

Fusarium Head Blight Resistance in Winter Wheat: Insights from Genome-Wide Transcriptome Analysis

Christian Wagner¹, Jimmy Omony², Tetyana Nosenko², Thomas Nussbaumer³, Barbara Steiner¹, Mina Samad-Zamini^{1,4}, Maria Buerstmayr¹, Klaus F.X. Mayer², Hermann Buerstmayr¹

University of Natural Resources and Life Sciences, Vienna
Department of Agrobiotechnology, IFA-Tulln



¹Institute of Biotechnology in Plant Production, IFA Tulln, University of Natural Resources and Life Sciences Vienna (BOKU), Austria
²PGSB Plant Genome and Systems Biology, Helmholtz Center Munich, German Research Center for Environmental Health, Neuherberg, Germany
³Institute of Network Biology (INET), Helmholtz Center Munich, Ingolstädter Landstraße 1, 85764 Neuherberg, Germany
⁴Saatgut Edelhof, Edelhof 1, 3910 Zwettl, Austria

HelmholtzZentrum münchen
Deutsches Forschungszentrum für Gesundheit und Umwelt

Introduction

Fusarium head blight (FHB), caused by *Fusarium graminearum* and other *Fusarium* species, is a major crop disease of global concern, causing:

- yield loss, reduced baking and malting properties
- mycotoxin contamination (e.g. deoxynivalenol, zearalenone) which is harmful for humans and livestock

FHB resistance in wheat & transcriptomic response

FHB is a quantitative trait controlled by many loci. To date more than 500 resistance QTL have been mapped [1], but still little is known about the Fusarium response on the expression level. To study the transcriptomic response of winter wheat, we sequenced the transcriptome of 96 lines after *F. graminearum* or water (mock) treatment.

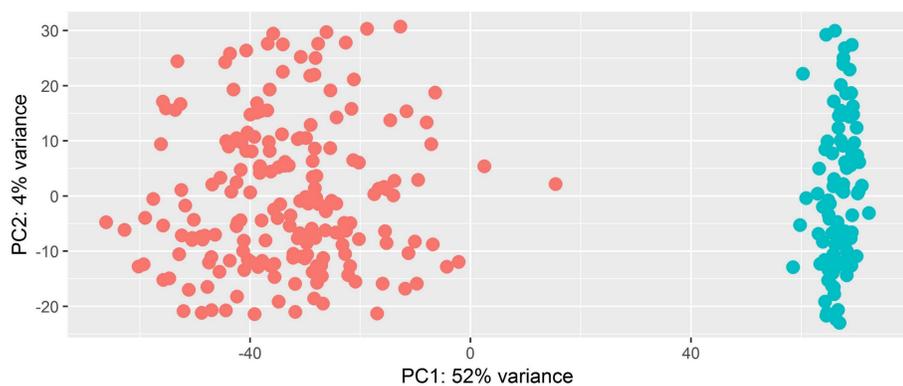


Figure 1: PCA plot of variance stabilized counts indicate large expression differences between mock (blue) and Fusarium treated samples (red).

Results

Transcriptomic response to *F. graminearum*

- Many genes are involved in the Fusarium defense mechanism – most are up regulated, only very few are down regulated
- A total of 12273 Fusarium responsive genes were identified, thereof 8040 DEG were common across all resistance groups, indicating that the Fusarium response is largely independent of the resistance level.

Most frequently identified gene families and pathways:

- Transcription factors (especially WRKY and ethylene responsive TF)
- DUF538 family proteins (putative chloroplast degeneration)
- Tryptophan pathway and kinases, especially receptor kinases
- Detoxification proteins, cytochrome P450, glycosyltransferases
- Disease resistance proteins, pathogenesis-related proteins
- Enriched biological process GO-terms include fungal recognition, defence, cell signalling, communication (Figure 3)
- *TraesCS5A01G211300LC*, a stress-response-NST1-like protein, was constitutive expressed only in lines with the resistant allele of the major QTL *Qfhs.ifa-5Ac* designating therefore a promising candidate gene.

A total of 7681 (2181 local and 5500 distant) Fusarium responsive eQTL could be identified that were evenly distributed across the wheat genome, without showing distinct regulatory hotspots (Figure 4).

Conclusion: A multitude of genes orchestrate the transcriptomic response of *F. graminearum* resistance and their defined biological processes are opening up a plethora of favourable pathways for the genetic improvement of elite winter wheat germplasm.

