STUDY OF GENETIC DIVERGENCE IN INDIGENOUS EDIBLE AROIDS OF NAGALAND USING MORPHOLOGICAL AND SSR DNA FINGERPRINTING.

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Dedicated

To

My Parents

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Chapter 1
Introduction

The Araceae belongs to the monocotyledonous, which is a large family, comprising some hundred genera and more than fifteen-hundred species. Mostly tropical or subtropical plants, the aroids grow mainly in moist or shady habitats. Some are terrestrial plants while others are vines, creepers, or climbers. Many species of the Araceae are also epiphytes. The major edible aroids are classified in two tribes and five genera; Lasioideae (*Cyrtosperma* and *Amorphophallus*) and Colocasiodeae (*Alocasia*, *Colocasia*, and *Xanthosoma*). Among tuber crops, edible aroids form an important group constituting mainly of taro (Colocasia esculenta (L.) Schott), tannia (Xanthosoma sagittifolium(L.) Schott), giant taro (Alocasia macrorrhiza (L.) Schott), swamp taro (Cyrtosperma spp. Griff.), elephant foot yam (Amorphophallus paeoniifolius (Dennst.) Nicolson) etc. *Colocasia esculenta* (L.) Schott commonly known as Taro or Cocoyam is considered as a single polymorphic species. *Colocasia* and *Xanthosoma* are the most important of the edible genera. *Colocasia esculenta* (L.) Schoot, is a vegetatively propagated root crop, although it is propagated vegetatively, it can also flower and set seed. Individual shoots of *C. esculenta* will reach a height and spread of 1.5m x 60cm (RHS, 1999) but eventual size is very much dependent on climate and cultivation factors. The morphology of Aroideae, which contains *C. esculenta,* includes the characteristic spadix and spathe inflorescence present in all members of this subfamily (Lebot, 2009). A spadix is a specialised form of spike inflorescence where small, sessile, individual flowers are tightly packed onto a fleshy core. *Colocasia* species are monoecious; the female flowers are situated at the base of the spadix with the male flowers above. The spathe, which is a large bract

partially enclosing the spadix, surrounds the spadix and the space formed between these two structures provides a resting place and shelter for insect pollinators.(Lebot, 2009)

The leaf shape is peltate in almost all genotypes and the leaf lamina can vary from 30 to over 80cm long; in part the variation is due to genotype but environmental and cultivation factors also have a significant effect on length and breadth of both lamina and petiole. Leaves are somewhat glaucous with reticulate, sometimes prominent, venation. Leaf colour can vary from pale green to deep purple with the laminae and petioles not necessarily exhibiting the same colour.

There are two botanical varieties characterised by their corm shape and described as the Eddoe, with a smaller central corm where the side cormels are eaten, and the Dasheen with a large central corm (which is eaten) and small cormels which are discarded. The Eddoe may correspond to the *esculenta* varieties and the Dasheen to the *antiquorum,* with the *esculenta* (Eddoe) varieties bearing the most similarity to wild forms of taro (Lebot, 2009). It has been suggested that of the two varieties, *C. esculenta* var. *esculenta* is diploid and var. antiquorum is triploid (Kuruvilla and Singh 1981; Irwin *et al.*, 1998). It is generally accepted that the majority of triploids are of Asian origin (Matthews 1990). It is believed to have been originated in the Indo-Malayan region perhaps in Eastern India (de la Pena, 1970). Saner (1969) and Spier (1951) also believed that Colocasia originated in the lands along the Northern edge of the Bay of Bengal is an important root crop throughout the world (Mace *et al.,* 2006). Generally, cocoyams are considered to be either a variety of taro or a variety of tannia (*Xanthosoma sagittifolium*). Tannia is an aroid that bears tubers resembling the taro. The best way to tell tannia and taro apart is to examine where the leaf is attached to the

stem. The tannia stalk starts at the base of the leaf blade, while the taro stalk starts further toward the center of the leaf. According to Bown (2000) there are two main species, *X. sagittifolium* and *X. violaceum.* This division into species is based on the colour of the corm, cormels and leaves and on the shape of the cormels. The foliage of *X. violaceum* is purple-flushed and the corms and cormels are purple-grey with reddish eyes and purple, red, pink, yellow or white flesh. *X. sagittifolium* has green leaves and the corms and cormels have white, yellow or pink flesh and pale brown skin. The shape of the cormels from *X sagittifolium* is globose, and for *X violaceum* ovateelliptic (Bown, 2000).

According to the estimate, the world area under Colocasia (taro) is 9.88 lac hectares with an annual production of 5.7 million tones of tuber (FAO, 1987). World-wide, it is the fifth most consumed root vegetable (FAOSTAT, 2005) with over 25% produced in Oceania and South-East Asia.

Until recently, Colocasia has been a vegetable of minor importance .However, now different cultivars of Colocasia are being grown throughout the tropics, sub-tropics and to some extent in the temperate regions. The corms and the cormels are usually consumed after boiling, curing or frying. Occasionally, the petioles and runners are used as vegetables and considered as a rich source of carbohydrates, proteins, minerals and vitamins. They are a good source of thiamin, riboflavin, iron, phosphorus, zinc and a very good source of vitamin B6, vitamin C, niacin, potassium, copper, and manganese. The digestibility of Colocasia starch is quite good and considered equal to that of potato starch (Standal, 1983). Colocasia makes a good substitute for potato and somewhat sweeter and easily cooked then potato. The flour of taro can be mixed with wheat flour in the ratio 1:3 (Jain *et al.,* 1950). Taro chips which are similar to the potato chips are popular snack food in Hawaii. The tubers are rich source of starch (up to 21 percent total

carbohydrate), protein (above three percent) and minerals, the leaves contain protein (3.9 per cent) and minerals (Gopalan *et al.,* 1977). Taro in its raw form, the plant is toxic due to the presence of calcium oxalate, and the presence of needle-shaped raphides in the plant cells. However the toxin can be minimized and the tuber rendered palatable by cooking or by steeping in cold water overnight. Corms of small variety are peeled and boiled, sold either frozen, bagged in its own liquids or canned. The leaves are rich in vitamins and minerals. It is also used for Anthocyanin study experiments especially with reference to abaxial and adaxial anthocyanic concentration. Taro is often fed to babies as their first whole and natural healthy food, as well as to the elderly, for it is easy to digest and has high vitamin content. Some people call poi the "soul food" of Hawaii. Poi is prepared by cooking the corms and mashed with water. In the old days, a person might consume up to five pounds of poi per day. MacCaughey, 1990 recognized how easily poi was digested in 1917, and explained that this was due to the small size of the taro starch granule. This was confirmed by the studies of Langworthy and Deuel, 1922, who found that the raw starches of rice and taro root were notably more digestible; they also determined that this was the result of the smaller size of the starch granules. Early human studies with poi ingestion showed no undigested starch in feces, even if large quantities of poi were consumed. Food allergies most frequently afflict children, with cow's milk being the most common allergenic food for infants, followed by eggs, peanuts, tree nuts, and soybeans. Feingol, (1942) was one of the first researchers to suggest that poi be considered a substitute for soy milk in infants allergic to both soy and cow's milk. Poi may also be useful for people with celiac disease, who are allergic to the protein gluten in wheat.

Taro is cultivated not only for its edible root stalks, but also for its

medicinal properties (Nadkarni, 1927). Hot tubers are locally applied to the painful parts in "rheumatism". The ash obtained from the root stalks is mixed with honey and locally applied for 'Aphathae' in mouth. Medicinal use of taro includes pressed juice of the petioles is used as a stypic or astringent. The corms are rubifacient and laxative and used in otalgia, internal haemorrhages. Another potential medicinal use of poi is as a probiotic because it contains the predominant lactic acid bacteria (*L. lactis*). Perhaps poi also deserves to be researched as having a possible beneficial role in those medical conditions shown to improve with the use of fermented dairy products: diarrhea, gastroenteritis, irritable bowel syndrome, and inflammatory bowel disease (Crohn's disease and ulcerative colitis), cancer, depressed immune function, and inadequate lactase digestion. In addition, the easy digestibility and other characteristics of poi might make it a nutritional supplement for weight gain in patients with conditions such as failure-to-thrive, cancer cachexia, AIDS, pancreatitis (cystic fibrosis), and some of the induced weight loss conditions of the gastrointestinal tract, such as inflammatory bowel disease.

India holds a rich genetic diversity of tropical root and tuber crops viz. Cassava, Sweet potato, Aroids, Yams and several minor tuber crops. The two hot spots of global biodiversity in India are viz. North Eastern Himalayas and Western Ghats are particularly rich in wild relatives of tropical root and tuber crops. Safe conservation and sustainable use of plant biodiversity is essential for meeting the present and future needs of tuber crop improvement in India. Colocasia is a versatile crops found grown (wild as well as cultivated) throughout the country. It prefers moist soil condition and flourishes under flooded conditions. Again it is well adapted to shade and can withstand drought to a great extent. Although colocasia had been in India for a sufficiently long time mainly in hilly areas, it is

only during the last few years that this crop assumed considerable importance. Keeping the view of the economic importance of the crops, the Indian Council of Agricultural Research has launched a Coordinated Tuber Crop Improvement Programm (other than potato).

Germplasm collection of Aroids from North-east and their maintenance was done at NBPGR, Shillong and their total germplasm collection of 233 aroids is maintained (Pandey *et al*., 1992). The 216 accessions of taro cultivars that have been collected from various parts of NEH region (Hore and Sharm, 1986-92) show variability in their tuber shape, petiole colour, colour of leaf margin and petiole attachment.

Taro is mostly cultivated in Asia, Africa and Pacific as well as Caribbean Islands. In Pacific Islands it is an important economic crop besides being a staple in countries like Fiji, Papua New Guinea, Western Samoa, Vanuatu etc in the South pacific region. In India, taro is cultivated in almost all the states, right from the foot hills of Himalayas to the coastal areas in the South. Taro is believed to have originated in South East Asia including India.

Colocasia popularly known as '*Kochu*' (Assamese), *Dziinuo* (Angami), *Manii* (Ao) etc, in Nagaland it is one of the secondary stable food and most important vegetable which is extensively consumed by most of the farmers in the hilly region and also used as feeds for animals particularly piggery. It is generally grown in Jhum field and in kitchen garden as its cormels, petiole and

leaves serve the important purpose as an instant vegetable for household consumption. The average yield is about 10,000 – 15,000 kg/ha (State Agriculture Research Station, Yisemyong, Mokokchung, Nagaland). In Nagaland, a wealth of diverse genetic material has been observed. Within a region one often finds different kinds of cultivars cultivated by the farmers which may vary in color, size or texture of the corms and cormels etc. Of all the districts in Nagaland, Taro is mostly eaten as a staple food in Mon especially during the taro harvesting season as well as during the plantation season wherein Taro's are dried in the sun and stored in the bamboo basket for almost 2 months and are eaten during these seasons. Though it has got a wide genetic diversity in Nagaland, but due to lack of information available regarding the potentiality not much research have been done. It needs hardly be emphasized that genetic variability is the prerequisite to undertake any breeding programm. Again for planning successful breeding programme, it is very much essential to have information on the association of important yield attributing characters as reflected by varieties adapted to various agro climatic conditions, further the magnitude of direct and indirect effects of various character on the product of economic worth as revealed by the path analysis, would be important in formulating the effective selection indices.

Due to the vegetative nature of the crop and as a result of fixing somatic mutations, morphotypes are quite distinct even when they share the same genetic material. Hence, for breeding purposes, selection of the most divergent parents becomes difficult if one goes by morphological characterization alone, it is in this regard that molecular characterization attains its relevance. Here, the actual genetic diversity exhibited by the crop can be measured and utilized for breeding and conservation of genetic resources. Molecular marker is an effective technique

in genetic analysis of a plant variety. Molecular markers have been applied widely in plant breeding programs. Molecular marker that is often used to distinguish plant diversity is a marker of isozyme and DNA. Cytologically, though, separation of taro varieties into diploid and triploid types (x 5 14) has been possible, Onyilagha *et al*. (1987) have reported unpredictable changes in the chromosomes during cell division resulting in the lack of uniformity in this crop. They reported 2n 5 22,26,28,38 and 42 in the plants collected from various locations. Lebot and Aradhya (1991) studied the genetic relationships between taro cultivars from Asia and the Pacific using isozymes. Their results showed a higher level of genetic variation in Asia than in the Pacific, with Indonesia being the area with the greatest diversity. Irwin *et al*. (1998) screened taro germplasm with RAPD markers and also found that Asian cultivars were genetically distant from the Pacific genotypes. Molecular marker-based genetic diversity analysis, using hyper variable markers, allows enhanced resolution and objectivity. Microsatellite loci, also known as simple sequence repeats (SSRs) are among the most commonly used and technically efficient PCR-based markers (Abdelkrim *et al.*, 2009). The development of molecular markers as a tool for taro germplasm characterization and early progeny selection is highly desirable for developing an efficient breeding program to speed the integration of new genetic material into elite germplasm. Breeders are now attempting to broaden their working populations and morpho-agronomic characterisation has to be followed by molecular analyses in order to provide an accurate picture of the diversity within cultivars as well as in the wild genepool. In addition, taro germplasm characterization using molecular markers will contribute to knowledge of the genetic relationships between accessions of the wild and cultivated genepool, and hence facilitate the breeding of taro cultivars to satisfy market needs and to respond to diverse biotic (e.g., taro leaf blight) and abiotic (e.g., drought) challenges. Significant progress

has been made in recent years in the application of molecular markers to plant genetic resources characterization and evaluation (Gupta and Varshney, 2000). Microsatellites, also known as SSRs (simple sequence repeats), STRs (short tandem repeat), STMSs (sequence tagged microsatellite site), and VNTRs (variable number of tandem repeats), are short (1–8 bp long) tandemly repeated DNA sequences. Conservation of the flanking sequence of each microsatellite locus allows the design of primers for PCR amplification, and the amplification products are separated by electrophoresis to detect the polymorphism in repeat length. Till now, no systematic study has been carried out to determine the extent of genetic variation present at the DNA level by molecular marker technique in landraces of Taro germplasm in Nagaland. Therefore attempt has been made in the present investigation to analyse the genetic diversity using morphological characters and microsatellite marker technique.

Keeping the points in view the present investigation was planned with the following objectives:

- To collect and evaluate the germplasm scattered in different localities.
- To study the extent of variability of agro morphological characters.
- To find out the degree and direction of relationship of different characters.
- To find out direct and indirect contribution of independent variable on dependent one.
- Characterization of genetic diversity through DNA fingerprinting.
- To identify the promising lines.

Chapter 2
Review of Literature

Colocasia esculenta (L.) Schott until recently have been a vegetable of minor importance, but now different cultivars of Colocasia are cultivated extensively for their root stalk and medicinal properties. However limited studies have been done in this crop. The pertinent literature available on variability, heritability genetic advance correlation, path analysis studies and microsatellite, DNA marker studies in Colocasia along with other crops have been review as follows:

2.1. Genetic Variability

Variability refers to the existence of phenotypic differences among genotypes of a population. Variability differs from diversity in the sense that the former has observable phenotypic differences, whereas the later may or may not have such an expression (Ahlawat *et al*., 2008). Development of an effective breeding programme is dependent upon the existence of genetic variability. The success of genetic improvement in any character depends on the nature and extent of genetic variability present in the gene pool. For initiating a breeding programme on any crop, a survey of variation within the species may help the breeder in choosing the most appropriate breeding procedure. Among the two types of variability (phenotypic and genotypic) present in the materials, genotypic variability is of importance to the breeder.

Biradar and Venkateshwaralu (1979) studied eight quantitative characters in Colocasia *viz.,* number of suckers, petiole thickness, number of leaves retained at harvest time, plant height, harvest index, cormel number, mean cormel weight and

corm number along with yield per plant. They reported that 91.95% of variability in yield was accounted for by its association with other eight characters. Cormel number, mean cormel weight and corm number accounted for 87.24% of total variability.

Abraham and Nair (1980) working on lesser yam (*Dioscorea esculenta* Burk) considering eight characters (in 47 accession) *viz.,* tuber yield per plant, number of tubers per plant, individual tuber weight, tuber length, tuber diameter, neck length, internodes length and petiole length found that lowest amount of variation was recorded for tuber diameter and high value of CV for number of tubers, neck length, individual tuber weight and tuber weight per plant thus offering ample scope for improvement of these characters through selection.

Akorda (1984) working on yellow yam estimated the phenotypic variances, genetic co-efficient of variation, etc. and found high value of variation for leave size and yield per plant. He also observed high value of genetic co-efficient of variation for corm weight and leaf size.

Unnikrishnan and Nair (1984) recorded variation in Colocasia regarding morphological character such as plant height, petiole and lamina colour, petiole junction pattern colour, sheath colour etc.

Sreekumari and Abraham (1984) studied thirteen characters in Coleus and reported high variation in six characters (above 30%) *viz.,* number of branches, spike length, number of tuber per plant, tuber length, tuber girth and tuber yield. Less

amount of variation was observed in petiole length, leaf size and biochemical qualities of the tuber.

Singh and Naskar (1988) evaluated forty three strains of Colocasia for different useful characters and found that the strain differed significantly in height, length of petiole, breath of leaf, length of tuber, girth of tubers number of tuber per plant, size of the main tuber and yield per plant.

Dwivedi and Sen (1995) study the growth characters, yield attributes and cormel yield of 15 improved local taro cultivars grown in West Bengal, BCC-1, BCC-2, BCC-4, BCC-5, BCC-8, BCC-9, BCC-10, BCC-11, BCC-13, BCC-16, BCC-17, BCC-18, BCC-19, BCC-20 and BCC-21. Cultivar BCC-13 was found superior to all other cultivars in terms of the length and girth of the main sucker. However, the number of side suckers and petioles per plant were greatest in BCC-1 and BCC-11. BCC-19 produced the most cormels per plant. The highest corm weight and corm:cormel ratio were recorded in BCC-13, while the weight of cormels per plant was greatest in BCC-16. The largest cormel was produced by BCC-17. BCC-16, BCC-19 and BCC-20 yielded the most cormels per hectare.

Pandey and Dobhal (1997) reported the genetic variation of *C. esculenta* collected from Assam, Meghalaya and Nagaland. They found that significant differences occurred between the genotypes which, using Mahalanobis' D2 statistic, were grouped into 11 clusters irrespective of geographical origin. Genotypes IC-87168(M), IC-87042(M) and IC-89548(A) were distinct and classed as separate clusters. IC-89548(A) exhibited the highest mean values for yield/plant (933.8 g) and weight of mother cormels (640.5 g). The cluster containing IC-87132(A) and IC-87163(M) also exhibited high yields (875.2 g) and cormel weight (449.8 g) combined

with greater plant height, leaf length and leaf width than IC-89548(A). These genotypes are recommended for use in breeding programmes.

Sarma and Narzary (2000) studied the tubers of 5 *Colocasia esculenta* cultivars, Bor Kachu, Ahina-Black, Mohkhuti, Tekeli Kachu and Koni Kachu, and analyzed for moisture, dry matter and ash contents at various stages of growth under 4 different spacing (60 x 35, 60 x 45, 60 x 55 and 60 x 65 cm) and reported that the most significant changes were observed in immature tuber with a decreased in moisture content and increase in dry matter and ash content with increasing maturity. At harvest, oxalic acid, total acid, ascorbic acid, reducing sugar, non-reducing sugar and starch content were determined and all the cultivars showed varying amount of these contents. Oxalic acids, which responsible for acidity, was minimum in Ahina-Black. The spacing had no effect on quality attributes in *C. esculenta* cultivars.

Dwivedi and Sen (2001) conducted a comparative study of some local taro (*Colocasia esculenta var. antiquorum)* of 15 improved local taro cultivars BCC-1, BCC-2, BCC-4, BCC-5, BCC-8, BCC-9, BCC-10, BCC-11, BCC-13, BCC-16, BCC-17, BCC-18, BCC-19, BCC-20 and BCC-21. Cultivar BCC-13 was found cultivars of West Bengal. Cultivar BCC-13 was found superior to all other cultivars in terms of the length and girth of the main sucker. However, the number of side suckers and petioles per plant were greatest in BCC-1 and BCC-11. BCC-19 produced the most cormels per plant. The highest corm weight and corm:cormel ratio were recorded in BCC-13, while the weight of cormels per plant was greatest in BCC-16. The largest cormel was produced by BCC-17. BCC-16, BCC-19 and BCC-20 yielded the most cormels per hectare.

Singh *et al.* (2003) study the variability and character association in Colocasia. The reported that the phenotypic and genotypic variation coefficients showed that selection may be made for petioles per plant, leaf area and cormels per clump. The value of heritability and genetic advance showed that effective selection may be made for leaf area, corms per plant and clump weight per plant Corms per clump and cormels per clump had a strong positive correlation with corm yield. Corm yield may be increased through selection for this trait.

Singh *et al.* (2003) studied the genetic variability of 36 *C. esculenta var. antiquorum* in terms of phenotypic and genotypic coefficients of variation, heritability and genetic advance. They reported that significant differences were observed among the cultivars studied. The highest phenotypic and genotypic coefficients of variation was recorded for cormel weight per plant, number of cormels per plant and weight of corm per plant.

Mukherjee *et al.* (2003) conducted an experiment on genetic variability and causal relationships in dasheen taro (*Colocasia esculenta* var. esculenta (L.) Schoot) on fourteen diverse genotypes of dasheen type taro (*Colocasia esculenta* var. esculenta) for genetic variability and character association among 9 quantitative traits (plant height, number of leaves, length of leaf lamina, breadth of leaf lamina, number of cormels per plant, weight of mother corms per plant, weight of cormels per plant, dry matter of tuber, and total tuber yield per plant). They found that significant differences were observed for all the traits. The number of cormels per plant and dry matter content of mother tubers exhibited high genetic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance as percent of mean, indicating the presence of additive genes controlling the characters. The genotypic and phenotypic correlations showed good agreement. The weight of

cormels per plant, number of cormels per plant and dry matter content of mother tubers exhibited significant positive correlations with total tuber yield per plant.

Singh *et al.* (2004) studied the genetic variability in Banda (*Colocasia esculenta*). Observations were recorded for 20 characters, i.e. plant height, petiole length, sheath length, plant diameter, leaf number per plant at 90 days after planting (DAP), leaf number per plant at 120 DAP, leaf length at 120 DAP, leaf breadth at 120 DAP, number of suckers per plant, cormel number per plant, corm length, corm diameter, cormel length, cormel diameter, corm dry matter and starch contents, cormel weight per plant, average corm weight, average cormel weight and corm weight per plant. Highly significant differences amongst the genotypes for all the characters were observed. A wide range of variation was observed for all the characters. The phenotypic coefficients of variation (PCV) were higher in magnitude than the genotypic coefficients of variation (GCV) for all the traits. The highest estimates of GCV and PCV were observed in the case of cormel number per plant followed by average weight of corm. The lowest estimates of GCV and PCV were recorded in the case of starch percentage in corm.

Mandal *et al.* (2013) conducted an experiment on genetic variability in Taro (*Colocasia esculenta* (L.) Schoot) on twenty diverse genotypes of d taro for genetic variability and character association among 9 quantitative traits (Length of main sucker, Girth of main sucker, No of side sucker, No of petioles per clump, Length of leaf lamina, breath of leaf lamina, No of side tuber, weight of side tuber, corm yield. They found that significant differences were observed for all the traits. The highest estimates of GCV and PCV were observed in the case of Length of main sucker followed by Girth of main sucker. The lowest estimates of GCV and PCV were recorded in the case of length of leaf and breath of leaf lamina. Number of

petioles/clump. Number of side tuber/plant and weight of side tubers/plants and corm yield had high GCV and PCV (>30%).

Bhattachrarjee *et al.* (2014) studied the genetic variability in Upland taro (*Colocasia esculenta var antiquorium(L.)Schott*). Observations were recorded for 9 characters, i.e. Length of main sucker, Girth of main sucker, No of side sucker, No of leaf lamina per clump, Length of leaf lamina, breath of leaf lamina, No of side tuber, weight of side tuber, corm yield. Highly significant differences amongst the genotypes for all the characters were observed. A wide range of variation was observed for all the characters. The phenotypic coefficients of variation (PCV) were higher in magnitude than the genotypic coefficients of variation (GCV) for all the traits. The highest estimates of GCV and PCV were observed in the case of Length of main sucker followed by Girth of main sucker. The lowest estimates of GCV and PCV were recorded in the case of length of leaf and breath of leaf lamina.

Assessment of genotypic variability is usually made by high genotypic coefficient of variation, wide range among genotypes with high mean values. The literature consulted on this aspect are summarized as under:-

2.2. Heritability and genetic advance

Heritability and genetic advance are two important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will also exibit high genetic advance (Johnson *et al*., 1955)

Heritability is an index of the transmission of the characters from the parents to their off-springs (Falconer, 1981) and generally it is expressed in percentage. Heritability estimates help the plant breeder in selection of elite genotypes from diverse population. This also measures the degree of resemblance between relatives and correspondence between phenotypic and breeding values. Heritability is of two types depending on the components of variance used in the calculation-

Heritability in broad sense ($(h^2_{b.s})$)

It is a ratio of genotypic variance to the total phenotypic variance. This type of heritability is used for study of homozygous lines (Lush 1940)

Heritability in narrow sense ($(h^2_{n.s})$)

It is the ratio of additive or fixable portion of genetic variance to the total phenotypic variance. This is essential from additive genetic variance as it plays important role in selection of elite genotypes from the segregating population.

The concept of heritability indicates whether the phenotypic difference among the individuals are due to genetic or non-genetic (environmental) causes. High heritability estimates of any particular character indicates more genetic variance or additive components of variance for that character. Such characters can be included in crop improvement programme as the gain under selection based in those characters is likely to be more. On the other hand, low heritability estimate of a character indicates less contribution of genetic variance to the total phenotypic variance of that character. Such characters are highly affected by environment. Gain under selection based on these character is less and hence such characters cannot be included in crop improvement programmes.

Genetic advance is the improvement in mean genotypic value of the selected individuals over the parental population. It is the measure of genetic gain under selection. Allard (1960) expressed the genetic advance as the product of selection intensity, heritability and phenotypic standard deviation of a character. He further reported that genetic advance under selection depends on –

i. Magnitude of genetic variability
ii. Magnitude of the heritability of the character
iii. Intensity of selection.

Burton (1952) suggested that genetic co-efficient of variance (GVC) along with heritability estimate would provide the best pick of the amount of the advance to be expected from the selection.

Lin (1983) observed that in sweet potato that dry matter weight, length of main stem/R(Stem per tuber weight),inter node length and yield showed heritability estimates more than 65% T/R value and number of large tubers had the highest GCV and greatest genetic advance followed by yield per plant , length of main stem and branch number.

Rhishi *et al.* (1984) reported high estimates for heritability in broad sense for weight of vine per plant, leaf area per plant and tuber yield per plant in *Dioscorea deltoidea*.

Akorda (1984) also observed high estimates of variability and genetic advance (over 50%) for plant leafiness, number of tubers and tuber yield in *Dioscorea cayenensis*.

Thankamma and Easwari (1988) reported that in sweet potato, heritability and genetic advance estimates were comparatively high for yield and medium or low for other characters. High heritability estimates were obtained for tuber length and tuber yield followed by numbers of branches, tuber girth and weight of the vine, indicating that additive genetic variance was relatively more important than non additive genetic variance. Low heritability estimates were observed for vine length, vine girth, number of leaves per branch, leaf length, leaf breadth, petiole length and number of tubers. Low heritability is attributed to non additive genetic variance.

Pandey *et al.* (1996) conducted an experiment in taro (*Colocasia esculenta* L.). They reported that a wide variability was observed for yield/plant, weight of mother cormels and weight of cormels. High heritability coupled with high genetic advance was estimated for weight of mother cormels, weight of cormels and yield/plant.

Matthews (1997) developed this guide is designed to encourage research on wild and possibly natural varieties of taro (wild-types). An apparently natural form of taro and the wild habitats in which it has been found are described. A short form is provided for recording a single plant from each site. It is suggested that, with practice, this form can be completed in 10 minutes. The form can also be used to record cultivated varieties of taro, but is not intended as a substitute for the longer FAO descriptor list.

Singh *et al.* (2003) in their studies reported that the value of heritability and genetic advance showed that effective selection may be made for leaf area, corms per plant and clump weight per plant, corms per clump and cormels per clump had a strong positive correlation with corm yield. Corm yield may be increased through selection for this trait.

Singh *et al.* (2003) studied heritability and genetic advance for yield and its attributing traits in arvi (*Colocasia esculenta* var. antiquorum). The genetic variability of 36 *C. esculenta* var. antiquorum in terms heritability and genetic advance was determined in a field experiment conducted in Uttar Pradesh, India during 1998-99. Significant differences were observed among the cultivars studied. High heritability and genetic advance were obtained for corm weight per plant, number of cormels per plant, weight of cormels per plant and dry matter content of cormels.

Singh *et al.* (2004) studied the extent of genetic variation present in 35 genotypes of Banda (*C. esculenta*). They reported that the heritability estimates ranged from 63.10 to 99.90%, indicating high heritability for all the traits. The heritability was highest for cormel number per plant and average weight of corm. The highest genetic advance was noticed in respect of corm weight per plant. Among the economic characters, the highest genetic advance was noticed in corm weight per plant followed by average weight of corm and cormel weight per plant. The high heritability coupled with high genetic advance made the component traits corm weight per plant, average weight of corm, cormel weight per plant and average weight of cormel, the most reliable bases of selection programme.

Mandal *et al.* (2013) conducted an experiment on genetic variability in Taro (*Colocasia esculenta* (L.) Schoot). The genetic variability of 20 *C. esculenta* in terms of heritability and genetic advance was determined in a field experiment. Significant differences were observed among the cultivars studied. High heritability were obtained from Length of main sucker followed by weight of side tubers per plant, corm yield, number of petioles per clump and breath of leaf lamina. The highest genetic advance was notice in weight of side tubers per plant. The high heritability coupled with high genetic advance made the component traits Length of main sucker and girth of main sucker indicating improvement of character through selection programme.

Bhattacharjee *et al.* (2014) studied the extent of genetic variation present in 20 genotypes of (*C. esculenta*). The heritability was highest for Leaf main sucker and Girth of main sucker. Among the economic characters, the highest genetic advance was noticed in corm yield per plant followed by No of petioles/clump, no of side tuber/plant and weight of side tuber/plant. The high heritability coupled with high genetic advance made the component traits Length of main sucker and girth of main sucker the most reliable bases of selection programme.

2.3. Correlation studies and path analysis

Correlation refers to the degree and direction of linear association between two or more variables. It, however, does not measure the dependence of one variable over the other. Important properties of correlation as outlined by Elhance and Elhance (1990) are-

i. It is independent of unit of measurement.
ii. Its value lies between -1 and +1.
iii. It measure the degree and direction of linear relationship between two or more variables.

The correlation study of a given crop is important because most of the economic characters such as yield and yield attributing traits are correlated eith eacg other. Correlation may be phenotypic, genotypic and environmental. Phenotypic correlation is the observable association between two variables. It includes both genotypic and environmental effect and it is mostly due to genetic causes for the high heritable characters.

Genotypic or genetic correlation is the heritable association between two variables. This type of correlation may be either due to pleiotropic action of the genes or due to linkage or more likely both. The main genetic cause of such correlation is pleiotropy, which refers to many fold effect of gene (Falconer, 1960). This type of correlation is more stable and is of paramount importance for a plant breeder to bring about genetic improvement in one character by selecting another genetically correlated character. While, environmental correlation is entirely due to environmental effects. In other words, this is due to error variance. This type of correlation is not important to a plant breeder, as it is not heritable and stable.

2.4 Path Coefficient analysis

The concept of Path analysis was originally developed by Wright (1921) but the technique was first used for plant selection by Dewy and Lu (1959). Path coefficient is simply a standardized partial regression coefficient, which splits the correlation coefficient into measures of direct and indirect effects.

It is now an established fact that one gene governs not only one major character but also several other minor characters through its pleiotropic action. For this reason, correlation study alone does not provide a clear picture about the contribution of a particular character towards its association with another character. Two positively correlated characters may have negative direct effect. In such cases, correlation coefficient is the result of positive indirect effects, which masked the direct effect of the character. Under such situation, indirect effects should be taken into account while planning a selection programme. Knowledge of direct and indirect contributions of any character is, therefore, very essential for any selection programme.

Karikari (1974) had also reported a very high linear correlation between LAI and cormel yield in cocoyam. The result on path analysis of yield components and yield indicated that the direct effect of number cormel per plant with yield was high, but the indirect effect was low .the negative indirect effect though the mean weight of the cormel led to a reduction in the magnitude of correlation. The direct effect of mean weight of cormel was high and as correlation with yield was positive and high but the effect was less. The correlation was attributed to the sum total of the plant and mean cormel weight of cormel.

Parthasarathy and Medhi (1981) studied correlations between tuber weight, diameter, length and volume, number of tuber per plant and yield per plant for 10 cultivars of *Colocasia esculenta* and found that yield per plant was significantly and positively correlated with weight and numbers of tubers per plant. There were significant positive correlation between tuber length or tuber weight and volume, tuber diameter or volume and number of tuber per plant and between tuber weight and tuber volume.

Anonymous (1984) worked correlation co-efficient and path analysis on taro and reported that mean cormel weight per plant, number of cormels per plant and LAI were positively and significantly correlated with yield.

Unnikrishnan *et al*. (1984) worked on Colocasia for various characters associated with total yield and reported that strong correlation exists between sheath length, size of the leaf, weight of corm, number and weight of the cormels with yield. Correlation also existed between number of suckers, leaves and girth of mother plant, but negative correlation was observed in the case of number of corms with yield.

Agueguia (1986) studied the association of metric traits and path analysis in cocoyam, *Xanthosoma saggittifolium* (L.) Schott and reported that genotypic correlation were generally higher then the phenotypic ones excepts for number of cormels with other characteristic such as dry matter content of corms and cormels, corm + cormel fresh weight, leaf area and number of leaves. Number of leaves, leaf area and total cocoyam yield was positively correlated with each other. However, co-efficient analysis showed that number of leaves had the highest genotypic correlation with cocoyam yield. Leaf area and number of cormels had high positive direct effect on cocoyam yield whole dry matter content of corm exhibited high negative direct effect.

Singh and Naskar (1988) studied phenotypic and genotypic correlation between different quantitative character of Colocasia and reported that the plant height was significantly and positively correlated at phenotypic as well as genotypic level with their character except yield. Number of corm was found to have negative but non - significant association with the length of petiole, length of leaf and yield of corms at phenotypic and genotypic levels. However, this character had positive but non- significant association with the diameter of petiole and breadth of leaf.

Pillai *et al.* (1995) studied correlation and path analysis in taro. Information on yield correlations is derived from data on 11 characters in 22 accessions of *Colocasia esculenta* grown in Trivandrum during 1989-89. Of the traits studied, number of cormels/plant had the maximum direct effect on yield, followed by mean cormel weight.

Sarkar *et al.* (1996) conducted an experiment on correlation and path coefficient analysis on yield and yield components of *Colocasia esculenta* (L.). They reported that plant height, number of tillers, number of cormels and weight of cormels were positively correlated with yields. The number of tillers/plant had the highest positive direct effect on cormel yield. Plant height and cormels/plant had indirect effects on cormel yield.

Pandey *et al.* (1996) studied the genetic variability, correlation and path analysis in taro (*Colocasia esculenta* L.). They found that a wide variability was observed for yield/plant, weight of mother cormels and weight of cormels. Yield/plant was significantly and positively correlated with most characters at both phenotypic and genotypic levels. Path analysis revealed that weight of mother cormels and weight of cormels had the highest direct and indirect effects, respectively, and could therefore be used as selection criteria for higher yielding genotypes.

Dwivedi and Sen (1999) studied thirty genotypes of taro for correlation and path analysis. The results indicated that cormel yield had positive and significant association with the length and girth of main sucker, number of cormels per plant and corm weight but it was negatively correlated with corm:cormel ratio. Path coefficient analysis revealed that corm weight had the highest direct effect on the cormel yield and positive indirect effect via girth of main sucker. Highest negative direct effect

was recorded by length of main sucker. Selection based on corm weight and higher girth of main sucker will be efficient to maximize the cormel yield in taro.

Singh *et al.* (1999) in their studies reported the association between plant traits related to corm yield and the total marketable yield. The total marketable yield per plant was positively correlated with corm yield per plant. These two traits were positively correlated with leaf availability period, number of leaves and corms per plant, leaf length and breadth, petiole girth and length, and cormel length and diameter. Positive correlations were also observed between the number of corms per plant and the length and breadth of leaves, petiole girth and cormel length, leaf length and cormel length, and leaf breadth and cormel length.

Singh *et al.* (1999) studied correlation and path coefficient analysis in Colocasia (*Colocasia esculenta*) from ten genotypes of Colocasia collected from different districts of Uttar Pradesh, evaluated for 8 yield components at Kanpur in 1996-97. Positive correlations were observed between yield and tubers/plant. It is recommended that selection should focus on tubers/plant, tuber length and plant height.

Velayudhan *et al.* (2000) studied the correlation and path analysis in Taro (*Colocasia esculenta* (L.) Schott) morphotypes for twelve characters using representatives of 72 morphotypic groups (one accession each) of indigenous Taro germplasm. The characters cormel number, cormel thickness, plant height, leaf length and leaf width were found to have high positive correlation with cormel yield whereas leaf number was negatively correlated with yield. Cormel number showed maximum positive direct effect on cormel yield. Selection based on the characters

like number of cormels, plant height and cormel thickness appeared to be most desirable for yield in Taro.

Mukherjee *et al.* (2003) studied genetic variability and causal relationships in dasheen taro (*Colocasia esculenta* var. esculenta L. Schoot). Fourteen diverse genotypes of dasheen type taro (*Colocasia esculenta* var. esculenta) were evaluated, for genetic variability and character association among 9 quantitative traits (plant height, number of leaves, length of leaf lamina, breadth of leaf lamina, number of cormels per plant, weight of mother corms per plant, weight of cormels per plant, dry matter of tuber, and total tuber yield per plant). Significant differences were observed for all the traits. The path coefficient analysis revealed that cormel weight per plant was the most important component because of its high positive direct effects on total tuber yield. Attention should be paid on selection based on cormel weight per plant for total tuber yield improvement.

2.5 Genetic Divergence

Darwin. C (1959) used the expression divergence in characters to record variation in genera, species and varieties. Huxley (1955) used another term genetic polymorphism which means co-existence of different genetic forms in a population.

A number of scientist (Griffing and Lindstrom 1954; Arunachalam 1981 and Hawkes 1981) have emphasized the importance of genetic diversity in plant breeding for obtaining broad spectrum of desirable variability in segregating generations. The presence of potential genetic variability in early and advance generation is an important pre-requisite for the success of selection procedures in attaining objectives of breeding programs.

The varieties which come from widely separated localities are usually presumed to be diverse and are utilized in hybridization program. Earlier workers regarded this geographical isolation as a reasonable index of genetic diversity (Joshi and Dhawan 1966). However, several workers have emphasized that there is no parallelism in geographical distribution and genetic diversity (Murthy and Anand 1966, in linseed; Maurya and Singh 1977 in rice), advocating that varieties with the same geographical origin could have undergone changes under selection pressure. Thus the estimation of variation within the germplasm in divergence study in the form of classification into different homogeneous groups is an important practice.

Conservation of germplasm resource is basic to crop improvement programme. However, to understand the usable variability, grouping or classification of genetic stocks based on suitable scale is quite imperative. Similarly, the major consideration for hybridization under transgressive breeding programme is the choice of genetically divergent parents, which depends on categorization of breeding materials based on the magnitude of genetic diversity among them. Genetically divergent parents are likely to produce higher heterotic effect and also desirable recombinants in the segregating generations.

Multivariate analysis through Mahalanobi's (1936) D^2 statistic methodology has been realized as a powerful tool in qualifying the degree of divergence among biological population. It has a unique place in plant breeding programmes and has been utilized by several breeders (Murthy and Arunachalam, 1966; Arunachalam and ram, 1967; Murthy *et al.,* 1967; Chandrasekhariah *et al.,* 1969; Ram and Panwar, 1970 etc). Mahalanobi's D^2 technique, further elaborated by Rao (1952), has been widely utilized by several workers in both self and cross pollinated crops to measure the statistical distance among genotypes.

Bhatt (1973) compared the D^2 method with the conventional selection based on performance of the parents, random selection based on eco-geographic divergence in wheat breeding programme. Out of the four methods investigated, D^2 technique of selecting parents with high inter genotypic divergence for utilization in crossing programmes was found to be the most effective.

Several breeders studied whether geographic diversity may be consider as an index of genetic diversity. Murty and Arunachalam (1966); Gupta *et al* (1991); Park *et al* (2007) and many others did not find any parallelism between genetic diversity and geographic distribution.

Mandal *et al.* (2013) conducted an experiment on genetic variability and genetic divergence in Taro (*Colocasia esculenta* (L.) Schott). On the basis D^2 statistics the twenty genotypes were grouped into six clusters. Most of the local taro genotypes collected from different locations was placed in Cluster II with moderate intra cluster distance indicating their closeness, and showed similar phenotypic characters. Some genotypes were found to distantly relate to other genotypes and were grouped into Cluster III.

Devi *et al*. (2013) analyse the genetic diversity of edible aroid accessions of India based on morphological characters. Diversity analysis using cluster package (R package) was done for 45 taro accessions on the basis of six tuber characters and 26 elephant foot yam accessions on the basis of 14 above ground characters. The results showed that five clusters were formed in taro based on six tuber characters,

whereas, in elephant foot yam, six major clusters were formed. No duplicates could be identified within the accessions screened.

Bhattacharjee *et al.* (2014) conducted an experiment on genetic variability and genetic divergence in Taro (*Colocasia esculenta* (L.) Schoot). The genetic diversity of 20 *C. esculenta* in terms of D^2 analysis grouped them into 6 clusters. The inter cluster distances in all the clusters were higher than the intra cluster distances suggesting wider genetic diversity among the genotypes of different groups. There was existence of variation for almost all of the characters among different cluster

2.6 Molecular studies:

Genetic diversity in a crop species is basic to the improvement of the species and can be estimated at the molecular level. Genetic markers are of great value in breeding programmes and research. DNA based markers provide powerful tools for discerning variations within crop germplasm and for studying evolutionary relationship (Gepts.1993). For an effective breeding programme, information concerning extend and nature of genetic diversity within a crop species is essential. It is practically useful for characterizing individual accessions and cultivar and as a general guide in the selection of parents for hybridization. Molecular markers like Random amplified DNA (RAPD), Restriction Fragment Length polymorphism (RFLP), Amplified Fragment Length Polymorphism (AFLP), Simple Sequence Repeat (SSR) etc can detect genetic variation at DNA sequence level and reveal genetic variability between closely related individuals. Molecular marker based probes have introduced a new dimension to obtain information ranging from diversity relationship among germplasm to development of genetic maps. The major strength of DNA probes which are exclusively used in Restriction Fragment length Polymorphism (RFLP) is that they have potential to reveal almost unlimited number

of polymorphism. Kan and Dozy, (1978) and Botstein *et al*., (1980) for the first time suggested using RFLPs for mapping of human genome. Later on its potential was recognized in plant breeding and experimentally tested in tomato and maize.

After the discovery of PCR, modern biology has been revolutionized in each and every aspect. It is also applied in diagnosis of plant diseases. A large number of plant pathogens in various host and environment samples are detected by using PCR e.g. viroids (associated with apple, pear, grapes, citrus etc.), viruses such as TMV, Cauliflower mosaic virus, mycoplasmas, bacteria (*Agrobacterium tumifaciens, Pseudomonas solanacearum; Rhizobium leguminosarum, Xanthomonas* spp), and Nematodes e.g. (*Meloidogyne incoginta, M.Javanica* etc. (Hension and French, 1993). Williams *et al.*, (1990) found that the two genetically distinct individuals differ as they show different polymorphism in pattern of amplified bands.

The development of molecular markers as a tool for taro germplasm characterization and early progeny selection is highly desirable for developing an efficient breeding program to speed the integration of new genetic material into elite germplasm. Breeders are now attempting to broaden their working populations and morpho-agronomic characterisation has to be followed by molecular analyses in order to provide an accurate picture of the diversity within cultivars as well as in the wild genepool. In addition, taro germplasm characterization using molecular markers will contribute to knowledge of the genetic relationships between accessions of the wild and cultivated genepool, and hence facilitate the breeding of taro cultivars to satisfy market needs and to respond to diverse biotic (e.g., taro leaf blight) and abiotic (e.g., drought) challenges. Significant progress has been made in recent years in the application of molecular markers to plant genetic resources characterization and evaluation (Gupta and Varshney 2000). Microsatellites, also known as SSRs (simple sequence repeats), STRs (short tandem repeat), STMSs (sequence tagged microsatellite site) and VNTRs (variable number of tandem repeats) are short , 2-8

nucleotide repeats such as CA or AGC, which are repeated in tandem upto hundred of times at many independent loci, and are ubiquitous in eukaryote genomes (Lagercrantz *et al*., 1993). They are generally very highly polymorphic, mainly based on the number of tandem repeat units. SSR markers can be assayed in a similar manner to RFLPs using a short synthetic oligonucleotide probe such as $(CA)_{20}$ to hybridize to blots. However, to speed up and simplify the process, SSR marker can be sequenced tagged (Morgante and Oliveiri,1993). This requires sequencing the flanking regions of a specific SSR locus and designing primers which will amplify the SSR. Polymorphism will be based on either the flanking sequence of more usefully, the number of repeats.

SSRs are very powerful markers in that they are single locus, co-dominant and Multi-allelic. They do not require radioactivity for detection, although this is sometimes used on polyarylamide gels to detect accurately alleles which differ by one repeat unit (as little as 2 bp). They are extremely robust and easily exchanged between labs, and multiplex reactions can be run to speed up the assay, where the products have non overlapping size ranges. The greatest disadvantage is the initial cost in finding and sequencing loci because although SSRs are ubiquitous, there needs to be considerable effort put into their isolation. Hence they have a higher cost of establishment than other systems. SSRs also have limited use for phylogenetic analysis because of their high mutation rate. It is considered by some that due to the limited cross-transferability and long start up time, where speed is essential, SSRs are not the best choice (Karp and Edwards, 1997). However once they are establish, SSR markers are not only permanent, highly informative resource for germplasm fingerprinting and management, but they will be useful for mapping, as has been demonstrated in many plant species including eucalyptus (Brondani *et al*., 1998), soyabean (Akkaya *et al*., 1995), wheat (Korzun *et al*., 1999), rice (Chen *et al*.,1997;

Temnykh *et al*., 2000), maize (Taramino and Tingey, 1996) and triticum (salina *et al*., 2000).

