Genetic analysis of leaf spot resistance in species of the genus Beta

Background

Sugar beet (*Beta vulgaris*) and its fungal pathogen *Cercospora beticola* provide an informative model system to study the impact of domestication, intensive crop cultivation and fungicide applications on the evolution of plant pathogens. This pathogen is important in beet production worldwide and fungicide resistance is a growing concern. *B. vulgaris* was domesticated in Germany approximately 200 years ago and is cultivated world-wide for sugar production. Leaf spot disease, as caused by *C. beticola,* is also a common pathogen of the wild progenitor of sugar beet, *B. vulgaris ssp. maritima*. The impact of host domestication on plant resistance and pathogen virulence can be studied in a comparative framework of wild and agricultural host-pathogen systems.

Objectives

- Dissect the genetics of *C. beticola* resistance in wild and cultivated beet species (QTL-, association mapping)
- Clone and functionally analyze candidate genes from the QTL

Workprogram

The project started March 2020. A core diversity set of 350 wild and cultivated Beta accessions has been assembled and will be grown under field conditions. Resistance and other phenotypic characters will be determined. Accessions will be sequenced for performing genome wide association mapping.

Project team

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Scientific Partners

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