

Marker-trait associations of agronomic traits from the Cerealméd durum wheat panel as assessed in multi-environment trials under conservative agriculture

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Objectives

Developing a biodiversity-based agriculture is currently considered an innovation target to enhance cropping sustainability and food security in the frame of climate changes. The constant reduction of biodiversity, due to intensive agriculture, is affecting all components of the farming ecosystem (crop varieties, crop species, soil microbioma, etc) and is increasingly considered a constraint for the development of sustainable cropping systems. Conservation agriculture (CA) is a promising option for solving soil degradation and fertility and sustainable management of water resource, however genotypes adapted to this specific agronomic practice need to be selected. In the frame of the Cerealméd Project (PRIMA2019) dedicated to "Enhancing diversity in Mediterranean cereal farming systems", a wide and largely underutilized phenotypic diversity present in durum wheat germplasm is being characterised towards the identification of genotypes fitting with the current principles of agriculture sustainability and genetic determinants of the relevant traits.

Methods

A 300 lines germplasm panel made of elite, cultivars/ breeding lines originated from stress-prone durum growing area was selected for evaluation in a multi-environmental trial network across a range of Mediterranean environments (Morocco, Egypt, Turkey, Italy) for two years (2019/20, 20/21) based on augmented field design and 4m² plots. The panel is a selected subset of the Global Durum Panel previously established by the EWG of Wheat Initiative "Durum wheat genomics and breeding" and provided with Illumina 90k SNP data.

Traits considered for phenotyping were agronomic traits relevant for adaptation and grain yield, but also resistance to wheat fungal diseases. Meteorological data and soil humidity have been registered during the entire plant growth cycle.

Genome-wide association analyses (GWAS) are on going based on a large panel of SNP by fitting a Mixed Linear model, that includes a kinship matrix as random term to account for genetic relatedness.

Results

Phenotyping: the following traits were scored according to shared protocols: heading date (HD), plant height (PH), canopy growth rate through several rounds of RGB and estimation of vegetation index, canopy leaf posture (angle and orientation) and size, canopy temperature, plant height, number of fertile culms/m², grain yield, grain yield components such as grain weight and volume grain weight, straw biomass production, quality traits (Poster XM-40120), disease resistance. A good variability was observed in all environments (Fig. 1 and 2), statistic significant differences among the genotypes for most of the traits, and a good uniformity of the field, as seen through the behaviour of the repeated checks (Tab. 1).

Structure analysis and GWAS

The Cerealméd wheat collection was analysed for the population structure while single environment GWAS analyses are on going. Around 11K polymorphic Illumina 90K SNP markers with MAF >0.05 are available for such analysis. Four groups were identified (Fig. 3) that can be related to improvement status or geographic/ breeding program origin. Italian genotypes provide most of the genetic diversity (Fig. 4). Significant marker associations have been identified for most of the traits in Italy (Fig. 5 and 6). Significant associations will be assessed across environments and year upon the second-year field trials (season 2021-2022).

Discussion & Conclusions

- The collection showed a wide variability and some genotypes were selected for good performance across the environments or for specific adaptation
- Single environment GWAS analyses identified significant associations for most of the traits
- Stability of GWAS results in respect to environment is being assessed through a second-year experimental fields, as well as the agronomic performance of the best genotypes.

