Genetic Characterization of Locally Cultivated Taro Germplasm from Eleven District of Nagaland, India

Thejazhanuo Lulu Mezhii¹, Sapu Changkija¹, A. Pattanayak², H.P. Chaturvedi¹, S. Vimala Devi³ and Pravas R. Kole⁴*

¹Department of Genetics and Plant Breeding, Nagaland University, SASRD, Medziphema- 797106, India
²ICAR RC for NEHR, Umiam, Meghalaya- 793103, India
³Division of Germplasm Conservation, National Bureau of Plant Genetic Resources, New Delhi, India
⁴Protection of Plant Variety and Farmer Right Act, NASC Complex, DPS Marg, New Delhi, India
*Corresponding author

A B S T R A C T

Colocasia or taro (Colocasia esculenta L.) is one of the important tuber crops, which has been grown by farmers in rain-fed ecosystem and considered as an important food crop after rice in Nagaland. The characterization of taro from 11 districts of Nagaland, Northeast India has been analyzed using microsatellite markers. Twenty eight microsatellite markers were used to analyze 50 accessions of taro collected from 11 district of Nagaland. A total of 53 alleles were amplified at an average of 1.89 alleles per locus. Both altered alleles and null alleles were observed. The number of alleles ranged from one to four. The overall size of amplified products ranged from 117bp to 685bp. Dendrogram based on UPGMA analysis separated the accessions into five clusters. Four definite clusters were identified at a level of 35% similarity among the individuals. A three dimensional plot prepared from the principal component analysis of fifty-three alleles with PIC values ranging from 0.41 - 0.93 indicating high specificity and discriminatory power of the markers. Analysis of molecular variance (AMOVA) revealed most variation among individuals within population at 100%. It appears that high within population variation is a characteristic of colocasia. The present study showed that the germplasm of Nagaland was diverse but somewhat uniformly distributed across the state. Further exploration and collection of colocasia germplasm is required.

Keywords: Taro, Colocasia esculenta, Microsatellite, Molecular marker.

Article Info

Accepted: 26 June 2017
Available Online: 10 August 2017

Introduction

Northeast India is the home for large numbers of tribal communities with rich culture and traditional knowledge system. In northeast India, the state of Nagaland (25º6’-27º0’4N and 93º0’20-95º0’15E) with a geographical area of 16527 km² is the home for large number of Naga tribal communities with rich culture and traditional knowledge system. Nagaland is rich in biodiversity. It has a very large number of non-traditional or underutilized horticultural crops. The abundant rainfall and different agro-ecological climate condition prevailing in different altitude in various districts favor the diversity both in cultivated and the wild horticultural crops. The wide range of underutilized fruits and vegetables are available in Nagaland. From these fruits and vegetables farmers can meet their...
household needs like food, nutrition, medicine and general livelihood balancing. Among these crops colocasia or taro (Colocasia esculenta L.), a member of the Araceae family, is one of the important tuber crops which has been grown by farmers in rainfed (>2,000 mm rainfalls) ecosystem and considered as an important food crop after rice in Nagaland. Taro has basic chromosome number 14 and two cytotypes: diploid with 28 chromosomes and triploid with 42 chromosomes (Coates et al., 1988). Like most other root and tuber crops, taro is vegetatively propagated, although seed production is possible. Natural breeding and production spread have been reported for wild taro (Hunt et al., 2013). Cultivars are propagated with corms, cormela (also known as suckers), and while vegetative propagation occurs through stolons in the wild (Ramanatha et al., 2010).

According to Lebot (2009) taro is probably one of the oldest crops. Archaeological studies indicate its usage as early as 28,000 years ago in the Solomon Islands (Loy et al., 1992). The origin of center of taro is still unresolved. Research continues to elucidate the center of origin of this global crop, northeast India and New Guinea being the potential separate centers of domestication (Jianchu et al., 2001; Kuruvilla and Singh 1981 and Coates et al., 1988).