Molecular markers (RAPD) have been used more recently to analyze a subset of 44 accessions from diverse origins (Irwin *et al*., 1998) but no clear geographical or morphological structure was obtained. A combination of isozymes and RAPDs was also used to study Asian taros and the differentiation of the studied regions (Nepal, Yunnan, Japan) was obvious although the relationships between the different populations was far from being evident. Interestingly, their data gave support to an autopolyploid origin of the triploids. More reliable dominant markers (AFLP), have been used to study the diversity of a core sample including 255 accessions from seven countries (Kreike *et al*., 2003). Most accessions could be clearly differentiated by using three primer pairs and few duplicates were found. A differentiation between Southeast Asian and Melanesian taros was obtained, confirming the isozyme results. Thirty-eight wild genotypes were analysed and only those from Thailand (16 acc.) showed a significantly higher genetic diversity as compared to the cultivars. For Indonesia and Malaysia, cultivated and wild genotypes were not clearly differentiated, indicating a possible feral origin of some wild genotypes. Triploids were not associated to diploids and their origin remains unknown. In fact, two clusters of triploids were identified, indicating the possibility of different polyploidisation processes. In Vanuatu, AFLPs were used on a core sample (40 acc.) aiming at validating a stratification approach for germplasm collections. No correspondence was found between the structure of the dendrogram produced and the major morpho-agronomic traits (Quero Garcia, 2000).

Bastide (2000), constructed another microsatellite-enriched library following a hybridisation-based capture methodology using biotin-labelled microsatellite oligoprobes and streptavidin-coated magnetic beads (Billote *et al.,* 1999).

Mace and Godwin (2002) have developed a microsatellite-enriched library following the hybridization method described by Edwards (1996). These microsatellite markers were tested on a sample (17 accession) from several Pacific countries. They proved to be a valuable tool for the identification of duplicates although the geographical structure produced was not very informative, probably due to the small size of the sample.

Lakhanpaul *et al* (2003) collected thirty two Taro [*Colocasia esculenta* (L.) Schott] germplasm accessions from different parts of India and were subjected to RAPD (Random Amplified Polymorphic DNA) analysis to assess the genetic diversity prevalent and also to test the genetic basis of morphotypic classification. Thirteen random decamer primers out of the 22 tested were used to analyse 32 taro accessions belonging to 28 morphotypes. Three out of these thirteen primers analysed showed 100 per cent polymorphism. Dendrogram obtained from UPGMA analysis grouped 32 accessions in four clusters and three accessions were placed as outliers. Clustering pattern did not show any strict relationship with geographical distribution, morphotype classification and genotypic diversity. Further, accessions classified, as belonging to the same morphotypic group did not always cluster together. Presence of a very close genepool of the wild, weedy and cultivated forms with extreme levels of phenotypic and genotypic variation is suggested as the reason for high genetic diversity reported.

Mace *et al.* (2006) have developed a core collection of taro germplasm based on phenotypic and molecular characterization. In total, 2199 accessions of taro germplasm have been collected by TaroGen (Taro Genetic Resources: Conservation and Utilisation) from 10 countries in Oceania. The larger collections from Papua New Guinea,Vanuatu and New Caledonia were analysed based on phenotypic characters, and a diverse subset representing 20% of these collections was fingerprinted. In total, 515 accessions were genotyped (23.4% overall) using taro specific simple sequence repeat (SSR) markers. DNA fingerprint data showed that great allelic diversity existed in Papua New Guinea and the Solomon Islands. Interestingly, rare alleles were identified in taros from the Solomon Islands province of Choiseul which were not observed in any of the other collections. Overall, 211 accessions were recommended for inclusion in the final regional core collection based on the phenotypic and molecular characterization.

Singh *et al.* (2008) collected Taro (*Colocasia esculenta*) accessions from 15 provinces of Papua New Guinea (PNG). The collection, totalling 859 accessions was collected for characterization and a core collection of 81 accessions (*10%) was established on the basis of characterization data generated on 30 agro-morphological descriptors, and DNA fingerprinting using seven SSR primers. The selection of accessions was based on cluster analysis of the morphological data enabling initial selection of 20% accessions. The 20% sample was then reduced and rationalized to 10% (ie. 163 accession) based on molecular data generated by seven SSR primers. Molecular analysis showed that it was not unusual in many instances that contrasting morphological characteristics can cluster together, and conversely, accessions with the same morphological characteristics tend not to cluster together. This could be a manifestation of the clonally propagated behaviour of taro, and ‘sports’ type mutations, Under such situations, the level of similarity based on the molecular analyses was considered a better indicator of genetic similarity than the agro-

morphological characterization. The core collection is a valuable resource for food security of the South Pacific region and is currently being utilized by the breeding programmes of small Pacific Island countries to broaden the genetic base of the crop.

Beevi *et al.* (2011) collected sixty accessions of taro (*Colocasia esculenta* (L.) Schott.) from the three South Indian states and were analyzed using nine Random Amplified Polymorphic DNA (RAPD) primers at Central Tuber Crops Research Institute, Thiruvananthapuram, Kerala, India. The results obtained were utilized for assessing the extent and pattern of intraspecific variation within the species complex. Out of the nine primers, four proved to be highly informative as they could detect high levels of polymorphic fragments and were able to differentiate the accessions. The phylogenetic tree generated using UPGMA cluster analysis revealed that genetic diversity in taro was correlated with the wild and the cultivated forms. The accessions were separated into five major clusters. Out of the five clusters obtained in the dendrogram at 40% level of similarity coefficient, cluster I and cluster II included mainly cultivars. Cluster IV included almost exclusively wild accessions, majority of them being true wild ones with frequent flowering and significant stolon production. The primers were able to distinguish between diploids/triploids accessions. The diploid (clusters I, II, III and IV) and triploid (cluster V) group of accessions tended to form independent clusters and this may be suggestive of agro ecological and sexual separation between them.

Mandal *et al.* (2013) conducted an experiment on genetic diversity using RAPD in Taro (*Colocasia esculenta* (L.) Schoot). The genetic diversity study of 20 *C. esculenta* in terms of RAPD analysis showed the high degree of polymorphism which is effective for assessment of diversity among the local genotypes of West Bengal.

Bhattacharjee *et al.* (2014) studied the genetic diversity on 20 genotypes of Upland taro (*Colocasia esculenta var antiquorium(L.)Schott*) using RAPD technique. Analysis revealed that 9 primers out of 10 amplified total 41 bands, out of them 5 bands were monomorphic. 9 primers were highly informative because they either amplified more than 4 polymorphic or monomorphic bands, which could differentiate between specific Colocasia accessions. Thus showing high degree of polymorphism which is effective for assessment of diversity among the local genotypes.

Macharia *et al*. (2014) studied the genetic diversity of East African taros (*Colocasia esculenta* (L.) Schoot) consisting of 98 taro cultivars from East Africa using six microsatellite primers to analyse five population of taro. Population estimate was relatively very low with the highest being 0.27. Analysis of molecular variance (AMOVA) revealed most variation among individuals with population at 79%. SSR analysis showed that the sampled populations of *Colocasia esculenta* are not significantly different, despite concerns of genetic erosion due to clonal propogation, the accessions obtained from the same variety harbored some genetic difference.

Mace and Godwin (2002) have developed a microsatellite-enriched library following the hybridization method described by Edwards (1996). These microsatellite markers were tested on a sample (17 acc.) from several Pacific countries. They proved to be a valuable tool for the identification of duplicates although the geographical structure produced was not very informative, probably due to the small size of the sample. While several microsatellite locus for Taro are published (Quero-García *et al.,* 2006 ; Hu *et al.,* 2009)

Another microsatellite-enriched library was constructed (Bastide, 2000) following a hybridisation-based capture methodology using biotin-labelled microsatellite oligoprobes and streptavidin-coated magnetic beads (Billote *et al.,* 1999). This second source of microsatellite markers was used in order to analyze a subset of the sample previously characterized by Kreike *et al*. (2003). Microsatellite loci, also known as simple sequence repeats (SSRs) are among the most commonly used and technically efficient PCR-based markers (Abdelkrim *et al.* 2009). Availability of SSR marker sequences for oligonucleotide synthesis, involvement of PCR amplification, the simplicity of protocol that produces reliable and highly detectable amplification products, their co-dominance and single genome location constitutes their advantage over AFLP (Hamza *et al.* 2004).

Singh *et al.* (2008) assess and rationalize the genetic diversity of Papua New Guinea taro using SSR DNA fingerprinting comprising of 163 accessions of the most diverse based on agro morphological characterization was further characterized using taro specific SSR markers. Seven SSR primers resulted in the amplification of 35 total alleles of which 30 (86%) were found to be polymorphic. PIC values ranged from 0.0 for Xuqtem91 to 0.87 for Xuqtem84, with an average PIC value of 0.59.

Lu *et al.* (2011) isolated SSR markers from the genomic DNA of *Colocasia esculenta.* Eighteen of the 19 primers pairs yielded polymorphic amplification products in three populations. The number of alleles varied from two to seven per polymorphic locus. 19 nuclear microsatellite markers developed specifically from taro. These newly developed nuclear microsatellite markers will be a useful tool for studying the population genetics and evolutionary history of Taro in southwestern China. In addition, the set of novel markers are also helpful for the improvement of Taro germplasm and identifying commercial germplasm.

Chapter 3
Materials and Methods

3.1 Collection and documentation

A survey was conducted during the year 2008-2009 for collection of all the edible aroids of Nagaland. Altogether 50 landraces of colocasia, two variety of Xanthosoma, two variety of Alocasia and 1 variety of Amorphophallus were collected from all the eleven districts of the state. Each accession was given a code name of CV-1 to CV-50, XN1 and XN2, AL1 and AL2 and AM1. All the 55 edible aroids were documented. The detailed list of place of collection, village name, with their altitudes and special features are presented in Table 3.1

3.2 Morphological studies

3.2.1 Site and season

The study was conducted during the kharif season of 2008-2009 and 2009-2010 at the Experimental Farm, Department of Genetics and Plant Breeding, School of Agricultural Sciences and Rural Development, Medziphema, Nagaland situated at 23° 45'49" N latitude and 90°33'04" E longitude with an altitude of 305 meter above the mean sea level bearing sub-tropical climate. The soil of the experiment area was sandy loam with a pH of 4.5. The meteorological data for the period of experimentation are given in the appendix I and II.

3.2.2 Experimental materials

The materials for the present investigation comprises of 50 cultivars of *Colocasia esculenta* (L.) Schott indigenous local type collected from all the 11

districts of Nagaland. The list of the genotypes along with their place of collection is given in the table 3.1. Variation in corm morphology of the collected landraces is presented in Plate 1.

3.2.3 Experimental design

An experimental field design (Agro Techniques of taro) recommended by Central Tuber Crop Research Institute, Tiruvanthampuram, Kerala, India was carried out following the Randomised Block Design as randomization gives equal chance to all treatments of a population for being allotted to a more fertile plot and to a less fertile plot. The RBD was carried out in such a way that a homogenous piece of land, as far as possible, was selected and the principal of local control or error control was adopted in the design by forming homogenous blocks. All the fifty accessions were sown in a Randomised Block Design (RBD) with three replications. A plot consisted of 2 rows of plot size 2.25*1.20 m^2, spaced row to row distance 60 cm and plant to plant distance 45cm. Distance between plots 50 cm and distance between replications 100 cm. Overview of the experimental field is presented in Plate 2.

Summary of the field layout

The detail specification of one field experimentation is given below.

i.	Design	: Randomized Block Design (RDB)
ii.	Number of replications	: 3
iii.	Number of entries	: 50
iv.	Plot size	: 2.25m * 1.20m
v.	Number of rows per plot	: 2
vi.	Number of plants per row	: 2
vii.	Number of plants per plot	: 10

viii. Spacing :

a. Row to row distance : 60 cm

b. Plant to plant distance : 45 cm

ix. Distance between plots : 50 cm

x. Distance between replications : 100 cm

3.2.4 Time and method of sowing

The experimental land was ploughed and then harrowed to make it loose and friable. In each plot two rows or trenches were made with a spacing of 60 cm and the corms were placed in these trenches with a depth of 5-7cm and covered. Planting was done in the first week of May 2008. Prior to sowing the seeds were treated with Bavistin @ 1gm per litre plantomycin 3 gm per litre as prophylactic measure against fungal diseases.

3.2.5 Manures and fertilizers

FYM @ 10-15 tonnes per ha was applied to the experimental area about one week prior to planting. No other chemical fertilizers were applied in the experimental area and the crops were raised in natural condition of fertility.

3.2.6 Cultural operations

The experimental area was kept weed free by manual weeding when required. Earthing up was done during the crop growth. During the early period of crop growth mulching was done with straw.

3.2.7 Tagging

Five plants in each plot were sampled randomly and were tagged. Observations were taken on these tagged plants for different morphological traits.

3.2.8 Harvesting

The crop was harvested from 2nd week of November when almost all the entries were matured and the leaves turned yellow and the plants started dying.

3.2.9 Observations recorded

According to the descriptors for Colocasia (1980) prepared by International Bureau for Plant Genetic Resources Institute, Rome, Italy observation for 14 quantitative characters and 19 qualitative characters were made on five randomly sampled plants from each plot and the average was recorded.

3.2.10 Quantitative characters.

3.2.10.1 Plant height

The plant height was measured in cm from the ground surface to the tip of the main shoot on five randomly sampled plants.

3.2.10.2 Petiole length

The petiole length of each of the petiole per plant was recorded from the base of the plant to the leaf and their average length was used in the analysis. The unit was taken in cm.

3.2.10.3 Leaf length (cm)

The leaf length was recorded on fully extended leaves at full foliage stage.

3.2.10.4 Leaf breadth (cm)

The leaf breadth was recorded on fully extended leaves at full foliage stage.

3.2.10.5 Number of leaves per plant

The number of the leaves per plant was recorded and their average was used for the analysis.

3.2.10.6 Number of inflorescence

The number of the flowers per plant was recorded and their average was used for the analysis.

The characters 1-6 were recorded at 120 days.

3.2.10.7 Shoot number

The number of suckers per plant was recorded and their average are calculated and used in the analysis.

3.2.10.8 Corm weight

The corm of the individual plants was weighted out and the average weight of randomly sampled plants was worked out in grams.

3.2.10.9 Cormel number

Total number of cormels per plant was recorded for five randomly sampled plants and their average was used in the analysis.

3.2.10.10 Cormel weight

The total cormels number recorded per plant was weighted and their average weight was worked out (in gram).

3.2.10.11 Corm girth

The girth or the circumference of the mother corms from each plant was recorded in centimetres and the average girth was worked out.

3.2.10.12 Length of Corm (cm)

The length of corm was measured on the mother corm and the average length worked out for analysis.

3.2.10.13 Breath of Corm (cm)

The breath of corm was measured on the mother corm and the average length worked out for analysis.

3.2.10.14 Yield per plant

The average yield of five randomly sampled plants represents the yield per plant of a cultivar and was recorded in grams. The yield per plant included both the weight of the corms and the cormels per plant.

The characters 6-14 were recorded at the time of harvest.

3.2.11 Qualitative characters

3.2.11.1 Leaf blade margin

Leaf blade margin was found to be undulate for all the genotypes

3.2.11.2 Leaf blade colour

Six classes of leaf blade colour were recognised during the late vegetative stage as follows:

Code	Type of observation
1	White
2	Yellow/ yellow green
3	Green
4	Pink
5	Purple
6	Blackish(Violet blue)

3.2.11.3 Leaf blade colour variegation

Leaf blade colour variegation was observed during the late vegetative stage and was observed to be either 0-absent or 1-present.

3.2.11.4 Flower formation

Flower formation was observed during the maximum vegetative growth and was observed to be 0-absent or 1-flowering.

3.2.11.5 Predominant position of leaf lamina surface.

Predominant position of the leaf lamina surface was observed on fully open young leaves:

Code	Type of observation
1	Drooping
2	Horizontal
3	Cup shaped
4	Erect apex up
5	Erect apex down

3.2.11.6 Leaf main vein colour

Leaf main vein colour was observed on the upper side of leaf blade beyond junction as follows:

Code	Type of observation
1	White
2	Purple
3	Green
4	Pink

3.2.11.7 Leaf vein pattern

Leaf vein pattern was observed on the surface of the leaf and classified as follows:

Code	Type of observation
1	V-pattern
2	I-pattern
3	Y-pattern

3.2.11.8 Petiole basal ring colour

Four classes of Petiole basal colour were observed on fully developed leaves as follows:

Code	Type of Observation
1	Green
2	Purple
3	White
5	Dark brown

3.2.11.9 Petiole junction colour

Petiole junction colour was observed on the upper side of the leaf as follows:

Code	Type of observation
0	Absent
1	Green
2	White
3	purple

3.2.11.10 Petiole junction pattern

Petiole junction pattern was observed as area of spots at vein junction on upper surface as follows:

Code	Type of observation
0	Absent
1	Small
2	Medium
3	Large

3.2.11.11 Petiole lower colour

Petiole lower colour was observed on the middle third of the petiole and its colour are as follows:

Code	Type of observation
1	Green
2	Purple
3	Brown

3.2.11.12 Presence of petiole stripe

Presence of petiole stripe was observed as follows:

Code	Type of observation
0	Absent
1	Present

3.2.11.13 Petiole stripe colour

Petiole stripe colour was observed as follows:

Code	Type of observation
1	Purple
2	Green

3.2.11.14 Petiole top colour

Petiole top colour was observed from the top third of the petiole as follows:

Code	Type of observation
1	Green
2	Purple
3	Light green
4	White

3.2.11.15 Taro leaf blight resistance

Taro leaf blight resistant was observed as follows:

Code	Type of observation
T	Tolerant for leaf blight
NT	Not tolerant for leaf blight

3.2.11.16 Corm flesh colour

Two classes of corm flesh colour were observed as follows:

Code	Type of observation
1	White
2	Pink

3.2.11.17 Corm flesh fibre colour

Two classes of corm flesh fibre colour were observed as follows:

Code	Type of observation
1	White
2	Yellow

3.2.11.18 Corm shape

Three classes of corm shape were observed as follows:

Code	Type of observation
1	Round
2	Flat and multifaced
3	Elongated

3.2.11.19 Corm cortex colour

Two classes of corm cortex colour were observed as follows

Code	Type of observation
1	White
2	Pink

3.3 Statistical analysis of the data

The mean values of the observations recorded on each plot for different characters were subjected to the following statistical and biomaterial analysis like analysis of variance, coefficient of covariance, correlation, path coefficient analysis, genetic divergence (D^2)

3.3.1. Analysis of variance

The analysis of variance for RBD as described in Panse and Sukhatme (1958). In this method analysis of variance is worked out by using the mean performance of the genotypes.

ANOVA for RBD was tabulated as follows

Source of variation	Degree of freedom (df)	Sum of square (SS)	Mean square (MS)	Variance ratio
Replication	(r-1)	SSr	MSr	MSr/MSe
Genotype	(g-1)	SSg	Msg	MSg/MSe
Error	(r-1)- (g-1)	SSe	MSe	
Total	(rg-1)	TSS		

Where,

r : Number of replications
g : Number of genotypes under study
SSr : Sum of square for replications
SSg : Sum of square for genotypes
SSe : Sum of square for error
TSS : Total sum of square
MSr : Mean square due to replication
MSg : Mean square due to genotypes
MSe : Mean square due to error

F-test for significance was tested using the mean square due to genotype against the mean square due to error. In order to test whether there is significant difference between any of the two genotypes, the Critical Difference (C.D) for each of the character was calculated.

CD = S.Ed x t .0.05 or t 0.01 at error degree of freedom

$$S.\ Ed = \sqrt{\frac{2\ MSe}{r}}$$

Where,

S.Ed = Standard error of the difference between two treatment means

MSe = Error mean square

r = Number of replications

3.3.2. Estimation of genotypic and phenotypic variance (Fisher, 1918)

3.3.2.1. Genotypic variance (σ_g^2)

$$\sigma_g^2 = \frac{MSg - MSe}{r}$$

Where,

MSg = Mean square due to genotype

MSe = Mean square due to error

r = Number of replication

3.3.2.2. Phenotypic variance (σ_p^2)

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

Where,

σ_g^2 = Genotypic variance

σ_e^2 = Environmental variance

3.3.2.3. Environmental variance (σ_e^2)

σ_e^2 = MSe

Where,

MSe = Mean square due to error

3.3.3. Coefficient of variation (CV)

The Genotypic, phenotypic and environmental coefficients of variations were calculated following the method given by Burton (1952).

3.3.3.1. Genotypic coefficient of variation (GCV) (%)

$$GCV = \frac{\sqrt{\sigma_g{}^2}}{Mean} \; x \; 100$$

3.3.3.2. Phenotypic coefficient of variation (PCV) (%)

$$PCV = \frac{\sqrt{\sigma_p{}^2}}{Mean} \; x \; 100$$

3.3.3.3. Environment coefficient of variation (ECV) (%)

$$ECV = \frac{\sqrt{\sigma_e{}^2}}{Mean} \; x \; 100$$

Where,

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

σ_e^2 = Environmental variance

3.3.4. Heritability (%)

Heritability in broad sense (h_{bs}^2) was calculated by following Allard's formula (1960). According to this method heritability in broad sense is computed as the ratio of genotypic variance (σg^2) to the phenotypic variance (σp^2) and expressed in percentage.

$$h_{bs}^2 = \frac{\sigma_g{}^2}{\sigma_p{}^2} x\ 100$$

Where,

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

3.3.5. Genetic Advance (GA)

The expected genetic advance was calculated by using the formula suggested by Johnson, Robinson and Comstock (1958). The genetic advance was expressed as per cent of the mean to facilitate the comparison between different characters under study

$GA = K\sigma p\ h_{bs}^2$

Where,

K = Selection differential, the value of which is 2.06 at 5 per cent selection intensity.

σp = Phenotypic standard deviation

h_{bs}^2 = Heritability in broad sense

3.3.6. Correlation studies

The correlation coefficient at phenotypic, genotypic and environmental levels was calculated according to the formula given by Karl Pearsons (1961).

3.3.6.1. Genotypic correlation coefficient between character x and y

$$rg_{xy} = \frac{Cov.xy\ (g)}{\sqrt{Var.x(g)\ X\ Var.y\ \ (g)}}$$

3.3.6.2. Phenotypic correlation coefficient between character x and y

$$rp_{xy} = \frac{Cov.xy\ (p)}{\sqrt{Var.x(p)\ X\ Var.y\ \ (p)}}$$

Where,

Cov.xy (g) and cov.xy (p) denotes genotypic and phenotypic co-variance for the character x and y respectively.

Var.x (g) and var.x (p) denotes genotypic and phenotypic variance for the character x.

Var.y (g) and var.y (p) denotes genotypic and phenotypic variance for the character y.

The calculated genotypic and phenotypic correlation coefficients were tested for 't'.

$'t' = \frac{r\sqrt{n-2}}{\sqrt{(1-r)^2}}$ at (n-2) degree of freedom

Where,

n = number of genotypes

The calculated 't' value was compared with 't' value at 5% or 1% probability level with (n-2) degree of freedom for its significance.

3.3.7. Path Coefficients

Path coefficients were calculated by using the formula given by Dewey and Lu (1959).

To estimate various direct and indirect effects, the following sets of simultaneous equation were formed and solved.

3.3.7.1. Direct effect

$ry_1 = Py_1 + Py_2r_{12} + Py_3r_{13} + ... + Py_nr_{1n}$

$ry_2 = Py_1r_{12} + Py_2 + Py_3r_{23} + ... + Py_nr_{2n}$

.

.

$ry_n = Py_1r_{1n} + Py_2r_{2n} + Py_3r_{3n} + ... + Py_n$

Where,

ry_i is the total genotypic correlation between x_i's (independent variable) and y (dependent variable)

py_i is the direct effect of x_i variable on y and

Py_1r_{1n} is the indirect effect of x_i variable on y through the variable x_n

3.3.7.2. Indirect effect

Indirect effects of n^{th} variable (x_n) via i^{th} variable (x_i) were worked out as :

$Py_i + rn_i$

i.e. Py_2r_{12} is the indirect effect on x_i on y via x_2

P_y2r_{12} is the indirect effect of x_2 on y via x_3 and similarly all the indirect effects were calculated

3.3.7.3. Residual effect

Variation in y may be due to variables not studied or due to pseudo variables. The degree of determination of pseudo-variable/variables on the dependent variable was calculated as follows :

$$(P^2yr) = 1 - \{P^2y_1 + 2Py_1.\ r_{12}\,P_{y2} + 2Py_1.\ r_{13}\ .\ Py_3 + \ .....$$
$$+ P^2y_2 + 2Py_2.\ r_{23}\ .\ Py_3 + \ .....$$
$$+ P^2y_3 + 2Py_3.\ r_{34}\ .\ Py_4 + \ .....$$
$$.$$
$$+ P^2y_n\}$$

3.3.8. Genetic divergence

Conservation of germplasm resources is basic to crop improvement programmes. However to understand the usable variability, grouping or

classification of genetic stocks based on suitable scale is quite imperative. Similarly choice of divergent parents for hybridization under transgressive breeding programme is also dependent upon categorization of breeding materials on the basis of appropriate criteria. Systematic classification rests exclusively upon easily distinguishable quantitative attributes, but it does not consider quantitative traits showing continuous variation which constitutes the backbone of plant breeding practices.

Genetic divergence among 50 genotypes of experiment was analyzed by using Mahlanobis D^2 statistics (Rao, 1952). D^2- statistics is a measure of genetic distances among groups or varieties based on multiple characters. Genetic diversity plays an important role in plant breeding because hybrids between lines of diverse origin generally display a greater heterosis than those between closely related parents. Genetic diversity arises due to geographical separation or due to genetic barriers to crossability. The purpose of D^2 statistics is to identify genotypes which can be grouped together as one genetic group. If there are 'p' characters measured on each individual, and 'ds' are the difference between means of two groups, then D^2 statistics (Mahalanobis, 1928) is defined as:

pD^2=b1d1+b2d2+……+bpdp _____(1)

Where,

The bi values are to be estimated such that the F ratio of variance 'between groups' and 'within groups' is maximized. In terms of variances and covariances of the I and j traits of two groups, 1 and 3, the D^2 value is obtained as follows:

$pD^2 = w^{ij}\ (x^1\text{i} — x^2\text{i})\ (x^1 j - x^2\text{j})$

where,

w^{ij} is the inverse of estimated variance-covariance matrix.

For each pair of mean deviation i.e. Yi^1- Yi1 with i = 1,2,……P. is computed and the D^2 is calculated as the sum of this diviation i.e.

$D^2 = \sum (yi^1 - yi^2)^2$

Traits					
Group	1	2	2		P
1	Y11	Y21	Y31	……	Yp1
2	Y12	Y22	Y32	……	Yp2
……	…….	……..	……..	……	……...
Difference	Y11-Y12	Y21-Y22	Y31-Y32	…….	Yp1-Yp2

$D^2 = (Y11-Y12)^2 + (Y21-Y22)^2 + \ldots\ldots\ldots (Yp1-Yp2)^2$

$= \sum (yi^1 - yi^2)^2$

Similarly, the D^2 value for all the other combination of group pairs, 1 and 3, 1 and 4, 2 and 3, etc. are calculated. The D^2 values obtained for a pair of group is taken as the calculated value of x^2 for p degrees of freedom, where p is the number of character considered.

Each character is ranked on the basis of di = Yij – Yij values. Ranked one is given to the highest mean difference, where p is the number of characters. These ranks are given in the parenthesis in the calculation of D^2 values for all the contribution of pairs.

Percent contribution is calculate d taking pq = 100.

3.3.8.1. Tocher's method of cluster grouping.

Treating these D^2 values as the square of generalized distance, all the genotypes were grouped into a number of clusters following the method described by Tocher (Rao, 1952). A table is made with each group heading a column and changing their group in the same column in order of their distances. First column is headed by group or variety 1. In this column, the group or variety nearest to the group or variety 1 is placed next row below and so on for the 3^{rd}, 4^{th} ,…… p^{th} rows of the same column. Second column is headed by group 2 and the group nearest to the group 2 is placed in the 2^{nd} row and so on. In this way groups belonging to the same are now grouped into different clusters according to D^2 values. The average D^2 value in the first row is arbitrarily taken as the maximum permissible values for being placed in the same cluster. The first two are automatically of the same cluster. When the third is added, the average D^2 value due to addition of the third and fourth group from the previous average should not exceed the permissible limit set above. If the increase in the average D^2 value over the previous combination is less than the permissible value, it is excluded in the cluster, otherwise stays out. The rest of the group is then considered for making a second cluster. Any pairs which shows least distances between them is taken and the same procedure is followed for the inclusion of other group.

Forces of differentiation at genotypic and inter cluster levels are demonstrated by CV values.

Cluster means of each of the cluster were calculated as the average values of were tabulated.

3.4. MOLECULAR STUDIES (Simple Sequence Repeat Analysis)

3.4.1 Materials

3.4.1.1. Plant material

Fourty- eight accessions of *C. esculenta* var.*esculenta* collected from all the districts of Nagaland were used to investigate the level of polymorphism by SSR method (table 3.2). Plant DNA was extracted from these accessions. Young unrolled leaves were harvested for DNA extraction. Total genomic DNA was extracted using the DNeasy Plant Mini (QIAGEN).

3.4.1.2. Chemicals:

(i) Twenty eight Oligonucleotide primer sequence were used in the present investigation. The details of the primers used are presented in table-3.3

(ii) DNease Plant Mini kit (QIAGEN)

(iii) PCR Master mix

(iv) 100 bp DNA ladder

(v) Agarose

(vi) Ethidium bromide

(vii) Gel loading buffer

3.4.1. 3. Equipment:

i. Centrifuges: Eppendorf centrifuge

ii. Vortex-SPINIX

iii. Microwave oven

iv. Digital balance

v. Incubator

vi. Electrophoretic gel system.

vii. Deep freezer

viii. Spectrophotometer

ix. Veriti PCR

3.4.1.4. Lab Wares

i. Microcentrifuge tubes (1.0ml, 2 ml)

ii. Digital Mocropipettes

iii. Eppendorf tubes

iv. PCR tubes

3.4.1.5. PCR reaction mixture:

The reaction mixture for PCR and their concentrations are as follows

Chemicals	**Amount taken**
5X buffer	: 5.0µl
$MgCl_2$	: 1.5µl
dNTP	: 0.4µl
Taq DNA polymerase	: 0.2µl
Forward primer	: 1.0µl
Reverse primer	:1.0µl
Template DNA	:1.0µl
Nuclease free water	:14.9µl
Total volume	: 25.00 µl

3.4.2. Methods.

3.4.2.1. Isolation of genomic DNA

For SSR analysis of Genetic diversity at molecular level, total genomic DNA was isolated from young unfurled leaves of fifty genotypes of colocasia using mini protocol for purification of total DNA from plant tissue.

3.4.2.2 Protocol:

Leaf tissue of Colocasia of 150-200 mg was weighed, the leaf material was grounded in a mortar and pestle using liquid nitrogen. The grounded tissue was then transferred into a 1.5 ml micro centrifuge tube.

i. To this add 400 µl of buffer AP1 and 4 µl RNase A. Vortex and incubate for 10 mins at 65^0C and inverted the tubes 2-3 times during incubation.
ii. Add 130 µl buffer P3. Mix and incubate for 5 mins on ice. Centrifuge the lysate for 5 mins at 20,000 xg (14,000 rpm)
iii. Pipet the lysate into a QIA shredder Mini spin column in a 2ml collection tube. Centrifuge for 2 min at 20,000xg (14,000 rpm).
iv. Transfer the flow through fraction into a new tube without disturbing the pellet. Add 1.5 volumes of buffer AW1 and mix by pipetting.
v. Transfer 650 µl of the mixture into a DNeasy Mini spin column in a 2 ml collection tube. Centrifuge for 1 min at ≥ 6000xg (≥8000 rpm). Discard the flow-through. Repeat this step with the remaining sample.
vi. Place the spin column into a new 2 ml collection tube. Add 500 µl buffer AW2 and centrifuge for 1 min at 6000xg. Discard flow through.
vii. Add another 500 µl buffer AW2.Centrifuge for 2 min at 20,000 xg. Remove the spin column from the collection tube carefully so the column

does not come into contact with the flow through.

viii. Transfer the spin column to a new 1.5 ml or 2 ml micro centrifuge tube and add 100 µl buffer AE for elution. Incubate for 5 mins at room temperature. Centrifuge for 1 min at ≥ 6000xg. Repeat this step.

3.4.2.3. Quantification of isolated DNA

The DNA isolated was then run in a 2% Agarose gel and observed in a Gel documentation unit to check the quality of the isolated DNA.

3.4.2.4. SSR analysis

Twenty eight colocasia microsatellite markers were used for amplification. The sequence details of the markers are presented in table 3.3. PCR was carried out in a 25-µl reaction mixture consisting of 1 µl of template DNA, 5 pmol of each reverse and forward primer, 7.1 µl PCR Master-mix (Qiagen), 0.2 µl of Taq DNA polymerase and nuclease-free water. Amplification was carried out in a thermal cycler (thermal Scientific , Veriti PCR) with a 5 min initial denaturation at 94ºC followed by 30 cycles of 94ºC for 40 sec, annealing at primer-specific temperature(for 1 min and extension at 72 for 32 sec. A final extension at 72ºC for 5 min was given after the last cycle. After the completion of the PCR, The products were stored at -4ºC until the gel electrophoresis was done. The details of annealing temperature for each primer used are given below.

Annealing Temperature (°C)	Primer
49	COLGCC209-120
53	COLGCC132-147, COLGCC233-167,
54	COLGCC56-191, COLGCC82-117, COLGCC111-300, COLGCC192-245,
55	COLGCC88B-94, COLGCC75-100, COLGCC75-100, COLGCC118-22
56	COLGCC77-174, COLGCC95-219, COLGCC98-294, COLGCC206-122, COLGCC223-157, COLGCC220-211.
56.5	COLGCC105-267, COLGCC208-253
57	COLGCC91-262, COLGCC249-155
58	COLGCC110-283, COLGCC211-202, COLGCC228-110, COLGCC240-223,
60	COLGCC90-102
61.5	COLGCC73-164
63	COLGCC103-220

3.4.2.5. Gel Electrophoresis

10 µl of the PCR product was electrophoresed in 3% ISSR 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'.

3.4.2.6. 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;

$$PIC = 1-\Sigma x2i$$

where, xi 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).

Canonical discriminate analysis was carried out on the band scoring data and grouping (clustering) data using the SPSS16.0 statistical package to determine the optimal number of clusters in the dendrogram. Discriminate analysis was carried out using the equation:

$$Z = W1X1 + W2X2 + \ldots + WiXi$$

Where, Z = discriminate score

Wi = discriminate weight for variable i and

Xi = ith independent variable.

The method averages the discriminate scores for all individuals (accessions in this case) within a particular group, to arrive at the group mean, referred to as 'centroid'. The centroid indicates the most typical location of any individual from a particular group, and the comparison of group centroids shows how far apart the groups are along the dimensions being tested (Hair, *et al.* 1995). Subclusters within the clusters were also determined following the same method.

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. For average gene diversity, PCA (populations) and AMOVA, the computer program GenAlEx 6.5 Beta (Peakall and Smouse 2012) was used.

Chapter 4
Experimental Findings

The result obtained through the statistical and biometrical analysis of the data of the present investigation is presented in this chapter.

4.1 Collection and documentation

Edible aroids of Nagaland state was surveyed in the year 2008-2009 for collection of all the edible aroids of Nagaland. Altogether 11 districts of Nagaland were surveyed covering a total of 35 villages. Out of the 11 districts, Kohima possess good amount of germplasm as compared to the area explored. Altogether 14 cultivars were collected from Kohima district followed by Dimapur- 12 cultivars, Peren-5 cultivars, Mokokchung-5 cultivars, Phek- 4 cultivars, Zunheboto-3 cultivars, Wokha-3 cultivars, Mon-3 cultivars, Tuensang-3 cultivars, Kiphire-2 cultivars and Longleng-1 cultivars, making up to a total of 50 cultivars of colocasia. Other edible aroids collected includes two variety of Xanthosoma namely *Xanthosoma sagittifolium* cultivar and *Xanthosoma violeceum* cultivar, Two variety of Alocasia namely *Alocasia macrorrhizos* and *Alocasia Odora* and one variety of *Amorphophallus paeoniifolius* .

Brief description of the edible aroids which were documented during the survey apart from Colocasia are mentioned below. Variation in their morphological characters are presented in Plate 3 and Plate 4.

4.1.1 Scientific classification of *Xanthosoma sagittifolium*

Kingdom: Plantae

Order: Alismatales

Family: Araceae

Subfamily: Aroideae

Tribe: Caladieae

Genus: Xanthosoma

Species: *X.sagittifolium*

- There are two main species of Xanthosoma which is found in Nagaland, *X.sagittifolium* and *X.violaceum.* This division into species is based on the colour of the corm, cormels and leaves and on the shape of the cormels.
- The cocoyam, (Xanthosoma sp.) also known as tannia, tannier, yautia, malanga or new cocoyam belonging to the family Araceae.
- *X. sagittifolium* has green leaves and the corms and cormels have white, yellow or pink flesh and pale brown skin. The shape of the cormels for *X. sagittifolium* is globose.
- The sagittate-ovate leaves are between 1-2 m long and arise directly from the corm, with long ribbed petioles.
- Flowering is rare, but when it occurs, the inflorescence consists of a cylindrical spadix of flowers enclosed in a 12-15 cm spathe.
- The crop originated from Tropical America since the pre-Columbian times (Purseglove, 1972).

- Cocoyam (*Xanthosoma* spp.) is one of the six most important root and tuber crops world-wide (Jennings, 1987; Onwueme & Charles, 1994). The corm, cormels, and leaves of cocoyam are an important source of carbohydrates for human nutrition, animal feed (Ndoumou *et al.*, 1995; Nyochembeng & Garton, 1998)
- *Xanthosoma* spp., is cultivated in Nagaland as a source of carbohydrates for human nutrition, for animal feed, and cash income for the farmers.

4.1.2 Scientific classification *of Xanthosoma violaceum.*

Kingdom: Plantae

Order: Alismatales

Family: Araceae

Subfamily: Aroideae

Tribe: Caladieae

Genus: Xanthosoma

Species: *X.violeceum*

- The foliage of *X. violaceum* is purple-flushed and the corms and cormels are purple-grey with reddish eyes and purple, red, pink, yellow or white flesh.
- The shape of the cormels for *X violaceum* ovate elliptic.
- Flowering is rare, but when it occurs, the inflorescence consists of a cylindrical spadix of flowers enclosed in a 12-15 cm spathe.
- *X. Violaceum* is cultivated in Nagaland as a source of carbohydrates for human nutrition as well as animal feed .

4.1.3 Scientific classification of *Alocasia macrorrhizos*

- Kingdom: Plantae
- Order: Alismatales
- Family: Araceae
- Subfamily: Aroideae
- Tribe: Caladieae
- Genus: Alocasia
- Species: *A. macrorrhizos*
- The genus contains about 65 species occurring through Sri Lanka and India, through Indochina to China and southern Japan, the Malesian archpelago, Australia and Oceania.
- There are two main species which are found in Nagaland are *A. macrorrhizos* and *A.Odora.*
- In Nagaland, *A macrorrhizos* is found growing in moist shady areas and is mostly consider as weed as it is neither consumed as vegetable nor use as feed for domestic animals.
- In India, *A macrorrhizos* (together with *Colocasia*) occurs mostly in the humid tropical habitats of the Western and Eastern Ghats and in the northeast
- *A. macrorrhizos* is a massive perennial, huge "elephant ear" leave, 3-6 feet in length, 2-4 feet wide stalks and 2-4 feet long. Stalks emerge from an upright trunk to 6-feet tall. Whole plant can be 12-15 feet tall and 6-10 feet wide.

- Leaves are glossy medium green with paler veins, arrow-shaped at the bases. The leaves stand upright, pointing skyward, unlike her large “elephant ears.”
- Alocasia is commonly grown in upland areas, high islands, or drier areas of atolls. In Bangladesh and many parts of India, Alocasia is grown for the leaves as well as the stems. The stems are cut into cubes and used in curry and the young leaves are used in soups or fritters

4.1.4 Scientific classification of *Alocasia odora*

- Kingdom: Plantae
- Order: Alismatales
- Family: Araceae
- Subfamily: Aroideae
- Tribe: Caladieae
- Genus: Alocasia
- Species: *A. odora*
- *Alocasia odora* (also called Night-scented Lily or giant upright elephant ear) is a flowering plant native to East and South East Asia. The plant is a member of the genus Alocasia, and is thus related to taro.
- In Nagaland, It is grown in kitchen gardens and is its leaves are consumed after thorough cooking.
- The plant grows 3 to 8 feet tall; its leaf-blade can be 4 feet 3 inches long and 3 feet wide, with a leaf-stalk 5 feet long, its flowers are fragrant and its leaves are peltate.

- It is used as medicine for the treatment of common cold in North Vietnam. Compared to *Alocasia macrorrhizos,* this is smaller; less cold-hardy.

4.1.5 Scientific classification of *Amorphophallus paeoniifolius*

Kingdom: Plantae,

Order: Alismatales,

Family: Araceae ,

Subfamily: Aroideae,

Genus: Amorphophallus

Species: *A. paeoniifolius*

- *Amorphophallus paeoniifolius* is a perennial, terrestrial underground hemispherical depressed dark brown corm of approximately 20-25 cm in diameter
- The solitary leaf, which emerges after the flowering parts, resembles a small tree, Stem-like structure, which bears the lamina, is merely the petiole, 1 meter or more high, radically developed from the corm.
- Leaves are usually solitary, the blades up to 1 meter in diameter, trisected, the segments dichotomous, the ultimate ones pinnately divided into oblong to oblong-obovate, acuminate lobes.
- The tuberous roots of the plant posses blood purifier properties and have been used traditionally for the treatment of piles, abdominal disorders, tumours, enlargement of spleen, asthma and rheumatism.
- They are traditionally used in arthralgia, elephantiasis, tumors, inflammations, hemorrhoids, hemorrhages, vomiting, cough, bronchitis, asthma, anorexia, dyspepsia, flatulence, colic,

constipation, helminthiasis, hepatopathy, spleenopathy, amenorrhea, dysmenorrhoea, seminal weakness, fatigue, anemia and general debility.

- Grown mostly in West Bengal, Kerala, Andhra Pradesh, Maharashtra and Orissa. It is also found in Nagaland and its corm is consumed as a vegetable.
- In India, it has attended the status of a cash crop and the area under its cultivation is increasing fast. (Nedunchezhiyan *et al.,* 2006).

All the 50 cultivars were collected based on popularity within the district. The altitudes from where the cultivars were collected ranges from 450-1980m msl indicating diverse adaptability. According to the information collected at the time of germplasm collection, 7 cultivars out of 50 produce stolon namely CV3, CV4, CV18, CV27, CV33, CV42 and CV44, while CV13 and CV 26 possesses small thin running stolons.

4.2 Qualitative characters studies

The details of nineteen qualitative characters under studies are presented in Table 4.1.Variation in corm morphology presented in Plate 5(a), 5(b), 5(c) and 5(d).

4.2.1 Leaf blade margin

All the genotype of Colocasia leaf blade margin was found to be undulate.

4.2.2 Leaf blade colour

The genotype**s** showed a wide range of variation with respect to leaf blade margin. Six classes of leaf blade color were presented with

majority of the genotypes were found to possess green leaf blade color followed by white, purple, yellow green, pink and black.

4.2.3 Leaf blade colour variegation

Leaf blade color variegation was found in all the genotypes.

4.2.4 Flower formation

Flower formation was present in 13 genotype out of the total 50 genotype in the experiment.

4.2.5 Predominant position of leaf lamina surface

Predominant position of leaf lamina surface was found to be erect apex down in all the cultivars.

4.2.6 Leaf main vein colour

Four classes of Leaf main vein color were present with majority of the genotype were found to possess white color followed by purple, green and pink.

4.2.7 Leaf vein pattern

Leaf vein pattern was found to be V pattern for all the genotypes.

4.2.8 Petiole basal ring colour

Four classes of Petiole basal ring color were presented with majority of the genotypes were found to possess green petiole basal ring color followed by purple, white and dark brown.

4.2.9 Petiole junction colour

Three classes of Petiole junction color were presented with majority of the genotypes were found to possess green petiole junction color followed by purple and white Petiole junction color.

4.2.10 Petiole junction pattern

Petiole junction pattern was found to be small for all the genotypes.

4.2.11 Petiole lower colour

Three classes of Petiole lower colour were presented with majority of the genotypes were found to possess green petiole lower colour followed by purple and brown Petiole lower colour.

4.2.12 Presence of petiole stripe

16 genotypes were found to have petiole stripe out of the 50 genotypes.

4.2.13 Petiole stripe colour

Three classes of Petiole stripe colour were presented with majority of the genotypes were found to possess purple petiole stripe colour followed by green and black.

4.2.14 Petiole top colour

Four classes of Petiole top colour were presented with majority of the genotypes were found to possess green petiole top colour followed by purple, Light green and white.

4.2.15 Taro leaf blight resistant

All the genotype were found to be tolerant for Taro leaf blight resistant.

4.2.16 Corm flesh colour

Two classes of corm flesh colour were presented with majority of the genotypes were found to possess white corm flesh colour followed by pink.

4.2.17 Corm flesh fiber colour

Two classes of corm flesh fiber colour were presented with majority of the genotypes were found to possess white corm flesh fiber colour followed by yellow.

4.2.18 Corm shape

Three classes of corm shape were presented with majority of the genotypes were found to possess round corm shape followed by flat and multi faced and elongated shape.

4.2.19 Corm cortex colour

Two classes of corm cortex colour were presented with majority of the genotypes were found to possess white corm cortex colour followed by pink.

