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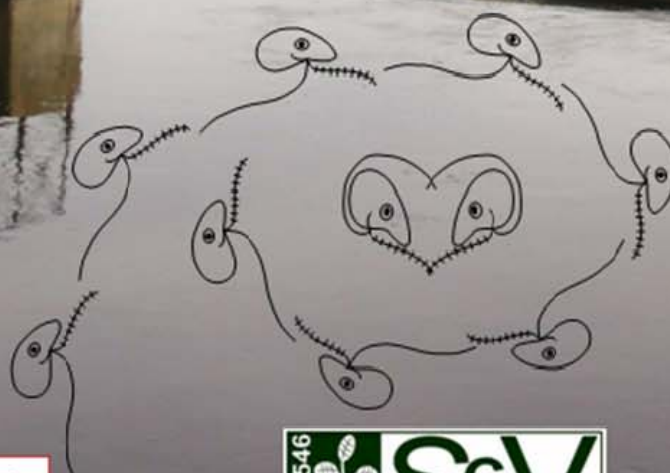
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Genes flow in populations of *Bremia lactucae*, the causal agent of downy mildew of lettuce, in France

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Bremia lactucae, the causal agent of downy mildew on *Lactuca sativa*, is an important economic problem for lettuce crops. Breeders used genetic control to limit damages of this pathogen and more particularly specific resistances. However, under selection pressure, *B. lactucae* populations showed a rapid adaption to host resistances. A better knowledge is necessary to understand this rapid virulence evolution. A study was initiated to evaluate genetic diversity of this biotrophic, heterothallic and diploid pathogen, and to determine the impact of recombination and migration on the structure of pathogen populations. More than four hundred isolates were recovered in France from different regions and different varieties (carrying different resistance genes) from *L. sativa* and *L. serriola* which is a wild host species. More than one hundred isolates were characterized for their virulence. Neutral markers, microsatellites, were developed to assess population structure and gene flow in french populations of *Bremia*. Moreover, polymorphism in RxLR candidate genes was evaluated in relation with genotypic and phenotypic diversity. Results showed an important polymorphism for virulence in *B. lactucae* french populations and the occurrence of gene flow between populations and between the wild and crop pathosystems. These results will be discussed regarding durable resistance management.