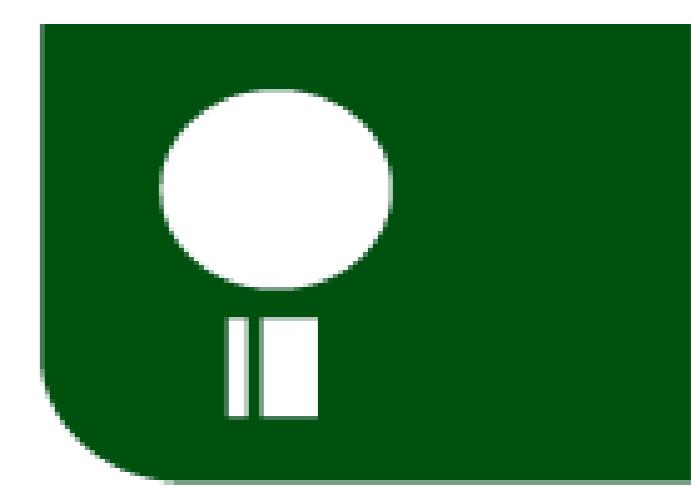


# **Fusarium graminearum and Deoxynivalenol resistance in Aegilops tauschii: a preliminary study**



Rizky Pasthika Kirana<sup>1,3</sup>, Barbara Steiner<sup>1</sup>, Sebastian Michel<sup>1</sup>, Kumar Gaurav<sup>2</sup>, Sanu Arora<sup>2</sup>, Marc Lemmens<sup>1</sup>, Branded BH Wulff<sup>2</sup>, Hermann Buerstmayr<sup>1</sup>

<sup>1</sup>Institute of Biotechnology in Plant Production, Dept. of Agrobiotechnology (IFA-Tulln), University of Natural Resources and Life Sciences, Vienna (BOKU), Austria

<sup>2</sup>John Innes Centre, Norwich Research Park, Norwich, UK

<sup>3</sup>Institute of Plant Breeding, Department of Agronomy, Faculty of Agriculture, Universitas Gadjah Mada, Indonesia

## Introduction

The bread wheat progenitor, *Aegilops tauschii* ( $2x=2n=14$ , DD), is a promising source of resistance genes for use in wheat improvement (Arora et al. 2019). Fusarium head blight (FHB), caused by *Fusarium graminearum*, is an important disease in wheat because it not only damages plants but also produces deoxynivalenol (DON), which is the major *Fusarium* mycotoxin with high toxicity effect. This study aims is to evaluate the variation for Fusarium and DON resistance within a diverse panel of *Ae. tauschii* accessions.

## Materials and Methods

Phenotyping for *F. graminearum* and DON resistance was carried out on 152 *Ae. tauschii* accessions. At anthesis, one spikelet per head was inoculated with *F. graminearum* or infiltrated with DON solution. The severity of the fungal infection and the DON-induced bleaching were evaluated at several time points after treatment. Furthermore DON and the conjugated non-toxic DON-3-O-glucoside (D3G) contents for a subset of the material were determined. For association mapping analysis, the whole genome sequencing (WGS) of *Ae. tauschii* that developed at the John Innes Centre was used.



Fig. 1: Greenhouse trial management and point inoculation/infiltration with wounding method for *Ae. tauschii*.