4.3 Quantitative character studies

4.3.1 Analysis of variance

The analysis of variance of the mean value revealed significant difference among the genotype for all the traits except corm number per plant, which indicated the presence of considerable amount of variability amongst the genotypes. The analysis of variance for all the traits studied is presented in Table 4.2 and Table 4.3 and also diagrammatically presented in fig.1.

4.3.2 Mean performance

The mean performance of all the 50 genotypes and range of variation for yield and yield related traits are presented in Table 4.4 and discussed as follows.

4.3.2.1 Plant height

Differences in plant height were observed among the genotypes. Dziinuo III was found to be the tallest among all the genotypes during both the years, 2008 (145.87cm) and 2009 (145.84cm).On the other hand, the minimum plant height was observed for the genotypes, Dzii dziinuo (29.97 cm)during 2008 and Bao (37.47cm)during 2009. The general mean for the character was 61.03cm and 71.68cm, recorded during 1st and 2nd year, respectively.

4.3.2.2 Petiole Length

Dziinuo III was found to have the tallest petiole during both the years, 2008 (86.80cm) and 2009 (122.33cm). the minimum petiole length was observed in Obei for both the year, 2008 (23.67cm) and 2009 (34.00cm). Grand mean for the character was found to be 46.07cm for 2008 and 56.82cm for 2009.

4.3.2.3 Leaf length

The minimum leaf length was observed in Dziidziinuo for the year 2008 (8.74cm) and Obei (19.4cm) for the year 2009, while maximum leaf length was recorded for the genotype, Tefiidzii (51.27cm) and Tino I (55.67cm) during 2008 and 2009 respectively.

4.3.2.4 Leaf width

The minimum leaf width (17.87cm) was recorded for the genotype, Chugoma during 2008, while the genotype Dziinuo I produce the narrowest leaf (12.84cm) for among all the test genotype during 2009. The maximum Leaf width was recorded for the genotype, Bei I (42.00cm) for the year 2008 and Banu sam sam (42.96cm) for the year 2009.General mean for the character was estimated to be 28.09cm during 2008 and 23.78cm during 2009.

4.3.2.5 Number of inflorescence per plant

The number of inflorescence per plant was recorded minimum in Dziitii for the year 2008 (0.14 number) and for the year 2009 (0.10 number), while the maximum number of inflorescence was observed in Bei I (2.60 number) for the year 2008 and Banu sam sam (23.17 number) for the year 2009. Infloresence was observed in Dziirinuo II (0.27), Dziinuo III (0.94), Chucha (0.47), Dziirinuo III (0.54), Tinopang (0.50), Atsantu (1.94), Chuyali (0.47) while the general mean was recorded 0.187. The general mean for the character was found to be 0.19 and 0.79 during 2008 and 2009, respectively.

4.3.2.6 Number of suckers

The maximum number of suckers was recorded in Lijalanii (3.54) for the year 2008 and banu sam sam (24.30) for the year 2009. The minimum number of sucker was recorded in Dziitii (0.13) during both the years of experimentation. Grand mean for the character was found to be 1.00 and 1.68 during 2008 and 2009, respectively.

4.3.2.7 Number of leaves

The genotype, Chugoma produced the maximum number of leaves (6.10) for the year 2008 and Banu Sam sam (26.37) for the year 2009, while Beidimai II produced the minimum number of leaves (4.00) for the year 2008 and Bei I (4.17) produced the minimum number of leaves for the

year 2009. Grand mean for the character was found to be 4.76 and 5.19 during 2008 and 2009, respectively.

4.3.2.8 Corm weight

A wide range of variation was obtained for corm weight. Corm weight was recorded maximum in Lijalanii (354.67g) and Bei I (337.00g) during 2008 and 2009, while minimum corm weight was observed in Dziinuo I (72.00g) for the year 2008 and Thegabeizii (32.67g) for the year 2009. While, the grand mean of corm weight was recorded 144.89g and 143.76g during 2008 and 2009, respectively.

4.3.2.9 Number of cormels

The genotype, Beidimai I produced the maximum number of cormels (14.74) during the year 2008 and Banu sam sam(28.94) during 2009, while the minimum number of cormels was recorded in Dziitii (0.10) during the year 2008 (0.10) and 2009 (0.14).Grand mean for the character was found to be 4.01 during 2008 and 6.28 during 2009.

4.3.2.10 Cormel weight

The maximum cormel weight was recorded in the genotype Thegabeizii (292.22g) during 2008 and Bei I (478.34g) during 2009, while Dziitii recorded the minimum cormel weight during 2008 (28.34g) and 2009 (37.34g). The general mean for the character was 163.81g for 2008 and 193.42g during 2009, respectively.

4.3.2.11 Corm Girth

The minimum corm girth was recorded in Sama (3.78 cm) during 2008 and Tinopang (4.20cm) during 2009, while genotype Banu sam sam showed the maximum corm girth during 2008 (21.74 cm) and 2009 (37.77cm). General mean for the character was found to be calculated at 8.14cm and 14.21cm during 2008 and 2009, respectively.

4.3.2.12 Length of corm

The genotype, Dziinuo V (18.40cm) and Banu sam sam (26.87cm) were found to produced the longest length of corm and the shortest length of corm was recorded in the genotype Beidimai I (2.00cm) and Chiicha (2.34cm) respectively during 2008 and 2009. General mean for the character was found to be 6.08cm during 2008 and 6.79cm during 2009.

4.3.2.13 Breath of corm

The maximum breath of corm was recorded in the genotype, Tejongnii (14.50 cm) and Banu Sam sam (26.24cm) during 2008 and 2009, while the genotype Manie I (1.33cm) and Beidimai II (1.50cm) recorded the minimum breath of corm during 2008 and 2009 respectively. The mean value for the character was found to be 3.23cm during 2008 and 3.99cm during 2009.

4.3.2.14 Yield per plant

The highest corm yield per plant was observed for the genotype Loudoubei during 2008 (549.34g) and Bei I during 2009 (815.34g), respectively. On the other hand, the genotype Dziitii (156.67g) and Pajo (144.00g) produced the minimum corm yield per plant. General mean for the character was found to be 307.23g during 2008 and 336.65g during 2009.

4.3.3 Estimation of coefficient of variation, heritability and genetic advance.

An appreciable magnitude of variability among the genotype was observed for all the traits except corm number and leaves per plant. The estimates of mean range, genotypic and phenotypic coefficient of variation, heritability in broad sense and genetic advance expressed as percentage of mean for all the traits are present in Table 4.5 and 4.6. It is also diagrammatically represented in fig. 2, 3, 4, 5 and 6 respectively.

It was observed that for most of the characters the estimates of genotypic coefficient of variation was almost at par with phenotypic coefficient of variation, but genotypic coefficient of variation for plant height, and leaf length was rather lower than their respective phenotypic coefficient of variation.

4.3.3.1 Phenotypic coefficient of variation (PCV)

The estimates of phenotypic coefficient of variation ranged from 9.83-278.60% during 2008 and from 9.83-247.65% during 2009. High to moderate PCV estimates were recorded for the characters, number of inflorescence per plant (278.60 and 247.65%), followed by number of suckers per plant (108.9 and 95.57%), number of cormels per plant (84.69 and 78.27%), length of corm per plant (68.24 and 84.04%) and breath of corm per plant (89.61 and 78.54%). Moderate to low estimates for these parameters were recorded for the character, plant height, petiole length, leaf length, leaf width, corm weight, cormel weight, corm girth and yield per plant. On the other hand, low PCV estimate was recorded for number of leaves during both the years of experimentation.

4.3.3.2 Genotypic coefficient of variation (GCV)

The estimates of GCV followed almost similar trend with those of PCV estimates, being highest for number of inflorescence per plant (189.92% during 2008and 246.53% during 2009) followed by number of suckers, number of cormels per plant, length of corm per plant and breath of corm per plant. Like PCV estimates, the characters, plant height, petiole length, leaf length, leaf width, corm weight, cormel weight, corm girth and yield per plant also exhibited moderate to low estimates of GCV during both the years. Similarly, number of leaves showed low estimates for these parameters during both the years of experimentation.

4.3.3.3 Heritability

The Heritability estimates (Table 4.5 and Table 4.6) revealed high heritability values for almost all the characters under study during both the years. During 2008, the characters, length of corm (99.23%), breath of corm (98.55%) and number of cormels (90.59%) exhibited high heritability values. Rest of the character showed moderate to high heritability estimates, while the leaf width showing the minimum heritability value (42.54%) during 2008. On the other hand, during 2009, corm girth exhibited the highest heritability estimate (91.58%) followed by breath of corm (88.15%), number of cormels (80.11%) and leaf length (79.25%). Rest of the trait exhibited moderate to high heritability, while number of leaves per plant exhibiting the minimum heritability estimate (49.42%) during 2009.

4.3.3.4 Genetic advance

The estimate of Genetic advance as expressed in percentage of mean (Table 4.5 and Table 4.6) were found comparatively higher for number of infloresence per plant (449.39%) followed by breath of corm (181.92%), number of cormels (158.05%), length of corm (139.49%), number of suckers (107.48%) and corm weight (71.53%) during 2008. During this year, moderate estimate of this parameter were recorded for cormel weight (65.71%), corm girth (64.57%), plant height (58.13%), petiole length (51.84%), leaf length (50.98%), yield per plant (49.95%) and leaf width

(22.46%), while low estimate of GA as percent of mean was recorded for number of leaves (9.78%).

During 2009, the estimates of GA as per cent of mean followed almost similar trend as observed during 2008. High estimates of this parameter was recorded for number of inflorescence (300.03%), followed by number of suckers (143.75%), breath of corm (142.62%), corm weight (129.17%), length of corm (89.78%), corm girth (85.18%) and corm weight (76.23%). High to moderate estimates were recorded for cormel weight (65.02%), yield per plant (59.30%), petiole length (51.24%), plant height (45.97%), leaf length (43.15%) and leaf width (41.44%). Low estimate of GA as per cent of mean was recorded for number of leaves (10%) during 2009.

4.3.3.5 ASSOCIATION AMONG DIFFERENT CHARACTERS

The estimates of genotypic and phenotypic correlation coefficients among fourteen morphological characters and yield traits in Colocasia are presented in Table 4.7 and fig.7 for the year 2008 and in Table 4.8 and fig.8 for the year 2009. It is evident from the tables that the estimates of genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients for almost all the characters during both the years.

4.3.3.5.1 Association between yield per plant and its attributing trait.

The Table 4.7 reveals that during 2008, corm yield per plant showed significant and positive correlations with cormel weight (0.80 and 0.81), followed by corm weight at both genotypic and phenotypic levels.

On the other hand this corm yield trait showed significant but negative correlation with number of leaves, number of cormels and breath of corms at both genotypic as well as phenotypic levels.

During 2009, corm yield per plant showed significant positive correlation with cormel weight (0.88 and 0.88) and corm weight (0.81 and 0.80) (Table 4.8). On the other hand, during 2009 as evident from Table 4.8 leaf length (-0.05 and -0.04) and number of leaves (-0.30 and -0.17) showed significant but negative correlation with corm yield per plant at both genotypic and phenotypic levels.

4.3.3.6 Association among component characters

4.3.3.6.1 Plant height

Plant height was found to be significantly and positively correlated with petiole length (0.95), followed by leaf length (0.29), leaf width (0.46), number of inflorescence (0.53), number of suckers (0.55), and length of corm (0.29) at genotypic level during 2008. At phenotypic level also it showed significant positive correlation with these six characters, petiole length (0.93), leaf length (0.27), leaf width (0.32), number of inflorescence (0.42), number of suckers (0.39) and length of corm (0.26). On the other hand plant height showed significant negative correlation with number of leaves (-0.18 and -0.03), number of cormels (-0.10 and -0.09) and corm girth (-0.12 and -0.07) at both genotypic and phenotypic levels and with cormel weight per plant (-0.01) at only genotypic level during 2008.

During 2009, plant height was found to be significantly and positively correlate with petiole length (0.99), cormel weight (0.25), length of corm (0.43), yield per plant (0.25) at the genotypic level and with petiole length (0.97), length of corm (0.32) at the phenotypic level. On the other hand, plant height showed significant negative correlation with number of leaves (-0.07), number of cormels (-0.07) and corm girth (-0.14) at the genotypic level and number of leaves (-0.06), number of cormels (-0.0) and corm girth (-0.11) at the phenotypic levels.

4.3.3.6.1 Petiole length

Table 4.7 revealed that petiole length was significantly and positively correlated with leaf length (0.35), leaf width (0.47), number of inflorescence (0.61) and length of corm (0.27) at the genotypic level during 2008. At the phenotypic level also it showed significant positive correlation with these traits. On the other hand, petiole length showed significant negative correlation with only number of leaves (-0.24) at the genotypic level. During 2009, petiole length was significantly correlated with only length of corm (0.41) at the genotypic level. On the other hand, at the phenotypic level petiole length did not show any significant positive correlation with these characters. While petiole length showed significant negative correlation with number of cormels (-0.27) and corm girth (-0.52) at the phenotypic level.

4.3.3.6.2 Leaf length

During 2008, leaf length showed significant positive correlation with leaf width (0.35) and number of suckers (0.32) at the genotypic level, while it showed significant positive correlation with leaf width (0.50) and number of suckers (0.44) at the phenotypic level. On the other hand significant negative correlation was observed in number of leaves (-0.23) at the genotypic level, while it showed significant negative correlation with length of corm (-0.72) at the phenotypic level. During 2009, leaf length showed significant positive correlation with only leaf width at the genotypic (0.97) and phenotypic (0.94) levels. On the other hand, it showed significant negative correlation with number of leaves (-0.25), number of cormels (-0.37) and corm girth (-0.60) at the genotypic level and significant negative correlation with only corm girth (-0.47) at the phenotypic level.

4.3.3.6.3 Leaf width

During 2008, significant positive correlations of this character was observed with number of inflorescence (0.40), followed by cormel weight (0.58) and yield per plant (0.50) at the genotypic level, while a significant positive correlation was observed in number of inflorescence (0.34), followed by number of suckers (0.40), cormel weight (0.27) and yield per plant (0.27) at the phenotypic level. On the other hand during 2009, leaf width did not show any significant positive correlation with any of the traits at the genotypic and phenotypic level, while it showed significant negative correlation with number of leaves (-0.31), number of cormels (-0.27)and corm girth (-0.55) at the genotypic level. Leaf width did

not show significant negative correlation with any of the traits at the phenotypic level.

4.3.3.6.4 Number of inflorescence

Number of inflorescence showed significant positive correlation corm weight (0.32) followed by length of corm (0.43) and yield per plant (0.29) at the genotypic level, while number of inflorescence showed significant positive correlation with corm weight (0.27), length of corm (0.37) and yield per plant (0.25) at phenotypic level. On the other hand number of inflorescence showed significant negative correlation with number of suckers (-0.26), number of leaves (-0.32) and number of cormels (-0.32) at the genotypic level, while significant negative correlation was observed only for the character number of cormels (-0.27) at the phenotypic level. During 2009, number of inflorescence showed significant positive correlation with only cormel weight (0.25) at the genotypic level, while number of inflorescence showed significant positive correlation with number of cormels (0.38) and corm girth (0.25) at the phenotypic level. On the other hand, number of inflorescence did not show any significant negative correlation with any of the traits at the genotypic and phenotypic levels.

4.3.3.6.5 Number of suckers

During 2008, number of suckers showed significant positive correlation with number of cormels at the genotypic (0.36) and phenotypic (0.24) levels. While, non significant negative correlation was observe with the other traits. During 2009, number of suckers showed significant positive

correlation with number of cormels (0.54), cormel weight (0.27) and corm girth (0.28) at the genotypic level. While no significant positive correlation was observe for all the traits at the phenotypic level. On the other hand, number of suckers showed significant negative correlation with only corm weight (-0.27) at the phenotypic level.

4.3.3.6.6 Number of leaves

Number of leaves showed no significant positive correlation with any of the traits at the genotypic and phenotypic level during 2008, while a significant negative correlation was observe for yield per plant at the phenotypic level. On the other hand, during 2009, number of leaves did not show significant positive correlation with any of the traits at the genotypic and phenotypic levels. While, number of leaves showed significant negative correlation with corm weight (-0.47) and yield per plant (-0.30) at the genotypic level and corm weight (-0.27) at the phenotypic levels.

4.3.3.6.7 Corm weight

During 2008, in addition to petiole length, leaf length and leaf width, corm weight was found to be significantly positively correlated with length of corm (0.52), breath of corm (0.34) and yield per plant (0.65) at the genotypic level. While it showed significantly negative correlation with number of cormels at both genotypic (-0.39) and phenotypic level (-0.29). During 2009, corm weight showed significant positive correlation with cormel weight (0.44), corm girth (0.44), length of corm (0.50), breath of

corm (0.40) and yield per plant (0.81). While corm weight showed significantly negative correlation with number of cormels at genotypic (-0.24) level.

4.3.3.6.8 Number of cormel

Number of cormels showed non significant positive correlation with any of the traits. While number of cormels showed significantly negative correlation with length of corm (-0.35) and breath of corm (-0.27) at genotypic level, While it showed significantly negative correlation with length of corm (-0.33) and breath of corm (-0.25) at the phenotypic level during 2008. On the other hand, during 2009, number of cormels showed significant positive correlation with only corm girth (0.41) at the genotypic level, while number of cormels showed significant positive correlation with cormel weight (0.30) and corm girth (0.38) at the phenotypic level. On the other hand it was found to exhibit significantly negative correlation with only breath of corm (-0.23) at the genotypic level.

4.3.3.6.9 Cormel weight

During 2008, cormelweight showed significant positive correlation with corm girth (0.25) and corm yield per plant (0.81) at the genotypic level. While cormel weight showed significantly negative correlation with only breath of corm at both the genotypic (-0.47) and phenotypic (-0.36) levels. During 2009, cormel weight showed significant positive correlation with corm girth (0.55), length of corm (0.32) and corm yield per plant (0.88) at the genotypic level. While cormel weight showed

significantly negative correlation with only breath of corm at the genotypic (-0.28) levels.

4.3.3.6.10 Corm girth

Corm girth showed significant positive correlation with only corm yield per plant (0.33) at the genotypic level but non significant correlation with other traits during 2008. On the other hand, during 2009, corm girth showed significant positive correlation with only corm yield per plant at the genotypic (0.60) and phenotypic (0.52) levels, but non significant correlation with other traits was observed.

4.3.3.6.11 Length of corm

During 2008, length of corm showed significant positive correlation with breath of corm (0.44) and corm yield per plant (0.33) at the genotypic level. While it showed significant positive correlation with breath of corm (0.43) and corm yield per plant (0.27) at the phenotypic level. On the other hand, during 2009 length of corm showed significant positive correlation with only corm yield per plant at the genotypic (0.46) and phenotypic (0.26) levels, but non significant correlation with other traits was observed.

4.3.3.6.12 Breath of corm

Breath of corm showed non significant correlation with all the traits at the genotypic and phenotypic levels during both the years 2008 and 2009 of experimentation.

4.3.3.7 Path coefficient analysis

The genotypic and phenotypic coefficient among several characters and yield per plant were subjected to path coefficient analysis to identify the causative characters and their direct and indirect influence on the dependent characters. In order to have a clear picture of the inter relationships between different characters, Path analysis was used to work out the direct and indirect effects on corm yield per plant at the genotypic and phenotypic levels during 2008 and 2009 separately (Table 4.9 and 4.10) The result are describe as under-

4.3.3.7.1 Corm yield per plant vs. plant height

Plant height showed positive but non-significant correlations with corm yield per plant at genotypic level during 2008, while plant height showed significant correlation with corm yield at the phenotypic level during 2009. These non significant correlation were also indicated by its low direct as well as indirect effects on corm yield per plant via most of the other traits. Plant height also showed moderate positive indirect effects through petiole length (0.20) at the genotypic level. During 2009, plant height showed low positive direct effects and low to moderate positive direct effects through petiole length (0.10) and corm weight (0.11) at the genotypic level.

4.3.3.7.2 Corm yield per plant vs. petiole length

The data reveal non significant positive correlation between these two traits during 2008 at genotypic level (0.09).This was attributed by

its positive direct effect (0.21) on corm yield per plant. On the other hand, petiole length did not show positive direct effects on corm yield per plant at the genotypic level during 2009, which were nullified by negative indirect effects via plant height (-0.11), leaf length (-0.01), number of suckers (-0.00), number of cormels (-0.00) and length of corm (-0.00), resulting its weak association with corm yield per plant.

4.3.3.7.3 Corm yield per plant vs. leaf length

Leaf length showed low positive direct effect (0.03) on the corm yield per plant at the genotypic level during 2008. During this year leaf length showed negative indirect effect through leaf width (-0.02), number of inflorescence (-0.02), number of suckers (-0.05), cormel weight (-0.01) and breath of corm (-0.00) at the genotypic level. On the other hand it showed low positive indirect effects on corm yield per plant via petiole length (0.07), number of leaves (0.01) and corm weight (0.01) at the genotypic level.

During 2009, leaf length showed negative correlation with corm yield per plant at the genotypic (-0.07) level. It also showed low negative indirect effects on corm yield per plant via plant height (-0.02), number of cormels (-0.00), cormel weight (-0.05) and length of corm (-0.00) at the genotypic level. On the other hand, it showed low positive indirect effects on corm yield per plant via petiole length (0.02), leaf width (0.04) and corm weight (0.02) at the genotypic level.

4.3.3.7.4 Corm yield per plant vs. leaf width

The data reveal significant positive correlation with corm yield per plant during 2008 (0.55**). During the first year, leaf width showed low negative direct effect on corm yield per plant at the genotypic (-0.06) level. This trait also showed low negative indirect effects through number of inflorescence (-0.05) and number of suckers (-0.02) at the genotypic level. Such negative indirect effects were minimize by its moderate to low positive indirect effects mainly through petiole length (0.10), leaf length (0.01), corm weight (0.02) and cormel weight (0.49) at the genotypic level.

During 2009, leaf width showed low positive direct effect (0.04) on the corm yield per plant at the genotypic level. During this year leaf width showed low positive indirect effects on corm yield per plant via petiole length (0.02) and corm weight (0.01) at the genotypic level. On the other hand it showed negative indirect effect through plant height (-0.02), leaf width (-0.07), and cormel weight (-0.03) at the genotypic level.

4.3.3.7.5 Corm yield per plant vs. number of inflorescence

The data reveal moderate positive correlation with corm yield per plant during 2008 (0.29*). During the first year, number of inflorescence showed low negative direct effect on corm yield per plant at the genotypic (-0.14) level. This trait also showed low negative indirect effects through leaf width (-0.02) and length of corm (-0.01) at the genotypic level. Such negative indirect effects were minimize by its moderate to low positive indirect effects mainly through petiole length

(0.11), number of suckers (0.04), number of leaves (0.01), corm weight (0.19) and cormel weight (0.10) at the genotypic level.

During 2009, the data reveal low positive correlation with corm yield per plant (0.15). During the second year, number of inflorescence showed low positive direct effect on corm yield per plant at the genotypic (0.01) level. This trait also showed low negative indirect effects through plant height (-0.01) at the genotypic level. On the other hand, number of inflorescence also show low positive indirect effects mainly through cormel weight (0.17) at the genotypic level.

4.3.3.7.6 Corm yield per plant vs. number of suckers

The data reveal low positive correlation with corm yield per plant during 2008 (0.07). During the first year, number of suckers showed low negative direct effect on corm yield per plant at the genotypic (-0.17) level. This trait also showed low negative indirect effects through leaf width, number of leaves and breath of corm at the genotypic level. Such negative indirect effects were minimize by its moderate to low positive indirect effects mainly through petiole length (0.13), number of inflorescence (0.03), corm weight (0.19) and cormel weight (0.05) at the genotypic level.

During 2009, the data reveal low positive correlation with corm yield per plant (0.08). During the second year, number of suckers showed low negative direct effect on corm yield per plant at the genotypic (-0.03) level. This trait also showed low negative indirect effects through plant height (-0.02) and corm weight (-0.06) at the genotypic level. On the other hand, number of suckers also show low positive indirect effects mainly

through petiole length (0.01), leaf length (0.01) and cormel weight (0.18) at the genotypic level.

4.3.3.7.7 Corm yield per plant vs. number of leaves

Number of leaves showed low negative direct effect (-0.20) on the corm yield per plant at the genotypic level during 2008. During this year number of leaves showed negative indirect effect through petiole length (-0.05), corm weight (-0.04) and cormel weight (-0.11) at the genotypic level. On the other hand, it showed low positive indirect effects on corm yield per plant via leaf width (0.01) and number of inflorescence (0.04) at the genotypic level.

During 2009, number of leaves showed significant negative correlation with corm yield per plant at the genotypic (-0.30*) level. It also showed moderate and low negative indirect effects on corm yield per plant via leaf width (-0.01), corm weight (-0.24) and cormel weight (-0.06) at the genotypic level. On the other hand, it showed low positive indirect effects on corm yield per plant via leaf length (0.04) at the genotypic level

4.3.3.7.8 Corm yield per plant vs. corm weight

The data reveal significant positive correlation with corm yield per plant during 2008 (0.65**). During the first year, corm weight showed significant positive direct effect on corm yield per plant at the genotypic (0.61) level. This trait also showed low negative indirect effects through number of inflorescence (-0.04) and length of corm (-0.01) at the genotypic level. Such negative indirect effects were minimize by its moderate to low

positive indirect effects mainly through petiole length (0.04), cormel weight (0.05) and breath of corm (0.01) at the genotypic level.

During 2009, the data reveal significant positive correlation with corm yield per plant (0.81**). During the second year, corm weight showed moderate positive direct effect on corm yield per plant at the genotypic (0.52) level. This trait also showed low negative indirect effects through plant height (-0.02) at the genotypic level. On the other hand, corm weight showed moderate to low positive indirect effects mainly through petiole length (0.01) and cormel weight (0.29) at the genotypic level.

4.3.3.7.9 Corm yield per plant vs. number of cormels

Number of cormels showed low negative but non-significant corr elation with corm yield per plant at genotypic (0.01) level during 2008, while number of cormels showed low positive correlation with corm yield at the phenotypic level during 2009. These non significant correlation were also indicated by its low direct as well as indirect effects on corm yield per plant via most of the other traits. Number of cormels also showed moderate positive indirect effects through number of inflorescence (0.04), cormel weight (0.17) and length of corm (0.01) at the genotypic level.

During 2009, number of cormels did not show significant correlation with corm yield per plant. Number of Cormels showed low positive direct effects on corm yield per plant at the genotypic (0.01) level and low positive indirect effects through cormel weight (0.12) at the genotypic level. On the other hand, number of cormels showed low to

moderate negative indirect effects through leaf width (-0.01), number of suckers (-0.02) and corm weight (-0.12) at the genotypic level.

4.3.3.7.10 Corm yield per plant vs. cormel weight

The data reveal significant positive correlation with corm yield per plant during 2008 (0.80**). During the first year, cormel weight showed significant positive direct effect on corm yield per plant at the genotypic (0.85) level. This trait also showed low negative indirect effects through petiole length (-0.01), leaf width (-0.03), number of inflorescence (-0.01) and breath of corm (-0.01) at the genotypic level. Such negative indirect effects were minimize by its moderate to low positive indirect effects mainly through corm weight (0.03) at the genotypic level.

During 2009, the data reveal significant positive correlation with corm yield per plant (0.88**). During the second year, cormel weight showed moderate positive direct effect on corm yield per plant at the genotypic (0.68) level. This trait also showed low negative indirect effects through plant height (-0.02) and number of suckers (-0.01) at the genotypic level. On the other hand, cormel weight showed moderate to low positive indirect effects mainly through petiole length (0.01) and corm weight (0.22) at the genotypic level.

4.3.3.7.12 Corm yield per plant vs. corm girth

The data reveal moderate positive correlation with corm yield per plant during 2008 (0.33**). During the first year, corm girth showed low negative direct effect on corm yield per plant at the genotypic (-0.02)

level. This trait also showed low negative indirect effects through plant height, petiole length, leaf length, leaf width, number of cormels and length of corm at the genotypic level. Such negative indirect effects were minimize by its low positive indirect effects mainly through length width (0.01), number of leaves (0.13) and cormel weight (0.21) at the genotypic level.

During 2009, the data reveal moderate positive correlation with corm yield per plant (0.60**). During the second year, corm girth showed low negative direct effect on corm yield per plant at the genotypic level. This trait also showed low negative indirect effects through leaf width (-0.02) and number of suckers (-0.01) at the genotypic level. On the other hand, corm girth also showed low positive indirect effects mainly through plant height (0.01), petiole length (0.02), leaf length (0.04), corm weight (0.22) and cormel weight (0.37) at the genotypic level.

4.3.3.7.13 Corm yield per plant vs. length of corm

Length of corm showed moderate positive correlations with corm yield per plant at genotypic (0.33**) level during 2008, while length of corm showed low negative direct correlation with corm yield at the genotypic (-0.03) level. Length of corm also showed low negative indirect effect through number of inflorescence (-0.06), on the other hand, length of corm also showed moderate to low positive indirect effects through petiole length (0.05), number of suckers (0.02), number of leaves (0.01), corm weight (0.32) and breath of corm (0.01) at the genotypic level.

During 2009, length of corm show moderate correlation with corm yield per plant at the genotypic (0.46) level. Length of corm showed low negative direct effects on corm yield per plant at the genotypic (-0.01) level. Length of corm also show moderate to low positive indirect effects through plant height (0.04), petiole length (0.04), corm weight (0.25) and cormel weight (0.22) at the genotypic level. On the other hand, length of corm also showed low negative indirect effects through leaf length, number of cormels and corm girth at the genotypic level.

4.3.3.7.14 Corm yield per plant vs. breath of corm

The data reveal low negative correlation with corm yield per plant during 2008 (-0.13). During the first year, breath of corm showed low positive direct effect on corm yield per plant at the genotypic (0.03) level. This trait also showed moderate to low negative indirect effects through cormel weight (-0.40) and length of corm (-0.01) at the genotypic level. Such negative indirect effects were minimize by its low positive indirect effects mainly through number of inflorescence (0.01), number of suckers (0.02) and corm weight (0.20) at the genotypic level.

During 2009, the data reveal low positive correlation with corm yield per plant (0.03). During the second year, breath of corm showed low positive direct effect on corm yield per plant at the genotypic (0.01) level. This trait also showed low negative indirect effects through leaf length (-0.01) and cormel weight (-0.19) at the genotypic level. On the other hand, breath of corm also showed low positive indirect effects mainly through corm weight (0.20) at the genotypic level. The residual effect was 0.06 in the year 2008 and 0.03 in the year 2009.

4.3.3.8 GENETIC DIVERGENCE

The study of genetic divergence of 50 genotypes of Colocasia was done through Mahalanobi's D^2 statistic as described by Rao, 1952. The analysis of variance revealed significant differences among the 50 genotypes for all the characters studied.

4.3.3.8.1 Clustering pattern

All the fifty genotypes were grouped into ten clusters depending on their genetic distance for the year 2008 and into nine clusters for the year 2009. The criterion used in clustering was that any two genotypes belonging to the same cluster must, at least on the average show a smaller intra cluster distance than those belonging to two different clusters, so they would vary very little from one another with regard to the aggregate of characters.

Cluster composition for the year 2008 is given in Table 4.11. It is evident from the clustering pattern that the entries usually did not cluster according to their geographical distribution. Applying Tocher's method, all the 50 genotypes were group into ten clusters (Table 4.11). Cluster VI had maximum number of 19 genotypes followed by cluster II with 13 genotypes, cluster IV with 6 genotypes, cluster I,III,V,VII,VIII with 2 genotypes and cluster IX and X had 1 genotype each. Cluster I comprised of 2 genotypes.

Cluster composition for the year 2009 is given in Table 4.12. Cluster VIII had maximum number of 21 genotypes followed by cluster VII with 14 genotypes, cluster I,II,III,IV,V and IV with 2 genotypes, cluster I,III,V,VII,VIII with 2 genotypes and cluster IX and X had 1 genotype each. Cluster I comprised of 2 genotypes.

4.3.3.8.2 Intra and inter cluster distance

The average intra and inter cluster distance is presented in Table 4.13 for the year 2008. The intra cluster distance was maximum in cluster IV (D^2 =20.4).The divergence at inter cluster level was maximum between cluster I and III (D^2=50.65), followed by cluster I and V (49.51) indicating greater diversity between these clusters. The genotype belonging to cluster I was collected from Peren and Mokokchung, while that belonging to cluster III was collected from Dimapur and Mon. The divergence was found to be minimum between cluster I and I (D^2 =1.98), followed by between clusters III and III (D^2 =3.77), V and V (D^2 =4.69), I and IX (D^2 =5.17), III and V (D^2 =5.47), VII and VII(D^2 =6.45), V and X (D^2 =7.64), VI and X (D^2 =8.68), V and VII (D^2 =9.56) and clusters III and X (D^2=9.77). This indicated that the genotypes belonging to these clusters were very close to each other.

The average intra and inter cluster distance is presented in Table 4.14 for the year 2009. The intra cluster distance was maximum in cluster IX (D^2=11.65). The divergence at inter cluster level was maximum between cluster III and IX (D^2=14.58), followed by cluster VI and IX (13.94) indicating greater diversity between these clusters. The genotype belonging to cluster III was collected from Wokha and Mon, while that belonging to

cluster IX was collected from Mokokchung, Phek and Dimapur. The divergence was found to be minimum between cluster II and II (D^2 =2.48), followed by between clusters III and III (D^2 =3.14), I and IV (D^2 = 3.18), I and II (D^2 =3.92), V and IV (D^2 =3.21), V and V (D^2 =3.28), VI and VI (D^2 =3.49), III and VI (D^2 =4.18) and clusters II and IV (D^2 =4.89). This indicated that the genotypes belonging to these clusters were very close to each other.

4.3.3.8.3 Cluster mean

The cluster mean of ten groups and the relative contribution of different characters toward divergence for the year 2008 is presented in table 4.15. It was observed that cluster I consisted of the genotype with longest breath of corm (14.32) (Waipong,Tejongnii). Cluster III consisted of the genotypes with longest leaf length(43.87) and maximum no of suckers (1.50) (Dziirinuo II, Tong I), Cluster IV consisted of the genotype with maximum leaf width (32.89), number of cormels (6.31), cormel weight (259.33) and yield per plant (397.17) (Dzii Dziinuo, Manie I, Dziinuo II, Thupela, Tino III and Tong II). Cluster V consisted of genotypes with maximum number of leave (5.07) (Beyo and Pajo). Cluster VIII consisted of genotypes with longest plant height (70.50), longest petiole length (55.77), maximum number of inflorescence (0.97) and longest length of corm (16.82) (Dziinuo VI and Atsantu) and cluster IX consisted of genotypes with maximum corm weight (256.33) and corm girth (10.73) (Beizo).

The contribution of different characters towards the expression of total genetic divergence indicated that yield per plant contributed a maximum level of (45.88). It was followed by length of corm (21.06%), number of cormels (12.41%), breath of corm (8.16%), cormel weight (3.02%), corm girth (2.29%), leaf length (1.39%), corm weight (1.31%), plant height (1.14), leaf width (1.06%), petiole length (0.90%), number of leaves (0.65), number of suckers (0.41) and number of inflorescence (0.33%) contributed the least towards the total genetic divergence.

The cluster mean of nine groups and the relative contribution of different characters toward divergence for the year 2009 is presented in table 4.16. It was observed that cluster II consisted of the genotype, among others with longest leaf length (41.43) and leaf width (29.50) (Tinopang, Kotaknii). On the other hand, cluster III consisted of the genotype with maximum number of suckers (2.73), cormel weight (268.72) and corm girth (18.92) (Manie I and Tong I), cluster V consisted of the genotypes with maximum number of leaves (4.88) (Obei, Dziinuo I), cluster VI consisted of the genotype with maximum number of inflorescence (0.50) and number of cormel (13.08) (Ati, Dziinuo II). Cluster VII consisted of genotypes with maximum yield per plant (412.67) (Waipong, Chugoma, Bei I, Beithola, Dziirinuo I, Tephfii dziinuo, Thegabeizii, Beidimai I, Loudoubei, DziiDziinuo, DziirinuoII, Thupela, Sama, Banu sam sam) and cluster IX consisted of genotypes with longest plant height (79.30), petiole length (65.74), maximum corm weight (190.44), longest length of corm (9.00) and breath of corm (9.90) (Tejongnii, Beizo, Dziitii).

The contribution of different characters towards the expression of total genetic divergence indicated that corm girth contributed a maximum level of (31.92%). It was followed by yield per plant (16.25%), number of cormels (15.27%), breath of corm (8.25%), cormel weight(7.76%), number of suckers(4.98%), plant height(4.00%), number of inflorescence (2.53%), corm weight (2.29%), length of corm (1.96%), leaf length (1.88%), number of leaves (1.71%) and leaf width (1.06%).

4.4 Molecular studies

4.4.1 Simple Sequence Repeat (SSR) analysis ;

Out of the 50 colocasia genotypes collected, 48 genotypes germinated and were selected for Simple Sequence Repeat analysis. CV5 and CV38 could not be analysed in molecular studies due to non germination of corm as the corm got rot. Altogether twenty eight colocasia markers were used to study the genetic diversity. All the primers used produce scorable amplicons. Band size amplified by the markers are presented in table 4.17. As seen from the Table, out of 28 markers, 16 showed considerable variation from the expected band sizes (last 6 digits of the marker name). 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.

The banding pattern of forty eight landraces with different primers are describe below;

Primer COLGCC56-191 produced three scorable amplicon in all the colocasia landraces. The primer showed good polymorphism. In several landraces there was no amplification ie., null alleles in genotypes 1, 4, 6, 7, 9, 11, 13, 17, 18, 19, 22, 23, 26, 28, 29, 30, 31, 33, 35, 36, 37, 40, 41, 42, 44, 45, 46, 47 and 48.The banding pattern is presented in plate-6(a).

Primer COLGCC82-117 produced one scorable amplicon in all the colocasia landraces. Null allele was showed by 13, 35, 44, 45, 46 and 47. The banding pattern is presented in plate-6(b).

Primer COLGCC111-300 produced two scorable amplicon in all the Colocasia landraces. Null allele was showed by 6, 7, 13, 17, 31, 35, 37, 44, 45, 46, 47 and 48. The banding pattern of COLGCC111-300 is presented in plate-7(a).

Primer COLGCC192-245 produced two scorable amplicon in almost all the colocasia landraces. Null allele was showed by 3, 6, 7, 13, 17, 23, 30, 31, 33, 35, 37, 40, 45, 46, 47 and 48. The banding pattern is presented in plate-7(b).

Primer COLGCC132-147 produced one scorable amplicon in almost all the Colocasia landraces. All the bands produced by the primer were monomorphic. Null alleles were showed by 16, 31, 35, 40, 44, 45, 46, 47 and 48. The banding pattern of primer COLGCC 132-147 is presented in plate-8(a).

Primer COLGCC233-167 produced two scorable amplicon in some genotype of colocasia landraces. Heterozygote was detected for landraces 11, 16 and 23. Null alleles were showed by 4, 6, 12, 17, 19, 31, 35, 37, 44, 45, 46, 47 and 48, the banding pattern is presented in plate-8(b).

Primer COLGCC88B-94 produced two scorable amplicon in some genotype of colocasia landraces. Heterozygote was detected for landraces 16, 20 and 32. Null alleles were showed by 4, 6, 13, 14, 17, 22, 35, 44, 45, 46, 47and 48. The banding pattern is presented in plate-9(a).

The banding pattern of Primer COLGCC75-100 is presented in Plate-9(b), primer COLGCC75-100 produced two scorable amplicon in almost all the Colocasia landraces. The primers produced amplified fragments much below the expected band size, some genotype of colocasia landraces. Null alleles were showed by 4, 6, 13, 17, 31, 35, 44, 45, 46 and 47.

Primer COLGCC118-221 produced only one scorable amplicon in almost all the Colocasia landraces. All the bands produced by the primer were monomorphic. Null alleles were showed by 7, 13, 19, 35, 36, 44and 45. The banding pattern is presented in plate-10(a).

Primer COLGCC103-220 produced only one scorable amplicon in almost all the Colocasia landraces. All the bands produced by the primer were monomorphic. Null alleles were showed by 1, 2, 4, 6, 7, 10, 13, 23, 26, 30, 31, 33, 35, 37, 41, 44, 45, 46, 47and 48.

Primer COLGCC77-174 produced two scorable amplicon in some genotype of colocasia landraces. Null alleles were showed by 6, 7, 13, 17, 23, 25, 35, 44, 45, 46, 47and 48. The banding pattern is presented in plate-10(b).

Primer COLGCC95-219 produced one scorable amplicon in almost all the Colocasia landraces. All the bands produced by the primer were monomorphic. Null alleles were showed by 6, 7, 13, 16, 24, 35, 44,

45, 46, 47 and 48. The banding pattern of primer COLGCC 132-147 is presented in plate-11(a).

Primer COLGCC98-294 produced three scorable amplicon in some genotype of colocasia landraces. Null alleles were showed by 2, 4, 6, 13, 17, 19, 20, 23, 30, 31, 33, 35, 40, 44, 45, 46, 47and 48. The banding pattern is presented in plate-11(b).

Primer COLGCC206-122 produced four scorable amplicon in some genotype of colocasia landraces. Null alleles were showed by 4, 6, 7, 8, 9, 10, 11, 16, 17, 35, 44, 45, 46, 47and 48. The banding pattern is presented in plate-12(a).

Primer COLGCC223-157 produced one scorable amplicon in almost all the Colocasia landraces. All the bands produced by the primer were monomorphic. Null alleles were showed by 2, 6, 7, 13, 17, 19, 22, 23, 26, 30, 31, 33, 35, 44, 45, 46, 47, 48 and 50.

Primer COLGCC220-211 produced two scorable amplicon in almost all the colocasia landraces. Null alleles were showed by 6, 7, 13, 14, 15, 16, 17, 22, 35, 44, 45, 46, 47and 48. The banding pattern is presented in plate-12(b).

Primer COLGCC119-367 produced only one scorable amplicon in almost all the Colocasia landraces. All the bands produced by the primer were monomorphic. Null alleles were showed by 2, 4, 6, 7, 13, 14, 19, 20, 21, 25, 31, 32, 34, 35, 40, 42, 44, 45, 46, 47 and 48. The banding pattern is presented in plate-13(a).

Primer COLGCC91-262 produced two scorable amplicon in some genotype of colocasia landraces. Heterozygote was detected for landraces

24. Null alleles were showed by 6, 9, 11, 30, 44, 45, 46 and 47. The banding pattern is presented in plate-13(b).

Primer COLGCC249-155 produced three scorable amplicon in some colocasia landraces. Null alleles were showed by 1, 2, 3, 4, 6, 7, 10, 11, 12, 13, 14, 16, 1 7, 18, 19, 20, 21, 22, 23, 24, 25, 26, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 40, 42, 43, 44, 45, 46, 47, 48, 49and 50. The banding pattern is presented in plate-14(a).

Primer COLGCC110-283 produced two scorable amplicon in some genotype of colocasia landraces. Heterozygote was detected for landraces 48. Null alleles were showed by 4, 6, 8, 9, 11, 15, 16, 18, 20, 25, 26, 44 and 47. The banding pattern is presented in plate-14(b).

Primer COLGCC211-202 produced three scorable amplicon in almost all the colocasia landraces. Null alleles were showed by 22, 24, 44, 45, 46 and 47. The banding pattern is presented in plate-15(a).

Primer COLGCC228-110 produced one scorable amplicon in almost all the colocasia landraces. Null alleles were showed by 1, 6, 7, 9, 14, 20, 22, 25, 26, 27, 34, 46, 47 and 48. The banding pattern is presented in plate-15(b).

Primer COLGCC240-223 produced only one scorable amplicon in almost all the Colocasia landraces. All the bands produced by the primer were monomorphic. Null alleles were showed by 2, 6, 7, 8, 9, 10, 14, 18, 21, 24, 33, 34, 47 and 48. The banding pattern is presented in plate-16(a).

Primer COLGCC105-267 produced two scorable amplicon in some genotype of colocasia landraces. Heterozygote was detected for landraces 2,

9, 14, 37, 39 and 50. Null alleles were showed by 6, 9, 11, 13, 17, 35, 45, 46, 47 and 48. The banding pattern is presented in plate-16(b).

Primer COLGCC208-253 produced four scorable amplicon in some genotype of colocasia landraces. Heterozygote was detected for landraces 2, 14, 24 and 25. Null alleles were showed by 6, 9, 13, 17, 23, 35, 45, 46, 47 and 48. The banding pattern is presented in plate-17(a).

Primer COLGCC209-120 produced one scorable amplicon in almost all the Colocasia landraces. All the bands produced by the primer were monomorphic. Null alleles were showed by 2, 3, 10, 13, 15, 17, 21, 33, 35, 44, 45, 46, 47 and 48. The banding pattern is presented in plate-17(b).

Primer COLGCC90-102 produced one scorable amplicon in almost all the Colocasia landraces. All the bands produced by the primer were monomorphic. Null alleles were showed by 6, 13, 17, 44, 45, 46, 47 and 48. The banding pattern is presented in plate-18(a).

Primer COLGCC73-164 produced two scorable amplicon in almost all colocasia landraces. Heterozygote was detected for almost all the landraces except in 6, 10, 14, 20, 27, 32 and 43. Null alleles were showed by 36 and 45. The banding pattern is presented in plate-18(b).

Highest number of heterozygote 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 (range 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).

Dendrogram (Fig 9) based on UPGMA analysis separated the accessions into five clusters with a Jaccard's similarity co-efficient indicating high genetic variability among the accessions. Four definite clusters were identified at a level of 35% similarity among the individuals. As may be seen from fig 9-D, beyond cluster discrimination at CUT-3 (solid line on the dendrogram) the clusters overlapped. 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 (Fig 9). Clusters were determined based on discriminate analysis with the genotypic data. Clusters 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 no. 45 was unique as it formed a single genotype cluster at levels of cluster discrimination. At the discrimination level CUT-3, genotype no. 6 also produced a single genotype cluster. The discriminate analysis showed a clear distinction 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

vertical distinction was less prominent. There was no overlapping of group centroid, (Fig 10).

All genotypes were grouped into six hypothetical populations based on their location of collection (Table 4.18 and Fig 11). 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 4.19). Within population variation accounted for 100% of the observed molecular variation (Fig.12). A principal co-ordinate analysis was carried out to visualize the distribution of different hypothetical population across the regions. As seen from fig 13, the populations were uniformly distributed which supported the observation from AMOVA that within population variation accounts for the observed molecular variation.

