ISSR marker based genetic diversity in *Morinda* spp. for its enhanced collection, conservation and utilization

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**Abstract**  *Morinda* (Rubiaceae) is considerably recognized for its multiple uses viz. food, medicine, dyes, firewood, tools, oil, bio-sorbent etc. The molecular characterization of such an important plant would be very useful for its multifarious enhanced utilization. In the present study, 31 *Morinda* genotypes belonging to two different species *Morinda citrifolia* L. and *Morinda tomentosa* B. Heyne exRoth collected from different regions of India were investigated using inter simple sequence repeat (ISSR) markers. Fifteen ISSR primers generated 176 bands with an average of 11.7 bands per primer, of which (90.34%) were polymorphic. The percentage of polymorphic bands, mean Nei’s gene diversity and mean Shannon’s information index in *M. tomentosa* and *M. citrifolia* was [(69.89%, 30.68%); (0.21 ± 0.19, 0.12 ± 0.20) and (0.32 ± 0.27 0.17 ± 0.28)] respectively, revealing higher polymorphism and genetic diversity in *M. tomentosa* compared to *M. citrifolia*. These diversity rich genotypes of *M. tomentosa* can be evaluated for nutraceutical, nutritional and other nonfood purposes to identify trait specific genotypes for its enhanced utilization. ISSR markers based Structure, and UPGMA cluster analysis placed the *M. tomentosa* and *M. citrifolia* genotypes into well-defined separate clusters. Further, distinct ecotypes within a particular species could also be inferred. Priority regions identified can be earmarked for exploration and collecting substantial number of genotypes for ex-situ conservation. In-situ conservation of *Morinda* genotypes in hotspots to preserve the diversity in their natural habitats vis-à-vis evolution and increased adaptation of newer diversity with respect to changing environment was also emphasized.

**Keywords** Genetic diversity · ISSR markers · *Morinda citrifolia* · *Morinda tomentosa*

**Introduction**

*Morinda* genus (Rubiaceae) is distributed throughout the tropics and subtropics. It is an important underutilized fruit plant; *Morinda citrifolia* L. (commonly known as noni) and *Morinda tomentosa* B. Heyne exRoth are its two well recognized species. Although according to the official site of plant taxonomy (http://www.worldfloraonline.org/), *Morinda tomentosa* B. Heyne ex Roth is a synonym of *Morinda citrifolia* L., but there are other published references based on key to species/morphological data/molecular data (Natho 2001; Arya et al. 2012; Kesonbuaaa and Chantaranoothai 2013) which prove otherwise. Also, in the present study based on ISSR molecular markers *Morinda citrifolia* and *Morinda tomentosa* are...
different species as revealed by their grouping in different clusters. So, it is a taxonomic opinion of one or the other school of thought or group. These two species especially *M. citrifolia* are known for their immense health benefits because of the presence of secondary metabolites of medicinal importance and nutritional value due to excellent source of minerals and vitamins. Other than this, its multifarious uses as food, medicine, dyes, firewood, tools, toys, bio-sorbent, oil etc. are also renowned. *M. citrifolia* have broad range of therapeutic effects (Wang and Su 2001; Duke et al. 2002; McClatchey 2002). West et al. (2008), reported the utility of oil (average oil content of 124.9 g/Kg) extracted from the seeds of *M. citrifolia* as a potential source of vegetable oil containing healthy linoleic (59.4%) and oleic fatty acids. In another study by Palu et al. (2012), the utility of noni seed oil for human skin health was also reported. Lee et al. (2015) compared the physico-chemical properties of oil from the seeds of noni, lady’s finger, spinach, mustard, bitter gourd and the dried kernel (copra) of coconut and stated that noni seed oil contained palmitic acid (10.9%), oleic acid (17.1%), linoleic/octadecadienoic acid (72.1%) and no stearic acid and erucic acid was detected. Further the potential application of noni oil as whipped-soft margarine or salad oil as well as in nonfood industries was reported. In a recent review by Jahurul et al. (2021) utility of noni fruit seeds as a potential source of functional foods (due to the presence of many bioactive compounds) and oil was emphasized. Regarding *M. tomentosa* (syn. *M. coreia* Buch; *M. tinctoria* Roxb.) its fruits are consumed; wood is used for making dishes, plates and toys and a red dye is made from its root bark (Anonymous 1962; Jukema et al. 1991). *M. tomentosa* is also being fed to cattle and buffaloes to improve milk yield by livestock owners in tribal and semiarid belt of east of Gujarat (Rangnekar 1991). There are also reports available on its usage as an environmentally safe bio-sorbent (Suneetha and Ravindhranath 2012; Vijayalakshmi et al. 2013). In India, *Morinda* spp. are distributed in Kerala, Tamil Nadu, Andaman and Nicobar Islands, Maharashtra, Rajasthan, Gujarat and Madhya Pradesh etc. and the available diversity should be assessed using molecular markers for its proper utilization. Molecular markers like restriction fragment length polymorphism (RFLPs), amplified fragment length polymorphism (AFLPs), random amplified polymorphic DNA (RAPD), inter simple sequence repeats (ISSRs), start codon targeted (SCoT), simple sequence repeats (SSRs) etc. are very well recognized for assessing the level of genetic diversity (Powell et al. 1996). There are also few reports available in *Morinda* spp. wherein molecular markers such as RAPD, ISSR, SCoT (Singh et al. 2011; Arya et al. 2013, 2014; Bordallo et al. 2017) have been used to evaluate the genetic diversity.

