GENETIC FIDELITY ASSESSMENT OF TISSUE CULTURE-DERIVED Neolamarckia cadamba PLANTLETS USING DNA-BASED MARKERS

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ABSTRACT

Neolamarckia cadamba is one of the fast-growing tree species selected for industrial tree plantations (ITPs). As demand and supply of true-to-type planting material are increasing, micropropagation of elite *N. cadamba* planting material is required for the sustainable development of ITPs. However, somaclonal variation among tissue culture-derived plantlets is a bottleneck in micropropagation. The present study described the genetic fidelity of *in vitro* regenerated *N. cadamba* plantlets from first, second, third and sixth subcultures. These plantlets were obtained from axillary shoot multiplication and repeated subcultures of microshoots with three weeks interval period, which initially developed from nodal explants. By using five random amplified length polymorphism (RAPD) and two inter-simple sequence repeats (ISSR) primers, a total of 9,334 bands and 2,760 bands were amplified respectively, from a total number of 164 tested plantlets. The banding profiles for each primer was highly uniform, and the DNA bands were monomorphic across all tissue culture-derived plantlets from every four subcultures compared to the stock plants. A target gene-specific marker was also employed to detect single nucleotide polymorphism (SNP) within the targeted genomic sequence of *Susy* gene. There was no SNP detected from all the analysed plantlets. The current findings ascertained the efficiency and reliability of the *N. cadamba* micropropagation protocol at least up to six subculture cycles for mass production of true-to-type plantlets.

Key words: Neolamarckia cadamba, genetic fidelity, DNA marker, SNP, micropropagation

INTRODUCTION

Micropropagation of Neolamarckia cadamba (Roxb.) Bosser is vital for large scale commercial production of quality planting material for industrial tree plantations (ITPs) in Malaysia in order to fulfil the increasing demand for timber in future. This tree species is belonging to Rubiaceae family and widely distributed in South Asia and Southeast Asia, such as Malaysia, Indonesia, China, India, Thailand, Vietnam and Papua New Guinea (Krisnawati et al., 2011; Tchin et al., 2018). It is a light hardwood species that frequently harvested as raw materials for plywood, hardboard, paper, and furniture. It is also used for ornamental purposes, while its leaf and fruit extracts and dried bark are used for pharmaceutical purposes (Zaky et al., 2014; Dwevedi et al., 2015; Pandey & Negi, 2016).

Micropropagation is a well-established plant tissue culture technique that adopted to propagate commercially important plants by using part of the plants as explants. This technique is widely used for rapid clonal propagation in order to supply a large scale of planting material for afforestation and elite genotypes preservation (Kataria et al., 2013; Alizadeh et al., 2015). Hence, a high degree of genetic fidelity among the tissue culture-derived plantlets is very critical. The somaclonal variations could be detected in tissue culture-derived plantlets, which is the major bottleneck in the micropropagation of plants. Level of plant growth regulators, types of explants, time in tissue culture conditions and subculture number are frequently reported as the main factors of this variation (Bairu, 2011; Krishna et al., 2016). It is reported that shoot proliferation from explants with pre-existing meristems poses a lower genetic instability risk (Mohanty et al., 2012; Behera et al., 2018). Besides,

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studies have shown that prolonged inorganized cell cultures are prone to somaclonal variations than shoot cultures (Khan *et al.*, 2011; Devi *et al.*, 2014). Somaclonal variations are often heritable and represent permanent genetic changes that occurred within the genetic makeup of propagated plantlets (Leva *et al.*, 2012; Kasim *et al.*, 2018). Such changes may lead to the loss of desired traits from the mother plants and produce variants that are not accepted by the end-users (Krishna *et al.*, 2016).

