



Multi-environmental Genome-Wide Association Study for response to Fusarium Head Blight in bread and durum wheat panels

Viviani A.¹, Condorelli G.¹, Novi J. B.¹, Bruschi M.¹, Gadaleta A.², Giove S.², Prodi A.¹, Senatore M. T.¹, Ravaglia S.³, Laidò G.⁴, Scarano D.⁴, Buerstmayr H.⁵, Steiner B.⁵, Maccaferri M.¹, Tuberosa R.¹, Cattivelli L.⁶

¹ Department of Agricultural and Food Sciences, Alma Mater Studiorum - Università di Bologna, Viale G. Fanin 44, 40127 Bologna, Italy

² Department of Agricultural and Environmental Science, University of Bari 'Aldo Moro', Via G. Amendola 165/A, 70126 Bari, Italy.

³ S.I.S. Società Italiana Sementi S.P.A, Via Mirandola, 5, 40068 San Lazzaro di Savena BO

⁴ ISEA s.r.l. - Agroservice S.P.A., Località Rocchetta, 62027 San Severino Marche MC

⁵ Department IFA-Tulln, University of Natural Resources and Applied Life Sciences Vienna, Konrad Lorenz Str. 20, A-3430 Tulln, Austria

⁶ CREA Research Centre for Genomics and Bioinformatics, Via San Protaso 302, Fiorenzuola d'Arda, PC, Italy

Corresponding author: ambra.viviani@unibo.it

Introduction

Fusarium head blight (FHB) is a fungal disease caused by pathogens belonging to the genus *Fusarium*. In particular, *Fusarium culmorum* (FC) and *Fusarium graminearum* (FG) species cause severe grain yield losses and accumulation of mycotoxins (e.g., deoxynivalenol or DON) in wheat that compromise food safety and animal health. Two main **types of resistance** to FHB have been reported in wheat (Schroeder and Christensen, 1963): **Type I** acts against initial infection, while **type II** against spread within the head. **Type III** (DON content) is directly related to the final kernel contamination levels and it is therefore worth to assess. **Durum wheat** (*Triticum turgidum* ssp. *durum*) is known to be highly susceptible to FHB compared to bread wheat (*Triticum aestivum*). None of the selected durum wheat varieties or lines show a level of **resistance** to FHB comparable to Sumai-3. Over 250 QTL/genes for FHB resistance have been identified in bread wheat, such as *Fhb1* and *Fhb5* but only a small number of FHB resistance loci have been mapped in durum wheat. The **aim** of this work is to find loci of partial resistance to FHB already present in durum wheat germplasm and therefore easily cumulative. In addition, an attempt was made to assess the heritability of DON content.

Materials and Methods

- 200 cultivars from the Sofia-Project durum panel and 1000 cultivars from the Global Durum Panel (GDP) were evaluated in multiple field trials located in Cadriano (BO, Fig.1a), Idice (BO), Tolentino (MC), BOKU (Austria) and University of Bari, over four seasons (2015-2016-2019-2021-2022).
- **Selected check** cultivars (Claudio, Karim, Normanno, Saragolla and Simeto) were chosen and repeated within the experimental blocks.
- **50 ml of inoculum** (macroconidia of FC and FG isolates) was sprayed on the heads when 50% of the plants had reached anthesis.
- **FHB-related traits** such as: plant height, harvest date, FHB incidence, FHB severity, and DON content were evaluated for each accession (Fig. 2).
- The **DON content** was measured using a Ridascreen DON (R-Biopharm AG, Darmstadt, Germany) enzyme linked immune-assay (ELISA).
- **Genotypic analysis** was performed using the Illumina wheat 90K SNP array.
- **GWAS** was performed using **GAPIT3** R package for the traits collected, using five different models (GLM, MLM, MLM, BLINK, FarmCPU) and including the K kinship array in the mixed models (Fig. 3).

