GENETIC DIVERGENCE STUDIES THROUGH MULTIVARIATE ANALYSIS AND MOLECULAR MARKER IN TURMERIC (*Curcuma longa* L.)

Thesis submitted in part fulfillment of the requirements for the degree of
DOCTOR OF PHILOSOPHY IN HORTICULTURE
to the Tamil Nadu Agricultural University, coimbatore.

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CERTIFICATE

This is to certify that the thesis entitled **"GENETIC DIVERGENCE STUDIES THROUGH MULTIVARIATE ANALYSIS AND MOLECULAR MARKER IN TURMERIC** (*Curcuma longa* L.)" submitted in partfulfillment of the requirements for the degree of **Doctor of Philosophy in Horticulture** to the Tamil Nadu Agricultural University, Coimbatore is a record of *bonafide* research work carried out by **Miss. K.R.VIJAYALATHA** under my supervision and guidance and that no part of her thesis has been submitted for the award of any degree, diploma, fellowship or other similar titles or prizes and that the work has not been published in part or full in any scientific or popular journal or magazine.

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(K.R.Vijayalatha)

Abstrac

ABSTRACT

GENETIC DIVERGENCE STUDIES THROUGH MULTIVARIATE ANALYSIS AND MOLECULAR MARKER IN TURMERIC (*Curcuma longa* L.)

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Turmeric genotypes (two twenty three) were investigated for the extent of genetic diversity, extent of variability, heritability, genetic advance, correlation of components on rhizome yield and quality at Department of Spices and Plantation Crops, Horticultural College and Research Institute, TNAU, Coimbatore during 2000-2002.

A significant level of variability was established for most of the biometric characters except quality characters (curcumin, essential oil and oleoresin).

The genetic diversity assessed by D^2 statistic and K-means clustering for 22 quantitative traits exhibited significant contribution of these characters towards divergence. The cluster mean in conjunction with inter and intra cluster distance interpreted yield, weight of primary and secondary rhizomes as the major contributing characters that need to be emphasized during selection programme.

The principal component analysis (PCA) revealed 80 per cent total variability by three components of which weight of primary and secondary rhizomes contributed for more variation.

The traits yield, girth of secondary rhizomes, weight of primary and secondary rhizomes expressed higher order of GCV coupled with high heritability and genetic gain

suggesting additive gene action to be exploited for improvement of genotypes in turmeric. The correlation study established that all biometrical traits except oil, oleoresin, rhizome-core ratio, curcumin, number of mother rhizomes and curing percentage are amenable for simultaneous improvement. Path analysis projected girth of secondary rhizomes, breadth of leaf, weight of primary and secondary rhizomes and core diameter as dominating contributors towards yield.

The genetic diversity was assessed for 30 genotypes to detect variations at morphological and DNA level (RAPD marker). The clustering pattern based on 22 quantitative traits and RAPD markers revealed considerable level of congruence among them. The RAPD profiles revealed 68.5 per cent polymorphism and 4 primers (OPB 08, OPC 20, OPE 09 and OPG 19) showed more than 90 per cent polymorphism while OPC 18 was completely monomorphic. All the genotypes were found susceptible to the pest (scale) and disease (leaf spot) with variation in degree of tolerance. Both pest and disease exerted non-significant correlation with yield.

Introductio

CHAPTER I

INTRODUCTION

Turmeric of commerce is the dried rhizome of *Curcuma longa* L. (syn. *Curcuma domestica* Val.) belonging to the family Zingiberaceae that traces its origin to tropical rain forests of South East Asia. Turmeric, the Indian saffron, is cultivated throughout the length and breadth of the country (Thampi, 1997). It is mainly valued for its coloring constituent, the 'curcumin'. Being a unique natural dye, curcumin imparts color (Zachariah and Babu, 1992) and is indispensable in food industry, confectionary, pharmaceuticals and cosmetics as well. Awareness has propped up for the intrinsic quality of the natural ones replacing the synthetic coloring materials and has put in demand, the turmeric, as whole and value added products.

Turmeric occupies a dominant position due to its matchless properties accounting for 70 per cent of global production. India is a major exporter to a tune of 21600 t, which earned a foreign exchange of Rs.54.71 crores (Rajeshkumar, 1998). States like Andhra Pradesh, Tamil Nadu, Orissa, Karnataka, Kerala, Maharashtra and West Bengal are in the forefront in turmeric cultivation. In Tamil Nadu, Erode, Coimbatore, Salem and Namakkal are the major contributing districts accounting for 85 per cent production (Anon., 1997).

Turmeric is vegetatively propagated and hence systematic efforts on introduction and evaluation of improved varieties have not been undertaken consistently. The varietal improvement work so far attempted is only through selection and to a limited extent, mutations since hybridization is impossible due to sterility.

The commercial types are sterile triploids of *Curcuma longa* L. (3n = 63) and the cultivars of *Curcuma aromatica* are tetraploids (2n = 84), which set seed. With recently reported success of viable seed set in turmeric (under Kerala conditions) recombination breeding programme can take shape in this clonally propagated crop (Sasikumar *et al.*, 1994).

The first step in the improvement of this clonally propagated crop is to exploit the already existing land race variability and create more variability through mutation and somaclonal variation. The simpler approach to create new genotypes is to take advantage of the available genetic diversity and document clear-cut information on the extent of genetic diversity available. Till date, genetic improvement of the crop have been enforced conventionally and pivotal to these improvement efforts, is the collection and evaluation of its germplasm.

For any selection programme, it is useful to have information on the causative factors of genetic diversity. As all the characters do not contribute equally to yield, the researchers evince keen interest in studying few important traits at greater length. When intercorrelations exist, multiple regression analysis gives biased estimates in identification of characters affecting yield. So the crop improvement programme should focus to build up a rigorous basis for choice of traits.

The extent of genetic diversity among the genetic materials was estimated by adopting various methods over a period of time. Based on the knowledge of biometrics and genetics, tools like variance component analysis, D^2 statistic, non-hierarchial clustering, principal component analysis in assessing variability, are effective in reducing the environment effect substantially and projecting the real genetic effects and discrimination of better genotype. However, the existence of multiple local names and lack of authentic identity of materials have narrowed the genetic background. Distinguishing the genotypes solely based on morphological traits is cumbersome owing to ontogeny.

The recent developments in the field of molecular biology provide splendid possibilities in developing high yielding varieties with durable resistance to pest and disease. The advent of molecular markers has opened up new avenues that could revolutionize and hasten the traditional breeding programmes. The universal acceptance of PCR based markers have geared up the use of molecular markers, more specifically DNA based markers that are valid in assessing genetic diversity as they reflect on the genetic structure that is stable and detectable during all stages, thus giving new dimensions to concerted efforts of breeding.

It is imperative to conduct elaborate research involving conventional and molecular techniques for monitoring the genetic variability.

Considering the above issues, the study was formulated with the following objectives.

1. estimate the extent of genetic variability in the available germplasm for various traits.
2. assess the magnitude of diversity in the germplasm by multivariate statistics.
3. assess the genetic diversity at molecular level using RAPD marker.
4. reduce the number of attributes of importance to essential ones.
5. comprehend the nature of association among the attributes.
6. screening the genotypes for resistance to disease (leaf spot) and pest (scale).

Review of Literature

CHAPTER II

REVIEW OF LITERATURE

Turmeric is one of the ancient and sacred versatile natural products combining the properties of a spice, cosmetic and a drug. In recognition of the importance of turmeric as a whole and value added product, emphasis in evolving new varieties with high yield and quality have been on the forefront. Though, research has been focused on the genetic variability, crop improvement and quality in this clonally propagated crop, estimation of genetic variation between genotypes within germplasm collections, within geographical areas are targeted towards deliberate selection for genetic homogeneity.

In conjunction with the earlier research carried out, a brief review on the crop improvement is outlined in this chapter.

1.Variability

2. Genetic diversity studies

3. Heritability and Genetic Advance

4. Correlation

5. Path coefficient analysis

6.Screening studies against leaf spot disease and scale insect.

2.1 Variability

2.1.1. Height of the plant

Muralidharan and Ramankutty (1976) found that there was not much variation among the aerial parts except on the height of turmeric. Shah *et al.* (1982) reported that plant height ranged between 40.10 and 59.20 cm in CO1 cultivar.

Philip (1983) recorded the highest plant height (41.00 cm) in the cultivar Chayasupa followed by Amruthapani Kothapeta (40.00 cm) and Nandyal (40.00 cm), whereas the lowest height was recorded in the case of NBPGRT 17 (21.00 cm).

Philip and Nair (1983) observed the highest plant height in case of Chayasupa (41.10 cm) closely followed by Nandyal (40.20 cm).

Balashanmugam *et al.* (1986) found that the plant height varying from 41.40 to 106.20 cm in BSR 1 cultivar. Pujari *et al.* (1986) recorded plant height that varied from 86.00 to 150.00 cm in the cultivar Krishna. Ratnambal and Nair (1986) observed plant height of 69.40 in cultivar PCT 8 cultivar over PCT 2. Satyanarayana and Reddy (1986) reported considerable variations in plant height and among the sixteen varieties studied CII 325 recorded the highest. Pujari *et al.* (1987) recorded a higher plant height of 84.43 cm in cv. Krishna and lower in Duggirala (59.87 cm).

According to Jalgaonkar *et al.* (1988), cultivar Sugandham was found to be the tallest (111.47 cm) followed by Allepey (107.00 cm) and Waigon was the shortest (80.90 cm). Reddy *et al.* (1989) found that the highest plant height was observed in PCT 8 (35.70 cm) among the short duration cultures screened under Andhra Pradesh conditions and the least in PCT 10 (19.10 cm).

In a study under coastal regions of Karnataka, PCT 8 registered a plant height of 98.50 cm and the least in M 221 (46.26 cm), (Indiresh *et al.*, 1990). In an evaluation programme, Cholke (1993) found that the highest plant height in CO1 (55.22 cm) followed by Bidar 4 (53.00 cm) and least in PCT 13 (20.65 cm).

Sheshagiri and Uthaiah (1994) opined that BSR 1 were taller and was significantly superior over other varieties tested. Radhakrishnan *et al.* (1995) reported that the plants of BSR 1 were the tallest (48.25 cm) among the varieties studied.

Plant height exhibited significant differences among the turmeric types; the tallest plant was observed in VK 146 (141.67 cm), (Kurian and Valsala, 1995). Ramakrishna *et al.* (1995) indicated that the variety PCT 13 recorded the tallest plant (95.30 cm) while that PCT 10 was the shortest (47.70 cm).

Kurian and Nair (1996) pointed that plant height alone exhibited significant deviation among the traits studied. Highest plant height was recorded in VK 112

(156.00 cm) followed by VK 99 (141.00 cm). Rajeshkumar and Jain (1998) opined that Roma was the tallest one (103.00 cm) followed by Suroma (102.67 cm) and Sonali (92.00 cm) under plateau regions of Bihar. Shanmugasundaram (1998) found that PTS 43 was the tallest (102.85 cm) and the lowest in VK 5.

2.1.2. Number of tillers

Pillai and Nambiar (1975) recorded 2-3 tillers in longa types. Subbarayudu *et al.* (1976) were of the opinion that there was no significant difference in tiller production among short and medium duration types, whereas marginal differences were observed in long duration types. Shah *et al.* (1982) noted 3.70 to 5.00 tillers per plant in the case of CO1 cultivar.

According to Philip (1983), Mannuthy local recorded more number of tillers per plant (3.40) and the lowest in Dindrigram (2.15). Satyanarayana and Reddy (1986) obtained greater number of tillers in the clone Cls 3D (3.20) and the least in CII 326 (1.20).

Reddy *et al.* (1989) could not find significant differences in tiller production among the short duration cultures. The culture PCT 8 showed the highest number of tillers (1.40) and the least in Kasturi (0.40). Cholke (1993) registered for the cultivar Rajapuri, the highest number of tillers (7.15) and it was of the lowest order in PCT 14 (0.85) and PCT (0.86).

Sheshagiri and Uthaiah (1994) found that the number of tillers was larger in BSR 1 and CO1 (3.50 each). Venkatesha (1994) had reported that the variety BSR 1 (5.36) expressed the highest number of tillers followed by CO1 whereas the PCT 13 exhibited the least number of tillers (2.93). Kurian and Valsala (1995) found the highest number of tillers per plant in VK 5.

Patil *et al.* (1995) reported that the cultivar Suvarna possessed the largest number of tillers (4.76) however it was found to be inferior to other cultivars with regard to other attributes. The various cultivars of turmeric did not exhibit any significant deviation with respect to tiller production. (Philip and Nair,1983; Jalgaonkar *et al.,* 1988; Indiresh *et al.,* 1990; Ramakrishna *et al.,* 1995; Kurian and Nair, 1996).

2.1.3. Number of leaves

Rao *et al.*(1975) observed 8-9 leaves per plant in the variety Dindrigram. Pillai *et al.* (1976) reported that the longa types produced 9-12 leaves per plant in CO1 cultivar. Duggirala showed that the highest number of leaves (21.00) and the lowest in Mannuthy local (5.60) (Philip,1983).

Philip and Nair (1983) found that the number of leaves per plant ranged between 11.20 in Ca 89 and 20.70 in Mannuthy local under Kerala conditions. Pujari *et al.* (1987) in an evaluation trial observed that the variety Tekurpeta produced the highest number of leaves per plant (8.66) while it was the least in case of Sugandham (8.13) under Maharashtra conditions.

Jalgaonkar *et al.* (1988) observed significant variation in the leaf number per plant. The leaf number was more in case of Erode cultivar (18.70) followed by Allepey (17.30). On the other hand, it was lowest in Waigon (11.70) under Konkan conditions of Maharashtra. According to Reddy *et al.* (1989) the leaf number varied from 8.27 in PCT 11 to 7.10 in PCT 5 among the short duration types.

Studies by Indiresh *et al.* (1990) on the number of leaves under coastal regions of Karnataka have indicated that Sugandham produced more leaves (24.88) followed by Duggirala (24.66). In contrast, very low number of leaves was seen in PCT 8 (16.59). Hegde (1992) observed the highest number of leaves per main shoot in the cultivar Cuddapah and Bidar (9.10) and the lowest in Moovattupuzha (6.93). Much higher value for number of leaves were recorded in Rajapuri (33.20) under Northern transition region of Karnataka (Cholke,1993).

Sheshagiri and Uthaiah (1994) found that the number of leaves per clump was high in BSR 1 (17.10) followed by Waigon (14.90). Kurian and Valsala (1995) were of the opinion that the number of leaves were high in VK 5. The highest number of leaves

(6.16) was reported in BSR 1 by Patil *et al.* (1995). Ramakrishna *et al.* (1995) reported that the variety PCT 13 exhibited significant highest score in Reshmi, which was on par with Suroma, and Morangia (Rajeshkumar and Jain,1998). Shanmugasundaram (1998) recorded more number of leaves in PTS 43 (25.56).

2.1.4. Leaf area

Philip and Nair (1983) reported significant variation in leaf area that varied from 696.60 cm^2 in Armoor CII 324 to 1214.3 cm^2 in Amruthapani of the 19 types studied in Kerala. Pujari *et al.* (1987) noticed larger leaves with greater breadth (18.53 cm) and leaf area (1177.10) dm^2 per plant in an improved land race, Tekurpeta. The highest leaf length was observed in Krishna (49.20 cm) whereas Duggirala produced the smallest leaves (36.59 cm length and 12.85 cm breadth and 614.71 cm^2 leaf area per plant).

Jalgaonkar *et al.* (1988) noticed significant variation in leaf area among the different cultivars of turmeric tested. The highest leaf area was recorded in Salem local (433.23 cm^2) and the least in case of Waigon (256.23 cm^2). Reddy *et al.* (1989) found the highest leaf area in PCT 11 and the least in case of PCT 13 and PCT 10.

Kurian and Valsala (1995) noticed the highest leaf length and breadth in VK 5 cultivar. Similarly, Kurian and Nair (1996) reported on the possession of lengthy leaves in VK 112 and the broadest leaf was found in the cultivar VK 121. The larger leaf area (529.00 cm^2) was recorded in Sonali (Rajeshkumar and Jain, 1998). Shanmugasundaram, 1998 found greater leaf area in PTS 43 (602.39 cm^2) and lower in RH 5 (172.57 cm^2).

2.1.5. Mother rhizome

Muthuswamy and Shah (1982) reported the circumference (girth) of mother rhizome were similar in both Salem and Erode local types. Philip and Nair (1983) recorded that the girth at the centre of mother rhizome varied from 11.5 cm in Armoor Ca 324 to 17.3 cm in Kodur. Indiresh *et al.* (1990) found the largest mother rhizome in PCT 8 and the smallest in Duggirala.

Hegde (1992) noticed the largest mother rhizome in Rajapuri and the smallest in Moovattupuzha. Cholke (1993) recorded significant variation in girth and number of mother rhizomes in different cultivars of turmeric. Bidar 4 produced more number of mother rhizomes (3.85) followed by CO1 (2.87) and the least by PCT 13 (1.10). The highest girth was observed in PCT 8 (11.70 cm) followed by Rajapuri (11.62 cm) and the least in PCT 14 (9.21 cm).

2.1.6. Primary rhizome

Dhandar and Varde (1980) registered the highest length of finger in clone C1-FC (10.30 cm) and the least in clone C1-204 (7.40 cm). The girth of the finger varied from 4.00 - 9.00 cm in C1-24 D to 8.00 cm in C1-94 under Goa conditions. Philip and Nair (1983) reported that the number of primary fingers per plant varied from 4.20 in Tekurpeta to 7.20 in Mannuthy local and their girth varied from 7.10 in Dindrigram to 10.50 cm in Chayasupa. The number of nodes per primary finger varied narrowly from 9.10 in Rajapuri to 11.90 in Kuchupudi and the internodal length varied from 0.79 cm in Duggirala to 1.11 cm in Dindrigram.

Jalgaonkar *et al.* (1988) could not establish any significant differences in the weight of primary fingers per plant however significant variation in the length ranging between 5.62 cm in Salem and 9.04 cm in Krishna were observed. The girth was the highest (8.32 cm) in Kasthuri and the lowest (6.19 cm) in case of Erode local. Reddy *et al.* (1989) indicated in his study among the various short duration cultivars, the number of primary fingers were more in PCT 8 (8.20) followed by PCT 5 (7.30) and the least in PCT 12 (4.50).

Indiresh *et al.* (1990) recorded the highest number of primary fingers per plant (8.61) in PCT 8 followed by Chintamani (7.22) and the least in Duggirala (4.16). They also observed the longest primary finger in PCT 8 (9.91 cm) and the shortest in Erode local (5.50 cm). While the girth of the primary finger was the highest in PCT 8 (10.08 cm) and it was the least (6.24 cm) in Duggirala. Nandi (1990) reported that Cls 9 produced the highest number of fingers per plant (18.93) followed by PTS 25 (18.87) and the lowest in case of local (5.00). In addition, it recorded higher finger length of 9.11 cm and the least in Cls 2 (6.75 cm).

According to Hegde (1992), cultivar BSR 1 registered the highest number of primary fingers (13.00) and the land race Moovattupuzha (3.26), the least. He also noticed the longest finger length of 9.07 cm in Amalapuram and the shortest in 46 T (3.17 cm). The girth of finger was the greatest in Rajapuri (7.86 cm) while it was the least in Moovattupuzha (5.03 cm).

Cholke (1993) reported the highest number of primary fingers (9.80) in cultivar Amalapuram followed by Cuddapah (8.85) and Bidar (8.80) and the lowest number in PCT 13 (3.20). Further, the length and girth of primary fingers varied from 5.77 cm in Rajapuri to 9.22 cm in Cuddapah and 6.72 cm in BSR 1 to 8.51 cm in Rajapuri respectively under Dharwad conditions.

Sheshagiri and Uthaiah (1994) found Waigon to be superior to other varieties with regard to length of primary fingers (7.54 cm) followed by BSR 1.

Performance of 25 genotypes studied for 19 characters indicated that weight of primary finger rhizome exhibited the highest level of variability (38-94 %) followed by number of primary and secondary fingers per clump. (Chandra *et al,* 1999).

2.1.7. Secondary rhizome

Philip and Nair (1983) found significantly higher number of secondary fingers per plant in Mannuthy local (20.90) followed by Chayasupa (19.80), Armoor (19.80) and the least number was recorded in G.L.Puram (8.30) and Armoor C11-24 (7.90). The number of the nodes per finger ranged between 4.50 and 8.70 and the internodal length varied from 0.73 to 1.01 cm among the 19 cultivars studied.

Indiresh *et al.* (1990) recorded the highest number of secondary fingers in PCT 8 (9.51) followed by Allepey (8.83) and it was least in Kasturi (3.99). The length of secondary finger varied from 4.00 cm in Erode to 7.50 cm in PCT-8.

Hegde (1992) found that the highest number of secondary fingers was produced in Bidar (19.46) and the lowest in Moovattupuzha (4.60). According to Cholke (1993), the cultivar BSR 1 (19.45) recorded significantly higher number of secondary fingers followed by PCT-8 (18.25), Cuddapah (18.10) and the lowest number was seen in PCT-13 (9.55) and PCT-14 (8.10). He also reported that the length of the finger varied from 3.04 cm in Rajapuri to 6.30 cm in PCT-14 and the girth of the finger varied from 4.87 cm in PCT-14 to 6.37 cm in Amalapuram.

Sheshagiri and Uthaiah (1994) found that Waigon was superior with respect to length of secondary finger (4.90 cm) followed by BSR 1.

2.1.8. Rhizome Yield

Satheesan and Ramadasan (1982) registered a yield of 4.80 t ha^{-1} as an intercrop and 7.00 t ha^{-1} as a pure crop in turmeric selection 24. Philip and Nair (1986) observed variation for fresh yield (3.85-28.86 kg). Among the cultivars of *Curcuma longa* studied, Cls 94 (27.08 t ha^{-1}), Cls 24 (26.98 t ha^{-1}) and Ca 66 J (25.91 t ha^{-1}) recorded the highest yield of fresh turmeric and Cls 3D, Cls 8D and Cls 21A (14.04 -14.14 t ha^{-1}), the least as opined by Satyanarayana and Reddy (1986).

Pujari *et al.* (1987) evaluated eight turmeric cultivars under Andhra Pradesh conditions and reported that cultivar Krishna gave the highest fresh rhizome yield (42.72 t ha^{-1}) followed by Duggirala (32.92 t ha^{-1}) and the least yield in Rajapuri (21.70 t ha^{-1}).

Jalgaonkar *et al.* (1988) studied the performance of different varieties of turmeric under Konkan conditions of Maharashtra and found that cultivar Krishna produced the highest fresh rhizome yield (53.86 t ha^{-1}) followed by Waigon (48.93 t ha^{-1}) and the lowest by Kasturi (31.56 t ha^{-1}).

Among the short duration cultures evolved under Andhra Pradesh conditions by Reddy *et al.* (1989), it was found that cultures PCT 13 and PCT 14 recorded the highest fresh rhizome yield (28.04 t ha^{-1}; 26.71 t ha^{-1} respectively) and cured rhizome yield of 5.69 t ha^{-1}; 5.43 t ha^{-1} respectively.

Indiresh *et al.* (1990) found that among the different cultivars studied under coastal conditions of Karnataka, cultivar PCT 8 gave the highest yield (32.27 t ha^{-1}) followed by Waigon (31.64 t ha^{-1}) and it was lowest in the case of M 211 (4.00 t ha^{-1}). The highest quantity of cured turmeric was obtained in PCT 8 (6.5 t ha^{-1}) and Waigon (6.20 t ha^{-1}) and the lowest in M 211 (1.38 t ha^{-1}). Nandi (1990) recorded the highest rhizome yield of 27.0 t ha^{-1} for PTS-25 followed by Cls-9 (24.60 t ha^{-1}).

Hegde (1992) observed the highest fresh rhizome yield in case of Cuddapah (22.19 t ha^{-1}) followed by Bidar (21.69 t ha^{-1}) and the lowest in cultivar Moovattupuzha (3.73 t ha^{-1}). Ratnambal *et al.* (1992) reported a fresh rhizome yield of 29.00 t ha^{-1} and 28.82 t ha^{-1} by PCT-13 and PCT-14 respectively.

Cholke (1993) indicated that the cultivar Cuddapah exhibited the highest fresh rhizome yield of 33.37 t ha^{-1} followed by Amalapuram (31.44 t ha^{-1}) and the lowest in PCT-13 (10.87 t ha^{-1}). However, the cured yield was higher in case of Amalapuram (7.30 t ha^{-1}) followed by Cuddapah (6.34 t ha^{-1}) and the lowest in PCT 13 (2.26 t ha^{-1}).

Sheshagiri and Uthaiah (1994) observed that BSR 1 was the best in fresh rhizome yield (16.57 t ha^{-1}) followed by Waigon (15.45 t ha^{-1}) under rainfed conditions. Venkatesha (1994) indicated that Mydukur produced the highest fresh rhizome yield (46.19 t ha $^{-1}$) followed by CO 1 (39.65 t ha $^{-1}$) and the least in PCT 13 (19.51 t ha $^{-1}$).

Kurian and Valsala (1995) reported that VK 5 was superior in fresh rhizome yield (5.85 Kg / m^2).

Latha *et al.* (1995) have indicated that the cultivar Chayasupa recorded the highest yield (43.73 t ha^{-1}) of fresh rhizome followed by VK 31 (42.41 t ha^{-1}). The yield of cured rhizome was the highest in VK 116 (5.63 t ha $^{-1}$) under 25-30 per cent of shaded conditions. However, under open conditions, VK 31 (35.06 t ha $^{-1}$)

and VK 55 (34.66 t ha^{-1}) were the highest yielder in terms of fresh rhizome yield. Ramakrishna *et al.* (1995) reported that with respect to fresh and cured rhizome yield, PCT 13 was superior (19.15 t ha^{-1}) to PCT 10 (9.00 t ha^{-1}). Patil *et al.* (1995) recorded the highest yield in BSR 1 (20.88 t ha^{-1} of fresh rhizome) followed by Suvarna (19.32 t ha^{-1}) and Suroma (19.04 t ha^{-1}).

Kurian and Nair (1996) recorded the highest fresh rhizome yield in VK 121 (43.02 t ha^{-1}) and cured yield in VK 116 (8.43 t ha^{-1}).

Ten selected high curcumin lines were reported to register a yield ranging from12.65 to 19.38 kg per 3 m^2. Among the 153 accessions of *Curcuma longa* studied, PTS 12, PCT 8 and PTS 45 (42.00 to 52.50 t ha^{-1}) were found promising at Pottangi, Orissa (Anon., 1996-97). In MLT trials at Pottangi, Orissa, PTS 43 and RH 5 registered high yield during the first year evaluation of 10 entries and at Jagital, significantly higher yield was recorded in JTS 2 (32.70 t ha^{-1}) followed by JTS 1 (30.00 t ha^{-1}). Among the long duration types involved under CYT at Pottangi, significantly higher yield was obtained from PTS 55 (20.77 t ha^{-1}), PTS 43 (17.09 t ha^{-1}), PTS 62 (16.88 t ha^{-1}) and turmeric No. 1 (16.88 t ha^{-1}) (Anon., 1996-97).

Maurya *et al.* (1998d) observed that entry RH 10 out yielded other varieties with a fresh rhizome yield of 40.01 t ha^{-1} whereas local check Morangia yielded only 30.17 t ha^{-1}.

Lynrah and Chakrabarty (2000) evaluated 25 genotypes of turmeric. Among them, black turmeric, a semiwild type showed most vigorous growth with highest number of tillers, leaves and leaf area per clump. Ouguri Nepali, Black turmeric and PCT 13 gave higher yield than other genotypes while tall clone was the lowest. Curcumin content was found to be high for VK 145 followed by CL 24.

Seven Turmeric varieties were evaluated by MutyalaNaidu *et al.* (2000) in high altitude area of Chintapalle in Andhra Pradesh. Among the varieties tested, BSR 1 exhibited greater productivity of fresh rhizomes (36.50 t ha^{-1}) and it was on par with the productivity of the selection PTS 62.

2.1.9. Curing Percentage

Turmeric yield also depends on the curing percentage. The curing percentage varies depending upon the type of cultivars and the conditions under which they were grown. The percentage of curing varied with groups of turmeric types, the highest score being recorded by early duration aromatica types and the lowest by medium duration types whereas the long duration longa types recorded medium values (Sarma and Krishnamurthy, 1965; Subbarayudu *et al.,* 1976). Though curing per cent varied in different studies, the widest ranged between 13.50 and 32.40 per cent was reported by Ratnambal (1986).

2.1.10. Quality characters

Parry (1962) reported that the quality, appearance and colour of whole turmeric varied according to its source. Rosengarten (1969) opined that fingers showed the best quality as compared to round and splits. Lewis (1973) also found distinct differences in quality and quantity of oil and oleoresin in different types of turmeric grown in India. Chaurasia *et al.* (1974) reported that turmeric was of better quality when grown in hills than raised in the plains. Pruthi (1976) reported that the quality attributes of the commercial produce were its colour, aroma, maturity, bulk density, length and thickness of the finger and aroma.

2.1.10.1 Essential Oil

Subbarayudu *et al.* (1976) have opined that the oil content was higher (5.30 % to 6.80 %) in medium duration types and it was low (2.20 % to 4.20 %) in long duration types and moderate (3.30 % to 6.00 %) in short duration types. Ghosh and Govind (1982) reported that the highest content of oil was recorded in cv. Sugandham and the lowest in

Kasturitanaka. Ratnambal (1986) found that the volatile oil content was more in *Curcuma aromatica* than *Curcuma domestica*.

Volatile oil was estimated in 23 collections of *Curcuma longa* by Pathania *et al.* (1990). Among them, the greatest was in IC 29909 (11.20 %) and the lowest in IC 29798 (10.90 %). Reddy *et al.* (1990) reported that variability for oil content was more in *Curcuma longa* than *Curcuma aromatica*.

Ratnambal *et al.* (1992) demonstrated that PCT 14 and PCT 13 expressed highest volatile oil content (7.00 % and 6.00 % respectively). Sasikumar *et al.* (1996) recorded an oil content of (6.50 % and 6.20 %) in IISR Prabha and Prathibha respectively. At Solan, the essential oil content was high in PTS 10 (9.50 %) (Anon., 1996-97).

Rumikotoky *et al.* (1999) evaluated the essential oil content of seven *Curcuma longa* cultivars under Manipur conditions, of which, Thoubal exhibited the highest essential oil content (4.00 %).

2.1.10.2 Oleoresin content

Krishnamurthy *et al.* (1972) found that the oleoresin content in turmeric varied from 4.00 to 7.50 per cent. Lewis (1973) reported that the turmeric contained 6-7 per cent oleoresin. Mathai (1974) estimated the oleoresin content of six types of turmeric and recorded the highest in Allepey finger turmeric (24.30 %). The rhizome of Allepey turmeric contained only 16.20 per cent.

Philip *et al.* (1980) observed significant variations among the cultivars evaluated for oleoresin content and Mannuthy local recorded the highest (1470.30 kg/ha). Ratnambal (1986) reported that the cultivar Konni expressed highest oleoresin content (19.20 %).

Ratnambal *et al.* (1992) found that the PCT 14 was superior in oleoresin content (15.00 %). Sasikumar *et al.* (1996) observed an oleoresin content of 15.00 per cent and 16.20 per cent in IISR Prabha and Prathibha respectively. The highest oleoresin content was obtained in PCT 1 (15.32 %) (Anon., 1996-97) at Solan.