DNA-based markers provide several benefits for genetic fidelity assessment of in vitro regenerated plants, such as high accuracy, environmental factors independent, high reliability and reproducibility (Kamle et al., 2014; Alizadeh et al., 2015). RAPD and ISSR are the common markers that widely applied for genetic uniformity assessment of plantlets in several genera derived from in vitro cultures (Kumar et al., 2011; Ahmed et al., 2017). They are easy to use and highly cost-effective, no requirement for radioactivity (Roostika et al., 2016). Although RAPD markers can produce a large number of loci, it also has a limited reproducibility (Costa et al., 2016). Besides RAPD and ISSR, the advances in DNA sequencing technology enable evaluation of genetic variation up to nucleotide level. SNP polymorphisms are identified through direct sequencing of DNA segments obtained by PCR amplification (Rafalski, 2002). This method allows reliable detection of SNPs; however, it requires enormous effort for the development of specific primers and a large number of samples needed to be amplified and sequenced (Ganal et al., 2009). A combination of different markers is efficient for genetic fidelity analysis as different regions of the whole DNA sequence are amplified (Martins et al., 2004).

The estimation of genetic diversity and relatedness of the selected N. cadamba trees from six natural forests and two planted forests in Sarawak had been reported using RAPD and ISSR markers (Tan et al., 2007; Tiong et al., 2014). However, there is no published report on the genetic fidelity assessment of tissue culture-derived plantlets of N. cadamba to date. Hence, the objective of this study was to assess the genetic fidelity of N. cadamba plantlets using DNA-based markers, namely: RAPD, ISSR and SNP markers. The plantlets of N. cadamba were propagated through direct shoot organogenesis by using nodal explants from in vitro-germinated seedlings of selected candidate plus tree. The subcultures of microshoots were done at three weeks interval period up to six times. Genetic fidelity assessment of tissue culturederived plantlets at an early stage can assist in getting rid of genetically unstable seedlings, and thus reducing the maintenance cost in the field until maturity.

MATERIALS AND METHODS

Shoot multiplication and plantlet regeneration

Shoot culture was established through direct shoot organogenesis by using nodal explants of N. cadamba seedlings from selected candidate plus tree. Briefly, the explants were cultured in Gamborg B5 medium supplemented with 0.8 mg/L of Benzylaminopurine (BAP). Four in vitro seedlings were selected as stock plants based on their vigorous growth and then subcultured as nodal cultures. This was denoted as Subculture 1 (S1). The microshoots that less than 1 cm height after four weeks were excised and then subcultured into the new fresh medium with the same composition of nutrients and BAP (S2). Subcultures of microshoots were conducted every three weeks. The shoots were then rooted in Gamborg B5 medium supplemented with 0.1 mg/L of Paclobutrazol (PBZ) for four weeks.

DNA extraction and molecular analysis

The fresh young leaves from four stock plants and 160 randomly selected plantlets from four subcultures (S1, S2, S3 and S6) of the respective stock plants were collected and used as a source of DNA to assess genetic fidelity of the plantlets after repeated subculturing. The total genomic DNA was extracted from fresh leaf samples as prescribed by Murray and Thompson (1980).

RAPD-PCR amplification

Five RAPD primers from the previous study (Tan *et al.*, 2007), namely OPA-05, OPA-08, OPA-10, OPA-15 and OPB-20, were used to evaluate the genetic fidelity of the plantlets. The 25 μ L PCR reaction mixture containing 1 ng DNA, 2.5 mM MgCl₂, 10.0 pmol/ μ L of primer, 1.0 unit of *Taq* DNA polymerase, 0.2 mM dNTPs and 1× PCR buffer. The thermal cycling profile was programmed with an initial denaturation at 94°C for 3 minutes and then 45 s in 35 cycles, annealing at 40°C for 60 s, extension at 72°C for 1 min and final extension for 7 min at 72°C.

ISSR-PCR amplification

Two ISSR primers from the previous study (Tiong *et al.*, 2014), which are $(GTG)_6$ and $(AC)_{10}$ were used to amplify the ISSR regions. The PCR amplifications were carried out in 25 µL reaction mixtures that containing 1 ng DNA, 2.5 mM MgCl₂, 10.0 pmol/µL of primer, 0.5 unit of *Taq* DNA polymerase, 0.2 mM dNTPs and 1× PCR buffer. The thermal cycling profile was programmed with initial denaturation at 95°C for 2 min and then 30 s in 40 cycles, the annealing of the primer (GTG)₆ and (AC)₁₀ at temperature of 60 and 57.8°C respectively for 30 s, extension at 72°C for 1 min and final extension for 10 min.

