Session 5

MAGIC-RESIST: Identification and mapping of effective resistance genes to rust diseases and Fusarium head blight in the MAGIC WHEAT population WM-800

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Due to their high potential for damage and regular occurrence, phytopathogenic fungi like leaf rust, stripe rust and *Fusarium ssp.* belong to the most important pathogens of wheat. In particular, Fusarium head blight (FHB) is of great importance in cereal cultivation due to its ability to generate mycotoxins such as deoxynivalenol (DON) and thus reduce the quality of the crop. Aim of the MAGIC-RESIST project is to identify and map effective resistance genes in the multiparental wheat population WM-800, which consists of 800 lines and is based on the eight elite varieties Patras, Meister, Linus, JB Asano, Tobak, Bernstein, Safari and Julius by genome-wide association studies (GWAS). Field trials at two locations (Halle and Quedlinburg) that had previously been inoculated with spore material from the three pathogens were evaluated over several years. Due to drought stress situations, both rust pathogens occurred with different intensities in the tested environments. The traits are heritable and usable for genome wide association studies (GWAS). Due to the broad genetic variability of the parental lines, their resistance to rust, QTL for unknown leaf rust resistances could be detected using GWAS.

In order to validate the data on quantitative characteristics, such as resistance to FHB, grain samples were examined after the harvest with the aid of hyperspectral imaging methods, the DON content was determined using ELISA and related to the thousand grain mass and grain size. In this way, reliable parameters can be identified based on reflection values in specific wavelengths of the shortwave and infrared range, which establish a reliable connection with the resistance of the genotypes to FHB. By including plant morphological data such as plant height, grains per ear and flowering time, purely physiological resistance mechanisms can also be excluded. The rating of thousand grain mass, grain size, results of hyperspectral analyses and DON content will be used for GWAS. Because there are also great phenotypic differences in the parent lines for all recorded traits after Fusarium inoculation, previously unknown resistance QTLs are expected based on the DON data and the hyperspectral analyses. Using the WM-800 population and the QTL found can accelerate the breeding of varieties with an improved level of resistance to these diseases.