

Marker assisted breeding in Coconut (*Cocos nucifera* L.)

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Abstract: Coconut improvement is a highly complicated and time consuming process. Breeding coconut for any desirable traits is hindered by the long generation time, low multiplication rate, ineffective clonal propagation, etc. Hence marker assisted breeding is the need of the hour for crop improvement programmes in coconut. Assessment of genetic diversity is an essential component in germplasm characterisation and utilisation. Markers such as RAPD, SSR, etc. are being utilized for assessing genetic diversity and interrelationships among coconut cultivars. SSR, RAPD and microsatellite markers associated with several resistance genes like mite resistance, resistance to lethal yellowing etc. are being utilised in coconut breeding programmes. Molecular markers closely linked to specific traits provide the opportunity to select promising genotypes at early seedling stage itself through marker assisted selection.

Key words: coconut, breeding, marker, variability, resistance, primer, RAPD, SSR, microsatellite

INTRODUCTION

Coconut (*Cocos nucifera* L.), popular as *kalpa vriksha*, is a versatile tree with myriad uses. Owing to its importance to the rural communities, it has been termed 'tree of life' since from the root to the frond all parts of the coconut palm are utilized for either nutritional or non-food purposes (Persley, 1992). Coconut improvement is a highly complicated and time consuming process. Breeding coconut for any desirable traits is hindered by several reasons viz., long juvenile period, long interval between generations, heterozygous nature, large area and long period for experimentation, low multiplication rate, ineffective clonal propagation, etc. Hence marker assisted breeding is the need of the hour for crop improvement programmes in coconut. Molecular markers closely linked to specific traits provide the opportunity to select promising genotypes even at early seedling stage itself through marker-assisted selection. Application of molecular marker technology in coconut breeding especially for assessing genetic diversity and resistance breeding is briefly reviewed hereunder.

APPLICATIONS OF MARKER TECHNOLOGY IN COCONUT

Marker technology is utilized for different purposes in coconut conservation and improvement. The major applications are in the assessment of genetic diversity and resistance breeding,

1 Assessment of genetic diversity

Assessment of genetic diversity is an essential component in germplasm characterisation and utilisation. Molecular markers are the appropriate choice to study and preserve the diversity in germplasm collections. DNA markers can be used to diagnose the presence of the gene without having to wait for gene effect to be seen (Peterson *et al.*, 1991). Various DNA marker technologies have been applied in coconut biodiversity analysis through DNA fingerprinting as shown in Table 1.

Table 1. Marker technology employed in coconut for biodiversity analysis

Sl. No.	Marker	Reference
1	Randomly Amplified Polymorphic DNA (RAPD)	Ashburner <i>et al.</i> , 1997.
2	Restriction Fragment Length Polymorphism (RFLP)	Lebrun <i>et al.</i> , 1998.
3	Simple Sequence Repeat (SSR)	Perera <i>et al.</i> , 1999.
4	Inverse Sequence-Tagged Repeat (ISTR)	Rohde <i>et al.</i> , 199; Duran <i>et al.</i> , 1997.
5	Amplified Fragment Length Polymorphism (AFLP)	Perera <i>et al.</i> , 1998.

Genetic relationship and diversity among fifteen Indian and five exotic coconut accessions were analysed based on RAPD markers by Anuradha *et al.* (2004). The 8 primers yielded 77 markers, with an average of 9.6 markers per primer. In general, tall accessions were more heterozygous as they had higher proportions of polymorphic bands and genetic diversity.

The genetic interrelationships among 33 coconut germplasm accessions collected from various coconut growing regions were analysed using RAPD markers by Manimekalai and Nagarajan (2006). Genetic diversity among and within Brazilian Tall coconut populations was accessed by investigating 13 simple sequence repeats (SSR) loci (Ribeiro *et al.*, 2010). Genetic variability of ten coconut (*Cocos nucifera* L.) accessions from six locations in Hainan province, China was assessed by 26 microsatellite (SSR) markers by Liu *et al.* (2011).