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Target gene-specific PCR amplification and DNA sequencing

For further validation, the stock plants and their plantlets from each subculture (S1, S2, S3 and S6) were subjected for target gene-specific PCR amplification. PCR amplification of *Susy* gene was performed as prescribed by Tan *et al.* (2014). The PCR products were then sent for sequencing in both forward and reverse directions.

Data analysis

The amplified products from the RAPD and ISSR primers were resolved through 1.5% agarose gel electrophoresis. The patterns of bands were documented via Geliance 200 Imaging System (PerkinElmer, USA). The pattern of amplicons was compared between the stock plants and plantlets, which then manually scored. For sequence variation analysis, the raw data of DNA sequences were checked to remove low-quality base calling sequences by using Unipro UGENE 1.31 (UniPro, Russia). The partial *SuSy* genomic sequences from each stock plant and their plantlets were aligned to detect the presence of single nucleotide polymorphisms.

RESULTS

RAPD and ISSR analysis

All the five RAPD primers and two ISSR primers were found capable of generating reproducible, distinct and scorable bands (Table 1). A total of 9,334 bands and 2,760 bands (total number of scorable bands \times total number of analysed plants) were generated by the RAPD markers and ISSR markers, respectively. All the bands produced were monomorphic across all the tissue culture-derived plantlets from all the four passages. The RAPD and ISSR banding profiles are shown in Figure 1(a, b) and Figure 1(c, d), respectively. The average number of scorable loci for each RAPD primer was varied from 9.8 to 13.0, with sizes ranged from 250 to 4,000 bp. Based on the fingerprinting profiles from the four stock plants, the five RAPD primers produced 56.8 scorable loci, with a mean of 11.4 loci per primer. Similarly, the average number of detectable loci from each ISSR primer was ranging from 8.0 to 8.5 within the size range of 600 to 2,500 bp. An average of 16.5 distinct and scorable bands was obtained from the two ISSR primers, with a mean of 8.3 loci per primer.

Target gene-specific PCR analysis

Sequence analysis was carried out to determine the nucleotide variation within the sequence of a selected gene in *N. cadamba* plantlets and the stock plants. The partial *SuSy* genomic sequence with a length of 708 bp was amplified and sequenced from four stock plants and 80 plantlets from four passages. The consensus sequences from the stock plants and plantlets were aligned to detect the presence of SNPs. No nucleotide polymorphism was detected among the analysed plantlets since these plantlets were derived from the respective stock plant. The alignment of partial *SuSy* genomic sequences from the four stock plants was also performed and found no variation among them. A part of the partial *SuSy* gene sequence alignment is shown in Figure 2.

DISCUSSION

For commercial utility, micropropagation is known to generate a mass number of clones from desired germplasms, which results in plantlets that are theoretically identical to the donor plant. However, the hindrance of micropropagation is frequently due to the *in vitro* stresses that might result in genetic instability of tissue culture-derived plantlets that commonly known as the somaclonal variation (Bello-Bello *et al.*, 2014; Akdemir *et al.*, 2016).

Table 1. Summary of RAPD and ISSR primers with their amplification products from four stock plants and 160 tissue culture-derived plantlets selected from four subcultures (S1, S2, S3 and S6)

Primer		T _a (°C)	Mean no. of loci	Size range	Polymorphic band (%)			
	Primer sequence (5'-3')			(bp)	S1	S2	S3	S6
RAPD:								
OPA-05	AGGGCTCTTG	40.0	13.0	400-2000	0.0	0.0	0.0	0.0
OPA-08	GTGACGTAGG	40.0	9.8	250-2500	0.0	0.0	0.0	0.0
OPA-10	GTGATCGCAG	40.0	12.5	400-4000	0.0	0.0	0.0	0.0
OPA-15	TTCCGAACCC	40.0	11.3	600-3500	0.0	0.0	0.0	0.0
OPB-20	GGACCCTTAC	40.0	10.3	750-3500	0.0	0.0	0.0	0.0
ISSR:								
GTG ₆	GTGGTGGTGGTGGTGGTG	60.0	8.5	600-2500	0.0	0.0	0.0	0.0
AC10	ACACACACACACACACACAC	57.8	8.0	700-2500	0.0	0.0	0.0	0.0



Fig. 1. PCR amplification profiles obtained by a) OPA-08, b) OPB-20, c) GTG_6 , and d) AC_{10} for the stock plant, N5(14) and tissue culture-derived plantlets. Lane M, stock plant; Lanes 1-10, tissue culture-derived plantlets from axillary shoot multiplication. Lane L1, 1 kb ladder; Lane L2, 100 bp ladder.

