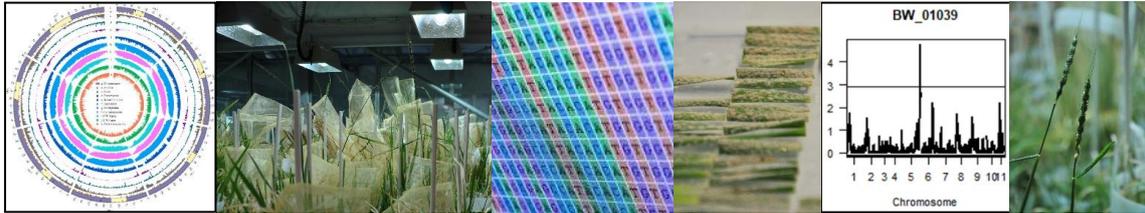


WHEAT AND RACE-SPECIFIC RESISTANCE TO FUNGAL PATHOGENS: WHAT CAN WE LEARN FROM WILD GRASSES?



Project description

Resistance breeding is gaining interest as a sustainable alternative to pesticides to combat crop diseases, such as wheat powdery mildew (*Blumeria graminis* f.sp. *tritici*; *Bgt*), one of the most important wheat disease-causing organisms threatening wheat production worldwide. Plant resistance largely depends on resistance (*R*) genes that usually encode for proteins that recognize fungal avirulence (*AVR*) effectors and activate immune response (Flor, 1971; Jones & Dangl, 2006).

The implementation of new genomic, genotyping and gene isolation tools allow the rapid identification and functional validation of *R* and *Avr* genes. In our lab, we identify both components to study their interaction and gain insights at molecular level on how host resistance works. Ultimately, the generated knowledge can be implemented in effective resistance breeding strategies.

The project revolves around a collection of *Aegilops tauschii*, a close relative of wheat proven to be a rich source of resistance genes, and a worldwide collection of *Bgt* isolates. The specific tasks for this project could include:

1. **Phenotyping** of the *Aegilops tauschii* collection with *Bgt* isolates from different regions of the world. The **identification of *R* genes** will be done following a novel genome wide association study (GWAS) approach (Arora et al. 2019) and the functional validation through transgenesis or virus-induced gene silencing.
2. **Identification of the corresponding *Avr* gene(s)** following a map-based cloning approach using a segregating population between two *Bgt* isolates. The validation will be done using by using transient expression assays in *Nicotiana benthamiana* via *Agrobacterium tumefaciens* infiltrations.
3. Study for possible interactions between the *R* and *AVR* proteins with **diverse biochemistry techniques**.
4. Help to develop a novel protocol for the **functional validation of *Avr* genes** using *Zymoseptoria tritici*, a transformable wheat pathogen. The successful establishment of such technique would represent a major breakthrough in the area of pathogen functional genomics.

The MSc Thesis project will be integrated in the lab of Prof. Dr. Beat Keller, a leading authority in wheat disease resistance and evolution-diversity studies in the wheat-powdery mildew pathosystem. Our group is part of the Department of Plant and Microbial Biology (UZH), located in the Botanical Garden (Zollikerstrasse 107, 8008 Zurich).

We are flexible and open for suggestions and project ideas. Please contact us if you have questions or inputs!

Prerequisites None, but motivation and interest in science!

Supervisor(s) Zoe Bernasconi (zoe.bernasconi@botinst.uzh.ch);
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For ETH students: an additional supervisor from ETH is needed. This can be arranged by asking a professor/group leader; we already had MSc students from ETH in the past, and we are ready to help with this organizational aspect.

Starting date Open

Language English is preferable

In case of interest or questions, feel free to contact Zoe per email.

Both UZH / ETH students are very welcome! 😊