CHARACTERISTICS OF PBA PROFILLING MARKERS IN THE ANALYSIS OF *ARACHIS HYPOGAEA* L. GENOME

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Aim

PBA technique was utilized to characterize its effectivity for the purposes of possible analysis of *Arachis hypogaea* L. genome polymorphism. Three different peanut genotypes were chosen that were characterized previously to have different profiles in iPBS fingerprints.

Materials and methods

Biological material: All of the genotypes were taken in Chuquisaca Department, Bolivia. Three different PBA primer combination were used in PCRs with the result of generating different PBA fingerprint profiles – CYP1A, CYP2B and CYP2C.

Results

A total of 83 amplicons were generated for the analysed peanut accessions with the higher 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 allelles 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 allelles 1.9780 and the Shannon's Information index 0.6876. See figure 1 and table 1.
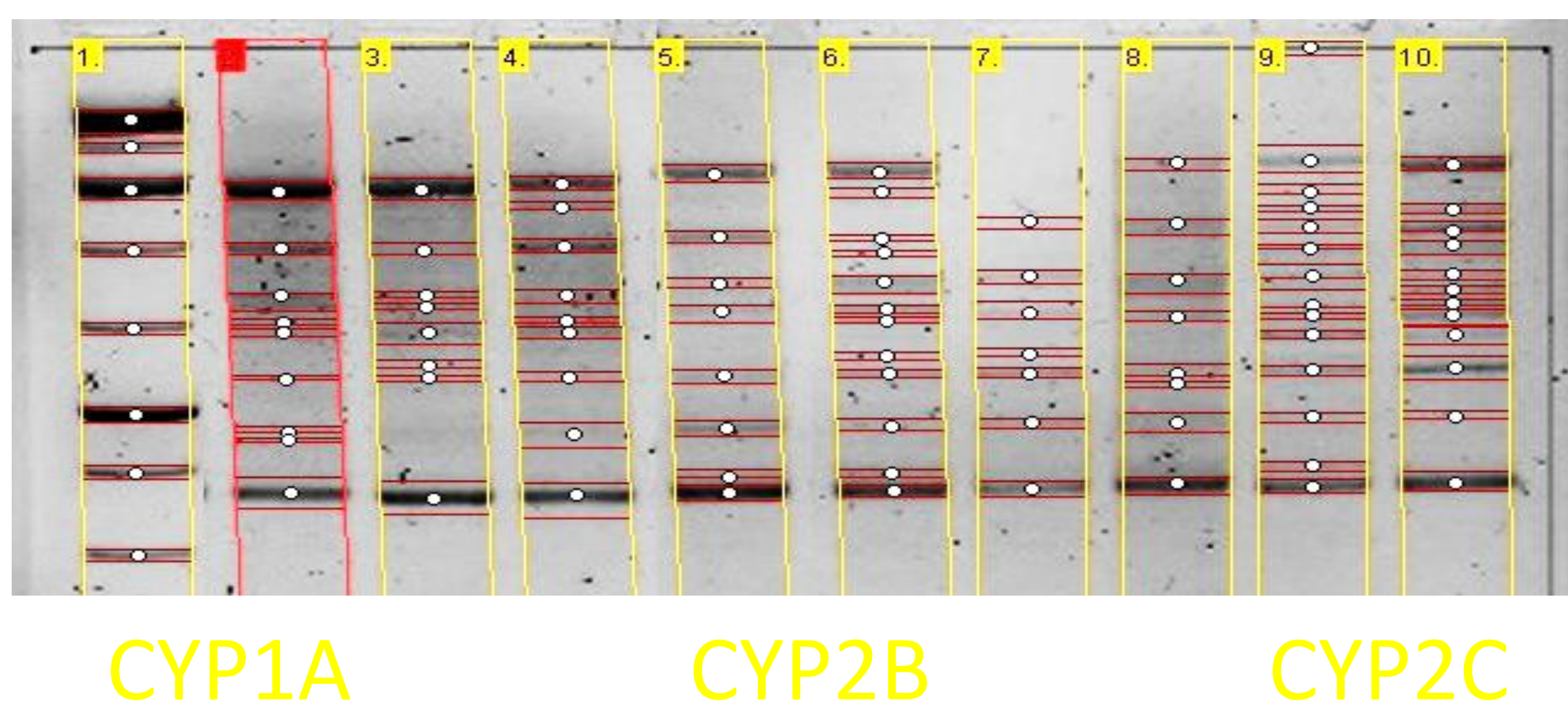

CYP1A   CYP2B   CYP2C

Figure 1: Three different PBA primer combination were used in PCRs with the result of generating different PBA fingerprints

Table 1: Characteristics of markers used in the study

MARKER/DATA	POLYMORPHISM	SHANNON'S INFORMATION INDEX	EFFECTIVE NUMBER OF ALLELLES
CYP1A	63 %	0.62	1.76
CYP2B	78 %	0.58	1.65
CYP2C	60 %	0.69	1.98

Conclusion

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 preferable.