		620		640		660		
N5(14)-SUSY	AAGTATOGOA	AGTTGGTGAG	TTOTTOTGTO	CTGGTCACTC	TGCATTGTTT	CTGCGTTCCT	CGTTCAAAAC	
N5(14)S1(6)-SUSY	AAGTATCGCA	AGTTGGTGAG	TTCTTCTGTC	CTGGTCACTC	TGCATTGTTT	CTGCGTTCCT	CGTTCAAAAC	
N5(14)S1(7)-SUSY	AAGTATCGCA	AGTTGGTGAG	TTCTTCTGTC	CTGGTCACTC	TGCATTGTTT	CTGCGTTCCT	CGTTCAAAAC	
N5(14)S1(8)-SUSY	AAGTATCGCA	AGTTGGTGAG	TTCTTCTGTC	CTGGTCACTC	TGCATTGTTT	CTGCGTTCCT	CGTTCAAAAC	
N5(14)S1(9)-SUSY	AAGTATCGCA	AGTTGGTGAG	TTCTTCTGTC	CTGGTCACTC	TGCATTGTTT	CTGCGTTCCT	CGTTCAAAAC	
N5(14)S1(10)-SUSY	AAGTATCGCA	AGTTGGTGAG	TTCTTCTGTC	CTGGTCACTC	TGCATTGTTT	CTGCGTTCCT	CGTTCAAAAC	
N5(14)S2(6)-SUSY	AAGTATCGCA	AGTTGGTGAG	TTCTTCTGTC	CTGGTCACTC	TGCATTGTTT	CTGCGTTCCT	CGTTCAAAAC	
N5(14)S2(7)-SUSY	AAGTATCGCA	AGTTGGTGAG	TTCTTCTGTC	CTGGTCACTC	TGCATTGTTT	CTGCGTTCCT	CGTTCAAAAC	
N5(14)S2(8)-SUSY	AAGTATCGCA	AGTTGGTGAG	TTCTTCTGTC	CTGGTCACTC	TGCATTGTTT	CTGCGTTCCT	CGTTCAAAAC	
N5(14)S2(9)-SUSY	AAGTATCGCA	AGTTGGTGAG	TTCTTCTGTC	CTGGTCACTC	TGCATTGTTT	CTGCGTTCCT	CGTTCAAAAC	
N5(14)S2(10)-SUSY	AAGTATCGCA	AGTTGGTGAG	TTCTTCTGTC	CTGGTCACTC	TGCATTGTTT	CTGCGTTCCT	CGTTCAAAAC	
N5(14)S3(6)-SUSY	AAGTATOGOA	AGTTGGTGAG	TTETTETGTE	CTGGTCACTC	TGCATTGTTT	CTGCGTTCCT	CGTTCAAAAC	
N5(14)S3(7)-SUSY	AAGTATCGCA	AGTTGGTGAG	TTCTTCTGTC	CTGGTCACTC	TGCATTGTTT	CTGCGTTCCT	CGTTCAAAAC	
N5(14)S3(8)-SUSY	AAGTATCGCA	AGTTGGTGAG	TTCTTCTGTC	CTGGTCACTC	TGCATTGTTT	CTGCGTTCCT	CGTTCAAAAC	
N5(14)S3(9)-SUSY	AAGTATCGCA	AGTTGGTGAG	TTCTTCTGTC	CTGGTCACTC	TGCATTGTTT	CIGCGIICCI	CGTTCAAAAC	
N5(14)S3(10)-SUSY	AAGTATCGCA	AGTTGGTGAG	TTOTTOTOTO	CIGGICACIC	TGCATIGITI	CIGCGIICCI	CGTTCAAAAC	
N5(14)S6(6)-SUSY	AAGTATUGUA	AGTTGGTGAG	TTUTTUTGTU	GIGGICACIC	TGCATIGITI	CIGCGITCCI	CGTTCAAAAC	
N5(14)S6(7)-SUSY	AAGTATUGUA	AGTTGGTGAG	TTOTTOTOTO	GIGGICACIC	TGCATIGITI		CGTTCAAAAC	
N5(14)50(0)-5051	AAGTATOGOA	AGTTGGTGAG	TTOTTOTOTO	OTCOTOACTO	TOCATTOTT	OTCOCTTOCT	CGTTCAAAAO	
N5(14)56(9)-5051	AAGTATUGUA	AGTTGGTGAG	TTETTETCTE	OTGGTCACTC	TGCATTGTTT	ercectreet	CGTTCAAAAO	
145(14)50(10)-5051	AAGTATUGUA	AGTIGGIGAG	TTOTTOTOTO	OTGOTOAOTO	TGOATTGTTT		GITGAAAAG	
Consensus	AAGTATCGCA	AGTIGGTGAG	TICTICTGTC	CIGGICACTC	IGCAITGTTT	CIGCGTTCCT	CGIICAAAAC	
Conservation								

