



Characterization of a Global Durum Resource for spike traits related to grain yield potential

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Introduction

Durum wheat (*Triticum turgidum* L. ssp. *durum*) is one of the major staple crops in the world. The ever-growing food demand of an increasing world population has brought in the need of an improved grain yield. Up to now the majority of the **yield improvement** has been obtained through increasing the number of spikes per area and the grain number per spike. **Spike traits** like fertile spikelet number, spike length, sterile spikelet number and floret fertility can determine the number of grains per spike and other quality-related traits, therefore they might as well affect quality and yield potential. Most importantly, the **genetic inheritance** of each of these component traits is largely independent from the others, thus allowing for fine tuning the components leveraging on a range of loci and alleles.

The **Global Durum Panel (GDP)** is a wheat collection composed mainly of nearly 800 durum modern cultivars and durum landraces while the **Tetraploid Global Collection (TGC)** samples 1800 diverse tetraploids from wild emmer wheat, domesticated emmer wheat, to durum landraces, and other durum subspecies. In this ongoing study, both collections collectively referred as the **Global Durum Genomic Resource** (https://wheat.pw.usda.gov/GG3/global_durum_genomic_resources) were evaluated in multiple field trials for several yield-related traits and a genome-wide association mapping study has been performed.

Materials and Methods

- The collections are being evaluated in **two different environments** over **two seasons** (2020 and 2021) in Grosseto (Central Mediterranean), Italy.
- Collections were grown under an **unreplicated modified augmented design** with blocks including 10 modern durum and landraces. Data were analyzed accounting for rows, columns and blocks with six durum cultivars and six durum landraces employed as checks in the field layout.
- Both collections were **genotyped** with the wheat high-density Illumina *iSelect* 90K SNP assay to provide a common genotype framework.
- For each accession of both collections, six spikes have been **imaged** and **characterized** for different yield-related traits (i.e. average spike length, sterile spikelet number, fertile spikelet number, number of florets per central spikelet, thousand grain weight, grain size, grain shape, grain color).
- A preliminary **GWAS** was performed for all traits with R package GAPIT3 using different models (**GLM, MLM, MLMM, Blink, FarmCPU**) and including the kinship *K* matrix of relatedness among accessions.

Results

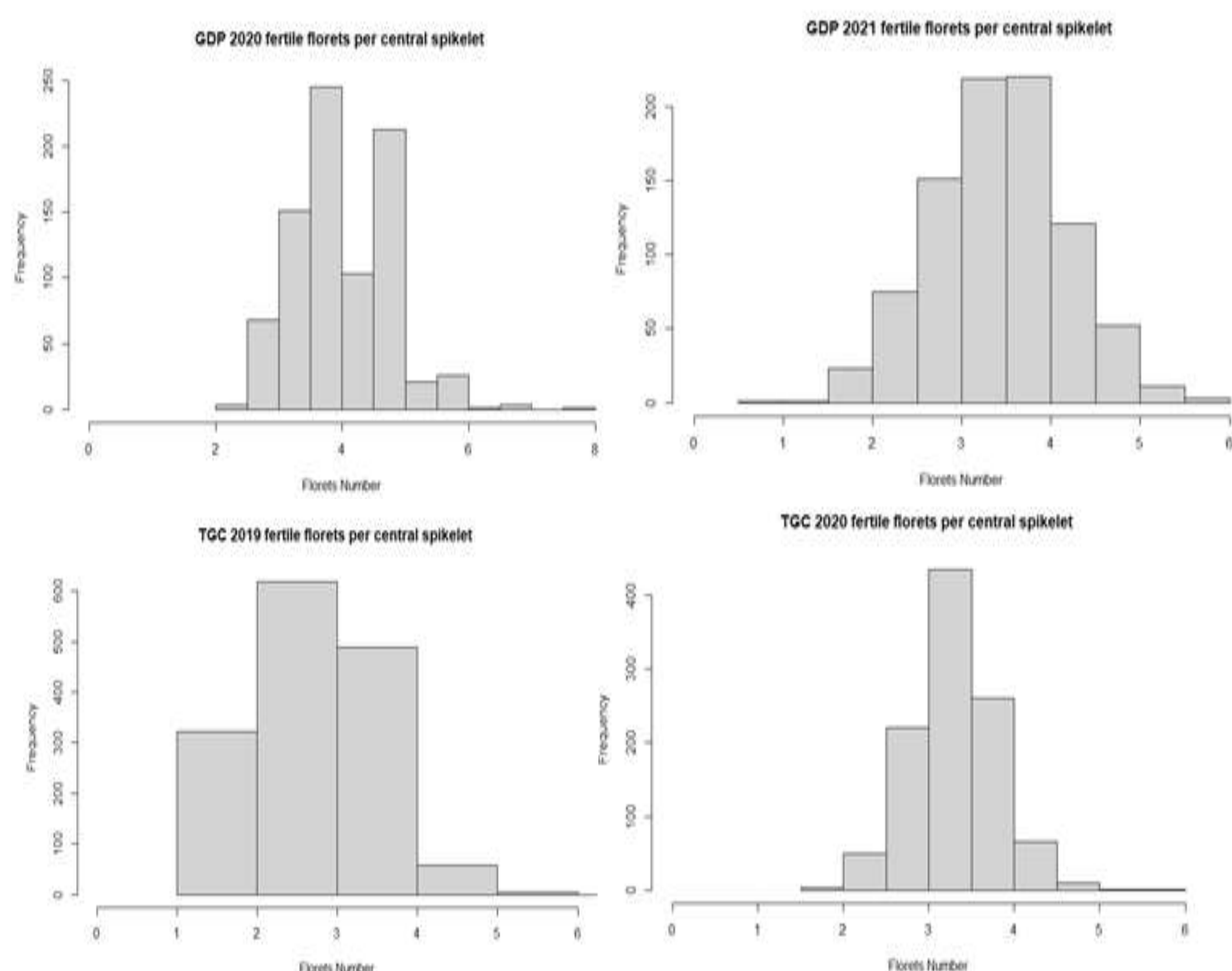


Figure 1. Phenotypic distribution in Global Durum Panel and Tetraploid Global Collection for Fertile Florets number per spikelet, one representative trait among those considered.

