

Genome-Wide Association Study Reveals Candidate Genes for Carbon Isotope Discrimination in Common Wheat

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Abstract: 【Background】

Drought and water shortage seriously threaten wheat production and render many land resources unusable for cultivation, thereby significantly restricting the development potential of wheat production. Therefore, the most effective measures to investigate the potential of wheat production include investigating genes associated with drought resistance and water-saving, as well as carrying out drought-resistant and water-saving breeding in wheat. 【Method】 In this study, 275 wheat natural populations were planted under three water conditions (well-watered, water-limited, and rain-fed), and the drought-resistant traits including fractional vegetation cover(FVC), canopy temperature(CT), SPAD(measured by SPAD 502 plus meter), YPFD(Yield Photon Flux Density), and CID(carbon isotope discrimination) were investigated during the important growth stages of the common wheat, including the seedling, anthesis, milk stage, and maturity stages, genome-wide association analysis was conducted using CID. 【Result】 The results showed that under the three different water conditions, except for the seedling vegetation coverage with a larger coefficient of variation in the rain-fed environment (57.87), the overall coefficient of variation for the other traits was normal, ranging from 2.48 to 29.64. The coefficient of variation of CID in the WW, WL, and RF environments was 2.88, 5.54, and 4.06, respectively, with a small variation range. GWAS of CID identified 233 SNP loci significantly associated with leaf CID under the three environments, distributed on chromosomes 1A, 2A, 3A, 3B, 4A, 5A, and 7A. These SNP loci explained the phenotype variation associated with the three environments and BLUE, ranging from 2.14 to 9.97 (WW), 2.56 to 8.3 (WL), 1.43 to 9.25 (RF), and 1.27 to 2.15 (BLUE). 【Conclusion】 Further analysis identified five candidate genes that encode peptidyl-prolyl cis-trans isomerase, MATE family protein, cation-chloride cotransporter gene, SRO protein, and flavin-containing monooxygenase. This result enriches the genetic resources for drought resistance and water-saving in wheat, providing a basis for effectively solving the problem of wheat drought at the molecular level.