REFERENCES

Cerealméd website: Cerealméd

Fig. 1 Distribution of phenotypes for different traits in Italy

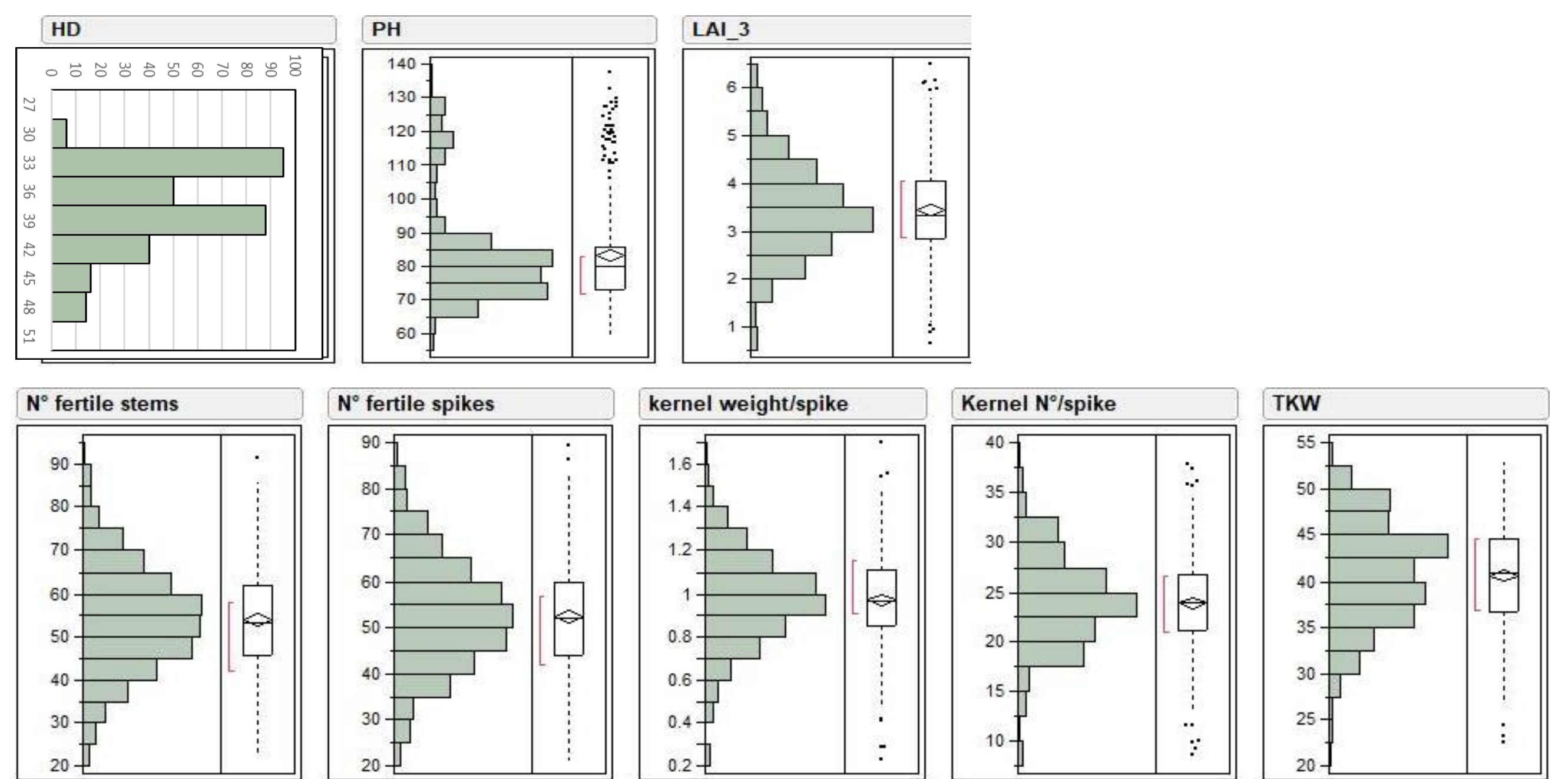
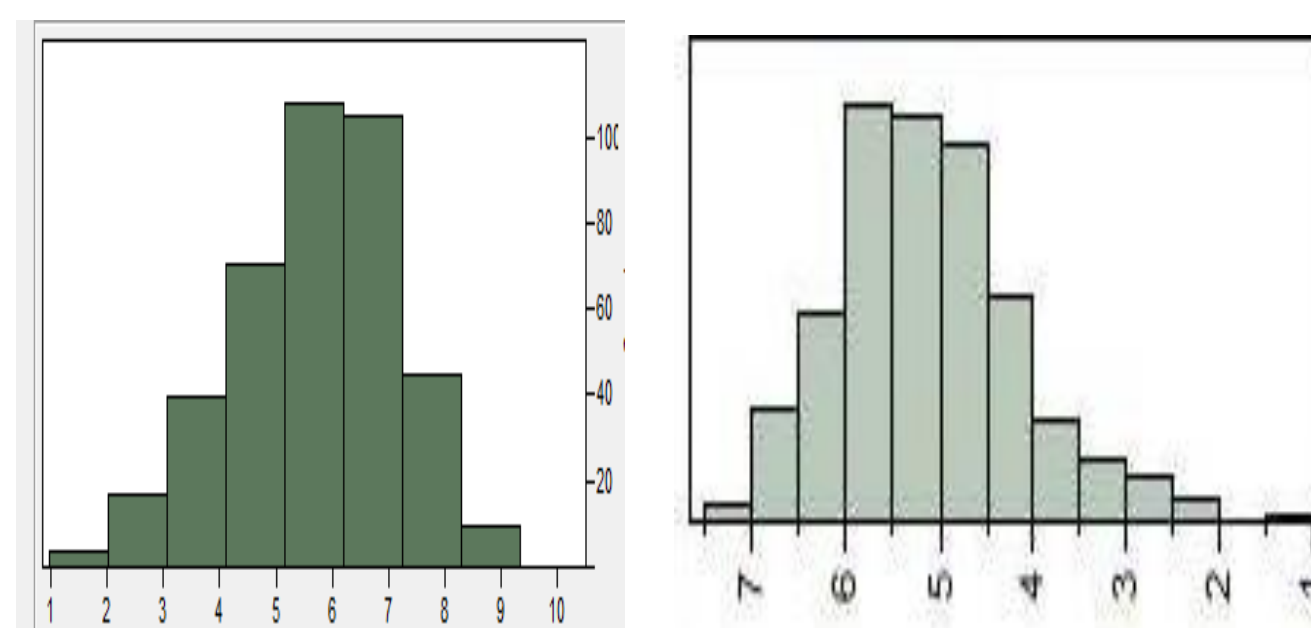