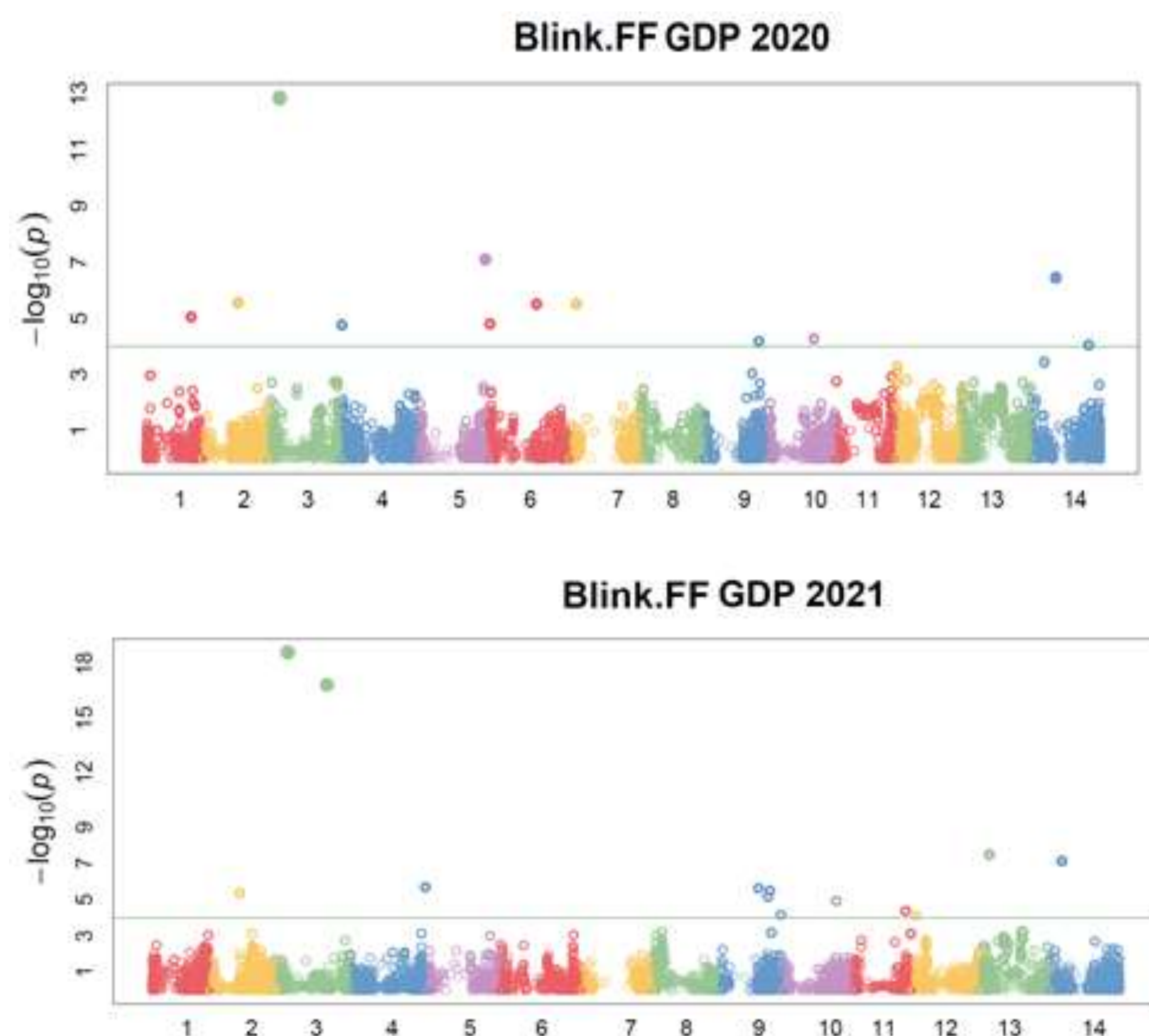


Figure 2. Manhattan plot representation of the preliminary GWAS results for the fertile floret number per spikelet trait in the two different years of the GDP. The x axis shows the fourteen durum chromosomes (1A – 7B). The y axis shows the $-\log_{10}(p)$ values. The horizontal green line is the Bonferroni corrected threshold value for association ($-\log P = 4.21$).

Discussion and Conclusions

- For the number of fertile florets per central spikelet, the tag SNP “BobWhite_c46780_84” was detected by three different models (GLM, FarmCPU and Blink) on **chromosome 2A** at position 130.385.623 bp as being **closely associated** with the increase in the number of fertile flowers in the spikelets.
- This could be a **putative QTL** for Grain Number Increase in the short arm of chromosome 2A with the favorable allele introduced by **CIMMYT breeding program**.
- A more **complete GWAS** will be performed for both GDP and TGC including population structure in order to detect novel loci involved in yield and its components.

Acknowledgments

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