Results

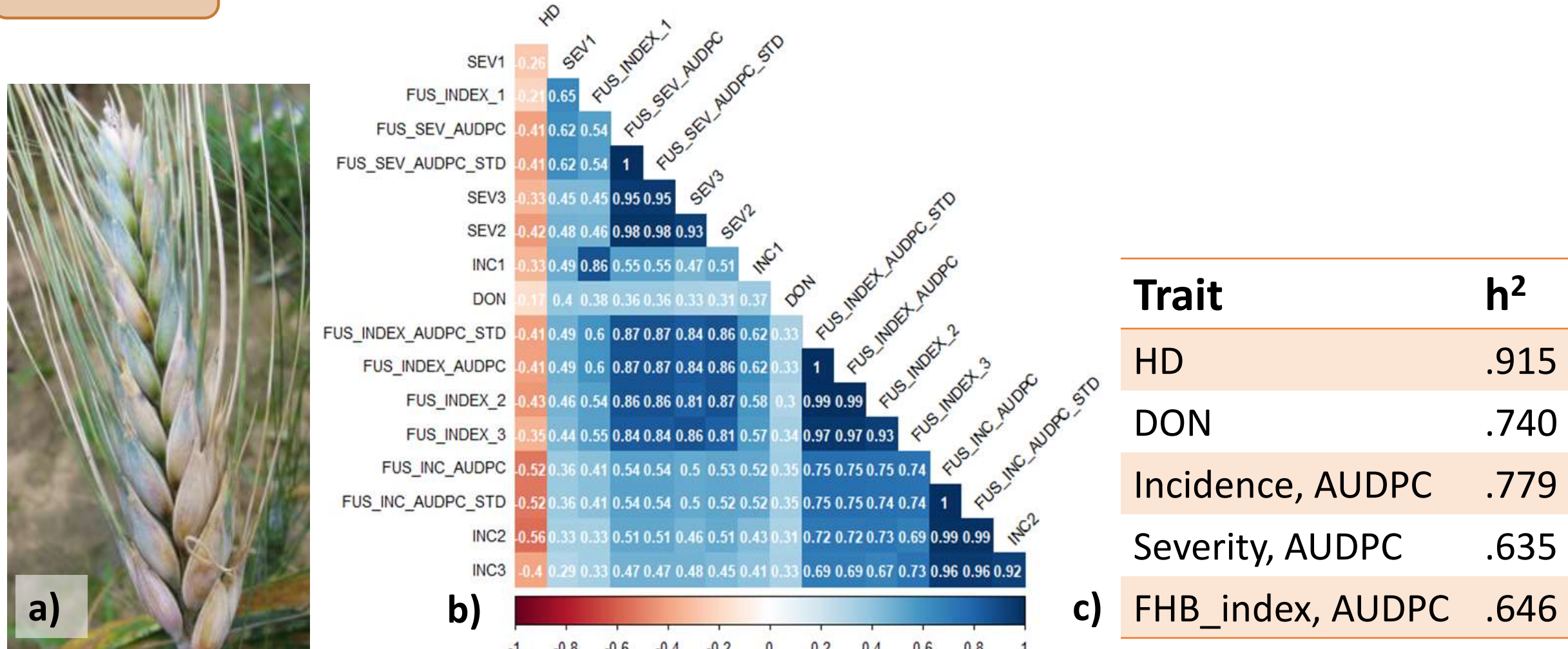


Figure 1. a) Plants heavily affected by FHB, b) Correlation graph as regards to the gene trial carried out in 2016, and c) Heritability table for the FHB-infection traits recorded in 2016.