The highest oleoresin was estimated in PTS 43 (8.47 per cent) followed by Acc. 361 (7.73 %) and the lowest in JTS 1 (3.53 %) as revealed by Shanmugasundaram (1998).

2.1.10.3. Curcumin content

Krishnamurthy *et al.* (1975) opined that curcumin content of *Curcuma longa* and *Curcuma aromatica* varied from 3.00 to 3.90 per cent and 1.20 to 1.50 per cent respectively. According to Rao *et al.* (1975), the curcumin content of eight varieties grown in Andhra Pradesh varied from 1.24 to 3.87 per cent. Krishnamurthy *et al.* (1976) noticed a variation of 1.80 to 5.40 per cent in curcumin content. Muralidharan and Ramankutty (1976) noticed the highest curcumin content from Allepey (6.20 %) followed by Etamulaka (5.63 %), Kharadi local (4.35 %) and Wynad local (4.17 %), among the 20 selected clones studied. Pillai *et al.* (1976) observed variation of 8.90 to 14.50 per cent in curcumin content among the 15 types of turmeric grown under Kasargod conditions.

Induced mutagenesis using single cell cultures to isolate chimera free mutant types for various characters including curcumin and yield was initiated by KaruvinaShetty *et al.* (1980). Muthuswamy and Shah (1982) reported that the cultivar Salem (4.75 %) recorded the highest curcumin than Erode type (3.90 %).

Ghosh and Govind (1982) noticed that the No.24 and C11-323Avamigadda exhibited the highest curcumin content (7.40 to 7.90 %). Philip (1983) observed significant differences in curcumin content among the 32 varieties. The highest content was found in Mannuthy local (7.58 per cent) and the lowest in Amalapuram (3.00 %).

Pujari *et al.* (1987) registered high curcumin in Salem (4.80 %) followed by Allepey (4.40 %) and Duggirala (3.80 %). Variations among the 23 varieties were the greatest for curcumin content (0.28 to 8.76 %). Environmental influence on the characters was the greatest for curcumin content (78.30 %) as reported by Pathania *et al.* (1988).

Hegde (1992) obtained the highest curcumin of 6.46 per cent in Moovattupuzha followed by Cls 114 (6.36 %) and the lowest in Bidar (2.37 %). Ratnambal *et al.* (1992) found that the PCT 14 was superior in curcumin content (7.90 %). VijayKumar *et al.* (1992) revealed that the Duggirala cultivar was found to be superior to Mydukur variety with respect to curcumin content. Suvarna (PCT 8) contained the highest curcumin content of 4.95 per cent.

Cholke (1993) evaluated turmeric cultivars under Dharwad conditions and reported that cultivar PCT 8 recorded the highest curcumin content (8.16 %) followed by PCT 14 (7.45 %) and the least in Bidar 4 (2.45 %).

Sasikumar *et al.* (1994) observed many land races that contained more than 6.00 per cent curcumin content. Among them, Aieng turmeric of Manipur, Wynad local, Edepalayam, Thodupuzha, Manathody, Pulally types of Kerala, Aizwal type of Mizoram, Sugandham of Gujarat were rich in curcumin content. Venkatesha (1994) reported that the highest curcumin was in PCT 8 (8.20 per cent) followed by PCT 13 (4.50 %), BSR 1 (4.20 %) and the least in Mydukur (1.69 %).

Ramachandra *et al.* (1994) opined that RCT 1 had 6.80 per cent curcumin content under Meghalaya conditions. Patil *et al.* (1995) recorded the highest curcumin content in Lakadong (5.44 %) followed by Suvarna (4.68 %) and CO 1 (3.79 %).

Kurian and Valsala in 1995 reported that VK 145, a collection from Kurrupampady of Kerala recorded the highest curcumin (7.82 %) closely followed by VK 188 (7.69 %).

Radhakrishnan *et al.* (1995) noticed the highest curcumin content in BSR 1 (4.40 %) under Idukki district of Kerala. Kurian and Nair (1996) recorded the highest curcumin content in VK 96 (7.85 %) followed by VK 112 (7.23 %) and these were the collections from Kerala representing Alleppey type. The curcumin content was the highest in PCT 1 turmeric (6.08 %) in Solan (Anon., 1996-97).

Rumikotoky *et al.* (1999) analysed the curcumin content of seven *Curcuma longa* culitvars of which Tamenlong recorded the highest curcumin content (7.30 %). Shanmugasundaram (1998) reported that curcumin level was of high order in RH 5 (4.87 %) and it was lower in VK 5 (1.29 %).

2.2. Genetic diversity studies

2.2.1. Multivariate analysis

Genetic architecture of a population is a result of prolonged natural selection. The populations, which exist in diverse environments, may be strongly diversified genetically. Among the several statistical methods developed for measuring the divergence between populations, multivariate analysis (D^2 statistic) developed by Mahalonobis in 1936 has been found to be a potent tool by Rao (1960), Cassie (1963) and Sokal (1965). An assessment of degree of divergence between populations by multivariate analysis helped to trace out the pattern of evolutionary process in crop plants (Chandrasekariah *et al.* 1969).

Chandra *et al.* (1997) interpreted that plant height, weight and internodal distance on primary finger rhizome had positive and significant correlation with yield, while dry matter was negatively correlated. The genotypes PCT 13 and Lakadong formed solitary groups and were genetically distant. Groups II and III consisted of greatest number of genotypes with moderate yield. The land races were clustered in low to moderate yielding groups. Sonajuli local types 1 and 2 were identified as important genotypes for North Eastern region.

Julian *et al.* (1997) studied the multivariate pattern of quantitative trait variation in triploid banana and plantain cultivars. Principal component analysis of 15 quantitative traits was carried out to establish a taxonomic relationship between cultivar groups and subgroups in the Musa germplasm. Fruit traits, number of neutral flowers, total number of leaves, plant growth at 50 cm, days to flowering and harvest were the discriminating traits in the germplasm. The principal components 1 and 2 accounted for 35.40 per cent and 28.30 per cent of the total variation in the dataset. The analysis grouped the germplasm into AAB plantains, AAA dessert bananas and ABB cooking bananas.

Metroglyph analysis showed wide genetic diversity among the genotypes. The genotypes PCT 13 and VK145 were superior in yield and curcumin content. Curcumin, tillers/clump and mother and finger rhizome yield exhibited genetic variations and high broad sense heritability on the investigation by Lynrah *et al.* (1998).

Singh *et al.* (2000) assessed the genetic diversity in the ginger germplasm available in Nagaland. The D^2 analysis was carried out on a set of 18 genotypes of ginger involving 8 metric traits. The genotypes got grouped into three clusters and the inter cluster D^2 values varied from 338.99 to 2029.63, intra cluster D^2 values ranged between 18.41 and 45.05. The major forces for divergence were rhizome yield per plant (49.02), oleoresin (17.65) and fibre contents (17.65).

Srivatsava *et al.* (2000) subjected 40 genotypes of coriander to multivariate analysis using D^2 statistic. The assessment revealed considerable variability among the stock for all characters except number of primary branches, umbellet per umbel and 1000 seed weight. They were grouped into four clusters and inter D^2 value ranged from 0.62 to 30.70 suggesting considerable diversity among the groups.

Kumaran *et al.* (2000) studied the clustering pattern in coconut using PCA. Coconut population of Indian Ocean islands of Madagascar, Mauritius and Seychelles were subjected to clustering for 28 biometric traits. The first five PCA accounted for 88 per cent of variations. Characters that contributed to the variations were breadth, length of leaflet, length of inflorescence and its stalk, length of spikelet bearing portion, length of spikelet and number of nuts/bunch. All the dwarfs were in one cluster based on vegetative and nut characters. Cluster analysis did not show any geographical affinity within the region.

Rekha *et al.* (2002) studied the genetic diversity based on PCA, which revealed a similar pattern of clustering of AAB and AB culitvars in *M.rubra, M.acuminata and*

M.acuminata spp. *malaccensis*. The cultivars of ABB were the third group and *M.balbisiana* clones (BB) formed a separate group.

2.3. Heritability and Genetic Advance

Natarajan (1975) found that heritability value for all the characters were high except for number of tillers. The genetic advance expressed in percentage mean was low for all characters except number of secondary fingers.

Mohanty (1979) reported that the values of heritability and expected genetic gain for rhizome yield, number of tillers, breadth of fully opened leaf and height of the aerial shoot to be high, that a large portion of the apparent variability was genetic and heritable.

Mukhopadhyay *et al.* (1986) opined that heritability estimates were the highest for shoots per clump (5.87 %). Philip and Nair (1986) noticed the fresh rhizome yield per plot, curing percentage and height of the plant gave a heritability estimate of 0.52,0.99 and 0.70 respectively and genetic advance as percentage of mean as high as 62.59, 44.96 and 29.64 respectively indicating high scope for improvement of these characters through selections. The oleoresin and curcumin content showed heritabiltity estimate of 0.96 each and gave percentage of mean as high as 27.08 and 54.0 respectively indicating scope for quality improvement.

Subramanian (1986) revealed that the diameter of the mother rhizome expressed the highest percentage of heritability and genetic advance. Geetha and Prabhakaran (1987) found that height of the plant exhibited high heritability combined with genetic advance and genetic gain, which indicated the importance of this character in selections.

Reddy (1987) revealed that rhizome yield, crop duration, number of leaves, number of primary fingers and height of pseudostem were having high heritability along with medium genetic advance per cent estimates.

Pathania *et al.* (1988) observed the highest estimates of heritability for volatile oil content, curcumin content, finger length and drying percentage. Selection can give better results based on these characters. Leaf size and yield per plant showed high heritability value with comparitively lesser genetic advance.

Jalgaonkar *et al.* (1990) showed that the characters like yield of cured turmeric, number of primary fingers and yield of secondary fingers showed high magnitude of heritability and appreciable expected genetic advance.

Pathania *et al.* (1990) recorded high heritability (99.54 %) and high genetic advance (90.33 %) for volatile oil content. Indiresh *et al.* (1992) stated that the rhizome yield, internodal distance of primary and secondary fingers and number of secondary fingers per plant recorded higher heritability estimates as well as high genetic advance. Yadav and Singh (1996) reported that per plant yield expressed high genetic advance, length and width of rhizome showed high heritability.

Lynrah *et al.* (1998) studied the pattern of genetic variability in 25 genotypes of turmeric collected in Assam, North Eastern hills and Shillong. Curcumin content, tillers per clump and mother rhizome yield exhibited high genetic variation and high broad sense heritability.

The highest phenotypic and genotypic variance for fresh rhizome per plant (34810.22 and 34679.48 respectively) while the lowest phenotypic and genotypic variance were recorded for number of mother rhizomes (1.19 and 0.63 respectively). The order of difference between PCV and GCV was high for leaf area (146.18) and the least for number of tillers (0.48). High Heritability estimates recorded for crop duration (99.65 %) followed by weight of mother rhizome (98.63 %). (Shanmugasundaram, 1998).

Investigation by Hazra *et al.* (2000) revealed that leaves per clump at 180 Days after planting exhibited high broad sense heritability and high genetic gain.

The genetic parameters and degree of mutual associations were assessed in relation to yield in cv. Nadia, West Bengal. The characters of fresh rhizome yield /ha, number of rhizomes, weight of secondary fingers / clump, weight of secondary fingers /

plant, exhibited genetic advance. The fresh rhizome yield was significantly correlated with length of secondary fingers and weight of primary and secondary fingers / clump. The findings were opined by Jana *et al.* (2001).

2.4. Correlation Studies

Natarajan (1975) noticed that leaf length exerted the highest influence on yield followed by leaf width, plant height, number of leaves, primary and secondary fingers.

Mohanty (1979) revealed from the studies of correlation coefficients, rhizome yield was positively and significantly associated with number of leaves and shoot height and negatively associated with number of tillers. The genotypic and phenotypic correlation coefficients between breadth of fully opened leaf and shoot height were significant and positive.

George (1981) found that the yield per plant was highly associated with length of primary finger, length and girth of secondary fingers. The correlation coefficients of these yield components were positive and significant. Pathania *et al.* (1981) also reported that the rhizome yield was positively and significantly correlated with plant height, number of secondary fingers, number of tillers, number of leaves and leaf size.

According to Philip and Nair (1983), plant height (0.63), number of leaves per tiller (0.59), leaf area (0.74) was highly significant and positively correlated with the yield of turmeric. The number of tillers (0.22) and leaves per plant (0.44) were not significantly correlated with yield. Among the yield components, though the girth of mother rhizome (0.56) and length of fingers were significant and positively correlated with yield, internodal length, girth of primary fingers and number of nodes did not have significant correlation with yield.

Subramanian (1986) reported that mother rhizome diameter exhibited significant and positive associations with rhizome yield. Geetha and Prabhakaran (1987) reported that most of the characters were highly intercorrelated among themselves.

Reddy (1987) showed that the number of leaves, number of primary fingers and period of crop duration expressed strong associations with rhizome yield at both genotypic and phenotypic levels. Jalgaonkar *et al.* (1988) observed significant and positive correlation between cured yield and with girth, weight of mother rhizome, length of primary finger and number and girth of secondary fingers.

Jalgaonkar *et al.* (1990) reported that the yield of cured turmeric was significantly correlated with yield of secondary fingers. The significant relationship of quantitative characters of secondary fingers among each other and with those of primary fingers suggested the scope for obtaining a good response to selection through direct as well as indirect means.

Cholke (1993) recorded significant and positive correlation between yield and primary fingers (0.95) and plant height (0.71). However, positive and non significant correlation were observed with number of leaves (0.58), number of tillers (0.42), number of mother rhizomes (0.61), number of secondary fingers (0.58) and length of primary fingers (0.55).

Venkatesha (1994) reported that plant height, leaf area and number of leaves exhibited positive correlation with fresh rhizome yield. Among the yield components, weight of mother rhizomes, primary and secondary fingers and length of primary and secondary fingers expressed positive and significant correlation with the yield.

Shanmugasundaram (1998) observed genotypic coefficient of variation for weight of secondary rhizomes (60.43) and weight of primary rhizomes (53.62). A significant and positive correlation with rhizome yield was exhibited for plant height, leaf area, number of leaves, number and weight of primary and secondary fingers, weight of mother rhizomes and duration except for number of tillers and number of mother rhizomes. Curing percentage exhibited a high negative association with core diameter.

Plant height, leaf length and breadth, weight of primary finger rhizomes and rhizome yield per hectare were significant and positively associated with fresh rhizome yield per clump. A negative correlation between dry rhizome recovery and fresh rhizome yield per clump was opined by Chandra *et al.* (1999).

Hazra *et al.* (2000) revealed that leaves/clump at 180 Days after planting exhibited positive phenotypic correlation and direct contribution to rhizome yield.

2.5. Path Coefficient Analysis

Natarajan (1975) reported that leaf length had exerted the highest direct effect on yield followed by number of secondary fingers and leaves.

Pathania *et al.* (1981) revealed that plant height had higher direct contribution towards yield followed by number of secondary fingers and number of leaves. Lal *et al.* (1986) reported that out of 9 yield contributing characters; rhizome length and fingers per rhizome expressed the highest direct and positive effect on yield among thirteen varieties evolved. Therefore greater emphasis should be given to these two characters for the improvement of turmeric by selection.

Subramanian (1986) recorded that the diameter of mother rhizome is the main determinant of the yield. According to Geetha and Prabhakaran (1987), path coefficient analysis indicated that height of the plant and length of secondary finger were the major contributors towards rhizome yield. Direct effects of number of leaves per tiller and length and girth of mother rhizome were positive whereas, number of nodes per primary finger showed high negative direct effects on rhizome yield.

Nandi *et al.* (1992) reported that the highest direct effect by girth of finger followed by weight of finger. Indirect effects of high magnitude were also exerted by girth of finger in relation to most of the other components.

Path coefficients analysis projected the characters like weight of primary fingers (0.482), weight of secondary rhizomes (0.459) and weight mother rhizomes (0.218) as the primary contributors of the yield (Shanmugasundaram, 1998).

2.6. Genetic diversity based on Markers

Genetic markers have been observed and used since the dawn of genetics. Markers are typically used as tools to characterize varieties and they should be heritable, discriminate between the individuals examined, and be easy to measure and evaluate, provide comparable results, known to be either neutral or unlinked.

2.6.1. Morphological markers

Morphological characters in various parts of plants have been used to distinguish one cultivar from other. Although the observation of phenotype undoubtedly represents a very successful means of variety identification, cannot be reliable under all circumstances, as they are subjected to environmental conditions, show differential expression that depends on ontogeny. Thus there are compelling reasons to seek more rapid and objective methods and in this respect, biometrical techniques have been widely explored.

2.6.2. Biochemical marker

Isozymes, the multiple molecular forms of an enzyme with similar or identical catalytic activities occurring within the same organism can be a rapid sensitive tool for cultivar identification. It is possible to characterize genetically distinct isozyme variants for much enzyme system in numerous species, however, they are subjected to ontogenic variations. (Tanksley and Orton, 1983).

Shamina *et al.* (1997) observed variability for twenty-five accessions of ginger for isozyme loci. Dendrograms indicated average similarity of the accession with respect to the isozyme profiles and accessions collected from the same geographical area exhibited a tendency to cluster together.

Shamina *et al.* (1998) studied the variation in fifteen accessions of turmeric based on isozyme polymorphism. A high degree of variability (63.80 – 96.00 % similarity) was observed. Two seedling progenies showed higher similarity and stood distinctly from the clonally propagated material.

2.6.3. Molecular marker (DNA level)

Molecular markers based on differences in DNA sequences between individuals generally detect more polymorphism than morphological and isozyme based markers (Botstein *et al.,* 1980 and Tanksley *et al.,* 1989). Restriction fragment length polymorphism (RFLP) technique has been used extensively to determine the genetic diversity, genome structure and evolutionary relationship between species.

However, the use of RFLP in germplasm studies is limited by several factors; for example, RFLP markers require large amounts of DNA for the assay; they are time consuming and labour intensive. (Beckmann and Soller, 1983). Alternatively with the development of Polymerase Chain Reaction (PCR technology), new molecular markers which use random oligo nucleotide primers for selective amplification of DNA, to generate Random Amplified Polymorphic DNA (RAPD) markers, that are shown to be good genetic markers (Williams *et al.,* 1990).

RAPD uses a decamer to amplify several segments of the target genome in a random fashion. It amplifies 5-15 bands of 200-400bp in length. An RAPD primer shows polymorphism most frequently by giving "n" products and therefore is a dominant polymorphism. DNA polymorphism generated by RAPDs has been used to identify the germplasm lines and cultivars (Margale *et al.,* 1995).

Rout *et al.* (1998) evaluated the genetic stability of micropropagated plants of ginger cv. V_3S_{18} using RAPD marker. Of the 15 decamers tested, three (OPC 04, OPC 19 and OPC 07) produced amplification products that were monomorphic. The twelve other primers did not yield good amplification product. The size of the monomorphic DNA fragments produced by these primers ranged from 0.40 to 1.00 kb (OPC 04), 0.97 to 0.75 kb (OPC 19) and 1.32 to 0.43 kb (OPC 07).

Boehm *et al.* (1999) studied the genetic differences among 11 cultivated and wild type population of North American ginseng (*Panax quinquefolium* L.) and four cultivated population of South Korean Ginseng (*Panax ginseng*) using RAPD markers. Evaluation of the germplasm using 10 decamer primers resulted in 100 polymorphic bands. The results indicated that there are no genetically distinct cultivated population of either species. The wild type population may present *Panax quinquefolium* with a source of genetic diversity for improving the populations.

DNA profiling of twenty accessions of turmeric among the turmeric germplasm were initiated by Sasikumar (2000-2001). The primer extension in PCR reaction was found to be optimal at 72 °C. Using 10 mer primers viz. OPQ 20, R 5, T 13 and X 7, DNA was profiled and work on suitable primers for amplification is in progress.

Rekha *et al.* (2002) studied the genomic relationship among the 28 genotypes using RAPD markers. Among the 10 primers used for amplification, 6 primers (OPA 03, OPA 04, OPA 10, OPA 13, OPE 18 and OPQ 18) gave scorable polymorphic bands. The dendrogram differentiated two main clusters that separated the AA genotypes from BB genotypes.

2.7. Screening Studies

2.7.1. Screening for resistance to Leaf spot disease (*Colletotrichum curcumae* syn. *Colletotrichum capsici*)

Patil and Patil (1983) carried out varietal resistance in turmeric to *Curcuma capsici*, in 11 cultivars of *Curcuma longa* and *Curcuma amada*. The percentage of leaf area damaged was the lowest in cv. Kasthuri (2.30 %) and Gadhavi (2.70 %) and the highest in Erode (10.60 %).

Fourteen turmeric cultivars were screened for resistance to *Curcuma capsici*. The cvs. Bhendi, Duggirala, Gadhavi, Kasturi, Rajapuri and Warangal were resistant. The genotypes of Erode were moderately resistant and Allepey, Brahmpuri, Jaweli, Krishna, Waigon and Sugandham were moderately resistant (Palarpawar and Ghurde, 1989).

Rao *et al.* (1994) reported that PCT 10, Suguna and Sudarshana have remained free from Colletotrichum leaf spot compared to Armoor and Duggirala.

Palarpawar and Ghurde (1995) studied the variability in *Colletotrichum curcumae*, the incitant of leaf spot of turmeric. Three different strains were identified and distinguished by their cultural, morphological and physiological characteristics in turmeric cv. Waigon. Strain 1 and 3 were more virulent than strain 2. Strain 1 produced symptoms on turmeric flowers too.

Screening of turmeric germplasm against leaf spot disease was carried out at four research centres. At Jagital, of the 50 cultivars (8 short duration, 26 medium duration and 16 long duration) tested against leaf spot disease, 46 cultivars (8 short duration, 26 mid duration and 12 long duration) were found to be free from Colletotrichum leaf spot under natural conditions, in comparison with susceptible check Duggirala, Telupu and Armoor (Anon., 2000-2001).

At Dholi, GL.Puram and Kohinoor were found to be resistant to leaf spot. At Raigarh, 4 entries exhibited resistance to Colletotrichum leaf spot. At Pundibari, Acc.584, Prathibha, PTS 52 and TCP 1 were immune to the foliar disease (Anon., 2000-2001).

Study on varietal resistance to leaf spot began as early in 1962 by Sarma and Krishnamurthy (1962). They screened four short duration types (*Curcuma aromatica*), 7 kesari types (*Curcuma longa*) and 7 long duration types (*Curcuma longa*). It was inferred that long duration types were susceptible to leaf spot.

Philip and Nair (1981) tested 19 cultures of turmeric in Kerala for resistance to leaf spot. Cultivars Mannuthy local, Tekurpeta, C11-324, Kodur were found to be tolerant to leaf spot while Rajapuri, Vontimitta and Kasturi Tanaka were susceptible.

Field studies were conducted in four districts of Karnataka, during the kharif season in 1994-95, showed that the percentage incidence of *Alternaria alternata* on turmeric was 16.50-46.50. Local turmeric varieties appeared more susceptible (40.50%)

than improved varieties like Rajapuri (16.50 %) (Mallikarjuna Gaddankeri and Srikant Kulkarni, 1998).

2.7.2. Screening for resistance to Scale (*Aspidiotus hartii*)

Regupathy *et al.* (1976) studied the reaction of 191 turmeric types to rhizome scale and found that 87 were free from infestation.

Tirumurthi *et al.* (1993), screened 3 varieties to its reaction to three major pests : scale (*Aspidiella hartii*) , shoot and root borer (*Conogethes punctiferalis)* and leaf folder (*Udaspes folus*). The BS 43 (2.02 %) appeared to be highly resistant to scale compared to cultivar CO1 (45.31 %) and BSR 1 (49.37 %) and fairly tolerant to other two pests.

Thus, there are plethora of methods and technologies available for assessing genetic variability which can be better exploited in the near future. With this overview, the investigation was contemplated to assess the genetic diversity combining the conventional and molecular techniques.

Materials and Methods

CHAPTER III

MATERIALS AND METHODS

Studies on the evaluation of the germplasm of turmeric (***Curcuma longa*** L. syn. ***Curcuma domestica*** Val.) for quality and resistance to leaf spot and scale insect and to assess its genetic variability were conducted during 2000-2002 at the Department of Spices and Plantation Crops, Horticultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore.

The methodologies adopted for the study are presented in this chapter.

3.1. MATERIALS

Two twenty four genotypes of turmeric, drawn from different states of India were maintained in the germplasm at the Department of Spices and Plantation Crops, Horticultural College and Research Institute, Tamil Nadu Agricultural University, Coimbatore, and were used as the materials. The details of the genotypes and their sources are furnished in Annexure -1.

3.2. METHODS

The experimental method consisted of two phases.

Phase I. Studies on the germplasm

1. Genetic divergence studies of the germplasm
2. Evaluation of the germplasm for yield and quality.
3. Screening the genotypes for resistance to leaf spot disease (*Colletotrichum curcumae* syn. *Colletotrichum capsici*) and scale insect (*Aspidiotus hartii*).

Phase II. Study on the selected genotypes

1. Assess the genetic diversity based on RAPD marker for genotypes selected from phase I.

2. Screening the selected genotypes for resistance to leaf spot disease (*Colletotrichum curcumae* syn. *Colletotrichum capsici*) and scale (*Aspidiotus hartii*).

3.2.1. PHASE I

3.2.1.1. Details of the Experiment

The study was conducted to assess the diversity among the germplasm and to screen the genotypes for quality parameters and level of resistance to leaf spot and scale. The design adopted was Randomized Block Design with 223 accessions and replicated twice. The trial was conducted during 2000 May – 2001 February. (Plate 1).

The experimental plot size was $3m^2$ with a spacing of 45x20 cm accommodating 30 plants per plot. Healthy, disease free, uniformly sized (20g) fingers with well-developed buds were used for planting (Edison *et al.*, 1991). The recommended package of practices for the crop was followed uniformly for all accessions (Anon., 1994). The plant protection sprays were not practiced so as to allow the natural incidence of leaf spot and scale.

3.2.1.2. Observations Recorded

Five plants in each accession per replication were tagged randomly for recording the observations on plant characters and mean values were subjected to statistical scrutiny. The following observations were recorded.

BIOMETRICAL CHARACTERS

Sprouting

The number of sprouts emerged after 45 days of planting were counted in each plot and the mean was expressed as per cent.

Height of the plant

The plant height was measured at 180 days from the collar region of the pseudostem to the tip of the fully opened top most leaf and the mean was expressed as cm per plant.

Plate 1. Field view of the experiment (phaseI)

Plate 2. Field view of the experiment (phase II)

Number of leaves

Fully opened leaves were counted and the mean was expressed as number per plant.

Number of tillers

The tillers arising from base of the pseudostem were counted and the mean was expressed as number per plant.

Leaf area

The length of the leaf was measured from the base of the lamina to the tip using a scale and width was measured at the broadest point on the lamina of the fully opened third leaf and the mean was expressed as cm.

RHIZOME CHARACTERS

Number of mother rhizomes

The number of mother rhizomes was counted and the mean was expressed as number per plant.

Weight of mother rhizomes

The mother rhizomes of five randomly selected plants were pooled, weighed and the mean was expressed as g per plant.

Girth of mother rhizome

The girth at the broadest point was measured using a non-stretchable string and scale on five randomly selected mother rhizomes and the mean was expressed as cm.

Number of primary rhizomes

The primary rhizomes arising from the mother rhizomes in five randomly selected clumps were counted and the mean was expressed as number per clump.

Weight of primary rhizome

The primary rhizomes arising from the mother rhizome in five randomly selected clumps were weighed and the mean was expressed as g per clump.

Length of primary rhizome

The length was measured in five randomly selected primary rhizomes using a scale and the mean was expressed as cm per rhizome.

Girth of primary rhizome

The girth was measured in five randomly selected primary rhizomes using non-stretchable string and a scale and the mean was expressed as cm.

Rhizome to core diameter

Five primary rhizomes were selected randomly from the produce of randomly selected plants that were measured for rhizome diameter and internal core diameter by making a cross section and the ratio of rhizome diameter to core diameter was computed.

Number of secondary rhizomes

The secondary rhizomes arising from the primary rhizomes in five randomly selected clumps were counted and the mean was expressed as number per clump.

Weight of secondary rhizomes

The secondary rhizomes arising from the primary rhizomes in five randomly selected clumps were pooled, weighed and the mean was expressed as g per plant.

Length of secondary rhizome

The length of secondary rhizome was measured in five randomly selected rhizomes using a scale and the mean was expressed as cm.

Girth of secondary rhizome

The girth of secondary rhizome was measured in five randomly selected secondary rhizomes using a non-stretchable string and a scale and the mean was expressed as cm.

Yield

The fresh rhizomes harvested from each plot (3 m^2) were weighed and the mean was expressed as kg per plot.

YIELD OF CURED RHIZOME

One kilogram of fresh rhizomes from each plot (comprising 30 per cent mother rhizomes and 70 per cent primary and secondary rhizomes) were boiled in pure water for 45-60 minutes till the rhizomes became soft and emitted a typical turmeric odour (Natarajan and Lewis, 1980). After boiling, the rhizomes were dried under sun to attain 8 per cent moisture content (Philip and Sethumadhavan, 1980).

QUALITATIVE TRAITS

Curcumin content

The curcumin content was estimated as per the methods of ASTA (Anon., 1968) proposed by Manjunath *et al.* (1991). Turmeric powder @ 0.1g was refluxed with 30 ml of 95 per cent ethanol for 2½ hours. The extract was cooled and filtered quantitatively into a 100ml volumetric flask; the residue was then transferred to the filter, washed thoroughly and volume was made upto 100 ml with alcohol.

Twenty ml of this filtered extract was pipetted out into a 250 ml volumetric flask and volume made up using alcohol. The extract and standard solution (25 mg of standard curcumin obtained from E.Merck. (India) Limited, Chennai) was taken in a 100 ml volumetric flask which was dissolved in alcohol after adding small quantity of acetone and the volume was made up with the same. Again one ml of this solution was transferred into 100 ml volumetric flask and volume made up with alcohol. This standard solution (containing 0.0025g/l) was read at 425 nm against alcohol blank in spectrophotometer and curcumin content was computed as below and expressed as per cent.

CALCULATION

$$\text{Absorptivity of curcumin (a)} = \frac{\text{Absorbance of standard solution at 425 m}\mu}{\text{Cell length (cm)} \times \text{Concentration (g/l)}}$$

$$\text{Curcumin (per cent)} = \frac{\text{Absorbance of extract at 425 m}\mu \times 125}{\text{Cell length (cm)} \times a \times \text{Sample weight (g)}}$$

3.2.2. D^2 ANALYSIS

Computation of D^2 values: All possible { n (n-1)/2 } D^2 values between 223 genotypes were calculated utilising the replicated values.

Determination of group constellations or clusters

A relatively simple criterion suggested by Tocher (Rao, 1952) was adopted in the determination of clusters. The criterion of grouping was that, any two populations belonging to the same cluster on the average should show smaller D^2 than those belonging to the different clusters. Starting with two closely associated varieties, a third variety having the smallest average D^2 from the first two was added. Similarly, the fourth one was chosen to have the smallest average D^2 from the first three and so on and at any stage the average D^2 of a group, from already included appeared to be high, it was considered that the group does not fit in with the former cluster and hence taken to be outside the first cluster. The groups of the first cluster were then omitted and the rest treated in the similar way.