Fig. 2. A Part of the alignment result for the partial genomic sequences of *SuSy* gene from the stock plant, N5(14) and tissue culture-derived plantlets.

Somaclonal variations with frequency ranging from 60% to 98% had been documented in several reports on plantlets that regenerated from apical meristems and axillary buds (Phulwaria *et al.*, 2014; Werner *et al.*, 2015; Venkatachalam *et al.*, 2018). Genetic variations may arise among the plantlets considering the factors that associated with tissue culture conditions, such as the type of explants and regeneration pathway (Linacero *et al.*, 2000; Bramhanapalli *et al.*, 2017). In the present investigation, propagation for *N. cadamba* was

through direct axillary shoot organogenesis from nodal explants and no variation in all the DNA profiles generated. This regeneration pathway from organised meristematic cells without any intermediate callus formation is known to produce plantlets in mass amount within a short span of time with high genetic integrity and fidelity, and hence it is likely to be selected for mass production of quality planting materials with desired economic traits (Saha *et al.*, 2014; Behera *et al.*, 2018).

Several publications inferred that somaclonal variations result from interactions of three main factors which are the initial explants, genotype and in vitro culture conditions. For clonal propagation of N. cadamba with the absence of somaclonal variations, a low BAP concentration was used for axillary proliferation and subcultures of microshoots, while a low PBZ concentration was used for rooting in the present study. According to Farahani et al. (2011) and Khan et al. (2011), plant growth regulators are reported to be associated with somaclonal variations in tissue culture-derived plantlets. However, Venkatachalam et al. (2007) had shown that exposure to a high level of cytokinins up to 10 mg/L of banana cv. Nanjanagudu Rasabale (AAB) culture did not lead to genetic variation in all the plantlets screened. In contrast, a high concentration of BAP had resulted in chromosomal number variation in banana cultivar 'Williams' (Halim et al., 2018).

Findings from several reports had shown that the number of subcultures and the length of the culture period are associated with the occurrence of somaclonal variants, which the higher the number of subcultures and the longer the culture period, the higher the frequency of polymorphisms (Khan et al., 2011; Zoghlami et al., 2012; Devi et al., 2014). It is suggested that increase in culture duration is causing the cells or tissues being frequently exposed to in vitro environmental factors as well as various chemicals including plant growth regulators that lead to somaclonal variations (Turner et al., 2001; Peng et al., 2015). Conversely, some studies revealed that the level of subculture and culture duration did not affect the genetic integrity of tissue culture-derived plantlets, especially among regenerated plantlets obtained through shoot cultures and axillary branching (Gantait et al., 2010; Asthana et al., 2011; Chhajer & Kalia, 2016), which are in concordance with the present findings.

