

Innovations in Genetics and Breeding of Capsicum and Eggplant

Proceedings of the 17th EUCARPIA Meeting on Genetics and Breeding of Capsicum and Eggplant,

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A decade of studies in France to decipher the genetic/molecular basis of eggplant resistance to bacterial wilt

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BACKGROUND Bacterial wilt (BW) is caused by strains of the *Ralstonia solanacearum* species complex (RSSC) and widespread in the world. RSSC strains are phytopathogenic bacteria of primary importance in the world, due to their global distribution, broad-spectrum of host plants and the severity of attacks on food crops of major economic interest such as tomato, eggplant, and pepper. The varietal resistance is a major method for a sustainable control of BW. However, this resistance is unstable because of strong interaction with the huge genetic diversity of RSSC, which is structured into three species and four phylogenetic groups: phylotypes I, II, III, and IV. During the last decade, several sources of resistance to BW have been identified in eggplant accessions by CIRAD-INRA.

MATERIALS & METHODS A core-collection of eggplant lines was challenged with a core-collection of BW strains characterized by molecular genotyping techniques and representing the phylogenetic diversity of RSSC (Table 1). The GBS method was used for QTL mapping studies on RILs and DH populations from crosses between resistant and susceptible lines. Anchoring genetic maps on the physical maps of eggplant and tomato and RNAseq data from the parental lines identified candidate R-genes [1]. Functional genetics with RSSC mutants highlighted an avirulence gene in bacteria [2]. Breeder-friendly markers were developed in the region of the major gene for both fine mapping and marker-assisted selection (MAS).

RESULTS A total of six phenotypes ranging from highly resistant to highly susceptible were recorded when testing the interactions between eggplant lines and BW strains representing three out of the four phylotypes (Table 1). The MT035 haplotype of phylotype I, recently found prevalent in South Western Indian Ocean islands, was represented in Réunion by the aggressive strain RUN 3012 (I-31) that was observed throughout the vegetable production area up to 1200 m altitude [3]. The dissection of the resistance in accession E6 (AG91-25) revealed the presence of a major locus, *EBWR9*, controlling three strains of phylotype I, and two QTLs that revealed partially effective against strains of phylotypes I, IIA and III (Figure 1). Five candidates R-genes, polymorphic between parents, were found in the EBWR9 genomic region, four of them being orthologs and in a syntenic position among eggplant, tomato, and potato. Studies with mutants of strains GMI1000 and PSS4 demonstrated that RipAX2 type III effector of *R. pseudosolanacearum* was necessary to trigger resistance in AG91-25 eggplants, suggesting an R/Avr- type interaction [2]. We saturated the region of *EBWR9* with molecular markers for fine mapping and facilitating its transfer in commercial cultivars.

DISCUSSION & CONCLUSION The eggplant AG91-25 carrying *EBWR9* major gene recognizes the avirulence gene *RipAX2* to trigger resistance to BW. This R/Avr-type interaction, which is not conserved within a same phylotype, should be highly strain-specific. The identification of the *EBWR9* gene by functional genetics is necessary to understand this interaction, to search for orthologs in the genetic diversity of tomato and potato, and to assist breeding using molecular markers closely linked to the gene. Identification of complementary QTLs controlling resistance to other bacterial strains is ongoing in order to set up innovative breeding pyramiding strategies for the creation of wide-spectrum resistances controlling the disease in large production areas.

REFERENCES

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	CLIMATIC CHAMBERS ASSAYS												GREENHOUSE ASSAYS		GREENHOUSE ASSAYS	
Strain	CMR134	P\$\$366	PSS4	P\$\$358	GM11000	CFBP3059	CNR32	CMR15	CFBP2957	CMR39	CIIR34	CFBP6783	RUN3012	RUN4509	RUN3012	RUN4509
Classification	1-13	1-15	1.15	1-15	i-18	11-23	11-29	11-29	IIA-36	IA-41	IB-1	IIB-4NPB	1-31	IIB-1	1-31	IIB-1
											HOT SEASON (La Reunion)		COOL SEASON (La Reunion)			
E1	1	2	2	2	1			2	- 1	1.	1	4	3,1		2	1
E2	1	- 4	4	2	1	2	1	3,1	1	1	3,2	100	2	2	3,2	3,1
E3	1	4	2	4	2	2	1	2	1	1	2	4	2	1	2	2
E4	1	1	2	1	1	1	1	- 4	1	2	2	2	2	1	2	2
E5	3.1	4	4	4	2	2	1	4	1	2	32	2	4	2	4	4
E6	2	1	5	2	3,1	4	1	5	2	1	5.	4	2	3,1	2	-4-
E7	4	4	5	4	3,2	5	1	4	1	3,1	3,1	3,1	4	1 1	4	2
EB	4	4	5	5	5	3	3,1	5	4	4	5	4	5	4	5	4
E9	2	2	2	2	3,2	1	1	4	1	10	1	4	2	1	1.11	1
E10	5	4	5	5	4	5	4	5	2	4	5.00	5	4	2	1.5	4

Table 1. Eggplant accessions rank from highly resistant in dark green (1) to highly susceptible in red (5) when inoculated with representative RSSC strains.



Figure 1.3 genetic factors of resistance in AG91-25 (E6) eggplant line

Grey, blue and red circles represent QTLs conferring resistance to phylotypes I, IIA and III strains (phenotypic variance = 13 to 38%); QTLs conferring resistance to phylotypes IIA and III strains (phenotypic variance = 17 to 45%) and EBWR9 major resistance gene conferring very high level of resistance to phylotype I strains.