After establishing the group constellations or clusters, the average inter and intra cluster divergences were worked out taking into consideration all the component D^2 values possible among the members of the two clusters taken for consideration. The square root of the D^2 values gave the distance (D) between the clusters.

Ranking of characters to D^2 values

Ranking of individual D^2 values, contributed by each character, was done as the highest contributor taking rank 1. The character with the least rank total was taken to contribute the maximum to genetic divergence and the one with highest rank total, the least to genetic divergence.

3.2.3. K means clustering

K means clustering is referred to as non-hierarchial clustering. These techniques are designed to group objects into a collection of K clusters. The number of clusters, K, may either be specified in advance or determined as part of the clustering procedure.

Because resemblance matrix need not be determined, these techniques can be applied to much larger data sets than hierarchial techniques.

The objects are initially divided into a user specified number (k) of equal sized groups. Centroids are calculated for each group as average of its expression. The objects are reassigned to the group with the highest similarity between the expression profiles and group centroid is then recalculated and the process is iterated until the group compositions converge. (Ian Davidson, 2002).

The distance to the cluster center is the Euclidean distance, which is measured between two instances X and Y, represented by m continuous attributes as

$$D(X,Y) = (X_1 - Y_1)^2 + (X_2 - Y_2)^2 \dots + (X_m - Y_m)^2$$

The algorithm uses the attribute values of the instances assigned to a cluster and recalculate the cluster's centroid. (Sneath and Sokal, 1973)

3.2.4. Principal Component Analysis (PCA)

PCA is a multivariate statistical method, originated with Pearson (1901) as a means of fitting planes by orthogonal least square but was later proposed by Hotelling (1933) for the purpose of analyzing correlation structure. PCA attempts to describe the total variation in a multivariate sample with fewer variables than in the original data set.

PCA selects linear combinations of the attributes, which retain the highest proportion of unexplained variability between the units. These linear combinations (the principal components) can explain relationships between units and attributes and by restriction, the dimensionality of the problem is reduced.

The major axis or vector is called the principal component 1 (PC 1) and subsequent orthogonal axes are numbered sequentially (PC 2, PC 3 . . . PCn). Each PC axis is defined in terms of linear transformation of original variable scores.

Coefficients of each transformation equation form a set of eigen vector and the total variance accounted by each equation is called the eigen value. The eigen values exceeding 1.0, the corresponding PC has inherently more information than any single variable alone. A significant PC interprets the percentage of total variation in the data set.

The data matrix for all the N objects of the population over p attributes is DNxp

Then DNxp =

$$\begin{vmatrix} X_{11} & X_{12} & X_{1p} \\ X_{21} & X_{22} & X_{2p} \\ X_{N1} & X_{N2} & X_{Np} \end{vmatrix}$$

A PCA about the p attributes associated with D generates p new variables. These p new variables are the principal components Y_1, ...Y_p with each principal component being a linear combination of the p attributes of D, that is

$$Y_1 = A_1'X = A_{11}X_1 + \ldots\ldots + A_{p1}X_p$$

.

.

$$Y_p = A_p'X = A_{1p}X_1 + \ldots\ldots + A_{pp}X_p$$

Where Aij's are coefficients similar to that of regression equations except that they are scaled so that $\sum Aij^2 = 1$. These Aij's can be viewed as weights defining the contribution of the i^{th} attribute of D to the j^{th} principal component. Like regression coefficients, their signs (+ / -) are indicative of the directions of contribution.

3.2.5. VARIABILITY ANALYSIS

a. Unit analysis

The statistical parameters such as mean, variance, standard deviation, coefficient of variation and standard error were calculated for each genotype. The following formula was utilized for the calculations as suggested by Panse and Sukhatme (1978).

$$\text{General mean} = \frac{\text{Grand total}}{N}$$

Where,

N = number of observations

$$\text{Variance} = \frac{SS - CF}{df}$$

Where,

SS = sum of squares of all observations of a variable

$$CF = \frac{(\text{Grand total})^2}{N}$$

df = Degrees of freedom

$$\text{Standard deviation (SD)} = \sqrt{\text{Variance}}$$

$$\text{Standard error (SE)} = \frac{SD}{\sqrt{N}} \times 100$$

$$\text{Coefficient of variation (CV)} = \frac{SD}{\text{Mean}} \times 100$$

b. Analysis of variance

The replicated values were subjected to statistical analysis of variance as prescribed by Panse and Sukhatme (1978).

i) Phenotypic and genotypic variances

The phenotypic and genotypic variances were computed as per the methods suggested by Johnson *et al.* (1955).

Phenotypic variance = $(\sigma^2p) = (\sigma^2g) + (\sigma^2e)$

Where,

(σ^2e) = error variance

$$\text{Genotypic variance } (\sigma^2g) = \frac{M_1 - M_2}{r}$$

Where,

M_1 = Mean sum of squares for genotypes

M_2 = Mean sum of squares for error

r = Number of replications

ii) Heritability and genetic advance as percentage of mean

Heritability in the broad sense (h^2) was derived based on the formula proposed by Lush (1940) and expressed in percentage.

$$h^2 = \frac{(\sigma^2 g)}{(\sigma^2 p)} \times 100$$

Where,

$(\sigma^2 g)$ = Genotypic variance

$(\sigma^2 p)$ = Phenotypic variance

Genetic advance was estimated by the following formulae as per the methods of Johnson *et al.* (1955).

$$\text{Genetic advance} = \sqrt{\sigma^2 p \times h^2 \times k}$$

Where,

$\sigma^2 p$ = Phenotypic variance

h^2 = Heritability

k = Selection differential constant, 2.06 at 5% selection intensity (Falconer, 1967).

iii) Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV)

The phenotypic and genotypic coefficient of variation was worked out as per the methods suggested by Burton (1952).

$$\text{Genotypic coefficient of variation} = \frac{(\sigma^2 g)}{\text{Mean}} \times 100$$

$$\text{Phenotypic coefficient of variation} = \frac{(\sigma^2 p)}{\text{Mean}} \times 100$$

Where,

$\sigma^2 p$ and $\sigma^2 g$ are phenotypic and genotypic variances respectively.

iv) Correlation coefficients

Phenotypic and Genotypic correlation coefficients were worked out using the following formula as outlined by Johnson *et al.* (1955).

Phenotypic correlation coefficient

$$rph\ 1.2 = \frac{Cov.p.1\ \&\ 2}{\sqrt{{}^2p^1 \times {}^2p^2}}$$

Where,

rph 1.2 = Phenotypic correlation coefficient

cov.p.1& 2 = Phenotypic covariance between the traits 1&2

${}^2p^1$ & ${}^2p^2$ = Phenotypic variance of the traits 1&2 respectively.

Genotypic correlation coefficient

$$rgh\ 1.2 = \frac{Cov.g.1\ \&\ 2}{\sqrt{{}^2g^1 \times {}^2g^2}}$$

Where,

rgh 1.2 = Genotypic correlation coefficient

cov.g.1& 2 = Genotypic covariance between the traits 1&2

${}^2g^1$ & ${}^2g^2$ = Genotypic variance of the traits 1&2 respectively.

The significance of these correlation coefficients was tested by referring to the table given by Panse and Sukhatme (1978).

c. Path coefficient analysis

The estimated genotypic correlation coefficients were partitioned into direct and indirect effects for all characters to rhizome yield as per the procedure given by Wright (1921) and later adopted by Dewey and Lu (1959).

3.2.6. SCREENING OF GENOTYPES FOR RESISTANCE TO LEAF SPOT (*Colletotrichum curcumae* syn. *C. capsici*)

The genotypes were scored against leaf spot at the time of incidence based on 0-5 grades in similarity to the scale adopted for leaf spot in vegetables.

Five randomly selected leaves per genotype per replication were selected and scored by giving grade. The mean values were pooled to work out the percent disease index as calculated by Wheeler (1969).

$$PDI = \frac{\text{Sum of individuals}}{\text{Number of leaves}} \times \frac{100}{\text{maximum disease grade}}$$

Rating scale

Grade	Leaf area infested	Reaction
0	No infestation	Highly resistant
1	1-10% of leaf area infested	Resistant
2	11-25% of leaf area infested	Moderately resistant
3	26-50% of leaf area infested	Susceptible
4	>50% of leaf area infested	Highly susceptible

The score chart was framed on similar lines to the work contributed by Panja *et al.* (2000) against leaf blotch (*Taphrina maculans*) in turmeric.

3.2.7. SCREENING OF GENOTYPES FOR RESISTANCE TO RHIZOME SCALE (*Aspidiotus hartii*)

The genotypes were screened for incidence of rhizome scale caused by ***Aspidiotus hartii***. Under natural conditions, the rhizomes were observed for infestation at the time of harvest. Infestation rating was done on five randomly selected rhizome clumps of each genotype following 0-5 grade based on number of scales on 5 cm long fingers. The mean values were pooled to calculate the percent infestation. This was followed in accordance with similar work carried out by Tirumurthy *et al,* (1993).

The rhizomes were artificially inoculated with scale insect. The infected rhizome finger (2 cm rhizome finger with scale infestation) along with five uniform healthy fingers were tightly packed in polybags and sealed for all the genotypes. The fingers were scored as below based on 0-5 grades after 30 days.

Grade	Percent infestation	Reaction
0	No infestation	Highly resistant
1	< 5 % area infested with scale	Resistant
2	6 - 15 % area infested with scale	Moderately resistant
3	16 - 30 % area infested with scale	Susceptible
4	> 31 % area infested with scale	Highly susceptible

3.3. PHASE II

3.3.1. Selection of genotypes

The number of entries made in the germplasm was high to assess the divergence at molecular level. The clustering technique was found to be a useful tool in grouping the genotypes phenotypically. Hence the 223 genotypes were subjected to Mahalonobis D^2 statistic to cull out the variable parameters. The analysis was carried out for 22 parameters excluding the quality traits. The genotypes got clustered into two groups, exhibiting wide variability for eight parameters of importance among them. The experimental data for those eight parameters were resubjected to Mahalonobis D^2 statistic. Five clusters were formed grouping all 223 genotypes. Based on clustering, genotypes at extremities were selected to represent each cluster based on its performance to growth and yield and its resistance reaction to leaf spot and scale. Thirty genotypes thus selected were used as the material for study in phase II.

3.3.2 EXPERIMENTAL DETAILS

Based on the diversity analysis carried, thirty genotypes were selected from five different clusters and were raised to assess the diversity pattern phenotypically and at the molecular level.

The thirty genotypes were raised in Randomized Block Design and replicated twice. The trial was laid out during May, 2001–February 2002. (Plate 2).

The experimental plot size was $4m^2$ with a spacing of 45x20 cm accommodating 40 plants per plot. All the cultural practices were carried out in similarity to the crop raised as in Phase I. (Plate 3).

3.3.3. OBSERVATIONS RECORDED

Five randomly selected plants in each genotype per replication were tagged for recording the observations on biometrical and rhizome characters as in phase I and the mean values were subjected to diversity analysis.

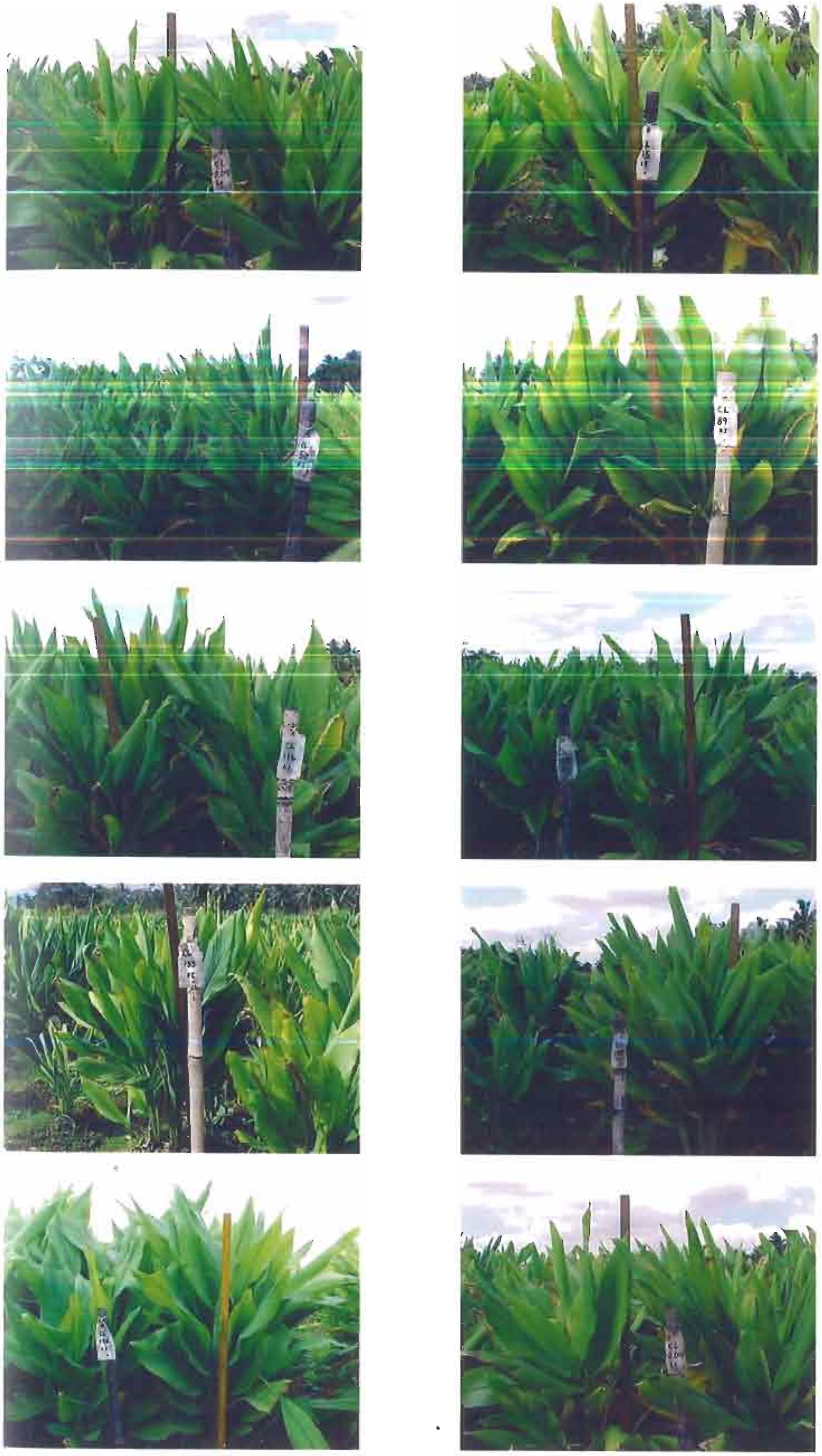
3.4. GENETIC DIVERSITY BASED ON RAPD MARKER

3.4.1. DNA Extraction

Molecular profiling of the selected genotypes was done using RAPD marker. DNA from all the 30 genotypes were extracted following the protocol described by McCouch *et al.* (1988) from leaves frozen at –20°C.

The leaves were cut into pieces and homogenized completely with liquid nitrogen. The leaf powder was filled in 50 ml centrifuge tubes to a volume of 15 ml to which 23 ml of preheated extraction buffer (100 mM tris-HCl-pH 8.0, 50 mμ EDTA – pH 2.0, 500 mμ NaCl, 1.25% SDS (w/v) and 3.8 g/l sodium bisulfite) was added and mixed well. The tubes were incubated at 65°C for 10-15 min with repeated shakings. Then 10 ml of 5 M potassium acetate was added and the tubes were incubated in ice for 20 min with shaking followed by centrifugation at 3000 rpm for 20 min. Two third volume of prechilled isopropanol was added to the supernatant. DNA was hooked out after half an hour and washed in 70 per cent alcohol and suspended in 5 ml of TE buffer (pH 8.0). To this, one

Plate 3. Variation in plot view of genotypes



tenth of 3 M sodium acetate and double the volume of prechilled absolute alcohol were added respectively. Tubes were incubated at 4°C for 30 min. After that DNA was resuspended in 0.5 ml of TE buffer in 1.5 ml tubes and stored at -20°C.

3.4.2. DNA quality and quantity check

Agarose gel electrophoresis on 0.8 per cent gel was performed to check the quality and quantity of DNA. DNA concentration for PCR amplification was estimated by comparing the band intensity of a sample with the band intensities of known dilutions that have good amplification.

3.4.3. RAPD ANALYSIS

Genomic DNA from 30 genotypes was amplified using a set of 20 arbitrary oligonucleotide decamer primers (Operon Technologies, Alameda, Calif., USA) (Table 1). Amplification reactions were in volumes of 20 µl containing 10 mµ Tris HCl (pH 8.3), 50 mM KCl, 1.5 mµ $MgCl_2$, 0.001 per cent gelatin, dATP, dCTP, dTTP and $dGTP_s$ each at 0.1 mM, 0.2 mM primer, 25-30 ng of genomic DNA and 0.5 unit of Taq DNA polymerase (Banglore Genei Pvt. Ltd., Bangalore). Amplifications were performed in 0.2 ml thin walled PCR tubes in a PTC 100 thermal cycler (MJ Research Inc.) programmed for 35 cycles. After initial denaturation for 2 min at 92°C, each cycle consisted of 1 min at 92°C, 1 min at 36°C and 2 min at 72°C. The 35 cycles were followed by 7 minute final extension at 72°C.

PCR amplified products (15 µl) were subjected to electrophoresis in 1.5 per cent agarose gels in 1 x TBE buffer at 120 V for 3.5 h using Apelex electrophoresis unit.

The electronic image of the ethidium bromide stained gel was captured using photo documentation system.

3.5. DATA ANALYSIS

3.5.1. Scoring

Amplified DNA fragments detected after electrophoretic separation in each genotype was scored for the presence (1) or absence (0) of clear and unambiguous bands.

Table 1. List of random primers used for RAPD analysis

Random Primer	5 ' to 3' sequence
OPB - 08	GTCCACACGG
OPB - 09	TGGGGGACTC
OPB - 11	GTAGACCCGT
OPB - 14	TCCGCTCTGG
OPB - 15	GGAGGGTGTT
OPC - 01	TTCGAGCCAG
OPC - 16	CACACTCCAG
OPC - 18	TGAGTGGGTG
OPC - 20	ACTTCGCCAC
OPE - 03	CCAGATGCAC
OPE - 09	CTTCACCCGA
OPF - 03	CCTGATCACC
OPE - 04	GGTGATCAGG
OPF - 09	CCAAGCTTCC
OPF - 13	GGCTGCAGAA
OPG - 10	AGGGVVGTCT
OPG - 13	CTCTCCGCCA
OPG - 14	GGATGAGACC
OPG - 17	ACGACCGACA
OPG - 19	GTCAGGGCAA
OPG - 20	TCTCCCTCAG

A data matrix comprising of '1' and '0' was formed and this data matrix was subjected to further analysis.

3.5.2. CLUSTER ANALYSIS

The two different sets of data gathered (quantitative and RAPD marker) were subjected to cluster analysis. Sequential Agglomerative Hierarchical Non-Overlapping (SAHN) clustering was performed and similarity matrix using Jaccard's similarity coefficient for binary data utilizing the Unweighted Pair Group Method with Arithmetic Average (UPGMA) for the RAPD marker data set and the quantitative data were subjected to cluster analysis using D^2 statistic, K means based on Euclidean distance and UPGMA method based on squared Euclidean distance.

3.6. SCREENING STUDIES

3.6.1. SCREENING FOR LEAFSPOT

The selected genotypes were screened against leaf spot at the time of incidence both under natural and artificial conditions.

Under artificial conditions, virulent isolate of ***Colletotrichum capsici*** was cultured on Potato Dextrose Agar (PDA) medium (Riker and Riker, 1936) and sprayed on the leaves of the potted plants after 90 days. The individual plants were covered with polybags to maintain a humid condition for the development of leaf spot disease. The leaves of the infected plants were scored based on 0-5 grade as in phase I.

3.6.2. SCREENING FOR RHIZOME SCALE

The genotypes were screened against scale insect at the time of harvest and under artificial condition as in phase I. The rhizomes were observed for the infestation and rating was done based on 0-9 grade on five randomly selected rhizome clumps of each genotype. The mean values were pooled to calculate the percent infestation.

Under artificial condition, the rhizomes were artificially inoculated with scale insect. The infected rhizome finger along with five uniform healthy fingers were tightly packed in polybags and sealed for all the genotypes. The fingers were scored based on 0-5 grade as in Phase I after 30 days.

3.7. Statistical analysis

The replicated data of the genotypes for the characters were subjected to analysis of variance using AGRES, D^2 statistic (Mahalonobis, 1936) was employed using GENRES, K means was followed using SYSTAT packages available at Horticultural college and Research Institute, Coimbatore.

Results

CHAPTER IV

RESULTS

Turmeric genotypes were evaluated in two phases for yield, quality and resistance to disease (leaf spot) and pest (scale). The mean data pertaining to biometrical characteristics and quality parameters were tabulated and results concerned to it are interpreted in this chapter.

MEAN PERFORMANCE OF TURMERIC GENOTYPES (Phase I)

4.1. Biometrical characters

4.1.1. Sprouting (Table 2)

The genotypes differed significantly with reference to sprouting which ranged between 45.00 and 100.00 per cent. The genotypes 2, 16, 17, 21, 22, 23, 24, 25, 29, 30, 31, 32, 33, 34, 35, 44, 45, 46, 50, 59, 60, 61, 66, 68, 69, 72, 74, 76, 78, 86, 89, 94, 95, 99, 100, 101, 106, 114, 121, 123, 125, 126, 132, 134, 135, 138, 139, 141, 144, 145, 147, 148, 149, 151, 153, 154, 163, 166, 173, 178, 183, 191, 193, 195, 209, 210, 213, 214, 221, 222 and 223 registered 100.00 per cent sprouting. However, this was on par with genotypes 3, 6, 7, 8, 13, 14, 15, 20, 26, 28, 38, 39, 40, 41, 42, 43, 47, 48, 51, 52, 53, 56, 57, 65, 67, 70, 71, 73, 75, 77, 80, 88, 91, 92, 103, 104, 107, 111, 112, 113, 116, 122, 124, 127, 130, 131, 133, 155, 157, 159, 161, 168, 170, 172, 174, 176, 179, 189, 192, 196, 197, 198, 199, 202, 203, 204, 205, 208, 211, 212, 215, 219, 220 and 221 valuing up to 92.86 per cent. The lowest per cent of sprouting was noticed in genotype 63 (45.00%), which was on par with genotypes 142 (49.00%). (Table 2)

4.1.2. Height of the plant (Table 3)

The plant height measured at 180 days of planting varied significantly from 29.05 to 48.56 cm. The genotype 2 was found to be the tallest (48.56 cm). However, it was on par with genotypes 3, 9, 15, 22, 29, 35, 41, 43, 55, 72, 74, 75, 76, 89, 101, 102, 114 and 198. The short stature plants were found in genotype 20 (29.05 cm), which was on par

Table 2. Mean performance of turmeric genotypes for sprouting

Geno types	Sprouting (%)	Geno types	Sprouting (%)	Geno types	Sprouting (%)	Geno types	Sprouting (%)	Geno types	Sprouting (%)
1	56.00	46	100.00	91	94.00	136	90.00	182	91.00
2	100.00	47	96.00	92	93.00	137	86.00	183	100.00
3	94.00	48	99.00	93	91.50	138	100.00	184	89.00
4	82.00	49	92.00	94	100.00	139	100.00	185	77.50
5	90.00	50	100.00	95	100.00	140	82.00	186	91.00
6	96.00	51	97.00	96	80.00	141	100.00	187	87.00
7	98.00	52	96.00	97	80.00	142	49.00	188	85.00
8	96.00	53	94.00	98	88.00	144	100.00	189	95.50
9	70.00	54	90.00	99	100.00	145	100.00	190	86.50
10	90.00	55	88.00	100	100.00	146	62.50	191	100.00
11	90.00	56	94.00	101	100.00	147	100.00	192	94.00
12	92.00	57	96.00	102	86.00	148	100.00	193	100.00
13	94.00	58	86.00	103	98.00	149	100.00	194	85.00
14	96.00	59	100.00	104	98.00	150	73.50	195	100.00
15	96.00	60	100.00	105	92.00	151	100.00	196	98.00
16	100.00	61	100.00	106	100.00	152	91.00	197	99.00
17	100.00	62	70.00	107	94.00	153	100.00	198	95.00
18	80.00	63	45.00	108	86.00	154	100.00	199	94.00
19	86.00	64	86.00	109	74.00	155	95.00	200	92.00
20	94.00	65	99.00	110	84.00	156	66.50	201	90.00
21	100.00	66	100.00	111	94.00	157	99.00	202	96.00
22	100.00	67	94.00	112	98.00	158	83.00	203	98.00
23	100.00	68	100.00	113	96.00	159	94.00	204	96.00
24	100.00	69	100.00	114	100.00	160	91.00	205	94.00
25	100.00	70	93.00	115	66.50	161	94.50	206	90.00
26	94.00	71	94.00	116	98.00	162	75.50	207	92.00
27	86.00	72	100.00	117	92.00	163	100.00	208	98.00
28	96.00	73	94.00	118	78.00	164	75.50	209	100.00
29	100.00	74	100.00	119	78.00	165	88.00	210	100.00
30	100.00	75	95.50	120	73.50	166	100.00	211	98.00
31	100.00	76	100.00	121	100.00	167	65.50	212	98.00
32	100.00	77	98.00	122	94.00	168	94.50	213	100.00
33	100.00	78	100.00	123	100.00	169	91.50	214	100.00
34	100.00	79	88.00	124	98.00	170	99.00	215	94.00
35	100.00	80	96.00	125	100.00	171	83.50	216	90.00
36	82.00	81	81.00	126	100.00	172	95.50	217	90.00
37	82.00	82	74.00	127	96.00	173	100.00	218	90.00
38	98.00	83	90.00	128	92.00	174	94.00	219	94.00
39	96.00	84	91.00	129	92.00	175	77.50	220	96.00
40	93.50	85	91.00	130	94.00	176	93.00	221	96.00
41	93.00	86	100.00	131	96.00	177	74.50	222	100.00
42	95.50	87	84.00	132	100.00	178	100.00	223	100.00
43	97.00	88	96.00	133	94.00	179	95.50	224	82.00
44	100.00	89	100.00	134	100.00	180	86.00		
45	100.00	90	67.00	135	100.00	181	91.50		

SEd 3.62 CD (.05) 7.14

Table 3. Mean performance of turmeric genotypes for height of plant

Geno types	Plant height (cm)	Geno types	Plant height (cm)	Geno types	Plant height (cm)	Geno types	Plant height (cm)	Geno types	Plant height (cm)
1	38.79	46	41.17	91	36.10	136	34.34	182	33.50
2	48.56	47	39.57	92	38.34	137	33.56	183	32.10
3	45.04	48	40.60	93	38.66	138	30.33	184	33.46
4	36.53	49	41.94	94	40.16	139	34.89	185	33.00
5	32.39	50	38.74	95	34.25	140	35.82	186	38.92
6	36.24	51	38.59	96	33.94	141	35.66	187	40.74
7	38.19	52	42.14	97	32.88	142	34.55	188	35.04
8	36.96	53	33.04	98	32.58	144	33.60	189	35.18
9	44.20	54	40.19	99	33.43	145	33.62	190	34.19
10	37.81	55	45.70	100	38.88	146	34.64	191	31.43
11	36.58	56	42.87	101	46.40	147	34.91	192	33.72
12	38.62	57	31.65	102	44.12	148	35.70	193	31.89
13	41.00	58	32.59	103	35.61	149	35.32	194	31.44
14	30.44	59	32.79	104	32.60	150	34.96	195	36.19
15	45.53	60	34.69	105	38.18	151	41.37	196	35.48
16	40.45	61	38.27	106	35.63	152	39.27	197	32.47
17	36.28	62	40.24	107	40.37	153	41.95	198	44.24
18	32.84	63	32.94	108	34.94	154	37.08	199	33.02
19	32.23	64	34.69	109	32.12	155	33.52	200	34.79
20	29.05	65	42.55	110	31.89	156	39.19	201	34.34
21	41.93	66	35.09	111	39.15	157	36.69	202	34.94
22	44.30	67	33.56	112	37.12	158	31.24	203	34.08
23	43.19	68	37.63	113	39.22	159	34.83	204	31.47
24	32.86	69	41.62	114	45.99	160	32.16	205	32.82
25	41.09	70	33.08	115	36.52	161	32.12	206	32.50
26	34.05	71	36.91	116	33.89	162	32.84	207	32.31
27	34.74	72	44.39	117	35.44	163	33.90	208	33.04
28	40.53	73	38.94	118	31.51	164	35.18	209	31.73
29	45.87	74	44.23	119	33.98	165	35.78	210	32.94
30	41.79	75	44.59	120	37.60	166	33.01	211	32.77
31	36.38	76	45.89	121	35.52	167	32.85	212	32.55
32	35.14	77	35.83	122	35.27	168	32.83	213	32.57
33	32.27	78	35.97	123	31.26	169	33.52	214	32.94
34	37.56	79	32.54	124	30.75	170	34.01	215	31.32
35	44.88	80	38.05	125	30.74	171	36.74	216	33.48
36	35.12	81	34.60	126	30.43	172	37.65	217	32.76
37	31.85	82	34.75	127	31.11	173	36.50	218	33.59
38	35.18	83	36.27	128	30.89	174	37.29	219	35.30
39	36.40	84	32.97	129	42.17	175	33.32	220	33.36
40	36.25	85	37.77	130	40.94	176	33.41	221	33.38
41	44.35	86	36.43	131	32.64	177	33.04	222	33.70
42	42.39	87	41.60	132	33.79	178	34.36	223	38.54
43	45.84	88	42.61	133	34.00	179	33.90	224	31.75
44	42.54	89	44.70	134	31.80	180	34.28		
45	43.04	90	34.25	135	33.45	181	33.49		

SEd 2.55 CD (.05) 5.04

with genotypes 5, 14, 18, 19, 24, 26, 33, 37, 53, 57, 58, 59, 63, 67, 70, 79, 84, 96, 97, 98, 99 and 104. 109, 110, 116, 118, 119, 123, 124, 125, 126, 127, 128, 131, 132, 133, 134, 135, 137, 138, 144, 145, 155, 158, 160, 161, 162, 163, 166, 167, 168, 169, 170, 175, 176, 177, 179, 181, 182, 183, 184, 185, 191, 193, 194, 197, 199, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 220, 221, 222 and 224. (Table 3 and Plate 4)

4.1.3. Number of leaves (Table 4)

The number of leaves at180 days after planting revealed significant variation among the genotypes. The difference in number of leaves among the genotypes ranged between 10.25 and 17.92. The highest number of leaves was scored in the genotype 47 (17.92) followed by 43 (17.59) and are on par with genotypes 15, 21, 22, 23, 29, 30, 31, 35, 39, 41, 46, 48, 51, 52, 54, 55, 56, 65, 68, 69, 70, 71, 72, 74, 75, 76, 83, 87, 88, 101, 102, 111, 114, 129, 130, 157, 186, 187 and 190. Genotype 149 exhibited the least number of leaves (10.25) and was on par with the genotypes 150 (10.50), 151 (10.75) and 224 (10.75). (Table 4)

