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Objectives

The CerealMed research project (Enhancing diversity in Mediterranean cereal farming systems 2020-2023) is aimed at implementing a biodiversity-based wheat cropping system in the Mediterranean area. Tan spot caused by *Pyrenophora tritici-repentis* (Died.) is an economically important disease in most wheat-growing regions worldwide, including Europe, North and South America, Australia, and Asia. On an average, losses due to tan spot vary from 10% to 15% but may reach up to 50% during epidemic years, with strong effects on total yield, grain weight, number of grains per head, total biomass, and grain quality (Kokhmetova et al. 2021). This study was aimed at identifying new sources of resistance to tan spot in durum wheat.

Methods

A population of nearly 130 introgression lines (genome of *T. dicoccoides* AG218) introgressed into durum wheat PR22D89) has been evaluated during 2020-2021 growing season in a field trial with two biological replicates in two locations: Foggia (South of Italy, 41° 27' 42" N, 15° 30' 2" E) and Fiorenzuola d'Arda (North of Italy, 44° 55' 22" N, 9° 54' 36" E). The experimental design consisted of a randomized complete block with two replicates; accessions were planted in single rows, 1 m long, using a sowing density of 25 seeds/m. Field was managed with fertilizer applications following the local agronomic practices. Heading date was considered and calculated as number of days from 1st April to when spikes appeared in 50% of the plants. A natural infection of tan spot caused by *Pyrenophora tritici-repentis* occurred in both locations, and it was recorded. Symptom expression was evaluated as surface of infected leaf in a scale with range 0.1-10.

Results

Looking at the frequency distribution of the tan spot disease severity in the two locations, the natural infection was more severe in Foggia than in Fiorenzuola, indeed a larger number of susceptible lines was identified in this location. Anyway, in both trials a significant difference for disease severity was observed between the two parents, with a more susceptible reaction in PR22D89 than in Ag218 (Figure 1).

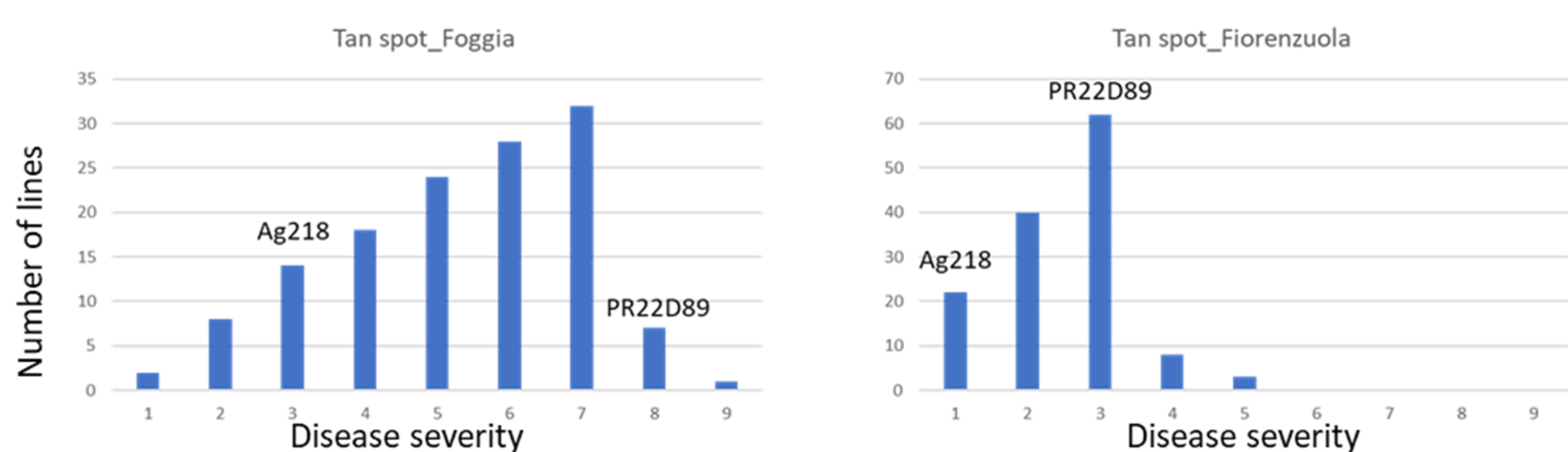


Figure 1. Frequency distribution of tan spot disease severity in the IL population grown in Foggia and Fiorenzuola.

Phenotypic and genotypic data for the IL population deriving from the 90 K wheat SNP iSelect assay, were analyzed to find ILs putatively carrying genes for resistance to tan spot. A first locus was identified on the long arm of chromosome 1B, as shown in the figure, between 647 and 664 Mb (referred to the 'Svevo' genome – Maccaferri et al. 2019). In this case a resistant phenotype was observed in 8 lines. A second locus was identified on chromosome 4A at 20-59 Mb. These loci, different from those identified for heading date and plant height, are under further investigation.