## Results

### *F. graminearum* resistance

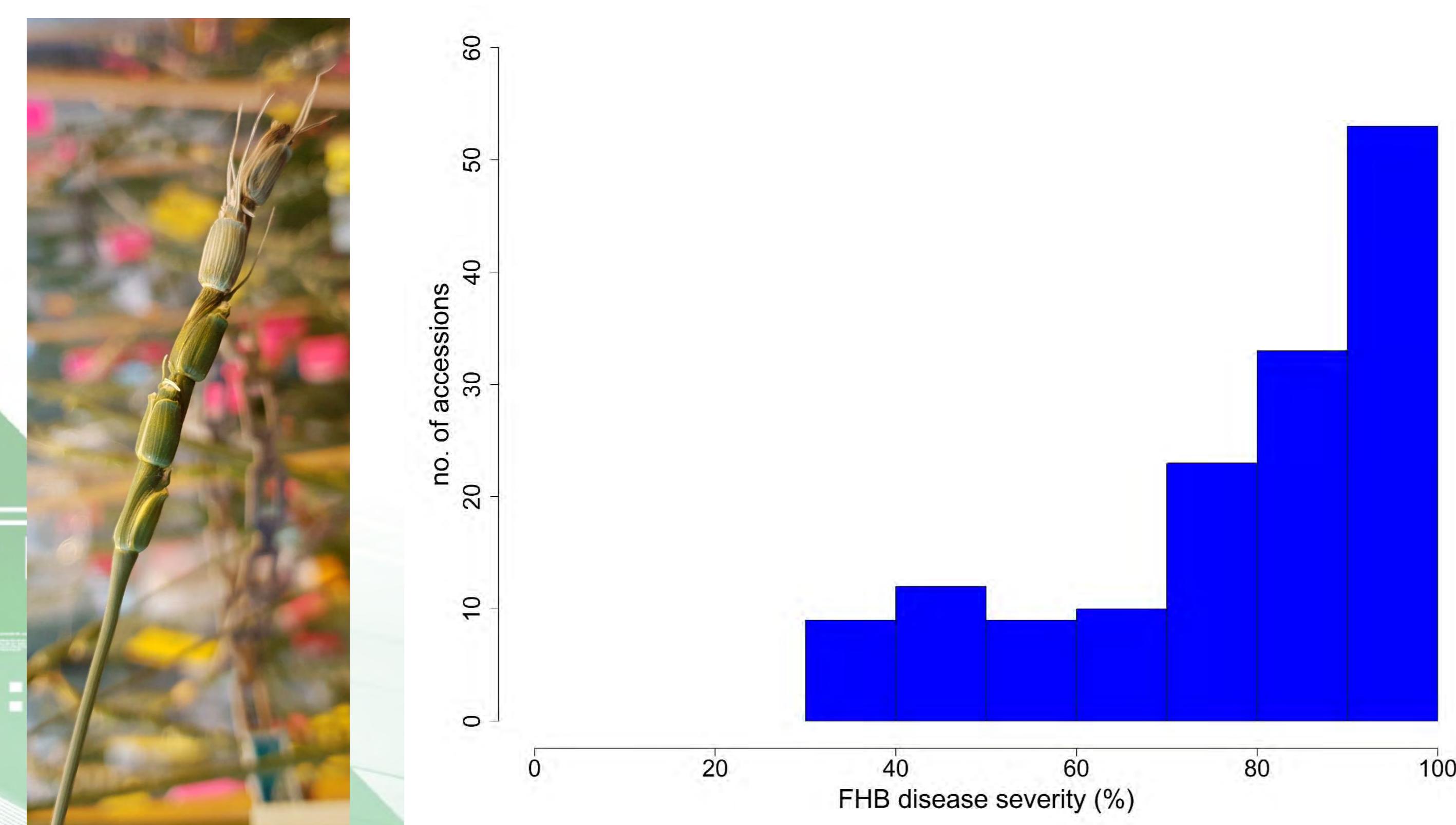


Fig. 2: Phenotypic variation for *F. graminearum* resistance in 152 *Ae. tauschii* accessions at 27 days after inoculation.

The accessions showed broad variation of the disease spreading within the spike, although no highly resistant accessions were identified and the fungal spreading promoted early 'spike shattering' (Fig. 2).