4.1.4. Length of leaf (Table 5)

The length of leaf measured at 180 days of planting among the different genotypes exhibited significant variations. The longest leaf was recorded in the genotype 43 (56.31 cm) followed by 101 (55.87 cm), which were on par with genotypes 2, 35, 41,74, 75, 89, 102, 107, 153, 156, 157, 189, 198 and 223. The shortest leaf was noticed in the genotype 213 (31.19 cm) which was on par with 4, 5, 8, 14, 19, 20, 23, 24, 25, 26, 27, 33, 36, 37, 40, 45, 53, 57, 58, 59, 63, 66, 67, 79, 84, 92, 96, 97, 98, 104, 109, 110, 116, 117, 118, 124, 126, 127, 131, 135, 136, 137, 138, 139, 140, 142, 147, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 169, 172, 173, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 189, 191, 192, 193, 196, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 223, 214, 215, 216, 217, 218, 220, 221, 222 and 224. (Table 5 and Plate 5)

Plate 4. Whole plant view of different genotypes

Table 4. Mean performance of turmeric genotypes for number of leaves

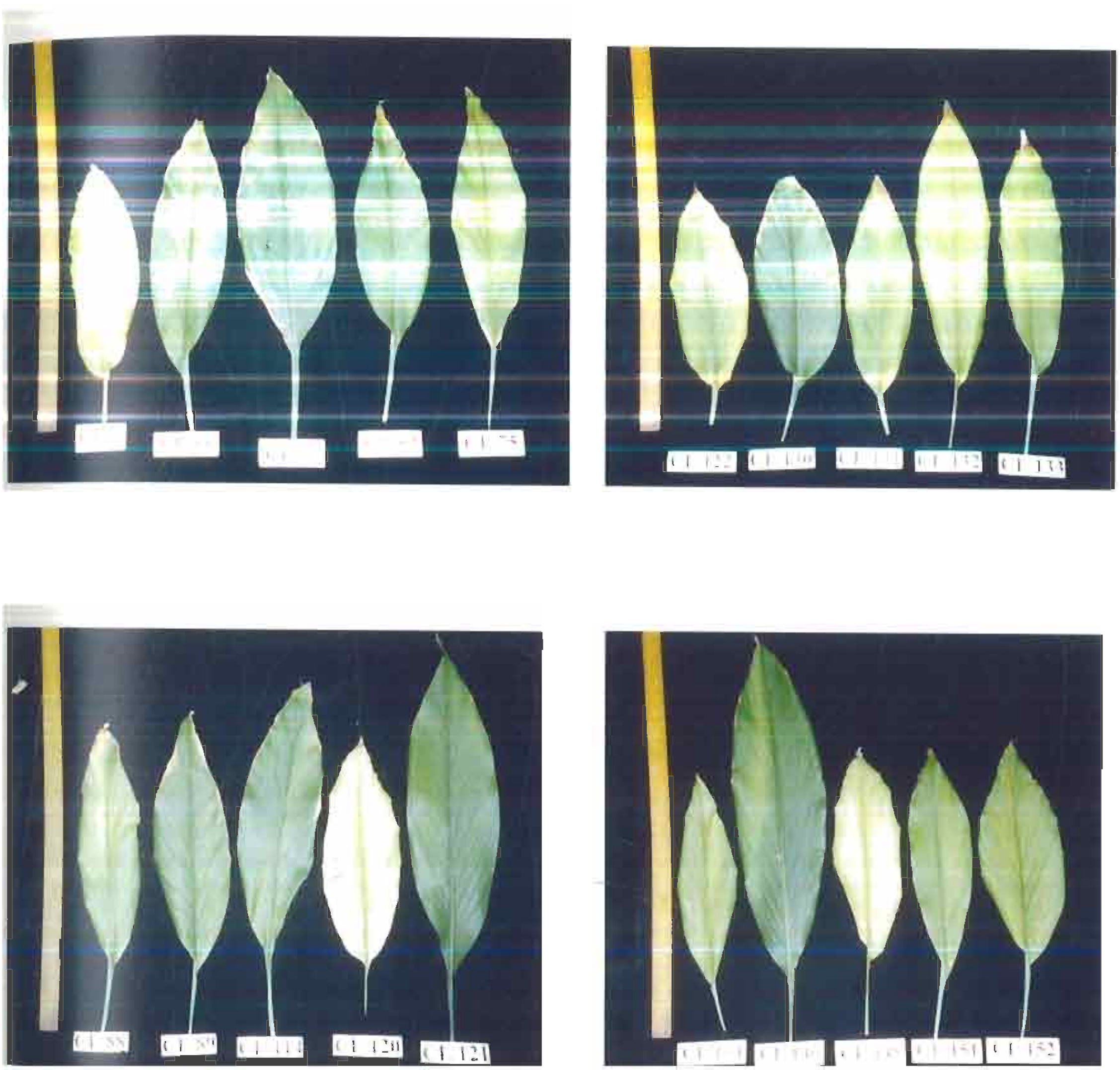
Geno types	Number of leaves	Geno types	Number of leaves	Geno types	Number of leaves	Geno types	Number of leaves	Geno types	Number of leaves
1	14.09	46	16.42	91	14.75	136	13.16	182	11.25
2	15.34	47	17.92	92	14.85	137	13.25	183	11.25
3	14.59	48	16.75	93	15.85	138	12.75	184	11.25
4	14.25	49	15.50	94	13.00	139	12.75	185	11.67
5	12.59	50	15.67	95	15.17	140	15.59	186	16.10
6	14.42	51	16.75	96	14.35	141	15.67	187	16.60
7	15.00	52	15.92	97	13.10	142	14.85	188	15.67
8	14.09	53	14.75	98	13.42	144	14.92	189	15.84
9	15.50	54	16.00	99	14.33	145	15.00	190	16.10
10	15.67	55	16.34	100	14.50	146	15.75	191	14.67
11	14.59	56	17.50	101	17.16	147	15.25	192	13.42
12	15.09	57	13.85	102	16.17	148	14.42	193	14.50
13	15.00	58	13.29	103	14.50	149	10.25	194	13.59
14	12.17	59	13.59	104	14.42	150	10.50	195	13.25
15	17.00	60	15.75	105	14.59	151	10.75	196	13.40
16	14.75	61	15.59	106	15.75	152	15.00	197	14.67
17	14.67	62	15.75	107	15.42	153	15.42	198	15.00
18	14.17	63	13.50	108	14.50	154	15.34	199	12.25
19	12.75	64	15.17	109	13.59	155	14.33	200	15.90
20	14.42	65	16.34	110	14.00	156	15.33	201	15.50
21	15.92	66	14.75	111	16.10	157	16.00	202	13.40
22	16.75	67	15.25	112	15.35	158	11.75	203	13.75
23	16.92	68	16.50	113	15.42	159	11.84	204	12.25
24	14.67	69	16.42	114	17.17	160	11.67	205	12.75
25	15.42	70	17.00	115	14.10	161	11.00	206	11.17
26	15.09	71	17.00	116	14.00	162	13.25	207	11.33
27	13.67	72	17.42	117	14.00	163	13.25	208	11.75
28	15.67	73	15.17	118	13.85	164	11.59	209	11.50
29	16.34	74	16.84	119	15.33	165	11.10	210	12.00
30	16.50	75	15.92	120	14.42	166	11.25	211	12.25
31	16.09	76	17.59	121	14.25	167	11.00	212	11.33
32	13.75	77	15.25	122	14.59	168	13.33	213	11.42
33	13.00	78	15.50	123	12.25	169	11.42	214	11.33
34	15.42	79	15.42	124	11.85	170	14.50	215	11.90
35	16.59	80	15.42	125	11.85	171	15.33	216	11.00
36	15.67	81	15.50	126	11.60	172	12.66	217	11.75
37	15.25	82	13.75	127	11.25	173	11.10	218	11.75
38	15.67	83	16.10	128	11.60	174	14.92	219	12.75
39	16.25	84	13.50	129	17.59	175	12.25	220	12.00
40	14.17	85	15.67	130	16.34	176	11.85	221	11.75
41	16.92	86	14.82	131	15.67	177	11.59	222	12.00
42	15.25	87	17.50	132	15.67	178	11.25	223	15.75
43	17.59	88	16.17	133	14.60	179	11.59	224	10.75
44	15.67	89	15.10	134	13.50	180	11.33		
45	14.67	90	14.00	135	14.17	181	11.25		
SEd 1.02		CD (.05) 2.01							

Table 5. Mean performance of turmeric genotypes for length of leaf

Geno types	Length of leaf (cm)	Geno types	Length of leaf (cm)	Geno types	Length of leaf (cm)	Geno types	Length of leaf (cm)	Geno types	Length of leaf (cm)
1	43.87	46	43.21	91	39.29	136	35.45	182	36.25
2	51.00	47	47.05	92	35.50	137	35.20	183	36.27
3	46.51	48	46.00	93	44.13	138	36.28	184	34.15
4	35.01	49	44.97	94	44.80	139	34.66	185	32.86
5	36.78	50	42.95	95	40.42	140	38.20	186	44.07
6	43.32	51	39.23	96	36.33	141	39.60	187	49.48
7	42.06	52	40.34	97	33.90	142	36.20	188	41.78
8	37.52	53	36.95	98	33.45	144	41.95	189	36.90
9	43.07	54	40.50	99	39.06	145	40.68	190	40.89
10	46.53	55	48.64	100	44.85	146	40.77	191	34.67
11	43.30	56	43.93	101	55.87	147	37.87	192	34.84
12	39.30	57	34.29	102	48.93	148	45.69	193	36.32
13	45.84	58	33.25	103	38.90	149	41.60	194	42.44
14	34.04	59	32.47	104	36.41	150	43.02	195	39.54
15	45.15	60	42.97	105	46.35	151	45.70	196	34.63
16	45.12	61	39.23	106	46.12	152	47.48	197	42.65
17	40.57	62	45.90	107	50.48	153	50.68	198	53.99
18	39.70	63	35.57	108	42.18	154	46.15	199	39.12
19	34.49	64	41.99	109	36.10	155	40.06	200	43.85
20	33.04	65	42.59	110	34.39	156	48.79	201	33.06
21	39.30	66	37.00	111	41.39	157	49.30	202	34.15
22	40.42	67	36.56	112	44.85	158	33.35	203	33.97
23	38.75	68	43.28	113	44.08	159	37.93	204	36.49
24	37.70	69	48.53	114	48.05	160	36.20	205	35.40
25	37.25	70	42.81	115	40.21	161	35.10	206	37.04
26	35.38	71	42.31	116	38.54	162	37.30	207	36.00
27	36.09	72	44.69	117	36.04	163	36.80	208	32.37
28	41.74	73	45.92	118	38.20	164	37.24	209	33.63
29	46.13	74	50.81	119	41.94	165	34.55	210	33.47
30	47.42	75	50.13	120	41.49	166	34.01	211	32.89
31	39.22	76	42.73	121	41.78	167	33.62	212	33.34
32	39.88	77	38.87	122	40.84	168	43.70	213	31.19
33	35.54	78	44.46	123	39.23	169	34.40	214	34.87
34	39.70	79	36.47	124	36.78	170	41.06	215	33.11
35	49.84	80	46.73	125	38.88	171	43.99	216	31.58
36	37.14	81	39.32	126	33.90	172	38.15	217	33.08
37	34.92	82	40.78	127	37.83	173	34.45	218	32.74
38	42.23	83	39.43	128	39.29	174	39.10	219	42.74
39	39.74	84	32.49	129	48.52	175	34.84	220	36.20
40	35.08	85	41.77	130	39.15	176	34.38	221	34.17
41	55.09	86	41.22	131	38.14	177	36.99	222	33.45
42	45.53	87	46.92	132	39.64	178	36.74	223	52.24
43	56.31	88	48.10	133	41.87	179	34.70	224	32.00
44	48.04	89	50.90	134	39.15	180	34.15		
45	38.80	90	43.92	135	35.89	181	38.40		

SEd 3.86 CD (.05) 7.62

Plate 5. Variation in leaf size of genotypes



4.1.5. Breadth of leaf (Table 6)

The breadth of leaf measured among the genotypes varied significantly from 10.05 cm to 16.05 cm. The broadest leaf was noticed in the genotype 129 (16.05 cm) and it is on par with genotypes 2, 15, 16, 23, 29, 35, 44, 46, 47, 65, 71, 72, 73, 74, 75, 76, 78, 82, 88, 89, 94, 102, 105, 106, 107, 111, 114, 123, 129, 130, 131, 142, 151, 153, 187, 219 and 223. The narrowest leaf was registered in the genotype 33 (10.05 cm) which was on par with 5, 7, 8, 10, 11, 12, 14, 18, 19, 20, 21, 24, 25, 27, 30, 31, 33, 34, 37, 38, 39, 40, 45, 59, 64, 66, 67, 77, 79, 80, 83, 84, 85, 90, 92, 96, 101, 109, 110, 115, 116, 118, 124, 125, 126, 127, 128, 134, 138, 139, 149, 150, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 169, 170, 171, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 191, 192, 193, 194, 195, 196, 197, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 212, 214, 215, 216, 217, 218, 220, 221, 222 and 224. (Table 6)

4.1.6. Number of tillers (Table 7)

Number of tillers counted among the genotypes ranged significantly between 1.00 and 5.50. It was of higher order in the genotype 69 (5.50), which was on par with genotypes 2, 7, 9, 16, 22, 23, 29, 36, 41, 43, 48, 49, 50, 51, 55, 56, 60, 62, 65, 69, 70, 71, 72, 79, 81, 82, 88, 89, 94, 102, 104, 107, 109, 112 and 113. Number of tillers was low in the genotypes 73, 131, 132, 133, 134, 135, 139, 142, 145, 150, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 164, 165, 166, 167, 168, 169, 170, 172, 173, 174, 175, 176, 178, 179, 180, 181, 182, 184, 185, 191, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223 and 224. (Table 7 and Plate 6)

4.1.7. Days to maturity (Table 8)

A significant variation was noticed for duration of genotypes. The duration of the crop extended from 218 to 261.50 days. The genotypes 9,10,14,15,16,17 exhibited longer duration (> 260 days) while genotypes with a duration period of 240 to 260 days were medium duration types in the present study. The short duration types were noticed for

Table 6. Mean performance of turmeric genotypes for breadth of leaf

Geno types	Breadth of leaf (cm)	Geno types	Breadth of leaf (cm)	Geno types	Breadth of leaf (cm)	Geno types	Breadth of leaf (cm)	Geno types	Breadth of leaf (cm)
1	13.15	46	13.87	91	12.99	136	12.80	182	11.48
2	14.16	47	13.75	92	11.40	137	13.35	183	11.53
3	13.19	48	13.16	93	13.05	138	11.38	184	12.04
4	12.89	49	13.29	94	13.77	139	12.30	185	11.10
5	12.05	50	13.26	95	12.43	140	12.60	186	11.92
6	12.60	51	12.44	96	12.15	141	12.70	187	13.88
7	12.29	52	13.66	97	13.20	142	14.95	188	12.48
8	12.11	53	12.60	98	12.95	144	12.82	189	12.60
9	13.33	54	13.34	99	12.45	145	12.78	190	12.80
10	12.39	55	13.26	100	12.75	146	12.65	191	12.34
11	12.20	56	13.05	101	12.35	147	12.57	192	11.47
12	12.02	57	12.71	102	15.50	148	12.68	193	12.00
13	13.36	58	13.67	103	12.82	149	11.85	194	12.24
14	10.31	59	10.76	104	12.74	150	11.21	195	12.20
15	14.22	60	13.30	105	13.71	151	14.43	196	12.20
16	14.18	61	13.03	106	13.88	152	13.54	197	12.35
17	12.99	62	12.94	107	13.90	153	14.22	198	12.44
18	10.85	63	13.15	108	12.90	154	13.47	199	13.20
19	10.36	64	11.88	109	11.73	155	13.64	200	10.68
20	11.27	65	13.83	110	10.69	156	13.04	201	12.15
21	12.19	66	11.93	111	13.77	157	13.36	202	12.38
22	13.18	67	12.28	112	13.22	158	11.00	203	11.54
23	14.00	68	12.70	113	12.77	159	11.18	204	11.05
24	11.48	69	12.64	114	14.56	160	11.50	205	11.80
25	11.81	70	12.98	115	12.37	161	11.54	206	11.73
26	12.71	71	13.75	116	12.40	162	12.28	207	11.43
27	11.19	72	13.75	117	13.35	163	11.32	208	12.22
28	13.59	73	13.94	118	12.10	164	11.95	209	12.08
29	15.08	74	13.91	119	13.30	165	11.52	210	11.08
30	12.32	75	13.85	120	13.13	166	11.69	211	12.56
31	12.23	76	13.95	121	12.45	167	11.50	212	11.72
32	13.20	77	12.04	122	12.75	168	12.69	213	12.50
33	10.05	78	15.27	123	14.50	169	11.53	214	10.68
34	11.79	79	10.67	124	11.64	170	12.10	215	10.48
35	13.97	80	12.10	125	11.50	171	11.64	216	12.06
36	12.50	81	13.50	126	10.59	172	12.68	217	11.54
37	10.85	82	13.95	127	11.15	173	11.58	218	10.95
38	11.00	83	11.77	128	11.63	174	12.25	219	13.95
39	11.13	84	12.13	129	16.05	175	11.60	220	11.74
40	10.75	85	11.02	130	15.15	176	11.69	221	11.60
41	12.99	86	12.42	131	13.82	177	11.23	222	11.06
42	13.18	87	13.43	132	13.40	178	11.37	223	14.63
43	12.74	88	14.46	133	12.77	179	11.63	224	11.29
44	14.35	89	14.27	134	12.19	180	11.22		
45	11.57	90	11.52	135	12.72	181	11.75		

SED 1.20 CD (.05) 2.36

Table 7. Mean performance of turmeric genotypes for number of tillers

Geno types	No.of tillers	Geno types	No.of tillers	Geno types	No.of tillers	Geno types	No.of tillers	Geno types	No.of tillers
1	3.92	46	4.10	91	3.50	136	2.25	182	1.92
2	5.09	47	4.10	92	3.85	137	2.67	183	2.25
3	3.84	48	5.34	93	2.85	138	2.25	184	2.00
4	3.09	49	5.00	94	4.50	139	2.10	185	1.33
5	3.00	50	4.75	95	3.25	140	2.33	186	2.92
6	3.50	51	5.09	96	3.59	141	3.10	187	3.41
7	4.50	52	4.33	97	3.84	142	1.92	188	3.33
8	2.75	53	3.25	98	2.75	144	3.85	189	2.59
9	4.59	54	3.84	99	3.10	145	1.92	190	2.92
10	3.50	55	4.42	100	3.59	146	2.33	191	2.00
11	3.09	56	4.50	101	3.92	147	2.60	192	2.25
12	3.17	57	2.75	102	4.50	148	3.25	193	2.25
13	3.75	58	3.00	103	4.25	149	2.17	194	3.25
14	2.50	59	3.50	104	4.59	150	1.66	195	1.92
15	4.25	60	5.17	105	3.35	151	2.84	196	2.00
16	4.50	61	4.00	106	4.25	152	4.00	197	1.50
17	3.75	62	4.59	107	4.42	153	1.84	198	2.00
18	4.17	63	2.92	108	3.92	154	1.00	199	1.50
19	2.92	64	3.34	109	4.35	155	1.34	200	1.58
20	3.50	65	4.67	110	4.00	156	1.92	201	1.41
21	3.25	66	2.67	111	2.92	157	1.42	202	1.41
22	5.09	67	3.17	112	4.92	158	1.17	203	1.41
23	4.42	68	3.42	113	5.10	159	1.67	204	1.41
24	3.92	69	5.50	114	4.25	160	1.17	205	1.75
25	4.17	70	5.00	115	3.50	161	1.17	206	1.00
26	3.84	71	4.67	116	3.42	162	1.00	207	1.00
27	3.42	72	5.25	117	2.60	163	2.17	208	1.59
28	4.25	73	1.92	118	4.00	164	1.75	209	1.59
29	4.50	74	3.85	119	3.75	165	1.75	210	1.25
30	4.34	75	4.25	120	4.00	166	1.25	211	1.00
31	4.00	76	4.25	121	3.10	167	1.42	212	1.00
32	3.34	77	4.33	122	3.10	168	1.34	213	1.41
33	3.34	78	4.33	123	3.10	169	1.67	214	1.17
34	3.92	79	4.67	124	2.59	170	1.00	215	1.00
35	4.17	80	2.67	125	2.85	171	2.25	216	1.59
36	4.42	81	4.92	126	2.85	172	1.59	217	1.25
37	4.00	82	5.42	127	2.67	173	1.42	218	1.17
38	3.84	83	2.92	128	2.17	174	2.00	219	1.00
39	3.92	84	3.35	129	3.25	175	1.67	220	1.41
40	4.09	85	2.60	130	2.75	176	1.75	221	1.17
41	4.75	86	3.84	131	1.85	177	2.25	222	1.41
42	3.59	87	2.84	132	1.60	178	1.50	223	1.75
43	4.67	88	4.84	133	1.60	179	1.92	224	1.00
44	3.25	89	4.60	134	1.85	180	1.67		
45	3.84	90	4.00	135	1.60	181	1.75		
SEd 0.58		CD (.05) 1.15							

Plate 6. Variation in number of tillers of genotypes

Table 8. Mean performance of turmeric genotypes for days to maturity

Geno types	Days to maturity	Geno types	Days to maturity	Geno types	Days to maturity	Geno types	Days to maturity	Geno types	Days to maturity
1	243.00	46	255.00	91	255.00	136	231.50	182	243.50
2	240.50	47	252.50	92	249.50	137	230.00	183	231.00
3	245.00	48	255.00	93	227.00	138	229.00	184	251.00
4	246.00	49	259.50	94	258.50	139	230.50	185	233.50
5	245.00	50	250.50	95	241.50	140	253.00	186	231.00
6	245.00	51	251.00	96	243.50	141	239.00	187	250.50
7	251.00	52	255.00	97	242.50	142	250.50	188	253.00
8	256.50	53	246.00	98	246.50	144	245.00	189	246.00
9	261.00	54	257.50	99	254.00	145	232.50	190	256.00
10	261.00	55	228.00	100	251.50	146	235.50	191	250.50
11	250.00	56	251.00	101	252.00	147	232.00	192	231.00
12	256.50	57	252.50	102	252.50	148	245.50	193	218.00
13	256.50	58	251.50	103	256.00	149	232.50	194	256.00
14	260.00	59	246.00	104	256.00	150	249.50	195	223.00
15	261.00	60	258.50	105	253.00	151	250.50	196	252.50
16	260.00	61	230.50	106	255.00	152	252.50	197	231.50
17	261.50	62	227.00	107	250.50	153	235.00	198	232.00
18	257.50	63	256.00	108	251.50	154	235.50	199	221.00
19	257.50	64	256.00	109	251.50	155	234.50	200	235.00
20	255.00	65	255.00	110	251.00	156	234.50	201	241.50
21	255.00	66	256.00	111	251.00	157	235.00	202	243.00
22	253.50	67	253.50	112	255.00	158	225.50	203	242.50
23	248.50	68	251.50	113	252.00	159	232.50	204	252.00
24	242.00	69	250.50	114	254.00	160	231.00	205	250.50
25	242.50	70	251.50	115	255.00	161	235.50	206	242.50
26	235.50	71	253.50	116	251.50	162	232.00	207	243.50
27	257.50	72	252.50	117	255.00	163	231.00	208	249.50
28	231.00	73	250.50	118	253.50	164	245.00	209	242.00
29	234.00	74	255.00	119	251.00	165	252.50	210	245.00
30	246.00	75	254.00	120	228.00	166	229.00	211	245.00
31	252.50	76	251.50	121	241.00	167	228.00	212	241.00
32	251.50	77	251.50	122	230.50	168	230.00	213	245.00
33	252.00	78	252.50	123	229.00	169	230.00	214	232.50
34	252.00	79	251.50	124	234.50	170	218.50	215	243.50
35	253.50	80	253.00	125	229.50	171	244.00	216	231.00
36	253.50	81	252.50	126	229.00	172	239.50	217	245.00
37	253.50	82	252.50	127	230.00	173	242.50	218	245.00
38	240.50	83	251.50	128	232.50	174	234.50	219	245.00
39	247.00	84	251.50	129	252.50	175	234.00	220	240.00
40	255.00	85	252.50	130	251.50	176	235.00	221	245.00
41	250.50	86	256.00	131	241.00	177	231.00	222	241.00
42	251.00	87	225.50	132	251.00	178	233.50	223	250.00
43	257.50	88	256.00	133	246.00	179	232.50	224	250.00
44	251.50	89	252.00	134	247.00	180	229.50		
45	253.50	90	232.00	135	245.00	181	235.50		
SEd 12.14		CD (.05) 23.95							

genotypes 193 (218.00 days), 170 (218.50 days), 195 (223.00 days) and 199 (221.00 days). (Table 8)

4.2. Rhizome characters

4.2.1. Number of mother rhizomes (Table 9)

The number of mother rhizomes counted was found to have significant variations among the genotypes. It was the highest in the genotype 193 (4.00) and that was on par with 4, 5, 23, 25, 26, 27, 32, 34, 36, 37, 53, 71, 79, 84, 92, 96, 103, 112, 119, 120, 126, 130, 137, 138, 193 and 219. The lowest number of mother rhizomes was noted in genotype 43 (1.67), which was on par with genotypes 110 and 123 (1.00 each). (Table 9)

4.2.2. Weight of mother rhizomes (Table 10)

A significant variation was recorded for weight of mother rhizomes among the genotypes, which ranged between 10.10 g and 110.00 g. The genotype 153 yielded heavier rhizomes (110.00 g) and was on par with 56 (104.17 g), 73 (103.33 g), 151 (100.50 g), 153 (110.00 g), 154 (102.33 g) and 168 (104.34 g). The genotypes 63 (22.50 g) and 195 (24.17 g) were noticed as the least order. The genotypes 110 and 123 were observed for poor rhizome formation (10.10 g and 11.20 g respectively). (Table 10)

4.2.3. Girth of mother rhizomes (Table 11)

The girth of mother rhizomes measured varied significantly from 2.12 cm to 13.29 cm. The widest rhizome was registered in the genotype 154 (13.29 cm). The rhizome that measured the least was noticed in the genotype 137 (5.05 cm) followed by 90 (6.07 cm) apart from 110 (2.25 cm) and 123 (2.12 cm). (Table 11)

4.2.4. Number of primary rhizomes (Table 12)

The number of primary rhizomes counted recorded a significant variation among the genotypes. The genotypes 82, 89, 92, 108, 112, 171, 174, 180, 190, 195, 212 and 213 were on par with the genotype 191 which registered the highest (9.14). The genotypes 5, 6, 38, 58, 63, 84, 90, 97 and 137 were on par with the genotype 197 which was found to be the lowest (3.00 each) apart from 110 (1.65) and 123 (1.82). (Table 12)

Table 9. Mean performance of turmeric genotypes for number of mother rhizomes

Geno types	No. of mother rhizome	Geno types	No. of mother rhizome	Geno types	No. of mother rhizome	Geno types	No. of mother rhizome	Geno types	No. of mother rhizome
1	3.17	46	2.00	91	3.00	136	2.33	182	2.67
2	3.00	47	2.67	92	3.67	137	3.67	183	3.17
3	2.83	48	3.00	93	2.85	138	3.33	184	3.00
4	3.33	49	3.17	94	2.67	139	3.17	185	3.00
5	3.50	50	3.00	95	2.85	140	3.00	186	3.17
6	2.83	51	3.17	96	3.50	141	2.83	187	2.33
7	3.17	52	2.85	97	2.67	142	3.00	188	2.50
8	2.17	53	3.50	98	3.00	144	3.00	189	2.67
9	3.17	54	3.00	99	2.50	145	2.50	190	3.17
10	2.67	55	3.00	100	2.33	146	3.00	191	2.33
11	3.00	56	3.00	101	2.50	147	3.00	192	2.17
12	2.83	57	3.17	102	3.00	148	2.50	193	4.00
13	2.66	58	3.17	103	3.33	149	2.84	194	3.17
14	2.33	59	2.85	104	3.00	150	3.17	195	2.00
15	3.16	60	3.00	105	2.50	151	2.50	196	2.66
16	2.83	61	3.17	106	2.50	152	2.50	197	2.50
17	2.67	62	2.85	107	2.50	153	2.33	198	2.17
18	3.17	63	2.67	108	2.50	154	2.00	199	2.50
19	3.00	64	2.85	109	3.17	155	2.50	200	2.50
20	2.83	65	3.17	110	1.00	156	2.50	201	2.17
21	3.17	66	3.17	111	3.17	157	2.50	202	2.50
22	2.50	67	3.00	112	3.33	158	2.67	203	2.33
23	3.50	68	2.85	113	2.17	159	3.17	204	3.17
24	3.17	69	2.50	114	2.17	160	2.33	205	2.00
25	3.50	70	3.17	115	2.17	161	2.33	206	2.50
26	3.67	71	3.33	116	3.00	162	2.67	207	2.50
27	3.33	72	3.00	117	3.00	163	2.85	208	2.33
28	2.83	73	2.85	118	3.00	164	3.00	209	3.17
29	3.17	74	3.17	119	3.67	165	3.17	210	3.00
30	2.33	75	3.17	120	3.50	166	3.17	211	2.50
31	2.33	76	2.00	121	3.17	167	2.85	212	3.17
32	3.50	77	3.17	122	2.50	168	2.83	213	3.17
33	3.00	78	3.00	123	1.00	169	2.50	214	3.17
34	3.33	79	3.33	124	2.85	170	2.33	215	3.00
35	3.00	80	2.85	125	3.00	171	2.85	216	3.00
36	3.33	81	3.00	126	3.50	172	2.67	217	2.67
37	3.83	82	3.17	127	3.17	173	2.50	218	3.17
38	3.00	83	3.17	128	2.17	174	2.50	219	3.33
39	2.85	84	3.33	129	3.17	175	3.17	220	2.50
40	2.67	85	2.85	130	3.50	176	2.50	221	3.17
41	2.33	86	2.50	131	3.17	177	2.33	222	2.50
42	2.50	87	2.50	132	2.00	178	2.85	223	2.50
43	1.67	88	2.80	133	2.85	179	2.67	224	2.00
44	2.00	89	2.17	134	3.00	180	2.85		
45	2.50	90	2.50	135	3.00	181	2.67		