Estimation of the genetic diversity widespread in the germplasm needs immediate attention for the improvement of taro. Very few reports are available on the analysis of genetic diversity of this crop. Several studies have attempted to describe the use of molecular marker to study genetic diversity in taro such as restriction site variation in rDNA, mitochondrial DNA (Matthew et al., 1992) and RAPD markers (Irwin et al., 1998; Lakhanpal et al., 2003; Pillai & Lekha 2008; Sharma et al., 2008; Singh et al., 2012). Globally taro genetic studies has been done with isozymes (Lebot et al., 2000), AFLP (Kreike et al., 2004; Callion et al., 2006) and microsatellite makers (Mace and Godwin 2002; Singh et al., 2008; Macharia et al., 2014). Very few reports on the genetic resources of C. esculanta (L.) have been analyzed for diversity and evolutionary pattern, but only a few germplasm has been included from Nagaland in some of the studies. Therefore, the present study was conducted with objective of genetic diversity analysis in 50 accessions of C. esculenta collected from 11 district of Nagaland using microsatellite markers.

Materials and Methods

Fifty accessions of C. esculenta var. esculenta collected from all the 11 districts of Nagaland were used to investigate the genetic diversity by studying the level of polymorphism with SSR markers. For Plant DNA extraction, young unrolled leaves were harvested and 150-200 mg leaf tissue was used. Total genomic DNA was extracted using the DNEasy Plant Mini (QIAGEN). The isolated DNA was quantified and purity checked by running 0.8% agarose gel followed by spectrophotometer.

Twenty eight Colocasia microsatellite markers were used for amplification (Table 2). PCR was carried out in a 25-µl reaction mixture consisting of 1 µl of template DNA, 5 µmol of each reverse and forward primer, 7.1 µl PCR Master-mix (Qiagen) and nuclease-free water.

Amplification was carried out in a thermal cycler (Thermal Scientific, Veriti PCR) with a 5 min initial denaturation at 94°C followed by 30 cycles of 94°C for 40 sec, annealing at primer-specific temperature for 1 min and extension at 72 for 32 sec. A final extension at 72°C for 5 min was given after the last cycle. After the completion of the PCR, the
products were stored at 4°C refrigerator until the gel electrophoresis was done. 10 µl of the PCR product was electrophoresed in 3% agarose gel (with ethidium bromide) at 120V cm⁻¹ for 4 hours. The gels were then visualized and photographed using a gel documentation system (Alpha Innotech, USA). Bands in gel images were corrected for smiling effect using the Alpha Imager FC software (Alpha Innotech, USA) and were scored for the presence or absence in the genotypes. The presence of an amplified band in each position was scored as ‘1’; absence was scored as ‘0’.

**Data analysis**

The data were entered into an Excel sheet as a rectangular matrix. Polymorphism information content (PIC) of each marker was calculated using the formula;

\[ \text{PIC} = I - \sum x_i^2 \]

Where, \( x_i \) is the frequency of \( i^{th} \) allele for each SSR locus (Sajeev et al., 2011). Similarity index were calculated employing Jaccard’s coefficient to established genetic relatedness. Molecular weight of the amplified bands was determined based on their relative migration in comparison to the molecular weight standards and expressed in base pairs (bp). Genetic similarity (GS) matrix between accessions based on molecular data was computed using Jaccard’s (1908) coefficient.

Null alleles were treated as missing data. The similarity matrix was used to produce an agglomerative hierarchical clustering by employing UPGMA with average linkage (Sneath and Sokal 1973), which was then graphically converted into a dendrogram. To test the goodness of fit of clustering to the band scoring data, ‘cophenetic correlation coefficient’ was estimated. All the above calculations were made using NTSYS-pc software (Rohlf 2001). To get an idea about community / ecology-based preference of accessions / sharing of seeds/corms among communities, test accessions were grouped into six hypothetical populations (Pop. I–VI) based on their location of collection. Principal Coordinates (PCA) in different populations was calculated to get a first-hand idea about variations that exist within and among the hypothetical populations. A hierarchical analysis of molecular variance (AMOVA) with populations nested within types was performed (Excoffier et al., 2005). For average gene diversity, PCA (populations) and AMOVA, the computer program GenAlEx 6.5 Beta (Peakall and Smouse 2012) was used.

**Results and Discussion**

Out of the fifty *Colocasia esculanata* genotypes collected, forty-eight genotypes germinated and were selected for Simple Sequence Repeat (SSRs) analysis. CV5 and CV38 could not be analysed in molecular studies due to non-germination of corm as the corms were rotten. Altogether twenty eight colocasia SSRs markers were used to study the genetic diversity. All the primers used produce scorable amplicons. Band sizes amplified by the markers are presented in Table 2. Out of 28 markers, 16 showed considerable variation from the expected band sizes. A total of 53 alleles were amplified at an average of 1.89 alleles per locus. Both altered alleles and null alleles were seen. The number of alleles ranged from one to four. The overall size of amplified products ranged from 117bp to 685bp.