The genetic fidelity of the regenerated N. cadamba was confirmed by using five RAPD and two ISSR markers in the current study. Many studies on the molecular characterisation of micropropagated plantlets are conducted, especially in the assessment of clonal fidelity among the regenerated plants and donor plants by adopting the RAPD and ISSR techniques. Lattoo et al. (2006) had reported the 100% similarity among the Chlorophytum arundinaceum plantlets and the mother plant by using five RAPD marker. In a study by Kumar et al. (2013), the genetic uniformity of the micropropagated Catharanthus roseus plantlets was confirmed by five RAPD markers with no variation was detected. By using the cytogenetic and RAPD analysis from three primers, the genetic uniformity of regenerated Iris sibirica plantlets with identical profiles had been assessed in a study by

Stanišiæ *et al.* (2015). Sharma *et al.* (2014) and Ramírez-Mosqueda *et al.* (2016) had shown a high genetic homology among the *Tylophora indica* and *Stevia rebaudiana* plantlets, respectively after the genetic fidelity evaluation via six ISSR primers. Besides that, the true-to-type of *Citrullus lanatus* plantlets was ascertained by six ISSR markers in the report by Vinoth and Ravindhran (2016).

Three different DNA marker systems were used for genetic fidelity assessment in the present study. It is suggested that a combination of different markers is efficient for genetic fidelity assessment as different regions of the genome are amplified and compared (Martins et al., 2004). The numbers of RAPD bands (11.4 loci per primer) and ISSR bands (8.3 loci per primer) were fairly high when compared with the reports on the other species. Therefore, the number of bands amplified in the current study seemed to be sufficiently satisfied with the evaluation of genetic fidelity among the N. cadamba plantlets. Bhatia et al. (2011) detected an average of 5.5 and 4.5 bands per primer from ten ISSR primers and twelve RAPD primers, respectively in the genetic stability assessment of in vitropropagated gerbera. Saha et al. (2012) reported that an average of 4.11 fragments was obtained from nine RAPD primers. By using 31 RAPD and 11 ISSR primers, the average numbers of 2.96 and 4.81 bands per primer were generated in another study by Saha et al. (2014).

The PCR amplicons obtained in the present study were sequenced in both forward and reverse directions and aligned to distinguish the true single nucleotide polymorphisms (SNPs) from sequencing errors. SNPs are found in non-coding regions of the genome such as 3' untranslated regions (UTRs), introns and repetitive sequences; including in most of the coding sequences (Agarwal et al., 2008; Chagné et al., 2008). There was no SNP detected within the 708 bp of partial genomic sequence sucrose synthase (SuSy) gene among the analysed stock plants and plantlets. SuSy is a key enzyme that catalyses the reversible synthesis and degradation of sucrose (Carlson et al., 2002; Tan et al., 2014). Coleman et al. (2009) implicated that overexpression of SuSy gene resulted in increased cellulose synthesis in the secondary cells, which demonstrated the tight association of SuSy gene with cellulose production and secondary cell wall formation. The SNP result further verifies the genetic integrity of regenerated N. cadamba plantlets from micropropagation technique. Due to the same clonal origin, it is expected that no sequence variation should be detected between the plantlets and their respective mother plant (Negi & Saxena, 2010).

Several studies had been reported that tissue culture conditions might cause stresses to the plantlets and results in the development of variants that manifested from errors occurred in cellular control during plant regeneration process (Ruffoni & Savona, 2013; Khatun *et al.*, 2018). The tissue culture-induced genetic changes including activation of transposon elements, chromosome rearrangements, duplication and point mutations such as base deletion, insertion, and substitution (Bairu *et al.*, 2011; Krishna *et al.*, 2016). The changes occurred within the genome, especially the gene coding regions may result in the generation of off-type plantlets.

CONCLUSION

To the best of our knowledge, this is the first report on the genetic fidelity assessment of tissue culturederived plantlets of N. cadamba using DNA-based markers. The present study also successfully demonstrated the usefulness of molecular markers such as RAPD, ISSR and SNP in determining the trueness-to-type of tissue culture-derived plantlets of N. cadamba. The genetic integrity of tissue culture-derived plantlets could be maintained and stable up to at least the sixth subcultures. The findings proved that micropropagation of N. cadamba from axillary shoot buds is a rapid, safe and efficient method for large scale production of true-to-type plants, and thus aids to meet the demands for quality planting materials for industrial tree plantation development.

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