CFBP4834-R reveals that flagellar motility is not a general feature of xanthomonads.

Armelle Darrasse^{1,2,3}, Sébastien Carrère^{4,5,6}, Valérie Barbe⁷, Tristan Boureau^{1,2,3}, Adriana Bernal⁸, Sophie Bonneau^{1,2,3}, Chrystelle Brin^{1,2,3}, Stéphane Cociancich⁹, Karine Durand^{1,2,3}, Stéphanie Fouteau⁷, Lionel Gagnevin^{10,11}, Jérôme Gouzy^{4,5,6}, Fabien Guérin^{10,11}, Endrick Guy^{4,5,6}, Arnaud Indiana^{1,2,3}, Ralf Koebnik¹², Emmanuelle Lauber^{4,5,6}, Alejandra Munoz⁸, Laurent D. Noël^{4,5,6}, Isabelle Pieretti⁹, Stéphane Poussier^{1,2,3,a}, Olivier Pruvost^{10,11}, Isabelle Robène-Soustrade^{10,11}, Philippe Rott⁹, Monique Royer⁹, Boris Szurek¹², Marie-Anne Van Sluys¹³, Valérie Verdier¹², Christian Vernière^{10,11}, Matthieu Arlat^{4,5,6}, Charles Manceau^{1,2,3,b}, and Marie-Agnès Jacques^{1,2,3}.

(1) INRA, UMR1345 IRHS, F-49071 Beaucouzé, France.

(2) AGROCAMPUS OUEST, UMR1345 IRHS, F-49071 Beaucouzé, France.

(3) Université d'Angers, UMR1345 IRHS, SFR4207 QUASAV, PRES L'UNAM, F-49071 Beaucouzé, France.

(4) INRA, UMR LIPM, F-31326 Castanet-Tolosan Cedex, France.

(5) CNRS, UMR LIPM, F-31326 Castanet-Tolosan Cedex, France.

(6) Université Paul Sabatier, UMR LIPM, F-31326 Castanet-Tolosan Cedex, France.

(7) CEA, Genoscope, Centre National de Séquençage, F-91057 Evry Cedex, France.

(8) Universidad de Los Andes, Laboratorio de Micología y Fitopatología Uniandes, Bogotá, Colombia.

(9) CIRAD, UMR BGPI, F-34398 Montpellier Cedex 5, France.

(10) CIRAD, UMR PVBMT, F- Saint-Pierre, La Réunion, France.

(11) Université de la Réunion, UMR PVBMT, F-97715 Saint-Denis, La Réunion, France.

(12) IRD, UMR RPB, F-34394 Montpellier Cedex 5, France.

(13) GaTE Lab Botanica IBUSP 277 05508-900, São Paulo, SP, Brazil.

^(a) current address: Université de la Réunion, UMR PVBMT, F-97715 Saint-Denis, La Réunion, France.

^(b) current address: ANSES, Laboratoire de Santé des végétaux, F-49044 Angers, France.

Xanthomonads are plant-associated bacteria that establish neutral, commensal or pathogenic relationships with plants. The list of common characteristics shared by all members of the genus *Xanthomonas* is now well established based on the entire genome sequences that are currently available and that represent various species, numerous pathovars of *X. axonopodis* (sensu Vauterin *et al.*, 2000), *X. oryzae* and *X. campestris*, and many strains within some pathovars. These γ -proteobacteria are motile by a single polar flagellum. Motility is an important feature involved in biofilm formation, plant colonization and hence considered as a pathogenicity factor. *X. axonopodis* pv. *phaseoli* var. *fuscans* (Xapf) is one of the causal agents of common bacterial blight of bean and 4834-R is a highly aggressive strain of this pathogen that was isolated from a seed-borne epidemic in France in 1998. We obtained a high quality assembled sequence of the genome of this strain with 454-Solexa and 2X Sanger sequencing. Housekeeping functions are conserved in this genome that shares core characteristics with genomes of other xanthomonads: the six secretion systems which have been described so far in Gram negative bacteria are all present, as well as their ubiquitous substrates or effectors and a rather usual number of mobile elements. Elements devoted to the adaptation to the environment constitute an important part of the genome with a chemotaxis island and dispersed MCPs, numerous two-component systems, and numerous TonB dependent transporters. Furthermore, numerous multidrug efflux systems and functions dedicated to biofilm formation that confer resistance to stresses are also present. An intriguing feature revealed by genome analysis is a long deletion of 35 genes (33 kbp) involved in flagellar biosynthesis. This deletion is replaced by an insertion sequence called ISXapf2. Genes such as *flgB* to *flgL* and *fliC* to *fleQ* which are involved in the flagellar structure (rod, P- and L-ring, hook, cap and filament) are absent in the genome of strain 4834-R that is not motile. Primers were designed to detect this deletion by PCR in a collection of more than 300 strains representing different species and pathovars of *Xanthomonas*, and less than 5% of the tested xanthomonads strains were found non-motile because of a deletion in the flagellum gene cluster. We observed that half of the Xapf strains isolated from the same epidemic than strain 4834-R was non-motile and that this ratio was conserved in the strains colonizing the next bean seed generation. Isolation of such variants in a natural epidemic reveals that either flagellar motility is not a key function for fitness or that some complementation occurs within the bacterial population.