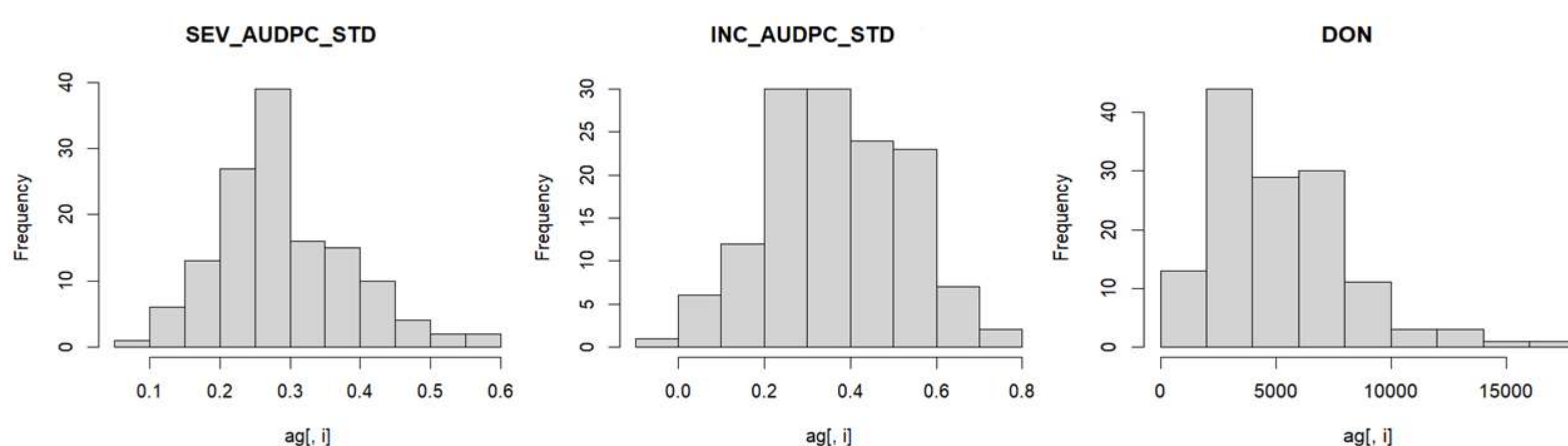


Figure 2. Phenotypic distribution for severity, incidence and DON content.

Based on the GWAS analysis (Fig. 3), **sixteen** QTL hotspots were detected.

- ❑ Six of them were specific for DON: *QFHB.ubo-1A.1*, *QFHB.ubo-1B.1*, *QFHB.ubo-2A.2*, *QFHB.ubo-3A.1*, *QFHB.ubo-6A.1*, *QFHB.ubo-7B.1*.
- ❑ Two of them were specific for FHB index: *QFHB.ubo-2A.1*, *QFHB.ubo-5A.2*.

