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Brigitte B. Maisonneuve

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Improvement of the differential lettuce set for *Bremia* virulence evaluation: new *sativa* monogenic lines

Maisonneuve Brigitte

INRA, UR 1052, Unité de Génétique et d'Amélioration des fruits et Légumes, Domaine Saint Maurice, 84143-Montfavet Cedex, France. Contact: Brigitte.Maisonneuve@avignon.inra.fr

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Several accessions of the actual set of host differentials are difficult to use to determine the virulence of *Bremia* isolates; some are *Lactuca serriola* with reflex capitula and slow germination, some are not monogenic, like Ninja (*Dm3*, *Dm4*, *Dm11*, and a resistance from *L. saligna* called here *Rsal-1*) or Discovery (*Dm7*, *Rsal-1*). Besides, some *Bremia* isolated recently on some cultivars do not sporulate on Cobham green, the accession used as universal susceptible. In collaboration with 5 breeding societies (Enza Zaden, Gautier Semences, Rijk Zwaan, Seminis, Syngenta) and the Geves-Snes, and with some financial support from French Agricultural Ministry, a project was developed to create some new differential lines: a susceptible line without the resistance from Cobham green (called *Rcg* here), a *sativa* monogenic line with *Dm16* to replace *L. serriola* LSE/18, and the *sativa* line CGDM16 (*Dm16*, *Rcg*), a monogenic line with *Rsal-1* to replace Ninja and Discovery.

To produce a universal susceptible line and to eliminate *Rcg* from the differential line CGDM16, the cross [CGDM16 x F₁ (Cobham green x LSE/18)] was produced. Progeny of that cross was tested with Serr84/99, a *Bremia* strain isolated by A. Lebeda in the French Alps which was not virulent on Cobham green. Only 18 I₁ progenies of 100 hybrid plants [CGDM16 x F₁ (Cobham green x LSE/18)] were in segregation for the resistance to Serr84/99; 8 out of these 18 I₁ families were homogeneous resistant and 10 showed segregation for *Dm16* resistance. In the progenies from these 18 selected hybrid plants, I₂ families were produced on 71 I₁ plants tested as susceptible to Serr84/99. The capitulum of these 71 plants was observed and the I₂ progenies were tested with Serr84/99; therefore 14 lines I₂ susceptible to Serr84/99 and with an erect capitulum were selected. A ring test was realized with Serr84/99 and BI:22 in 6 laboratories: one line without resistance (susceptible to BI:22 or NL2) and 8 lines with *Dm16* (resistant to BI:22 or NL2) were selected. These 9 lines were tested with the 16 UPOV strains of *Bremia* used for cultivar inscription in Europe, and 2 I₂ were selected: one line (*Rcg*⁺, *Dm16*⁺) and one line (*Rcg*⁺, *Dm16*). These two lines are good candidates as a susceptible genotype and as a *Dm16* line in the set of lettuce differentials for *Bremia* evaluation.

To create a differential line with only *Rsal-1*, a screening in the progenies from (Discovery x Angie) was realized with BI:17 to eliminate *Dm6* from Angie (a cultivar *Dm6*, *Rsal-1*) and the strain FR30/99 (sextet 63-62-16-01) to eliminate *Dm7* from Discovery. In a first step, 22 out of 287 F₃ families, issued from 287 harvested F₂ (Discovery x Angie) plants, were selected as homozygous for *Dm6*⁺ and *Dm7*⁺ (susceptible to BI:17 and to FR30/99). After a ring test in 6 laboratories, 5 F₃ were selected and tested with the 16 UPOV strains of *Bremia*; the results were up to expectation except with BI:5.

In conclusion, interesting candidates for *Bremia* differential lines were obtained to replace (1) Cobham green by a line susceptible to all know *Bremia* strains, called FrDm0, (2) CGDM16 by a monogenic *Dm16 sativa* line, called FrDm16, and (3) Ninja and Discovery by a monogenic *Rsal-1* line, called FrRsal-1. The partners of that project decided to improve the homogeneity of these F₃ lines with one extra generation of selfing and observations on the morphology of the lines. An extra control of the conformity of the susceptibility/resistance especially with Serr84/99 and with BI:5 will be also realized before proposing the material to the IBEB group.