### DON resistance

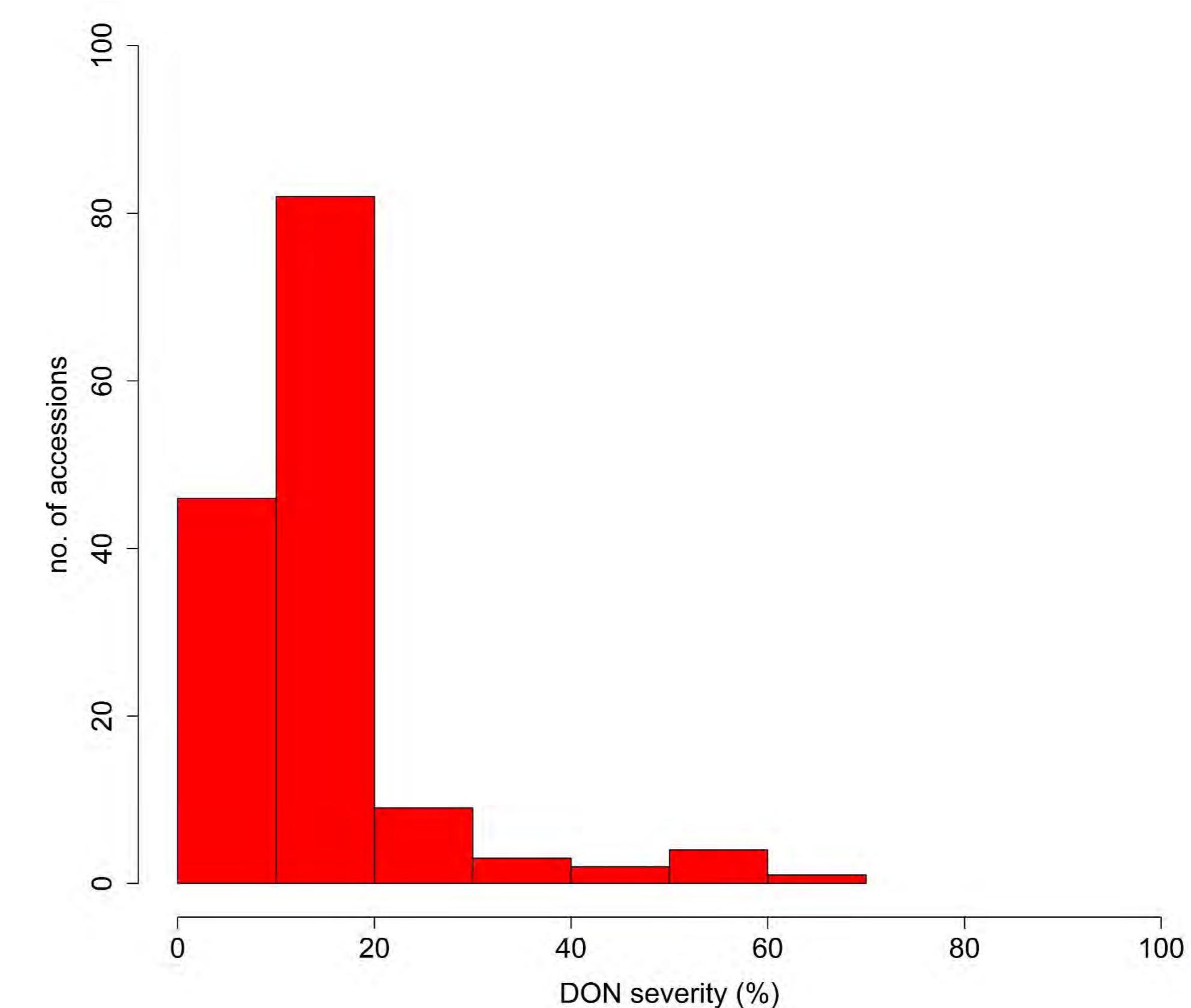


Fig. 3: Phenotypic variation for DON resistance in 152 *Ae. tauschii* accessions at 23 days after infiltration.

Compared to the *F. graminearum* resistance, the variation of DON resistance was very low. Most of the accessions showed bleaching symptoms only on the infiltrated spikelet (Fig. 3), but for nine genotypes the DON infiltration resulted in severe bleaching symptoms and for two genotypes no DON-induced bleaching was detected. Analysis of DON and D3G contents revealed higher amounts of D3G compared to DON in the resistant accessions whereas in the highly susceptible most of the applied DON was recovered.

WGS association mapping analysis for DON severity resulted in a significant peak on chromosome 5D in the centromeric region (Fig. 4).

