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Marker Assisted Backcrossing (MABC) in Peanuts: Identification and Validation of KASPar Markers based on 48K SNP Chip Analysis (*Arachis hypogaea* L.)

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[Introduction]

Peanut (*Arachis hypogaea* L.) is an allopolyploid species cultivated mostly in tropical, subtropical, and warm temperate areas, and it is the world's fourth most significant oilseed crop. The current peanut cultivar is originated from natural hybridization with a polyploid genome and two ancestral species, namely *A. duranensis* and *A. ipaensis*. Marker-assisted backcrossing (MABC) is one of the most effective strategies widely used for gene pyramiding or introgressing the favorable trait from donor to elite line. High oleic acid content (Hae-OI) and High yield (Sewon and Sinpalkwang) is a two major factor and key value-added trait in groundnut which improves the shelf-life of product besides offering nutrition and health benefits to the end-users.

[Materials and Methods]

Korean peanut cultivars Sewon, Sinpalkwang (High yield) and Hae-OI (High oleic acid content) were used and the experiment conducted in the RDA, National Institute of Crop Science, Miryang, Korea. Samples collected on seedlings stage and high-quality of genomic DNA extraction was performed using a Qiagen DNA kit (with minor medications). DNA quality and quantity were check and conducted polymerase chain reaction. *In-silico* analysis, genotyping with the Axiome array we selected best practices work flow and performed QC, SNP pass quality test were selected for further analysis. The high resolution SNPs allele selected based on polymorphism between cultivars. Further, we design 200 KASPar marker and validated.

[Results and Discussion]

High-density SNP array 'Axiom Arachis' with 48K SNPs and their usefulness in the analysis. MABC approach, study aim to improving Korean cultivars Sinpalkwang, Haeol, and Sewon for oleic acid content and yield. Based on the 'Axiom Arachis' 48 K SNPs genotyping, 47,837 total SNP identified, out of it 2060 poly high-resolution based SNP were identified throughout the genome. Furthermore, 758 SNPs were identified among the three genotypes based on high-polymorphism. From the cross1 between Sinpalkwang and Hae-OI, 200 SNP were selected for validation and we observed the 80% polymorphism. Whereas from the second cross between Sewon and Hae-OI, SNPs were selected for validation and 80% polymorphisms were observed. The polymorphic markers that will be used to evaluate peanut MABC and further population are arising in green house in RDA, National Institute of Crop Science, Miryang. In addition, developing the nutritional or dietary cultivars has the potential to deliver far reaching socio-economic benefits to farmers.

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