SEd 0.40 CD (.05) 0.78

Table 10. Mean performance of turmeric genotypes for weight of mother rhizomes

Geno types	Wt. of mother rhizome (g)	Geno types	Wt. of mother rhizome (g)	Geno types	Wt. of mother rhizome (g)	Geno types	Wt. of mother rhizome (g)	Geno types	Wt. of mother rhizome (g)
1	46.00	46	26.67	91	59.17	136	60.00	182	65.00
2	51.67	47	67.50	92	55.83	137	88.34	183	54.99
3	72.50	48	62.50	93	45.84	138	70.00	184	54.17
4	45.84	49	60.00	94	60.84	139	75.00	185	50.00
5	26.25	50	65.00	95	55.00	140	59.17	186	50.00
6	61.67	51	67.50	96	55.00	141	78.34	187	60.00
7	36.67	52	71.67	97	60.00	142	82.50	188	48.50
8	40.84	53	64.17	98	84.34	144	91.00	189	47.00
9	36.67	54	75.84	99	66.67	145	76.67	190	41.65
10	64.17	55	95.00	100	56.50	146	94.17	191	63.34
11	54.17	56	104.17	101	60.84	147	79.17	192	53.32
12	78.34	57	60.00	102	75.00	148	79.17	193	45.83
13	48.33	58	42.50	103	50.84	149	87.50	194	53.34
14	29.17	59	55.00	104	62.50	150	65.00	195	24.17
15	51.84	60	65.00	105	64.17	151	100.50	196	76.67
16	45.84	61	67.50	106	60.84	152	59.25	197	75.17
17	40.00	62	50.00	107	75.00	153	110.00	198	70.00
18	31.67	63	22.50	108	55.67	154	102.33	199	43.34
19	45.17	64	52.50	109	53.34	155	80.00	200	65.84
20	57.50	65	79.17	110	10.10	156	79.83	201	44.17
21	63.50	66	51.00	111	50.84	157	67.50	202	43.33
22	57.50	67	73.33	112	75.00	158	45.00	203	56.67
23	77.33	68	80.84	113	62.50	159	44.00	204	44.17
24	48.50	69	67.50	114	77.50	160	81.67	205	40.00
25	93.34	70	57.50	115	63.34	161	90.83	206	45.84
26	57.50	71	88.34	116	60.83	162	56.67	207	66.67
27	76.00	72	85.00	117	56.84	163	64.00	208	71.67
28	75.84	73	103.33	118	59.00	164	62.50	209	66.67
29	50.83	74	67.50	119	55.00	165	48.34	210	65.50
30	42.50	75	79.17	120	80.00	166	72.67	211	55.00
31	62.50	76	51.67	121	75.00	167	67.00	212	57.50
32	40.00	77	60.83	122	60.84	168	104.34	213	55.83
33	70.83	78	78.34	123	11.20	169	79.17	214	47.50
34	83.34	79	48.34	124	76.67	170	82.50	215	59.17
35	74.17	80	58.33	125	87.50	171	56.50	216	65.00
36	56.67	81	74.17	126	80.84	172	53.50	217	52.50
37	55.84	82	66.50	127	66.50	173	75.00	218	59.99
38	65.00	83	67.50	128	79.17	174	55.00	219	85.84
39	56.67	84	48.17	129	69.67	175	57.50	220	74.17
40	64.17	85	56.67	130	60.00	176	48.34	221	72.33
41	70.84	86	51.67	131	83.33	177	39.50	222	72.50
42	69.17	87	64.17	132	85.84	178	44.17	223	72.67
43	49.17	88	59.17	133	92.33	179	44.17	224	40.83
44	55.83	89	47.50	134	95.00	180	44.17		
45	49.34	90	48.50	135	79.17	181	50.50		

SEd 5.72 CD (.05) 11.28

Table 11. Mean performance of turmeric genotypes for girth of mother rhizomes

Geno types	Girth of mother rhizome (cm)	Geno types	Girth of mother rhizome (cm)	Geno types	Girth of mother rhizome (cm)	Geno types	Girth of mother rhizome (cm)	Geno types	Girth of mother rhizome (cm)
1	7.72	46	8.07	91	8.14	136	8.15	182	10.84
2	9.30	47	8.37	92	8.67	137	5.05	183	8.95
3	10.18	48	9.25	93	8.77	138	8.85	184	8.75
4	7.25	49	8.65	94	9.83	139	9.00	185	8.05
5	6.90	50	8.37	95	7.75	140	7.20	186	8.34
6	8.44	51	8.85	96	8.94	141	8.40	187	8.99
7	8.13	52	9.54	97	6.60	142	9.25	188	7.40
8	7.70	53	7.99	98	10.69	144	8.45	189	9.49
9	7.62	54	8.87	99	9.80	145	9.00	190	8.62
10	9.12	55	8.60	100	7.39	146	10.35	191	7.27
11	8.72	56	9.43	101	10.47	147	9.25	192	10.75
12	9.02	57	8.92	102	9.78	148	9.25	193	9.62
13	9.95	58	8.90	103	8.97	149	9.25	194	8.22
14	9.15	59	8.82	104	9.47	150	8.30	195	9.15
15	7.09	60	8.62	105	9.42	151	10.55	196	6.10
16	8.77	61	9.08	106	8.50	152	8.37	197	10.42
17	9.49	62	8.85	107	10.69	153	10.09	198	10.78
18	8.30	63	6.77	108	8.30	154	13.29	199	9.78
19	7.02	64	9.07	109	8.75	155	9.04	200	8.90
20	8.47	65	9.05	110	2.25	156	10.49	201	10.98
21	8.53	66	8.17	111	8.54	157	8.85	202	8.09
22	8.79	67	8.42	112	8.40	158	7.95	203	7.55
23	9.63	68	8.47	113	10.20	159	8.30	204	9.60
24	8.77	69	8.63	114	10.45	160	9.05	205	8.07
25	8.62	70	8.05	115	9.70	161	8.50	206	9.19
26	9.03	71	9.40	116	7.80	162	6.77	207	9.50
27	8.80	72	8.82	117	9.90	163	8.29	208	10.15
28	9.83	73	10.04	118	8.95	164	10.19	209	9.35
29	10.50	74	7.72	119	8.00	165	8.09	210	9.85
30	9.10	75	8.63	120	7.90	166	8.87	211	10.77
31	9.30	76	8.27	121	8.85	167	8.80	212	10.15
32	8.75	77	8.80	122	9.20	168	10.10	213	10.92
33	8.75	78	9.15	123	2.12	169	9.85	214	7.45
34	9.42	79	7.27	124	10.10	170	9.45	215	8.49
35	9.57	80	8.92	125	9.15	171	10.00	216	8.47
36	9.95	81	9.30	126	9.30	172	9.70	217	8.67
37	8.30	82	8.64	127	9.25	173	9.50	218	8.60
38	8.97	83	8.67	128	9.30	174	8.60	219	8.62
39	8.95	84	6.77	129	7.45	175	8.25	220	7.64
40	8.82	85	8.07	130	9.00	176	8.30	221	9.75
41	8.62	86	9.32	131	9.00	177	7.95	222	10.37
42	8.12	87	9.15	132	9.70	178	8.75	223	11.47
43	8.90	88	9.02	133	8.00	179	6.29	224	7.30
44	8.63	89	9.08	134	10.20	180	8.67		
45	8.15	90	6.07	135	8.75	181	8.67		

SEd 0.51 CD (.05) 1.04

Table 12. Mean performance of turmeric genotypes for number of primary rhizomes

Geno types	No. of primary rhizome	Geno types	No. of primary rhizome	Geno types	No. of primary rhizome	Geno types	No. of primary rhizome	Geno types	No. of primary rhizome
1	4.67	46	4.84	91	6.17	136	5.67	182	7.17
2	5.50	47	6.00	92	7.80	137	3.33	183	6.84
3	4.67	48	6.00	93	5.67	138	7.17	184	7.67
4	4.67	49	6.00	94	6.80	139	6.67	185	6.50
5	3.84	50	7.33	95	7.17	140	6.17	186	5.50
6	3.84	51	6.83	96	5.00	141	6.50	187	6.50
7	4.84	52	6.67	97	3.17	142	6.50	188	7.00
8	5.17	53	6.00	98	5.67	144	6.67	189	7.50
9	5.33	54	6.33	99	7.34	145	4.83	190	8.85
10	6.00	55	6.00	100	6.17	146	7.50	191	9.14
11	6.00	56	7.17	101	7.50	147	6.00	192	6.94
12	5.83	57	5.67	102	7.33	148	6.50	193	6.62
13	6.33	58	4.50	103	6.17	149	5.83	194	4.67
14	5.67	59	5.00	104	6.17	150	7.17	195	8.34
15	5.84	60	6.50	105	7.00	151	4.83	196	4.84
16	6.50	61	5.67	106	7.50	152	6.00	197	3.00
17	6.67	62	6.50	107	6.80	153	6.33	198	5.94
18	5.84	63	3.50	108	7.84	154	6.84	199	6.00
19	4.67	64	5.67	109	6.00	155	6.50	200	5.67
20	4.67	65	6.83	110	1.65	156	5.85	201	7.00
21	4.67	66	5.00	111	6.00	157	4.83	202	5.34
22	5.00	67	6.85	112	7.85	158	5.67	203	6.84
23	5.33	68	6.50	113	5.50	159	4.67	204	5.83
24	5.67	69	6.00	114	6.00	160	5.17	205	5.83
25	5.84	70	5.00	115	4.93	161	4.67	206	6.00
26	6.50	71	6.17	116	5.00	162	5.50	207	5.83
27	6.67	72	5.33	117	6.95	163	6.00	208	6.50
28	6.00	73	6.17	118	6.50	164	6.00	209	7.27
29	6.17	74	6.83	119	5.50	165	6.00	210	7.00
30	6.17	75	7.34	120	6.50	166	6.00	211	6.83
31	6.17	76	4.85	121	6.33	167	7.00	212	8.17
32	7.33	77	7.50	122	5.17	168	7.00	213	7.84
33	7.17	78	6.50	123	1.82	169	6.85	214	7.47
34	6.67	79	6.17	124	5.17	170	6.67	215	7.17
35	6.83	80	6.33	125	5.50	171	8.00	216	7.17
36	6.00	81	5.67	126	6.50	172	6.67	217	7.17
37	5.00	82	7.84	127	5.50	173	6.50	218	6.32
38	4.33	83	6.00	128	5.50	174	8.50	219	6.00
39	5.33	84	4.00	129	5.67	175	6.17	220	4.83
40	5.67	85	5.00	130	6.17	176	6.50	221	6.50
41	4.85	86	6.17	131	5.17	177	7.17	222	5.10
42	4.83	87	6.67	132	4.83	178	6.17	223	6.50
43	5.17	88	6.50	133	6.50	179	7.00	224	4.78
44	5.50	89	8.00	134	6.00	180	8.17		
45	5.67	90	3.17	135	7.00	181	6.84		

SEd 0.74 CD (.05) 1.45

4.2.5. Weight of primary rhizomes (Table 13)

The mean weight of the primary rhizomes indicated significant variation among the genotypes. The genotype 114 produced heavier rhizomes (219.50 g) and was the highest followed by genotype 89 (205.83 g). The weight of primary rhizomes was low in the genotype 123 (2.10 g) followed by 19 (3.10 g) and 110 (3.10 g), which were on par with the genotype 63 (9.45 g). (Table 13)

4.2.6. Length of primary rhizomes (Table 14)

The genotypes exhibited significant variation when measured for length of primary rhizomes that ranged between 1.20 and 10.77 cm. The longest rhizome was observed in the genotype 75 (10.77 cm) and that was on par with 2 (9.82 cm), 89 (10.07 cm), 101 (9.85 cm), 114 (9.85 cm) and 152 (9.74 cm). The shortest rhizomes were measured in the genotype 19 (1.20 cm) and it was on par with 110 (1.24 cm) and 123 (1.20 cm). (Table 14)

4.2.7. Girth of primary rhizomes (Table 15)

A significant variation was noticed within the genotypes for girth of primary rhizomes. It varied from 2.30 cm to 10.30 cm. The genotypes 135 recorded higher circumference (10.30 cm) and was on par with 198 (9.70 cm). The genotypes 19, 63, 110 and 123 showed the least circumference and were on par with each other (2.55 cm, 2.80 cm, 2.30 cm and 2.48 cm respectively). (Table 15)

4.2.8. Number of secondary rhizomes (Table 16)

The genotypes accounted a significant variation between 1.15 and 10.33 for number of secondary rhizomes. It was of the higher order in the genotype 175 (10.33) and that was on par with 52 (9.77), 101 (9.50) and 172 (9.47). The least order was noticed in the genotype 123 (1.15) and was on par with 19 (1.20), 63 (1.50) and 110 (1.22). (Table 16)

Table 13. Mean performance of turmeric genotypes for weight of primary rhizomes

Geno types	Wt. of primary rhizome (g)	Geno types	Wt. of primary rhizome (g)	Geno types	Wt. of primary rhizome (g)	Geno types	Wt. of primary rhizome (g)	Geno types	Wt. of primary rhizome (g)
1	46.67	46	99.17	91	80.00	136	88.50	182	124.17
2	137.50	47	86.67	92	79.17	137	52.50	183	122.50
3	99.17	48	119.17	93	145.84	138	107.50	184	90.00
4	72.50	49	104.17	94	117.50	139	102.67	185	79.00
5	21.25	50	106.67	95	90.84	140	100.84	186	133.33
6	75.00	51	117.50	96	84.00	141	110.84	187	156.67
7	52.50	52	135.00	97	84.00	142	190.00	188	79.17
8	67.50	53	72.50	98	95.00	144	138.00	189	92.50
9	101.67	54	112.50	99	93.34	145	140.17	190	107.50
10	105.00	55	108.33	100	133.33	146	156.00	191	114.17
11	77.50	56	124.17	101	178.50	147	95.83	192	151.00
12	97.50	57	70.83	102	141.50	148	95.00	193	62.50
13	90.84	58	25.00	103	98.50	149	60.17	194	119.17
14	61.67	59	68.34	104	110.00	150	84.84	195	40.00
15	117.50	60	152.50	105	113.33	151	137.50	196	80.84
16	89.00	61	120.83	106	158.33	152	122.50	197	122.50
17	71.67	62	100.00	107	106.50	153	178.50	198	156.84
18	19.60	63	9.45	108	96.67	154	160.00	199	119.17
19	3.10	64	62.50	109	88.33	155	192.33	200	105.00
20	67.50	65	108.34	110	3.10	156	163.33	201	60.00
21	85.84	66	30.84	111	93.33	157	100.84	202	70.84
22	130.00	67	105.84	112	136.67	158	105.67	203	110.00
23	77.50	68	152.50	113	193.33	159	92.50	204	84.17
24	74.17	69	161.67	114	219.50	160	100.00	205	95.00
25	83.34	70	60.00	115	132.00	161	95.00	206	96.67
26	91.50	71	107.50	116	143.33	162	92.50	207	112.50
27	80.84	72	106.67	117	105.17	163	91.67	208	83.34
28	122.50	73	134.17	118	91.50	164	76.67	209	130.00
29	120.00	74	145.00	119	138.84	165	90.84	210	119.17
30	108.33	75	155.00	120	118.34	166	95.83	211	116.67
31	68.34	76	135.00	121	110.50	167	109.00	212	123.33
32	91.67	77	102.00	122	58.34	168	108.34	213	112.50
33	100.03	78	100.01	123	2.10	169	105.00	214	106.17
34	85.84	79	70.00	124	94.00	170	111.84	215	107.00
35	105.83	80	133.30	125	79.00	171	100.83	216	110.00
36	76.67	81	133.33	126	62.50	172	149.17	217	115.00
37	44.99	82	125.17	127	94.00	173	117.36	218	120.00
38	65.00	83	79.17	128	118.34	174	106.00	219	119.83
39	75.00	84	45.00	129	137.17	175	92.50	220	120.00
40	59.17	85	87.50	130	62.50	176	74.00	221	100.67
41	127.50	86	77.50	131	149.50	177	80.84	222	146.67
42	114.17	87	131.00	132	184.50	178	78.34	223	85.84
43	139.17	88	122.50	133	167.84	179	96.50	224	70.84
44	110.84	89	205.83	134	190.00	180	80.84		
45	60.00	90	35.00	135	166.57	181	109.83		

SEd 5.23 CD (.05) 10.32

Table 14. Mean performance of turmeric genotypes for length of primary rhizomes

Geno types	Length of primary rhizome (cm)	Geno types	Length of primary rhizome (cm)	Geno types	Length of primary rhizome (cm)	Geno types	Length of primary rhizome (cm)	Geno types	Length of primary rhizome (cm)
1	7.09	46	8.85	91	6.95	136	7.25	182	7.17
2	9.82	47	8.09	92	6.27	137	7.20	183	6.13
3	8.77	48	7.65	93	8.82	138	7.17	184	7.09
4	6.85	49	8.30	94	8.00	139	7.74	185	9.15
5	2.45	50	8.87	95	6.25	140	8.25	186	7.33
6	6.85	51	8.47	96	6.89	141	6.20	187	6.15
7	7.44	52	9.00	97	4.88	142	8.40	188	6.10
8	6.75	53	6.50	98	9.55	144	9.05	189	6.87
9	7.84	54	7.29	99	7.37	145	8.95	190	6.30
10	9.29	55	8.64	100	9.30	146	7.13	191	7.00
11	7.44	56	8.97	101	9.85	147	8.07	192	7.80
12	6.70	57	7.33	102	8.60	148	8.15	193	5.73
13	8.62	58	5.80	103	8.97	149	6.35	194	6.14
14	6.87	59	6.00	104	8.77	150	6.15	195	4.77
15	8.79	60	9.28	105	8.17	151	8.50	196	6.54
16	6.29	61	8.72	106	9.22	152	9.74	197	7.17
17	7.79	62	9.00	107	7.09	153	9.25	198	9.10
18	6.10	63	5.24	108	7.97	154	9.29	199	7.17
19	1.20	64	5.40	109	6.77	155	8.00	200	5.95
20	6.44	65	7.54	110	1.24	156	8.99	201	5.58
21	9.03	66	7.22	111	7.52	157	8.90	202	5.47
22	9.38	67	6.70	112	8.19	158	7.05	203	6.95
23	8.22	68	8.15	113	9.04	159	8.17	204	7.84
24	8.70	69	9.17	114	9.85	160	6.28	205	5.85
25	7.85	70	5.38	115	6.60	161	6.50	206	7.07
26	6.70	71	6.37	116	7.90	162	7.17	207	7.14
27	9.04	72	7.50	117	7.50	163	8.05	208	6.97
28	7.97	73	9.10	118	7.33	164	6.25	209	6.97
29	9.50	74	9.37	119	8.05	165	7.09	210	8.22
30	8.05	75	10.77	120	7.79	166	7.95	211	8.12
31	7.50	76	9.39	121	7.10	167	8.15	212	8.00
32	6.88	77	7.45	122	5.25	168	7.75	213	7.20
33	8.97	78	8.33	123	1.20	169	7.17	214	6.65
34	6.13	79	7.30	124	8.00	170	7.17	215	7.57
35	8.63	80	8.67	125	7.25	171	6.50	216	8.32
36	8.29	81	9.55	126	5.25	172	7.59	217	7.23
37	6.88	82	8.22	127	6.92	173	7.39	218	6.60
38	7.03	83	7.25	128	7.79	174	6.98	219	8.07
39	8.90	84	7.30	129	7.27	175	6.97	220	7.30
40	7.57	85	7.69	130	5.70	176	6.75	221	6.37
41	7.62	86	7.15	131	8.45	177	6.35	222	8.30
42	8.90	87	9.33	132	8.67	178	5.74	223	5.75
43	8.90	88	8.45	133	7.42	179	6.50	224	4.75
44	8.84	89	10.07	134	7.67	180	7.60		
45	6.65	90	8.67	135	9.20	181	8.08		
SEd	0.59		CD (.05)	1.17					

Table 15. Mean performance of turmeric genotypes for girth of primary rhizomes

Geno types	Girth of primary rhizome (cm)	Geno types	Girth of primary rhizome (cm)	Geno types	Girth of primary rhizome (cm)	Geno types	Girth of primary rhizome (cm)	Geno types	Girth of primary rhizome (cm)
1	6.97	46	6.62	91	5.00	136	5.50	182	5.14
2	7.27	47	6.77	92	4.08	137	5.12	183	5.40
3	8.10	48	7.19	93	7.25	138	5.10	184	4.15
4	6.23	49	7.73	94	8.17	139	6.67	185	4.69
5	3.05	50	7.55	95	5.12	140	7.35	186	8.33
6	6.67	51	7.17	96	4.93	141	7.35	187	7.35
7	7.02	52	7.98	97	4.42	142	8.10	188	4.00
8	6.35	53	8.17	98	7.05	144	8.17	189	4.50
9	8.12	54	6.94	99	6.67	145	6.80	190	5.07
10	7.92	55	6.60	100	7.00	146	7.50	191	7.58
11	6.70	56	8.13	101	8.13	147	8.10	192	8.87
12	7.00	57	6.82	102	8.33	148	7.50	193	5.90
13	8.12	58	5.15	103	7.50	149	4.79	194	8.30
14	7.27	59	6.37	104	7.90	150	4.27	195	5.08
15	7.10	60	8.15	105	7.37	151	7.60	196	6.84
16	7.97	61	8.03	106	6.47	152	7.12	197	7.43
17	7.15	62	7.95	107	7.34	153	8.79	198	9.70
18	6.03	63	2.80	108	7.82	154	8.25	199	6.17
19	2.55	64	6.10	109	5.27	155	7.00	200	6.30
20	5.78	65	7.00	110	2.30	156	9.10	201	4.20
21	6.99	66	5.03	111	8.15	157	8.10	202	5.15
22	8.98	67	6.37	112	8.05	158	4.55	203	6.30
23	7.19	68	8.42	113	8.43	159	5.30	204	5.08
24	7.95	69	8.52	114	8.50	160	5.60	205	5.15
25	7.00	70	5.72	115	7.55	161	4.40	206	4.87
26	7.15	71	7.30	116	6.95	162	5.80	207	5.70
27	9.00	72	8.50	117	5.79	163	5.30	208	4.72
28	8.93	73	8.10	118	4.87	164	4.75	209	5.07
29	7.50	74	8.95	119	7.67	165	6.40	210	5.30
30	8.24	75	9.05	120	7.20	166	5.25	211	6.24
31	7.47	76	8.67	121	6.89	167	5.60	212	6.49
32	7.12	77	7.27	122	5.15	168	6.15	213	4.93
33	8.10	78	6.50	123	2.48	169	6.10	214	4.85
34	7.40	79	5.17	124	5.50	170	6.10	215	5.25
35	8.19	80	8.30	125	6.09	171	5.40	216	6.60
36	8.48	81	9.34	126	4.27	172	5.00	217	5.42
37	5.65	82	6.20	127	7.15	173	5.55	218	4.52
38	8.13	83	5.33	128	8.15	174	6.10	219	9.17
39	6.77	84	7.39	129	6.40	175	4.20	220	9.12
40	5.23	85	5.79	130	3.35	176	4.35	221	6.62
41	7.33	86	6.67	131	8.67	177	5.35	222	7.58
42	8.77	87	8.23	132	9.25	178	4.95	223	5.70
43	8.52	88	7.35	133	8.10	179	4.85	224	4.67
44	7.60	89	8.70	134	8.27	180	5.60		
45	7.14	90	3.98	135	10.30	181	6.07		

SEd 0.47 CD (.05) 0.92

Table 16. Mean performance of turmeric genotypes for number of secondary rhizomes

Geno types	No. of secondary rhizome	Geno types	No. of secondary rhizome	Geno types	No. of secondary rhizome	Geno types	No. of secondary rhizome	Geno types	No. of secondary rhizome
1	7.17	46	4.50	91	7.22	136	6.17	182	8.33
2	8.50	47	6.85	92	7.27	137	4.43	183	8.67
3	8.33	48	5.67	93	8.17	138	6.59	184	8.67
4	7.50	49	5.25	94	7.17	139	7.50	185	8.67
5	3.17	50	6.00	95	8.83	140	8.00	186	6.33
6	7.17	51	5.33	96	7.50	141	8.50	187	7.33
7	8.00	52	9.77	97	3.94	142	6.85	188	7.20
8	7.67	53	6.50	98	7.67	144	6.17	189	7.13
9	6.85	54	6.17	99	7.84	145	6.27	190	8.84
10	7.50	55	7.00	100	8.00	146	6.33	191	6.50
11	7.17	56	7.50	101	9.50	147	8.27	192	5.17
12	7.33	57	7.10	102	7.17	148	7.27	193	6.50
13	6.17	58	4.27	103	8.33	149	6.79	194	6.17
14	5.85	59	6.27	104	8.44	150	5.75	195	4.60
15	8.17	60	7.50	105	7.05	151	6.10	196	5.17
16	7.17	61	7.50	106	7.27	152	5.84	197	6.00
17	7.17	62	8.84	107	7.09	153	6.83	198	6.17
18	8.50	63	1.50	108	8.17	154	6.00	199	7.50
19	1.20	64	8.17	109	6.42	155	7.05	200	7.59
20	6.00	65	7.17	110	1.22	156	6.75	201	6.17
21	8.00	66	5.85	111	8.50	157	6.27	202	8.59
22	6.17	67	8.00	112	7.33	158	7.17	203	6.27
23	7.00	68	7.85	113	8.10	159	7.67	204	7.17
24	7.50	69	7.27	114	8.85	160	7.04	205	6.83
25	6.50	70	7.17	115	7.50	161	6.50	206	7.00
26	8.50	71	6.95	116	8.17	162	6.42	207	7.50
27	7.50	72	7.33	117	7.85	163	5.92	208	6.00
28	7.17	73	7.13	118	8.17	164	6.50	209	6.59
29	7.17	74	8.50	119	7.50	165	7.44	210	7.27
30	8.50	75	6.67	120	7.33	166	6.82	211	5.84
31	6.85	76	7.50	121	6.17	167	6.50	212	7.59
32	8.00	77	8.00	122	5.43	168	6.44	213	8.17
33	8.85	78	7.50	123	1.15	169	6.12	214	6.67
34	7.50	79	7.17	124	6.17	170	8.67	215	6.17
35	6.67	80	6.85	125	8.12	171	9.17	216	6.84
36	7.00	81	6.83	126	5.50	172	9.47	217	6.50
37	6.50	82	7.83	127	7.85	173	7.67	218	8.17
38	5.17	83	7.25	128	6.17	174	7.90	219	7.49
39	6.67	84	7.20	129	7.17	175	10.33	220	8.99
40	6.17	85	6.50	130	7.50	176	8.20	221	7.49
41	7.17	86	6.33	131	5.85	177	8.00	222	4.83
42	5.50	87	5.85	132	6.10	178	6.63	223	7.67
43	7.50	88	6.50	133	6.95	179	8.00	224	6.17
44	6.00	89	7.67	134	5.93	180	5.20		
45	6.17	90	4.77	135	7.10	181	6.33		

SEd 0.52 CD (.05) 1.03

4.2.9. Weight of secondary rhizomes (Table 17)

The difference in weight of secondary rhizomes extended from 2.37 g to 144.00 g within the genotypes. The genotype 114 exhibited heaviest rhizomes (144.00 g) and was significant from 156 (129.17 g). The genotypes 19, 63, 110 and 123 recorded the least weight and were on par with each other (2.37 g, 5.50 g, 3.62 g and 2.55 g respectively). (Table 17)

4.2.10. Length of secondary rhizomes (Table 18)

The genotypes showed a significant variation when measured for its length, which ranged between 1.95 cm and 8.52 cm. The lengthiest rhizome was accounted in the genotype 61 (8.52 cm), which was on par with 15 (8.28 cm), 51 (8.12cm), 76 (8.18 cm), 101 (8.20 cm) and 114 (8.15 cm). The shortest rhizome was measured in the genotype 123 (1.95cm) that was on par with 110 (2.20 cm) and 19 (2.30 cm). (Table 18)

4.2.11. Girth of secondary rhizomes (Table 19)

The girth of secondary rhizomes measured varied significantly from 1.00 cm to 8.09 cm. The largest rhizome was encountered in the genotypes 219 and 22 (8.09 cm and 8.08 cm respectively). The girth measured was the least in the genotypes 63, 110 and 123 (1.00 cm each) that was on par with 19 (1.05 cm). (Table 19)

4.2.12. Rhizome diameter (Table 20)

The genotypes differed significantly with reference to rhizome diameter, which ranged between 0.40 and 2.78 cm. The genotype 22 registered the highest rhizome diameter (2.78 cm) that was on par with genotypes 2 (2.55 cm), 3 (2.54 cm), 9 (2.60 cm), 27 (2.65 cm), 33 (2.55 cm), 43 (2.53 cm), 132 (2.55 cm), 133 (2.55 cm) and 142 (2.55 cm). The rhizome diameter was least in the genotype 123 (0.38 cm), which was on par with 19 (0.40 cm), 63 (0.49 cm), 110 (0.58 cm), 117 (0.60 cm), 118 (0.55 cm), 120 (0.50 cm) and 121 (0.65 cm). (Table 20)

Table 17. Mean performance of turmeric genotypes for weight of secondary rhizomes

Geno types	Wt. of secondary rhizome (g)	Geno types	Wt. of secondary rhizome (g)	Geno types	Wt. of secondary rhizome (g)	Geno types	Wt. of secondary rhizome (g)	Geno types	Wt. of secondary rhizome (g)
1	34.17	46	50.67	91	76.00	136	60.84	182	75.84
2	81.67	47	53.34	92	42.50	137	35.84	183	80.84
3	80.84	48	74.17	93	85.00	138	55.84	184	61.67
4	56.67	49	84.17	94	62.33	139	72.50	185	74.00
5	16.50	50	56.67	95	65.84	140	96.00	186	77.50
6	59.34	51	77.50	96	46.65	141	83.00	187	92.50
7	60.67	52	96.50	97	30.67	142	106.50	188	46.00
8	51.67	53	40.85	98	43.34	144	72.50	189	60.84
9	85.00	54	61.67	99	60.67	145	102.33	190	56.67
10	75.00	55	75.84	100	97.50	146	92.34	191	65.83
11	42.50	56	78.50	101	114.17	147	81.67	192	102.50
12	42.50	57	52.50	102	100.02	148	76.67	193	42.33
13	54.17	58	17.50	103	75.84	149	52.50	194	62.67
14	38.33	59	40.85	104	90.00	150	60.00	195	20.84
15	103.17	60	94.17	105	106.67	151	75.00	196	40.00
16	37.33	61	106.50	106	100.67	152	78.33	197	57.00
17	39.17	62	90.85	107	84.17	153	73.33	198	104.00
18	21.67	63	5.50	108	98.50	154	90.67	199	70.67
19	2.37	64	55.85	109	70.84	155	104.34	200	70.00
20	30.00	65	79.34	110	3.62	156	129.17	201	43.33
21	77.50	66	22.50	111	86.67	157	115.00	202	62.50
22	74.17	67	97.50	112	92.50	158	66.67	203	55.84
23	60.84	68	94.00	113	112.50	159	70.84	204	60.84
24	47.49	69	85.00	114	144.00	160	85.83	205	82.50
25	44.17	70	50.00	115	109.50	161	76.67	206	68.50
26	56.67	71	62.50	116	77.50	162	74.17	207	72.33
27	40.00	72	68.67	117	99.83	163	63.34	208	72.50
28	72.50	73	84.17	118	67.33	164	69.17	209	74.17
29	84.17	74	88.50	119	75.84	165	54.50	210	72.50
30	75.00	75	80.00	120	86.67	166	65.84	211	114.17
31	39.17	76	84.17	121	74.34	167	69.17	212	80.83
32	54.00	77	52.67	122	38.34	168	70.84	213	70.67
33	47.50	78	73.33	123	2.55	169	85.00	214	72.50
34	45.83	79	53.33	124	70.67	170	79.17	215	80.83
35	72.50	80	85.00	125	85.00	171	71.50	216	80.83
36	70.00	81	76.67	126	60.84	172	65.84	217	81.65
37	30.67	82	73.33	127	71.67	173	95.00	218	82.49
38	40.84	83	43.33	128	70.84	174	52.50	219	82.52
39	50.67	84	37.50	129	84.17	175	72.50	220	100.67
40	40.84	85	45.00	130	40.84	176	72.50	221	95.99
41	84.17	86	56.67	131	104.17	177	50.84	222	70.67
42	70.00	87	85.00	132	96.67	178	32.17	223	41.67
43	80.84	88	82.50	133	108.67	179	60.67	224	36.67
44	76.67	89	115.00	134	122.67	180	60.67		
45	39.17	90	32.50	135	102.33	181	74.17		
SEd	3.29	CD (.05)	6.50						