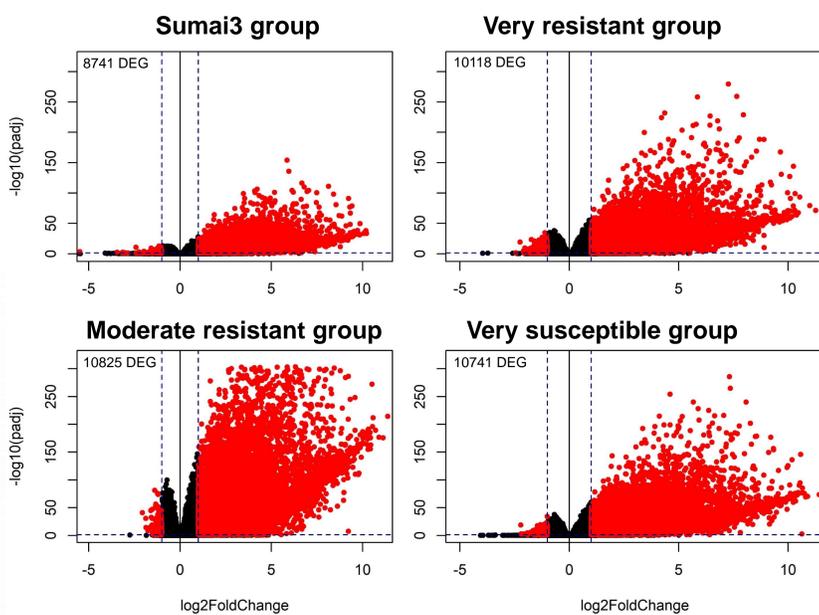


Figure 2: Volcano plots showing differentially expressed genes (DEG) for the different resistance groups.

Materials and Methods

A diversity set of 96 winter wheat lines was used for analysis, including 15 descendants of Sumai-3. RNA was extracted of water and *F. graminearum* treated spikelets 48 hours after inoculation and RNA reads were aligned to the IWGSCv1.0 reference sequence. Differentially expressed genes (DEG) analysis was subsequently performed with the R-package DESeq2 [2] using different resistance groups, comprising i) very resistant Sumai-3 derived lines (Sumai3 group), ii) very resistant lines, iii) moderately resistant lines and iv) very susceptible lines. The found DEGs were afterwards subjected to a gene set enrichment analysis and eQTL were finally mapped with the package MatrixeQTL for R [3].

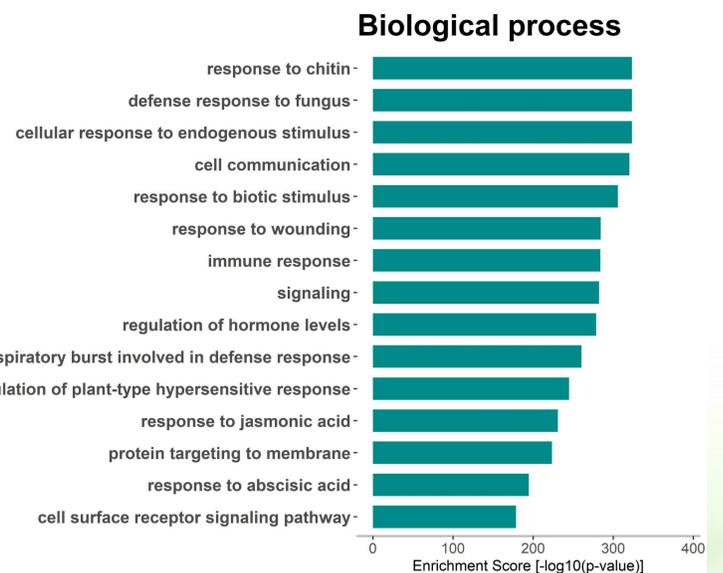


Figure 3: Top biological process enriched GO-Terms.

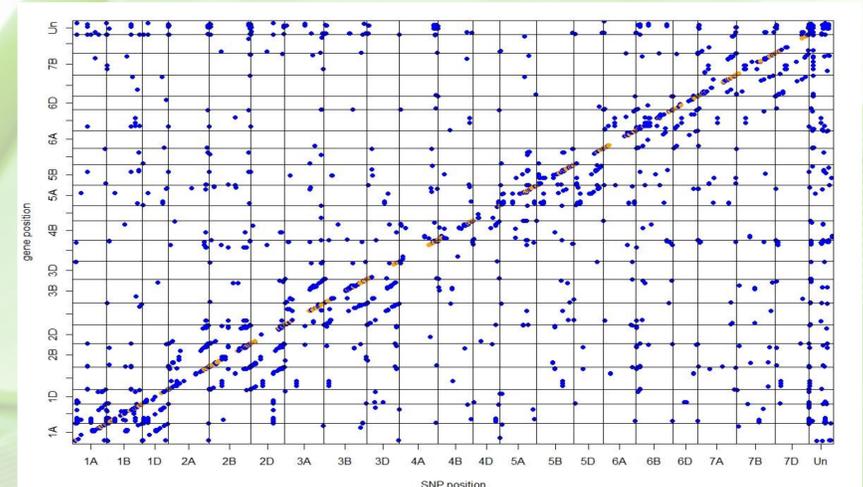


Figure 4: Genome-wide distribution of the 7681 mapped local (orange) and distal (blue) *F. graminearum* responsive eQTL.

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University of Natural Resources and Life Sciences, Vienna
Department of Agrobiotechnology, IFA-Tulln

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