

WHOLE GENOME WIDE ASSOCIATION ANALYSIS OF MAIZE (*ZEA MAYS L.*) IN RESPONSE TO GLUTAMINE

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Maize (*Zea mays L.*) plays a significant role in global food security and energy consumption. Nitrogen (N), an important macronutrient, exists in soils heterogeneously both as inorganic and organic form. Amino acids, a crucial organic nitrogen source for plants, are not only the structural components of biological proteins but also have biological functions to regulate hormone synthesis, nitrogen transport, resistance to external abiotic stress, and root morphology. Glutamine is an important intermediate in plant nitrogen metabolism. The nitrogen absorbed by plants from the soil is first converted to glutamine, and then to other biomolecules vital for various biological activities of plants. In addition, glutamine as a metabolite of NO is a negative signal for plants to absorb nitrate and induce nitrogen metabolism. Therefore, understanding the molecular and physiological mechanisms of amino acid absorption and transport in maize, using emerging biotechnological and analytical methods, is of great significance. There are large differences in the genomes of maize, which provide a good opportunity to study them using genome-wide association analysis (GWAS). With the development of high-throughput sequencing technology and the application of correlation analysis of plants, genetic basis of amino acid absorption in maize can be further analysed. Use of GWAS combined with genomics and metabolomics and other big data analysis methods for the analysis of amino acid absorption and metabolism in maize becomes worth studying. This study used 510 maize inbred lines under control and glutamine treatment. We found phenotypic indicators related trait of maize varied broadly. There was 2.23-8.96 fold change and 7.76-18.48 fold change SPAD value, shoot dry weight, root dry weight, total dry weight, root length and root to shoot ratio as a whole under control and glutamine treatment, respectively. A set of 27229 high quality SNPs were used to perform GWAS on the diverse panel of 510 maize inbred lines. 6 genetic loci were identified in control whereas 5 genetic loci were identified in glutamine treatment at $p \leq 3.35 \times 10^{-6}$ significant level.

Biography

Huilan Luo has completed her Undergraduate degree from Shihezi University and Masters' degree from China Agriculture University. Currently, she is a PhD student in Department of Plant Nutrition, College of Resources and Environmental Sciences, China Agricultural University, China.

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