Table 18. Mean performance of turmeric genotypes for length of secondary rhizomes

Geno types	Length of secondary rhizome (cm)	Geno types	Length of secondary rhizome (cm)	Geno types	Length of secondary rhizome (cm)	Geno types	Length of secondary rhizome (cm)	Geno types	Length of secondary rhizome (cm)
1	4.77	46	6.10	91	6.10	136	6.05	182	6.35
2	7.40	47	5.57	92	5.78	137	5.05	183	5.55
3	6.10	48	5.17	93	6.42	138	6.15	184	5.30
4	5.54	49	6.97	94	6.50	139	5.35	185	5.15
5	7.20	50	6.47	95	5.90	140	6.05	186	6.63
6	6.57	51	8.12	96	5.10	141	6.75	187	6.43
7	6.03	52	6.33	97	5.52	142	6.85	188	5.55
8	7.29	53	5.12	98	5.03	144	7.00	189	4.67
9	6.90	54	6.30	99	5.77	145	6.25	190	5.25
10	6.10	55	7.10	100	7.67	146	6.02	191	5.99
11	5.55	56	6.34	101	8.20	147	5.55	192	6.30
12	6.50	57	5.98	102	7.34	148	4.67	193	4.43
13	6.54	58	3.77	103	5.67	149	4.68	194	4.55
14	6.50	59	4.79	104	6.00	150	4.55	195	2.95
15	8.28	60	7.05	105	5.43	151	5.21	196	4.63
16	5.45	61	8.52	106	7.87	152	5.02	197	5.35
17	5.82	62	7.75	107	5.43	153	6.52	198	7.65
18	5.05	63	7.10	108	5.62	154	6.09	199	5.72
19	2.30	64	5.35	109	7.15	155	7.15	200	4.85
20	4.90	65	5.35	110	2.20	156	5.97	201	4.17
21	6.69	66	3.99	111	6.74	157	4.87	202	4.80
22	7.10	67	6.40	112	5.10	158	5.79	203	5.02
23	7.19	68	6.05	113	6.33	159	6.58	204	5.62
24	6.69	69	7.40	114	8.15	160	5.88	205	6.25
25	4.43	70	4.75	115	6.30	161	4.60	206	4.95
26	5.98	71	5.93	116	6.55	162	5.05	207	5.15
27	5.30	72	6.74	117	6.35	163	5.14	208	5.15
28	6.17	73	5.98	118	5.50	164	5.32	209	5.30
29	5.70	74	6.98	119	5.40	165	4.84	210	5.62
30	7.85	75	7.28	120	6.10	166	4.32	211	6.28
31	4.72	76	8.18	121	4.65	167	5.43	212	5.57
32	7.57	77	6.15	122	5.45	168	6.05	213	5.75
33	6.89	78	6.15	123	1.95	169	4.92	214	4.43
34	7.05	79	5.98	124	5.10	170	5.42	215	6.09
35	7.07	80	5.75	125	5.35	171	6.25	216	7.75
36	5.47	81	6.10	126	5.35	172	5.05	217	5.99
37	4.47	82	5.55	127	5.00	173	5.04	218	6.58
38	5.09	83	4.65	128	6.35	174	4.95	219	5.70
39	6.60	84	5.17	129	5.65	175	4.85	220	5.64
40	4.12	85	5.82	130	5.10	176	4.80	221	6.80
41	6.09	86	5.15	131	6.30	177	5.00	222	5.58
42	6.42	87	7.25	132	6.35	178	5.60	223	5.21
43	6.55	88	7.27	133	6.15	179	5.15	224	4.43
44	5.57	89	7.37	134	7.05	180	6.25		
45	4.99	90	4.72	135	7.30	181	6.30		
SEd	0.24	CD (.05)	0.47						

Table 19. Mean performance of turmeric genotypes for girth of secondary rhizomes

Geno types	Girth of secondary rhizome (cm)	Geno types	Girth of secondary rhizome (cm)	Geno types	Girth of secondary rhizome (cm)	Geno types	Girth of secondary rhizome (cm)	Geno types	Girth of secondary rhizome (cm)
1	4.67	46	4.95	91	5.12	136	5.10	182	4.50
2	6.40	47	5.04	92	4.30	137	2.90	183	4.75
3	6.60	48	4.87	93	6.59	138	4.95	184	4.25
4	5.12	49	6.35	94	5.14	139	3.70	185	3.27
5	5.37	50	6.20	95	4.60	140	4.55	186	4.65
6	5.95	51	6.02	96	4.08	141	4.25	187	5.58
7	5.67	52	6.55	97	3.63	142	4.60	188	3.60
8	6.07	53	6.47	98	2.97	144	3.70	189	3.55
9	7.30	54	5.75	99	3.85	145	3.45	190	4.15
10	7.12	55	6.90	100	5.70	146	6.70	191	4.28
11	5.48	56	7.33	101	4.68	147	4.99	192	7.09
12	6.27	57	4.77	102	6.81	148	3.40	193	4.55
13	6.60	58	2.43	103	4.99	149	3.89	194	4.90
14	5.85	59	4.67	104	4.00	150	3.18	195	1.89
15	6.79	60	6.17	105	4.89	151	3.89	196	4.42
16	5.30	61	6.45	106	5.10	152	3.68	197	4.17
17	4.74	62	6.55	107	3.67	153	4.99	198	7.05
18	3.92	63	1.00	108	5.00	154	4.55	199	4.81
19	1.05	64	1.95	109	5.20	155	3.89	200	4.87
20	5.45	65	5.12	110	1.00	156	4.85	201	3.00
21	7.17	66	4.15	111	4.27	157	3.10	202	4.19
22	8.08	67	5.20	112	3.42	158	4.19	203	3.10
23	6.95	68	5.70	113	4.59	159	4.59	204	4.17
24	5.17	69	6.62	114	4.75	160	4.17	205	4.92
25	4.90	70	6.85	115	4.35	161	2.92	206	3.09
26	5.82	71	4.95	116	4.55	162	3.62	207	2.99
27	6.17	72	6.15	117	4.90	163	4.17	208	3.40
28	5.70	73	5.11	118	4.35	164	3.59	209	4.42
29	6.85	74	5.03	119	4.45	165	4.10	210	5.07
30	6.75	75	6.73	120	4.70	166	2.97	211	3.26
31	5.50	76	6.05	121	6.10	167	5.55	212	4.00
32	6.37	77	6.17	122	3.90	168	5.43	213	4.30
33	5.15	78	4.48	123	1.00	169	4.67	214	2.90
34	7.15	79	4.35	124	5.25	170	4.08	215	4.50
35	7.30	80	4.22	125	5.20	171	3.97	216	4.53
36	6.40	81	5.77	126	3.45	172	3.55	217	3.70
37	4.68	82	5.17	127	3.35	173	4.15	218	5.55
38	4.60	83	2.79	128	4.15	174	3.89	219	8.09
39	4.64	84	3.65	129	3.80	175	4.25	220	4.19
40	4.06	85	4.35	130	2.95	176	4.42	221	5.68
41	5.35	86	3.40	131	6.95	177	3.47	222	5.54
42	6.94	87	4.70	132	6.25	178	4.15	223	4.89
43	5.84	88	5.95	133	7.35	179	3.30	224	4.47
44	6.17	89	5.42	134	7.00	180	4.28		
45	4.77	90	2.05	135	5.15	181	5.09		
SEd	0.36	CD (.05) 0.71							

Table 20. Mean performance of turmeric genotypes for rhizome diameter

Geno types	Rhizome Diameter (cm)	Geno types	Rhizome Diameter (cm)	Geno types	Rhizome Diameter (cm)	Geno types	Rhizome Diameter (cm)	Geno types	Rhizome Diameter (cm)
1	2.00	46	2.15	91	1.88	136	2.05	182	1.75
2	2.55	47	2.05	92	1.79	137	1.20	183	1.52
3	2.54	48	2.17	93	1.83	138	1.23	184	1.45
4	2.45	49	2.30	94	2.15	139	1.43	185	1.19
5	1.40	50	2.44	95	1.48	140	1.55	186	1.90
6	2.30	51	2.35	96	1.85	141	2.10	187	2.12
7	2.05	52	2.29	97	1.75	142	2.55	188	1.50
8	2.07	53	2.19	98	1.86	144	1.68	189	1.45
9	2.60	54	2.14	99	1.89	145	1.94	190	1.75
10	2.50	55	2.23	100	1.92	146	1.87	191	2.06
11	1.68	56	2.17	101	2.10	147	2.01	192	2.28
12	2.00	57	1.90	102	1.95	148	1.98	193	1.42
13	2.25	58	1.80	103	2.09	149	1.50	194	2.15
14	2.03	59	1.85	104	1.59	150	1.65	195	1.15
15	2.50	60	2.17	105	2.20	151	1.82	196	1.58
16	1.58	61	2.02	106	1.70	152	2.17	197	2.02
17	1.74	62	2.00	107	1.92	153	2.22	198	2.20
18	1.25	63	0.49	108	2.25	154	2.00	199	1.72
19	0.40	64	1.62	109	1.80	155	1.75	200	1.72
20	1.97	65	1.75	110	0.58	156	1.85	201	1.45
21	2.15	66	1.60	111	2.00	157	1.55	202	1.27
22	2.78	67	2.09	112	2.15	158	1.35	203	1.77
23	1.55	68	2.28	113	2.37	159	1.47	204	1.35
24	2.12	69	2.06	114	1.20	160	1.50	205	1.65
25	1.59	70	1.83	115	1.10	161	1.42	206	1.50
26	2.00	71	2.05	116	1.25	162	1.57	207	1.48
27	2.65	72	2.02	117	0.60	163	1.55	208	1.35
28	2.40	73	2.05	118	0.55	164	1.49	209	1.45
29	2.08	74	2.38	119	1.35	165	1.80	210	1.68
30	2.50	75	2.20	120	0.50	166	1.42	211	1.79
31	1.95	76	2.17	121	0.65	167	1.39	212	1.65
32	1.88	77	1.87	122	0.90	168	1.40	213	1.55
33	2.55	78	2.19	123	0.38	169	1.50	214	1.45
34	1.98	79	1.95	124	1.85	170	1.55	215	1.48
35	2.49	80	2.38	125	1.90	171	1.50	216	1.40
36	2.29	81	2.18	126	1.45	172	1.90	217	1.45
37	1.72	82	1.85	127	2.10	173	1.77	218	1.42
38	1.97	83	1.80	128	2.15	174	1.80	219	2.17
39	1.89	84	1.85	129	2.05	175	1.59	220	1.60
40	1.94	85	1.91	130	1.45	176	0.97	221	1.44
41	2.17	86	1.85	131	2.50	177	1.50	222	2.27
42	2.33	87	2.28	132	2.55	178	1.61	223	2.05
43	2.53	88	2.22	133	2.55	179	1.60	224	2.02
44	2.47	89	2.37	134	2.15	180	1.39		
45	2.13	90	1.59	135	2.25	181	1.90		

SEd 0.14 CD (.05) 0.27

4.2.13. Core diameter (Table 21)

The genotypes indicated significant variations for core diameter that varied from 0.23 cm to 1.80 cm. The genotype 80 recorded the highest core diameter (1.80 cm) that was on par with genotypes 9 (1.72 cm), 22 (1.75 cm), 43 (1.72 cm) and 44 (1.75 cm). The least core diameter was measured in genotype 19 (0.23 cm) that was on par with genotypes 63 (0.35 cm), 110 (0.30 cm), 123 (0.30 cm), 185 (0.40 cm) and 195 (0.40 cm). (Table 21)

4.2.14. Rhizome core ratio (Table 22)

There was significant variation for rhizome core ratio among the genotypes ranging between 0.65 and 3.46. It was of higher order in the genotype 90 (3.46), which was on par with 178 (3.22), 189 (3.26) and 193 (3.41). The least order was noticed in the genotypes 114 (0.76), 115 (0.76), 120 (0.71) and 121 (0.65). (Table 22)

4.2.15. Oil (Table 23)

The difference in quality of rhizomes with reference to oil was found to be non-significant among the genotypes. The genotypes quantified for oil varied from 1.00 to 1.48 per cent. (Table 23)

4.2.16. Oleoresin (Table 24)

The genotypes exhibited non-significant variation when estimated for oleoresin content. The oleoresin content ranged between 2.90 and 5.55 per cent. (Table 24)

4.2.17. Curcumin (Table 25)

A significant variation was noticed for curcumin among the genotypes, which varied from 1.73 to 5.94 per cent. The genotype 146 possessed the highest curcumin content of 5.94 per cent and was significant from the genotype 67 (5.23 %). The least curcumin content was noticed in the genotype 26 (1.73 %) that was on par with 44 (1.85 %). (Table 25)

Table 21. Mean performance of turmeric genotypes for core diameter

Geno types	Core Diameter (cm)	Geno types	Core Diameter (cm)	Geno types	Core Diameter (cm)	Geno types	Core Diameter (cm)	Geno types	Core Diameter (cm)
1	1.30	46	1.45	91	0.72	136	0.95	182	0.65
2	1.62	47	1.29	92	0.84	137	0.60	183	0.67
3	1.35	48	1.40	93	1.04	138	0.65	184	0.56
4	1.00	49	1.40	94	1.25	139	0.45	185	0.40
5	0.49	50	1.53	95	0.67	140	0.60	186	1.17
6	1.59	51	1.25	96	0.92	141	1.10	187	1.15
7	0.98	52	1.30	97	0.93	142	1.55	188	0.59
8	0.86	53	0.95	98	0.90	144	0.95	189	0.45
9	1.72	54	1.15	99	1.04	145	1.15	190	0.65
10	1.40	55	1.05	100	0.84	146	1.05	191	0.85
11	1.01	56	0.93	101	0.97	147	0.95	192	1.28
12	0.86	57	0.95	102	0.90	148	0.95	193	0.42
13	1.55	58	0.55	103	1.15	149	0.50	194	1.22
14	1.30	59	0.95	104	0.90	150	0.65	195	0.40
15	1.45	60	1.50	105	1.47	151	0.95	196	0.88
16	1.19	61	0.98	106	0.57	152	1.45	197	0.88
17	1.03	62	1.27	107	0.95	153	1.17	198	0.82
18	0.50	63	0.35	108	1.45	154	1.17	199	0.74
19	0.23	64	0.55	109	0.90	155	0.80	200	0.74
20	1.40	65	0.65	110	0.30	156	0.85	201	0.60
21	1.28	66	0.70	111	1.05	157	0.75	202	0.53
22	1.75	67	0.91	112	1.47	158	0.55	203	0.57
23	1.10	68	1.35	113	1.45	159	0.74	204	0.67
24	1.13	69	1.18	114	1.58	160	0.54	205	0.57
25	0.70	70	0.74	115	1.45	161	0.63	206	0.62
26	1.05	71	1.02	116	1.37	162	0.95	207	0.55
27	1.40	72	1.05	117	0.55	163	0.50	208	0.59
28	1.34	73	1.40	118	0.55	164	0.56	209	0.47
29	1.20	74	1.38	119	1.15	165	0.90	210	0.88
30	1.50	75	1.10	120	0.70	166	0.57	211	0.90
31	1.05	76	1.18	121	1.00	167	0.58	212	0.67
32	1.13	77	0.82	122	0.65	168	0.55	213	0.51
33	1.30	78	1.27	123	0..30	169	0.60	214	0.46
34	1.10	79	0.98	124	0.85	170	0.50	215	0.55
35	1.40	80	1.80	125	0.95	171	0.63	216	0.88
36	1.48	81	0.72	126	0.55	172	0.88	217	0.65
37	0.71	82	1.00	127	1.25	173	0.58	218	1.39
38	1.37	83	0.90	128	1.20	174	0.61	219	1.37
39	0.87	84	0.80	129	0.85	175	0.62	220	0.78
40	0.98	85	0.96	130	0.50	176	0.62	221	0.88
41	1.38	86	0.85	131	1.60	177	0.50	222	1.15
42	1.49	87	1.27	132	1.50	178	0.50	223	1.10
43	1.72	88	1.48	133	1.40	179	0.56	224	1.05
44	1.75	89	1.45	134	1.10	180	0.54		
45	0.68	90	0.46	135	1.10	181	0.87		

SEd 0.08 CD (.05) 0.17

Table 22. Mean performance of turmeric genotypes for rhizome core ratio

Geno types	Rhizome Core - ratio	Geno types	Rhizome Core - ratio	Geno types	Rhizome Core - ratio	Geno types	Rhizome Core - ratio	Geno types	Rhizome Core - ratio
1	1.54	46	1.48	91	2.61	136	2.16	182	2.71
2	1.58	47	1.59	92	2.13	137	2.00	183	2.29
3	1.80	48	1.55	93	1.87	138	1.89	184	2.59
4	1.50	49	1.64	94	1.72	139	3.18	185	2.97
5	2.88	50	1.59	95	2.24	140	2.58	186	1.64
6	1.44	51	1.80	96	2.01	141	1.83	187	1.84
7	2.12	52	1.76	97	1.88	142	1.65	188	2.57
8	2.95	53	2.12	98	2.07	144	1.77	189	3.26
9	1.67	54	1.86	99	1.82	145	1.80	190	2.71
10	1.78	55	2.15	100	2.29	146	1.78	191	2.43
11	1.65	56	2.15	101	2.16	147	2.12	192	1.79
12	2.33	57	2.17	102	2.17	148	2.08	193	3.41
13	1.45	58	2.01	103	1.82	149	2.91	194	1.77
14	1.57	59	3.10	104	1.77	150	2.48	195	2.89
15	1.70	60	1.95	105	1.50	151	1.92	196	1.80
16	1.33	61	1.45	106	3.01	152	1.46	197	2.30
17	1.70	62	2.07	107	2.02	153	1.91	198	2.70
18	2.50	63	1.55	108	1.55	154	1.72	199	2.35
19	1.73	64	2.45	109	2.00	155	2.50	200	2.31
20	1.41	65	2.69	110	1.35	156	2.19	201	2.42
21	1.69	66	2.70	111	1.91	157	2.08	202	2.40
22	1.76	67	2.27	112	1.43	158	2.45	203	3.05
23	1.04	68	1.75	113	1.63	159	2.00	204	2.02
24	1.88	69	1.74	114	0.76	160	2.78	205	2.82
25	2.25	70	2.19	115	0.76	161	2.26	206	2.31
26	1.50	71	2.03	116	0.91	162	1.67	207	2.69
27	1.88	72	1.93	117	1.09	163	3.10	208	2.33
28	1.89	73	1.48	118	1.00	164	2.65	209	3.13
29	1.73	74	1.73	119	1.18	165	2.02	210	1.91
30	1.66	75	2.01	120	0.71	166	2.53	211	1.99
31	1.86	76	1.84	121	0.65	167	2.40	212	2.48
32	1.67	77	2.28	122	1.07	168	2.33	213	2.74
33	1.97	78	1.72	123	1.28	169	2.51	214	3.14
34	1.80	79	1.99	124	2.18	170	3.10	215	2.72
35	1.78	80	1.32	125	2.00	171	2.38	216	1.59
36	1.55	81	3.03	126	2.24	172	2.12	217	2.07
37	2.42	82	1.85	127	1.68	173	3.05	218	2.18
38	1.44	83	2.00	128	1.79	174	2.93	219	1.01
39	2.18	84	2.31	129	2.41	175	2.58	220	1.05
40	1.97	85	1.99	130	2.90	176	1.57	221	2.48
41	1.56	86	2.18	131	1.56	177	3.00	222	1.98
42	1.58	87	1.80	132	1.70	178	3.22	223	1.78
43	1.47	88	1.50	133	1.82	179	2.86	224	1.83
44	1.45	89	1.63	134	1.95	180	2.57		
45	3.21	90	3.46	135	2.05	181	2.19		

SEd 0.12 CD (.05) 0.24

Table 23. Mean performance of turmeric genotypes for oil

Geno types	Oil (%)	Geno types	Oil (%)	Geno types	Oil (%)	Geno types	Oil (%)	Geno types	Oil (%)
1	1.30	46	1.20	91	1.11	136	1.19	182	1.21
2	1.48	47	1.21	92	1.21	137	1.11	183	1.17
3	1.30	48	1.17	93	1.15	138	1.31	184	1.11
4	1.21	49	1.18	94	1.25	139	1.12	185	1.20
5	1.24	50	1.29	95	1.19	140	1.25	186	1.19
6	1.18	51	1.26	96	1.25	141	1.37	187	1.12
7	1.29	52	1.26	97	1.21	142	1.16	188	1.25
8	1.27	53	1.26	98	1.23	144	1.24	189	1.21
9	1.25	54	1.27	99	1.25	145	1.35	190	1.24
10	1.19	55	1.19	100	1.26	146	1.34	191	1.11
11	1.21	56	1.19	101	1.16	147	1.34	192	1.18
12	1.23	57	1.20	102	1.12	148	1.36	193	1.25
13	1.20	58	1.17	103	1.14	149	1.27	194	1.23
14	1.18	59	1.26	104	1.16	150	1.21	195	1.32
15	1.25	60	1.16	105	1.25	151	1.28	196	1.19
16	1.25	61	1.27	106	1.27	152	1.32	197	1.30
17	1.25	62	1.26	107	1.21	153	1.11	198	1.29
18	1.24	63	1.20	108	1.29	154	1.28	199	1.26
19	1.23	64	1.25	109	1.25	155	1.29	200	1.25
20	1.21	65	1.26	110	1.26	156	1.30	201	1.23
21	1.20	66	1.17	111	1.21	157	1.29	202	1.22
22	1.19	67	1.11	112	1.29	158	1.28	203	1.25
23	1.18	68	1.21	113	1.23	159	1.27	204	1.19
24	1.28	69	1.26	114	1.25	160	1.29	205	1.12
25	1.29	70	1.18	115	1.21	161	1.21	206	1.16
26	1.30	71	1.25	116	1.19	162	1.25	207	1.19
27	1.24	72	1.16	117	1.17	163	1.24	208	1.21
28	1.25	73	1.20	118	1.11	164	1.20	209	1.24
29	1.20	74	1.17	119	1.19	165	1.22	210	1.25
30	1.19	75	1.25	120	1.28	166	1.19	211	1.23
31	1.20	76	1.20	121	1.36	167	1.19	212	1.22
32	1.21	77	1.11	122	1.45	168	1.19	213	1.19
33	1.24	78	1.07	123	1.35	169	1.12	214	1.12
34	1.25	79	1.25	124	1.25	170	1.25	215	1.07
35	1.25	80	1.20	125	1.26	171	1.26	216	1.24
36	1.19	81	1.25	126	1.32	172	1.16	217	1.11
37	1.20	82	1.26	127	1.30	173	1.11	218	1.23
38	1.19	83	1.20	128	1.28	174	1.26	219	1.20
39	1.19	84	1.17	129	1.24	175	1.30	220	1.24
40	1.29	85	1.16	130	1.40	176	1.21	221	1.00
41	1.20	86	1.11	131	1.37	177	1.19	222	1.19
42	1.26	87	1.18	132	1.36	178	1.16	223	1.19
43	1.11	88	1.24	133	1.33	179	1.19	224	1.20
44	1.17	89	1.25	134	1.24	180	1.19		
45	1.19	90	1.20	135	1.25	181	1.24		

SEd 0.09 CD (.05) 0.18

Table 24. Mean performance of turmeric genotypes for oleoresin

Geno types	Oleoresin (%)	Geno types	Oleoresin (%)	Geno types	Oleoresin (%)	Geno types	Oleoresin (%)	Geno types	Oleoresin (%)
1	4.21	46	4.22	91	3.94	136	4.26	182	4.51
2	5.55	47	4.26	92	4.17	137	3.94	183	4.61
3	4.70	48	4.00	93	3.99	138	4.34	184	4.71
4	4.62	49	4.17	94	4.24	139	3.89	185	4.78
5	4.81	50	4.11	95	4.16	140	4.21	186	4.30
6	4.18	51	4.18	96	4.17	141	4.22	187	4.18
7	4.16	52	4.66	97	4.22	142	3.97	188	4.30
8	4.32	53	4.26	98	4.21	144	3.87	189	3.87
9	3.90	54	4.25	99	4.18	145	4.21	190	4.79
10	4.31	55	4.41	100	4.18	146	4.59	191	4.46
11	4.09	56	4.34	101	4.04	147	4.63	192	4.29
12	4.04	57	4.25	102	4.11	148	4.36	193	5.18
13	4.34	58	4.14	103	4.04	149	4.24	194	3.89
14	4.22	59	4.16	104	4.11	150	4.04	195	4.21
15	4.09	60	4.11	105	4.26	151	4.71	196	4.16
16	4.56	61	4.31	106	4.24	152	4.74	197	3.91
17	4.22	62	4.45	107	4.21	153	3.90	198	4.47
18	4.05	63	4.30	108	4.18	154	4.65	199	4.31
19	4.14	64	4.66	109	4.16	155	4.73	200	4.12
20	4.19	65	4.61	110	4.26	156	4.68	201	4.00
21	4.16	66	4.39	111	4.34	157	3.89	202	4.01
22	4.74	67	4.35	112	4.24	158	3.82	203	3.89
23	4.15	68	4.31	113	4.17	159	4.02	204	4.17
24	4.74	69	4.20	114	4.35	160	4.17	205	4.09
25	4.24	70	4.31	115	4.21	161	4.41	206	3.92
26	4.16	71	4.12	116	4.17	162	4.48	207	3.89
27	4.09	72	4.20	117	4.00	163	4.56	208	3.79
28	3.87	73	4.22	118	3.94	164	4.32	209	3.56
29	4.18	74	4.11	119	4.00	165	4.40	210	3.58
30	4.28	75	4.29	120	4.31	166	4.39	211	3.60
31	4.42	76	4.16	121	4.40	167	4.59	212	3.81
32	4.47	77	4.18	122	4.59	168	4.37	213	4.08
33	4.72	78	4.01	123	4.41	169	3.90	214	4.18
34	4.66	79	4.16	124	4.37	170	4.01	215	3.81
35	4.09	80	4.14	125	4.37	171	3.98	216	4.05
36	4.30	81	4.13	126	4.26	172	4.48	217	4.07
37	4.19	82	4.22	127	4.29	173	5.05	218	3.81
38	4.05	83	4.11	128	4.16	174	2.90	219	3.48
39	4.01	84	3.94	129	4.21	175	4.61	220	3.67
40	4.05	85	4.00	130	4.64	176	3.56	221	3.50
41	4.22	86	3.84	131	4.77	177	4.52	222	3.68
42	4.24	87	4.00	132	4.71	178	4.21	223	3.56
43	4.27	88	4.20	133	4.55	179	4.05	224	3.70
44	4.28	89	4.21	134	4.22	180	3.90		
45	4.09	90	4.18	135	4.16	181	3.92		

SEd 0.29 CD (.05) 0.58

Table 25. Mean performance of turmeric genotypes for curcumin

Geno types	Curcumin (%)	Geno types	Curcumin (%)	Geno types	Curcumin (%)	Geno types	Curcumin (%)	Geno types	Curcumin (%)
1	3.82	46	4.70	91	3.86	136	3.90	182	4.51
2	4.55	47	4.74	92	3.99	137	4.19	183	4.61
3	3.23	48	4.60	93	4.15	138	5.18	184	4.78
4	4.87	49	4.38	94	4.28	139	4.72	185	4.71
5	3.67	50	3.90	95	4.40	140	3.89	186	4.30
6	2.79	51	4.01	96	4.40	141	4.48	187	4.18
7	4.13	52	2.87	97	4.56	142	3.98	188	4.30
8	4.56	53	3.58	98	4.00	144	4.14	189	3.87
9	2.83	54	4.27	99	3.94	145	4.32	190	4.79
10	2.68	55	4.44	100	3.93	146	5.94	191	4.46
11	4.92	56	4.01	101	4.18	147	5.12	192	4.29
12	4.62	57	4.01	102	4.21	148	4.30	193	5.18
13	2.97	58	3.90	103	4.02	149	3.99	194	3.89
14	4.04	59	3.84	104	3.99	150	3.92	195	4.21
15	4.37	60	4.18	105	4.02	151	5.08	196	4.16
16	3.90	61	3.86	106	3.90	152	5.19	197	3.91
17	3.79	62	4.34	107	4.10	153	4.47	198	4.47
18	4.57	63	3.90	108	4.20	154	4.65	199	4.31
19	4.45	64	4.03	109	4.34	155	4.73	200	4.12
20	4.63	65	4.20	110	2.89	156	4.68	201	4.00
21	4.53	66	4.69	111	2.80	157	3.89	202	4.01
22	4.81	67	5.23	112	3.19	158	3.82	203	3.89
23	4.72	68	3.83	113	3.56	159	4.02	204	4.17
24	4.03	69	3.88	114	3.86	160	4.17	205	4.09
25	4.61	70	2.71	115	4.87	161	4.41	206	3.92
26	1.73	71	2.62	116	3.70	162	4.48	207	3.89
27	3.89	72	4.76	117	3.89	163	4.56	208	3.79
28	3.79	73	3.21	118	3.96	164	4.32	209	3.56
29	4.76	74	4.60	119	5.28	165	4.40	210	3.58
30	3.38	75	3.48	120	4.77	166	4.39	211	3.60
31	4.54	76	4.49	121	4.71	167	4.59	212	3.81
32	4.35	77	4.18	122	4.61	168	4.37	213	4.08
33	4.13	78	4.00	123	2.60	169	3.90	214	4.18
34	4.01	79	2.90	124	4.70	170	4.01	215	3.81
35	4.20	80	5.21	125	4.46	171	3.98	216	4.05
36	4.47	81	3.24	126	4.44	172	4.48	217	4.07
37	3.99	82	2.59	127	4.60	173	5.05	218	3.81
38	4.49	83	3.22	128	4.57	174	2.90	219	3.48
39	3.92	84	4.21	129	4.80	175	4.61	220	3.67
40	4.06	85	4.21	130	4.77	176	3.56	221	3.50
41	3.67	86	3.97	131	4.59	177	4.52	222	3.68
42	3.77	87	3.82	132	3.97	178	4.21	223	3.56
43	2.66	88	3.90	133	4.62	179	4.05	224	3.70
44	1.85	89	3.83	134	3.80	180	3.90		
45	4.72	90	3.93	135	3.88	181	3.92		

SEd 0.14 CD (.05) 0.28

4.2.18. Curing percentage (Table 26)

The genotypes differed significantly with respect to curing percentage that was shown to vary from 12.23 per cent to 23.35 per cent. The genotype 157 exhibited the highest curing percentage of 23.35 that was on par with genotype 7 (22.92 %), 50 (23.24 %), 146 (22.70 %), 197 (23.11 %) and 224 (23.24 %). The lowest per cent was observed in the genotype 187 (12.23 %) that was on par with 130 (12.43 %), 15 (12.78 %), 78 (12.45 %), 86 (12.62 %), 123 (12.76 %), 137 (12.79 %), 139 (12.81 %) and 222 (12.67 %). (Table 26)

4.2.19. Yield (Table 27)

The yield of rhizomes varied significantly from 0.15 kg to 12.82 kg/plot. The genotype 101 registered the highest yield of 12.82 kg followed by 154 (12.44 kg) and 47 (12.11 kg). The genotype 110 recorded the lowest yield of 0.15 kg that was found to be on par with genotypes 5 (0.42 kg), 18 (0.62 kg), 19 (0.37 kg), 58 (0.20 kg), 61 (0.55 kg), 63 (0.20 kg), 70 (0.60 kg), 90 (0.55 kg), 97 (0.66 kg), 122 (0.57 kg), 137 (0.50 kg), 138 (0.55 kg), 195 (0.28 kg), 201 (0.60 kg) and 224 (0.60 kg). (Table 27 and Plate 7)

4.3. Genetic divergence as measured by D^2 statistic

By using Mahalonobis D^2 statistic, the two twenty three genotypes were subjected to divergent analysis based on twenty-two traits. The characters analyzed were sprouting, plant height, number of leaves, length of leaf, breadth of leaf, number of tillers, days to maturity, number of mother rhizomes, weight of mother rhizomes, girth of mother rhizomes, number of primary rhizomes, weight of primary rhizomes, length and girth of primary rhizomes, number, weight, length and girth of secondary rhizomes, rhizome and its core diameter, rhizome-core ratio and yield. The quality parameters were excluded from the analysis, as there was no significant contribution of these characters towards variability. The mean values of these characters have been discussed and furnished in tables 2-22 and 27.

