

Cassava Plant Architecture: Insights from Genome-Wide Association Studies

Authors : Abiodun Olayinka, Daniel Dzidzienyo, Pangirayi Tongoona, Samuel Offei, Edwige Gaby Nkouaya Mbanjo, Chiedozie Egesi, Ismail Yusuf Rabbi

Abstract : Cassava (*Manihot esculenta* Crantz) is a major source of starch for various industrial applications. However, the traditional cultivation and harvesting methods of cassava are labour-intensive and inefficient, limiting the supply of fresh cassava roots for industrial starch production. To achieve improved productivity and quality of fresh cassava roots through mechanized cultivation, cassava cultivars with compact plant architecture and moderate plant height are needed. Plant architecture-related traits, such as plant height, harvest index, stem diameter, branching angle, and lodging tolerance, are critical for crop productivity and suitability for mechanized cultivation. However, the genetics of cassava plant architecture remain poorly understood. This study aimed to identify the genetic bases of the relationships between plant architecture traits and productivity-related traits, particularly starch content. A panel of 453 clones developed at the International Institute of Tropical Agriculture, Nigeria, was genotyped and phenotyped for 18 plant architecture and productivity-related traits at four locations in Nigeria. A genome-wide association study (GWAS) was conducted using the phenotypic data from a panel of 453 clones and 61,238 high-quality Diversity Arrays Technology sequencing (DARTseq) derived Single Nucleotide Polymorphism (SNP) markers that are evenly distributed across the cassava genome. Five significant associations between ten SNPs and three plant architecture component traits were identified through GWAS. We found five SNPs on chromosomes 6 and 16 that were significantly associated with shoot weight, harvest index, and total yield through genome-wide association mapping. We also discovered an essential candidate gene that is co-located with peak SNPs linked to these traits in *M. esculenta*. A review of the cassava reference genome v7.1 revealed that the SNP on chromosome 6 is in proximity to Manes.06G101600.1, a gene that regulates endodermal differentiation and root development in plants. The findings of this study provide insights into the genetic basis of plant architecture and yield in cassava. Cassava breeders could leverage this knowledge to optimize plant architecture and yield in cassava through marker-assisted selection and targeted manipulation of the candidate gene.

Keywords : *Manihot esculenta* Crantz, plant architecture, DARTseq, SNP markers, genome-wide association study

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