

Literature survey of quantitative trait regions (QTLs) in common wheat

Sustainable agriculture requires a greater emphasis on particular traits, such as plant height or resistance against various rust fungus species in common wheat (*Triticum aestivum* conv. *aestivum*). Plant breeding can make use of various sources (gene pools) for the crossing of these trait genes. A classical reservoir are varieties of common wheat or the closest crop wild relatives (CWR). In order to provide specific support to breeders, e.g., with 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 of gene loci influencing the resistance of one of the most important rust fungus species (brown rust: *P. triticina*, black rust: *P. graminis*, yellow rust: *Puccinia striiformis* s. str.) of common wheat as well as the corresponding genetic markers.

Master thesis:

Literature survey of gene loci that influence the resistance of all important rust fungus species (brown rust: *P. triticina*, black rust: *P. graminis*, yellow rust: *Puccinia striiformis* s. str.) or the plant height, as well as the corresponding genetic markers.

- Elaboration of the principles of the specific traits and the localization 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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