Table 26. Mean performance of turmeric genotypes for curing percentage

Geno types	Curing (%)	Geno types	Curing (%)	Geno types	Curing (%)	Geno types	Curing (%)	Geno types	Curing (%)
1	21.17	46	14.60	91	13.19	136	13.16	182	18.48
2	16.71	47	13.34	92	15.10	137	12.79	183	17.40
3	20.90	48	14.05	93	14.43	138	16.53	184	14.23
4	14.91	49	16.63	94	15.46	139	12.81	185	16.19
5	15.41	50	23.24	95	14.92	140	16.19	186	14.56
6	14.06	51	16.90	96	16.79	141	21.20	187	12.23
7	22.92	52	16.64	97	16.56	142	15.19	188	15.30
8	20.50	53	16.80	98	15.65	144	16.51	189	18.20
9	20.17	54	15.86	99	16.32	145	20.21	190	17.21
10	15.92	55	14.47	100	16.56	146	22.70	191	22.02
11	15.98	56	14.47	101	14.10	147	21.84	192	20.16
12	17.04	57	15.39	102	13.91	148	21.42	193	18.55
13	16.02	58	16.37	103	14.21	149	21.02	194	16.21
14	13.73	59	14.67	104	14.63	150	16.19	195	21.27
15	12.78	60	16.20	105	16.03	151	22.18	196	16.47
16	13.67	61	14.99	106	16.68	152	21.71	197	23.11
17	13.12	62	14.25	107	15.87	153	15.91	198	22.63
18	13.33	63	13.27	108	20.58	154	20.69	199	20.70
19	13.19	64	15.69	109	16.21	155	21.13	200	18.22
20	15.06	65	15.72	110	11.60	156	22.52	201	16.81
21	15.49	66	16.68	111	21.63	157	23.35	202	15.85
22	14.62	67	13.21	112	19.77	158	17.23	203	17.90
23	14.68	68	14.25	113	22.24	159	15.95	204	16.58
24	15.02	69	16.33	114	16.40	160	22.52	205	15.22
25	20.51	70	14.67	115	15.65	161	15.50	206	16.98
26	20.77	71	16.59	116	14.46	162	17.20	207	15.67
27	15.80	72	13.41	117	13.40	163	16.41	208	15.34
28	17.03	73	15.88	118	12.99	164	21.60	209	17.19
29	14.69	74	13.19	119	15.31	165	15.75	210	18.61
30	13.70	75	16.35	120	21.74	166	14.73	211	15.65
31	14.44	76	15.69	121	22.40	167	14.99	212	15.19
32	14.97	77	12.99	122	21.31	168	20.04	213	14.00
33	16.49	78	12.45	123	10.76	169	13.73	214	14.31
34	17.03	79	15.81	124	16.61	170	16.31	215	13.90
35	16.61	80	14.78	125	16.58	171	16.76	216	16.58
36	16.04	81	16.38	126	17.65	172	22.00	217	16.24
37	13.00	82	18.32	127	18.19	173	17.25	218	15.23
38	14.32	83	15.91	128	18.35	174	16.72	219	20.50
39	14.95	84	13.94	129	15.52	175	20.53	220	19.16
40	21.23	85	13.76	130	12.43	176	18.49	221	17.20
41	17.35	86	12.62	131	13.27	177	16.10	222	12.67
42	16.10	87	13.41	132	19.24	178	14.76	223	22.18
43	13.19	88	15.69	133	21.42	179	14.25	224	23.24
44	17.13	89	16.38	134	15.40	180	15.78		
45	16.35	90	15.59	135	16.70	181	16.20		
SEd 0.36		CD (.05) 0.71							

Table 27. Mean performance of turmeric genotypes for yield

Geno types	Yield (Kg)	Geno types	Yield (Kg)	Geno types	Yield (Kg)	Geno types	Yield (Kg)	Geno types	Yield (Kg)
1	1.02	46	4.58	91	3.89	136	1.00	182	1.26
2	7.25	47	12.11	92	1.10	137	0.50	183	1.88
3	4.60	48	4.08	93	5.60	138	0.55	184	4.30
4	1.95	49	3.85	94	4.37	139	1.47	185	1.90
5	0.42	50	10.60	95	3.16	140	1.51	186	6.12
6	2.49	51	8.40	96	3.08	141	1.43	187	5.44
7	2.55	52	4.27	97	0.66	142	3.05	188	1.26
8	2.30	53	2.01	98	1.55	144	4.43	189	1.75
9	4.58	54	2.99	99	5.05	145	3.95	190	1.56
10	4.50	55	4.52	100	8.96	146	2.55	191	1.78
11	1.12	56	6.77	101	12.82	147	2.24	192	1.45
12	2.53	57	2.42	102	6.32	148	1.63	193	2.90
13	2.06	58	0.20	103	2.55	149	1.12	194	2.64
14	1.37	59	1.55	104	3.55	150	1.60	195	0.28
15	6.50	60	5.47	105	5.95	151	3.04	196	0.92
16	2.88	61	0.55	106	6.45	152	3.81	197	5.29
17	2.65	62	3.90	107	1.65	153	6.90	198	5.32
18	0.62	63	0.20	108	2.69	154	12.44	199	5.23
19	0.37	64	1.85	109	1.56	155	4.43	200	2.11
20	2.15	65	3.48	110	0.15	156	7.39	201	0.60
21	5.59	66	6.00	111	2.11	157	3.18	202	1.47
22	8.77	67	3.83	112	7.15	158	4.15	203	3.15
23	3.30	68	6.69	113	5.05	159	4.68	204	2.95
24	2.45	69	1.11	114	4.18	160	3.66	205	1.65
25	3.53	70	0.60	115	6.90	161	2.49	206	4.40
26	11.38	71	2.98	116	1.42	162	5.50	207	3.80
27	2.50	72	4.76	117	2.55	163	1.95	208	3.45
28	2.82	73	5.90	118	1.05	164	1.55	209	3.15
29	2.64	74	8.21	119	6.58	165	2.05	210	4.68
30	2.10	75	9.00	120	1.68	166	4.39	211	7.57
31	0.96	76	8.04	121	1.37	167	5.05	212	5.42
32	2.06	77	5.55	122	0.57	168	5.21	213	5.17
33	3.82	78	6.25	123	1.00	169	5.42	214	3.22
34	4.15	79	8.27	124	1.14	170	3.66	215	3.74
35	9.41	80	3.05	125	2.00	171	7.42	216	4.86
36	4.26	81	5.56	126	3.08	172	1.93	217	2.41
37	1.45	82	2.55	127	2.55	173	7.51	218	4.25
38	3.78	83	1.50	128	1.07	174	4.08	219	3.79
39	2.50	84	1.08	129	5.27	175	10.45	220	2.35
40	2.06	85	4.65	130	3.71	176	1.65	221	4.08
41	6.99	86	3.34	131	4.75	177	2.01	222	2.50
42	7.57	87	7.69	132	4.16	178	4.19	223	0.89
43	6.96	88	8.07	133	2.36	179	5.46	224	0.60
44	5.17	89	8.16	134	2.17	180	3.84		
45	1.90	90	0.55	135	1.95	181	2.78		

SEd 0.26 CD (.05) 0.52

Plate 7. Rhizome of different genotypes

4.3.1. Cluster composition of genotypes (Table 28)

Mahalonobis D^2 analysis provides the information on the nature of different clusters accommodating various genotypes. The 223 genotypes were grouped into 8 clusters. The cluster 1 comprised 109 genotypes followed by cluster 8 being the next largest group with 89 genotypes. The clusters 2, 3, 4, 6 and 7 were the least comprising only 2 genotypes per cluster. The cluster 5 accommodated 15 genotypes.

The cluster 1 included genotypes only from Bhavanisagar while cluster 5 grouped Bhavanisagar genotypes with that of Kerala and Orissa. The cluster 8 exhibited genotypes from North India (Bihar, Orissa and West Bengal), Bangalore and Kerala along with genotypes from Erode.

4.3.2. Inter and Intra cluster D^2 values (Table 29)

The inter and intra cluster D^2 and D values among the 8 clusters are presented in table 29. The genetic divergence (D^2) between the cluster 3 and 5 were the highest (919.106) followed by cluster 5 and 8 (877.046) and cluster 5 and 7 (813.055). The lowest value was recorded by the cluster 2 and 4 (101.107). The intra cluster D^2 value ranged between 43.703 and 1021.742. The cluster 5 registered the highest D^2 value of 1021.742 followed by cluster 1 (682.244) and cluster 8 (587.311). The least value was recorded for the cluster 2 (43.703).

Intra cluster distance was the largest for the cluster 5 (31.965) followed by cluster 1 (26.120) and cluster 8 (24.234). Distance between the clusters indicated that cluster 3 and 5 were separated at 30.317 followed by cluster 5 and 8 (29.615) and 4 and 7 (28.514). The clusters 2 and 4 (10.055) and 4 and 6 (11.626) expressed the least distance among them.

4.3.3. Cluster mean values for twenty two characters (Table 30)

The cluster mean values for different characters are furnished in Table 30. Variation was observed among the clusters for all the characters except for length of primary rhizomes, number of secondary rhizomes, rhizome and its core diameter.

Table 28. Cluster composition of turmeric genotypes based on D^2 statistic

Cluster number	Number of genotypes	Genotypes
1	109	1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26, 27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48, 49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70, 71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92, 93,94,95,96,97,98,99,100,101,102,103,104,105,106,107,108,109
2	2	212, 213
3	2	140, 163
4	2	184, 206
5	15	110,111,112,113,114,115,116,117,118,119,120,121,122,150,164
6	2	158, 167
7	2	174, 203
8	89	123,124,125,126,127,128,129,130,131,132,133,134,135,136,137,138, 140,141,142,144,145,146,147,148,149,151,152,153,154,155,156,157, 158,159,160,161,162,165,166,168,169,170,171,172,173,175,176,177, 178,179,180,181,182,183,185,186,187,188,189,190,191,192,193,194, 195,196,197,198,199,200,201,202,204,205,207,208,209,210,211,214, 215,216,217,218,219,220,221,222,223,224.

Table 29. Inter and Intra Cluster D^2 and D values

Cluster	1	2	3	4	5	6	7	8
1	682.244 **26.120**	526.746 (22.951)	755.341 (27.486)	489.262 (122.119)	964.503 (31.056)	604.777 (24.592)	555.428 (23.568)	724.684 (26.920)
2		43.703 **6.611**	395.722 (19.893)	101.107 (10.055)	769.439 (27.739)	170.667 (13.064)	196.383 (14.014)	416.985 (20.420)
3			46.512 **6.820**	315.454 (17.761)	919.106 (30.317)	327.597 (18.100)	176.240 (13.276)	472.087 (21.728)
4				55.632 **7.459**	696.610 (26.393)	135.158 (11.626)	148.415 (28.514)	390.872 (19.770)
5					1021.742 **31.965**	779.367 (27.917)	813.055 (14.205)	877.046 (29.615)
6						64.338 **8.021**	201.779 (14.205)	429.584 (20.726)
7							66.020 **8.125**	406.887 (20.171)
8								587.311 **24.234**

Values in paranthesis indicate inter cluster distances
Values bold are intra cluster distances
Others are inter cluster values

Table 30. Cluster mean values of twenty two characters for turmeric genotypes.

Cluster / Character	1	2	3	4	5	6	7	8	% contribution
Sprouting (%)	92.88	99.00	100.00	89.50	86.73	74.25	96.00	92.97	0.48
Plant height (cm)	38.12	32.56	34.39	32.98	36.21	32.05	35.68	34.39	0.01
Number of leaves	15.27	11.38	13.00	11.21	14.31	11.38	14.33	13.27	0.28
Length of leaf(cm)	41.79	32.26	35.74	35.59	4080	33.48	36.53	38.55	0.00
Breadth of leaf (cm)	12.77	12.11	11.81	11.88	12.67	11.28	11.90	12.24	0.00
Number of tillers	3.92	1.21	2.13	1.50	3.47	1.29	1.71	1.94	0.13
Days to maturity	250.47	243.00	230.75	246.75	278.20	226.75	238.50	239.05	3.98
Number of Mother rhizomes	2.91	3.17	3.00	2.75	2.73	2.75	2.42	2.72	0.00
Girth of Mother rhizomes (cm)	8.72	10.53	8.64	8.97	8.43	8.38	8.08	8.90	0.09
Weight of Mother rhizomes (g)	60.34	56.67	69.50	50.00	60.28	56.00	55.83	65.87	1.22
Number of Primary rhizomes	5.92	8.00	6.08	6.83	5.69	6.34	7.67	6.16	0.02
Weight of Primary rhizomes (g)	96.07	117.92	97.17	93.33	113.49	107.33	108.00	110.20	5.95
Length of Primary rhizomes (cm)	7.75	6.73	7.89	7.08	6.97	7.61	6.97	7.21	0.08
Girth of Primary rhizomes (cm)	7.04	5.71	5.99	4.51	6.28	5.08	6.20	6.27	1.22
Number of Secondary rhizomes	6.97	7.88	6.97	7.84	6.84	6.54	6.97	6.85	0.32
Weight of Secondary rhizomes (g)	63.83	75.75	67.92	65.08	79.61	67.92	54.17	74.16	4.96
Length of Secondary rhizomes (cm)	6.07	5.66	5.24	5.13	5.49	5.61	4.98	5.57	4.62
Girth of Secondary rhizomes (cm)	5.32	4.15	3.93	3.67	4.07	4.37	3.49	4.39	4.14
Rhizome diameter (cm)	2.02	1.60	1.48	1.48	1.18	1.37	1.78	1.72	2.10
Core diameter (cm)	1.10	0.59	0.48	0.59	0.95	0.57	0.59	0.82	3.45
Rhizome Core ratio (cm)	1.91	2.61	3.13	2.45	1.22	2.43	2.99	2.21	5.58
Yield (Kg/plot)	4.13	5.30	1.71	4.35	2.93	4.60	3.62	3.32	61.62

Genotypes of cluster 3 exhibited the highest mean value for sprouting (100 %) followed by cluster 2 (99.00 %) and 7 (96.00 %). While the cluster 6 scored the least value (74.25 %). Plant height was found to be the highest in case of cluster 1 followed by cluster 5 (38.12 cm and 36.21 cm respectively), short stature plants were noticed in cluster 6 (32.05 cm). Number of leaves, length of leaf and breadth of leaf were found to be high for cluster 1 (15.27, 41.79 cm and 12.77 cm respectively). The lowest mean value was recorded for the cluster 2 (11.38, 32.26 cm for number of leaves and length of leaf respectively).

The number of tillers was high in the genotypes in cluster 1 followed by cluster 5 (3.92 and 3.47 respectively). Similar trend was observed for days to maturity. The longer duration genotypes were accommodated in cluster 1 and 5 (250.47 and 278.20 respectively). The short duration types were grouped in cluster 6 (226.75). The number of mother rhizomes and girth of mother rhizomes were high for cluster 2 (3.17 and 10.53 cm respectively). While the lowest was recorded for cluster 7 (2.42 and 8.08 cm respectively). Heavier mother rhizomes were recorded for cluster 3 (69.50 g) and the least for cluster 7 (55.83 g).

Cluster 2 revealed the highest value for number of primary rhizomes and weight of primary rhizomes (8.00 and 117.92 g respectively). The length of primary rhizomes was found to be the greatest for cluster 3 (7.89 cm) and the least for cluster 2 (6.73 cm). Girth of primary rhizomes was high for the genotypes of the cluster 1 (7.04 cm) and the least for cluster 4 (4.51 cm). Weight, length and girth of secondary rhizomes were high for cluster 1 (63.83 g, 6.07 cm and 5.32 cm respectively) while more number of secondary rhizomes were attributed to cluster 2 and 4 (7.88 and 7.84 respectively).

Rhizome and core diameter measured the highest for genotypes of cluster 1 (2.02 cm and 1.10 cm respectively) while the other clusters did not exhibit much variation for its mean value. The rhizome core ratio was found to be high for cluster

3 (3.13) and the least for cluster 5 (1.22). The yield values were high for the genotypes of cluster 2 (5.30 kg) followed by cluster 6 (4.60 kg) and the least for cluster 3 (1.71 kg).

4.3.4. Ranking of characters in relation to their contribution to genetic divergence (Table 30, Fig.1)

The D^2 values ranked character wise for each character indicated their contribution to total genetic divergence is furnished in Table 30. Accordingly, yield showed the highest contribution (61.62%) followed by weight of primary rhizomes (5.95%) and rhizome core ratio (5.58%). While length of leaf and breadth of leaf showed no effect on genetic divergence. Sprouting, plant height, number of leaves, number of tillers, number of primary rhizomes, length of primary rhizomes and number of secondary rhizomes contributed the least to genetic divergence.

4.4. K means clustering

The two twenty three genotypes of turmeric were subjected to K means clustering to analyze the variables contributing for divergence and also for the existing genetic diversity. The clustering technique was followed as a measure of Euclidean distance. The K means splitted the genotypes into 8 clusters based on 22 characters.

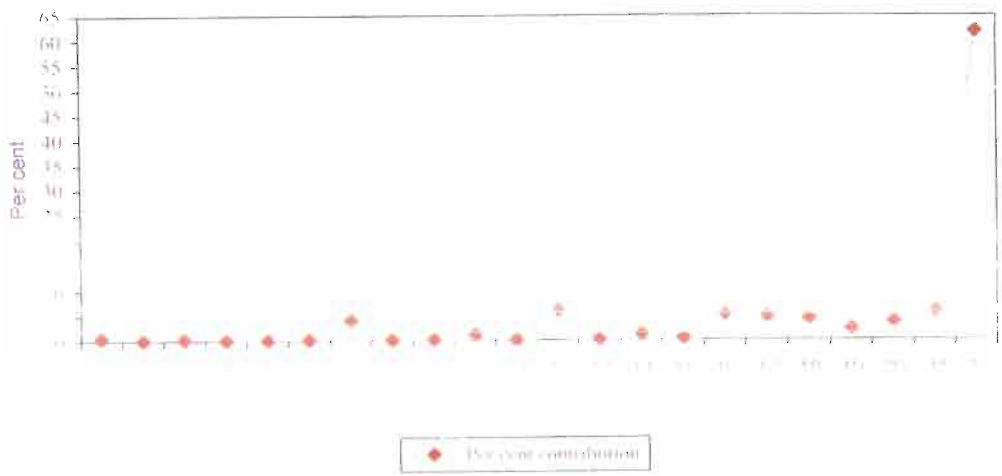
The characters analyzed were the biometrical traits excluding quality characters as they exhibited negligible variation and did not have direct influence on yield.

4.4.1. Pattern of clustering of genotypes (Table 31, Fig. 2)

The cluster 1 contained 47 genotypes and cluster 2 accommodated 44 genotypes. The cluster 3 exhibited 2 genotypes while nine of the genotypes were accorded to cluster 4. The cluster 5 and 7 were the lowest groups, each having a single genotype without being linked to any other cluster. The cluster 6 was the largest, exhibiting 78 genotypes and cluster 8 produced 41 genotypes.

The cluster 5 and 7 contained single genotype from Bhavanisagar and cluster 3 included Bhavanisagar genotype with VK 112 genotype from Kerala. The cluster

Fig 1. Relative contribution of characters towards genetic divergence

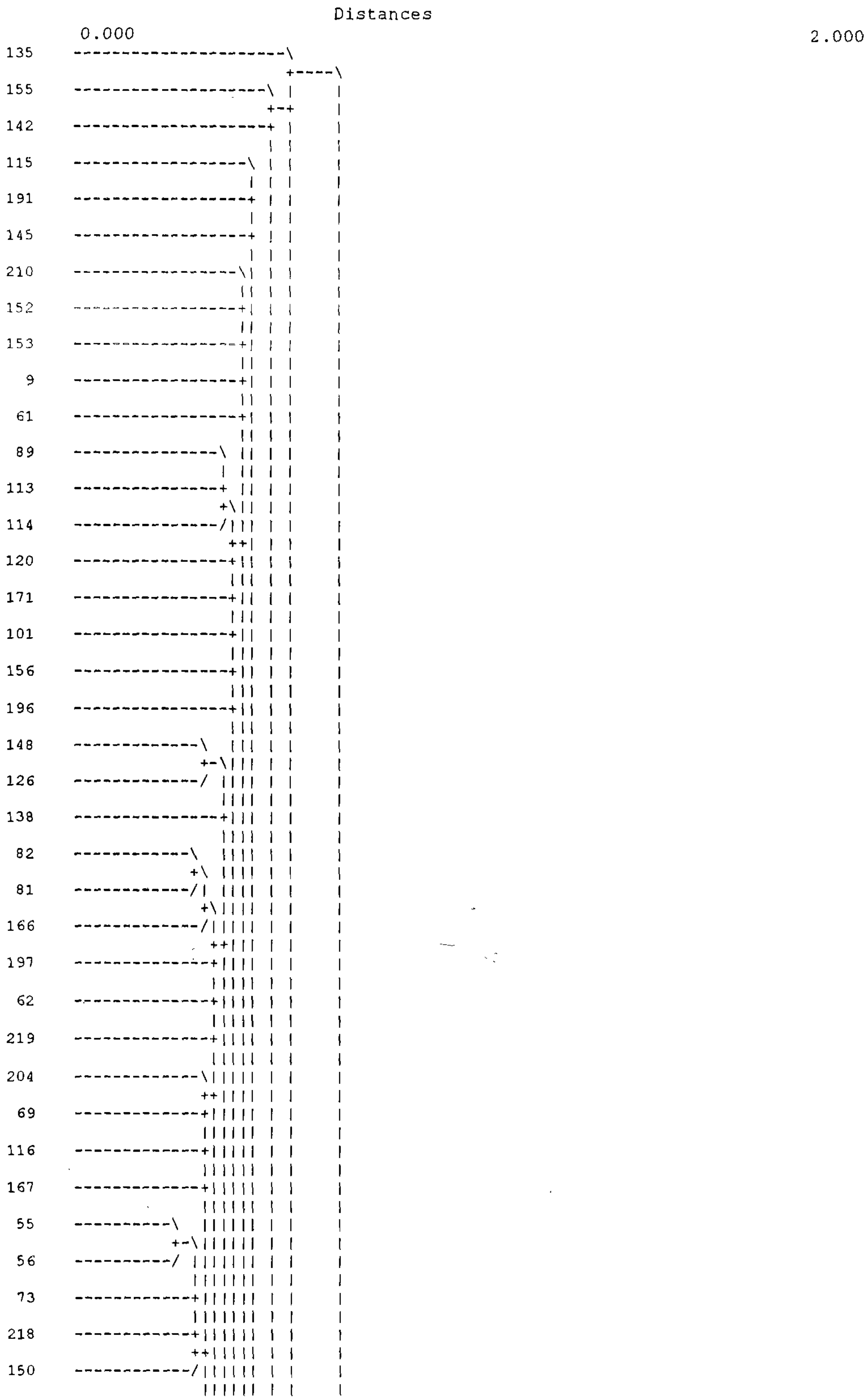


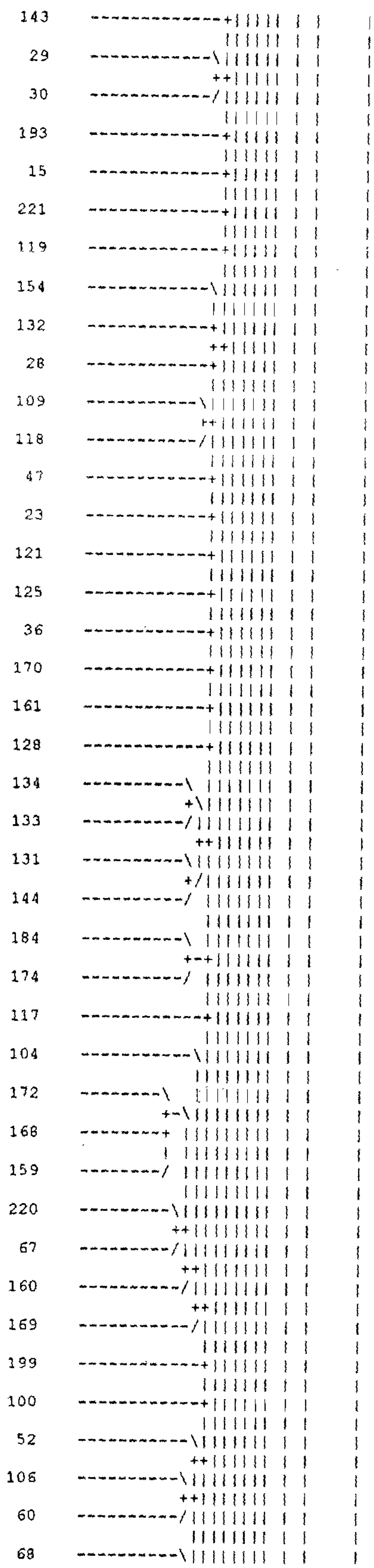
1 Sprouting
2 Plant height
3 Number of leaves
4 Length of leaf
5 Leaf breadth
6 Number of tillers
7 Days to maturity
8 Number of mother rhizomes
9 Weight of mother rhizomes
10 Girth of mother rhizomes
11 Number of Primary rhizomes
12 Weight of Primary rhizomes
13 Length of Primary rhizomes
14 Girth of Primary rhizomes
15 Number of Secondary rhizomes
16 Weight of Secondary rhizomes
17 Length of Secondary rhizomes
18 Girth of Secondary rhizomes
19 Rhizome diameter
20 Core diameter
21 Rhizome Core ratio
22 Yield

Table 31. Cluster composition of turmeric genotypes based on K means clustering

Cluster	Number of genotypes	Cluster members
1	47	3,12,23,25,28,33,34,54,55,56,65,71,72,73,78,98,99,107,121,124, 125,126,127,128,136,13,138,139,141,144,147,148,149,150,151, 161,163
2	44	4,6,7,8,11,13,14,16,17,20,24,31,32,38,39,40,45,46,53,57,59,64, 70,79,83,85,86,92,96,97,122,130,165,177,178,188,193,196,201, 204,223,224
3	2	110, 123
4	9	1,5,18,37,58,66,84,90,195
5	1	63
6	78	2,9,10,15,21,22,26,29,30,35,36,41,42,43,44,47,48,49,50,51,62, 67,76,77,80,82,88,91,94,95,100,103,104,105,108,109,111,117, 118,140,152,157,158,162,167,171,173,174,175176,179,180,181, 182,183,184,185,189,190,191,194,199,203,205,206,207,209,210, 211,212,213,214,215,216,217,218,221
7	1	19
8	41	52,60,61,68,69,74,75,81,87,89,93,101,102,106,112,113,114,116, 119,120,129,131,132,133,134,135,142,145,153,154,155,156,172, 186,187,192,198,220,222

Fig 2. Cluster Tree based on Euclidean distance

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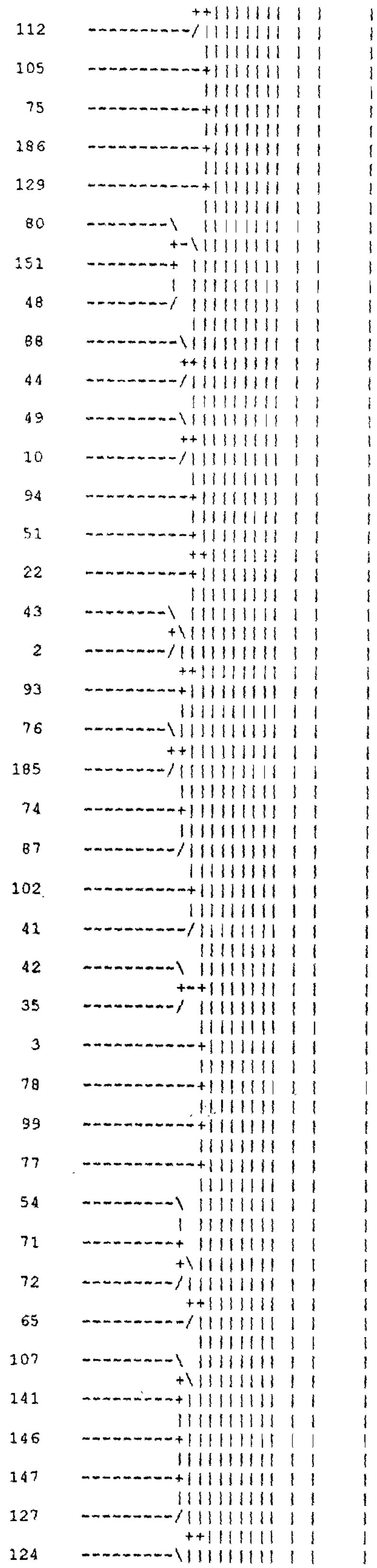
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178    -----------+||||||||  | |     |
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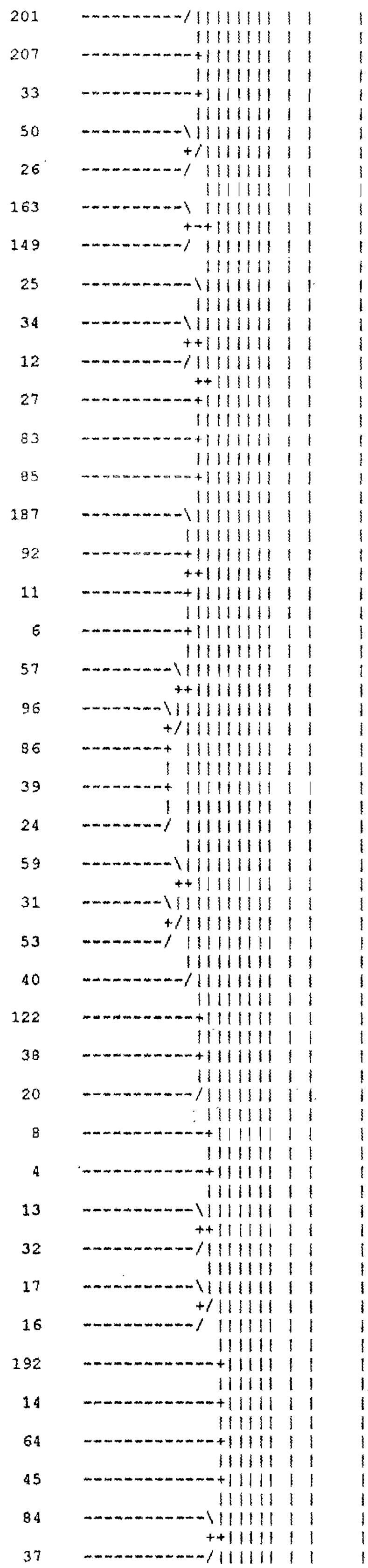
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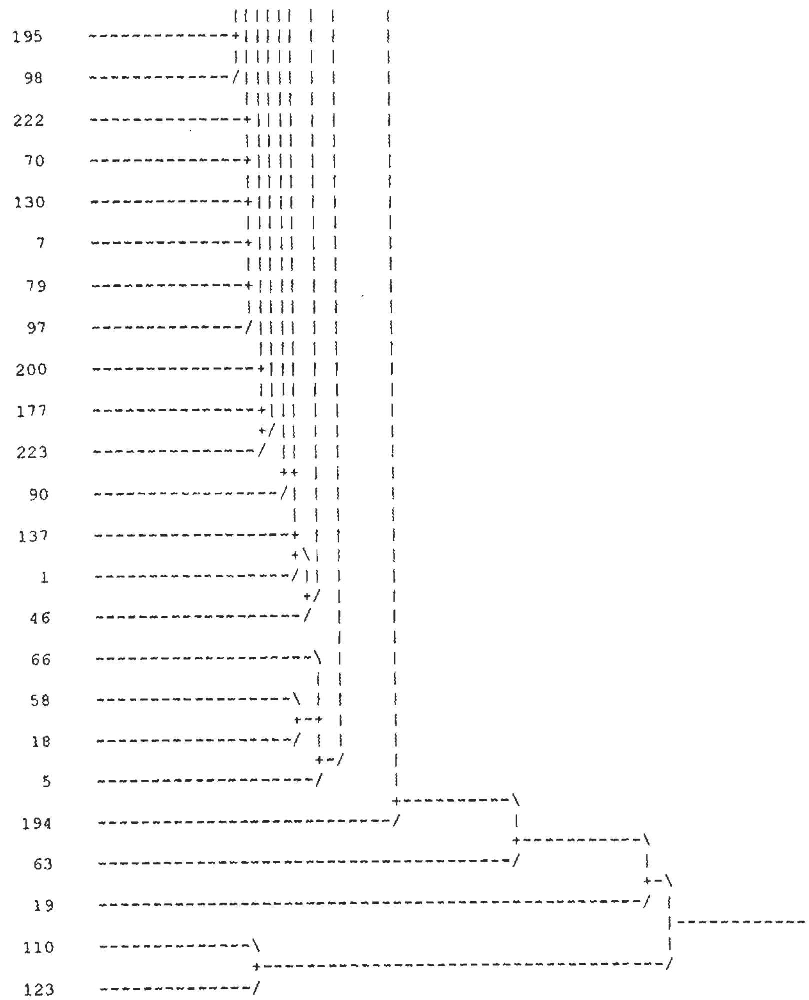
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63
19
110
123

1, 2, 6 and 8 grouped genotypes from Bhavanisagar, genotypes from Kerala, Orissa, West Bengal and Erode. The cluster 4 contained genotypes from Bhavanisagar and Bihar.

