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Association genetics of kernel size, a competent of sink strength, in a historical US population wheat

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Kernel weight in wheat is a component of sink strength. We studied genetics of kernel weight in a historical US wheat population that represents 200 years of selection and breeding history. Kernel weight, from 290 field-grown historical accessions, was estimated on the basis of 5 randomly chosen spikes from one-meter rows. Kernel average weight was 37.2 mg, with standard deviation of 5.6 mg. The largest kernel (56 mg) was 2.8 fold heavier than the lightest kernel (20 mg) accession in this study. Genomic sequences were used to make reduced representation libraries for next generation sequencing. SNP calling following reference genome-based alignment yielded a total of 33992 polymorphic markers with minimum allele frequency of greater than 5% and maximum missing data of not more than 25%. Genome-wide association genetics analysis, in TASSEL environment, was conducted using Kinship and the first two principal components to partially account for population structure. One locus, encompassing multiple markers, was identified on chromosome 7A and four other loci were identified on chromosomes 4A, 4B, 5D, and 7D. Favorable allele effects of these loci ranged from 3-6 mg. The diversity of QTL controlling kernel weight in the past will be compared with the diversity of QTL in the most recent germplasm, which will be useful to identify prospects of germplasm and QTL utilization in breeding programs. Sequence search using the wheat genome Ensembl and wheat gene models returned candidate genes such as sugar phosphate translocator, hexokinase, ureide permease, and ripening related protein for further functional validations.

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