Tropentag, September 9-11, 2020, virtual conference

"Food and nutrition security and its resilience to global crises"

Characteristics of PBA Profiling Markers in the Analysis of *Arachis hypogaea* L. Genome

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Abstract

In this study, the PBA technique was utilised to characterise its effectivity to be used for the possible analysis of *Arachis hypogaea* L. genom polymorphism. Three different peanut genotypes were chosen that were characterised previously to have different profiles in iPBS fingerprints. All the genotypes were collected from Chuquisaca Department, Bolivia as original plant sources. The seeds were transferred to the Faculty of Tropical Agrisciences, CULS in Prague, Czech Republic and planted in pots. Young plants were transferred to the AgroBioTech Research Centre; SUA in Nitra, Slovak Republic where biological material was analysed. Three different PBA primer combinations were used in PCRs with the result of generating different PBA fingerprint profiles – CYP1A, CYP2B, and CYP2C. A total of 83 amplicons were generated for the analysed peanut accessions with the highest number of 33 amplicons for marker CYP2C, but for this marker, the lowest percentage of polymorphism was obtained on the level of 60 %. CYP1A marker achieved the polymorphism on the level of 63 % and CYP2B marker on the level of 79 %. CYP1A marker achieved the value of effective number of alleles 1.7634 and the Shannon's Information index 0.6245. CYP2B marker achieved the value of effective number of alleles 1.6500 and the Shannon's Information index 0.5830. CYP2C marker achieved the value of effective number of alleles 1.9780 and the Shannon's Information index 0.6876. None of the markers used in this study has generated the same profile for any of the analysed peanut accessions, that is why all of them should be useful for DNA based profiling of *Arachis hypogaea* L. germplasm, but CYP2B should be used preferably.

Keywords: *Arachis hypogaea*, genome, germplasm, PBA markers, polymorphism

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