



MGBS

Molecular Genetics & Biotechnology Seminars

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Mining the global diversity of barley for Fusarium resistance using leaf and spike inoculations



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Published in *Euphytica* (2018) 214:18
IF =1.71

Hosted by Dr. Ahmed Sallam
Seminar co-sponsored by
Department of Genetics
Faculty of Agriculture
Assiut University

Fusarium graminearum is a devastating fungal pathogen that causes significant yield and quality losses in cereals. We utilized a diversity set of barley (140 genotypes) to explore vital resistance alleles against this aggressive pathogen. The resistance assessment was carried out on spikes and leaves via artificial inoculations under control conditions. The phenotypic data was subjected to genome-wide association analysis using a genetic map based on DArT and SNP markers. This analysis revealed eleven and nine marker trait associations for leaf disease scoring (LDS) and spike disease scoring (SDS), respectively. The strongest QTL for LDS was found on chromosome 1H where a minor allele of wild origin decreased disease symptoms by 78%. The major QTL allele for SDS was linked with marker locus SCRI_RS174710 on chromosome 5H. In addition, four favorable epistatic interactions effects were found in decreasing disease symptoms. Overall, three QTL were common for LDS and SDS, which indicates a partial genetic relatedness of these resistances in barley. The QTL alleles for LDS and SDS will help to establish organ specific resistances in cultivated barley.

Monday, 08.10.2018

Seminar 12:00 pm

Location: Training Hall beside the Main
Conference Hall at the Faculty of
Agriculture, Assiut University

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