

# Breeding driven enrichment of genetic variation for key yield components and grain starch content under drought stress in winter wheat

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## Abstract

Drought is one of the major abiotic stress factors limiting wheat production worldwide, thus threatening food security. The dissection of the genetic footprint of drought stress response offers strong opportunities toward understanding and improving drought tolerance in wheat. In this study, we investigated the genotypic variability for drought response among 200 diverse wheat cultivars (genotypes) using agronomic, developmental, and grain quality traits, and conducted genome-wide association studies (GWAS) to uncover the genetic architectures of these important traits. Results indicated significant effects of genotype, water regime and their interactions for all agronomic traits. Grain yield was the most drought-responsive trait and was highly correlated with kernels number per meter square. GWAS revealed 17 and 20 QTL regions under rainfed and drought conditions, respectively, and identified one LD block on chromosome 3A and two others on 5D associated with breeding progress. The major haplotypes of these LD blocks have been positively selected through breeding and are associated with higher starch accumulation and grain yield under drought conditions. Upon validation, the identified QTL regions carrying favorable alleles for high starch and yield will shed light on mechanisms of tolerance to drought and can be used to develop drought resistant cultivars.

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