Chapter 5
Discussion

Nagaland is rich in genetic diversity of colocasia owing to its ecological diversity offered by its dense forest and hilly tracts/terrains. Farmers cultivate several locally adapted landraces of colocasia. These landraces are not only numerous, fulfilling a varieties of needs and adapted to different conditions, but also genetically viable. To efficiently conserve, manage and use such germplasm resources, an understanding of structure and dynamics of local landraces variation is required. Studies carried out by workers to examine the genetic variation of colocasia of the region is very limited and little or no information is available so far on how genetic diversity is structured within a given landraces.

The present investigation was undertaken to gather knowledge on the variability and diversity among the local landraces, through collection, documentation and also by evaluation and characterization of the genotype at both the morphological and molecular levels.

5.1 Collection and documentation

Collection and exploration of edible aroids of Nagaland indicated the presence of large number of germplasm in the region especially colocasia. Local adaptation plays an important role in maintaining yields in traditional agricultural system. It was observed during the collection that different germplasm were grown under varying altitudes ranging from 450-

1980m mean sea level indicating the diverse adaptability. Out of all the districts, Mon district maintained a good amount of local germplasm.

5.2 Qualitative characters

The genotypes under study showed wide range of variability for all the qualitative characters studied. In all the genotypes of Colocasia leaf blade margin was found to be undulate. Six classes of leaf blade color were presented with majority of the genotypes were found to possess green leaf blade color followed by white, purple, yellow green, pink and black. Leaf blade color variegation was found in all the genotypes. Flower formation was present in 13 genotype out of the total 50 genotype in the experiment. Predominant position of leaf lamina surface was found to be erect apex down in all the cultivars. Four classes of leaf main vein color were present with majority of the genotype were found to possess white color followed by purple, green and pink. Leaf vein pattern was found to be V pattern for all the genotype. Four classes of Petiole basal ring colour were presented with majority of the genotypes were found to possess green petiole basal colour followed by purple, white and dark brown. Five classes of Petiole junction colour were presented with majority of the genotypes were found to possess green petiole junction colour followed by purple, white, light purple and dark purple Petiole junction colour. Petiole junction pattern was found to be small for all the genotypes. Three classes of Petiole lower colour were presented with majority of the genotypes were found to possess green petiole lower colour followed by purple and brown Petiole lower colour.16 genotypes were found to have petiole stripe. Three classes of Petiole stripe colour were presented with majority of the genotypes were

found to possess purple petiole stripe colour followed by green and black. Five classes of Petiole top colour were presented with majority of the genotypes were found to possess green petiole top colour followed by purple, light green, white and greenish purple. All the genotypes were found to be tolerant for Taro leaf blight resistant. Two classes of corm flesh colour were presented with majority of the genotypes were found to possess white corm flesh color followed by pink. Two classes of corm flesh fiber colour were presented with majority of the genotypes were found to possess white corm flesh fiber colour followed by yellow. Three classes of corm shape were presented with majority of the genotypes were found to possess round corm shape followed by flat and multi faced and elongated shape. Two classes of corm cortex colour were presented with majority of the genotypes were found to possess white corm cortex colour followed by pink. Similar results were also reported by Tanimoto *et al.* (1986), Ivancic *et al.* (2003), Trimanto *et al*. (2010) and Bhattacharjee *et al*. (2014).

5.3 Quantitative characters

Analysis of variance for various morpho-agronomic characters revealed high significant variation among the 50 genotypes with respect to all the character studied. The presence of large amount of variability might be due to diverse source of materials as well as environmental influence affecting the phenotypes. A wide range of variability and co-efficient of variation in this crop had also been found for yield and its components by Biradar *et.al.* (1978), Unnikrishnan *et. al.* (1984), Sree Kumarie Abraham (1984) and Bhattacharjee *et. al.* (2014)

5.3.1 Mean performance of the genotypes

From the study of the mean performance of the genotypes, the highest corm yield per plant was exhibited by CV27 (Lijalanii) during 2008 and CV3 (Bei I) during 2009. The above mentioned yield attributing character showed significant positive correlation with yield per plant at both the phenotypic and genotypic level. Therefore, the genotype CV27 and CV3 could be considered as one of the potential cultivars among the genotypes.

Based on the mean performance of 2008 and 2009, following genotypes showed high corm yield per plant along with high value for yield attributing characters. Therefore, these cultivars could be considered as promising genotype:

2008	2009
CV10 (Thegabeizei)	CV1 (Waipong)
CV12 (Louduobei)	CV2 (Chugoma)
CV13 (Dziinuo II)	CV3 (Bei I)
CV18 (Thupela)	CV4 (Beithola)
CV27 (Lijalanii)	CV15 (Dziirinuo II)
CV33 (Bao)	CV21(Sama)
CV39 (Tino II)	CV29 (Beidimai II)
CV42 (Atsantu)	CV30 (Diirinuo III)

5.3.2 Genetic variability and related parameters

Presence of genetic variability may it be natural or induced is the first pre-requisite for success of any breeding program. Hence, it is essential for the breeder to assess the genotypic variation and genetic value of the material under investigation by estimating the genotypic variance, genotypic coefficient of variation, heritability, genetic advance etc. Again,

the genotypic component are accessed from the phenotypic value, which reflect both genetic (heritable) and non-genetic (non-heritable) influence. Thus it is important to estimate genotypic variance and phenotypic variance and genotypic coefficient of variation and phenotypic coefficient of variation to have a clear idea about the genetic worth of the breeding material.

5.3.3 Genotypic and Phenotypic variance

In the present investigation, phenotypic variance was higher than the genotypic variance for all the characters thus indicating the influence of environmental factor on these traits. The maximum phenotypic and genotypic variation was obtained from corm yield per plant, cormel weight and corm weight. While moderate variation was observed for plant height, petiole length, leaf length and leaf width. Values of phenotypic and genotypic variance were very close for number of inflorescence and number of suckers indicating least influence of environment on these traits. These results are in accordance with Kumar *et al* (2000) and Paul *et.al*. (2011).

5.3.4 Genotypic and phenotypic coefficient of variation

A better comparison of the characters regarding the extent of genetic variation could be made from the estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). Among the characters considered in the present investigation, phenotypic coefficient of variation (PCV) was found to be higher than genotypic coefficient of variation (GCV) indicating the influence of environment for

the expression of these characters. In this context, Kumar *et al.,* (2000) reported that in Arvi (*Colocasia esculenta* L. Schott) phenotypic coefficient of variation was higher than corresponding genotypic component for all the traits studied. Paul *et al.,* (2011) studied the extent of genetic variation in taro (*C. esculenta*) and reported that the phenotypic coefficient of variation (PCV) were higher in magnitude than the genotypic coefficient of variation (GCV) for all the traits. Similarly petiole length, leaf length, leaf width, corm weight, corm girth and yield per plant exhibited higher phenotypic coefficient of variation than the genotypic coefficient of variation. This was partly supported by Akorda (1984). Moderate estimates of GCV and PCV were observed for plant height, corm weight, cormel weight and corm girth. This finding is in agreement with those recorded by Bhattacharjee *et al.,*(2014). These result indicates that selection will be effective for these characters and sufficient improvement could be achieved if selection is practiced based on these traits.

5.3.5 Heritability and genetic advance

To determine the relative amount of heritable portion of the total variance, the estimates of heritability in broad sense ($h^2_{b.s}$) and genetic advance as percent of mean were taken into account so that emphasis could be laid on highly heritable characters for further improvement of the populations. High heritability indicates greater correspondence between phenotypic and genotypic values. However, for effective selection, high heritability of a character should be accompanied by high genetic advance (Johnson *et al.,* 1955) because such characters are mostly controlled by additive gene action as reported by Panse (1957).

A fairly reliable idea of the relative amount of heritable variation in the population for a particular character can be obtained from the heritability estimates for the character concerned. In the present investigation, high estimates of heritability were observed for length of corm, breath of corm, number of cormel and plant height for the year 2008 and com girth, breath of corm, and number of cormels for the year 2009 suggesting that selection should be effective for these characters as high heritability implies low influence on environment. However, rather low estimates of heritability were recorded for leaf width, number of suckers and number of leaves for the year 2008 and number of leaves and length of corm for the year 2009. Rhishi *et al*., (1984) reported high estimates of heritability for leaf area and tuber yield per plant in *Dioscorea deltoidea*. Mathura *et al*., (1988) also observed high heritability for tuber weight per plant. Other reports available regarding the estimates of heritability are quite contradictory. In this investigation high heritability was observed for length of corm during 2008 and corm girth during 2009, this may be due to different locations and environmental condition in which the experiment were conducted. Since heritability is the proportion of the total variability that is describable to the genotype, it gives only the idea of the relative amount of heritable variation to the total variation. Thus based on heritability estimates alone, no precise suggestion can be made.

Burton (1952) suggested that the genotypic coefficient of variation together with heritability in a broad sense is perhaps a better index of the extent of advance that can be expected from a given selection scheme. In the present investigation high heritability was associated with high genotypic coefficient of variation for length of corm and breath of corm for the year 2008 and corm girth for the year 2009.

For reliable selection, high heritability of a character needs to be accompanied by high genetic advance (Johnson *et al*., 1955), because such characters are mostly controlled by additive gene action, as reported by Panse and Sukhatme (1957). Selection for such a character is highly effective. In the present investigation high heritability coupled with high genetic advance was found to be associated with all the traits except leaf width, number of suckers and number of leaves during 2008 and number of leaves during 2009, suggesting predominance of additive variance for these characters. Simple selection based on phenotypic value can be useful for improving these characters.

5.3.6 Correlation studies

Interrelationship among various plant characters has an important bearing on formulation of effective breeding strategy. To improve complex traits like yield which is influenced by a number of component characters, it is necessary for the breeders to have a clear idea about the degree and direction of association of yield with these components and also among them. Hence after getting information regarding the variability present in the material it was considered worthwhile to study the interrelationships of different characters and the associations were worked out at genotypic and phenotypic levels.

Yield per plant showed significant positive genotypic correlation with leaf width, number of inflorescence, corm weight, cormel weight, corm girth and length of corms during 2008 and with plant height, corm weight, cormel weight, corm girth and length of corm during 2009. Hussian *et al*., (1983) reported positive correlation between yield per plant and leaf

size, plant height and petiole length in Colocasia. Sreekumari and Abraham (1973) in their studies in Coleus also reported a significant positive correlation between tuber yields with plant height.

Petiole length exhibited significant positive genotypic correlation with leaf width, number of inflorescences and number of suckers during 2008. Plant height exhibited a positive significant correlation both at genotypic and phenotypic with petiole length during both the years. Leaf breadth also exhibited a positive significant correlation with number of inflorescences during 2008. A positive significant correlation was also exhibited between number of inflorescences with length of corm during 2008 at genotypic and phenotypic level and a positive significant correlation at phenotypic level with number of cormels during 2009. Corm weight exhibit a positive significant correlation both at genotypic and phenotypic level with length of corm during 2008 and cormel weight and corm girth during 2009. Number of cormels exhibit a positive significant correlation both at genotypic and phenotypic level with corm girth during 2009. Cormel weight exhibit a positive significant correlation both at genotypic and phenotypic level with corm girth during 2009. Length of corm exhibited a positive significant correlation both at genotypic and phenotypic level with breath of corm during 2008 and at the genotypic level during 2009. This was partially supported by Parthasarathy and Medhi (1981). They reported a significant correlation between tuber weight with corm girth and leaf length. A negative significant correlation also exist between number of cormels and length of corm both at genotypic and phenotypic levels during 2008. A negative significant correlation also exist between leaf length and corm girth both at genotypic and phenotypic levels during 2009. Thus this present investigation reveals that among the

characters which were significantly correlated with each other, all of them were positively correlated with each other, except for number of cormels and corm weight and leaf length and corm weight which showed a significant negative genotypic and phenotypic correlation with each other. Thus it is clearly indicated that improvement of one character may also improve another correlated character.

The information with regard to estimates of genotypic and phenotypic coefficient of variation, heritability and genetic advance together with estimates of correlation suggest a greater possibility of inclusion of number of cormels, length of corm, leaf length and corm girth in the breeding programme for desired improvement of these characters as well as for the improvement of their correlated characters.

5.3.7 Path coefficient analysis

Path coefficient analysis of yield and yield attributes depicts the cause and effect relationship and accordingly measures the relative importance of each variable. Correlation values between yield and its component traits are equivocal due to interrelationships existing among the components. As a result the direct contribution of each component trait on yield and the indirect effects through its association with other component traits cannot be discerned entirely from correlation studies. In other words, correlation studies reveal only the general relationship between any two variables without tracing possible causes of such associations. A positive correlation between a particular trait and yield need not necessarily lead to a direct positive effect. Hence knowledge of the association of various

quantitative characters and their direct and indirect effects on seed yield would be of immense help to breeders (Rao, *et al.*, 1980) particularly in formulating an indirect selection program for seed yield based on component traits. Keeping all these points in view, path coefficient analysis was carried out to resolve the direct and indirect effects of different characters on yield at both genotypic and phenotypic levels. At genotypic level, the path analysis revealed that cormel weight had the highest positive direct effect on yield for both the year, 2008 and 2009 this was supported by Unnikrishnan *et al*., (1984) on Colocasia. This was followed by corm weight and petiole length for both the years, which exerted a positive effect and exhibit significant positive correlation with yield indicating a true relationship among the traits. Mohankumar *et al*., (1990) reported that leaf area and cormel weight had a positive direct effect on yield in taro. Cormel weight and corm weight exerted positive direct effect and also exhibited significant positive correlation with yield indicating a true relationship between the traits. This suggested that the direct relation for cormel weight and corm weight would likely be effective in increasing seed yield.

The residual effect was 0.06 during 2008 and 0.03 during 2009 indicating 94% and 97% of the variability in corm yield per plant could be explained by the variables included in study.

5.3.8 Genetic Divergence

Genetic diversity in the available gene pool is the source of variation, which is raw for the improvement work. For effective conservation and utilization of colocasia genetic resources, a clear understanding of genetic diversity and relationships of varieties is essential.

Precise information on the nature and degree of genetic divergence of the parents is the prerequisite for an effective breeding program. Several measures of distance have been propose to suit the various objectives of which Mahalanob's generalized distance had occupied a unique place in plant breeding.

Using this technique, 50 genotype of colocasia were classified into 10 clusters for the year 2008 and 9 cluster for the year 2009. The distribution of entries in various clusters showed that there was considerable amount of genetic divergence among the genotypes for all the characters studied. During 2008, Out of the 10 clusters, cluster VI had maximum number of 19 genotypes followed by cluster II with 13 genotypes, cluster IV with 6 genotypes, cluster I,III,V,VII,VIII with 2 genotypes and cluster IX and X had 1 genotype each. During 2009, out of the 9 clusters, cluster VIII had maximum number of 21 genotypes followed by cluster VII with 14 genotypes, cluster I,II,III,IV,V and IV with 2 genotypes, cluster I,III,V,VII,VIII with 2 genotypes and cluster IX and X had 1 genotype each.

The inter-cluster distance were greater than intra-cluster distances revealing considerable amount of genetic diversity among the genotypes studied for both the years. The results are in agreement with the previous reports Singh *et al.,* (1985) and Rahman *et al.*, (1997). During 2008, the intra cluster distance was maximum in cluster IV (D^2 =20.4). The divergence at inter cluster level was maximum between cluster I and III (D^2 =50.65), followed by cluster I and V (49.51) indicating greater diversity between these clusters. Choosing of genotypes belonging to distant clusters was expected to produce highly variable population. The minimum inter

cluster distance was recorded between I and IX (D^2 =5.17), III and V (D^2 =5.47), VII and VII (D^2 =6.45), V and X (D^2 =7.64), VI and X (D^2 =8.68), V and VII (D^2 =9.56) and clusters III and X (D^2 =9.77). The genotypes in these clusters are genetically very close.

During 2009, the intra cluster distance was maximum in cluster IX (D^2 =11.65). The divergence at inter cluster level was maximum between cluster III and IX (D^2 =14.58), followed by cluster VI and IX (D^2 =13.94) indicating greater diversity between these clusters. Choosing of genotypes belonging to distant clusters was expected to produce highly variable population. The minimum inter cluster distance was recorded between I and IV (D^2 = 3.18), I and II (D^2 =3.92), V and IV (D^2 =3.21), V and V (D^2 =3.28), VI and VI (D^2 =3.49), III and VI (D^2 =4.18) and clusters II and IV (D^2 =4.89). The genotypes in these clusters are genetically very close.

During 2008, the maximum cluster mean value was observed in cluster IV for leaf width, number of cormels, cormel weight, and yield per plant. Cluster VIII also have the highest mean for plant height, petiole length, number of inflorescence and length of corm. Cluster V consisted of genotypes with maximum number of leave. Cluster IX consisted of genotypes with maximum corm weight and corm girth.

During 2009, the maximum cluster mean value was observed in cluster IX for plant height, petiole length, corm weight, length of corm and breath of corm. Cluster III consisted of the genotype with maximum number of suckers, cormel weight and corm girth. Cluster VI consisted of the genotype with maximum number of inflorescence and number of cormel. Cluster II consisted of the genotype, among others with longest leaf length and leaf width. Cluster V consisted of the genotypes with maximum

number of leaves and number of inflorescence contributed the least towards the total genetic divergence.

In several instances, clusters aggregated cultivars that are highly likely to be genetically distant, such as varieties with or without stolons, branched or unbranched, variegated or non-variegated. Singh *et al*. (2008) also reported similar result.

The selection and choice of parents mainly depends upon contribution of characters towards divergence. Among the characters studied the maximum contribution towards divergence among the local land races was corm yield per plant during 2008. This was followed by length of corm, number of cormels, breath of corm, cormel weight, corm girth, leaf length, corm weight, plant height, leaf width, petiole length, number of leaves, number of suckers. During 2009, the maximum contribution towards divergence among the landraces was corm girth .This was followed by number of cormels, breath of corm, cormel weight, number of suckers, plant height, number of inflorescence, corm weight, length of corm, leaf length, number of leaves, leaf width and petiole length (0.16%) contributed the least towards the total genetic divergence. Bhattacharjee *et al*. (2014) also reported similar findings.

Therefore, character such as corm yield per plant, length of corm, number of cormels, breath of corm, cormel weight, corm girth, leaf length, corm weight, plant height, leaf width can be used for selecting parents from distinctly placed clusters to obtain high yielding genotypes.

5.4 Molecular studies

Here we report genetic characterization of colocasia germplasm of Nagaland using molecular markers, which 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. In another two studies (Pillai & Lekha 2008, Sharma *et al*. 2008) 14 and 45 genotypes were studied respectively and the RAPD primers were reported to show 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.

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 7 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. Twenty three clusters were identified in their study. Macharia *et al.* (2014) identified 31 alleles in 98 East African germplasm accessions using 6 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. Within 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, informative and the germplasm of Nagaland was diverse but somewhat uniformly distributed across the state.

5.5 Comparative discussion of D^2 analysis and molecular diversity analysis.

In the D^2 analysis all the fifty genotypes were grouped into ten clusters depending on their genetic distance in the year 2008 (Table4.11) and into nine clusters in the year 2009 (Table 4.12). In D^2 analysis the two clusters that have the highest number of genotypes for both the years are thirteen genotype in cluster II and nineteen genotypes in cluster VI for the year 2008 whereas in the year 2009, clusters VII have 14 genotypes and cluster VIII have 21 genotypes. From these two years the similar genotype present in cluster II of 2008 and cluster VII of 2009 were selected and these similar genotypes present in the clusters were compared with molecular diversity analysis genotype which were group into six hypothetical population based on their location of collection (Table 4.18). In the comparison, the genotype Chugoma, Beithola, Dziirinuo I, Thegabeizii,

Beidimai I, Tephfii dziinuo, and Loudoubei were present in both the cluster II of 2008 and cluster VII of 2009 whereas only Chugoma and Beithola were present in pop1 of the genotype group in molecular diversity. Dziirinuo I was present in pop 6, Thegabeizii and Tephfii dziinuo were in pop 5 and Beidimai I and Loudoubei were present in pop 4. Similarily, the genotype of cluster IV of 2008 and cluster VIII of 2009 of D^2 analysis were compared with the molecular diversity analysis where Dziinuo III, Keriila, Sama, Dziinuo IV, Lijalanii, Tefiidzii, Chiicha, Beidimai II, Dziirinuo III, Manie II, Bao, Aiie, Wolikhuo, Kotaknii, Tino I and Tino II were present in both the cluster VI and cluster VIII of 2009. Among these genotypes Dziinuo III, Keriila and Chiicha genotypes were grouped in pop 6, Sama, Dziinuo IV, Tefiidzii and Wolikho were grouped in pop 5, Lijalanii, Manie II and Kotaknii were grouped in pop 2, Tino I and Tino II were grouped in pop 3 and Bao and Aiie were grouped in pop 1.

Thus the fifty genotypes in the D^2 analysis and molecular diversity shows that some of the genotypes present in the clusters of both the years were also present in the population group of molecular analysis, but most of the genotypes were scattered in different cluster and population group indicating role of diverse environmental condition.

Chapter 6
Summary and Conclusion

The present investigation entitled “Study of genetic divergence in indigenous edible aroids of Nagaland using morphological and SSR DNA fingerprinting” was carried out during Kharif season of two consecutive years, 2008 and 2009, in the Experimental Farm of Department of Genetics and Plant Breeding, Nagaland University, School of Agricultural Sciences and Rural Development using a total of 50 genotypes of Taro (*Colocasia esculenta* (L.)Schoot) comprising of local germplasm of Nagaland which were laid out in Randomized Block Design with three replications. Other edible aroids namely two Xanthosoma species, two Alocasia species and one Amorphophallus species were also documented.

The investigation was undertaken on two broad aspects:

i) Morphological evaluation, evaluation of genetic variability, character association and diversity based on fourteen morphological and yield traits viz, plant height, petiole length, leaf length, leaf width, number of inflorescence, number of suckers, number of leaves, corm weight, number of cormels, cormel weight, corm girth, length of corm, breath of corm, yield per plant and

ii) Characterization of genetic diversity through SSR DNA fingerprinting.

Morphological characterization

Variability analysis revealed highly significant difference among the genotypes for all the characters. The present study revealed highest mean for yield per plant was recorded from the local cultivar Lijalanii during 2008(549.34g) followed by Bei I (520.00g) and Thegabeizii (491.67g) and Bei I during 2009 (815.34g) followed by Beidimai (671.67g) and Sama (528.67g). Among the quantitative characters, number of inflorescence gave the highest estimates of both genotypic and phenotypic coefficient of variation for both the year, during 2008 (246.53 and 278.6 respectively) followed by breath of corm (88.96 and 89.61) and during 2009 (189.92 and 247.65) followed by breath of corm (73.74 and 78.54). Higher estimates of GCV and PCV were recorded for number of inflorescence, breadth of corm, number of cormels and number of suckers; medium estimates for corm girth, length of corm and cormel weight.

High estimates of heritability coupled with high genetic advance as percent of mean was recorded for length of corm, corm girth, breath of corm, number of cormels, leaf length, number of inflorescence per plant, number of suckers, corm weight, cormel weight, plant height, petiole length and yield per plant, showing possibility for improvement of these traits through selection.

Correlation coefficient studies reveal that yield per plant was positively and significantly correlated with only cormel weight and corm weight. The path analysis reveal that cormel weight and corm weight

exerted positive direct effect and also exhibited significant positive correlation with yield at genotypic level indicating a true relationship among the traits. This suggested that the direct selection for cormel weight and corm weight would likely be effective in increasing seed yield.

Genetic divergence was accessed through Mahalanobis (1936) D^2 statistic and the 50 genotype were grouped into ten cluster for the year 2008. The analysis revealed maximum contribution of corm yield per plant, length of corm and number of cormels towards genetic divergence. For the year 2009, the 50 genotype were grouped into nine clusters. The analysis revealed maximum contribution of corm girth, corm yield per plant and number of cormels towards genetic divergence. The clustering pattern indicates that geographic diversity has impact on genetic diversity.

Molecular studies

1. A total of 53 alleles were amplified by the 28 SSR markers in the 48 genotypes with an average of 1.89 alleles per locus.
2. The number of alleles ranged from one to four. The overall size of amplified products ranged from 117bp to 685bp.
3. The PIC value of COLGCC206-122 and COLGCC211-202 are noticeable as they showed PIC values above 0.9. The high polymorphism detected in this study supported our assumption that colocasia is highly variable.
4. The most frequent allele were 231bp, 312bp, 166bp, 278bp COLGCC105-267, COLGCC119-367, COLGCC223-157,COLGCC98-

294. Therefore this marker can be used as disgonostic marker for Colocasia.

5. Primer COLGCC56-191 showed good polymorphism for almost all the genotypes.
6. Maximum no of rare alleles were detected for landraces 2, 9, 13, 20, 24, 25, 48 and 50.
7. UPGMA dendrogram resulted in five major clusters with several subclusters.
8. Among the 48 genotypes, genotype CV 45 was unique as it formed a single genotype cluster at levels of cluster discrimination. At the discrimination level CUT-3, genotype CV 6 also produced a single genotype cluster.
9. Principal Coordinates (PCA) of the marker data (grouped on population basis) distinctly separated the populations from different locations indicating the role of habitat heterogeneity in genotype selection for colocasia cultivation.
10. Genotypes that form tiny separated groups or taxonomic units are potential germplasm for broadening genetic base of cultivated varieties. In this regard, the genotypes CV45, CV44 (Population 2), CV6 (population 5), CV46 (Population 1) and CV47 (Population 3) are important.

Conclusion

The result of the investigation revealed the presence of substantial variation in the experimental materials for all the characters under study.

- Collection and morphological studies of colocasia landraces indicates the presence of good diversity of colocasia germplasm in the region. Further exploration and collection of colocasia germplasm is required.
- Among the genotypes studied Lijalanii, Bei I, Thegabeizii, Beidimai II and Sama may be considered as the potential genotypes for incorporation in Colocasia breeding programme.
- High estimates of GCV and PCV were recorded for number of inflorescence, breadth of corm and number of cormels indicating the presence of ample variation for these traits in the present material.
- High heritability coupled with high genetic advance as percent of mean was recorded for length of corm, corm girth, breath of corm, number of cormels, leaf length, number of inflorescence per plant, number of suckers, corm weight, cormel weight, plant height, petiole length and yield per plant. Thus simple selection based on phenotypic performance for these traits would be effective as these are apparently under the control of additive gene action.
- The corm yield per plant exhibited significant positive correlation with cormel weight and corm weight indicating relative utility of this trait for selection.

- Cormel weight and corm weight exerted maximum positive direct effect and exhibited significant positive correlation with yield indicating a true relationship among the traits.
- Genetic divergence was accessed through Mahalanobis (1936) D^2 statistics and the 50 genotype were grouped into ten clusters for the year 2008. Most of the local genotypes collected from the districts (Dziinuo III, Keriila, Sama, Dziinuo IV, Bei II, Tefiidzii, Chiicha, Lijalanii, Beidimai II, Dziirinuo III, Manie II, Banu sam sam, Bao, Aiie, wolikhuo, Tinopang, Kotaknii, Tino I, Tino II) were placed in cluster VI with moderate intra cluster distance indicating their closeness. The genotypes collected from Peren and Mokokchung (Waipong and Tejongnii) were grouped into cluster I with least intra cluster distance indicating their closeness and similarity. The analysis revealed maximum contribution of corm yield per plant, length of corm and number of cormels towards genetic divergence. For the year 2009, the 50 genotype were grouped into nine clusters. Most of the local genotypes collected from the districts (Dziinuo III, Keriila, Sama, Beyo, Dziinuo IV, Tefiidzii, Chiicha, Lijalanii, Pajo, Beidimai II, Dziirinuo III, Manie II, Bao, Aiie, Wolikhuo, Kotaknii, Tino I, Tino II, Tino III, Dziinuo V, Atsantu, Tong II) were placed in cluster VIII with moderate intra cluster distance indicating their closeness. The genotypes collected from Mokokchung and Zunheboto (Wasiinii and Chuyali) were grouped into cluster I with least intra cluster distance indicating their closeness and similarity.
- The analysis revealed maximum contribution of corm girth, corm yield per plant and number of cormels towards genetic divergence.

The clustering patterns indicate that geographic diversity has impact on genetic diversity.

- The estimates of high PIC value showed high level of genetic diversity in germplasm.
- Both morphological and genetic variations exist between indigenous edible aroids.
- The information about the genetic diversity of these landraces will be useful for future work related to proper identification for selection in breeding programs.

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APPENDIX I

Meteorological data of Medziphema area during the period of investigation 2008 and 2009

Month	Temperature(°C)				Total rainfall (mm)		Relative humidity (%)	
	Maximum		Minimum					
	2008	2009	2008	2009	2008	2009	2008	2009
January	22	24.5	10	9.5	30.1	0	78	78
February	22.4	23.7	10	10	14.2	5.1	78	77
March	28.1	27.9	13.2	13.7	29.2	24	80	74
April	32	29.7	20	19.5	15.2	31.6	45	79
May	31.6	32.35	25.5	23.05	61.1	130.8	50.5	62.73
June	31	32.7	23.9	23.05	99	116.7	67	65.69
July	31.4	32.55	24.4	25.77	66	219	63.1	70.39
August	31.6	31.32	24.9	25.24	67	169.8	67.7	74.79
September	30.79	31.67	22.91	24.46	286.6	188.7	66.86	73.1
October	28.62	29.85	20.89	21.8	171.3	74.9	64.1	69.97
November	26.72	26.72	14.11	15.63	0	7.5	47.2	65.52
December	24.59	24.26	12.53	10.49	6.56	0	50.26	61.33

Source : ICAR Complex for NEH, Jharnapani

APPENDIX II

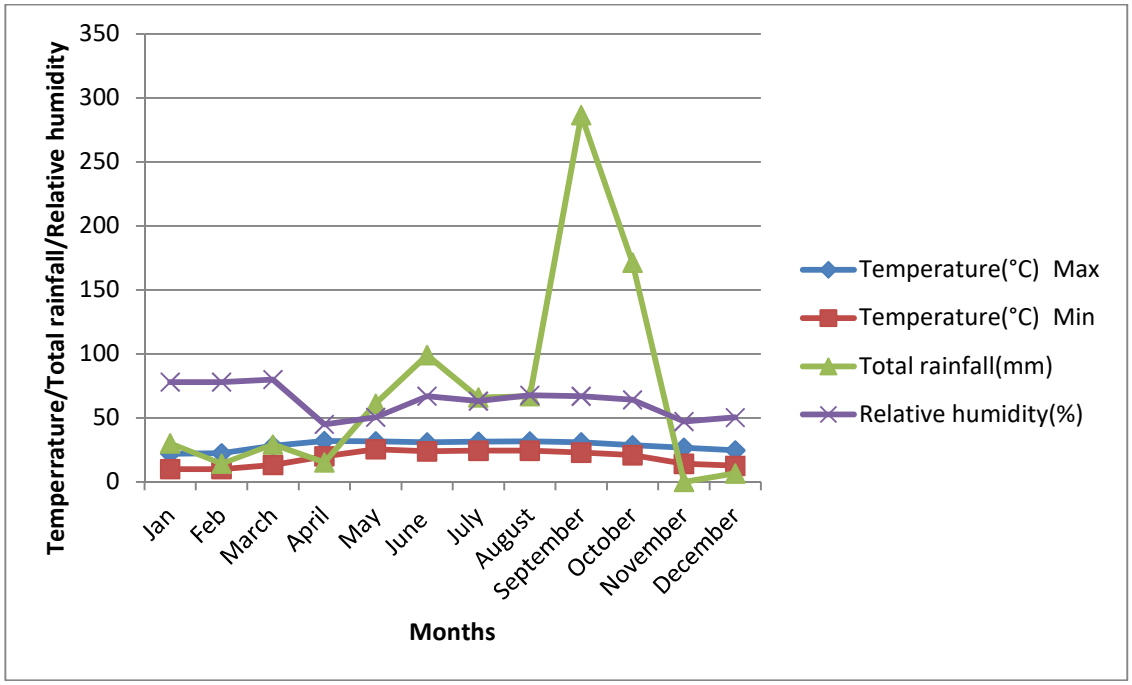


Fig: Meteorological data of Medziphema area during the period of investigation (January 2008 to December 2008).

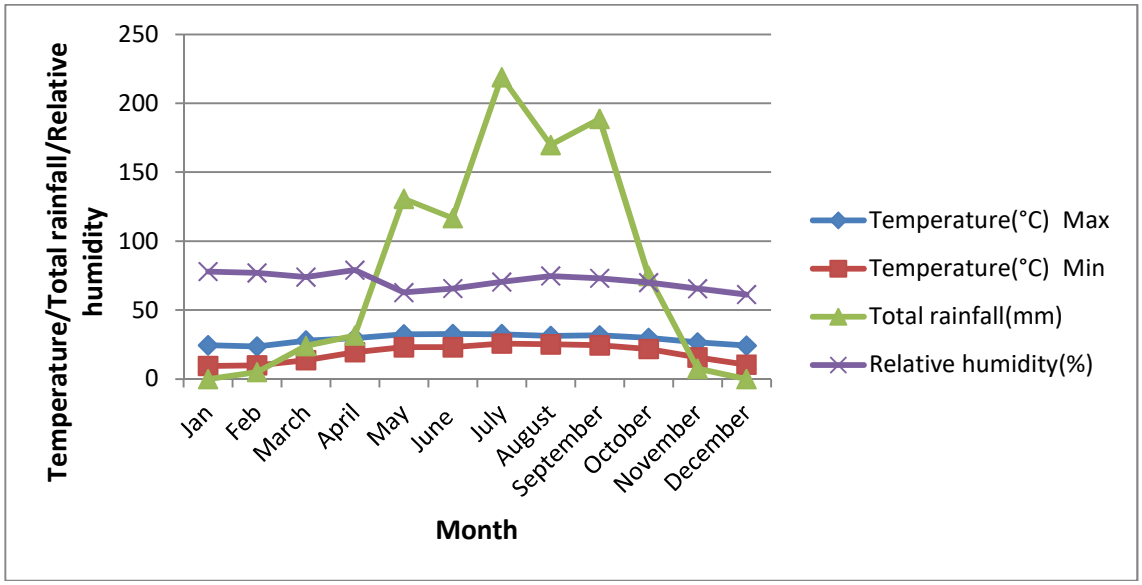


Fig: Meteorological data of Medziphema area during the period of investigation (January 2009 to December 2009).

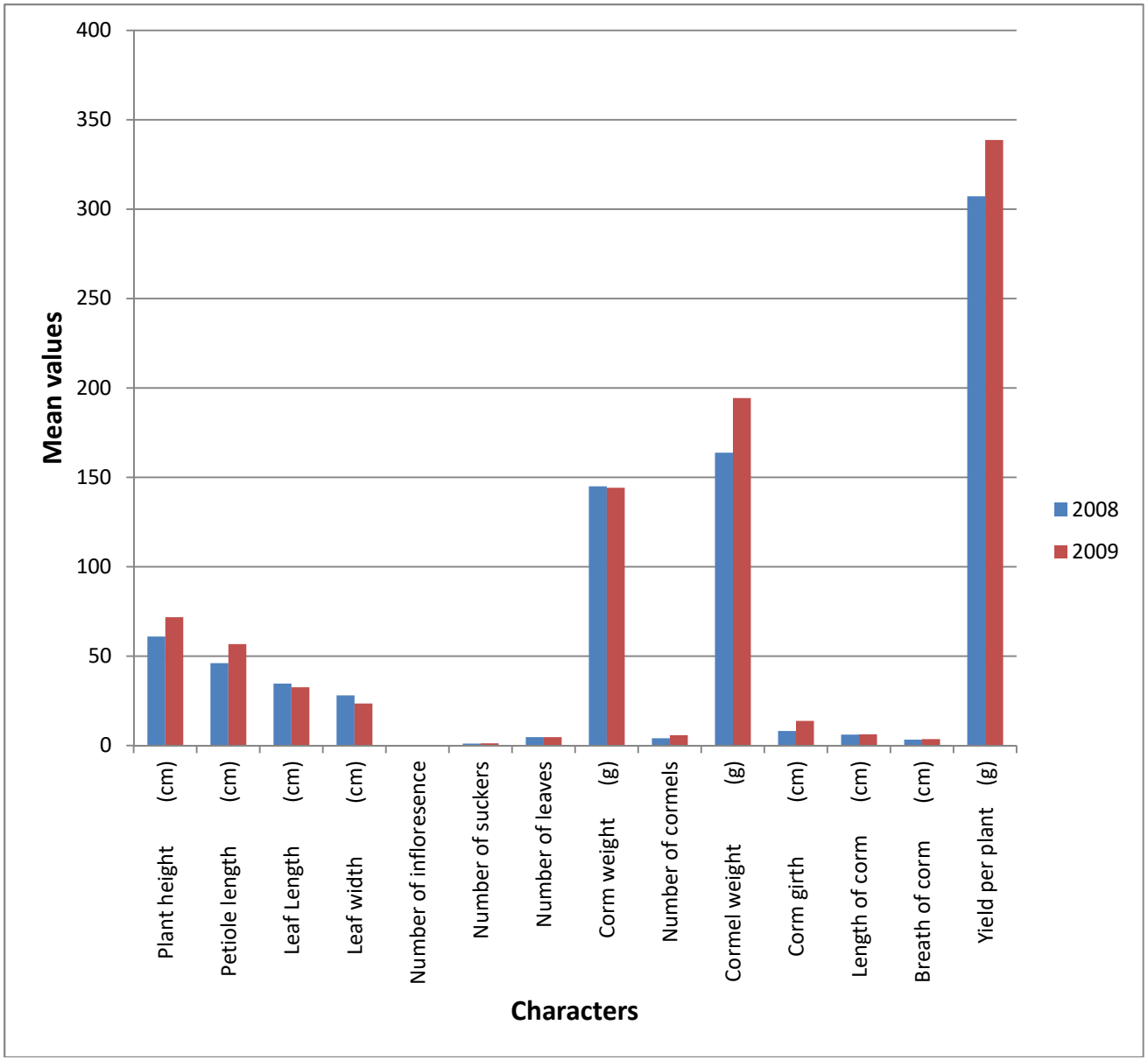

400
350
300
250
200
150
100
50
0
Mean values
2008
2009
Plant height (cm)
Petiole length (cm)
Leaf Length (cm)
Leaf width (cm)
Number of inflorescence
Number of suckers
Number of leaves
Corm weight (g)
Number of cormels
Cormel weight (g)
Corm girth (cm)
Length of corm (cm)
Breath of corm (cm)
Yield per plant (g)
Characters

Fig.1 Grand mean for 14 morphological and yield traits in *Colocasia* during 2008 and 2009.

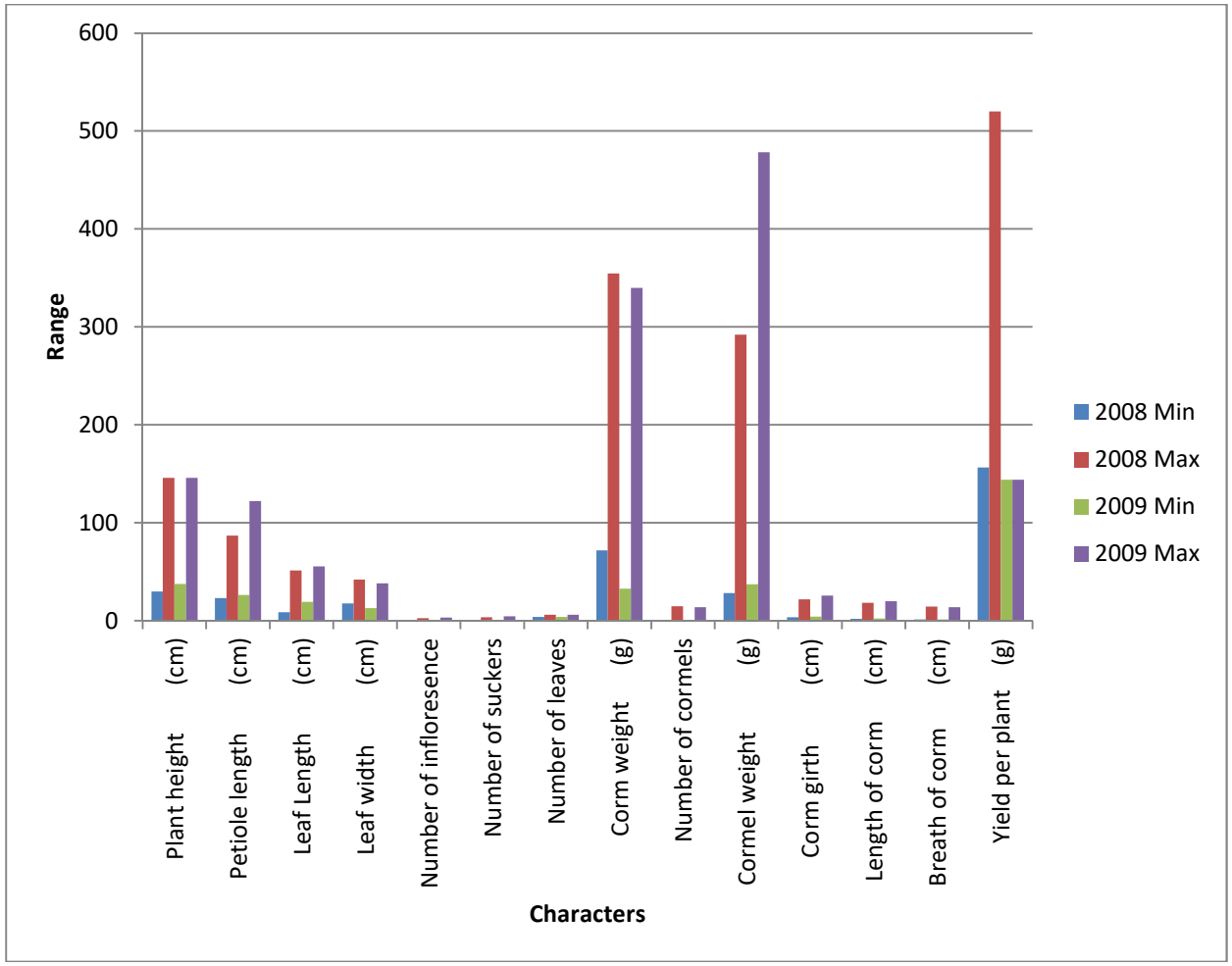


Fig.2 Range of 14 morphological and yield traits in *Colocasia* during 2008 and 2009.

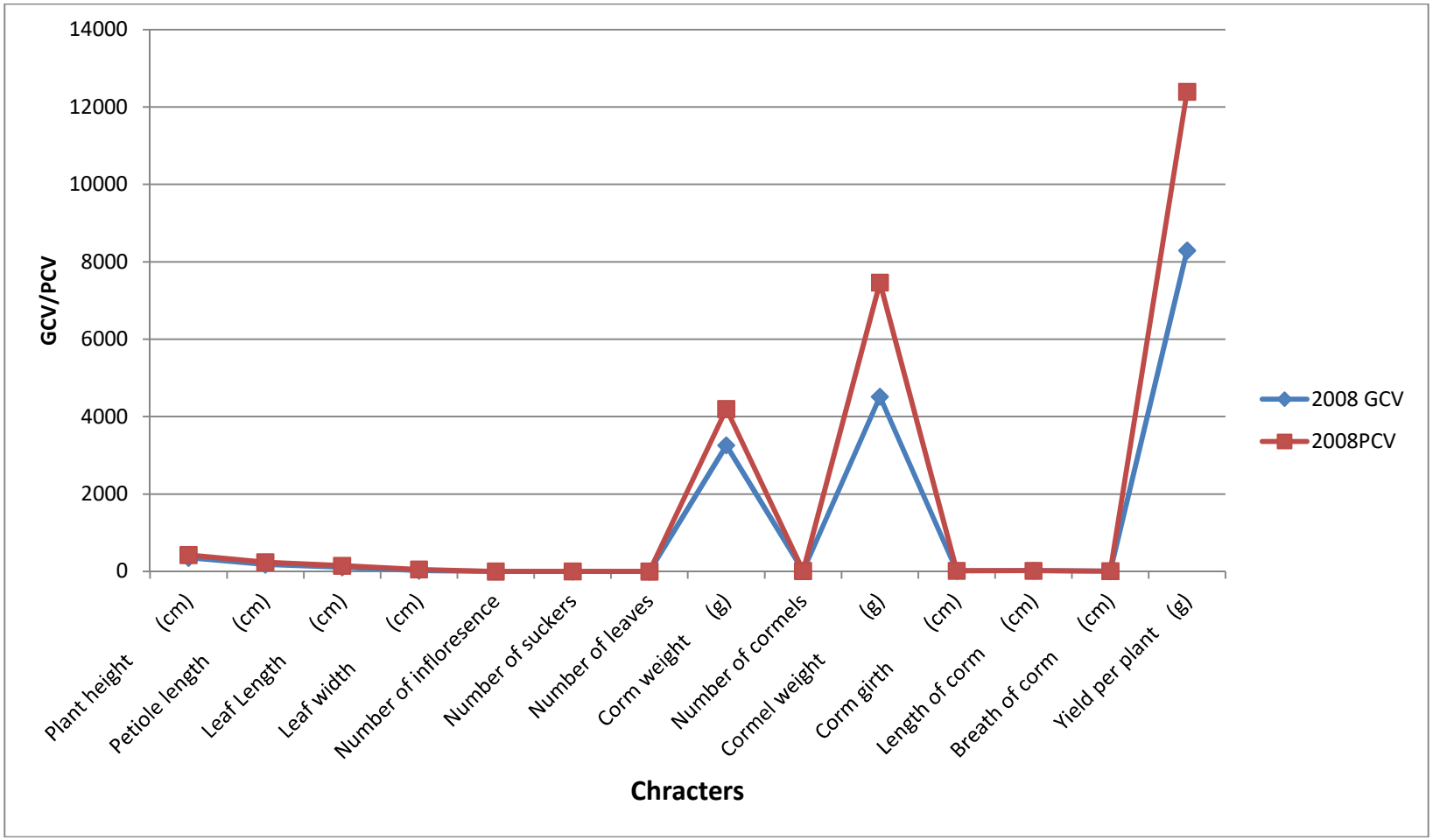


Fig.3 Diagramatic representation of PCV and GCV for 14 morphological and yield traits in *Colocasia* during 2008.