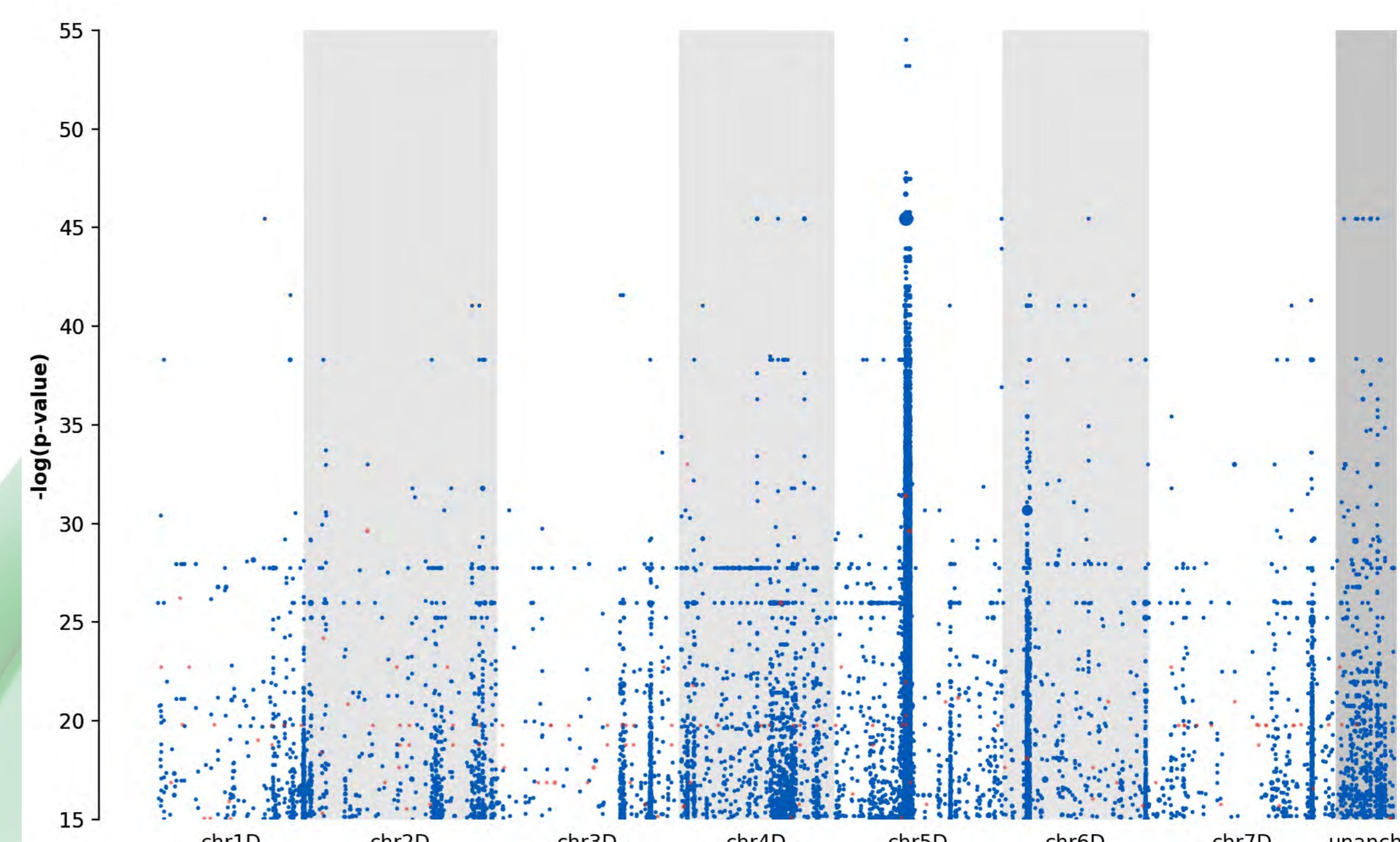


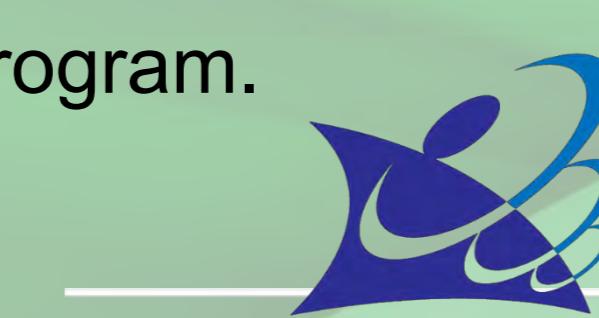
Fig. 4: Whole genome sequencing association mapping for DON severity using the *Ae. tauschii* reference genome AL8/78.

## Reference

Arora S, et.al. (2019) Resistance gene cloning from a wild crop relative by sequence capture and association genetics. *Nature Biotechnology* 37:139-143.

## Acknowledgements

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