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Identification of the Variants for Carotenogenesis Genes in Hexaploid Sweetpotato

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[Introduction]

Sweetpotato (*Ipomoea batatas* [L.] Lam) has a high heterozygous hexaploid genome ($2n = 6x = 90$). According to recent studies, the three diploid subgenomes exhibited a high degree of similarity or were partially homologous. As a major source of carotenoids, the investigation of variants related to the responsive genes is still elusive. Furthermore, obtaining a haplotype-resolved assembly is still a challenge due to the genome complexity. The present study was designed to (i) generate draft assembly (ii) identify carotenogenesis genes and; (iii) their variants structure at nucleotide level.

[Materials and Methods]

The assembly was generated by hifiasm from trimmed Pacbio hifi reads of sweetpotato cv. Jinyulmi. The assembly quality was checked with BUSCO. Afterward, Exonerate and Augustus were employed for homology-based carotenogenesis genic regions detection. To find out potential carotenoid co-linear genes, we performed an ALL vs ALL alignment with NUCmer. Besides, a reads-mapping approach was implemented to dive into variants detection by using Minimap2. In the next step, we extracted reads mapped on the region including the target gene by Samtools view. And then, We chose clean variants (number of reads about per variant > 6) for haplotyping by the command line we made.

[Results and Discussion]

As a result, a genome assembly (99.3% BUSCO) was produced with an N50 of 828,807 bp. The homology-based annotation revealed the presence of carotenogenesis genes including PSY, GGPS, et al. This analysis of some carotenogenesis genes shows variants of homoeologous copies. The preliminary results from this study pave the way for the genetic determinant of color in sweetpotato. Additional variants including diverse accessions will be performed to accurately characterized the genetic basis of color variation in sweetpotato.

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