In the present study, ISSR markers were particularly used due to their high level of polymorphism, random distribution throughout the genome, non-requirement of prior crop specific sequence data information for primer designing, better reproducibility than RAPD markers, advantages of both SSRs and AFLP markers, low cost and easy usage. And most of the *M. citrifolia* and *M. tomentosa* genotypes from Gujarat, Rajasthan, Kerala and Dharmapuri (Tamil Nadu) used in the present work were not reported in earlier studies. Only six of the accessions from Gujarat are common with the earlier report by Arya et al. (2013) and these were included in the present study for assessing the genetic relatedness/uniqueness and comparison among the *Morinda* genotypes collected from different regions of India.

### Materials and methods

#### Plant material

The experimental material (leaves) used in the present study consisted of 31 *Morinda* genotypes collected from Gujarat, Rajasthan, Kerala and Dharmapuri (Tamil Nadu) regions of India (Table 1). Genotypes collected from Kerala and Jodhpur (Rajasthan) belonged to *M. citrifolia*, while genotypes from Gujarat, Kota and Bundi (Rajasthan) and Dharmapuri (Tamil Nadu) belonged to *M. tomentosa* (Fig. 1a, b).

#### DNA extraction

DNA was extracted from 100 mg of leaf samples of *Morinda* spp. using AuPrep DNA easy plant mini kit. DNA quantification was done using NANODROP 1000 (Thermo Scientific) spectrophotometer. Stock DNA was stored at − 20 °C and 20 ng working DNA solution was prepared for ISSR profiling.
ISSR analysis

PCR amplification was carried out with 100 ng of genomic DNA, 2.5 mM MgCl₂, 1U Taq DNA polymerase, 1 × PCR buffer without MgCl₂, 1.0 μM ISSR primer and 0.2 mM dNTP mix. The volume was made up to 25 μl with sterile distilled water. Thermocycling conditions used for PCR were as follows: denaturation at 94 °C for 5 min; thirty-five cycles of denaturation at 94 °C for 1 min, primer annealing at 48–55 °C for 1 min and primer extension at 72 °C for 2 min and final extension step at 72 °C for 7 min. PCR products were run on 1.6% agarose gel and photographs were taken on SYNGENE G: Box Chemi XT4 Gel Documentation unit.

Data analysis

ISSR bands were scored as absent (0) or present (1). Genetic similarity among genotypes was evaluated by calculating the Jaccard’s similarity coefficient and cluster analysis was performed using the UPGMA.
(Unweighted Pair Group Method of Arithmetic Means) algorithm (Rohlf 1998). Genetic parameters were estimated by Nei’s gene diversity statistics (Nei 1973) using POPGENE version 1.32 (Yeh et al. 2000). Structure 2.3.4 (Prichard et al. 2000) and Structure Harvester (Earl and vonHoldt 2012) were used to know the genetic structure existing among the Morinda genotypes at K ranging from 1 to 10 with five iterations each (burn-in period of 100,000 and number of Markov Chain Monte Carlo (MCMC) repetitions of 100,000) using the admixture model.

