

GENOME-WIDE ASSOCIATION STUDY OF YIELD-RELATED TRAITS IN A NESTED ASSOCIATION MAPPING POPULATION GROWN IN KAZAKHSTAN

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This study evaluated 290 recombinant inbred lines (RILs) from the Nested Association Mapping (NAM) population in the UK, consisting of 24 hybrid families. All genotypes were grown in southeastern Kazakhstan (Kazakh Research Institute of Agriculture and Plant Growing, Almaty region, 2021-2022) and northern Kazakhstan (Alexandr Barayev Scientific-Production Center for Grain Farming, Akmola region, 2020). The studied traits included six yield-related characteristics: spike length (SL, cm), number of productive spikes per plant (NPS, pcs), number of kernels per spike (NKS, pcs), weight of kernels per spike (WKS, g), thousand kernel weight (TKW, g), and yield per square meter (YM2, g/m²). The significant phenotypic variability among genotypes was observed, which was suitable for the genome-wide associa-

tion study of yield-related traits. Pearson's index showed positive correlations among most yield-related traits, although a negative correlation was found between NKS and TKW in southeastern, and no correlation was recorded for northern regions. Top-performing RILs, surpassing local checks, were identified for NKS, TKW, and YM2, suggesting their potential for breeding programs. The application of GWAS allowed the identification of 72 quantitative trait loci (QTLs), including 36 QTLs in the southeastern region, 16 QTLs in the northern region, and 19 in both locations. Eleven QTLs matched those reported in previous QTL mapping studies and GWAS for studied traits. The results can be used for further studies related to the adaptation and productivity of wheat in breeding projects for higher grain productivity.