

Genetic Diversity and Population Structure of Peanut (*Arachis hypogaea* L.) Accessions from Korea, China, and South American Countries

Kunyan Zou¹, Nayoung Kwon¹, Tae-Hwan Jun^{1*}

¹Department of Plant Bioscience, Pusan National University, Miryang, South Korea

[Introduction]

Peanut (*Arachis hypogaea* L.) is an allotetraploid ($2n = 4x = 40$, AABB), and the single recent polyploidization caused significant decrease in genetic diversity. Development of SNP-based markers such as CAPS are widely applied in next-generation sequencing (NGS). This study aimed 1) to evaluate the availability of SNP markers and 2) to identify the peanut genetic diversity and structure populations using molecular markers and 116 peanut accessions from Peru, China, Argentina, Brazil, and Korea for data analyses.

[Materials and Methods]

A total of 116 peanut accessions were obtained from the National Agrobiodiversity Center, Jeonju, South Korea. In 2017, all peanut accessions were planted in a greenhouse at Pusan National University, Miryang, South Korea. Thirteen individual peanut samples from Peru (PRE), thirteen individual peanut samples from China (CHN), sixteen individual peanut samples from Argentina (ARG), twenty-five peanut samples from Brazil (BRA) and forty-nine from Korea (KOR) for the purpose of data analyses.

A total 30 CAPS markers were used for this study. These CAPS markers selected from laboratory developed in 2017, which were derived from 13 different chromosomes (A01, A03, A05, A06, A07, A06, A08; B01, B03, B04, B06, B07, B08). Twenty-eight of the CAPSs were in intergenic and two CAPSs were in coding sequence. PCR product was digested with enzyme (AseI, DraI, HpaII, MseI, MspI, PstI, Taq. I). PCR products and the restriction enzyme-digested PCR products were resolved on 1.5 % agarose gels to detect the polymorphism.

[Results and Discussion]

The UPGMA placed the peanut individuals into two major clusters. Results indicated that one cluster contained five country populations, only eight genotypes from Korea show a small group in this cluster. Most of Korea genotypes grouped mostly in other cluster, while with three exceptions from China and one exceptions from Peru. Genetic diversity indices all show that Korean peanut varieties have fewer common origins with others, while those from the other four regions have more closely related origins. The pattern of PCoA showed a similar result with clusters in UPGMA, peanuts from Korea form a less sticky block with other populations and there is no location-specific grouping between populations BRA and ARG. At $K = 2$, we found maximum Δk , which mainly separates the two types of peanut from Korea and other origins. Another lower peak was shown at $k = 9$, PCoA was also performed on the dataset. The most divergent subgroups by origin were formed at $K = 9$, but 8 subgroups are mixed in origin, which coincided with analysis of the UPGMA tree and PCoA.

In the next study, we will use 384 peanut germplasms including Korean varieties and core collections from USDA for genetic diversity study and genome-wide association analysis.

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*Corresponding author: Tel. +82-55-350-5507, E-mail. thjun76@pusan.ac.kr