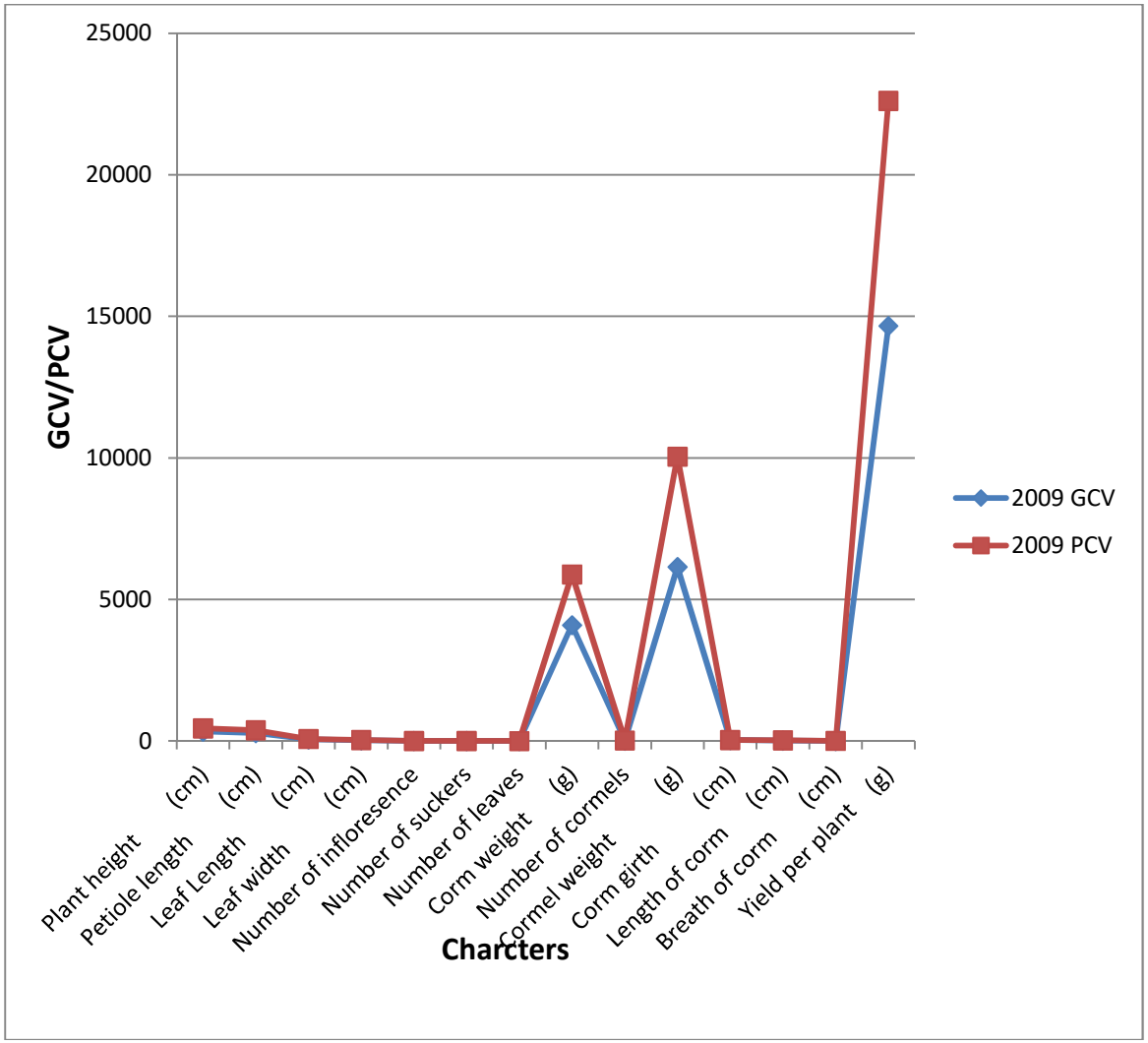


Fig.4 Diagramatic representation of PCV and GCV for 14 morphological and yield traits in *Colocasia* during 2009.

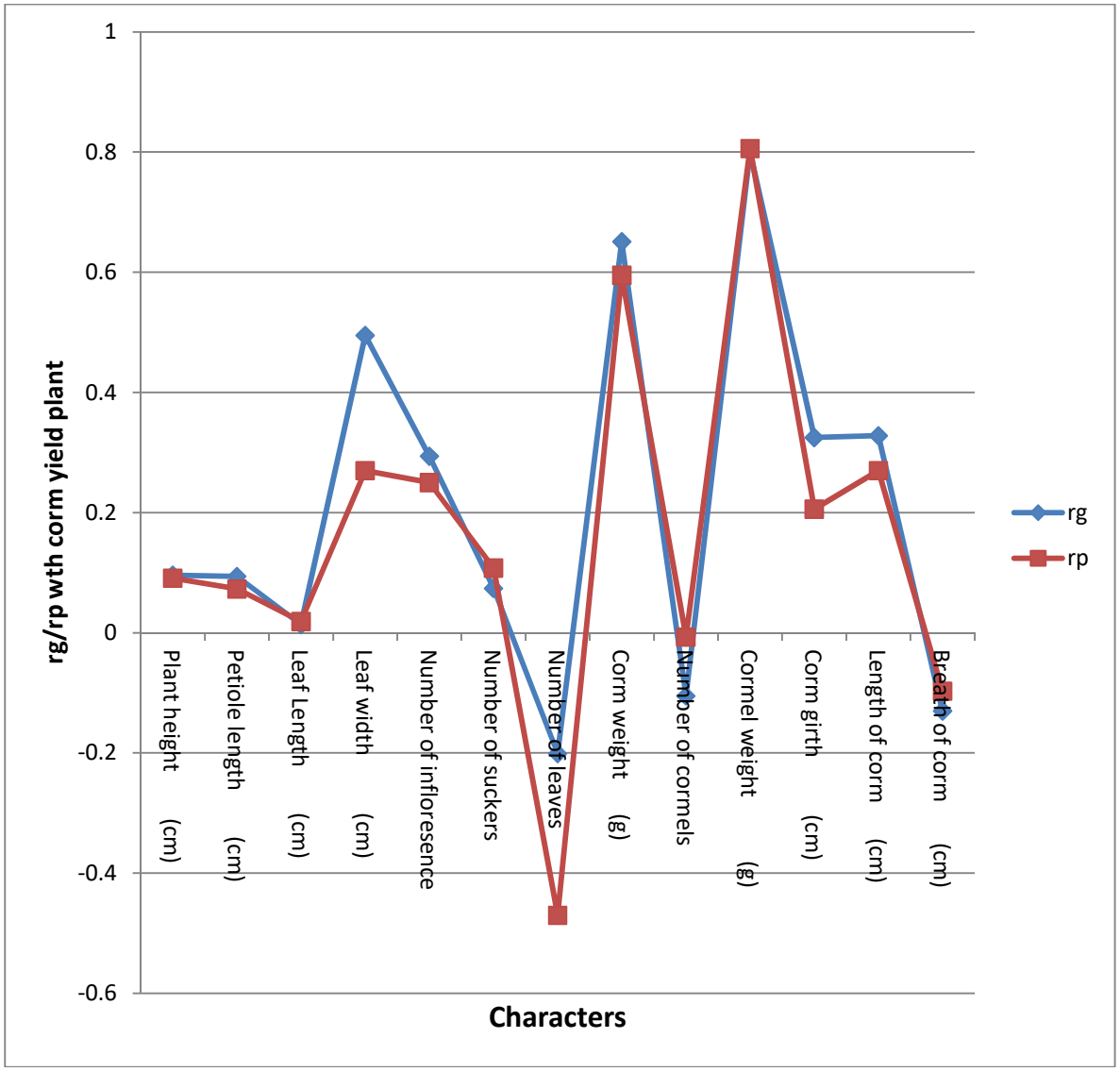

1
0.8
0.6
0.4
0.2
0
-0.2
-0.4
-0.6
rg/rp wth corm yield plant
Characters
Plant height (cm)
Petiole length (cm)
Leaf Length (cm)
Leaf width (cm)
Number of inflorescence
Number of suckers
Number of leaves
Corm weight (g)
Number of cormels
Cormel weight (g)
Corm girth (cm)
Length of corm (cm)
Breath of corm (cm)
rg
rp

Fig. Diagrammatic representation of genotypic (rg) and phenotypic (rp) correlation coefficients between corm yield/plant with different characters during 2008.

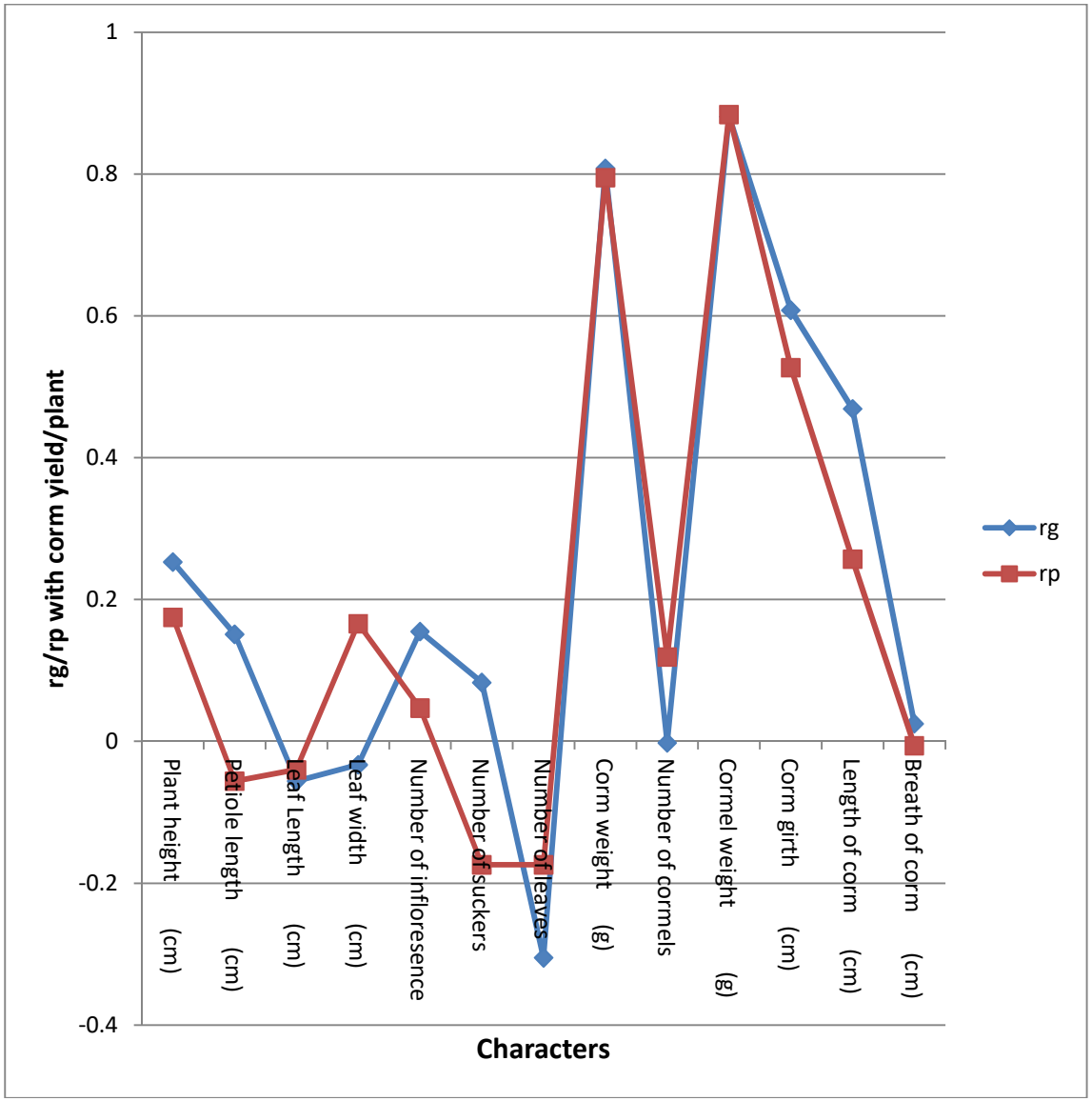

1
0.8
0.6
0.4
0.2
0
-0.2
-0.4
rg/rp with corm yield/plant
Plant height (cm)
Petiole length (cm)
Leaf Length (cm)
Leaf width (cm)
Number of inflorescence
Number of suckers
Number of leaves
Corm weight (g)
Number of cormels
Cormel weight (g)
Corm girth (cm)
Length of corm (cm)
Breath of corm (cm)
Characters
rg
rp

Fig. Diagrammatic representation of genotypic (rg) and phenotypic (rp) correlation coefficients between corm yield/plant with different characters during 2009.

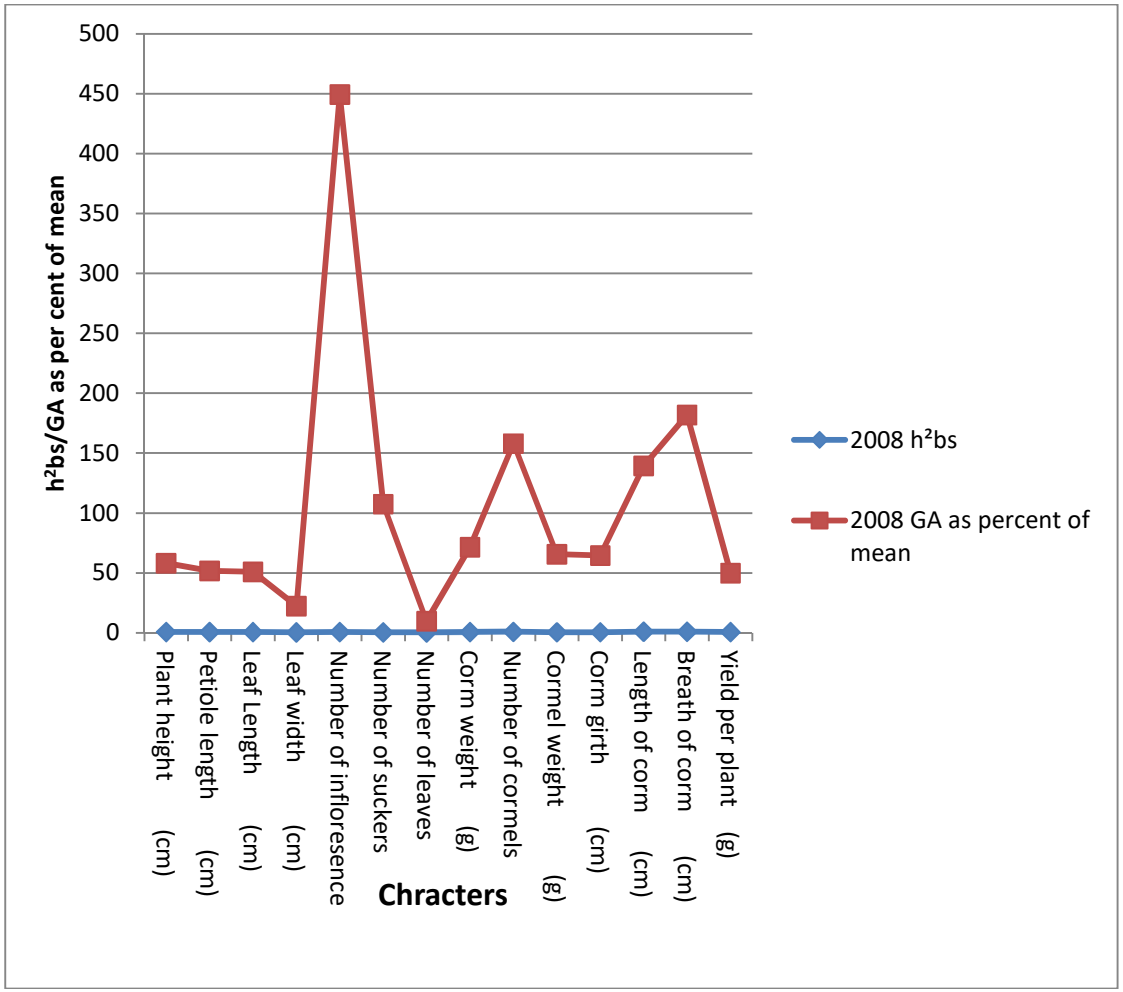


Fig. Diagrammatic representation of heritability and genetic advance as percent of mean for 14 morphological and yield traits in colocasia during 2008.

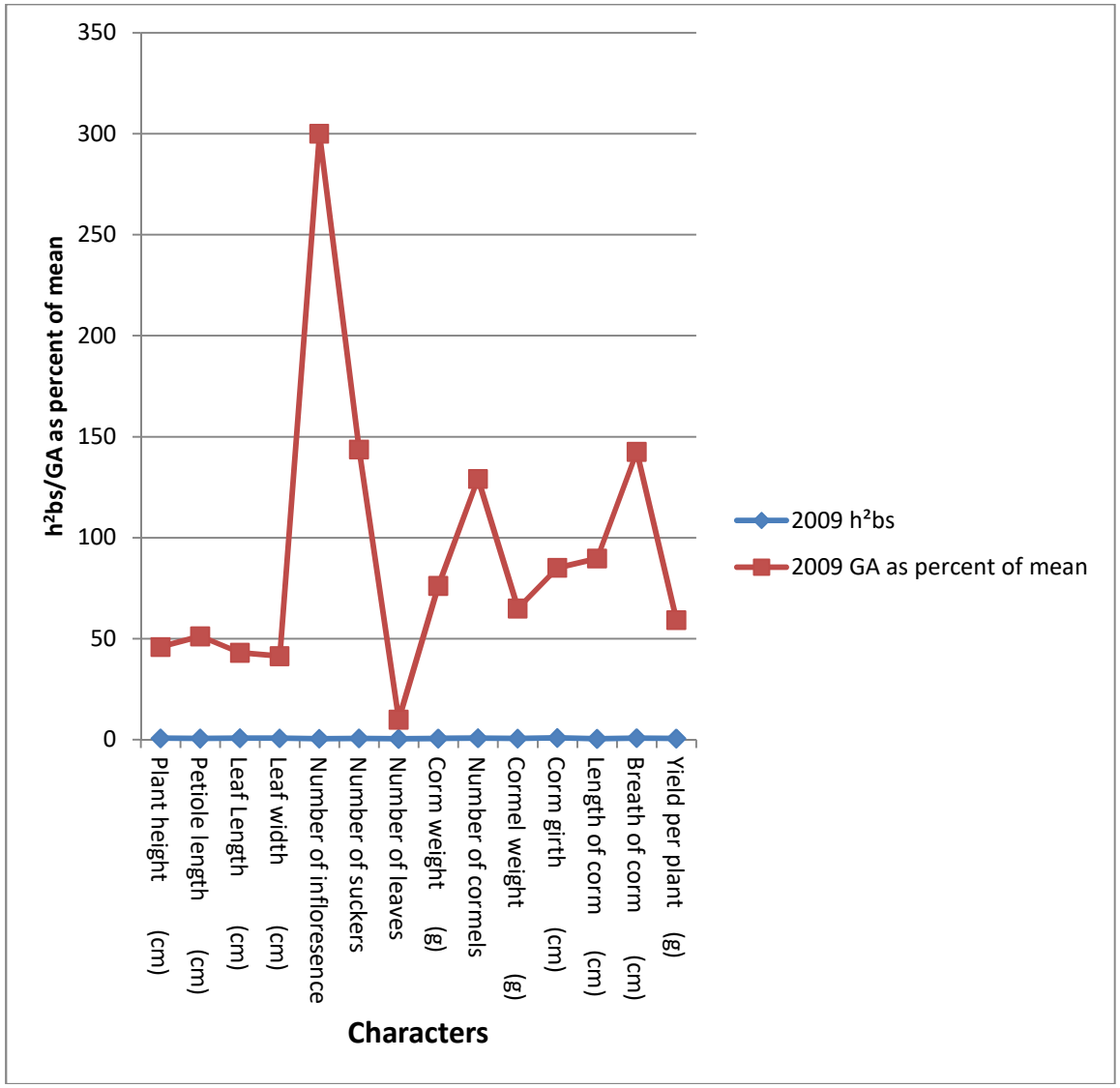

350
300
250
200
150
100
50
0
h²bs/GA as percent of mean
Plant height (cm)
Petiole length (cm)
Leaf Length (cm)
Leaf width (cm)
Number of inflorescence
Number of suckers
Number of leaves
Corm weight (g)
Number of cormels
Cormel weight (g)
Corm girth (cm)
Length of corm (cm)
Breath of corm (cm)
Yield per plant (g)
Characters
2009 h²bs
2009 GA as percent of mean

Fig. Diagrammatic representation of heritability and genetic advance as percent of mean for 14 morphological and yield traits in colocasia during 2008.

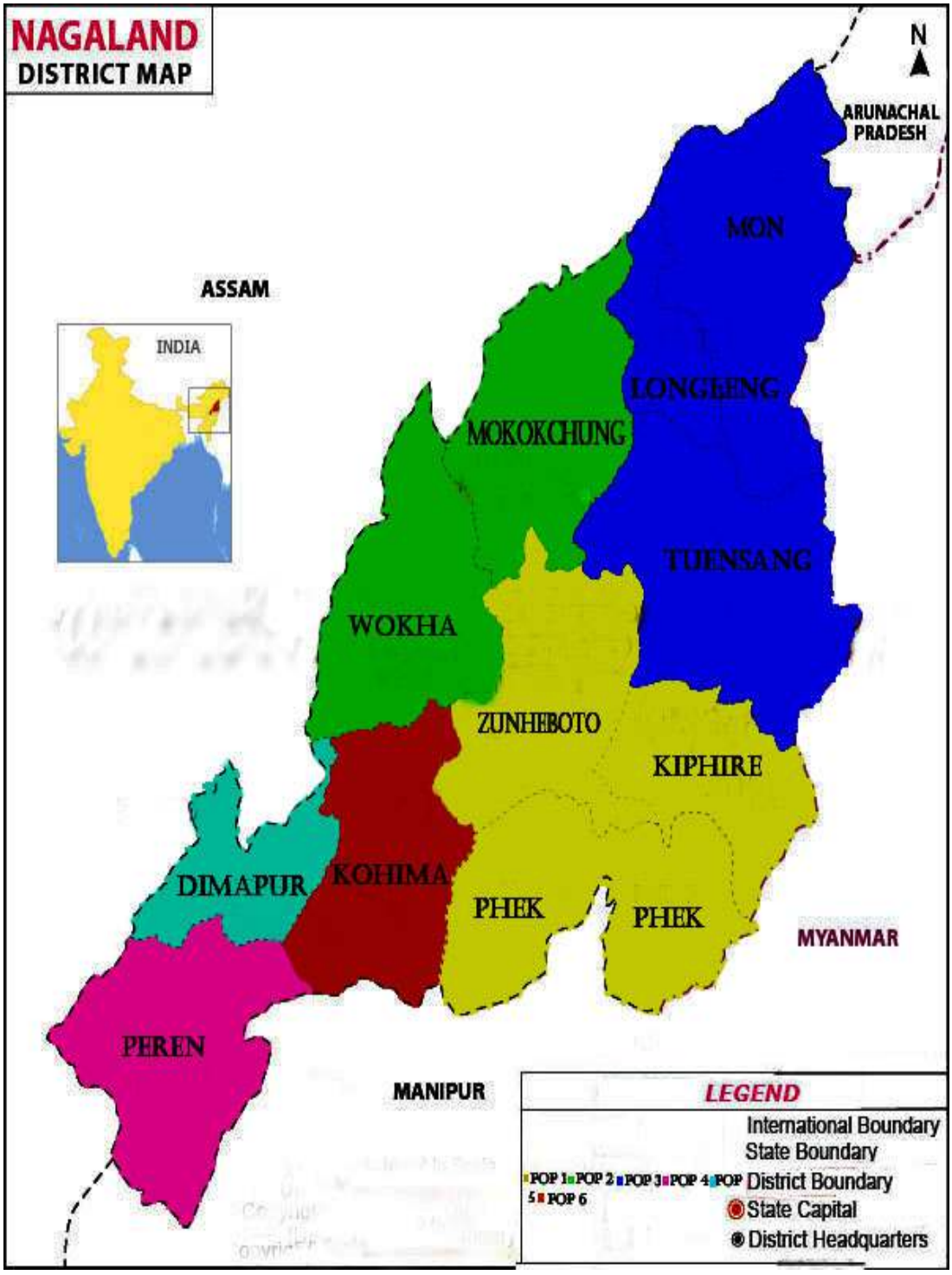


Fig. 10 Map of Nagaland showing the genotypes grouped into six hypothetical population based on their location of collection.

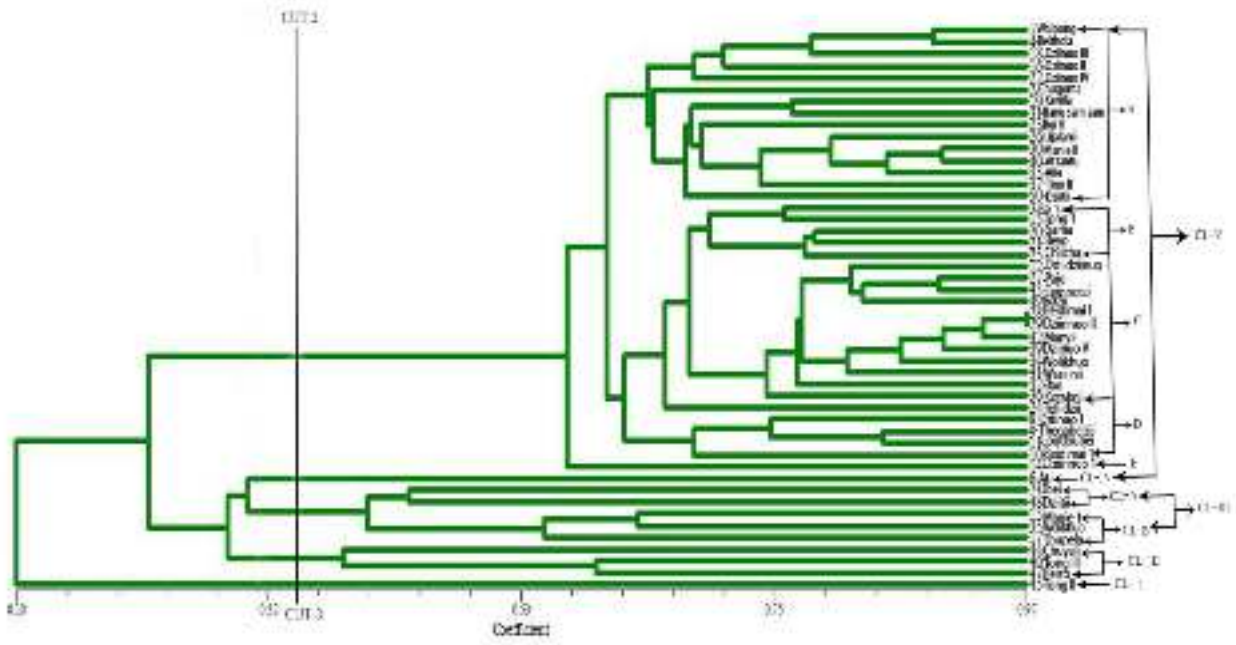


Fig. 9 Dendrogram of colocasia varieties obtained by UPGMA cluster analysis based on microsatellite data.

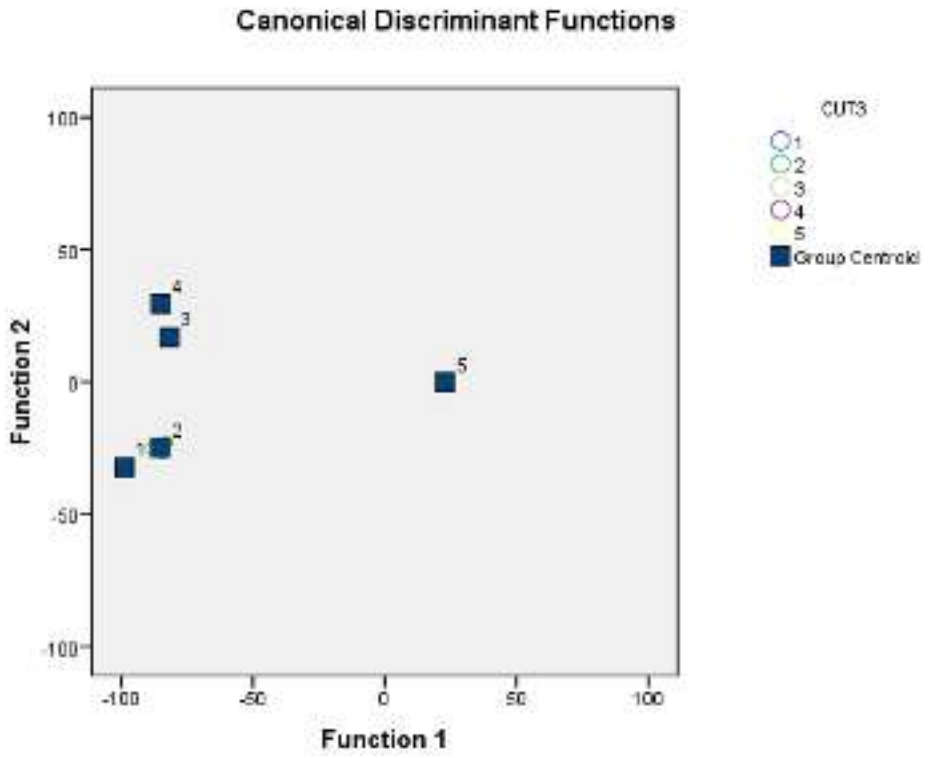


Fig 11. The discriminate analysis showed a clear distinction of the accessions of different clusters with the group (cluster) centroids placed distinctly apart from one another.

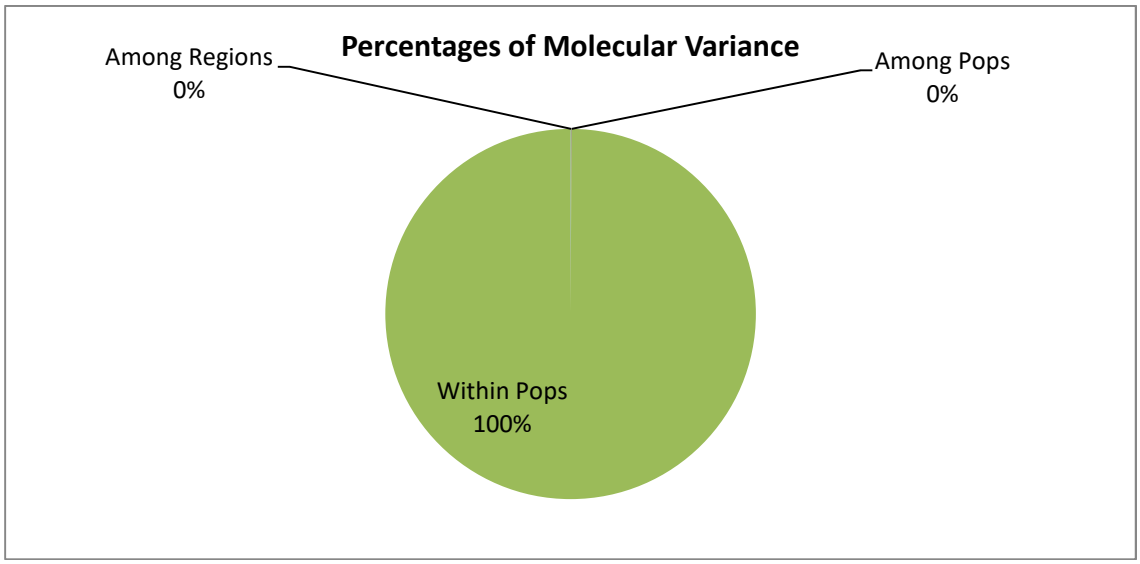


Fig 12. Showing the percentage of analysis of molecular variance.

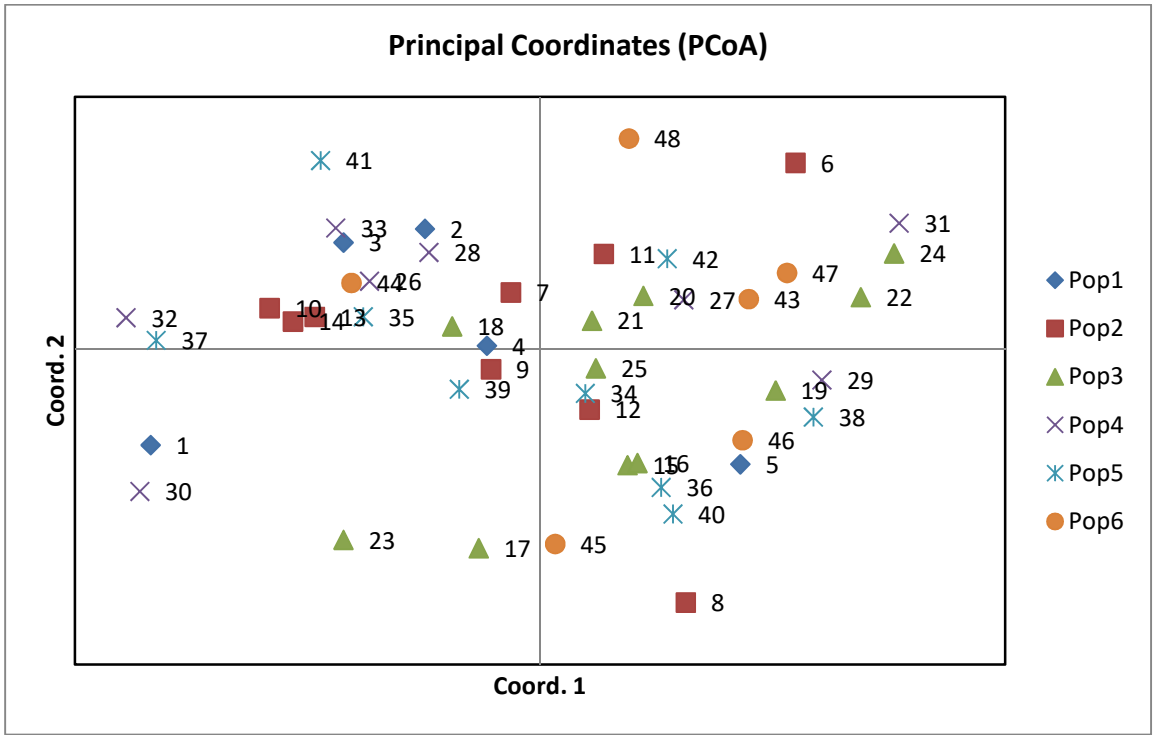


Fig 13. Distribution of population on the scatter plot.

PLATE 1(a): Variation in corm morphology of the collected landraces (Scale in mm)

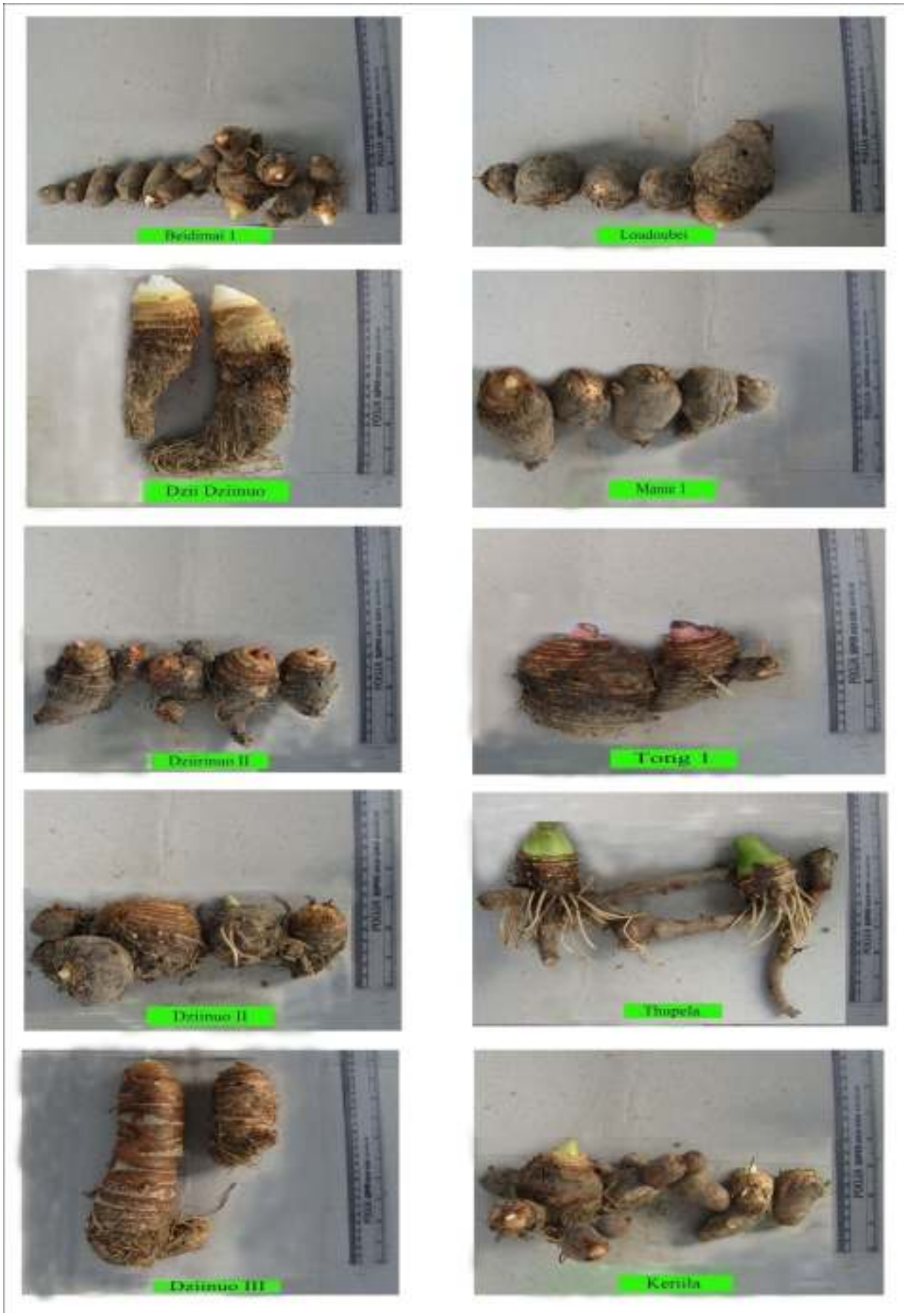


PLATE 1(b): Variation in corm morphology of the collected landraces (Scale in mm)

PLATE 1(c): Variation in the corm morphology of the collected landraces. (Scale in mm)

PLATE 1(d): Variation in the corm morphology of the collected landraces (Scale in mm)

PLATE 1(e): Variation in the corm morphology of the collected landraces (Scale in mm)

PLATE 3: Variation in the corm morphology of edible aroids

(Scale in mm)

Xanthosoma sagittifolium *Xanthosoma violaceium*

Alocasia maccharizo *Alocasia odora*

Amorphophallu paeoniifolius

PLATE 4: Showing edible aroids found in Nagaland.

(a) (b)

Fig. *Colocasia esculenta* (a) White colour corm flesh, (b) Pink colour corm flesh

Fig. Colocasia antiquorum, White colour corm flesh

PLATE 5(a). Showing variation in corm flesh colour



PLATE 5(b): Plants showing different morphological characters.