Highest number of heterozygotes was detected by the primer COLGCC73-164 (Plate-26). Highest variation was seen in COL-GCC 211-202, where the most common band size was 414bp (rang 139-414 bp
compared to 202-211 bp expected). Similarly high variations were seen in COL-GCC 249-155 and COL-GCC-220-211. On the other hand, COL-GCC 233-167, COL-GCC 118-221, COL-GCC 77-174, COL-GCC 95-219 etc., showed similarity/closeness with the expected band size. PIC values of the markers ranged from 0.41 (COL-GCC228-110) to 0.93 (COL-GCC 211-202). Two markers amplified 4 alleles each (COL-GCC 208-253 and COL-GCC 206-122) while three markers amplified 3 alleles each (COL-GCC 56-191, COL-GCC 98-294 and COL-GCC 211-202). Pic values of the markers ranged from 0.41 (COL-GCC228-110) to 0.93 (COL-GCC 211-202). Two markers amplified 4 alleles each (COL-GCC 208-253 and COL-GCC 206-122) while three markers amplified 3 alleles each (COL-GCC 56-191, COL-GCC 98-294 and COL-GCC 211-202).

Dendrogram (Figure 2) based on UPGMA analysis separated the accessions into five clusters with a Jaccard’s similarity coefficient indicating high genetic variability among the accessions. Four definite clusters were identified at a level of 35% similarity among the individuals. A three dimensional plot prepared from the principal component analysis of the genotypic data also showed similar results. Cluster V was the biggest containing 38 genotypes followed by cluster-III with 5 genotypes. Cluster II contained 3 genotypes while both cluster I and cluster IV contained 1 genotype each (Figure 2). Clusters were determined based on discriminate analysis with the genotypic data. Cluster V showed 5 subclusters of which subcluster A was the biggest and subcluster E contained a unique genotype- 14. Cluster-III also showed two small subclusters. Among the 48 genotypes, genotype Tong II was unique as it formed a single genotype cluster at levels of cluster discrimination. At the discrimination level CUT-3, genotype Ati also produced a single genotype cluster. The discriminate analysis showed a clear distinction of the accession of the accessions of different clusters with the group (cluster) centroids placed distinctly apart from one another. The groups were placed distinctly apart both horizontally and vertically although the distinction was less prominent. There was no overlapping of group centroid. (Figure 2)

All genotypes were grouped into six hypothetical populations based on their location of collection (Table 1, Figure 1). These were again grouped into two regions based on altitude. Analysis of molecular variation (AMOVA) indicated that there were no variations among population or between the regions (Table 3). Within population the variation accounted for 100% of the observed molecular variation. A principal co-ordinate analysis was carried out to visualize the distribution of different hypothetical population across the regions. As seen from Figure 4, the populations were uniformly distributed which supported the observation from AMOVA that within population variation accounts for the observed molecular variation.

The present report on genetic characterization of colocasia germplasm of Nagaland using molecular markers is the first of its kind. Amplification pattern of the markers indicated that although some of the markers behaved as expected, others showed prominent variation. This indicated that in the population of Nagaland there is a large amount of inherent variation which might have accumulated due to vegetative propagation. There are four previous studies on the genetic diversity of Indian colocasia using either or a combination of random markers like RAPD, ISSR or isozyme. The current study is the first of its kind using the robust SSR marker with Indian germplasm. In the first study with Indian germplasm, Lakhanpal et al., (2003) analyzed
32 colocasia genotypes and showed 100% polymorphism among the RAPD primers. Pillai & Lekha (2008) and Sharma et al., (2008) studied 14 and 45 genotypes respectively and the RAPD primers showed 97% polymorphism. In a more recent study, Singh et al., (2012) reported diversity analysis using RAPD and ISSR markers in 24 colocasia genotypes collected from Andaman Islands. They also reported 70.60% and 77.30% polymorphism in the RAPD and ISSR markers, respectively. The present study is the first of its kind with a collection from North East India. Also, this is so far the only study with largest number of germplasm from India using the robust SSR marker. The markers showed 100% polymorphism indicating the extent of diversity in the genotypes studied.