Results

ISSR analysis

Fifteen ISSR primers were used to profile 31 Morinda genotypes belonging to two different species and yielded a total of 176 clear and bright bands and the number of bands varied from 5 (GT)$_8$ YG to 22 (AG)$_8$ T with an average of 11.7 bands per primer. Of 176 bands, 159 bands (90.34%) were found to be polymorphic and average number of polymorphic bands was 10.6. In case of M. tomentosa and M. citrifolia the %polymorphism was 69.89% and 30.68% respectively showing higher polymorphism in M. tomentosa.

Genetic diversity and differentiation

The mean Nei’s gene diversity value for all the 31 genotypes was 0.27 ± 0.18 and Shannon’s information index ranged from 0.03 to 0.52 with a mean of 0.42 ± 0.24 (Table 2) revealing considerable genetic diversity in Morinda spp. Averaged over all the markers and genotypes, M. tomentosa displayed higher genetic variation (0.21 ± 0.19) as compared to M. citrifolia (0.12 ± 0.20) and also higher mean Shannon’s information index for M. tomentosa (0.32 ± 0.27) as compared to M. citrifolia (0.17 ± 0.28). The ISSR primers varied in their power to detect diversity and the primers BDB(CA)$_7$, (GT)$_6$ AY, (AC)$_8$ YT, HVH(TG)$_7$ and (AC)$_9$ YA were selected as the most informative markers based on high Nei’s gene diversity. And the least informative primer was (GT)$_8$ YG, as it showed very low Nei’s gene diversity.
Cluster analysis

Genetic similarity was calculated among 31 Morinda genotypes belonging to M. citrifolia and M. tomentosa based on 176 scored bands. Genetic similarity coefficient between pairs of genotypes was obtained from the marker data based on Jaccard’s coefficients using NTSYS-pc. ver. 2.1 software. Jaccard’s similarity coefficients among the 31 genotypes ranged from a maximum of 1.0 (‘Kerala 2’ and ‘Kerala 4’) to a minimum of 0.186 (Dharampuri and Jodhpur City 2) with an average of 0.55. The two Kerala genotypes of M. citrifolia showing maximum similarity were from Thalikkulam and Valappadu (Thrissur) and the two genotypes showing maximum dissimilarity or variability were from Dharampuri (Tamil Nadu) (M. tomentosa) and Rajasthan (M. citrifolia).

Jaccard’s similarity coefficients generated from the ISSR marker data were used to construct a dendrogram. UPGMA clustering reflected the grouping of 31 genotypes into two clusters (Fig. 2). The cluster ‘I’ consisted of 15 genotypes of M. tomentosa, including Dharampuri (Tamil Nadu) genotype as outliers of cluster I. Cluster I was further subdivided into two subgroups Ia and Ib. All the genotypes except one (Popatpura, as outlier of cluster I) from Gujarat were present in subgroup Ia and genotypes from Rajasthan were placed in subgroup Ib and further in subgroup Ib also two genotypes from Bundi were present as outliers of Ib and all the genotypes from Kota were grouped together in Ib. The cluster ‘II’ consisted of 16 genotypes, from M. citrifolia species. Cluster II was further subdivided into two subgroups IIa and IIb. In subgroup IIb all the genotypes were from Jodhpur (Rajasthan). In subgroup IIa all the genotypes were from Thrissur (Kerala).

Structure analysis

STRUCTURE analysis revealed two groups G1 and G2 based on delta K value which was settled at 2. G1 (Ia and Ib of UPGMA cluster) contained all the genotypes from M. tomentosa and G2 (IIa and IIb of UPGMA cluster) consisted of all the genotypes from M. citrifolia (Fig. 3). In group G2 of M. citrifolia, four genotypes from Rajasthan showed admixture, while group G1 of M. tomentosa showed no admixtures.

