

Expression-QTL mapping in wheat to identify genes involved in resistance to *Fusarium graminearum*

Mina Samad-Zamini¹*, Wolfgang Schweiger, Erik Sam, Gerald Siegwart, Barbara Steiner, Marc Lemmens and Hermann Buerstmayr

Abstract

Fusarium head blight (FHB) caused by *Fusarium graminearum* frequently leads to large yield losses in wheat and other cereals but also reduces quality due to contamination with mycotoxins. Breeding for resistance against the disease in wheat provides the best means to protect yields. In the present study, we aim to identify genes which are differentially expressed in response to *Fusarium* in wheat. Therefore, we employ 200 doubled haploid lines and the two parents (the resistant line CM82036 and the susceptible European spring wheat cultivar Remus) in an expression quantitative trait loci (eQTL) mapping experiment using microarray technology. Expression QTL starts with generating a genetic map using differentially expressed genes between lines as molecular markers to identify genomic regions involved in *Fusarium* resistance. Microarrays allow to measure differential transcript abundance by detecting fluorescent emission of labeled-mRNA hybridized to complementary probe sets. We used a custom-build Agilent-microarray

to identify genes differentially regulated under varying experimental conditions (e.g. time, genotype, *Fusarium* vs. water inoculation). Our array-design allows to detect 44000 wheat genes, several hundred wheat candidate genes that have been reported upregulated in response to *Fusarium* stress in literature and the entire transcriptome of *Fusarium graminearum* (ca. 14000 genes). In total, we aim to hybridize about 400 microarrays. Once finished, we are able to compare and correlate the genetic map derived from conventional QTL analysis with the new eQTL map. We expect to identify new QTL involved in *Fusarium* resistance that encode for resistance genes or regulative hotspots controlling multiple genes not encoded on the eQTL. Such hotspots and the related genes cannot be detected by conventional QTL mapping and enables us to build biochemical pathways that are relevant for resistance against *Fusarium*.

Keywords

Expression QTL, microarray, QTL analysis, transcript abundance

References

- BUERSTMAYR H, STEINER B, HARTL L, GRIESSER M, ANGERER N, LENGAUER D, MIEDANER T, SCHNEIDER B, LEMMENS M, 2003: Molecular mapping of QTLs for *Fusarium* head blight resistance in spring wheat. II. Resistance to fungal penetration and spread. *Theor Appl Genet* 107: 503-508.
- CHEUNG VG, SPIELMAN RS, 2009: Genetics of human gene expression: mapping DNA variants that influence gene expression. *Nature Rev Genet* 10: 595-604.
- KLIEBENSTEIN D, 2009: Quantitative genomics: analyzing intraspecific variation using global gene expression polymorphisms or eQTL. *Ann Rev Plant Biol* 60: 93-114.

¹ BOKU - University of Natural Resources and Life Sciences Vienna, Department IFA-Tulln, Institute for Biotechnology in Plant Production, Konrad Lorenz Straße 20, A-3430 TULLN

* Ansprechpartner: Mina SAMAD-ZAMINI, mina.zamini@boku.ac.at