Table 1: The list of the Genotypes and their groups into six hypothetical population based on their location of collection

| Population | Sample ID | Genotype name | Place of collection | Population | Sample ID | Genotype name | Place of collection |
|------------|-----------|---------------|---------------------|------------|-----------|---------------|---------------------|
| pop 1      | CV2       | Chugoma       | Zunheboto           | pop2       | CV14      | Manie I       | Wokha               |
|            | CV34      | Aiie          | Zunheboto           | CV27       | Lijalani  | Mokokchung    |                     |
|            | CV46      | Chuyali       | Zunheboto           | CV28       | Pajo      | Wokha         |                     |
|            | CV4       | Beithola      | Phek                | CV31       | Manie II  | Wokha         |                     |
|            | CV22      | Beyo          | Phek                | CV37       | Kotaknii  | Mokokchung    |                     |
|            | CV24      | Beii II       | Phek                | CV43       | Wasii nii | Mokokchung    |                     |
|            | CV49      | Beixo         | Phek                | CV44       | Manyii    | Mokokchung    |                     |
|            | CV32      | Banu sam sam  | Kiphire             | CV45       | Tejongnii | Mokokchung    |                     |
|            | CV33      | Bao           | Kiphire             | CV3       | Waipong   | Peren         |                     |
|            | CV36      | Tong I        | Mon                 | CV16       | Beidimai I| Peren         |                     |
|            | CV39      | Tino II       | Tuensang            | CV12       | Loudoubei | Peren         |                     |
|            | CV40      | Tino III      | Tuensang            | CV29       | Beidimai I| Peren         |                     |
|            | CV47      | Tong II       | Mon                 | CV48       | Beidimai I| Peren         |                     |
|            | CV48      | Tong III      | Mon                 | CV47       | Beidimai I| Peren         |                     |
| pop 3      | CV3       | Beidimai      | Peren               | CV16       | Beidimai I| Peren         |                     |
|            | CV36      | Tino III      | Peren               | CV16       | Beidimai I| Peren         |                     |
|            | CV39      | Tino II       | Peren               | CV16       | Beidimai I| Peren         |                     |
|            | CV40      | Tino III      | Peren               | CV16       | Beidimai I| Peren         |                     |
|            | CV47      | Tong II       | Mon                 | CV47       | Beidimai I| Peren         |                     |
|            | CV48      | Tong III      | Mon                 | CV48       | Beidimai I| Peren         |                     |
| pop 5      | CV6       | Tepfii dziinuo| Kohima              | CV9        | Dziinuo I | Dimapur       |                     |
|            | CV7       | Ati           | Kohima              | CV13       | Dziinuo   | Dimapur       |                     |
|            | CV8       | Obei          | Kohima              | CV15       | Dziinuo I  | Dimapur       |                     |
|            | CV10      | Thegabeiizii  | Kohima              | CV17       | Dziinuo II | Dimapur       |                     |
|            | CV18      | Thupela       | Kohima              | CV19       | Dziinuo III| Dimapur       |                     |
|            | CV21      | Sama          | Kohima              | CV20       | Keriila    | Dimapur       |                     |
|            | CV23      | Dziinuo IV    | Kohima              | CV26       | Chiicha    | Dimapur       |                     |
|            | CV25      | Tefidzii      | Kohima              | CV41       | Dziinuo V  | Dimapur       |                     |
|            | CV30      | Dziirinuo II  | Kohima              | CV50       | Dziitii    | Dimapur       |                     |
|            | CV35      | Wolikhuo      | Kohima              |            |            |               |                     |
|            | CV42      | Atsantu       | Kohima              |            |            |               |                     |
Table 2. List of Colocasia SSR markers, their amplification pattern and PIC value in the accessions

