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Population structure of *Bremia lactucae* isolated from lettuce culture in France

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Bremia lactucae, the causal agent of lettuce downy mildew is an important economic problem for the lettuce crops. To limit the damages caused by this pathogen, breeders used race-specific monogenic resistances. However, under selection pressure, *B. lactucae* populations showed a rapid adaptation to host resistances. Characterizing of the population genetic structure could be an important step toward the identification of the evolutionary strategy used by *Bremia* to overcome host resistance. Thus, in collaboration with Gautier Semences and Rijk Zwaan, we compared the genetic diversity of *Bremia* isolates collected in France since 2006 with the diversity of European isolates and official races (BI: races). We also studied the population structure of French *Bremia* isolates.

Twelve microsatellites were specifically developed for *B. lactucae* in order to analyze the genetic diversity of the lettuce downy mildew. Isolates were recovered from different varieties of lettuce, carrying different resistance genes, from the most important production areas of lettuce in France. More than 400 isolates were genotyped using these twelve markers.

Eighteen different multilocus genotypes (MLG) were observed for 20 different official BI: races, 17 MLG were observed for 30 European isolates, whereas only twelve different MLG were identified for 340 isolates collected in France. Two out of these twelve MLG were found the most frequently at French scale and were observed in almost all the lettuce production areas that had been sampled. This low genetic diversity in France indicated high clonality in all populations and important gene flow between populations. However, different indexes suggested that rare events of sexual recombination occurred, especially in populations of Western France, where genotypic diversity was slightly higher. Moreover, analyzing the population genetic structure suggested the presence of different clonal lineages, possibly resulting from selection pressure of resistance genes.

These results will be discussed considering the impact of host resistance gene on the population structure of *B. lactucae*.