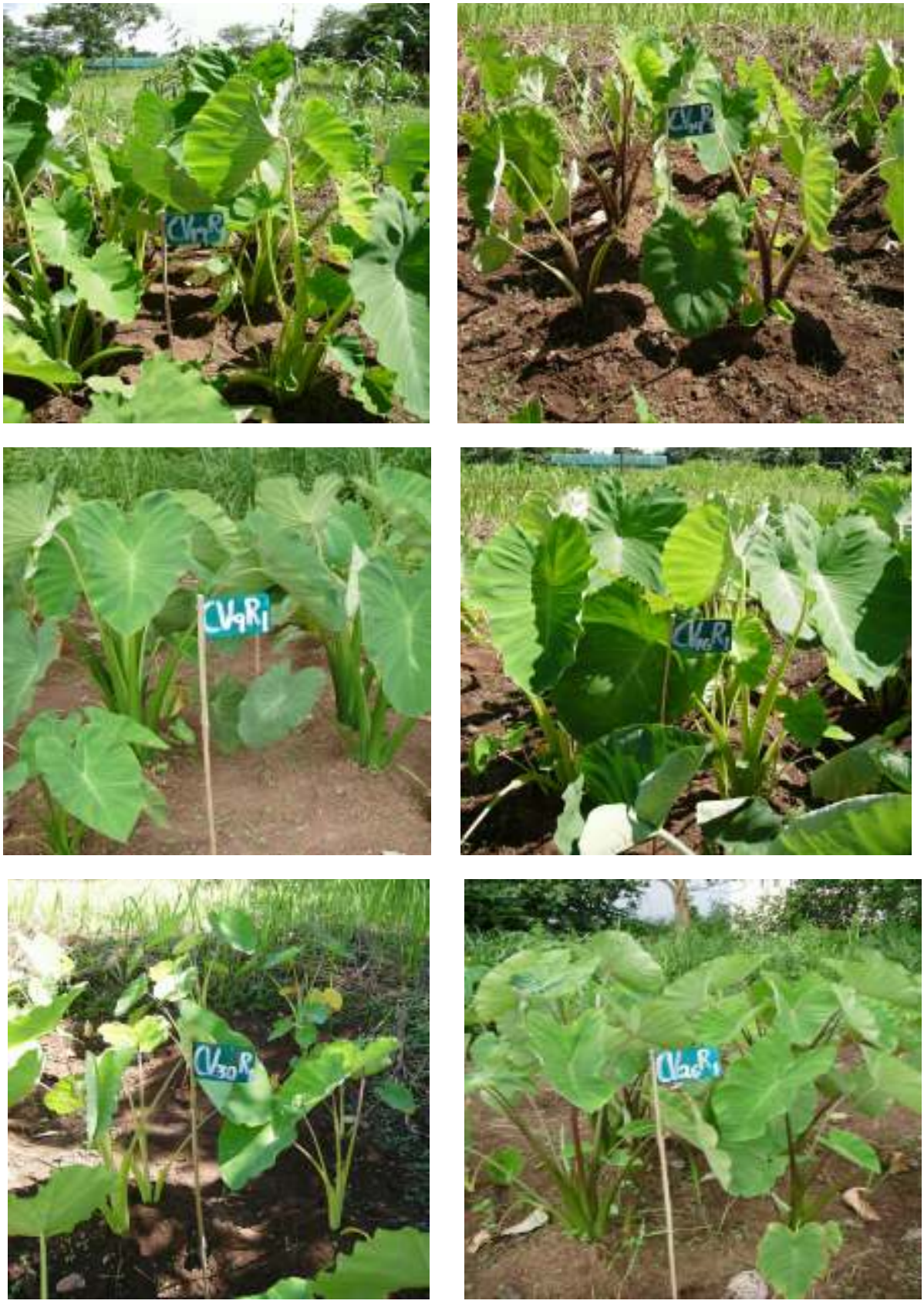


PLATE 5(c): Plants showing different morphological characters

PLATE 2: Overview of the experimental field

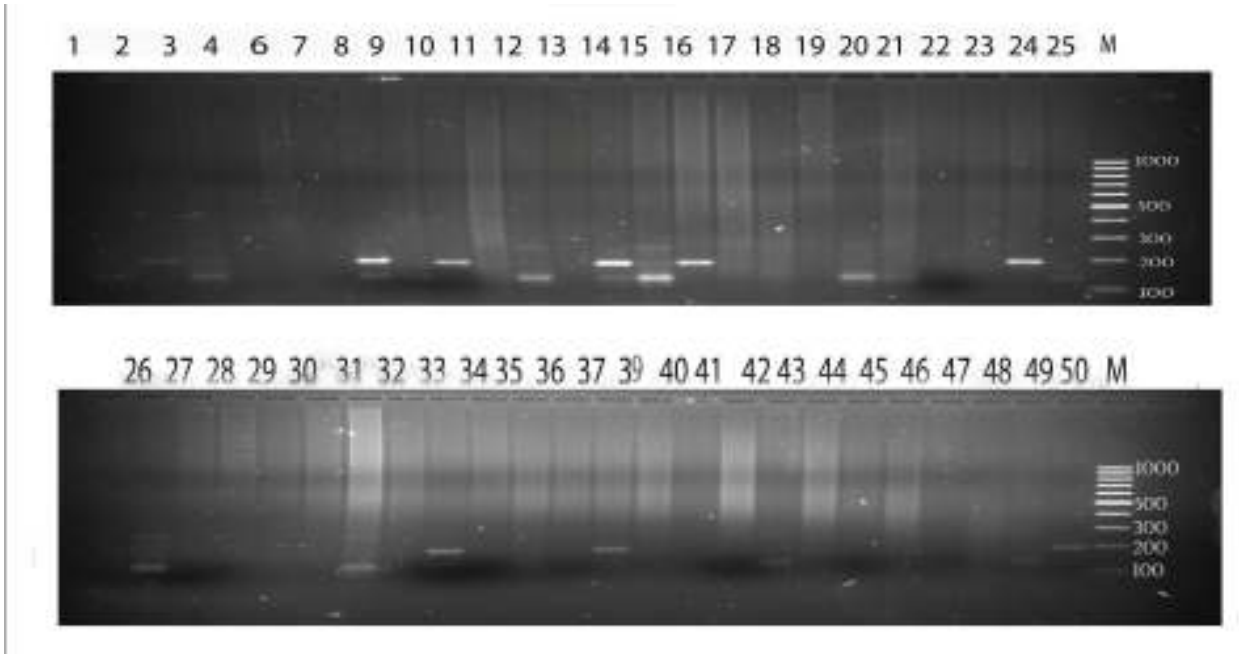
(i) Plants showing runners

(ii)Flower bud

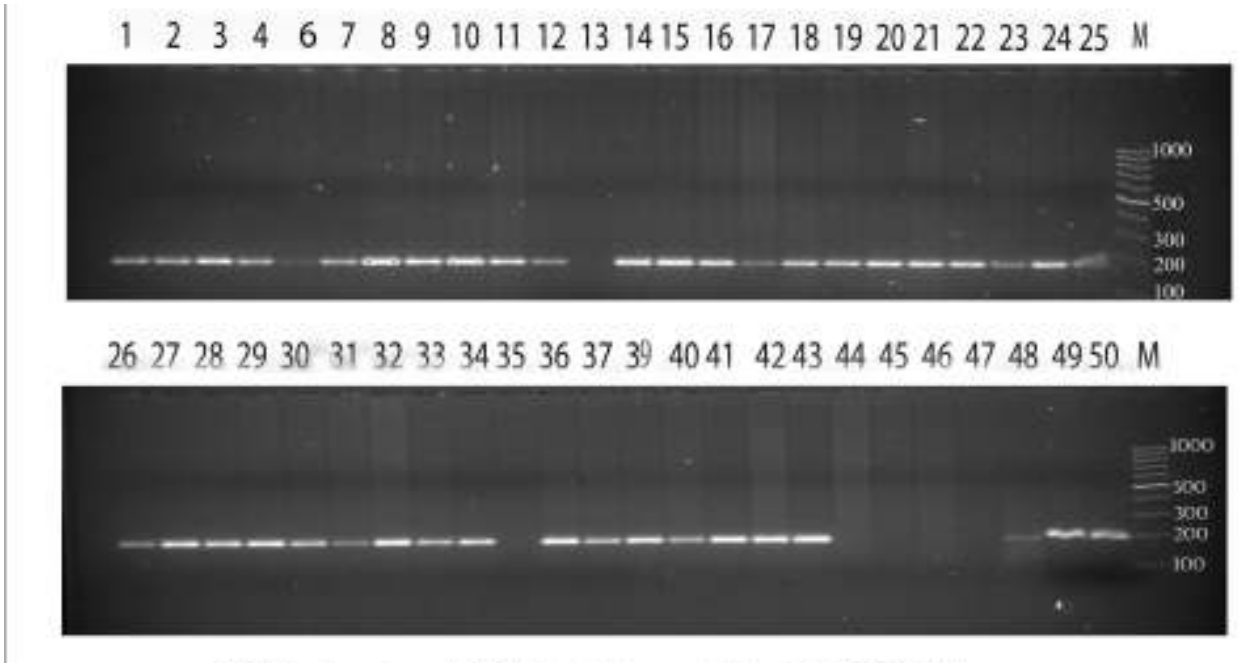
(iii)Flower

PLATE 5(d): Showing runners and flower morphology

PLATE 6

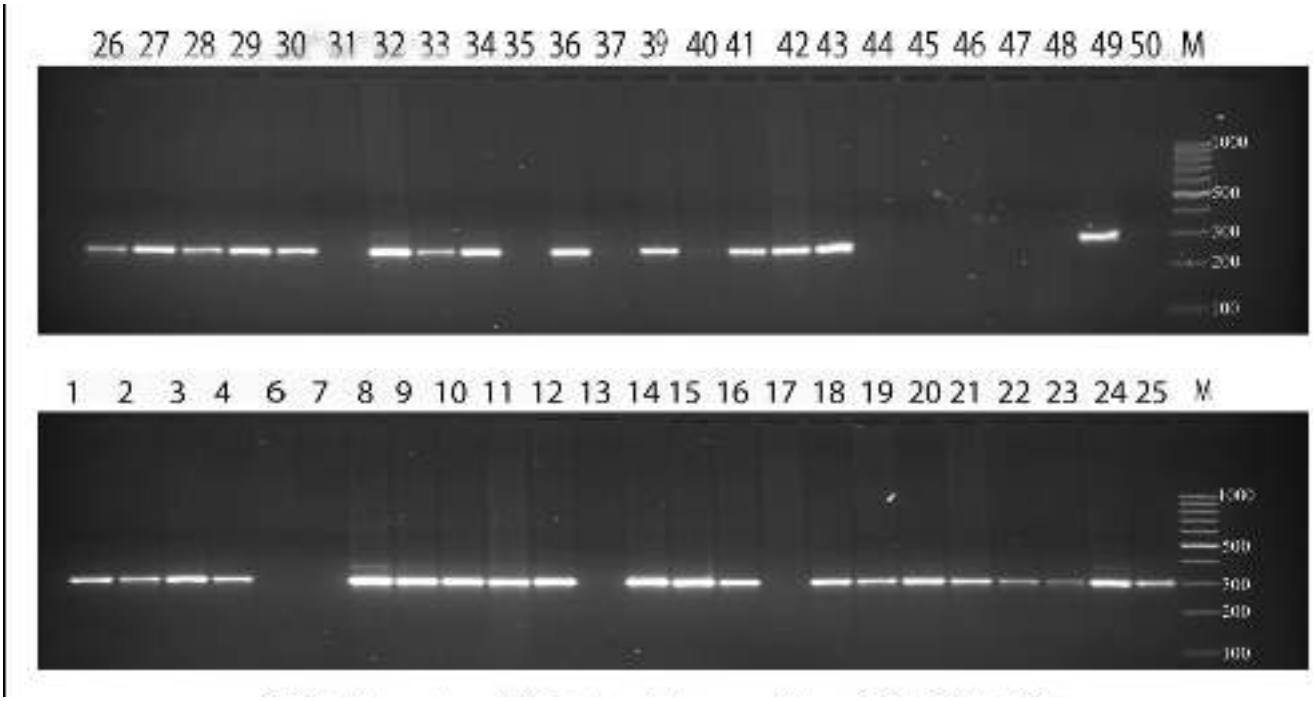


(a) SSR banding pattern of 48 colocasia landraces using primer COLGCC56-191, M- Molecular weight marker

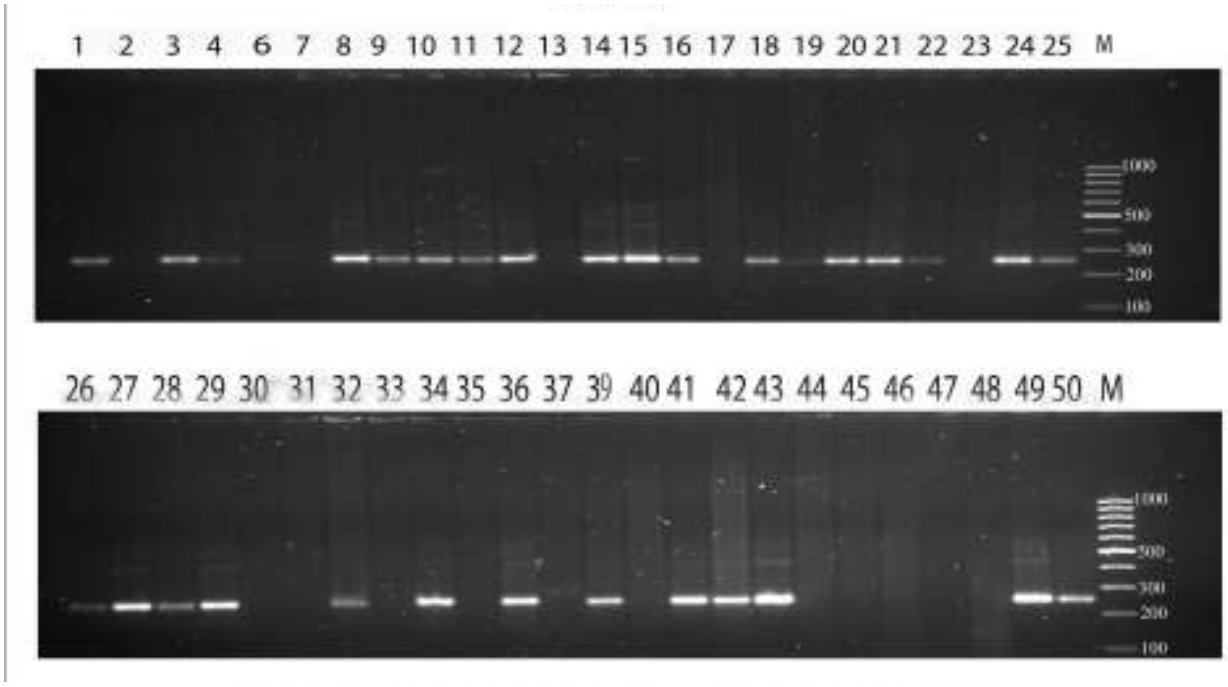


(b) SSR banding pattern of 48 colocasia landraces using primer COLGCC82-117, M- Molecular weight marker

PLATE 7

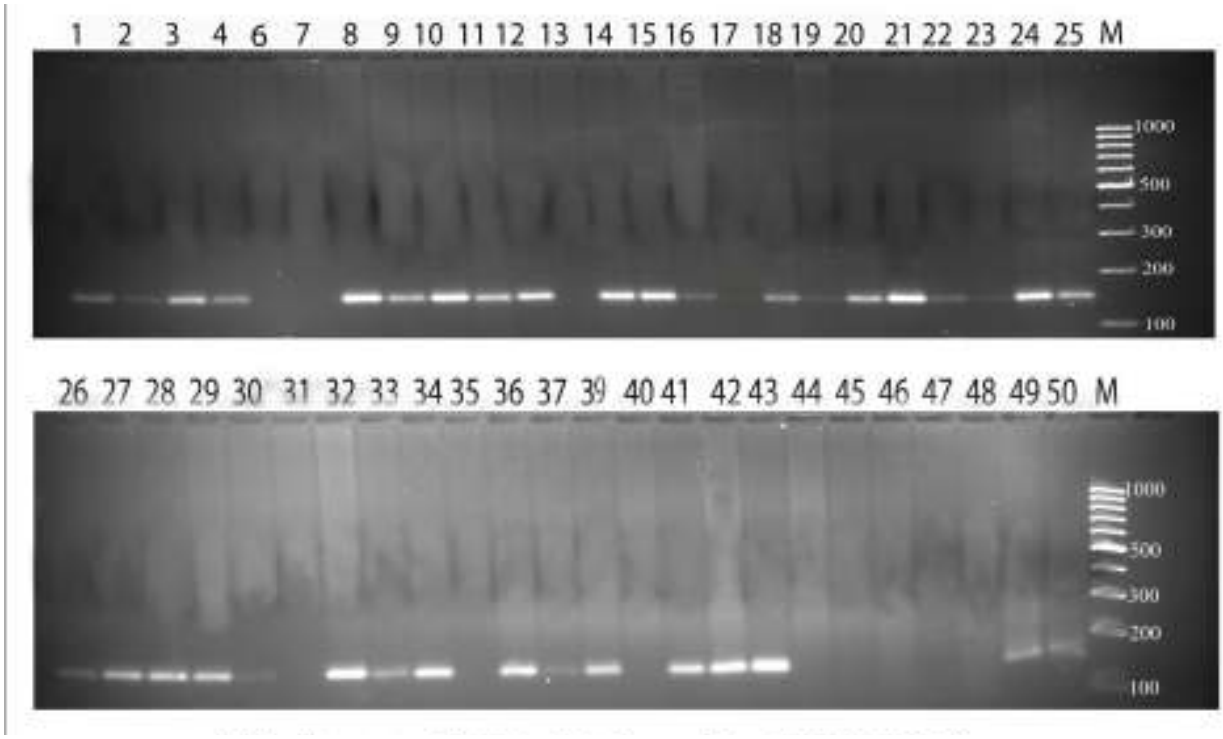


(a) SSR banding pattern of 48 colocasia landraces using primer COLGCC111-300, M-Molecular weight marker

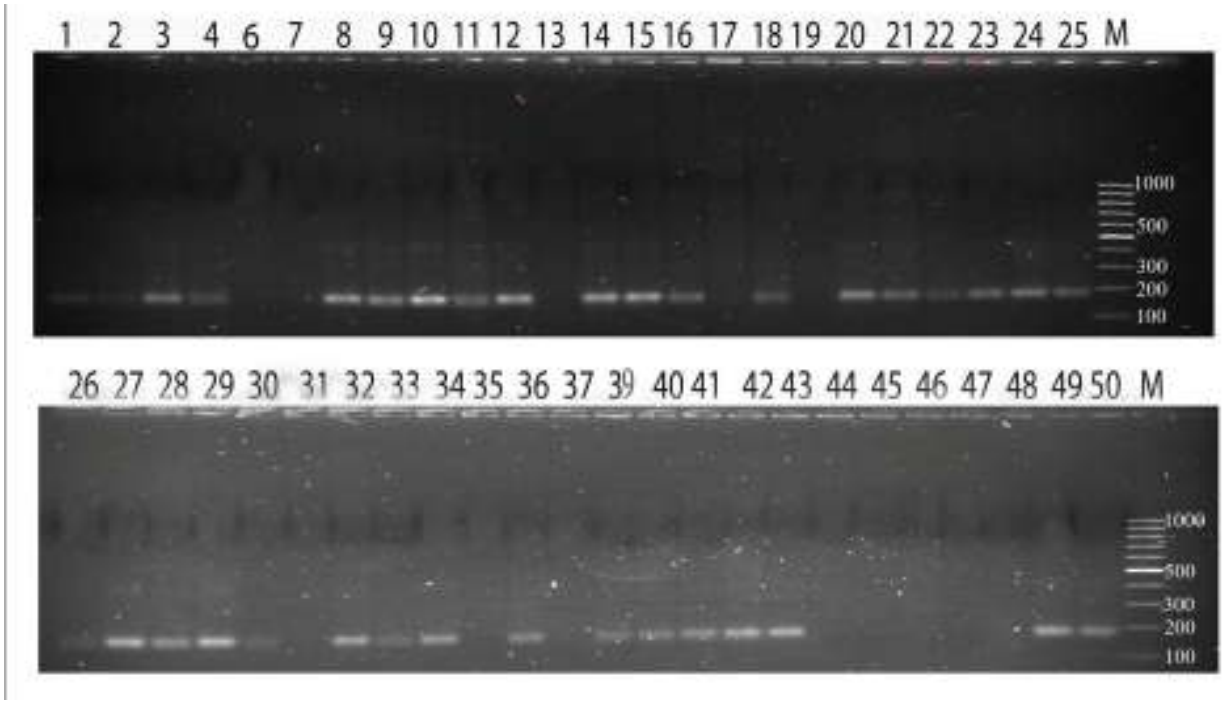


(b) SSR banding pattern of 48 colocasia landraces using primer COLGCC192-245, M-Molecular weight marker.

PLATE - 8

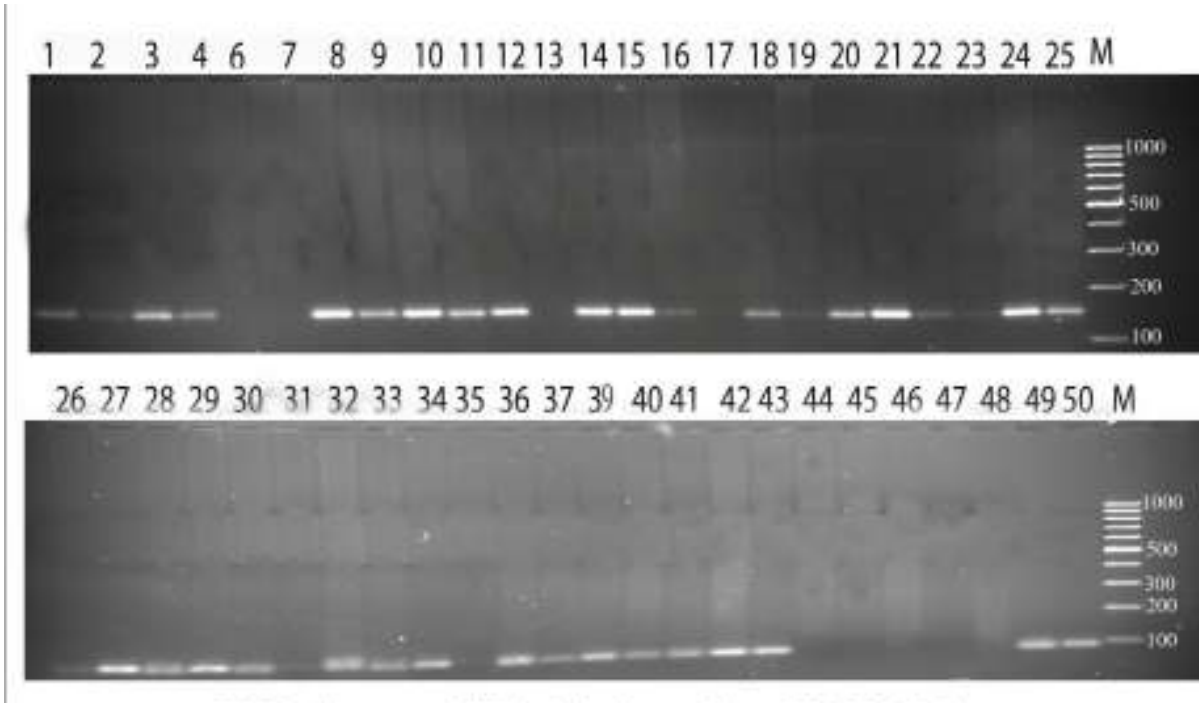


(a) SSR banding pattern of 48 colocasia landraces using primer COLGCC132-147, M- Molecular weight marker.

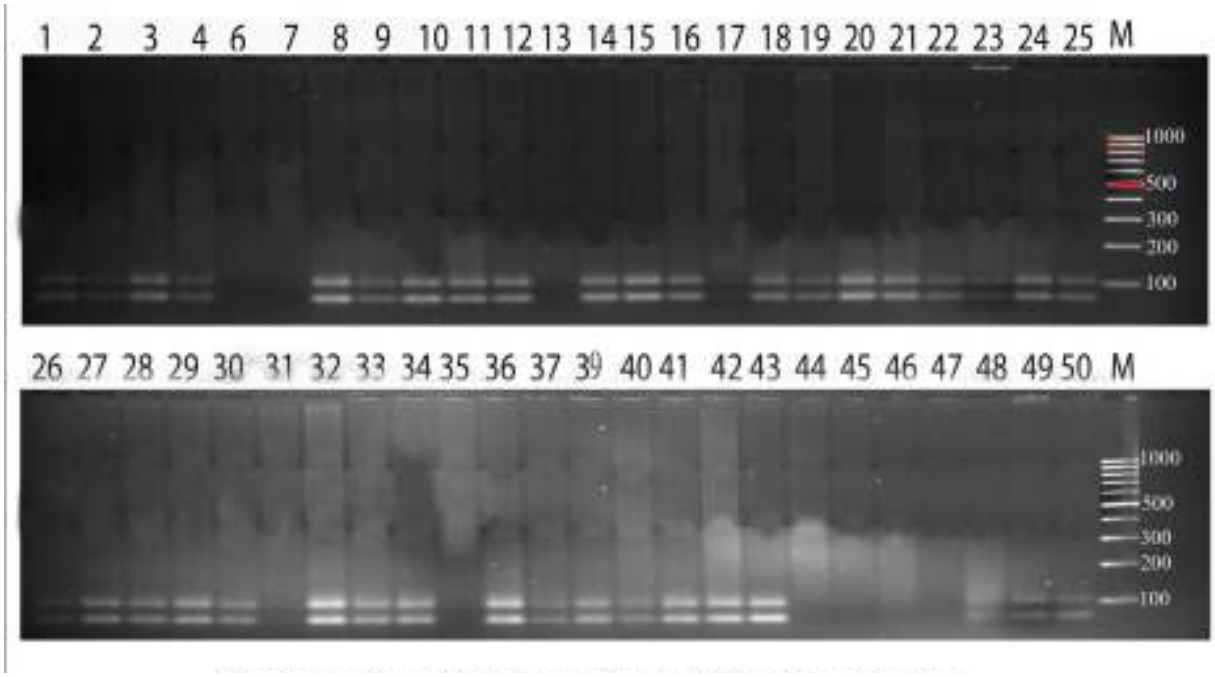


(b) SSR banding pattern of 48 colocasia landraces using COLGCC233-167, M- Molecular weight marker.

PLATE – 9

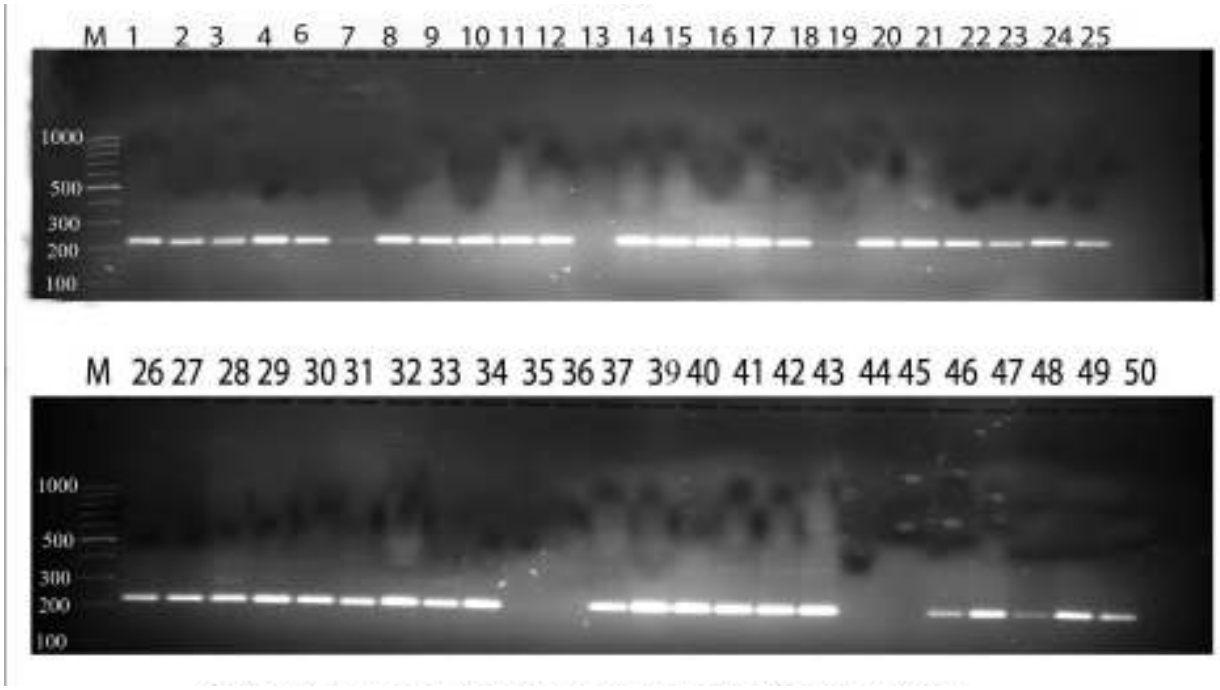


(a) SSR banding pattern of 48 colocasia landraces using Primer COLGCC88B-94, M-Molecular weight marker.

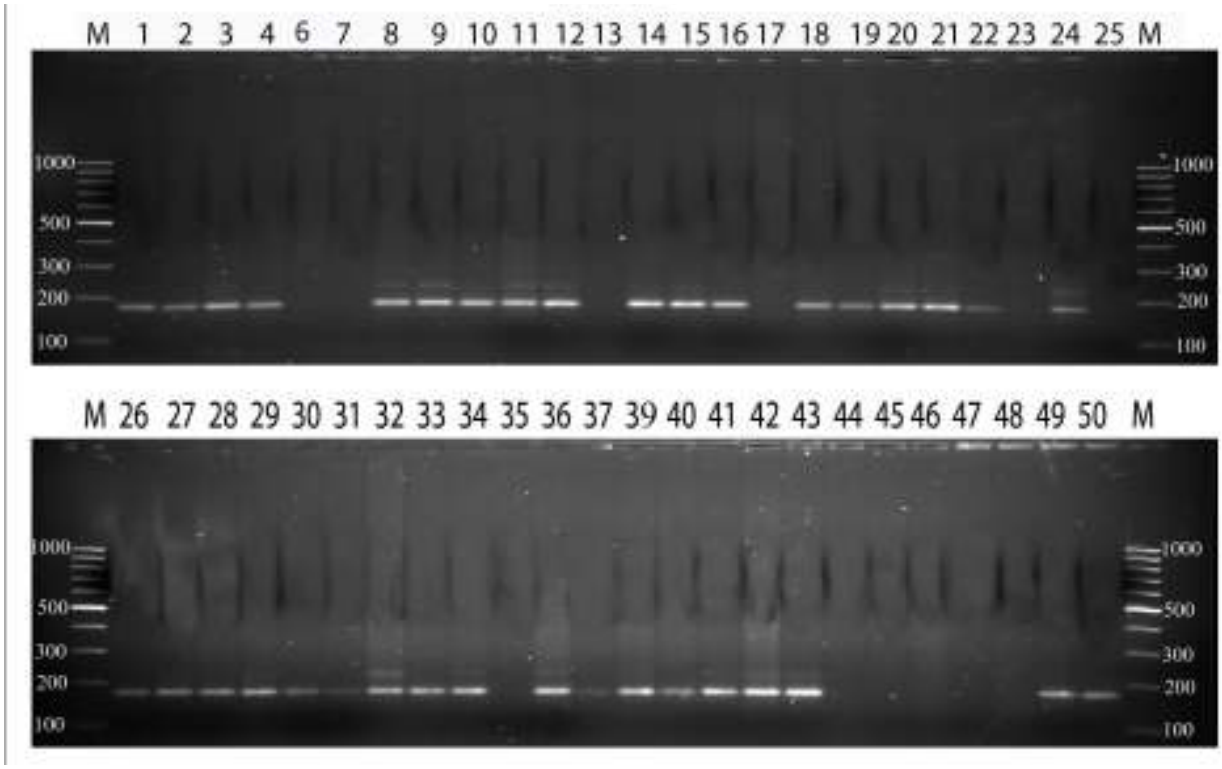


(b) SSR banding pattern of 48 colocasia landraces using Primer COLGCC75-100, M-Molecular weight marker.

PLATE – 10

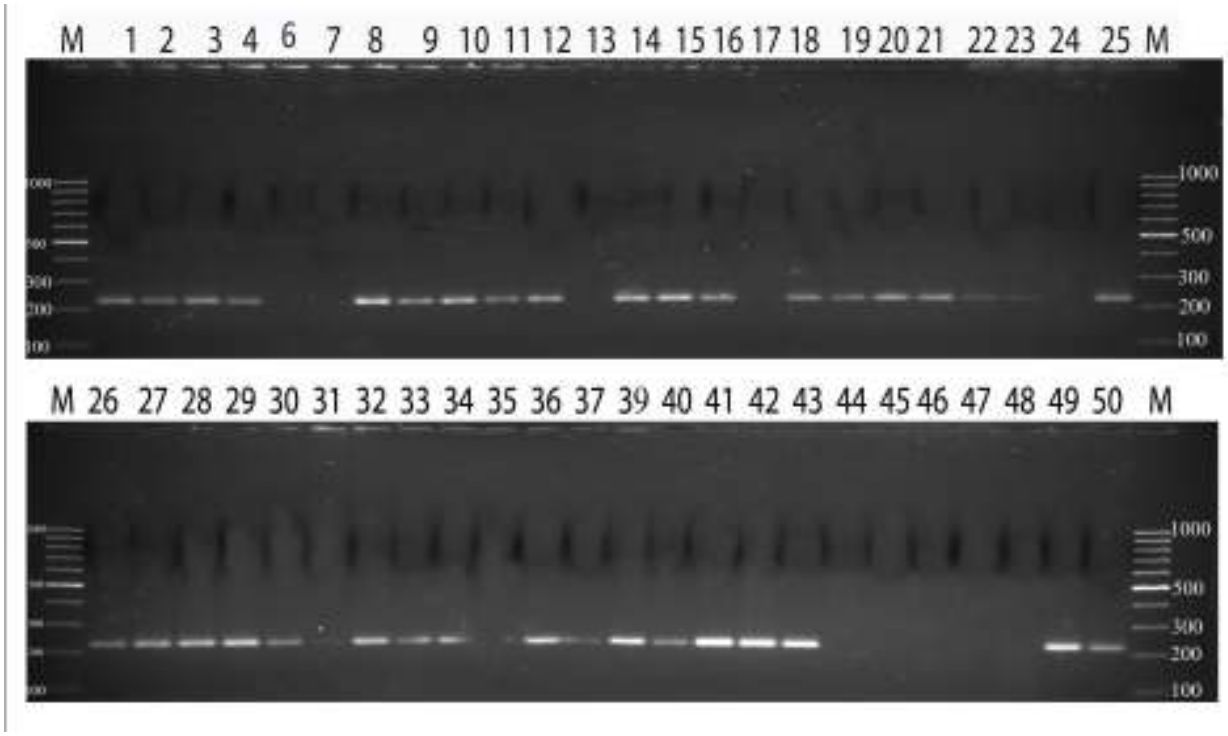


(a) SSR banding pattern of 48 colocasia landraces using Primer COLGCC118-221, M-Molecular weight marker.

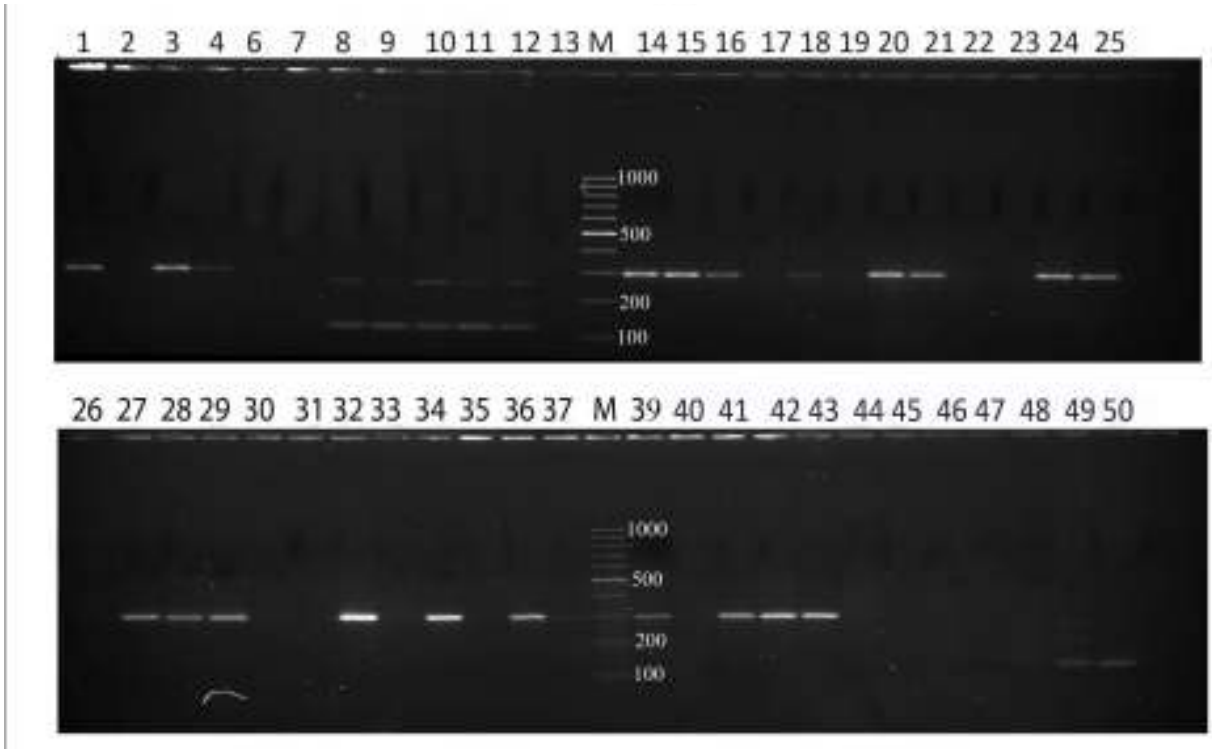


(b) SSR banding pattern of 48 colocasia landraces using Primer COLGCC77-174, M-Molecular weight marker.

PLATE – 11

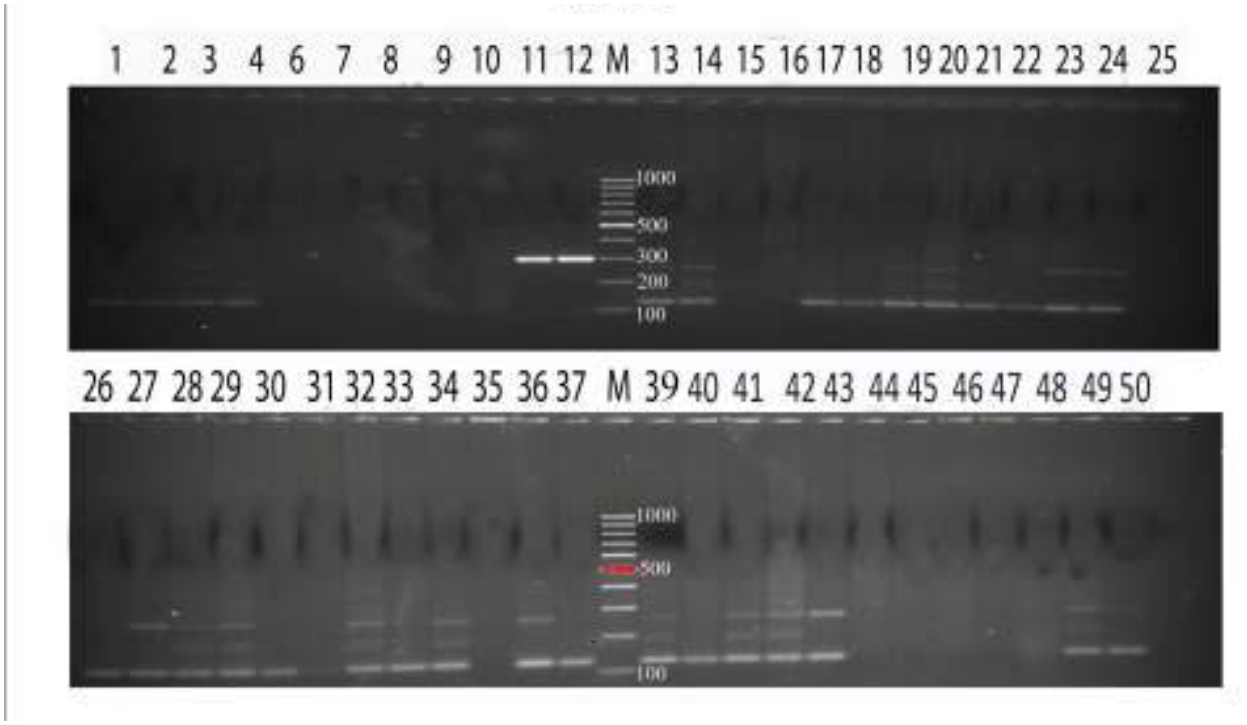


(a) SSR banding pattern of 48 colocasia landraces using primer COLGCC95-219, M- Molecular weight marker.

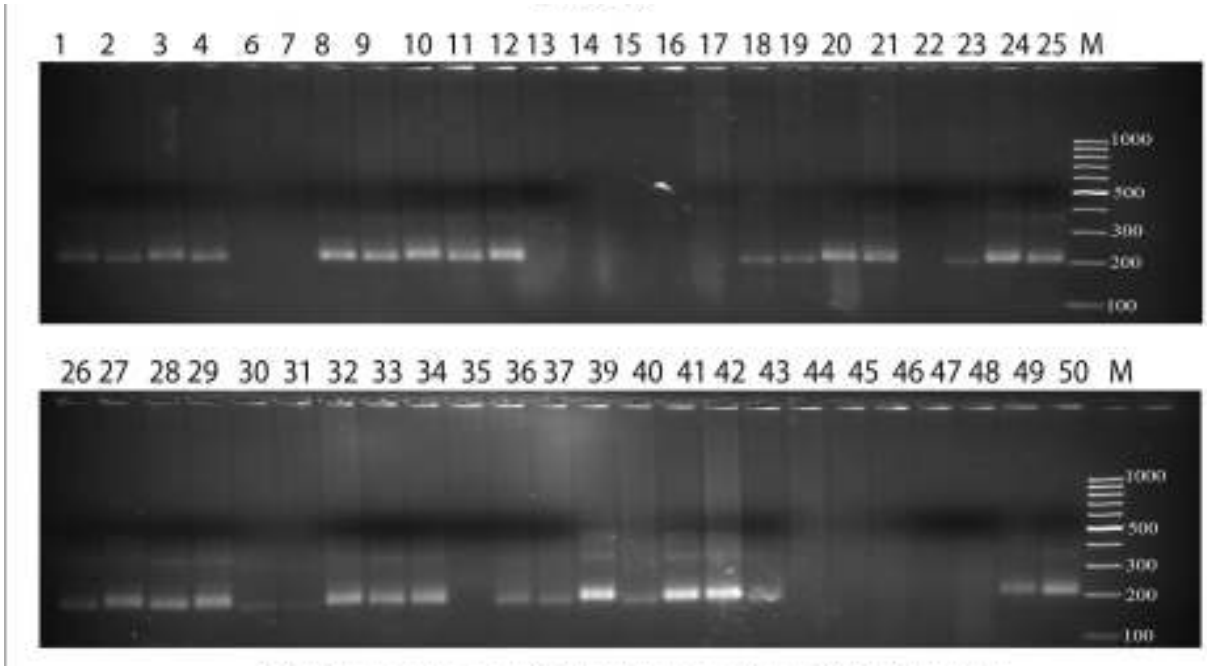


(b) SSR banding pattern of 48 colocasia landraces using Primer COLGCC98-294, M- Molecular weight marker.

PLATE – 12

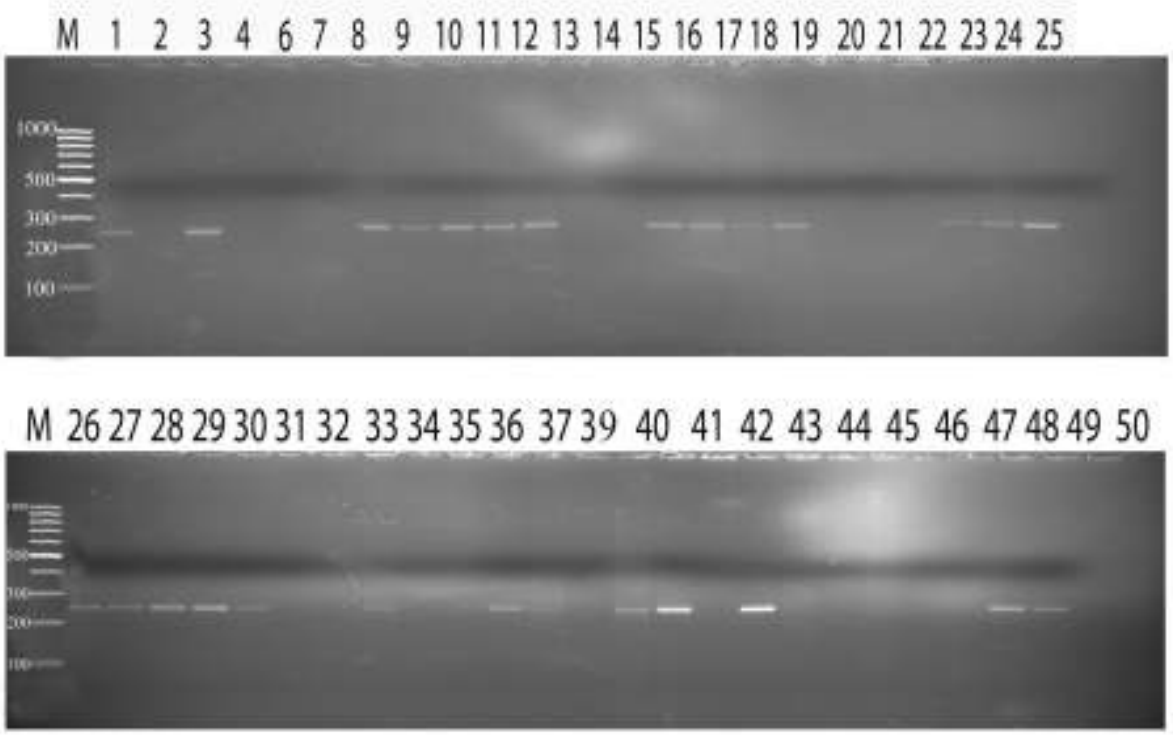


(a) SSR banding pattern of 48 colocasia landraces using Primer COLGCC206-122, M-Molecular weight marker.

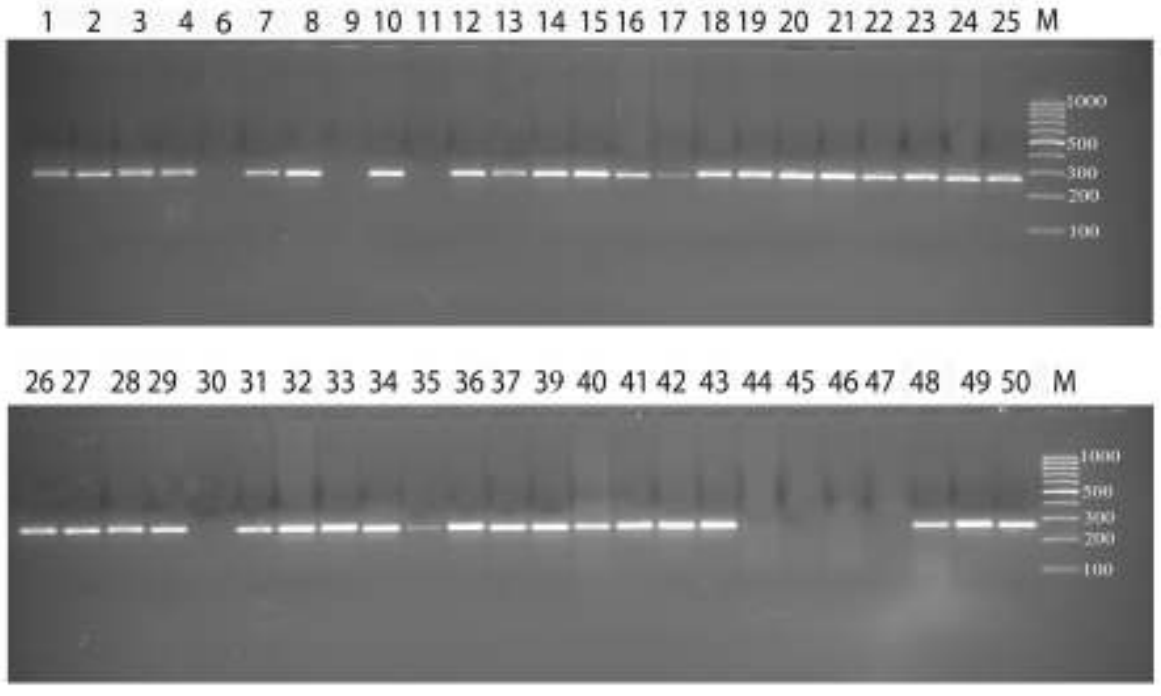


(b) SSR banding pattern of 48 colocasia landraces using Primer COLGCC220-211, M-Molecular weight marker.

PLATE – 13

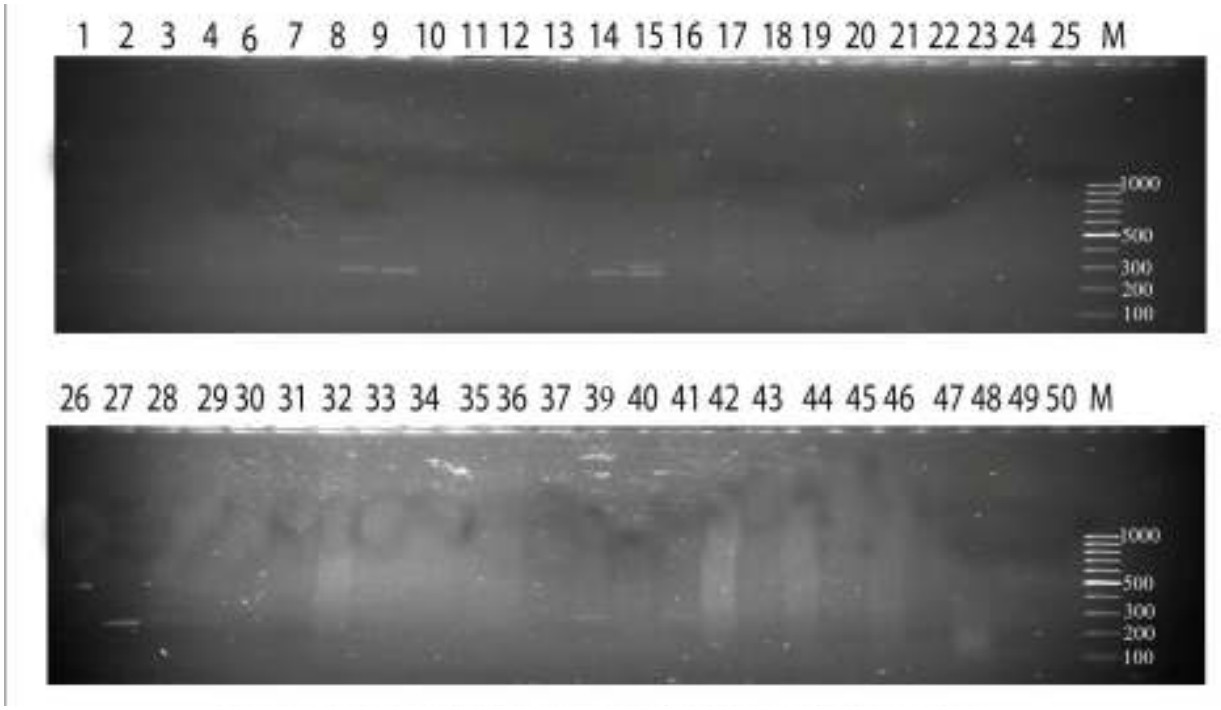


(a) SSR banding pattern of 48 colocasia landraces using Primer COLGCC119-367, M-Molecular weight marker.