| Marker      | Primer sequences                      | No. of alleles amplified | Expected band size | Size of bands (bp) | PIC value |
|-------------|---------------------------------------|--------------------------|--------------------|--------------------|-----------|
| COL-GCC56-191 | TGTCCCTTTTGTACCTGTACAAG - CTCACGGGCTCATACACAC | 3                        | 56-191             | 249 115 134        | 0.78      |
| COL-GCC82-117 | TCAAGCCTAGGGAAAAAAC - CACAACCAAAAATGAAACC | 1                        | 82-117             | 193 153 188        | 0.52      |
| COL-GCC111-300 | AGTGTATTCTACGATCCAGC - CAACCCTTCTCATCACTGAC | 2                        | 111-300            | 367 221 289        | 0.89      |
| COL-GCC192-245 | GGACTAACCGTTATGCTGC - CTAATCCTGCGACATTG | 2                        | 192-245            | 427 202 236        | 0.73      |
| COL-GCC132-147 | ACCCGAAAAGGCAATAG - CATACGTGGCTCTCCATCCTTC | 1                        | 132-147            | 156 113 139        | 0.65      |
| COL-GCC233-167 | TGACACAGTACAACTGAGC - ATCTCAAAGCCAAATCTCC | 2                        | 233-167            | 182 140 164        | 0.73      |
| COL-GCC88B-94 | CACATACCCACACACACAG - CCAGGCCTCTAATGATGATG | 2                        | 88-94              | 117 66 108         | 0.59      |
| COL-GCC75-100 | TTTGTGACATGAGGCTAGAG - GACACACTACACACACACAG | 2                        | 75-100             | 117 73 88          | 0.54      |
| COL-GCC118-221 | GACTAACCCTATGCTGACC - TAGATGGAGCCCTTGAGC | 1                        | 118-221            | 217 156 213        | 0.71      |
| COL-GCC103-220 | GGATTCCTGGTGTGGCTCC - ATGATGCCTCACACCCAC | 1                        | 103-220            | 351 169 176        | 0.48      |
| COL-GCC77-174 | GATCTCAACAGCAAGAGAGAGC - TCAACCTTCTCCATGCTCC | 2                        | 77-174             | 178 158 167        | 0.66      |
| COL-GCC95-219 | ACAACGTGTTGATGAAAGAGAAC - TGGACTACTAGACGAGAG | 1                        | 223-157            | 190 163 166        | 0.46      |
| COL-GCC220-211 | CTAAGGAGGAGGAGATCCGAC - CGTATACCATTTGCTGCC | 2                        | 220-211            | 361 153 351        | 0.72      |
| COL-GCC119-367 | GTCGTCAGCTAGGAAAAAAC - AGCTAGGGAGCAGGACAC | 1                        | 119-367            | 355 302 312        | 0.58      |
| COL-GCC91-262 | GTCAAGTCTGGATAAAAAACAC - AGTCAAGGGCGACCAAACAC | 2                        | 29-262             | 311 219 239        | 0.73      |
| COL-GCC249-155 | GACGCTCAACAAAGTGTAG - CCAAGGAGATATTACCAAAG | 3                        | 249-155            | 454 224 234        | 0.76      |
| COL-GCC110-283 | AGCCACAGACACATCTATAC - GCCAGATATATCTGCTCTCC | 2                        | 110-283            | 257 222 243        | 0.65      |
| COL-GCC211-202 | CTAACCACACACACATGAGCAC - TACTGTCCTGTCATCCCTC | 3                        | 211-202            | 414 139 414        | 0.93      |
| COL-GCC228-110 | CCAGACTCTCTTCTACACCAAG - GATCATGTGAAGGATCCTGAG | 1                        | 228-110            | 126 104 116        | 0.41      |
| COL-GCC240-222 | ACTAACACACAGACACCTCCT - ACCATTTCTACCACTCCT | 1                        | 240-223            | 250 199 203        | 0.52      |
| COL-GCC105-267 | CACCAAGGCATGGAACAAAC - CCTGAAATGGCAAATAACTTTAC | 2                        | 105-267            | 341 231 231        | 0.66      |
| COL-GCC208-253 | TAGAGGTGGAAGGAGGAG - CTAAGGAGCACTGTATG | 4                        | 208-253            | 685 229 244        | 0.89      |
| COL-GCC209-120 | CTAACCACACACACATTATGAGC - GTGAGTGAAAGGATGAAATG | 1                        | 209-120            | 130 67 70          | 0.51      |
| COL-GCC90-102 | TGGTTGGTTGGTCATACAGAGG - ACAACACACACACAGAGAC | 1                        | 90-102             | 185 92 94          | 0.57      |
| COL-GCC73-164 | ATGCCAATGGAGGATGAGCAG - CTCGACTGTTAGGACACATGC | 2                        | 73-164             | 184 137 140        | 0.68      |
Table 3 Analysis of Molecular variation

| Source       | df | SS     | MS   | Est. Var. | %   |
|--------------|----|--------|------|-----------|-----|
| Among Regions| 1  | 12.218 | 12.218 | 0.013     | 0%  |
| Among Pops   | 4  | 48.119 | 12.030 | 0.000     | 0%  |
| Within Pops  | 42 | 564.413| 13.438| 13.438    | 100%|
| Total        | 47 | 624.750| 13.451|           | 100%|

