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Developing a high-density molecular map of the A-Genome species Arachis duranensis

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Although markers have been mapped into linkage groups of both wild and cultivated peanut since the early 1990's, the maps have been extremely low density. To overcome difficulties associated with molecular polymorphism, Expressed Sequence Tag libraries were created to facilitate identifying Simple Sequence Repeats (SSR) and Single Nucleotide Polymorphism (SNP) markers in peanut. Arachis duranensis was used for genetic mapping experiments with the goal of utilizing the data for fine-mapping in the cultivated species. The objectives of this research were to first identify a large number of SSRs and SNPs in peanut and then to map polymorphic markers into linkage groups. Two A. duranensis accessions 15039 were used. Normalized cDNA was produced from leaf and root tissues of both accessions from which 22,356 and 21,487 long-read ESTs from leaves and roots, respectively, were produced for PI 475887 using the Sanger technology. Short-read ESTs also were produced from leaves (212,938 and 296,242 for PI 475887 and Grif. 15039, respectively) and roots (266,575 and 235,245 for PI 475887 and Grif. 15039, respectively). In addition, 2,134 SSR markers developed from an A. hypogaea EST database were evaluated for polymorphism in the two diploid accessions. 2,319 markers were mapped into 10 linkage groups, including 971 SSRs, 221 single-stranded DNA conformation polymorphism (SSCP) markers, and 1,127 SNPs. This represents the first high-density map for a peanut species. The linkages identified in this study will be an invaluable resource for sorting the A and B genomes and linkage relationships in the cultivated species.

ABSTRACT MUST BE RECEIVED BY January 15, 2017
Email Abstract to:
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