Fig. 2 Distribution of grain yield in Egypt (A) and Italy (B)



Tab. 1 ANOVA on check genotypes to assess field repeatability

	HD	Yield	TKW	Proteins
genotype	***	***	*	*
rep p	ns	ns	ns	***
H2	0.83	0.32	0.18	0.20

Fig. 3 Population structure of the Cerealméd collection

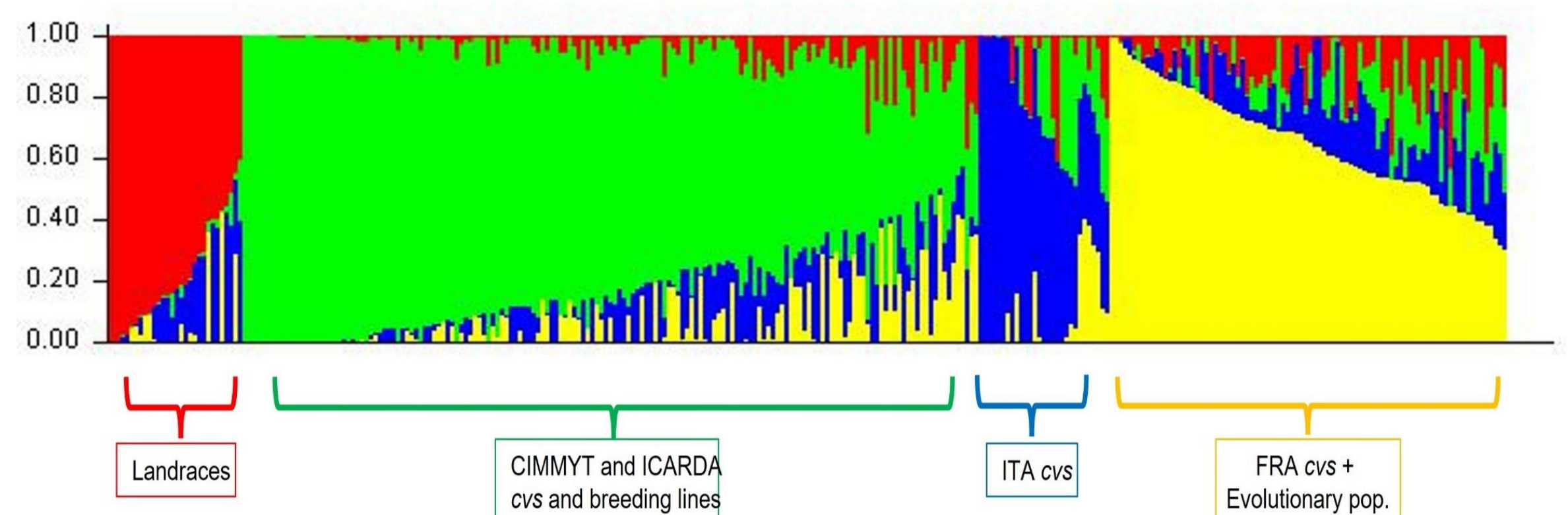


Fig. 4 Principal Component Analysis to show diversity of the collection

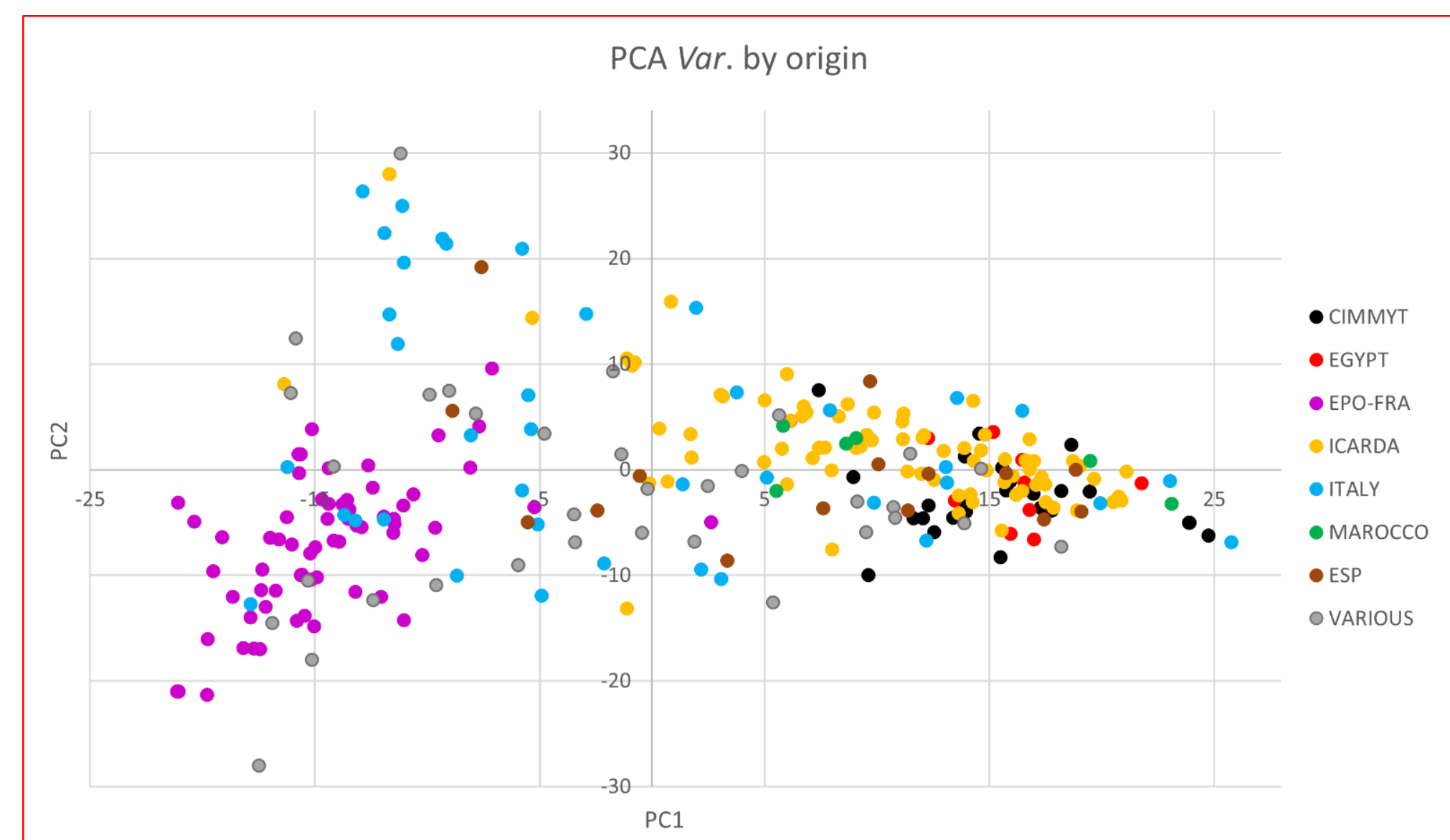