Fig.1 Map of Nagaland showing the genotypes grouped into six hypothetical population based on their location of collection.
**Fig. 2** Dendrogram of colocasia varieties obtained by UPGMA cluster analysis based on microsatellite data

**Fig. 3** The discriminate analysis showed a clear distinction of the accessions of different clusters with the group (cluster) centroids placed distinctly apart from one another
At the global level, genetic studies with isozymes (Lebot et al., 2000) and AFLP (Kreike et al., 2004) showed a greater diversity in the South East Asian germplasm compared to germplasm from Oceania. Another study on a set of 96 germplasm form Vanulatu Lava, a Pacific Ocean Island, using AFLP markers identified eight clusters with varying degrees of similarity (Callion et al., 2006). Macharia et al., (2014) studied 98 germplasm (5 populations) from East Africa using 6 microsatellite markers and amplified 31 alleles of which 85% were polymorphic.

The first set of 7 colocasia specific SSR markers was developed by Mace and Godwin (2002). Singh et al., (2008) used these seven markers to assess diversity in 859 Papua New Guinea colocasia collections. They obtained 30 polymorphic alleles with a PIC value ranging from 0.0 - 0.59 and twenty three clusters were identified in their study. Macharia et al., (2014) identified 31 alleles in 98 East African germplasm accessions using six micro satellite markers developed by Mace and Godwin (2002). In the present study, 28 SSR markers were used of which 4 were from the study of Mace and Godwin (2002). However, the new markers used in this study showed higher allelic variation. Fifty three alleles were identified with PIC values ranging from 0.41 - 0.93 indicating high specificity and discriminatory power of the markers. Four definite clusters were identified based on a discriminatory analysis. In none of the previous study, discriminatory analysis was done to delineate clusters. Two very distinct genotypes; genotype 9 from Dimapur and genotype 45 from Mokokchung were identified.

Six populations divided into two regions were hypothetically constituted to assess regional or altitudinal variation, if any, in the collection. However, AMOVA did not show inter-population or inter-regional variation. With-in population variation accounted for 100% of the molecular variation. This
supports the results obtained in all the previous studies (Singh et al., 2008, Kreike et al., 2004, Mace et al., 2006, Macharia et al., 2014) carried out in two different parts of the world where more than 80% of the variation was represented by within population variation. Thus, it appears that high within population variation is a characteristic of colocasia and movement/establishment of outside germplasm into a country or region specific population is low. However, it would be interesting to compare the two distinctly isolated population of India, one from the North East and the other from the Andaman Island.

The present study showed that the newly developed SSR markers were robust and informative, and also the germplasm of Nagaland was diverse but somewhat uniformly distributed across the state. Further exploration and collection of colocasia germplasm is required.

Acknowledgement

Authors are grateful to the Director, Indian Council of Agricultural Research, Umiam, Meghalaya for providing the facilities for conducting this research. The authors also thank GCC Biotech, Kolkata for providing the Colocasia SSR markers.

References

Caillon, S., Quero-García, J., Lescure, J.P. and Lebot, V. 2006. Nature of taro (Colocasia esculenta (L.) Schott) genetic diversity prevalent in a Pacific Ocean island, Vanua Lava, Vanuatu. Genet Res and Crop Evol. 53(6): 1273-1289.

Coates, D.J., Yen, D.E. and Gaffey, P.M. 1988. Chromosome variation in taro, Colocasia esculenta, implications for origin in the Pacific. Cytologia: 53(3):551–60.

Excoffier, L., Smouse, P. and Quattro, M. 2005. Analysis of molecular variance inferred from metric distances among DNA haplotypes: applications to human mitochondria DNA restriction data. Genetics. 131:479-491.

Hunt, H.V., Moots, H.M. and Matthews, P.J. 2013. Genetic data confirms field evidence for natural breeding in a wild taro population (Colocasia esculenta) in northern Queensland, Australia. Gen Resour Crop Evol. 60(5):1695–707.

