

## **P.19 - Selection pressures exerted by apple major resistance genes and QTLs on *Venturia inaequalis***

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Apple scab, caused by the fungal pathogen *Venturia inaequalis*, is one of the most important diseases of apple. Most commercial cultivars are susceptible to the disease and require up to 15 fungicides per season. The development of apple cultivars having a durable resistance is therefore needed. Major genes and quantitative trait loci have been identified in apple, and genotypes combining different resistance factors have been constructed. Our aim is to determine which resistance factors (alone or in combination) will provide the highest durability in relation to spatial deployment of apple genotypes. In the present study, we will assess the selection pressure of these genotypic constructions on isolates of *Venturia inaequalis* inoculated in mixtures in controlled conditions. Fifty apple genotypes have been chosen in one F1 progeny, which is segregated for 2 major genes and 6 QTLs (3 specific QTL and 3 general QTL). We classified the 50 genotypes: no resistance factor, one type of resistance factors (major, specific QTL or general QTL), two types of resistance factors, and three types of resistance factors together. Isolates of *V. inaequalis* were sampled from domesticated and wild apple from different geographic origins. A core collection was established in order to maximize the genetic diversity. Mixtures of 10 isolates will be inoculated on the 50 genotypes and 2 reference cultivars. After expression of symptoms, scabbed lesions will be sampled and the frequency of the isolates will be evaluated by genotyping in order to evaluate if there is a selection of more adapted *V. inaequalis* isolates.