

Biotic and/or abiotic factors? The driving force of genomic plasticity in *Albugo candidans* populations

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Obligate pathogens like *Albugo candida* and *Hyloperonospora parasitica* are ubiquitous in natural ecosystems. Although diversity has been studied between species and isolates of different origins, little is known about genome structure and genome plasticity within populations in natural environments.

It has been hypothesized that host resistance genes drive diversity and genome plasticity in pathogenic microbes. Yet, the influence of abiotic environmental conditions has vastly been ignored.

Our aim is to use comparative genomics and transcriptomics to study plasticity between isolates of one population with isolates of other geographic locations.

We would like to address the following questions:

Is there a difference in genome plasticity 'within populations' of *A. candida* and *H. parasitica* in comparison to 'between populations' in terms of hemizygoty, heterozygoty and extra chromosomal elements?

How is this influenced by environmental conditions?

Are biotic or abiotic factors the dominant driving forces of genome plasticity and diversity?



Albugo candida on inflorescences of *Capsella bursa-pastoris*



Hyloperonospora parasitica on *Capsella bursa-pastoris*