Table 2 Characteristics of ISSR markers used for diversity analysis in Morinda spp

| Primers | Total bands (no.) | No. of polymorphic bands | % Polymorphism | Size range of bands (bp) | Nei’s gene diversity | Shannon's Information Index |
|---------|-------------------|--------------------------|---------------|--------------------------|----------------------|---------------------------|
| (AC)₈ YT | 14 | 12 | 85.71 | 275–1500 | 0.33 | 0.48 |
| (GA)₉ AT | 12 | 12 | 100.00 | 350–2500 | 0.29 | 0.43 |
| BDB(CA)₇ | 17 | 17 | 100.00 | 250–950 | 0.35 | 0.53 |
| (AGC)₉ Y | 14 | 14 | 100.00 | 250–2250 | 0.34 | 0.51 |
| HVH(TG)₇ | 9 | 9 | 100.00 | 300–1000 | 0.36 | 0.53 |
| (CA)₉ RG | 14 | 13 | 92.86 | 275–1800 | 0.27 | 0.41 |
| (AG)₉ T | 22 | 20 | 90.91 | 275–2000 | 0.21 | 0.34 |
| VHV(GT)₇ | 11 | 10 | 90.91 | 260–1100 | 0.29 | 0.44 |
| (GT)₉ YG | 5 | 2 | 40.00 | 260–500 | 0.01 | 0.03 |
| (GT)₉ AY | 6 | 6 | 100.00 | 450–1250 | 0.35 | 0.52 |
| (GA)₉ T | 8 | 7 | 87.50 | 260–950 | 0.23 | 0.36 |
| (AC)₉ YA | 9 | 7 | 77.78 | 250–750 | 0.32 | 0.46 |
| AC₉ T | 11 | 7 | 63.64 | 300–3000 | 0.14 | 0.23 |
| (GA)₉ C | 6 | 5 | 83.33 | 325–900 | 0.23 | 0.37 |
| (AG)₉ C | 18 | 18 | 100.00 | 250–2000 | 0.25 | 0.39 |
| Average | 11.7 | 10.6 | 90.34 | 0.27 ± 0.18 | 0.42 ± 0.24 |
Fig. 2 UPGMA cluster analysis of *M. tomentosa* and *M. citrifolia*

Fig. 3 Structure Analysis of *M. tomentosa* and *M. citrifolia*
Discussion

ISSRs are one of the most reliable, low-cost molecular markers and have been used for diversity and population structure analysis, DNA fingerprinting, phylogenetic analysis etc. in different plant species (Ansari et al. 2012; Zhang et al. 2015; Kumar et al. 2016; Ana-Cruz et al. 2017). In Morinda spp. also ISSRs along with RAPD, and SCOT markers were used to find the level of genetic diversity from Andaman and Nicobar Islands, Chennai (Tamil Nadu), Karnataka, Gujarat and Madhya Pradesh (Singh et al. 2011, 2012; Arya et al. 2013, 2014). But in the present study, ISSRs were used to assess the genetic diversity of Kerala, Rajasthan and Dharmapuri (Tamil Nadu) regions, which were not explored earlier and the six common genotypes from Gujarat were included for comparing the diversity levels among the genotypes of Morinda spp. collected from different regions.

ISSR markers revealed 90.34% polymorphism among the 31 Morinda genotypes belonging to M. tomentosa and M. citrifolia. The mean Nei’s gene diversity and Shannon’s information index values also revealed considerable genetic diversity among the genotypes used in the present study. This may be due to the reason that genotypes used in this study were from two different species and different geographical locations of India (Gujarat, Rajasthan, Tamil Nadu and Kerala).

In an earlier study (Singh et al. 2011) based on ISSR markers and 22 accessions of M. citrifolia from Andaman and Nicobar Islands, Chennai (Tamil Nadu) and Bengaluru (Karnataka); M. tinctoria from Chennai (Tamil Nadu) and M. pubescens from Andaman and Nicobar Islands and Chennai (Tamil Nadu), polymorphism level of 56.02% was reported, which is very less than the polymorphism level reported in the present study. In another study by Singh et al. (2012), polymorphism range of 28.28–56.36% with an average of 43.21% was reported in 33 accessions of M. citrifolia from Andaman and Nicobar Islands based on ISSR markers, which is higher than the polymorphism level of 30.68% in M. citrifolia genotypes reported in our study, which is obvious due to its origin in Andaman and Nicobar Islands. Based on comparison with above cited earlier reports it is inferred that M. citrifolia from Andaman and Nicobar Islands are more diverse compared to Kerala and Rajasthan. And Gujarat, Rajasthan, Dharmapuri (Tamil Nadu) regions must be explored thoroughly to collect the maximum diversity available in M. tomentosa for conservation, characterization and utilization.