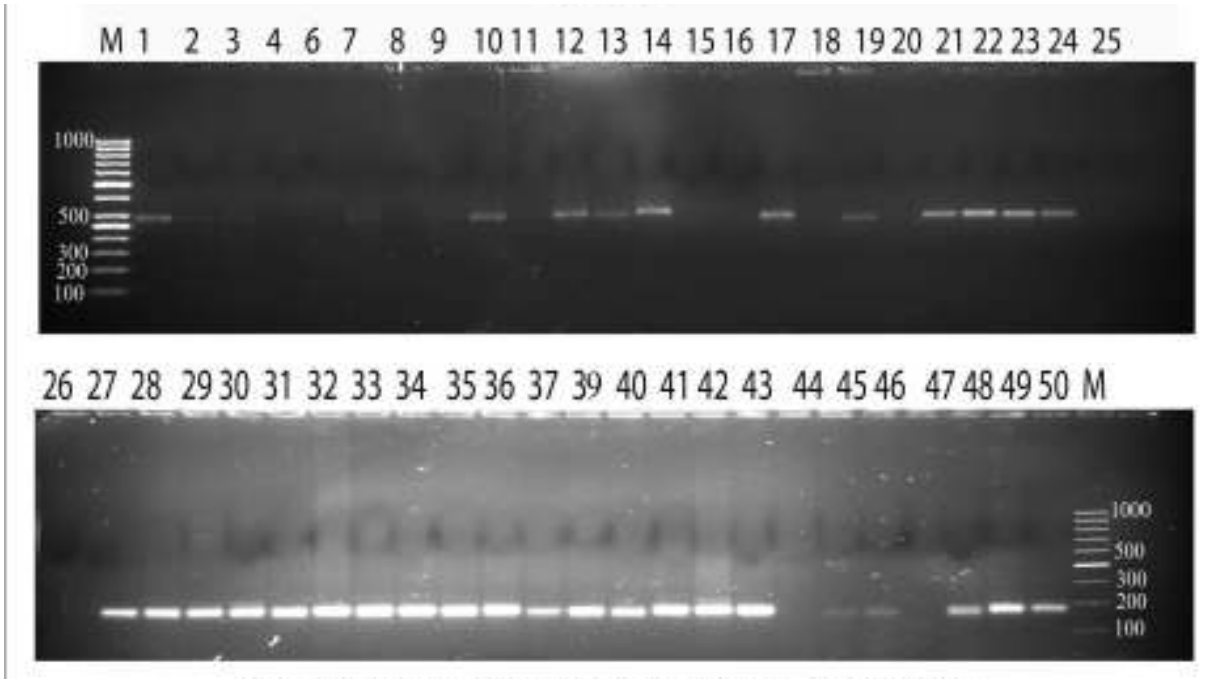


(b) SSR banding pattern of 48 colocasia landraces using Primer COLGCC91-262, M-Molecular weight marker.

PLATE – 14

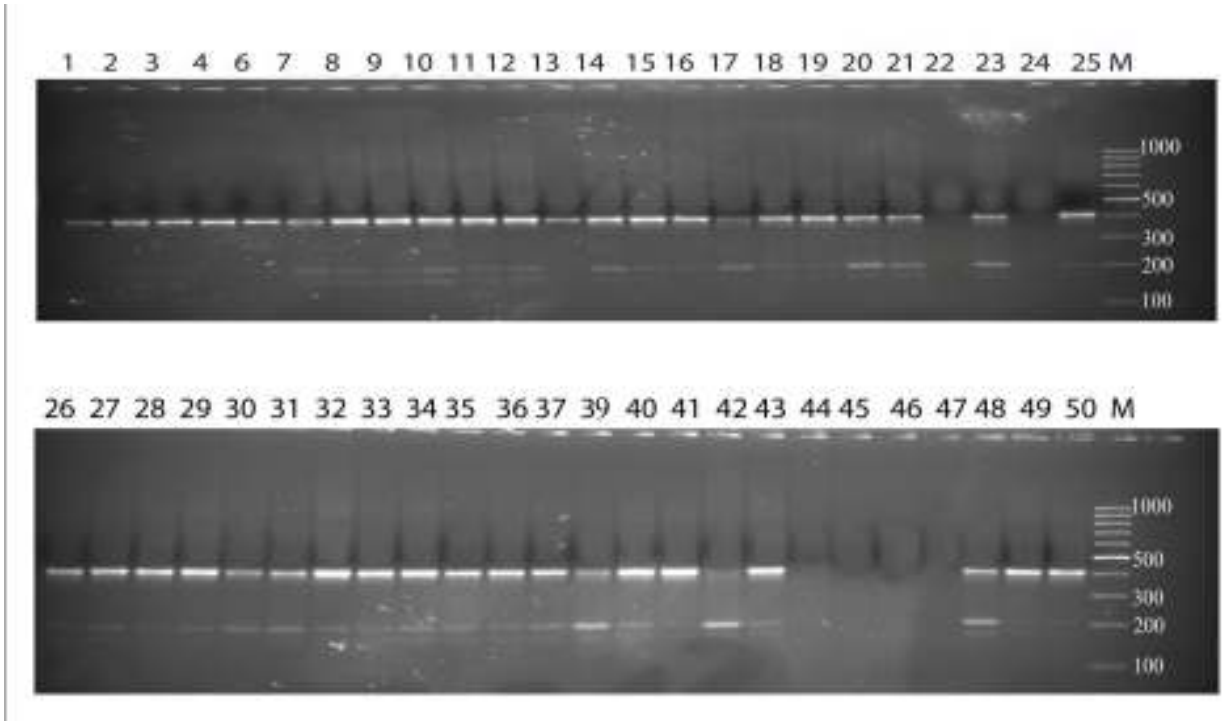


(a) SSR banding pattern of 48 colocasia landraces using Primer COLGCC249-155, M-Molecular weight marker.

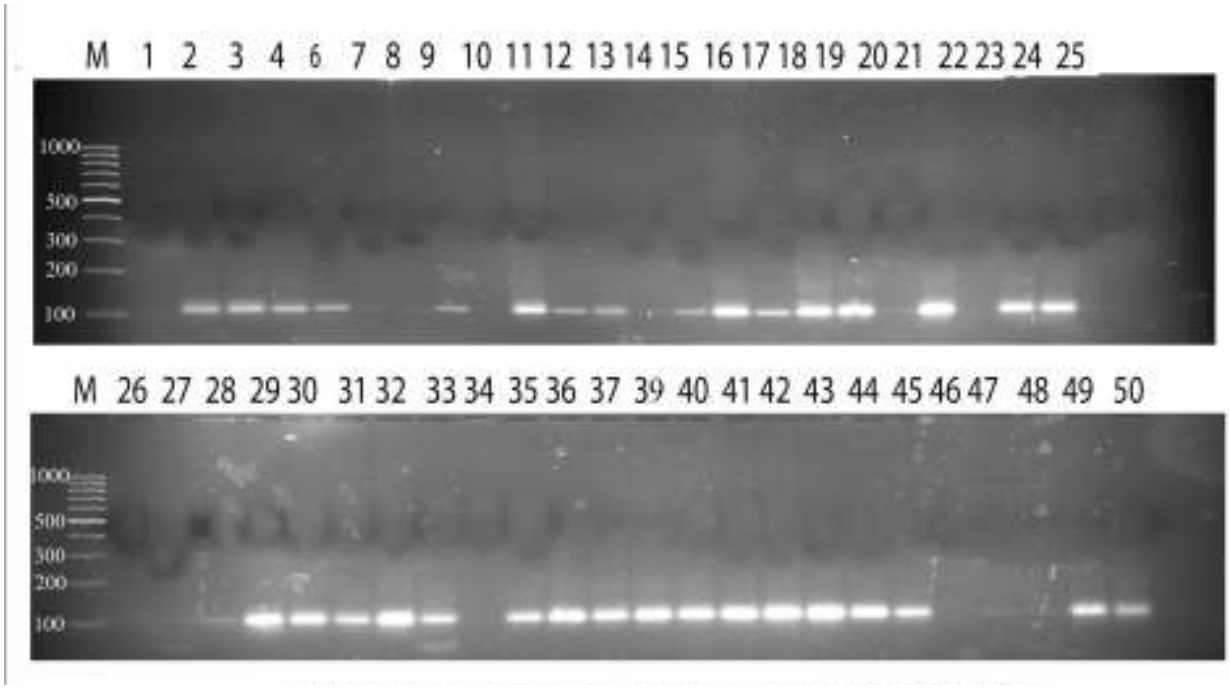


(b) SSR banding pattern of 48 colocasia landraces using Primer COLGCC110-283, M-Molecular weight marker.

PLATE – 15

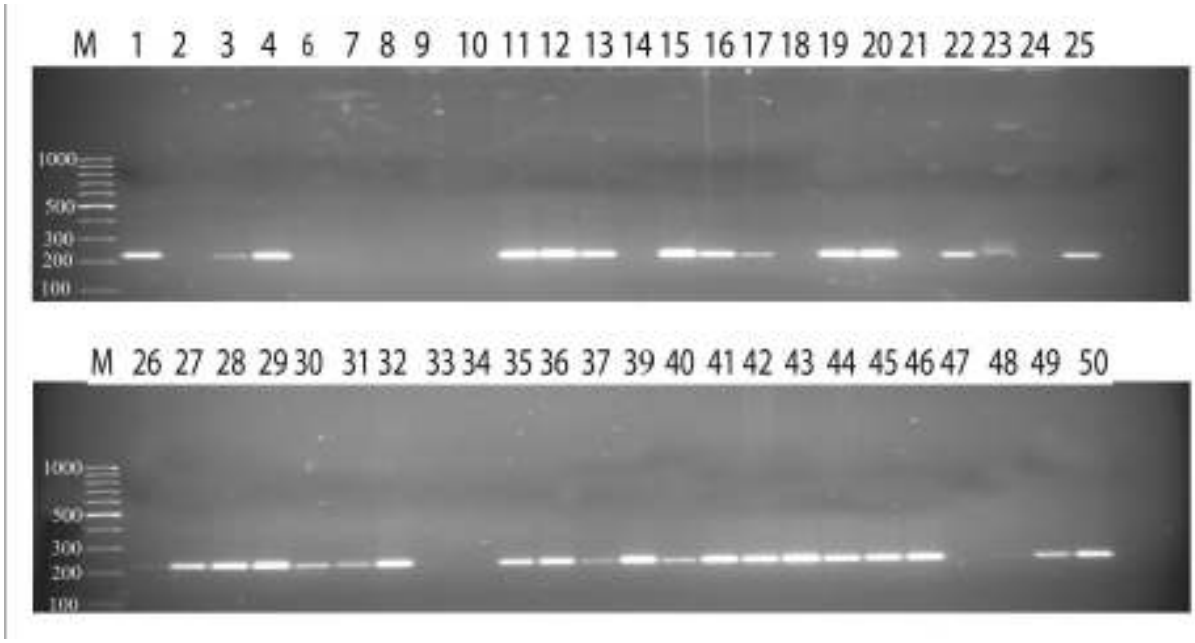


(a) SSR banding pattern of 48 colocasia landraces using Primer COLGCC211-202, M-Molecular weight marker.

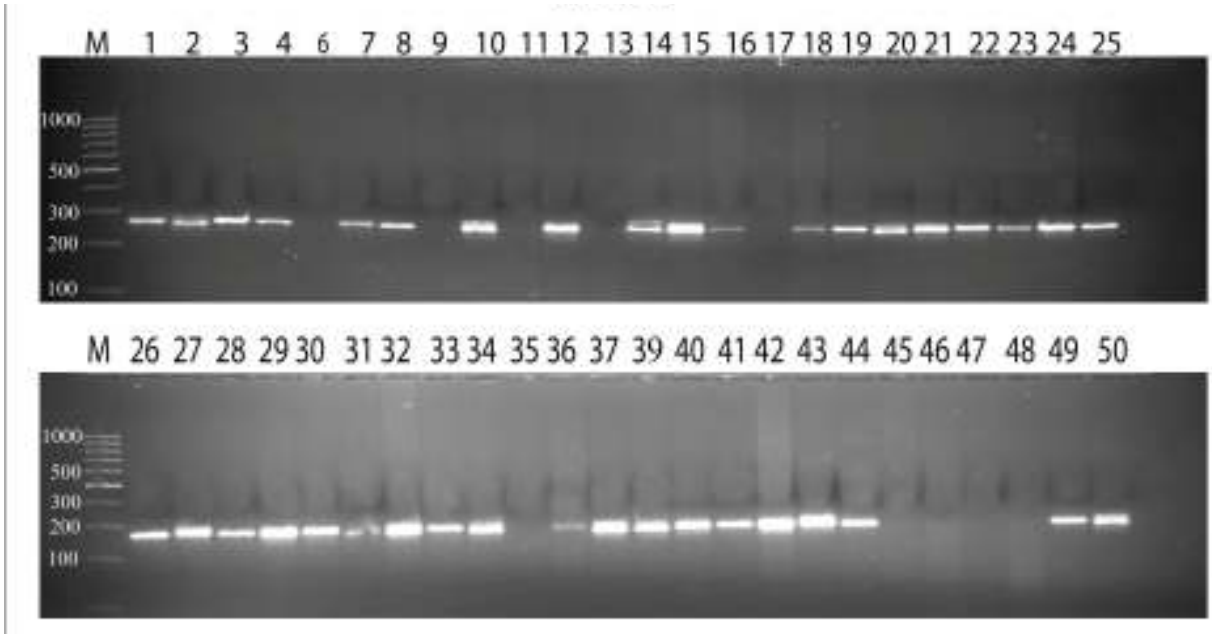


(b) SSR banding pattern of 48 colocasia landraces using Primer COLGCC228-110, M-Molecular weight marker.

PLATE – 16

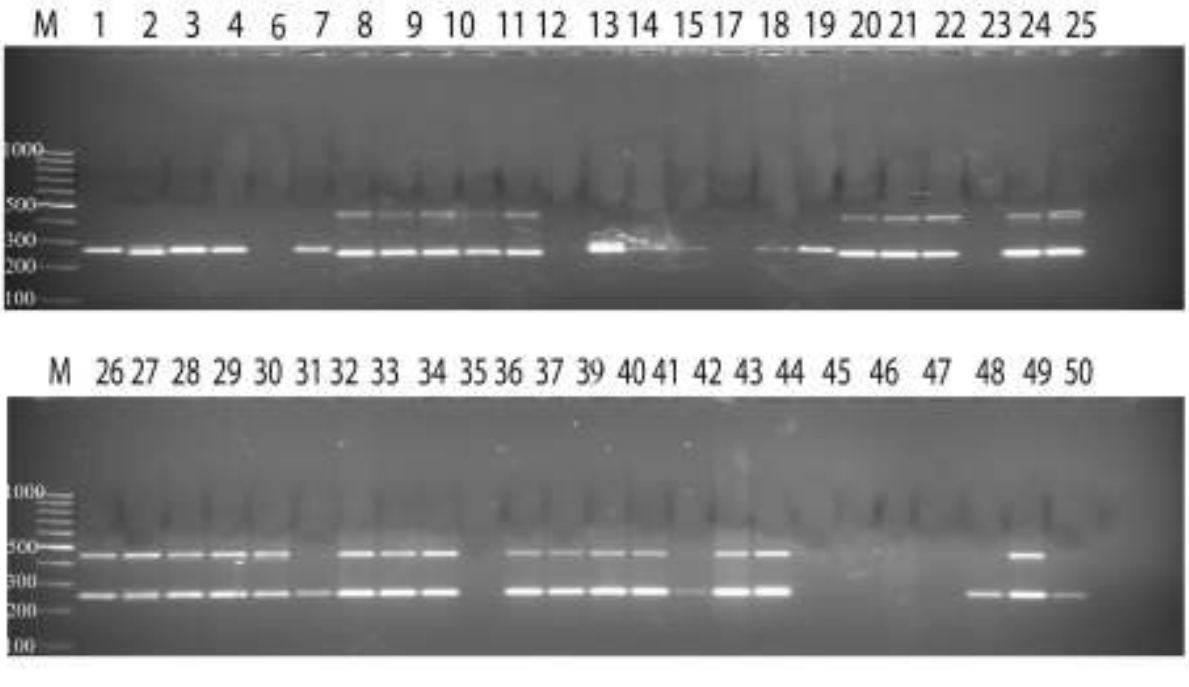


(a) SSR banding pattern of 48 colocasia landraces using Primer COLGCC240-223, M-Molecular weight marker.

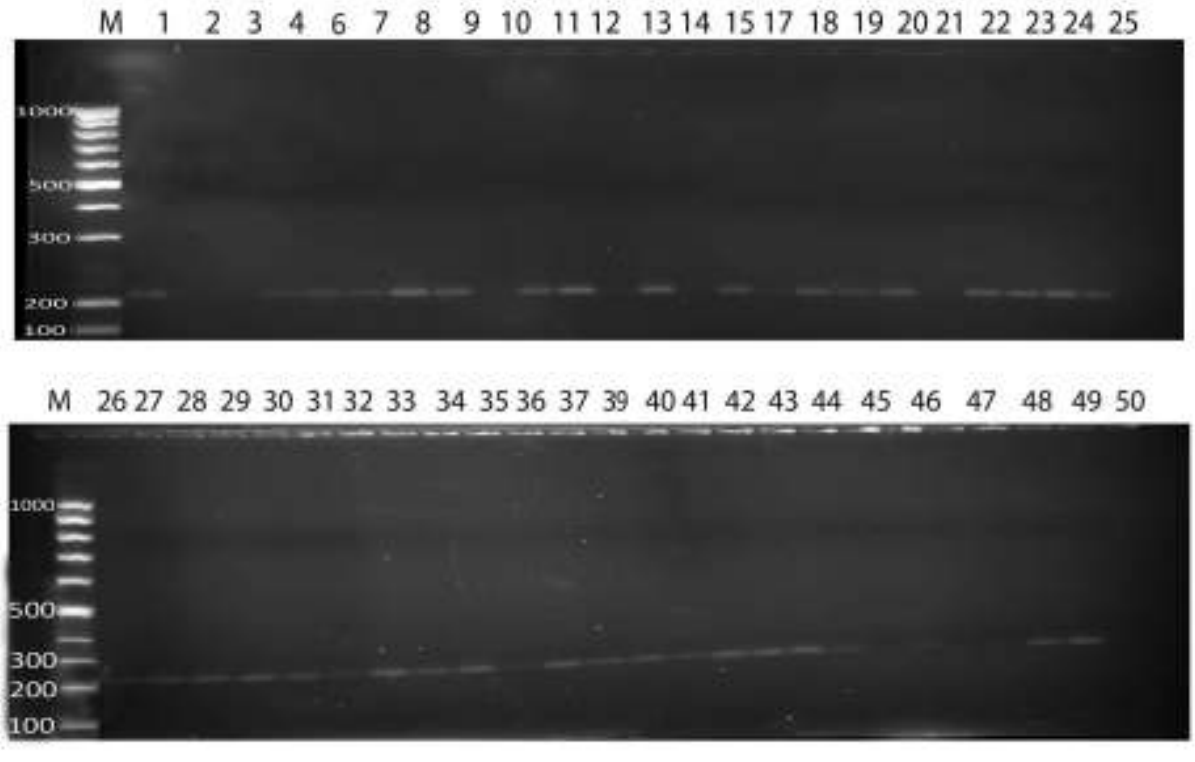


(b) SSR banding pattern of 48 colocasia landraces using Primer COLGCC105-267, M-Molecular weight marker.

PLATE – 17

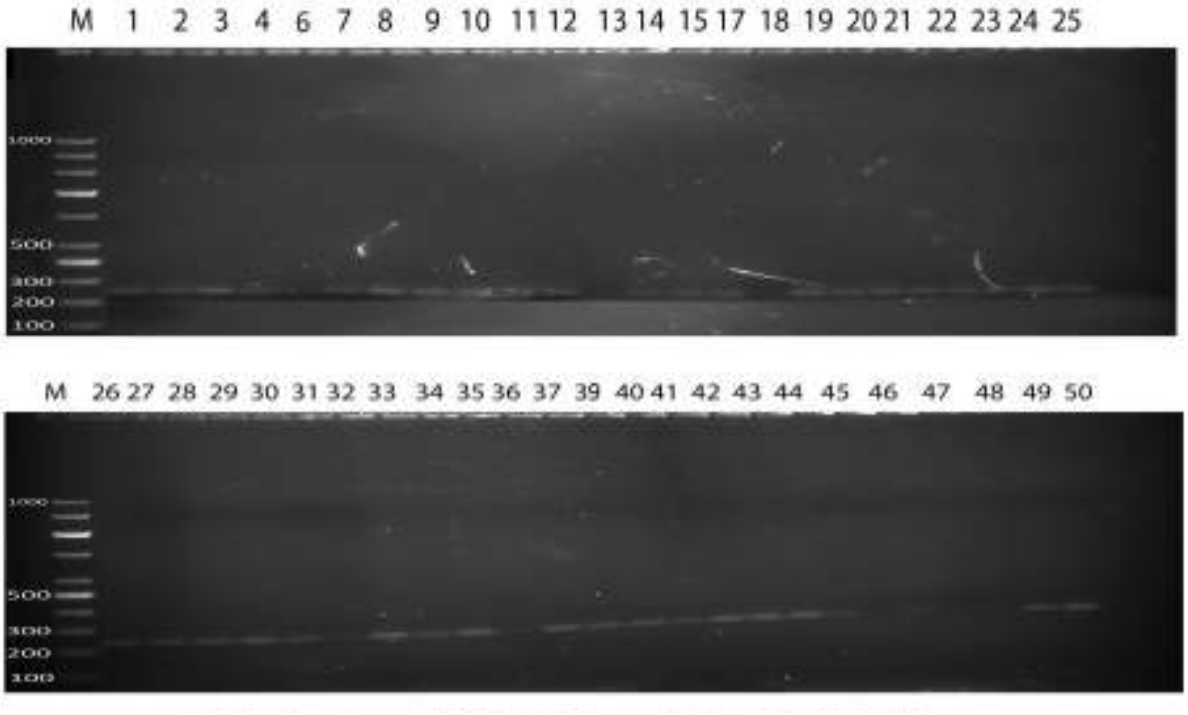


(a) SSR banding pattern of 48 colocasia landraces using Primer COLGCC208-253, M-Molecular weight marker.

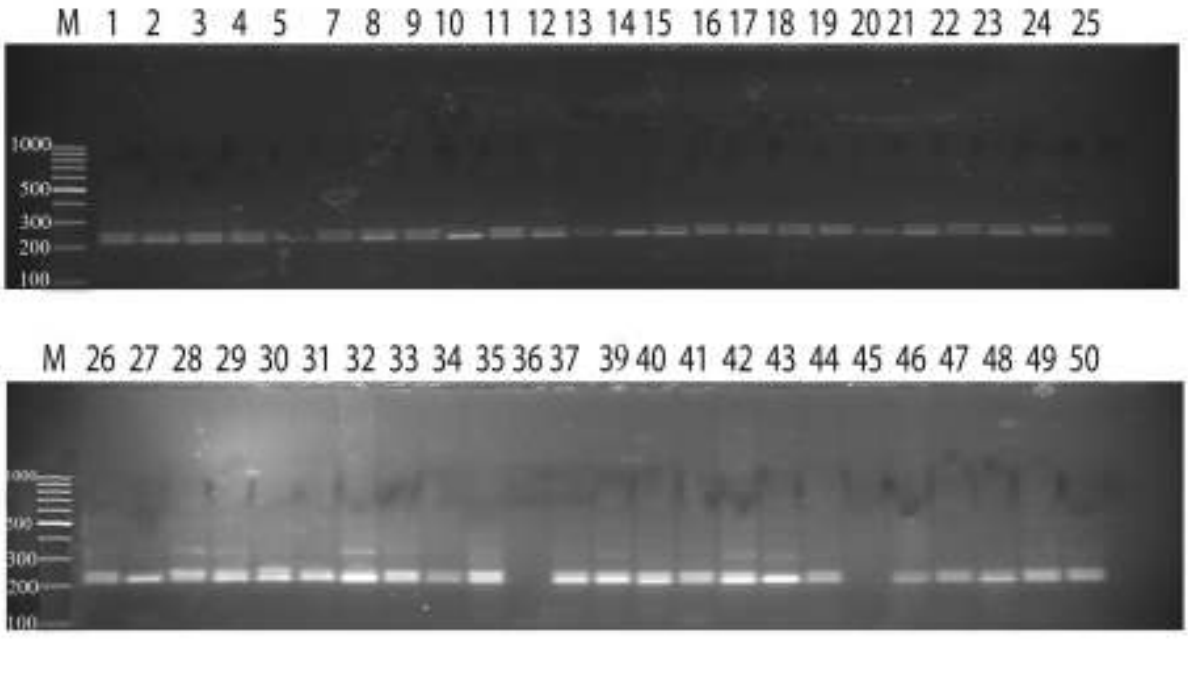


(b) SSR banding pattern of 48 colocasia landraces using Primer COLGCC209-120, M-Molecular weight marker.

PLATE – 18



(a) SSR banding pattern of 48 colocasia landraces using Primer COLGCC90-102, M-Molecular weight marker.



(b) SSR banding pattern of 48 colocasia landraces using Primer COLGCC73-164, M-Molecular weight marker.

Table 3.1 List of various cultivars of edible genotypes along with their respective codes and their source of collection.

Sl No	Code No	Local name	Place of collection	Headquater	Village	Distance from the Headquater (Km)	Altitude (MSL)	Special feature
1	CV1	Waipong	Peren	Tening	Tening village	10	750	
2	CV2	Chugoma	Zunheboto	Akuluto	Pishumi	36	1010	
3	CV3	Bei I	Peren	Tening	Tening village	10	750	Stolons
4	CV4	Beithola	Phek	Phek	Puraba village	15	1446	Stolons
5	CV5	Dziirinuo I	Kohima	Chiephobozou	Riisoma	13	1512	
6	CV6	Tephfii dziinuo	Kohima	Chiephobozou	Riisoma	13	1512	
7	CV7	Ati	Kohima	Tsiemenu	Tsiemenu	0	840	
8	CV8	Obei	Kohima	Jakhama	Khuzama	13	1512	
9	CV9	Dziinuo I	Dimapur	Cumukedima	Chumukedima	0	530	
10	CV10	Thegabeizii	Kohima	Jakhama	Khuzama		1512	
11	CV11	Beidimai I	Peren	Jalukie	Mainamshi	15	480	
12	CV12	Loudoubei	Peren	Jalukie	Hathipung		480	
13	CV13	Dzii Dziinuo	Dimapur	Chumukedima	Chumukedima	0	530	Small/Thin running stolon
14	CV14	Manie I	Wokha	Bhandari	Bhandari	0	701	
15	CV15	Dziirinuo II	Dimapur	Chumukedima	Razephema		600	
16	CV16	Tong I	Mon	Tobu	Tobu village	10	1296	
17	CV17	DziinuoII	Dimapur	Chumukedima	Chumukedima	0	530	
18	CV18	Thupela	Kohima	Chiephobozou	Chechama	3	840	Stolons
19	CV19	DziinuoIII	Dimapur	Dimapur	Shwoba	28	830	
20	CV20	Keriila	Dimapur	Medziphema	Medziphema	0	530	
21	CV21	Sama	Kohima	Chiephobozou	Riisoma	13	1512	
22	CV22	Beyo	Phek	Phek	Pholami		1446	
23	CV23	Dziinuo IV	Kohima	Jakhama	Jakhama	11	1512	
25	CV25	Tefiidzii	Kohima	Chiephobozou	Dziimetu	40	1512	
26	CV26	Chiicha	Dimapur	Medziphema	Medziphema	0	530	Small running stolons
27	CV27	Lijalanii	Mokokchung		Yachung	13	1512	Stolons
28	CV28	Pajo	Wokha	Wokha	Humtso	10	450	

Sl No	Code No	Local name	Place of collection	Headquater	Village	Distance from the Headquater (Km)	Altitude (MSL)	Special feature
30	CV30	Dziireinuo III	Kohima	Kohima	Kohima	10	1512	
31	CV31	Manie II	Wokha	Wokha	Humtso	10	450	
32	CV32	Banu sam sam	Kiphire	Amahator	Amahator	27	1980	
33	CV33	Boa	Kiphire	Amahator	Amahator	27	1980	Stolons
34	CV34	Aiie	Zunheboto		Sitimi village	10	1980	
35	CV35	Wolikhuo	Kohima	Kohima	Chedema	11	1512	
36	CV36	Tinopang	Longleng	Tamlu	Tamlu Village	10	1100	
37	CV37	Kotaknii	Mokokchung	Mokokchung	Yisemyong	17	1130	
38	CV38	Tino I	Tuensang	Noksen	Yangpi	10	1351	
39	CV39	Tino II	Tuensang	Noksen	Yangpi	10	1351	
40	CV40	Tino III	Tuensang	Chessore	Yangpi	8	1042	
41	CV41	Dziinuo V	Dimapur	Medziphema	Piphema	28	830	
42	CV42	Atsantu	Kohima	Tsiemenu	Tsiemenu	0	840	Stolons
43	CV43	Wasii nii	Mokokchung	Mokokchung	Yachang	20	1750	
44	CV44	Manyii	Mokokchung	Mokokchung	Changeongya	40	1130	Stolons
45	CV45	Tejongnii	Mokokchung	Mokokchung	Alichen	15	480	
46	CV46	Chuyali	Zunheboto	Akuluto	Gathashi	20	1010	
47	CV47	Tong II	Mon	Mon	Hangphoi	25	520	
48	CV48	Tong III	Mon	Tizit	Tela	18	570	
49	CV49	Beizo	Phek	Phek	Pholami	43	1446	
50	CV50	Dziitii	Dimapur	Dimapur	Dimapur	0	530	
51	XN 1	Jiimo	Kohima	Kohima	Riisoma	13	1512	
52	XN 2	Jiiti	Kohima	Kohima	Riisoma	13	1512	
53	AL1		Dimapur	Dimapur	Dimapur	0	530	
54	AL 2		Chumukedima	Dimapur	Chumukedima	0	530	
55	AM1		Showba	Dimapur	Showba	0	530	

Table 4.17 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
	Forward	Reverse			High	Low	Most frequent	
COL-GCC56-191	TGTCCCTTTTGATCTGTACAAG	CTCAACGGCTCATACACAC	3	56-191	249	115	134	0.78
COL-GCC82-117	TCAAGCGTAGGGGAAAAAC	CCACAACACAAAACTGTAAACC	1	82-117	193	153	188	0.52
COL-GCC111-300	AGTGTATCCTACGTCCACGG	CAACCTTCTCCATCAGTCCAG	2	111-300	367	221	289	0.89
COL-GCC192-245	GGACTAACCGTTATGCTGC	CTATGACTCGCCGTCATTG	2	192-245	427	202	236	0.73
COL-GCC132-147	ACCCCGAAAAAGCCAATG	CTATCACTTGTTCCTCCTTCTC	1	132-147	156	113	139	0.65
COL-GCC233-167	TGCACAGTCAACAATGTCG	ATCTCCAAGCCCAATCTCC	2	233-167	182	140	164	0.73
COL-GCC88B-94	CACACATACCCACATACACG	CCAGGCTCTAATGATGATGATG	2	88-94	117	66	108	0.59
COL-GCC75-100	TTGGTCAGATCAAGGCTAGAG	GACTAACATCACACACACACG	2	75-100	117	73	88	0.54

COL-GCC118-221	GACTAACCGTTATGCTGCC	TAGATTGGAGCCCTTGGAC	1	118-221	217	156	213	0.71
COL-GCC103-220	GGATCTCTGGATTGGCTTCC	ATGATGCACTCACACCCAC	1	103-220	351	169	176	0.48
COL-GCC77-174	GATCTCAAGCACAAGAGACG	TCAACCTTCTCCATCAGTCC	2	77-174	178	158	167	0.66
COL-GCC95-219	ACAACTCGTGTATCCTACATCC	TCAACTCTCAAACCCTTCCC	1	95-219	219	191	206	0.43
COL-GCC98-294	AGTCCAGAGCACTCAAGTCG	CACAACAGTGTATCCTACGTCC	3	98-294	339	125	278	0.83
COL-GCC206-122	CGTTCAACACAGACCACTAC	TCCTTTGGAAAGGAGGTCC	4	206-122	272	105	126	0.91
COL-GCC223-157	GAGATGGTGTGAGTAAAGGAAG	TGGACTACTACTGAAGCAGAG	1	223-157	190	163	166	0.46
COL-GCC220-211	CTAAGGAGAGGAGATCCGAAC	CTGATACCACTTGTTGCCC	2	220-211	361	153	351	0.72
COL-GCC119-367	GGTCAAGCGTAGGGGAAAAAC	AGCTAGGGAGCACCAAACAC	1	119-367	355	302	312	0.58
COL-GCC91-262	GTCCAGTGTAGAGAAAAACCAG	CACAACCAAACATACGGAAAC	2	91-262	311	219	239	0.73
COL-GCC249-155	GACGGTCCAAATGTTAG	CCAAGGAAGATATTACCAAG	3	249-155	454	224	234	0.76
COL-GCC110-283	AGCCACGACACTCAACTATC	GCCCAGTATATCTTGCATCTCC	2	110-283	257	222	243	0.65
COL-GCC211-202	CTAACCACACACACATGAGCAC	TACTGTCCTGCTTCATCCCTCC	3	211-202	414	139	414	0.93
COL-GCC228-110	CCAGACTTCTCTCTACACCAAG	GATCTGTTGAAGAGATCCGTTG	1	228-110	126	104	116	0.41
COL-GCC240-223	ACTAACACGAGCACTCTCC	ACCATTTCCTACCACCTCC	1	240-223	250	199	203	0.52
COL-GCC105-267	CACCAAGGCATGGGAAAC	CCTGAAAATGGCAAAATACTTTAC	2	105-267	341	231	231	0.66
COL-GCC208-253	TAGAGGGTGGACAGGAG	CTAGAGGCACTGATGTAAC	4	208-253	685	229	244	0.89
COL-GCC209-120	CTACTCTACTGCCATCTAC	GTGAGTGAGAAAGTGAATG	1	209-120	130	67	70	0.51
COL-GCC90-102	TGGTGCGTTGGTCAGATCAAGG	ACAACACACACACGAGCACAC	1	90-102	185	92	94	0.57
COL-GCC73-164	ATGCCAATGGAGGATGGCAG	CGTCTAGCTTAGGACAACATGC	2	73-164	184	137	140	0.68

Table 4. 18 **. Genotypes were grouped into six hypothetical population based on their location of collection**

Population	Genotype name		Place of collection
pop 1	CV2	Chugoma	Zunheboto
	CV34	Aiie	Zunheboto
	CV46	Chuyali	Zunheboto
	CV4	Beithola	Phek
	CV22	Beyo	Phek
	CV24	Bei II	Phek
	CV49	Beizo	Phek
	CV32	Banu sam sam	Kiphire
	CV33	Bao	Kiphire
pop2	CV14	Manie I	Wokha
	CV27	Lijalanii	Mokokchung
	CV28	Pajo	Wokha

	CV31	Manie II	Wokha
	CV37	Kotaknii	Mokokchung
	CV43	Wasii nii	Mokokchung
	CV44	Manyii	Mokokchung
	CV45	Tejongnii	Mokokchung
	CV16	Tong I	Mon
	CV36	Tinopang	Longleng
	CV39	Tino II	Tuensang
	CV40	Tino III	Tuensang
	CV47	Tong II	Mon
pop3	CV48	Tong III	Mon

	CV1	Waipong	Peren
	CV3	Bei I	Peren
	CV11	Beidimai I	Peren
	CV12	Loudoubei	Peren
pop4	CV29	Beidimai I	Peren
	CV6	Tephfii dziinuo	Kohima
	CV7	Ati	Kohima
	CV8	Obei	Kohima
	CV10	Thegabeizii	Kohima
	CV18	Thupela	Kohima
	CV21	Sama	Kohima
pop5	CV23	Dziinuo IV	Kohima

	CV25	Tefiidzii	Kohima
	CV30	Dziirinuo II	Kohima
	CV35	Wolikhuo	Kohima
	CV42	Atsantu	Kohima
	CV9	Dziinuo I	Dimapur
	CV13	Dzii dziinuo	Dimapur
	CV15	Dziirinuo I	Dimapur
	CV17	Dziinuo II	Dimapur
	CV19	Dziinuo III	Dimapur
	CV20	Keriila	Dimapur
	CV26	Chiicha	Dimapur
	CV41	Dziinuo V	Dimapur
pop6	CV50	Dziitii	Dimapur

Table 4.19 **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%

Table 4.1 Qualitative characters of the various genotypes.

Code no	Local name	Leaf blade margin(LBM)	Leaf blade colour(LBC)	Leaf blade colour variegation (LBV)	Flower formation(FFT)	Predominant position of leaf lamina surface (LPO)	Leaf main vein colour(LVC)	Leaf vein pattern(LVP)	Petiole basal ring colour(PBC)	Petiole junction colour(PJC)
CV1	Waipong	Undulate	White	1	0	Erect apex down	Whitish	Vpattern	green	Green
CV2	Chugoma	Undulate	Purple	1	1	Erect apex down	Pink	Vpattern	green	Purple
CV3	Bei I	Undulate	White	1	1	Erect apex down	White	Vpattern	green	Purple
CV4	Beithola	Undulate	White	1	1	Erect apex down	White	Vpattern	green	Green
CV5	Dziirinuo I	Undulate	White	1	0	Erect apex down	Pink	Vpattern	green	Purple
CV6	Tephfii dziinuo	Undulate	White	1	1	Erect apex down	White	Vpattern	green	Green
CV7	Ati	Undulate	White	1	1	Erect apex down	White	Vpattern	green	Green
CV8	Obei	Undulate	Pink	1	0	Erect apex down	Purple	Vpattern	Purple	Purple
CV9	Dziinuo I	Undulate	White	1	0	Erect apex down	White	Vpattern	White	Purple
CV10	Thegabeizii	Undulate	purple	1	0	Erect apex down	White	Vpattern	Purple	Purple
CV11	Beidimai I	Undulate	White	1	0	Erect apex down	White	Vpattern	green	Green
CV12	Loudoubei	Undulate	Purple	1	1	Erect apex down	Whitish	Vpattern	Purple	White
CV13	Dzii Dziinuo	Undulate	green	1	0	Erect apex down	green	Vpattern	White	White
CV14	Manie I	Undulate	Purple	1	0	Erect apex down	White	Vpattern	Purple	White
CV15	Dziirinuo II	Undulate	White	1	1	Erect apex down	White	Vpattern	green	White
CV16	Tong I	Undulate	White	1	1	Erect apex down	White	Vpattern	green	White
CV17	DziinuoII	Undulate	green	1	0	Erect apex down	White	Vpattern	Purple	White
CV18	Thupela	Undulate	Whitish	1	0	Erect apex down	White	Vpattern	green	White
CV19	DziinuoIII	Undulate	Green	1	1	Erect apex down	green	Vpattern	dark brown	Green
CV20	Keriila	Undulate	Purple	1	1	Erect apex down	White	Vpattern	Purple	Green
CV21	Sama	Undulate	Green	1	0	Erect apex down	White	Vpattern	green	Green
CV22	Beyo	Undulate	Green	1	0	Erect apex down	Purple	Vpattern	green	Green
CV23	Dziinuo IV	Undulate	Violet blue	1	0	Erect apex down	Purple	Vpattern	purple	Purple
CV24	Bei II	Undulate	Green	1	0	Erect apex down	White	Vpattern	green	Purple
CV25	Tefiidzii	Undulate	Green	1	0	Erect apex down	green	Vpattern	Purple	Purple

Continuation of Table 4.1

Code no	Local name	Petiole junctio pattern(PJP)	Petiole lower colour(LPC)	Presence of petiole stripe(PPS)	Petiole stripe colour(PSC)	Petiole top colour(PTC)	Taro leaf blight resistance(TLB)	Corm flesh colour(CFL)	Cormflesh fibre colour(CFI)	Corm shape(COS)	Corm cortex colour(CCC)
CV1	Waipong	Small	Green	0	0	green	T	White	yellow	Flat and multifaced	White
CV2	Chugoma	Small	Green	1	Purple	purple	T	Pink	White	Round	Pink
CV3	Bei I	Small	Green	0	0	green	T	White	White	Round	White
CV4	Beithola	Small	Green	0	0	Purple	T	White	White	Round	White
CV5	Dziirinuo I	Small	Green	1	Purple	Purple	T	White	White	Round	White
CV6	Tephfii dziinuo	Small	Green	0	0	green	T	White	White	Round	White
CV7	Ati	Small	Purple	0	0	green	T	White	White	Round	White
CV8	Obei	Small	Green	1	Purple	White	T	White	White	Round	White
CV9	Dziinuo I	Small	Purple	0	0	green	T	White	White	Round	White
CV10	Thegabeizii	Small	Green	1	green	green	T	White	White	Round	White
CV11	Beidimai I	Small	Purple	0	0	green	T	White	White	Round	White
CV12	Loudoubei	Small	Green	1	Purple	green	T	White	White	Round	White
CV13	Dzii Dziinuo	Small	Purple	1	purple	green	T	White	White	Round	White
CV14	Manie I	Small	Green	1	Purple	light green	T	White	White	Round	White
CV15	Dziirinuo II	Small	Green	1	Purple	light green	T	pink	White	Round	pink
CV16	Tong I	Small	Purple	0	0	green	T	pink	White	Round	pink
CV17	DziinuoII	Small	Green	1	Purple	green	T	White	White	Round	White
CV18	Thupela	Small	Green	0	0	green	T	White	White	Round	White
CV19	DziinuoIII	Small	Brown	1	green	green	T	White	White	Elongated	White
CV20	Keriila	Small	Green	1	Purple	green	T	White	White	Round	White
CV21	Sama	Small	Green	0	0	green	T	White	White	Round	White
CV22	Beyo	Small	Purple	0	0	green	T	pink	White	Round	pink
CV23	Dziinuo IV	Small	Green	0	0	Purple	T	White	White	Round	White
CV24	Bei II	Small	Purple	1	Purple	light green	T	White	White	Round	White
CV25	Tefiidzii	Small	Green	1	Purple	green	T	White	White	Round	White

Continuation of Table 4.1

Code no	Local name	Leaf blade margin(LBM)	Leaf blade colour(LBC)	Leaf blade colour variegation (LBV)	Flower formation(FFT)	Predominant position of leaf lamina surface (LPO)	Leaf main vein colour(LVC)	Leaf vein pattern(L VP)	Petiole basal ring colour(PBC)	Petiole junction colour(PJC)
CV26	Chiicha	Undulate	Purple	1	1	Erect apex down	Purple	Vpattern	green	green
CV27	Lijalanii	Undulate	White	1	0	Erect apex down	Whitish	Vpattern	green	Purple
CV28	Pajo	Undulate	green	1	1	Erect apex down	green	Vpattern	Purple	green
CV29	BeidimaiII	Undulate	green	1	0	Erect apex down	green	Vpattern	green	green
CV30	Dziireinuo III	Undulate	Purple	1	1	Erect apex down	Purple	Vpattern	green	Purple
CV31	Manie II	Undulate	Purple	1	0	Erect apex down	White	Vpattern	green	Purple
CV32	Banu sam sam	Undulate	green	1	0	Erect apex down	White	Vpattern	green	Purple
CV33	Boa	Undulate	White	1	0	Erect apex down	green	Vpattern	green	green
CV34	Aiie	Undulate	White	1	0	Erect apex down	green	Vpattern	green	purple
CV35	Wolikhuo	Undulate	green	1	0	Erect apex down	White	Vpattern	green	green
CV36	Tinopang	Undulate	green	1	1	Erect apex down	White	Vpattern	green	green
CV37	Kotaknii	Undulate	green	1	0	Erect apex down	White	Vpattern	green	purple
CV38	Tino I	Undulate	green	1	0	Erect apex down	White	Vpattern	green	green
CV 39	Tino II	Undulate	green	1	0	Erect apex down	White	Vpattern	green	Green
CV40	Tino III	Undulate	green	1	0	Erect apex down	White	Vpattern	purple	Green
CV41	Dziinuo V	Undulate	green	1	0	Erect apex down	White	Vpattern	green	Green
CV42	Atsantu	Undulate	green	1	1	Erect apex down	White	Vpattern	green	Purple
CV43	Wasii nii	Undulate	green	1	1	Erect apex down	White	Vpattern	green	Green
CV44	Manyii	Undulate	green	1	0	Erect apex down	White	Vpattern	green	Green
CV45	Tejongnii	Undulate	green	1	0	Erect apex down	White	Vpattern	green	Green
CV46	Chuyali	Undulate	Purple	1	1	Erect apex down	White	Vpattern	green	Purple
CV47	Tong II	Undulate	yellow green	1	0	Erect apex down	White	Vpattern	green	Green
CV48	Tong III	Undulate	Purple	1	1	Erect apex down	White	Vpattern	green	Purple
CV49	Beizo	Undulate	yellow green	1	0	Erect apex down	White	Vpattern	green	Green
CV50	Dziitii	Undulate	purple	1	1	Erect apex down	Purple	Vpattern	green	Green

Continuation of Table 4.1

Code no	Local name	Petiole junctio pattern(PJP)	Petiole lower colour(LPC)	Presence of petiole stripe(PPS)	Petiole stripe colour(PSC)	Petiole top colour(PTC)	Taro leaf blight resistance(TLB)	Corm flesh colour(CFL)	Cormflesh fibre colour(CFI)	Corm shape(COS)	Corm cortex colour(CCC)
CV26	Chiicha	Small	green	0	0	green	T	White	White	Round	White
CV27	Lijalanii	Small	Purple	0	0	green	T	White	White	Round	White
CV28	Pajo	Small	green	1	Purple	green	T	White	White	Round	White
CV29	BeidimaiII	Small	Purple	0	0	green	T	White	yellow	Flat and multifaced	White
CV30	Dziireinuo III	Small	green	1	Purple	purple	T	pink	White	Round	Pink
CV31	Manie II	Small	green	0	0	light green	T	White	White	Round	White
CV32	Banu sam sam	Small	green	0	0	green	T	White	White	Round	White
CV33	Boa	Small	green	0	0	green	T	White	White	Round	White
CV34	Aiie	Small	green	0	0	green	T	White	White	Round	White
CV35	Wolikhuo	Small	green	0	0	green	T	White	White	Round	White
CV36	Tinopang	Small	Purple	0	0	green	T	White	White	Round	White
CV37	Kotaknii	Small	green	1	Purple	white	T	pink	White	Round	Pink
CV38	Tino I	Small	green	0	0	green	T	White	White	Round	White
CV39	Tino II	Small	green	0	0	green	T	White	White	Round	White
CV40	Tino III	Small	green	0	0	green	T	White	White	Round	White
CV41	Dziinuo V	Small	green	0	0	green	T	White	White	Round	White
CV42	Atsantu	Small	green	0	0	green	T	White	White	Round	White
CV43	Wasii nii	Small	green	0	0	green	T	pink	White	Round	Pink
CV44	Manyii	Small	green	0	0	green	T	White	White	Round	White
CV45	Tejongnii	Small	green	0	0	green	T	White	yellow	Flat and multifaced	White
CV46	Chuyali	Small	green	0	0	White	T	pink	White	Round	Pink
CV47	Tong II	Small	green	0	0	green	T	White	White	Round	White
CV48	Tong III	Small	green	0	0	green	T	pink	White	Round	Pink
CV49	Beizo	Small	green	0	0	green	T	White	yellow	Flat and multifaced	White
CV50	Dziitii	Small	Purple	0	0	green	T	White	yellow	Flat and multifaced	White

Table 4.2. Analysis of variance for 14 characters based on 1st year (2008) data.