Irwin, S.V., Kaufusi, P., Banks, K., de la Pena, R. and Cho, J.J. 1998. Molecular characterization of taro (Colocasia esculenta) using RAPD markers. Euphytica. 99(3):183–9.

Jaccard, P., 1908. Nouvelles recherches sur la distribution florale. Bull Soc Vaud Sci Nat. 44: 223-270.

Jianchu, X., Yongping, Y., Yingdong, P., Ayad, W.G. and Eyzaguirre, P.B. 2001. Genetic diversity in taro (Colocasia esculenta Schott, Araceae) in China: An ethnobotanical and genetic approach. Econ Bot. 55 (1):14–31.

Kreike, C.M., Van Eck, H.J. and Lebot, V. 2004. Genetic diversity of taro, Colocasia esculenta (L.) Schott, in Southeast Asia and the Pacific. Theo and App Genet. 109(4): 761-768.

Kuruvilla, K.M. and Singh, A. 1981. Karyotypic and electrophoretic studies on taro and its origin. Euphytica. 30(2):405–13.

Lakhanpaul, S., Velayudhan, KC and Bhat, K.V. 2003. Analysis of genetic diversity in Indian taro [Colocasia esculenta (L.) Schott] using random amplified polymorphic DNA (RAPD) markers. Genet Res and Crop Evol, 50(6): 603-609.

Lebot, V., 2009. Tropical root and tuber crops: cassava, sweet potato, yams, aroids. CABI.
Lebot, V., Hartati, S., Hue, N.T., Viet, N.V., Nghia, N.H., Okpul, T. and Krieke, C.M. 2002. Genetic variation taro (Colocasia esculenta) in South East Asia and Oceania. 524-533.

Loy, T.H., Spriggs, M. and Wickler, S. 1992. Direct evidence for human use of plants 28,000 years’ ago-starch residues on stone artifacts from the northern Solomon-Islands. Antiquity. 66(253):898–912.

Mace, E.S., Godwin, I.D. 2002. Development and characterization of polymorphic microsatellite markers in taro (Colocasia esculenta). Genome. 45(5): 823-832.

Macharia, M.W., Runo, S.M., Muchugi, A.N. and Palapala, V. 2014. Genetic structure and diversity of East African taro [Colocasia esculenta (L.) Schott]. African J of Biotech. 13(29).

Matthew, P., Matsushita, Y., Sato, T. and Hirai, M. 1992. Ribosomal and mitochondrial variation in Japanese taro (Colocasia esculenta (L.) Schott). Jap. J. Breed. 42: 825–833.

Ramanatha, R.V., Matthews, P.J., Eyzaguirre, P.B. and Hunter, D. 2010. The Global Diversity of Taro: Ethnobotany and Conservation. Bioversity International, Rome, Italy. 202 p.

Rohlf, F.J., 2001. Comparative methods for the analysis of continuous variables: geometric interpretations. Evolution. 55(11): 2143-2160.

Sharma, K., Mishra, A.K. and Misra, R.S. 2008. The genetic structure of taro: a comparison of RAPD and isozyme markers. Plant Biotech Rep 2(3): 191-198.

Singh, S., Singh, D.R., Faseela, F., Kumar, N., Damodaran, V. and Srivastava, R.C. 2012. Diversity of 21 taro (Colocasia esculenta (L.) Schott) accessions of Andaman Islands. Genet Res and crop Evol.59 (5): 821-829.

Sneath, P.H., and Sokal, R.R. 1975. Numerical taxonomy. The principles and practice of numerical classification. Systematic Zoology. 24(2):263-268.

Sree Lekha, S., and Pillai, S.V. 2008. SSR marker variability in a set of Indian cultivars from a typical cassava growing area. Asian Austral. J. Plant Sci. Biotechnol, 2(2): 92-96.

How to cite this article:

Thejazhanuo Lulu Mezhii, Sapu Changkija, A. Pattanayak, H.P. Chaturvedi, S. Vimala Devi and Pravas R. Kole. 2017. Genetic Characterization of Locally Cultivated Taro Germplasm from Eleven District of Nagaland. Int.J.Curr.Microbiol.App.Sci. 6(8): 3338-3348.
doi: https://doi.org/10.20546/ijemas.2017.608.398