B-92: Search for RAPD markers linked to the sex expression in *Carica papaya*

E Niroshini[1], J M D T Everard[2], T L S Tirimanne[1], E H Karunanayake[3]
([1]*Dept of Botany, Faculty of Science, University of Colombo, Colombo 3,* [2]*Coconut Research Institute, Lunuwila,* [3]*Dept of Biochemistry, Faculty of Medicine, University Colombo, Colombo 8)*

Papaya (papaw) is dioecious, but hermaphrodite flowers and trees also occur. Sex in papaya is determined by 3 alleles, M_1 (dominant for male) M_2 (dominant for hermaphrodites) and m (recessive for female) where any diploid zygote with 2 dominant alleles cannot survive. Female plants produce large fruits of good flesh while bisexual trees produce uniform and medium sized fruits. Papaya is largely propagated by seeds and unproductive male plants are culled at the flowering stage after transplanting (3-4 plants per hole). Fruit characteristics being sex-dependent, a non-male population or a method for early identification of males is a major goal in papaya variety development. We report the success achieved in detection of RAPDs linked to sex locus in a study aimed towards developing an early sexing mechanism for papaya.

DNA was isolated from immature leaf tissue from 6 individuals each from male and female papaya trees using the procedure described by Doyle and Doyle. Male and female DNA was bulked and used in the RAPD-PCR with 60 Operon primers. All DNA profiles obtained by amplifying male and female DNA bulks were scored for both strongly and faintly amplified bands.

Among the 60 primers tested 26 primers detected a total of 55 polymorphisms between male and female papaya of which 5 appeared markedly strong in amplification. The other bands however, cannot be ruled out because they too can be made strong and reproducible by slight adjustments to the RAPD-PCR protocol.

The number of sex linked polymorphisms detected in papaya is remarkable indicating a strong likelihood of picking at least one or two loci with tight linkage to the sex locus. By assessing Mendelian segregation of these bands in male, female and bisexual parents and in F_1, BF_1, F_2 and BF_2 progenies, markers that satisfy required linkage to facilitate marker assisted selection of the papaya sex could be ascertained. Furthermore, this technique can be made more authentic by sequencing tightly sex linked fragments and by designing slightly longer and specific primers for use in the PCR.

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