



How gene flow between wild and cultivated lettuce can influence the dynamic of adaptation of *Bremia lactucae*

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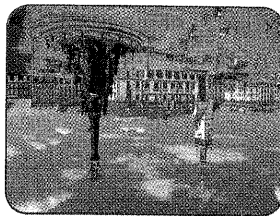
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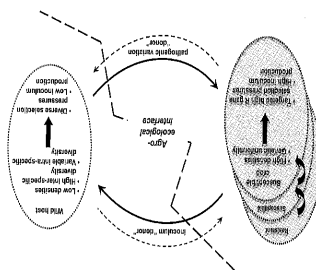
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How gene flow between wild and cultivated lettuce can influence the dynamic of adaptation of *Bremia lactucae*

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Host resistance may be considered as the main driving force of plant pathogens evolution, with pathogens evolving to overcome host resistance strategies. In the model system, *Bremia lactucae*, the causal agent of downy mildew on *Lactuca sativa*, several specific resistance genes are used to counter this pathogen. In turn, pathogens show a rapid adaptation to host resistances, and characterization of population genetic structure could be an important step to identify evolutionary strategies used by the pathogen to overcome host resistance.

Microsatellite markers were developed to study the genetic diversity of *B. lactucae*. More than 400 isolates were recovered in France from 23 regions; on different cultivars (carrying different resistance genes) of *L. sativa* and on the wild host *L. serriola*. Genotypic diversity and gene diversity were low in all the populations sampled; 14 multilocus genotypes (MLG) were identified in France and among them, two were predominant. Within the eight MLG observed on *L. serriola*, six MLG were specific to this host plant and two MLG were shared by isolates of the two host plants, suggesting the occurrence of gene flow between the wild and the cultivated pathosystems.

Virulence phenotypes of *B. lactucae* were characterized on a set of 19 differential hosts. The two pathotypes the most frequent matched respectively the two most frequent MLGs. Furthermore, clustering analyses revealed that *B. lactucae* populations could be clustered into three genetically distinct groups with good correlations with resistance genes. Each cluster corresponds mainly to different pathotypes. Isolates of MLG 1, found only in cluster 3, were not genetically closely related with the other isolates and pathotypes were very different. Moreover, MLG 1 isolates were also found on wild *L. serriola*. The hypothesis that new virulence may have emerged through migration from the wild host plant is discussed.

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