With respect to species, M. tomentosa and M. citrifolia were grouped separately and clearly distinguished based on UPGMA as well as Structure analysis based on ISSR markers. And the genotypes that showed maximum dissimilarity were from Tamil Nadu (M. tomentosa) and Rajasthan (M. citrifolia), which is obvious since these two genotypes were from two different species. Further, M. tomentosa showed higher polymorphism and genetic variation as compared to M. citrifolia. So, the advantage of higher diversity in M. tomentosa must be advanced for exploration and collecting more germplam from Gujarat, Rajasthan and Tamil Nadu covering newer regions as well and can be evaluated for nutritional, nutraceutical, and other qualities to identify the trait specific genotypes.

Within M. tomentosa the genotypes from Gujarat, Rajasthan and Dharmapuri (Tamil Nadu) were clustered as distinct ecotypes, with Dharmapuri genotype as the most diverse among the three regions. And the genotypes from Gujarat were more diverse compared to the genotypes from Rajasthan. Within Gujarat, the genotype Gujrat1A from Popatpura was the most diverse. Further, within Rajasthan, the two genotypes from Bundi were present as outliers and were more diverse compared to the genotypes from Kota. Based on these observations exploration and collecting activities should be prioritized from Dharmapuri (Tamil Nadu) and nearby areas followed by Popatpura (Gujarat) and other regions of Gujarat and then Bundi, Kota and other regions of Rajasthan. These regions should be earmarked for in-situ conservation to preserve the biodiversity in their natural habitats. And the genotypes collected should also be conserved ex-situ. Similarly, within M. citrifolia, the genotypes collected from Kerala and Rajasthan were grouped in separate clusters as distinct ecotypes. Kerala genotypes were found less diverse than Rajasthan genotypes, may be due to the uniformity in their habitat (partly disturbed saline). And within Kerala group, Kerala 5 and Kerala 6; Kerala 7 and Kerala 8 out of five genotypes from Kerayamparambu (Thrissur) were closely grouped though in separate subgroups in IIA and fifth genotype Kerala 9 from the same place was clustered in different subgroup. Similarly, the two genotypes Kerala 1 and Kerala 10 though from the
same place Thambakkadavu (Thrissur) were not closely grouped. Such groupings are based on the degree of relatedness between the genotypes and help in the selection of diverse genotypes from a particular place.

One more interesting information could be inferred based on Structure analysis. The four Rajasthan genotypes of *M. citrifolia* of group G2 showed admixtures, while no admixtures were observed in group G1 of *M. tomentosa*. The probable reason for this admixture can be explained as follows: *M. citrifolia* is commonly distributed in coastal areas and these four genotypes might have migrated/introduced to Rajasthan and in due course of time interspecific crossing might have occurred with *M. tomentosa* which is the prevalent species in that area. There are studies available wherein outcrossing based on expression of heterostyly (Waki et al. 2008; Liu et al. 2012) and pollination by bees, ants, flies etc. have been reported in *Morinda* (Rodri guez-Girones et al. 2013). Based on UPGMA analysis also, it is evident that Rajasthan genotypes were showing more diversity compared to Kerala genotypes which might be generated due to interspecific crossing and that will further increase the adaptive potential of such genotypes with respect to local/changing environment and their evolution. Such genotypes can also be evaluated for nutraceutical, nutritional as well as for other already known properties of *M. citrifolia* and can be compared for any differences. Further, in-situ conservation should be promoted to preserve such genotypes and more such regions should be explored and earmarked to collect substantial number of genotypes with higher diversity.