Source of variation	Degree of freedom	MEAN SUM OF SQUARES													
		Plant height (cm)	Petiole length (cm)	Leaf Length (cm)	Leaf width (cm)	Number of inflorescence	Number of suckers	Number of leaves	Corm weight (g)	Number of cormels	Cormel weight (g)	Corm girth (cm)	Length of corm (cm)	Breath of corm (cm)	Yield per plant (g)
Replications	2	72.08	60.24	429.03	165.7	0.03	2.83	0.15	835.99	1.68	1943.4	18.64	0.49	0.42	7891.7
Genotypes	49	1138.22**	599.96**	356.69**	95.95**	0.69	2.36**	0.43	10714.39**	32.57**	16491.91**	38.69**	51.39**	24.76**	289882.76**
Error	98	70.94	60.63	44.06	29.79	0.06	0.63	0.11	937.37	1.09	2949.6	6.77	0.13	0.12	4100.2

**** Significant at 1% level**

Table 4.3. Analysis of variance for 14 characters based on 2nd year (2009) data.

Source of variation	Degree of freedom	MEAN SUM OF SQUARES													
		Plant height (cm)	Petiole length (cm)	Leaf Length (cm)	Leaf width (cm)	Number of inflorescence	Number of suckers	Number of leaves	Corm weight (g)	Number of cormels	Cormel weight (g)	Corm girth (cm)	Length of corm (cm)	Breath of corm (cm)	Yield per plant (g)
Replications	2	110.50	56.64	57.97	22.60	0.78	0.41	0.27	5075.70	10.99	7905.43	4.63	16.38	1.19	23501.04
Genotypes	49	1128.74**	939.28**	191.52**	98.55**	1.41*	3.36**	0.43	14072.25**	54.8**	22345.49**	111.21**	57.99**	21.46**	51940.57**
Error	98	110.21	107.99	15.37	9.61	0.27	0.37	0.11	1791.94	4.19	3897.24	3.31	13.71	0.92	7950.96

**** Significant at 1% level**

Table 4.4. Mean performance of 50 genotypes of Colocasia for 14 characters during 2008 and 2009.

Varieties	Year	Plant height (cm)	Petiole length (cm)	Leaf Length (cm)	Leaf width (cm)	Number of infloresence	Number of suckers	Number of leaves	Corm weight (g)	Number of cormels	Cormel weight (g)	Corm girth (cm)	Length of corm (cm)	Breath of corm (cm)	Yield per plant (g)
Waipong	2008	60.2	45.67	32.74	26.35	0	1	5	198.67	1.8	40	8.59	12.37	14.14	238.67
	2009	66.1	49.37	29.63	21.62	0	1	5.03	314.33	5.67	220	23.78	13.33	13.2	534.33
Chugoma	2008	50.34	40	24.54	17.87	0	0.74	6.1	217.67	6.1	73	7.14	7.37	2.24	220.27
	2009	67.97	51.67	25.8	18.34	0.67	0.8	6.07	116.67	0	282.67	15.6	3.43	3.03	399.33
Bei I	2008	86.47	67.34	47.67	42	2.6	0	4.2	296.67	0	223.34	8.87	14.1	2.74	520
	2009	86.47	58.67	36.4	25.57	2.31	0	4.17	337	0	478.33	25.733	13.67	2.67	815.33
Beithola	2008	69.5	48	35.54	22.34	0.4	0	4.27	93.34	0	73.34	5.9	12.64	2.74	166.67
	2009	75.67	56.67	25.8	18.9	0.5	0	4.23	318.33	1.67	291.67	21.833	12.4	3.6	610
Dziirinuo I	2008	62.4	45	35	24.87	0	2.2	4.8	210.67	2.2	116.07	8.07	2.8	2.14	326.74
	2009	73.73	55	26.03	18.9	0	4.6	4.7	124.44	8.47	215.33	17.287	3.97	1.83	339.78
Tephfii dziinuo	2008	55.39	40	43.5	31.14	0	0.47	5.07	156.3	2.37	157.34	8.27	2.87	2.4	313.64
	2009	64.93	43.33	26.87	20.9	2	3.27	5.1	83.33	10.8	238.67	16.13	4.4	2.3	322
Ati	2008	51.61	44	40.6	28.67	0	1.54	4.87	134	4.67	148.67	7.34	3.57	1.4	282.67
	2009	67.33	58.33	30.4	24.13	1	2.03	4.83	107.11	12.29	213.89	17.53	4.03	2.93	321
Obei	2008	33.45	23.67	42.54	28.74	0	1.2	4.67	117.34	6.37	188.67	15.24	3.67	1.74	306
	2009	46.33	34	19.4	13.09	0	1	4.73	54.53	7.87	117.67	16.07	3.87	3.37	172.2
Dziinuo I	2008	43.34	32	33.94	21.27	0	0.7	5.04	72	5.3	119.34	10.17	3.54	1.77	191.34
	2009	60.33	40	20.73	12.83	0	0.8	5.03	78.67	6.13	126.33	18.47	3.53	2.67	205
Thegabeizii	2008	44.11	30.7	46.14	30.67	0	1.07	5.07	199.67	5.87	292.22	10	2.94	1.84	491.67
	2009	63	48	28.13	20.4	0	0.93	5.1	32.67	8.47	112.67	11.13	4.03	5.37	145.33
Beidimai I	2008	46	36	32.14	23.8	0	0.6	4.27	127.34	14.74	127.34	6.53	2	1.6	254.67
	2009	61.33	49	26.6	18.47	0	0.57	4.3	95	6.97	164.33	18.6	3.37	2.1	259.33
Loudoubei	2008	42.09	30.84	36.07	24.47	0	0.54	5	142.67	6.14	298.67	7.07	2.67	1.97	441.34
	2009	69.33	52.33	27.37	20.33	1	0.67	4.833	191.67	9.83	228.33	21	4.1	2.3	420
Dzii dziinuo	2008	29.97	23.1	8.74	28.47	0	0.3	5.1	188	6.34	236	6.9	14.24	2.34	424
	2009	53.67	41.33	26.47	22.52	0	0.37	5.2	150	13.87	208.33	15.53	14.67	2.27	358.33

Varieties	Year	Plant height (cm)	Petiole length (cm)	Leaf Length (cm)	Leaf width (cm)	Number of infloresence	Number of suckers	Number of leaves	Corm weight (g)	Number of cormels	Cormel weight (g)	Corm girth (cm)	Length of corm (cm)	Breath of corm (cm)	Yield per plant (g)
Manie II	2008	52.15	37.7	40.2	29.87	0	1.27	4.60	122	11	277.34	6.54	4.57	1.34	399.34
	2009	66.67	48.67	29.13	22.5	0	2.87	4.53	105.33	12.67	252.11	18.84	5.07	2.03	357.44
Dziirinuo II	2008	41.75	30.67	42.87	29.54	0.27	1.00	4.47	88.34	5.94	176	6.44	2.6	1.54	264.34
	2009	52.67	42	22.97	18.07	0	2.6	4.6	205	6.23	201.33	20	4.7	2.37	406.33
Tong I	2008	48.47	39.34	44.87	31.67	0	2	4.47	93	5.07	120	7.2	3.47	1.44	213
	2009	56.67	45.33	32.8	27.6	0.33	2.6	4.47	114.33	10.8	285.33	19	5.43	2.4	399.67
Dziinuo II	2008	75.67	54	48	33.87	0	1.87	4.6	150	4.74	282.67	6.17	2.9	1.64	432.67
	2009	78.17	64	30.53	24.73	0	0.87	4.4	116.67	13.87	206.67	18.27	3.77	2.2	323.33
Thupela	2008	34.14	23.97	12.24	32.07	0	0	4.8	150	0	286.67	8.6	6.17	1.84	436.67
	2009	45.67	37.67	27.26	17.77	0	0	4.77	88	0	146.67	14.73	5.77	3.07	232.67
Dziinuo III	2008	145.87	86.8	21.77	37.27	0.94	2.4	5.2	108	5.8	259.34	6.99	13.34	2.1	367.34
	2009	145.83	122.33	33.53	24.33	1	2.17	5.33	107.67	5.77	326.67	5.733	14.67	2.63	434.33
Keriila	2008	98.4	76.4	50.54	36.4	0.6	1.94	4.67	142	3.54	126	7.07	2.67	2.54	268
	2009	123.67	106.67	23.2	19.4	0	1.57	4.7	106	9.73	206.67	16.07	3.13	2.03	312.67
Sama	2008	71.86	53.08	48	28	0	2.8	4.87	61.34	9	166.67	3.73	3.2	1.94	228
	2009	68.33	53.67	30.97	22.6	0	1.47	4.83	163.33	11.43	365.33	22.08	5.27	4.93	528.67
Beyo	2008	65.84	46.84	29.14	19.94	0	1.8	5.07	93	3.67	105.34	5.87	2.97	2.17	200
	2009	74	53.33	27.73	20	0	2.47	5.07	182.5	5.58	165	18.17	4.37	3.3	347.5
Dziinuo IV	2008	41.68	34.7	14.74	23.34	0	0.44	4.7	104.44	3.4	122.77	4.67	3.34	1.74	225.54
	2009	55	39.67	24.07	17.6	0	0.37	4.8	124	7.88	169	19.87	3.27	1.67	326.33
Bei II	2008	60.84	39.69	36.94	25.4	0	1.2	5.4	105.34	6.8	138.67	5	4.57	3.7	246
	2009	50	43.33	23.13	14.17	0	2.67	5.33	105.73	10.88	195.33	17.7	3.37	2.73	301.07
Tefiidzii	2008	84.84	65.34	51.27	36.6	0	2.74	4.67	162.67	3.87	157.34	7.7	4.24	3.1	320
	2009	117.33	100.33	29.67	18.83	0	2.4	4.83	125.33	8.33	269.33	18.47	20	3.07	394.67
Chiicha	2008	64.04	53	18.67	24.2	0.47	0.64	4.94	84.34	4.94	106.34	9.5	2.74	1.7	190.67

	2009	63.13	51.63	31.49	20.87	0.43	0.47	4.9	92.67	5.53	105.67	10.47	2.33	2.07	201.67
Lijalanii	2008	80	63.11	33.47	24.87	0	3.54	4.37	354.67	2.07	194.67	11.37	12.2	2.34	549.34
	2009	89	73.78	34.2	28	0	2.5	4.3	152.33	3.47	238	11	3.17	3.43	390.33

Varieties	Year	Plant height (cm)	Petiole length (cm)	Leaf Length (cm)	Leaf width (cm)	Number of infloresence	Number of suckers	Number of leaves	Corm weight (g)	Number of cormels	Cormel weight (g)	Corm girth (cm)	Length of corm (cm)	Breath of corm (cm)	Yield per plant (g)
Pajo	2008	53	40.34	33.34	22.27	0	0.27	5.07	82.67	3.2	80	6.54	3.14	1.44	162.67
	2009	60.33	46.67	30	21.93	3.33	1.57	5	54.67	5.8	89.33	14.4	3.13	1.87	144
Beidimai II	2008	71.27	53.8	35	23.8	0	1.07	4	70.34	7.87	171.34	5.7	4.84	2.04	241.67
	2009	80.53	62.07	32.43	22.13	0	2.27	4	340	7.03	331.67	23.32	2.47	1.5	671.67
Dziirienuo III	2008	72.34	56.25	26.87	20.2	0.54	0.4	5.37	268.67	0.74	136	5.47	4.24	2.9	404.67
	2009	82	64.67	24.67	17.3	0.53	0.7	5.367	201.67	10.62	252.5	12.62	3.93	2.73	454.17
	2008	51.57	39.74	23.9	29.27	0	0.24	5.37	90.2	3.4	81.3	15.67	4.54	4.07	171.5
Manie II	2009	67	55	41.93	30.47	0	0.17	5.367	89.3	2.67	77.5	4.66	4.53	4.07	171.5
Banu sam sam	2008	69.44	60.34	25.54	30.6	0	1.6	4.67	147.34	8.37	253.34	21.74	5.34	4.57	400.34
	2009	69.67	56.83	41.4	30.27	0	1.73	4.667	146	8.47	250	21.43	5.13	4.43	406
Bao	2008	34	23.34	12.97	30.47	0	0	4.47	132.67	0	273.34	8.34	6.1	3.5	405.67
	2009	37.47	26.43	39.6	29	0	0	4.433	141	0	295	8.1	6.07	3.5	436
Aiie	2008	52.67	40.24	46.27	31.6	0	1	5.1	156.44	8.24	122.67	10.97	5.57	3.64	279.1
	2009	63	48.43	44.4	31.53	0	1.07	5.033	155.77	8.37	125.33	11.1	5.57	3.43	281.1
Wolikhuo	2008	55.84	43.17	45.57	30.87	0	0.57	4.84	163.67	2.97	141.67	8.6	8.14	4.1	305.34
	2009	69.67	56.83	42.47	29.2	0	1	4.833	164.5	2.93	146.67	10.83	8.23	4.13	311.17
Tinopang	2008	61.67	47	47.64	29.27	0.5	0.77	4.64	106	4.1	143.67	4.34	4.77	3.14	249.67
	2009	76	63	39.73	28.07	0.33	0.63	4.63	97.17	4.3	164	4.2	4.33	3.17	261.17
Kotaknii	2008	71.04	60.5	34.04	31.67	0	1.94	4.5	91	4.84	113	5.64	5.27	3.3	204
	2009	73.27	58.5	43.13	30.93	0	1.7	4.5	88.23	5	125.33	5.2	5.03	3.43	213.57
Tino I	2008	81.64	72.5	46.77	39.74	0	3.24	4.84	150.34	3.47	159.67	4.8	5.77	3.04	310

	2009	92.47	76.53	55.67	37	0	2.83	4.73	148.33	3.3	154	4.93	5.43	3.07	246.87
Tino II	2008	64.8	55.8	26.94	24.6	0	1.1	4.5	130.67	1.74	286.67	20.2	4.87	1.77	417.34
	2009	66.07	53.93	31.47	23.67	0	1.67	4.53	140.67	2.43	183.33	19.23	3.17	2	324
Tino III	2008	58.97	41.3	42.3	34.74	0	0.8	5.1	107.67	9.7	244	6.07	4.4	3.47	351.67
	2009	68.77	51.73	45.33	31.2	0	0.73	5.1	112.67	9.8	255.33	6.53	6.53	4.3	368
Dziinuo V	2008	56.7	43.4	38.1	18.27	0	0.47	4.47	161.07	1.4	188	10.07	18.4	3.24	349
	2009	62.33	51.23	26.07	17.87	0	1.53	4.47	169.9	10.03	195.5	10.03	17.33	2.97	365.23

Varieties	Year	Plant height (cm)	Petiole length (cm)	Leaf Length (cm)	Leaf width (cm)	Number of infloresence	Number of suckers	Number of leaves	Corm weight (g)	Number of cormels	Cormel weight (g)	Corm girth (cm)	Length of corm (cm)	Breath of corm (cm)	Yield per plant (g)
Atsantu	2008	84.3	68.14	47.54	33.6	1.94	0	4.24	201	0	222.67	8.2	15.24	3.04	423.67
	2009	98.9	82.9	46.27	32.93	1.77	0	4.23	171.67	0	198.33	8.17	15.13	3.07	370
Wasii nii	2008	68.6	51.94	28.2	26.2	0.3	0.47	4.54	112.34	0.37	133.67	6.5	4.27	2.87	245
	2009	74.73	59.07	35.33	26.2	0.43	0.43	4.47	113.67	0.4	113.67	6.97	3.97	2.9	239.67
Manyii	2008	36.74	25.5	14.57	24.2	0	0	4.8	151	0	219.34	8.74	4.74	3.04	370.34
	2009	54.6	39.73	38.53	24.13	0	0	4.83	145	0	209.67	8.4	4.97	3.07	354.67
Tejongnii	2008	59.4	46.1	35.44	26.47	0	0.84	4.57	200	1.74	53.34	9.47	12.37	14.5	253.34
	2009	64.9	49.9	35.93	26.47	0	0.7	4.5	187.33	1.13	43.67	8.87	12.33	13.67	232
Chuyali	2008	65.7	46.74	31	23.6	0.47	0.6	4.74	122.67	0.44	136.67	5.9	4.6	2.84	259.34
	2009	72.2	57.93	33.07	24	0.2	0.47	4.8	131	0.37	130	5.9	3.9	2.77	261
Tong II	2008	61.3	41.77	39.3	38.34	0	0.54	4.6	109.34	6.1	229.34	5.77	4.27	3.17	338.67
	2009	66.87	49.9	50.6	38.27	0	0.4	4.5	110.33	5.93	124.33	5.73	5.33	3.23	234.67
Tong III	2008	64.9	50.24	34.24	26.67	0.2	0.27	4.67	131.34	0.4	122	5.44	4.54	2.34	250
	2009	71.2	59.53	39	26.67	0.3	0.2	4.63	125	0.3	135.33	5.6	3.13	2.5	260.33
Beizo	2008	61.97	45.3	33.24	25.67	0	0.17	4.27	256.34	0.14	36.67	10.74	12.57	13.44	293
	2009	99.33	84	34.47	25.67	0	0.2	4.27	255.33	0.2	48.33	11.6	11.63	13.73	303.67

Dziitii	2008	53.47	39.6	28.6	19.27	0.14	0.14	4.37	128.34	0.1	28.34	5.04	2.47	3.64	156.67
	2009	73.67	63.33	26.4	18.8	0.1	0.13	4.7	128.67	0.13	37.33	7.033	3.033	2.3	166
Grand mean	2008	61.04	46.08	34.59	28.09	0.19	1.07	4.76	144.89	4.02	163.81	8.14	6.09	3.23	307.23
	2009	71.76	56.77	32.56	23.53	0.33	1.22	4.76	144.21	5.86	194.35	13.89	6.35	3.55	338.7
	2008	2.62	2.52	2.33	2.11	0.45	0.81	0.52	5.00	0.92	6.66	1.46	0.54	0.53	7.23
S.Ed±	2009	8.57	8.48	3.20	2.53	0.42	0.50	0.27	34.56	1.67	50.97	1.49	3.02	0.78	72.81
	2008	2.81	2.7	2.49	2.26	0.48	0.86	0.56	5.35	0.99	7.13	1.56	0.58	0.57	7.74
C.D at 5%	2009	8.54	8.45	3.19	2.52	0.42	0.49	0.27	34.42	1.66	50.77	1.48	3.01	0.78	72.51
	2008	6.85	6.33	5.40	4.44	0.20	0.65	0.27	24.90	0.85	44.17	2.12	0.29	0.28	52.07
C.D at 1%	2009	9.82	9.72	3.67	2.90	0.49	0.57	0.31	39.61	1.92	58.42	1.70	3.46	0.90	83.44

Table 4.5. Estimates of Mean, range, Genotypic Co-efficient of variance(GCV), Phenotypic Coefficient of variance(PCV),Heritability in broad sense(h^2bs) and Genetic advance(GA) as percentage of mean during 2008

Characters	Mean ±S.E	Range	Variance			GCV(%)	PCV(%)	(h^2bs)	GA%
			GV	PV	EV				
Plant height	61.03 ±2.62	29.97 - 145.87	355.76	426.69	70.74	30.9	33.86	83.38	58.13
Petiole length	46.08 ±2.52	23.10 - 86.80	179.77	240.4	60.62	29.09	33.65	74.78	51.84
Leaf length	34.58 ±2.33	8.73 - 51.27	104.2	148.2	44.06	29.52	35.21	70.28	50.98
Leaf width	28.09 ±2.11	17.87 - 42.00	22.05	51.84	29.78	16.71	25.62	42.54	22.46
Number of inflorescence	0.19 ±0.45	0.13 - 2.60	0.21	0.27	0.06	246.53	278.6	78.30	449.39
Number of suckers	1 ±0.81	0.13 - 3.53	0.58	1.20	0.63	75.38	108.9	47.91	107.48
Number of leaves	4.75 ±0.52	4.00 - 6.1	0.11	0.22	0.11	6.83	9.83	48.26	9.78
Corm weight	144.89 ±0.92	72.00 - 354.67	3259	4196.37	937.37	39.4	44.71	77.66	71.53
Number of cormels	4.01 ±6.66	0.10 - 14.73	10.49	11.58	1.09	80.61	84.69	90.59	158.05
Cormel weight	163.8 ±1.46	28.33 - 292.22	4514.11	7463.68	2949.57	41.01	52.74	60.48	65.71
Corm girth	8.13 ±0.54	3.77 - 21.73	10.64	17.41	6.77	40.09	51.29	61.11	64.57
Length of corm	6.08 ±0.53	2.00 - 18.40	17.08	17.21	0.13	67.97	68.24	99.23	139.49
breath of corm	3.22 ±0.53	1.33 - 14.50	8.21	8.33	0.12	88.96	89.61	98.55	181.92
yield per plant	307.22 ±7.23	156.67-520.00	8294.18	12394.38	4100.2	29.64	36.24	66.92	49.95

Note: High GCV(%) and PCV(%) in Number of inflorescence is due to flower formation in only 13 genotype out of the total 50 genotypes.

Table 4.6 Estimates of Mean, range, Genotypic Co-efficient of variance(GCV), Phenotypic Coefficient of variance(PCV),Heritability in broad sense(h^2bs) and Genetic advance(GA) as percentage of mean during 2009.

Characters	Mean	Range	Variance			GCV(%)	PCV(%)	(h^2bs)	GA%
			GV	PV	EV				
Plant height	71.75 ±8.52	37.46-145.833	339.51	449.72	110.21	25.68	29.56	75.49	45.97
Petiole length	56.77 ±8.48	26.43-122.33	277.09	385.08	107.99	29.32	34.57	71.96	51.24
Leaf length	32.56 ±3.20	19.40-55.67	58.71	74.08	15.37	23.53	26.43	79.25	43.15
Leaf width	23.52 ±2.53	12.83-38.27	29.64	39.25	9.6	23.15	26.63	75.53	41.44
Number of inflorescence	0.32 ±0.42	0.10-3.33	0.38	0.65	0.27	189.92	247.65	58.81	300.03
Number of suckers	1.22 ±0.50	0.13-4.60	1	1.37	0.37	81.67	95.57	73.02	143.75
Number of leaves	4.75 ±0.27	4.00-6.06	0.1	0.22	0.11	6.91	9.83	49.42	10
Corm weight	144.21 ±34.56	32.67-340.00	4093	5885.38	1791.94	44.36	53.19	69.55	76.23
Number of cormels	5.86 ±1.67	0.13-13.87	16.87	21.06	4.19	70.05	78.27	80.11	129.17
Cormel weight	194.35 ±50.97	37.33-478.33	6149.42	10046.66	3897.24	40.35	51.57	61.21	65.02
Corm girth	13.88 ±1.49	4.20-25.73	35.97	39.28	3.31	43.21	45.15	91.58	85.18
Length of corm	6.35 ±3.02	2.47-20.00	14.76	28.47	13.71	60.52	84.04	51.86	89.78
Breath of corm	3.55 ±0.78	1.50-13.73	6.85	7.77	0.92	73.74	78.54	88.15	142.62
Yield per plant	338.7 ±72.81	144-815.33	14663.21	22614.16	7950.96	35.75	44.39	64.84	59.3

Note: High GCV(%) and PCV(%) in Number of inflorescence is due to flower formation in only 13 genotype out of the total 50 genotypes.

Table: 4.7. Estimates of Genotypic and Phenotypic correlation coefficients for 14 characters in Colocasia during 2008.

Characters	Plant height (cm)	Petiole length (cm)	Leaf Length (cm)	Leaf width (cm)	Number of inflorescence	Number of suckers	Number of leaves	Corm weight (g)	Number of cormels	Cormel weight (g)	Corm girth (cm)	Length of corm (cm)	Breath of corm (cm)	Yield per plant (g)
Plant height (cm)	G	0.95**	0.29*	0.46**	0.53**	0.55**	-0.18	0.144	-0.10	-0.01	-0.12	0.29*	0.03	0.10
	P	0.93**	0.27*	0.32**	0.42**	0.39**	-0.03	0.113	-0.09	0.03	-0.07	0.26*	0.03	0.09
Petiole length (cm)		G	0.35**	0.47**	0.54**	0.61**	-0.24*	0.22	-0.13	-0.06	-0.03	0.27*	0.04	0.09
		P	0.30*	0.29**	0.41**	0.41**	-0.04	0.15	-0.10	-0.03	0.05	0.23*	0.04	0.07
Leaf Length(cm)			G	0.35**	0.20	0.32*	-0.23*	0.02	0.21	-0.02	-0.18	-0.09	-0.02	0.01
			P	0.50**	0.19	0.44**	-0.18	0.06	0.18	-0.03	-0.12	-0.72**	-0.01	0.02
Leaf width (cm)				G	0.40**	0.16	-0.19	0.05	0.14	0.58**	0.01	0.08	-0.05	0.50**
				P	0.34**	0.40**	-0.13	0.08	0.08	0.27*	-0.01	0.05	-0.03	0.27*
Number of infloresence					G	-0.26*	-0.32*	0.32*	-0.32*	0.20	-0.08	0.43**	-0.08	0.29*
					P	-0.14	-0.15	0.27*	-0.27*	0.11	-0.06	0.37**	-0.07	0.25*
Number of suckers						G	0.04	0.03	0.36**	0.06	-0.03	-0.16	-0.15	0.07
						P	0.02	0.07	0.24*	0.07	-0.01	-0.11	-0.10	0.11
Number of leaves							G	-0.07	0.21	-0.13	-0.05	-0.23	-0.09	-0.20
							P	0.03	0.15	-0.04	-0	-0.15	-0.06	-0.47**
Corm weight (g)								G	-0.39**	0.07	0.22	0.52**	0.34**	0.65**
								P	-0.29*	0.03	0.13	0.46**	0.31*	0.60**
Number of cormels									G	0.21	-0.03	-0.35**	-0.27*	-0.11
									P	0.21	-0.02	-0.33**	-0.25*	-0.01
Cormel weight (g)										G	0.25*	0.01	-0.47**	0.80**
										P	0.16	0.01	-0.36**	0.81**
Corm girth girth(cm)											G	0.14	0.16	0.33**
											P	0.11	0.13	0.21
Length of corm (cmv)												G	0.44**	0.33**
												P	0.43**	0.27*
Breath of corm (cm)													G	-0.13
													P	-0.01

Yield per plant (g)														G
														P

*, ** Significant at 5 and 1% levels

Table: 4.8. Estimates of Genotypic and Phenotypic correlation coefficients for 14 characters in Colocasia during 2009

Characters	Plant height (cm)	Petiole length (cm)	Leaf Length (cm)	Leaf width (cm)	Number of inflorescence	Number of suckers	Number of leaves	Corm weight (g)	Number of cormels	Cormel weight (g)	Corm girth (cm)	Length of corm (cm)	Breath of corm (cm)	Yield per plant (g)
Plant height (cm)	G	0.99**	0.19	0.20	0.17	0.20	-0.07	0.21	-0.07	0.25*	-0.14	0.43**	0.05	0.25*
	P	0.97**	0.12	0.14	0.12	0.14	-0.06	0.12	-0.0	0.18	-0.11	0.32*	0.03	0.16
Petiole length (cm)		G	0.20	0.20	0.09	0.18	-0.07	0.13	-0.08	0.16	-0.20	0.41**	0.05	0.15
		P	0.13	0.15	0.09	0.13	-0.07	0.03	-0.27*	-0.07	-0.52**	0.10	0.12	-0.06
Leaf Length (cm)			G	0.97**	0.01	-0.18	-0.25*	0.05	-0.37**	-0.08	-0.60**	0.10	0.14	-0.05
			P	0.94**	-0.02	-0.12	-0.15	0.03	-0.19	-0.05	-0.47**	0.09	0.12	-0.04
Leaf width(cm)				G	0.02	-0.14	-0.31*	0.04	-0.27*	-0.05	-0.55**	0.08	0.16	-0.03
				P	0.01	-0.07	-0.19	0.10	-0.10	0.17	0.07	0.08	-0.15	0.17
Number of inflorescence					G	-0.02	0.09	-0.02	-0.08	0.25*	0.12	0.13	-0.21	0.16
					P	-0.01	0.01	-0.09	0.38**	0.16	0.25*	-0.11	-0.17	0.05
Number of suckers						G	0.05	-0.13	0.54**	0.27*	0.28*	-0.12	-0.21	0.08
						P	0.08	-0.27*	0.12	-0.04	-0.08	-0.09	-0.02	-0.17
Number of leaves							G	-0.47**	0.25	-0.09	-0.13	-0.16	-0.07	-0.30*
							P	-0.27*	0.12	-0.05	-0.08	-0.09	-0.02	-0.17
Corm weight(g)								G	-0.24*	0.44**	0.44**	0.50**	0.40**	0.81**
								P	-0.15	0.43**	0.38**	0.29*	0.29*	0.80**
Number of cormels									G	0.19	0.41**	-0.08	-0.23*	-0.0
									P	0.30*	0.38**	-0.05	-0.22	0.12
Cormel weight (g)										G	0.55**	0.32*	-0.28*	0.88**
										P	0.48**	0.16	-0.23	0.88**
Corm girth (cm)											G	0.044	-0.045	0.60**
											P	0.009	-0.046	0.52**
Length of corm												G	0.438	0.46**

(cm)												P	0.294	0.26*
Breath of corm (cm)													G	0.03
													P	-0.01
Yield per plant (g)														G
														P

*, ** Significant at 5 and 1% levels

Table: 4.9. Direct and indirect effects of different characters on corm yield per plant at genotypic level in colocasia during 2008.

Characters	Plant height (cm)	Petiole length (cm)	Leaf Length (cm)	Leaf width (cm)	Number of inflorescence	Number of suckers	Number of leaves	Corm weight (g)	Number of cormels	Cormel weight (g)	Corm girth (cm)	Length of corm (cm)	Breath of corm (cm)	Genotypic correlation for yield/plnt
Plant height (cm)	**0.00086**	0.20398	0.00886	-0.02884	-0.07657	-0.09649	0.00744	0.08865	-0.0009	-0.00468	0.00333	-0.01016	0.00095	0.10
Petiole length (cm)	0.00082	**0.21458**	0.01078	-0.0298	-0.07849	-0.10738	0.01242	0.13356	-0.00119	-0.05439	0.00084	-0.0094	0.0013	0.09
Leaf Length (cm)	0.00025	0.0749	**0.0309**	-0.02214	-0.02843	-0.056	0.01181	0.01166	0.00198	-0.01883	0.00501	0.00311	-0.00067	0.01
Leaf width (cm)	0.00039	0.10152	0.01086	**-0.06298**	-0.05804	-0.02792	0.00963	0.02986	0.00129	0.49473	-0.00052	-0.00266	-0.00156	0.50**
Number of inflorescence	0.00045	0.11546	0.00602	-0.02506	**-0.14588**	0.04626	0.01657	0.19698	-0.00301	0.10187	0.00239	-0.01505	-0.00264	0.29*
Number of suckers	0.00047	0.13037	0.00979	-0.00995	0.03818	**-0.17674**	-0.00191	0.01985	0.00337	0.05929	0.00073	0.00572	-0.00528	0.07
Number of leaves	-0.00012	-0.05193	-0.00711	0.01181	0.04708	-0.00657	**-0.05134**	-0.04004	0.00193	-0.11112	0.00142	0.00796	-0.00306	-0.20
Corm weight (g)	0.00012	0.04642	0.00058	-0.00305	-0.04655	-0.00568	0.00333	**0.61736**	-0.00363	0.05518	-0.00621	-0.01848	0.01155	0.65**
Number of cormels	-0.00008	-0.02718	0.00652	-0.00863	0.04667	-0.06338	-0.01052	-0.23841	**0.0094**	0.17601	0.00082	0.01241	-0.00905	-0.11
Cormel weight (g)	0	-0.01364	-0.00068	-0.03642	-0.01737	-0.01225	0.00667	0.03983	0.00193	**0.85545**	-0.00703	-0.00014	-0.0161	0.80**
Corm girth (cm)	-0.0001	-0.00631	-0.00545	-0.00115	0.01227	0.00452	0.00256	0.13488	-0.00027	0.21153	**-0.02842**	-0.0049	0.00557	0.33**
Length of corm (cm)	0.00025	0.05723	-0.00273	-0.00475	-0.0623	0.02871	0.0116	0.32383	-0.00331	0.0033	-0.00395	**-0.03523**	0.01489	0.33**
Breath of corm (cm)	0.00002	0.0082	-0.00061	0.0029	0.01135	0.0275	0.00463	0.20989	-0.0025	-0.40553	-0.00466	-0.01545	**0.03397**	-0.13

Residual= 0.06

Table: 4.10 Direct and indirect effects of different characters on corm yield per plant at genotypic level in colocasia during 2009.

Characters	Plant height (cm)	Petiole length (cm)	Leaf Length (cm)	Leaf width (cm)	Number of inflorescence	Number of suckers	Number of leaves	Corm weight (g)	Number of cormels	Cormel weight (g)	Corm girth (cm)	Length of corm (cm)	Breath of corm (cm)	Genotypic correlation for yield/plnt
Plant height (cm)	**-0.11156**	0.10322	-0.01515	0.00854	0.00165	-0.00752	0.00053	0.10801	-0.00082	0.17024	0.00133	-0.00658	0.00099	0.25*
Petiole length (cm)	-0.11077	**0.10396**	-0.01537	0.00874	0.00081	-0.00701	0.00053	0.0691	-0.00087	0.10562	0.00192	-0.00639	0.00098	0.15
Leaf Length(cm)	-0.02141	0.02024	**-0.07894**	0.0419	0.00008	0.00693	0.00185	0.02641	-0.00411	-0.05593	0.00568	-0.0016	0.00261	-0.05
Leaf width (cm)	-0.02208	0.02106	-0.07668	**0.04314**	0.00023	0.00532	0.00229	0.02306	-0.00297	-0.03312	0.00522	-0.00116	0.00285	-0.03
Number of infloresence	-0.01922	0.00884	-0.00064	0.00105	**0.00957**	0.00093	-0.00069	-0.00967	-0.00084	0.1725	-0.0011	-0.00208	-0.00386	0.15
Number of suckers	-0.0218	0.01894	0.01423	-0.00597	-0.00023	**-0.03847**	-0.00036	-0.067	0.00597	0.18234	-0.00265	0.00187	-0.00396	0.08
Number of leaves	0.00792	-0.0073	0.01947	-0.01317	0.00087	-0.00182	**-0.00751**	-0.24641	0.00276	-0.06177	0.00122	0.00239	-0.00129	-0.30*
Corm weight (g)	-0.02317	0.01381	-0.00401	0.00191	-0.00018	0.00495	0.00356	**0.52014**	-0.0027	0.29863	-0.00413	-0.00764	0.00719	0.81**
Number of cormels	0.00831	-0.00819	0.0293	-0.01156	-0.00073	-0.02075	-0.00187	-0.12712	**0.01107**	0.12673	-0.00385	0.0012	-0.00433	0
Cormel weight (g)	-0.0279	0.01613	0.00649	-0.0021	0.00242	-0.0103	0.00068	0.22818	0.00206	**0.68073**	-0.00521	-0.00498	-0.00511	0.88**

Corm girth (cm)	0.01572	-0.02121	0.04764	-0.02391	0.00112	-0.01082	0.00098	0.22822	0.00453	0.37654	**-0.00941**	-0.00068	-0.00083	0.60**
Length of corm (cm)	-0.04779	0.04326	-0.00824	0.00327	0.00129	0.00469	0.00117	0.25896	-0.00087	0.22065	-0.00042	**-0.01535**	0.00796	0.46**
Breath of corm (cm)	-0.00609	0.00559	-0.01137	0.00678	-0.00203	0.0084	0.00053	0.20596	-0.00264	-0.19172	0.00043	-0.00673	**0.01815**	0.03

Residual= 0 .03

Table 4.11 Clustering pattern of 50 genotypes on the basis of genetic divergence in Colocasia during 2008.

Clusters	No of genotypes	Genotypes	Place of collection
I	2	Waipong,Tejongnii	Peren, Mokokchung
II	13	Chugoma,Bei I,Beithola,Dziirinuo I, Tephfii dziinuo, Ati,Obei, Dziinuo I, Thegabeizii,Beidimai I, Loudoubei, Wasii nii,Chuyali,	Zunheboto(2),Peren(3),Phek, Kohima (5),Dimapur, Mokokchung
III	2	Dziirinuo II, Tong I	Dimapur, Mon
IV	6	Dzii Dziinuo, Manie I,Dziinuo II,Thupela,Tino III,Tong II	Dimapur(2), Wokha,Kohima,Tuensang,Mon
V	2	Beyo, Pajo	Phek, Wokha
VI	19	Dziinuo III,Keriila,Sama,Dziinuo IV,Bei II,Tefiidzii,Chiicha,Lijalanii,Beidimai II,Dziirinuo III,Manie II,Banu sam sam,Bao,Aiie,wolikhuo,Tinopang,Kotaknii,Tino I,Tino II	Dimapur(3),Kohima(5),Phek,Mokokchung(2),Peren,Wokha,Kiphira(2),Zunheboto,Longleng,Tuensang(2).
VII	2	Manyii,Tong III	Mokokchung,Mon
VIII	2	Dziinuo4,Atsantu	Dimapur,Kohima
IX	1	Beizo	Phek
X	1	Dziiti	Dimapur
Total	50		

Table 4.12 .Clustering pattern of 50 genotypes on the basis of genetic divergence in Colocasia during 2009.

Clusters	No of genotypes	Genotypes	Place of collection of genotypes with number
I	2	Wasiinii, Chuyali	Mokokchung(1),Zunheboto(1)
II	2	Tinopang, Kotaknii	Longleng(1), Mokokchung(1)
III	2	Manie I, Tong I	Wokha(1), Mon(1)
IV	2	Manyii,Tong III	Mokokchung(1), Mon(1)
V	2	Obei, Dziinuo I	Dimapur(1),Kohima(1)
VI	2	Ati, Dziinuo II	Dimapur(1),Kohima(1)
VII	14	Waipong, Chugoma, Bei I, Beithola, Dziirinuo I, Tephfii dziinuo, Thegabeizii, Beidimai I, Loudoubei, Dzii Dziinuo, Dziirinuo II, Thupela, Sama, Banu sam sam.	Peren(3), Zunheboto(1),phek(1), Kohima(5), Dimapur(3), Kiphire (1)
VIII	21	Dziinuo III, Keriila,Sama,Beyo, Dziinuo IV,Tefiidzii,Chiicha, Lijalanii, Pajo, Beidimai II, Dziirinuo III, Manie II,Bao,Aiie, Wolikhuo,Kotaknii,Tino I,Tino II, Tino III,Dziinuo V,Atsantu,Tong II,	Dimapur(4)Kohima(5), Phek(1),Mokokchung(2), Wokha(2), Peren(1),Kiphire(1), Zunheboto(1),Tuensang(3), Mon(1)
IX	3	Tejongnii, Beizo, Dziitii	Mokokchung(1),Phek(1), Dimapur(1)
Total	50		

Table: 4.13 Average intra and inter Cluster distance in Colocasia during 2008

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX	X
I	3.93 (1.98)	2205.16 (46.96)	2565.57 (50.65)	2056.18 (45.34)	2451.39 (49.51)	1917.13 (43.79)	1981.79 (44.76)	1308.52 (36.17)	26.72 (5.17)	2096.85 (45.79)
II		387.99 (19.69)	241.48 (15.54)	375.43 (19.38)	240.67 (15.51)	323.19 (17.98)	218.86 (14.79	1469.06 (38.33)	2061.61 (45.41)	274.24 (16.56)
III			14.178 (3.77)	286.99 (16.94)	29.91 (5.47)	237.98 (15.43)	111.32 (10.55)	1838.82 (42.88)	2441.52 (49.41)	95.4 (9.77)
IV				404.16 (20.14)	296.31 (17.85)	318.44 (17.85)	238.97 (15.46)	1327.87 (36.44)	1922.61 (43.85)	349.42 (18.69)
V					22.015 (4.69)	223.45 (14.95)	91.35 (9.56)	1818.79 (42.65)	2329.95 (48.27)	58.35 (7.64)
VI						271.26 (16.47)	178.72 (13.37)	1309.39 (36.19)	1787.34 (42.27)	243.62 (15.61)
VII							41.82 (6.45)	1361.49 (36.89)	1828.69 (42.76)	75.34 (8.68)
VIII								156.26 (12.5)	1098.97 (33.15)	1801.12 (42.44)
IX									0 0	1974.09 (44.43)
X										0 0

D values are in parenthesis.

Table 4.14. Average intra and inter Cluster distance in colocasia during 2009

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX
I	3.94 (1.98)	15.34 (3.92)	104.97 (10.25)	10.09 (3.18)	100.37 (10.02)	105.97 (10.29)	116.09 (10.77)	68.67 (8.29)	130.26 (11.41)
II		6.13 (2.48)	100.90 (10.05)	23.89 (4.89)	118.34 (10.88)	101.74 (10.09)	133.30 (11.55)	70.53 (8.40)	141.33 (11.89)
III			9.83 (3.14)	126.77 (11.26)	38.68 (6.22)	17.48 (4.18)	73.63 (8.58)	87.55 (9.36)	212.44 (14.58)
IV				10.32 (3.21)	118.25 (10.87)	131.77 (11.48)	128.43 (11.33)	79.49 (8.916)	146.41 (12.1)
V					10.77 (3.28)	33.82 (5.82)	72.94 (8.54)	97.61 (9.88)	189.88 (13.78)
VI						12.15 (3.49)	76.16 (8.73)	87.63 (9.36)	194.34 (13.94)
VII							102.73 (10.14)	115.23 (10.73)	189.24 (13.76)
VIII								95.91 (9.79)	173.65 (13.18)
IX									134.88 (11.65)

Table: 4.15. Cluster wise mean value of 14 characters in Colocasia during 2008.

Cluster no	Plant height (cm)	Petiole length (cm)	Leaf Length (cm)	Leaf width (cm)	Number of inflorescence	Number of suckers	Number of leaves	Corm weight (g)	Number of cormels	Cormel weight (g)	Corm girth (cm)	Length of corm (cm)	Breath of corm (cm)	Yield per plant (g)
I	59.80	45.88	34.08	26.41	0.00	0.92	4.78	199.33	1.77	46.67	9.03	12.37	14.32	246.00
II	55.31	41.25	36.68	26.59	0.29	0.78	4.82	154.05	4.20	160.64	8.23	5.15	2.17	309.18
III	45.11	35.00	43.87	30.60	0.13	1.50	4.467	90.667	5.50	148.00	6.82	3.03	1.48	238.67
IV	52.03	36.97	31.79	32.89	0.00	0.79	4.80	137.83	6.31	259.33	6.67	6.09	2.29	397.17
V	59.42	43.58	31.23	21.10	0.00	1.03	5.07	87.833	3.43	92.67	6.20	3.05	1.80	181.33
VI	70.20	53.94	34.04	29.38	0.16	1.45	4.79	138.43	4.48	166.02	8.82	5.56	2.90	304.43
VII	50.82	37.87	24.40	25.43	0.10	0.13	4.73	141.17	0.20	170.67	7.08	4.63	2.68	310.17
VIII	70.50	55.77	42.82	25.93	0.97	0.23	4.35	181.03	0.70	205.33	9.13	16.82	3.13	386.33
IX	61.97	45.30	33.23	25.67	0.00	0.17	4.27	256.33	0.13	36.67	10.73	12.57	13.43	293.00
X	53.47	39.60	28.60	19.27	0.13	0.13	4.37	128.33	0.10	28.33	5.03	2.47	3.63	156.67
Contribution %	1.14	0.90	1.39	1.06	0.33	0.41	0.65	1.31	12.41	3.02	2.29	21.06	8.16	45.88

Table: 4.16. Cluster wise mean value of 14 characters in Colocasia during 2009.

Cluster no	Plant height (cm)	Petiole length (cm)	Leaf Length (cm)	Leaf width (cm)	Number of inflorescence	Number of suckers	Number of leaves	Corm weight (g)	Number of cormels	Cormel weight (g)	Corm girth (cm)	Length of corm (cm)	Breath of corm (cm)	Yield per plant (g)
I	73.47	58.5	34.2	25.10	0.32	0.45	4.63	122.33	0.38	121.83	6.43	3.93	2.83	250.33
II	74.63	60.75	41.43	29.50	0.17	1.17	4.57	92.70	4.65	144.67	4.70	4.68	3.30	237.36
III	61.67	47.00	30.97	25.05	0.17	2.73	4.50	109.83	11.58	268.72	18.92	5.25	2.22	378.56
IV	62.90	49.63	38.77	25.40	0.15	0.10	4.73	135.00	0.15	172.50	7.00	4.05	2.78	307.50
V	53.33	37.00	20.07	12.96	0.00	0.90	4.88	66.60	7.00	122.00	17.27	3.70	3.02	188.60
VI	72.75	61.17	30.47	24.43	0.50	1.45	4.62	111.89	13.08	210.28	17.90	3.90	2.57	322.17
VII	65.61	49.68	28.69	21.00	0.46	1.29	4.83	168.98	6.56	243.11	18.92	7.01	3.82	412.67
VIII	77.78	62.74	35.14	25.03	0.37	1.39	4.80	142.70	6.01	195.45	12.24	6.72	2.90	337.47
IX	79.30	65.74	32.27	23.64	0.03	0.34	4.49	190.44	0.49	43.11	9.17	9.00	9.90	233.89
Contribution %	4.00	0.16	1.88	1.06	2.53	4.98	1.71	2.29	15.27	7.76	31.92	1.96	8.25	16.25