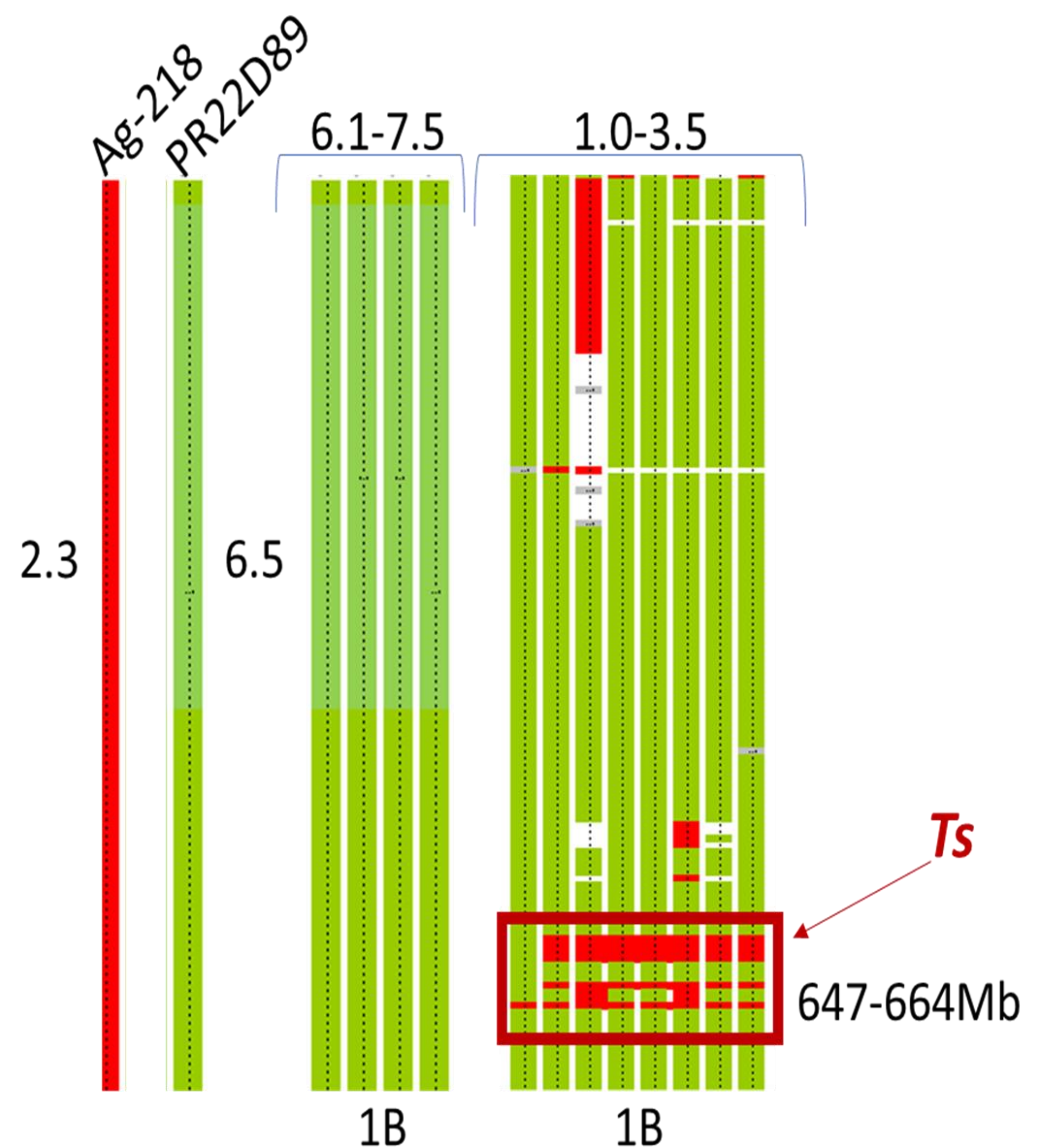


Figure 2. Genomic status for chromosome 1B of the two parents of the IL population and some susceptible and resistant lines.

Discussion & Conclusions

The identification of new sources of resistance to tan spot in wheat is of paramount importance, due to the continuous pathogen co-evolution process and the spreading of new virulent races in the frame of the current climate changes. Introgression lines carrying genomic portions of a wild/domesticated donor are a useful genetic tool to capitalize wheat biodiversity and represent a valuable pre-breeding genetic material carrying valuable resistant alleles.

REFERENCES

Kokhmetova et al. (2021) Front. Genet. 11:581214. doi: 10.3389/fgene.2020.581214
Maccaferri et al. (2019) Nature Genetics, 51: 885-895, <https://doi.org/10.1038/s41588-019-0381-3>.