**Conclusion**

Unique ISSR profiles were generated for genotypes from *M. tomentosa* and *M. citrifolia* species. Higher genetic variability and polymorphism was observed in *M. tomentosa* compared to *M. citrifolia*. Further genotypes collected from different eco-geographical regions were clustered in well-defined groups. And regions of higher diversity within a particular species were also identified. ISSR markers proved as excellent, informative and effective marker system for geographic patterning, genetic diversity and relatedness studies of *Morinda* spp. The information generated during the present study will certainly aid in proper management of *Morinda* genetic resources in terms of exploration, conservation and utilization.

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**Declarations**

**Conflict of interest** The authors declare that they have no conflict of interest.

**References**

Ana-Cruz MC, Helena ME, Yacenia MC (2017) Molecular characterization of *Chenopodium quinoa* Wild using Inter simple sequence repeat (ISSR) markers. Afr J Biotechnol 16(10):483–489

Anonymous (1962) The Wealth of India: raw materials, vol VI. Publications and Information Directorate, Council of Scientific and Industrial Research, New Delhi, p 425

Ansari SA, Narayanan C, Wali SA, Kumar R, Shukla N, Rahangdale SK (2012) ISSR markers for analysis of molecular diversity and genetic structure of Indian teak (*Tectona grandis* L.f.) populations. Ann for Res 55(1):11–23

Arya L, Ramya KN, Kak A, Pandey CD, Verma M, Gupta V (2012) Start Codon Targeted(SCoT) markers for species differentiation and diversity analysis in Morinda spp. In:Rethinam P, Marimuthu T (Eds.) Proceedings of seventh national symposium, Noni-thetool for wellness, Chennai, India, pp 8–15

Arya L, Ramya KN, Kak A, Pandey CD, Verma M, Gupta V (2013) Genetic diversity analysis in *Morinda tomentosa* collected from Gujarat using RAPD markers. Indian J Hortic 70(4):580–583

Arya L, Ramya KN, Verma M, Singh AK, Gupta V (2014) Genetic diversity and population structure analyses of *Morinda tomentosa* Heyne, with neutral and gene based markers. Genet Resour Crop Evol 61:1469–1479

Bordallo PN, Monteiro AM, Sousa JA, Ara ˜gao FA (2017) Molecular marker-based genetic diversity analysis of scantly studied Brazilian accessions of a medicinal plant, *Morinda citrifolia* L. (noni). Genet Mol Res 16:1. https://doi.org/10.4238/gmr16019531

Duke J, Bogenschutz M, Duke P (2002) Handbook of medicinal plants, 2nd edn. CRC Press, New York, p 529

Earl DA, vonHoldt BM (2012) Structure harvester: a website and program for visualizing STRUCTURE output and implementing the Evanno method. Cons Genet Resour 4(2):359–361

Jahurul MHA, Patricia M, Shihabul A, Norazlina MR, Ramlah George MR, Noorakmar AW, Lee JS, Junardi R, Jinap S, Zaidul ISM (2021) A review on functional and nutritional
properties of noni fruit seed (Morinda citrifolia L.) and its oil. Food Biosci. https://doi.org/10.1016/j.fbio.2021.101000

Jukema J, Wulijarni-Soetjipto N, Lemmens RHJM, Hildebrand JW (1991) Morinda L. [Internet] Record from Proseabase. Lemmens RHJM, Wulijarni-Soetjipto N (eds), PROSEA (Plant Resources of South-East Asia) Foundation, Bogor, Indonesia. http://www.proseanet.org

Kesonbuaa W, Chantaranothai P (2013) The genus Morinda (Rubiaceae) in Thailand. Sci Asia 39:331–339

Kumar A, Mishra P, Baskaran K, Shukla AK, Shasany AK, Velusamy Sundaresan V (2016) Higher efficiency of ISSR markers over plastid psbA-trnH region in resolving taxonomical status of genus Ocimum L. Ecol Evol 6:7671–7682

Lee ST, Radu S, Ariffin A, Ghazali HM (2015) Physico-chemical characterization of oils extracted from noni, spinach, lady’s finger, bitter gourd and mustard seeds, and copra. Int J Food Prop 18(11):2508–2527