2. Resistance Breeding

Coconut palm is highly susceptible and sensitive to various biotic and abiotic stresses. Planting resistant coconut cultivars is the most effective method of preventing yield loss and should form a major component of any integrated pest management strategy. Markers associated several resistance genes like mite resistance and resistance to lethal yellowing are being employed in coconut breeding programmes.

a. Mite resistance

Markers linked with mite resistance will facilitate the selection of mite resistant plants as well as mother plants at an early stage for breeding programmes. Nine SSR and four RAPD markers associated with mite resistance have been identified in a study employing coconut genotypes collected from various parts of South India by Shalini *et al.* (2007).

b. Lethal yellowing

Apart from fungal, bacterial, viral and viroidal pathogens attacking and causing substantial to losses in coconut, phytoplasma causing “lethal disease” or “lethal yellowing” is the most devastating pathogen in coconut. The only effective method for controlling lethal yellowing is replanting with resistant germplasm. Identification of RAPDs associated with resistance to lethal yellowing of the coconut (*Cocos nucifera* L.) palm was reported by Cardeña *et al.* (2003). Genetic differences between the tolerant genotypes Vanuatu Tall and Sri-Lanka Green Dwarf and the susceptible genotype West African Tall to lethal yellowing disease has been evaluated using twelve microsatellite markers (Konan *et al.*, 2007).

REFERENCES

- Anuradha U., Jayadev K., Manimekalai R. and Parthasarathy V.A., 2004. Genetic relationship and diversity in Indian coconut accessions based on RAPD markers. *Sci. Hort.* 99 (3-4): 353-362.
- Ashburner G.R., Thompson W.K. and Halloran G.M., 1997. RAPD analysis of South Pacific coconut palm populations. *Crop Sci.* 37:992-997.
- Cardeña R., Ashburner G.R. and Oropeza C., 2003. Identification of RAPDs associated with resistance to lethal yellowing of the coconut (*Cocos nucifera* L.) palm. *Sci. Hort.* 98 (3): 257-263.
- Duran Y., Rohde W., Kullaya A., Goikoetxea P. and Ritter E., 1997. Molecular analysis of East African Tall coconut genotypes by DNA marker technology. *J. Genet. Breed.* 51: 279-288.
- Konan K.J.N., Koffi K. E., Konan J.L., Lebrun P., Dery S. K. and Sangare A., 2007. Microsatellite gene diversity in coconut (*Cocos nucifera* L.) accessions resistant to lethal yellowing disease. *African J. Biotech.* 6 (4): 341-347.
- Manimekalai R. and Nagarajan P., 2006. Interrelationships among Coconut (*Cocos Nucifera* L.) accessions using RAPD technique. *Genetic Resources and Crop Evolution* 53 (6): 1137-1144.
- Lebrun P., N'Cho Y.P., Seguin M., Grivet L. and Baudouin L., 1998. Genetic diversity in coconut (*Cocos nucifera* L.) revealed by restriction fragment length polymorphism (RFLP) markers. *Euphytica* 101:103-108.
- Liu X., Tang H., Li D. and Hou L., 2011. Genetic diversity of coconut cultivars in China by microsatellite (SSR) markers. *Mol. Pl. Breed.* 2(12): 83-91.

Perera L., Russell J.R., Provan J., McNicol J.W. and Powell W., 1998. Evaluating genetic relationships between indigenous coconut (*Cocos nucifera* L.) accessions from Sri Lanka by means of AFLP profiling. *Theor. Appl. Genet.* 96:545–550.

Perera L., Russell J.R., Provan J. and Powell W., 1999. Identification and characterisation of microsatellite loci in coconut (*Cocos nucifera* L.) and the analysis of coconut populations in Sri Lanka. *Mol. Ecol.* 8:344–346.

Persley G.J. 1992. Replanting the Tree of Life. Cab Int., Wallingford, UK.

Peterson A. H., Tanksley S. D. and Sorrels M. E., 1991. DNA markers in plant improvement. *Adv. Agron.* 46:39-90.

Ribeiro F.E., Baudouin L., Lebrun P., Chaves L.J., Brondani C., Zucchi M.I., and Vencovsky R., 2010. Population structures of Brazilian tall coconut (*Cocos nucifera* L.) by microsatellite markers. *Genet. Mol. Biol.* 33 (4): 696-702.

Rohde W., Kullaya A., Rodriguez J. and Ritter E., 1995. Genetic analysis of *Cocos nucifera* L. by PCR amplification of spacer sequences separating a subset of *copia*-like *EcoRI* repetitive elements. *J. Genet. Breed.* 49:179–186.

Shalini K.V., Manjunatha S., Lebrun P., Berger A., Baudouin L., Pirany N., Ranganath R.M. and Theertha Prasad D., 2007. Identification of molecular markers associated with mite resistance in coconut (*Cocos nucifera* L.). *Genome National Research Council Canada* 50 (1): 35-42.