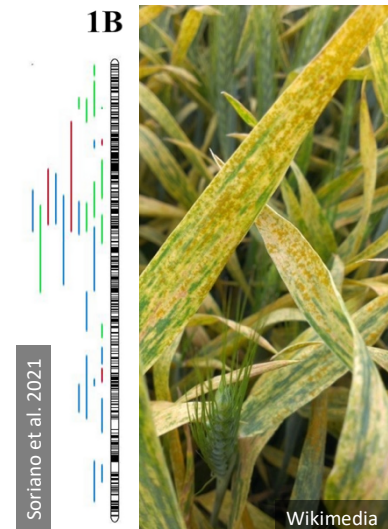


Project work, bachelor, and master thesis



# Meta analysis of regions of quantitative (resistance) trait (QRL) against yellow rust in common wheat

Sustainable agriculture requires a greater emphasis on particular traits, such as resistance against various rust fungus species (e.g., the obligate biotrophic yellow rust pathogen *Puccinia striiformis* s. str.) 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:** Literature survey of gene loci influencing the resistance of one of the most important rust fungus species, yellow rust (*P. striiformis* s. str.), of common wheat as well as the corresponding genetic markers.

**Project work:** All seven chromosomes of the D subgenome

**Bachelor thesis:** All seven chromosomes of the A or B subgenome

**Master thesis:** All chromosomes of the A, B, and D subgenome

- Elaboration of the principles of the specific trait and the localization of qualitative and quantitative genes
- Presentation of the found gene loci in genetic maps
- Conducting a meta-QTL analysis
- Based on a previously accomplished bachelor thesis
- Discussion of those gene loci

**Requirements:** Basic understanding of plant breeding and genomics

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

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