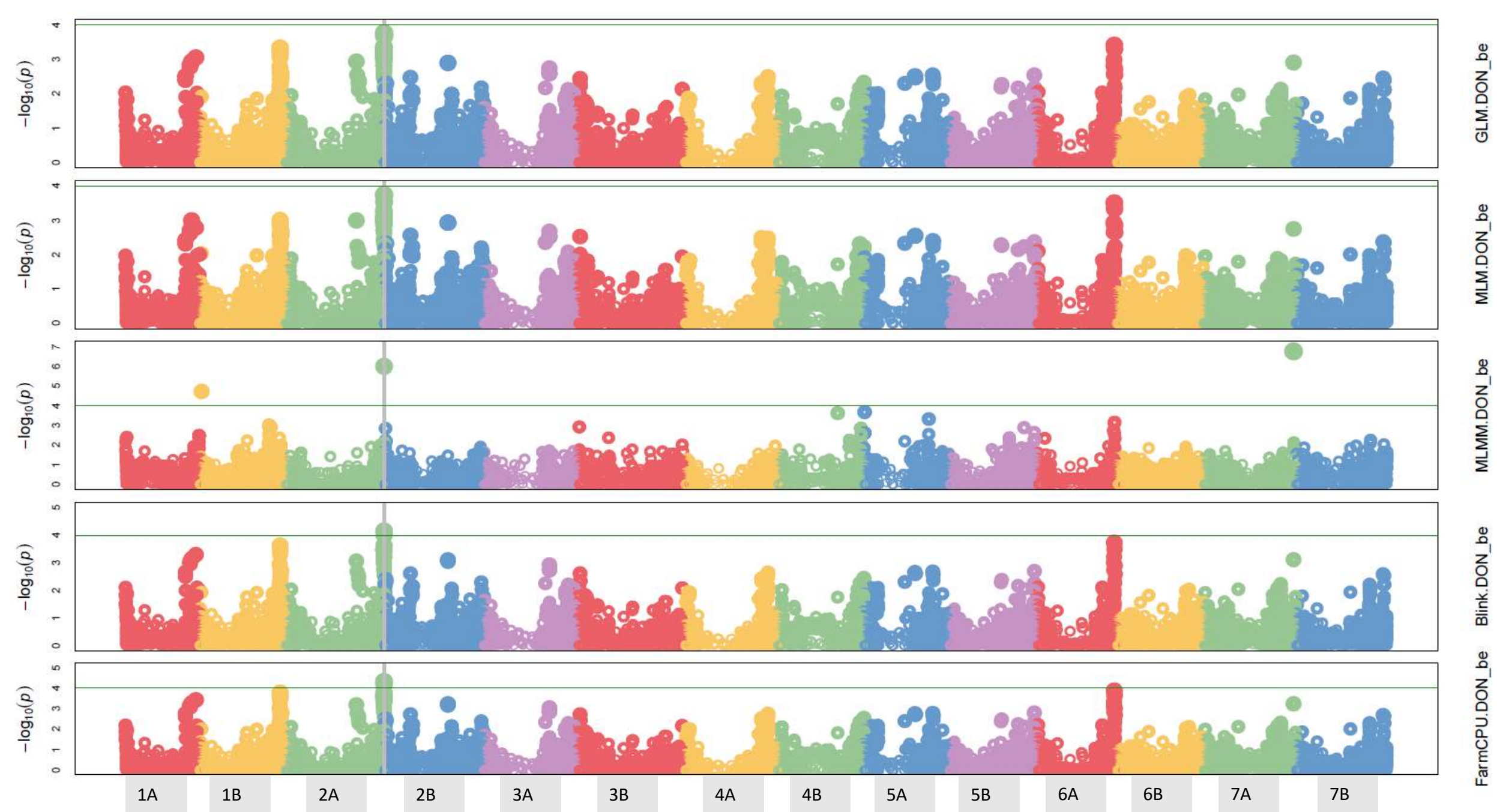


Figure 3. Manhattan plot - chromosomal representations of GWAS-QTL significance for FHB expressed as DON Content (DON) in one environment (Idice, 2016). The x axis shows durum chromosomes (1A - 7B). The y axis shows the $-\log_{10}(p)$ values. The green line for each Manhattan represents the significance threshold, set at $-\log P = 4$.

Discussion and Conclusions

- ❖ The **medium-to-high heritability** per trait (Fig. 1b) (referred to check cultivars repeated within the experimental blocks) showed how the variation in genetic factors highly affected the phenotypic values, while the **positive Pearson correlations** (r) (Fig. 1c) among traits reflected their common direction in FHB response.
- ❖ Preliminary GWAS revealed **several peaks** that can be attributed to QTL of interest for FHB resistance.
- ❖ GWAS peaks for **DON content** clearly showed that a dedicated **laboratory test** for DON is important to better identify chromosomal regions carrying favorable loci for DON content reduction. These loci can be directly targeted for selection/pyramidization in durum wheat germplasm.
- ❖ Of the several loci directly deputed to the control of DON content, most were found to be largely **independent** of other traits and heading date and thus potentially useful for marker-assisted selection directly aimed at rapidly enriching durum wheat with partial resistance QTL.

Acknowledgments

This research was supported by the Clust-ER AgriFood project, the project "CerealMed"- Enhancing diversity in Mediterranean cereal farming systems, funded by PRIMA2019-Section 2 and the project H2020 "INNOVAR" - Next generation variety testing for improved cropping on European farmland.