Liu Y, Luo Z, Wu X, Bai X, Zhang D (2012) Functional dioecy in Morinda parvifolia (Rubiaceae), a species with stigma-height dimorphism. Plant Syst Evol 298:775–785

McClatchey W (2002) From Polynesian healers to health food stores: changing perspectives of Morinda citrifolia (Rubiaceae). Integr Cancer Ther 1:110–120

Natho G (2001) Rubiaceae. In: Hanelt P, Institute of Plant Genetics and Crop Plant Research (eds) Mansfeld’s encyclopedia of agricultural and horticultural crops, 4th edn. Springer, Berlin, pp 1764–1789

Nei M (1973) Analysis of gene diversity in subdivided populations. Proc Natl Acad Sci USA 70(12):3321–3323

Palu AK, Brett JW, Jarakae Jensen C (2012) Noni seed oil topical safety, efficacy, and potential mechanisms of action. J Cosmet Dermatol Sci Appl 2:74–78

Powell W, Morgante C, Andre M, Hanafey M, Vogel J, Tingeys S, Rafalski A (1996) The comparison of RFLP, RAPD, AFLP, and SSR (microsatellite) markers for germplasm analysis. Mol Breed 2:225–238

Pritchard JK, Stephens M, Donnelly P (2000) Inference of population structure using multilocus genotype data. Genetics 155:945–959

Rangnekar DV (1991) In: Andrew S, Pugliese Pierre-Luc (eds) Legume trees and other fodder trees as protein sources for livestock. Feeding systems based on the traditional use of trees for feeding livestock. Food and Agriculture Organization of the United Nations, Rome, p 221 http://www.fao.org/DOCREP/003/T0632E/T0632E15.htm#ch15

Rodriguez-Girones MA, Gonzalez FG, Llandres AL, Corlett RT, L Santamarra (2013) Possible role of weaver ants, Oecophylla smaragdina, in shaping plant–pollinator interactions in South-East Asia. J Ecol. https://doi.org/10.1111/1365-2745.12100

Rohlf F (1998) NTSYSpc: Numerical taxonomy and multivariate analysis system, ver. 2.11. Exeter Software, New York

Singh DR, Srivastava AK, Srivastava A, Srivastava RC (2011) Genetic diversity among three Morinda species using RAPD and ISSR markers. Indian J Biotecnol 10:285–293

Singh DR, Singh S, Minj D, Anbanathan V, Salim KM, Kumari C, Varghese A (2012) Diversity of Morinda citrifolia L. in Andaman and Nicobar Islands (India) assessed through morphological and DNA markers. African J Biotecnol 11(86):15214–15225

Suneetha M, Ravindhranath K (2012) Removal of nitrite from polluted waters using bio-sorbents derived from powders of leaves, barks or stems of some herbal plants. Int J Chem Environ Pharm Res 3(1):24–34

Vijayalakshmi R, Venkatachalam R, Periyathamibi T, Saravanan P (2013) Biosorption of reactive red 198 from an aqueous solution using Morinda tinctoria. Int J Recent Trends Sci Technol 9(1):36–40

Waki J, Okpul T, Komolong MK (2008) Assessing the extent of diversity among noni (Morinda citrifolia L.) genotypes of Morobe Province, Papua New Guinea. S Pac J Nat Appl Sci 26:11–24

Wang MY, Su C (2001) Cancer preventive effect of Morinda citrifolia (Noni). Annal New York Acad Sci 952:161–180

West BJ, Jarakae Jensen C, Westendorf J (2008) A new vegetal oil from noni (Morinda citrifolia) seeds. Int J Food Sci Technol 43:1988–1992

Yeh FC, Yang R, Boyle TJ, Ye Z, Xiyang JM (2000) PopGene32: microsoft windows-based freeware for population genetic analysis, version 1.32. Molecular Biology and Biotechnology Centre, University of Alberta, Edmonton, Alberta, Canada

Zhang L, Cai R, Yuan M, Tao A, Xu J, Lin L, Fang P, Qi J (2015) Genetic diversity and DNA fingerprinting in jute (Corchorus spp.) based on SSR markers. Crop J 3:416–442

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