

Genome-Wide Association Study Reveals Novel Genomic Regions for Grain Yield and Yield-Related Traits in Drought-Stressed Synthetic Hexaploid Wheat

All supplementary materials are available online: <https://figshare.com/s/c448a2d5a559b3f6b462>

Figure S1. Pearson's correlation of grain yield and yield-related traits of 123 synthetic hexaploid wheat based on adjusted best linear unbiased predictors in 2016 (A) and 2017 (B) growing seasons in Konya, Turkey.

Figure S2. Population structure analysis of 123 synthetic hexaploid wheat.

Figure S3. Physical distribution of genotyping-by-sequencing-derived SNPs within a 1 Mb window size on 21 chromosomes of 123 synthetic hexaploid wheat.

Figure S4. Manhattan and quantile-quantile plots for 11 traits in 123 synthetic hexaploid wheat germplasm.

Table S1. Details of 123 synthetic hexaploid wheat used and subgroups obtained from the Bayesian clustering algorithm with population structure matrix (Q) and BLUPs from two-year (2016 and 2017) experiments conducted in Konya, Turkey.

Table S2. Crossing scheme of 123 synthetic hexaploid wheat.

Table S3. Genotyping-by-sequencing-derived SNP markers of 123 synthetic hexaploid wheats used in the present study.

Table S4. Combined analysis of variance with means squares and broad sense heritability (H^2) of 123 drought stressed synthetic hexaploid wheats grown in two seasons (2016 and 2017) in Konya, Turkey.

Table S5. Details of significant markers associated with 11 traits in 123 synthetic hexaploid wheat grown in two seasons (2016 and 2017) in Konya, Turkey.

Table S6. Details of potential candidate gene functions harboring SNPs affecting yield and yield-related traits under drought stress in 123 synthetic hexaploid wheat grown in two seasons (2016 and 2017) in Konya, Turkey.