

## Literature survey of regions of quantitative (resistance) traits (QRLs) against yellow (wheat) rust within the *Aegilops-Triticum* species complex (ATSC)

Sustainable agriculture requires a greater emphasis on disease resistance to reduce the spread of plant diseases. Plant breeding can make use of various sources (gene pools) for crossing resistance genes. A typical reservoir is the closest crop wild relatives (CWR). For common wheat (*T. aestivum* conv. *aestivum*), these are the (wild) species of the genera *Aegilops* (goatgrass) and *Triticum* s. str. (wheat), referred to as the *Aegilops-Triticum* species complex (*Triticum* s. lat.). In order to provide breeders with specific support, including marker-assisted selection (MAS), it is essential to identify these gene loci and to know where in the genome these loci are located.

**Aim:** Bachelor thesis

Literature survey on gene loci influencing yellow rust resistance in wheat for the di- and tetraploid species of the ATSC representing the genomes of common wheat as well as the associated genetic markers.



**Master thesis:**

Literature survey on gene loci influencing yellow rust resistance in wheat for all di- and tetraploid species of the ATSC, as well as the associated genetic markers.

- Elaboration of the principles of resistance traits and the localisation of qualitative and quantitative genes
- Focused literature survey
- Evaluation of the relevant publications
- Presentation of the found gene loci in genetic maps
- Conducting a meta-QTL analysis (master thesis only)
- Discussion of those gene loci

**Requirements:** Basic understanding of plant breeding

**Section:** Organic Plant Breeding and Agrobiodiversity (OPB)

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