

Genome Wide Association of Many Diverse Phenotypes in Nitrogen Limited Field Conditions

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Abstract

Nitrogen inputs can be an important cost consideration for farmers in terms of economic profit as well as environmental impact. Elucidating genetic regions that are associated with plant phenotype response to nitrogen stress can help in facilitating breeding approaches that can mitigate these costs. A diverse population of 272 maize lines was planted at a field site in Champaign, IL in two consecutive years in reduced nitrogen conditions. 302 phenotypes were recorded including: seed ionomic content, root structural traits derived from 2-dimensional images as well as a 3-dimensional representation generated from x-ray computed tomography (XRT) scans, root traits extrapolated from mini-rhizotron systems, drone images across the growing season and end of season agronomic traits such as biomass and yield. BLUP models were fit to obtain estimates of single year genotypic values as well as across years values both of which took into account year specific spatial variation. Individual years and combined years BLUP values were used as response variables in genome wide association studies (GWAS) to identify loci significantly associated with each set of values. Significant associations were identified for all phenotype categories.

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