Fig. 5 Manhattan plot for some yield related traits

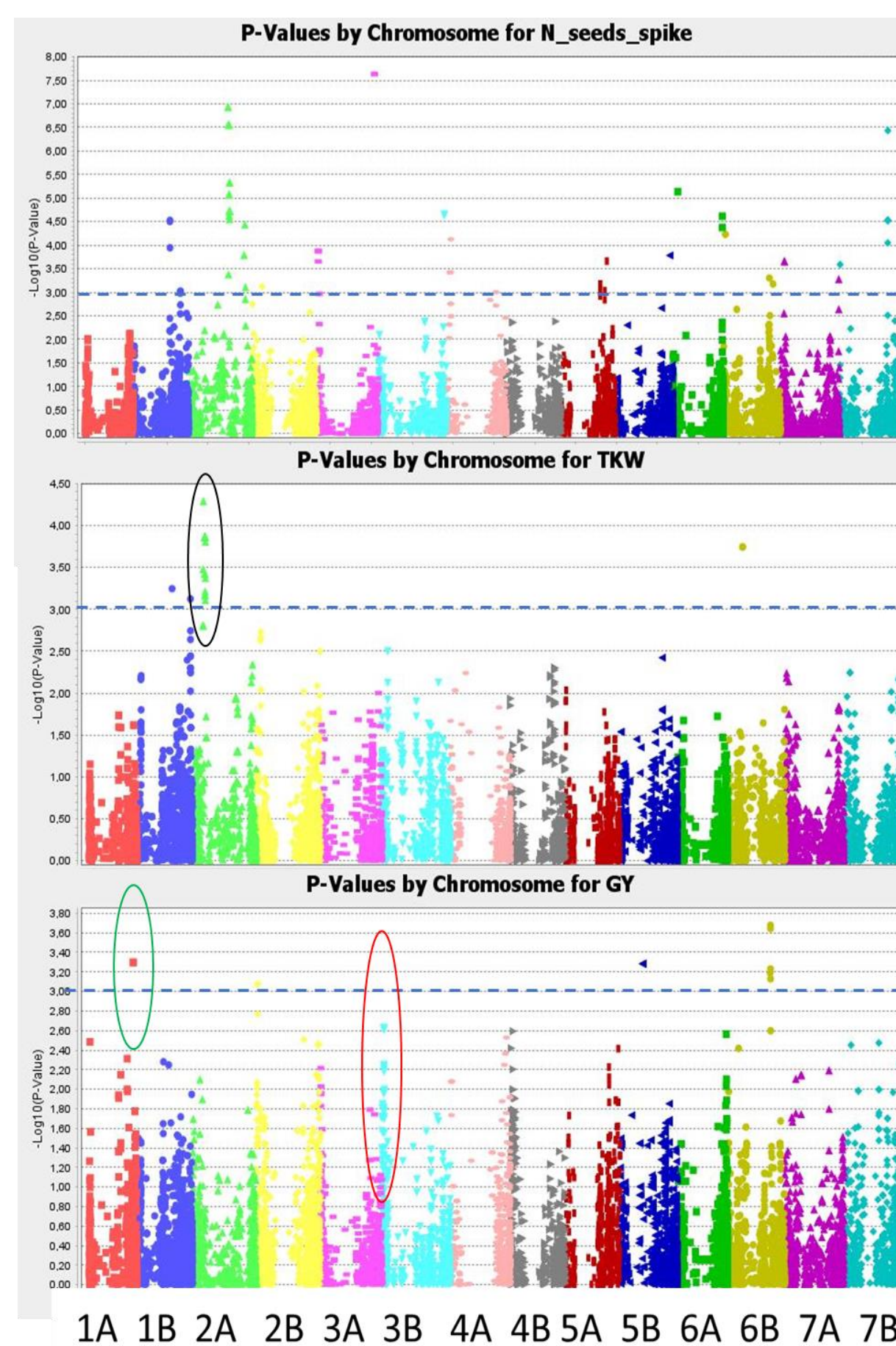


Fig. 6 Manhattan plot for yellow rust (YR) resistance (Infection type - IT, and disease severity DS), and Septoria (STB) resistance

