

POPULATION BIOLOGY OF THE APPLE SCAB PATHOGEN

Plant disease management is an essential component of agricultural production systems. Disease management strategies must target a **population of the pathogen** and not a single individual. Pathogen populations may be very diverse, in particular regarding to their **virulence**, or potential for causing disease. Therefore, it is of key importance to understand the interactions between crop genotypes and the pathogen population, and to integrate this information into disease management systems. Apple Scab, caused by the fungus *Venturia inaequalis*, is one of the most devastating diseases of apples worldwide and has been traditionally managed by fungicide applications. In apple production we are facing the transition of fungicide-based traditional systems into organic systems. As a consequence, as pesticides are less used, we face the need of alternative control strategies for managing apple scab.

Organic production systems must rely mainly on **resistant apple cultivars**. There is a great effort in breeding apples with efficient and durable resistance, and many of them are readily available. Most of these scab-resistant apple varieties carry a resistance gene found in the crabapple *Malus floribunda*. Current use of scab-resistant apple material has already promoted the appearance of pathogen populations that are able to cause disease on *Vf*-carrying apple varieties in several European countries. Due to globalization of Agriculture there is a risk of movement of such populations between countries, and the possibility of *V. inaequalis* virulent to scab resistant cultivars having entered the USA cannot be ruled out. Understanding the virulence level of the pathogen population present in a particular growing area is of key importance in effective integrated control of apple scab, and it is particularly crucial when initiating the establishment of new scab-resistant orchards, since the virulence status of resident *V. inaequalis* populations could render ineffective any host resistance.

We are using modern molecular techniques to define the genetic structure of *V. inaequalis* populations causing apple scab in North Eastern USA orchards, establish differences between production areas and seasons, and provide a better understanding on the population biology of this pathogen. Our ultimate goal is to determine the virulence level of genetically distinct individuals by using bioassays, and incorporate information on population structure and virulence levels to design best management strategies.

Another interesting question refers to host specificity and adaptation. Apart from apples, *V. inaequalis* can also infect other plants, including many ornamentals (crabapples, hawthorn, mountain ash, firethorn, and loquat.). Cultivates apples and crabapples (wild and ornamental) coexist in the North Eastern USA. Crabapples are often used as pollinators in apple orchard and there is no knowledge on how differentiated these populations may be. If there is no differentiation between populations, ornamental and pollinator crabapples may be serving as reservoir for the pathogen, as well as a source of inoculum for the initiation of primary or secondary epidemic cycles. We are comparing scab populations from both hosts, both genetically and pathogenically, to understand the role of alternative hosts in the development of apple scab epidemics.