4.4.2. Cluster range values of the characters (Table 32)

The cluster 1, 2, 3, 4, 6 and 8 (100.00 %) accounted for highest per cent of sprouting. The lowest values of sprouting were attributed to the cluster group 5 followed by cluster 8 (45.00 % and 49.00 % respectively). The cluster 3 projected genotypes of higher sprouting (84-100 %).

The genotypes of the cluster 6 registered tall stature plants (49.00 cm) followed by cluster 1 and 8 (46.00 cm). The shortest plants were noticed in cluster 2 (29.00 cm).

The highest number of leaves was recorded in the genotypes of cluster 1, 6 and 8 (18.00) while the lowest was observed in cluster 1 (10.00). Higher values for these characters ranged between 12 and 18 in the cluster 8.

The longest leaves were recorded in the clusters 6 and 8 (56.00 cm) and the shortest leaf was found in cluster 6 (31.00 cm). The cluster 8 expressed a range between 11.00 and 16.00 cm for breadth of leaf while the lowest was recorded in cluster 1.

More number of tillers was accounted by cluster 8 while the same measured the lowest number too, in addition to the clusters 1, 2 and 6. The duration of the genotypes extended from 218 to 262 days in cluster 2 followed by cluster 6 (221 to 261 days). Medium duration genotypes were noticed for cluster 5 and 7.

Higher girth for rhizomes were recorded for the genotypes of the cluster 8 (13.00 cm) followed by clusters 1 (11.00 cm). The least value was noticed in cluster 5 (7.00 cm). The heavier rhizomes exhibited the highest by cluster 8 (110.00 g) and the lowest for cluster 1 (60.00 g).

The greatest number of primary rhizomes was counted for the cluster 6 (9.00) while cluster 3 (1.00) recorded the lowest. Cluster 8 possessed genotypes of heavier

Table 32. Range values of turmeric genotypes based on K means cluster

Cluster / Character	1	2	3	4	5	6	7	8
Sprouting (%)	74 - 100	75 - 100	84 - 100	56 - 100	45	66 - 100	86	49 - 100
Plant height (cm)	30 - 46	29 - 43	31 - 32	32 - 39	33	31 - 49	32	32 - 46
Number of leaves	10 - 18	11 - 17	12 - 14	13 - 15	14	11 - 18	13	12 - 18
Length of leaf (cm)	32 - 50	32 - 52	34 - 39	32 - 44	36	31 - 56	34	33 - 56
Breadth of leaf (cm)	7 - 15	10 - 15	11 - 15	11 - 14	13	10 - 15	10	11 - 16
Number of tillers	1 - 5	1 - 5	3 - 4	2 - 4	3	1 - 5	3	1 - 6
Days to maturity	2 19 - 258	218 - 262	229 - 251	223 - 258	256	221 - 261	255	226 - 259
Girth of Mother rhizomes (cm)	5 - 11	6 - 11	10 - 11	6 - 9	7	6 - 11	7	7 - 13
Weight of Mother rhizomes (g)	60 - 104	27 - 77	2	24 - 56	23	37 - 75	45	46 - 110
Number of Primary rhizomes	3 - 7	3 - 8	1	3 - 8	4	5 - 9	5	5 - 8
Weight of Primary rhizomes (g)	53 - 138	53 - 99	2 - 3	20 - 47	9	74 - 139	3	118 - 220
Length of Primary rhizomes (cm)	5 - 10	5 - 9	1	2 - 7	5	6 - 10	1	6 - 11
Girth of Primary rhizomes (cm)	4 - 9	3 - 9	2	3 - 7	3	4 - 9	2	1 - 10
Number of Secondary rhizomes	4 - 9	4 - 9	1	3 - 9	2	5 - 10	1	5 - 10
Weight of Secondary rhizomes (g)	36 - 86	30 - 63	2 - 3	17 - 38	6	52 - 115	2	66 - 144
Length of Secondary rhizomes (cm)	4 - 7	4 - 8	1 - 2	3 - 7	1	4 - 8	2	5 - 9
Girth of Secondary rhizomes (cm)	3 - 8	2 - 7	1	2 - 5	1	3 - 8	1	3 - 7
Rhizome diameter (cm)	1 - 3	1 - 3	1	1 - 2	1	1 - 3	1	3
Core diameter (cm)	1	2	1	1	1	1 - 2	1	1 - 2
Rhizome Core ratio (cm)	1 - 3	1 - 3	1	2 - 3	2	1 - 3	1	1 - 3
Yield (Kg/plot)	1 - 7	1 - 8	1	1 - 6	1	1 - 12	1	1 - 13

rhizomes while the lowest was observed for cluster 5. Both the clusters 3 and 7 exhibited poor rhizome characteristics.

The length of primary rhizomes was higher varying from 6.00 to 11.00 cm in cluster 8 while the lowest was observed for cluster 4 (2.00 cm). The cluster 8 registered more girth (10.00 cm) whereas cluster 3 and 7 (3.00 cm) exhibited lesser values.

Higher values for number of secondary rhizomes were obtained for clusters 6 and 8 (10.00) and cluster 5 (2.00) projected the least value.

Similar trend was observed for weight and length of secondary rhizomes (144 g and 9.00 cm respectively) accounting the highest values for cluster 8 and the lowest for cluster 5 (6.00 g and 1.00 cm respectively). The genotypes of cluster 1 and 6 (8.00 cm) revealed the highest value for girth of secondary rhizome and the least in cluster 5 (1.00 cm).

The clusters 6 and 8 (12.00 kg and 13.00 kg) accommodated genotypes of higher yield. However, invariably all the clusters accommodated low yielding genotypes.

4.5. Principal Component Analysis (PCA)

The principal component analysis was applied to identify patterns in a data set containing many correlated variables into smaller sets of components of the original variables. The data were transformed to create new variables and axes are accounted for more variation in the original data than any single variable alone.

The mean values of twenty-two characters were subjected to PCA. The variables selected were sprouting, plant height, number of leaves, length of leaf, breadth of leaf, number of tillers, days to maturity, number of mother rhizomes, weight and girth of mother rhizomes, number, weight, length and girth of primary rhizomes, number, weight, length and girth of secondary rhizomes, rhizome and its core diameter, rhizome core ratio and yield. The quality characters were exempted, as their impact on yield was negative and contributed for lesser variation.

4.5.1. Component loadings

The PCA of the correlation matrix represented eleven components. The PCs showing eigen values lesser than one was considered non-significant. The component loadings that exhibited eigen values more than 1.00 and the per cent variability for each PC is furnished in Table 33.

The per cent total variability indicated that the first PC accounted for 75 per cent of variance and 90 per cent by the first three PCs and above 95 per cent by the first five PCs. The PCs from 6 to 21, which recorded eigen values less than one, were ignored, as they were unlikely to have any practical significance.

4.5.2. Variance contributed by components (Table 33, Fig. 3)

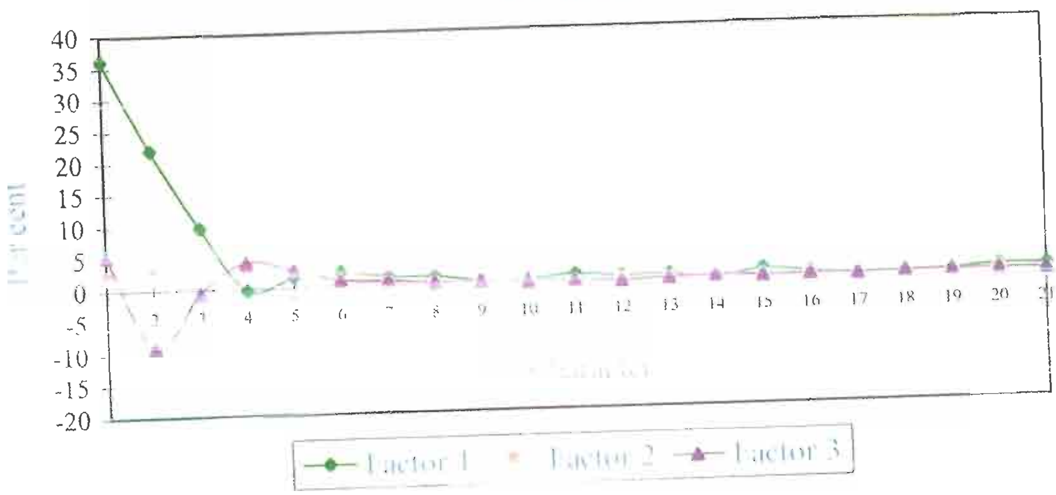
The significance of the variable in each PC was determined by comparing the loadings. The PC 1 accounted for 76.30 per cent of total variance and was an index of weight of primary rhizomes (36.15), weight of secondary rhizomes (22.02), girth of mother rhizomes (9.67), length of leaf (2.24), sprouting (1.60), plant height (1.46), yield (1.22), length of primary rhizomes (1.03), number of leaves, number of primary rhizomes, girth of primary rhizomes, number of secondary rhizomes, girth of secondary rhizomes, breadth of leaf, core diameter, length of secondary rhizomes and weight of mother rhizomes which were positively correlated. While the days to maturity, number of tillers and rhizome core ratio were negatively correlated.

The PC 2 recorded 8.59 per cent of total variability and together with PC 1, contributed about 80 per cent of the variance. The parameters that were positively correlated were weight of secondary rhizomes (2.62), weight of primary rhizomes (2.19), days to maturity (2.18), length of leaf, plant height, yield, number of leaves, number of primary and secondary rhizomes, number of tillers, breadth of leaf, core diameter and length of secondary rhizomes.

Table 33. Component loadings of attributes for first five principal components

Variable	Principal components				
	1	2	3	4	5
Weight of Primary rhizomes (g)	36.15	2.19	5.42	-2.49	-0.95
Weight of Secondary rhizomes (g)	22.02	2.62	-9.06	3.13	1.36
Girth of Mother rhizomes (cm)	9.67	-13.95	-0.44	1.51	-1.14
Days to maturity	- 0.31	2.18	4.18	8.62	-1.71
Sprouting (%)	1.60	-1.55	2.72	1.08	8.83
Length of leaf (cm)	2.24	0.30	1.02	1.42	-0.01
Plant height (cm)	1.46	0.43	0.85	1.43	0.20
Yield (kg/plot)	1.22	0.20	0.35	0.26	0.21
Number of leaves	0.44	0.08	0.48	0.75	-0.05
Number of Primary rhizomes	0.46	0.002	0.03	-0.002	0.06
Girth of Primary rhizomes (cm)	0.99	-0.14	0.22	0.41	0.02
Number of Secondary rhizomes	0.56	0.06	-0.20	0.23	0.14
Girth of Secondary rhizomes (cm)	0.60	-0.06	0.15	0.35	0.08
Number of tillers	- 0.03	0.14	0.33	0.61	-0.09
Length of Primary rhizomes (cm)	1.03	-0.07	0.07	0.26	0.03
Breadth of leaf (cm)	0.42	0.05	0.16	0.33	-0.01
Rhizome Core ratio	- 0.06	-0.05	-0.07	-0.14	0.04
Core diameter (cm)	0.17	0.03	0.09	0.13	-0.02
Rhizome diameter (cm)	0.20	-0.02	0.12	0.13	0.02
Length of Secondary rhizomes (cm)	0.77	0.11	0.01	0.21	0.12
Weight of Mother rhizomes (g)	0.63	-0.33	-0.01	0.07	0.09
Eigen value (variance)	1900.94	213.89	138.86	99.48	85.12
Per cent variability	76.30	8.59	5.57	3.99	3.42

Fig.3. Relative contribution of principal components to variability



1 Sprouting
2 Plant height
3 Number of leaves
4 Leaf length
5 Leaf breadth
6 Number of tillers
7 Days to maturity
8 Weight of mother rhizomes
9 Girth of mother rhizomes
10 Number of Primary rhizomes
11 Weight of Primary rhizomes
12 Length of Primary rhizomes
13 Girth of Primary rhizomes
14 Number of Secondary rhizomes
15 Weight of Secondary rhizomes
16 Length of Secondary rhizomes
17 Girth of Secondary rhizomes
18 Rhizome diameter
19 Core diameter
20 Rhizome Core ratio
21 Yield

The girth of mother rhizomes (-13.95), sprouting, girth of primary rhizomes and secondary rhizomes, length of primary rhizomes, rhizome core ratio, rhizome diameter and weight of mother rhizomes attributed for negative correlation.

The PC 3 which accorded 5.57 per cent of total variance reflected significant loadings on weight of primary rhizomes (5.42), days to maturity (4.18), sprouting, length of leaf, plant height, yield, number of leaves, number of primary rhizomes, number of secondary rhizomes, girth of secondary rhizomes, number of tillers, length of primary rhizomes, breadth of leaf, core diameter, rhizome diameter and length of secondary rhizomes being positive and the negative correlation noted for weight of secondary rhizomes (-9.06), number of secondary rhizomes, rhizome core ratio and weight of mother rhizomes.

The PC 4 was characterized by the conspicuous high load of weight of secondary rhizomes (3.13), weight of primary rhizomes, number of primary rhizomes and rhizome core ratio contributed for negative correlation while the other parameters were positively correlated.

The PC 5 relatively attributed high load for sprouting (8.83) and was in negative correlation with weight of primary rhizomes, girth of mother rhizomes, days to maturity, length of leaf, number of leaves, number of tillers, breadth of leaf and core diameter.

Among the PCs, for sprouting, PC 5 relatively contributed for higher loading even though PC 1 exhibited greater per cent of variance. Similarly PC 4 projected to score higher loading for number of leaves and number of tillers. The PC 3 accorded much of its variance through weight of primary rhizomes, days to maturity and sprouting. The PC 2 attributed its variance through days to maturity while PC 1 loadings were high for most of the variables, thus projecting higher variability.

4.6. Genetic variability (Table 34)

The estimates on genetic components of turmeric genotypes as furnished in Table 34 revealed highly significant variations for all the traits studied. The genotypic

Table 34. Genetic components of turmeric genotypes

Character	GV	PV	GCV	PCV	ECV
Sprouting (%)	85.09	98.17	9.98	10.72	3.91
Plant height (cm)	13.88	20.41	10.26	12.45	7.04
Number of leaves	2.88	3.92	11.89	13.87	7.13
Length of leaf (cm)	21.04	35.96	11.44	14.95	9.63
Breadth of leaf (cm)	0.63	2.06	6.34	11.47	9.56
Number of tillers	1.35	1.69	38.76	43.35	19.43
Days to maturity	98.27	104.84	4.04	4.18	1.05
Number of Mother rhizomes	0.16	0.32	14.17	20.02	14.13
Weight of Mother rhizomes (g)	275.56	308.29	14.52	15.64	5.79
Girth of Mother rhizomes (cm)	1.63	1.89	26.59	28.13	9.17
Number of Primary rhizomes	1.15	1.69	17.17	21.49	12.17
Weight of Primary rhizomes (g)	1334.71	1362.13	35.37	35.74	5.07
Length of Primary rhizomes (cm)	2.04	2.39	19.16	20.74	7.92
Girth of Primary rhizomes (cm)	2.60	2.82	24.38	25.39	7.07
Number of Secondary rhizomes	1.79	2.06	19.31	20.74	7.56
Weight of Secondary rhizomes (g)	579.88	590.73	34.84	35.16	4.77
Length of Secondary rhizomes (cm)	1.45	1.51	20.80	21.20	4.11
Girth of Secondary rhizomes (cm)	1.82	1.95	28.08	29.06	7.48
Rhizome diameter (cm)	0.21	0.23	25.01	26.11	7.49
Core diameter (cm)	0.13	0.14	37.44	38.53	9.10
Rhizome Core ratio (cm)	0.34	0.36	29.03	29.66	6.08
Oil (%)	-0.01	0.01	0.25	7.65	7.65
Oleoresin (%)	-0.01	0.09	0.25	6.93	6.93
Curcumin (%)	0.34	0.36	14.26	14.66	3.42
Curing per cent	7.68	7.81	16.65	16.79	2.16
Yield (Kg/plot)	6.28	6.35	67.39	67.77	7.14

variances were less than the phenotypic variances for all the characters involved. The highest phenotypic and genotypic variances were observed for weight of primary rhizomes (1362.13 and 1334.71 respectively) followed by weight of secondary rhizomes (590.73 and 579.88 respectively). The lowest phenotypic and genotypic variance was recorded for biochemical traits *viz.*, oil (0.01 and -0.01 respectively). The variance contributed by the environment was significant and the highest order of differences between phenotypic and genotypic variances were noticed for weight of mother rhizomes (32.73) followed by weight of primary rhizomes (27.42). The least order of differences was found for oil and oleoresin (0.01 and 0.09 respectively) (Table 34).

The phenotypic coefficients (PCV) were higher in magnitude than the corresponding genotypic coefficients (GCV) of variability for all the parameters under study. The highest per cent of PCV and GCV (67.77 and 67.39 respectively) were observed for yield followed by number of tillers (43.35 and 38.76 respectively). The lowest per cent of PCV and GCV were observed for oleoresin (6.93 and 0.25 respectively) followed by oil (7.65 and 0.25 respectively). The magnitude of difference between PCV and GCV estimates was less for days to maturity (1.05) followed by curing percentage (2.16) while the highest difference was observed for number of tillers (19.43) followed by number of mother rhizomes (14.13). (Fig. 4)

4.6.1. Heritability and genetic advance

Heritability (Table 35, Fig.5)

The heritability percentage ranged from -0.11 to 98.89. The percentage of heritability in broad sense was higher for yield, curing percentage, weight of secondary rhizomes and primary rhizomes (98.89, 98.35, 98.16 and 97.99 respectively). The least percentage of heritability was noticed for oil (-0.11), oleoresin (-0.13), breadth of leaf (30.53) and number of mother rhizomes (50.13) (Table 35).

Table 35. Heritability and Genetic advance of turmeric genotypes

Character	Heritability	Genetic advance	Genetic advance % of mean	Mean
Sprouting (%)	86.67	17.68	19.13	92.45
Plant height (cm)	68.01	48.04	17.44	36.30
Number of leaves	73.55	147.23	21.01	14.27
Length of leaf (cm)	58.51	44.93	18.02	40.11
Breadth of leaf (cm)	30.53	57.63	7.21	12.51
Number of tillers	79.91	2386.97	71.37	2.99
Days to maturity	93.73	3.29	8.06	45.16
Number of Mother rhizomes	50.13	734.54	20.67	2.81
Weight of Mother rhizomes (g)	86.27	316.44	27.79	62.42
Girth of Mother rhizomes (cm)	89.38	82.97	51.79	8.78
Number of Primary rhizomes	67.92	497.27	30.07	6.05
Weight of Primary rhizomes (g)	97.99	69.88	72.14	103.27
Length of Primary rhizomes (cm)	85.40	4.89	36.48	7.46
Girth of Primary rhizomes (cm)	92.25	729.69	48.24	6.61
Number of Secondary rhizomes	86.70	5.35	37.05	6.92
Weight of Secondary rhizomes (g)	98.16	102.88	71.11	69.12
Length of Secondary rhizomes (cm)	96.24	725.16	42.03	5.80
Girth of Secondary rhizomes (cm)	93.37	1164.13	55.89	4.80
Rhizome diameter (cm)	91.76	2707.62	49.36	1.82
Core diameter (cm)	94.42	7837.87	74.93	0.96
Rhizome Core ratio (cm)	95.83	2898.51	58.55	2.02
Oil (%)	-0.11	1.64	-0.02	1.22
Oleoresin (%)	-0.13	0.47	-0.02	4.22
Curcumin (%)	94.57	694.38	28.56	4.11
Curing per cent	98.35	2043.37	34.02	16.65
Yield (Kg/plot)	98.89	3712.02	138.05	3.72

Characters

1. Sprouting
2. Plant height
3. Number of leaves
4. Leaf length
5. Leaf breadth
6. Number of tillers
7. Days to maturity
8. Number of mother rhizomes
9. Weight of mother rhizomes
10. Girth of mother rhizomes
11. Number of Primary rhizomes
12. Weight of Primary rhizomes
13. Length of Primary rhizomes
14. Girth of Primary rhizomes
15. Number of Secondary rhizomes
16. Weight of Secondary rhizomes
17. Length of Secondary rhizomes
18. Girth of Secondary rhizomes
19. Rhizome diameter
20. Core diameter
21. Rhizome Core ratio
22. Oil
23. Oleoresin
24. Curcumin
25. Curing percentage
26. Yield

Fig 4. PCV, GCV and ECV in turmeric genotypes

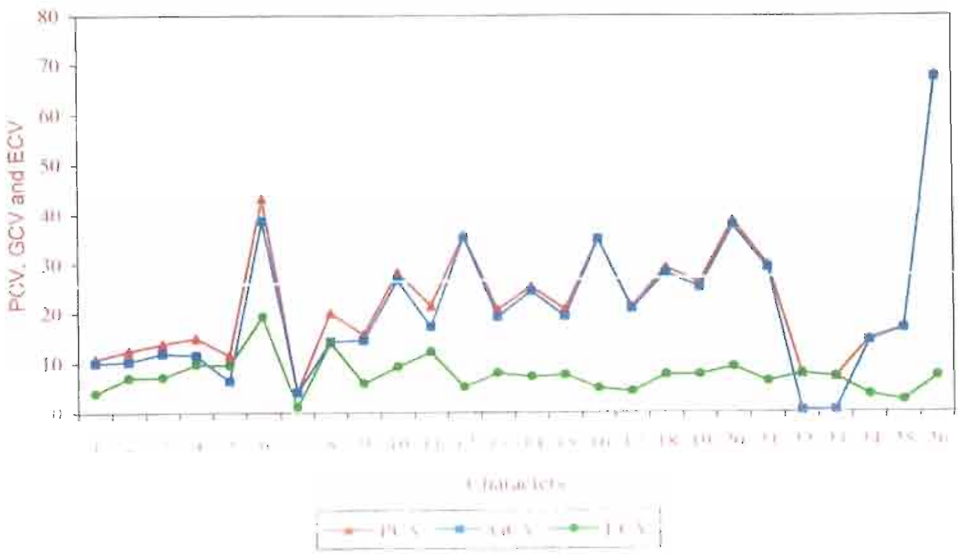
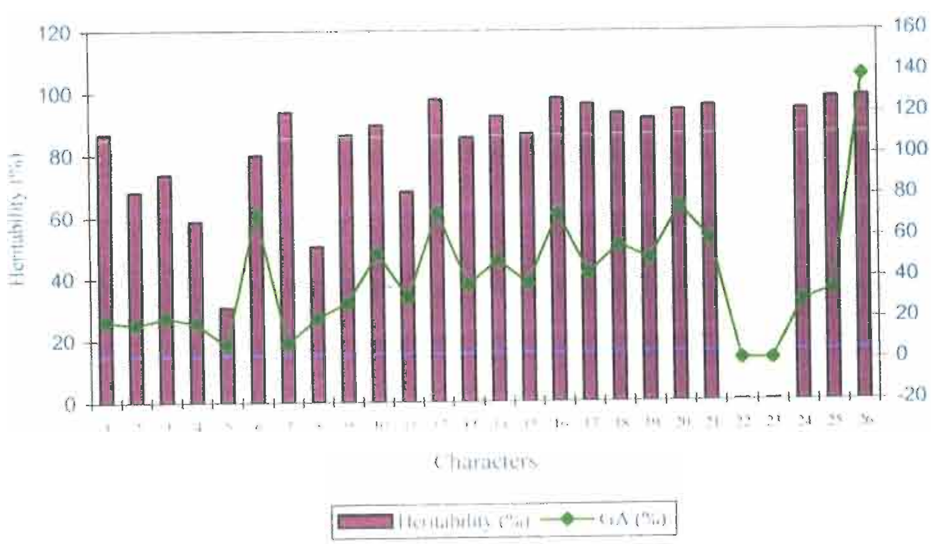


Fig 5. Heritability and genetic advance as per cent mean in turmeric genotypes



Genetic advance (Table 35)

The genetic advance ranged between 0.47 and 7837.87. The estimates of genetic advance were the highest for core diameter (7837.87) followed by yield (3712.02). The lowest was recorded for oleoresin (0.47).

High heritability coupled with high genetic advance was noticed for yield, weight of secondary rhizomes, weight of primary rhizomes and number of tillers.

4.6.2. Genetic advance as per cent of mean (Table 35, Fig. 5)

The values of genetic advance as per cent of mean varied from -0.02 to 138.05. Among all the characters studied, the highest value was noticed for yield (138.05) followed by core diameter (74.93). The lowest estimate of genetic gain was noticed for -0.02 (oil and oleoresin) followed by breadth of leaf (7.21).

4.7. Correlation studies

The interrelationships between twenty-six characters were established through their correlations both at phenotypic and genotypic levels and through simple correlation are furnished in Tables 36, 37 and 38.

In general, the genotypic correlation coefficients and simple correlation coefficients were higher than the phenotypic correlation coefficients. However, the simple correlation coefficients were lesser than the genotypic correlation coefficients.

4.7.1. Association of plant and rhizome characters on rhizome yield (Table 36 and 37)

The rhizome yield per plant exerted positive correlation both at phenotypic and genotypic levels for all the characters studied and is highly, significantly correlated with plant height (0.416, 0.513) followed by length of primary rhizomes (0.472 ,0.526), length of leaf (0.369,0.497), weight of primary rhizomes (0.488, 0.493), breadth of leaf (0.246, 0.455), weight of secondary rhizomes (0.413, 0.419), length of secondary rhizomes (0.405, 0.415), rhizome diameter (0.357, 0.374), girth of primary rhizomes (0.358, 0.373,), core diameter (0.353, 0.366), number of leaves (0.301, 0.362), girth of secondary rhizomes (0.287, 0.300), number of primary rhizomes (0.207, 0.262), weight

Table 36. Phenotypic correlation coefficients in turmeric genotypes

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17	X18	X19	X20	X21	X22	X23	X24	X25	X26
X1	1.000	0.140	0.099	0.105	0.031	0.026	0.022	-0.080	0.168	0.152	0.100	0.161	0.157	0.192	0.126	0.091	0.182	0.174	0.186	0.107	0.004	0.008	0.068	-0.031	-0.017	0.174
X2		1.000	0.621	0.679	0.478	0.488	0.251	-0.038	0.152	0.128	0.049	0.323	0.406	0.431	0.158	0.271	0.392	0.416	0.405	0.443	-0.179	-0.006	0.098	-0.059	-0.047	0.416
X3			1.000	0.599	0.462	0.590	0.358	0.041	0.044	0.112	-0.004	0.223	0.290	0.433	0.102	0.161	0.317	0.379	0.382	0.445	-0.247	0.019	0.094	-0.072	-0.104	0.301
X4				1.000	0.462	0.431	0.178	-0.141	0.165	0.170	0.012	0.369	0.338	0.443	0.110	0.309	0.320	0.311	0.359	0.428	-0.227	0.030	0.085	-0.077	0.065	0.369
X5					1.000	0.317	0.209	-0.020	0.078	0.157	0.011	0.284	0.242	0.298	0.050	0.250	0.206	0.205	0.232	0.315	-0.202	0.010	0.080	-0.064	-0.002	0.246
X6						1.000	0.485	0.115	-0.102	-0.066	-0.082	-0.015	0.186	0.295	0.047	-0.046	0.226	0.321	0.296	0.414	-0.334	0.000	0.119	-0.116	-0.195	0.144
X7							1.000	0.044	-0.035	-0.109	0.010	-0.010	0.100	0.178	0.061	-0.057	0.113	0.191	0.267	0.363	-0.224	-0.150	0.016	-0.180	-0.236	0.093
X8								1.000	0.187	0.195	0.259	-0.061	0.141	0.114	0.274	-0.026	0.170	0.210	0.096	0.037	0.139	-0.018	0.009	0.033	-0.094	-0.028
X9									1.000	0.447	0.445	0.433	0.451	0.410	0.392	0.405	0.377	0.313	0.316	0.242	0.163	0.011	-0.014	-0.012	0.177	0.233
X10										1.000	0.201	0.487	0.411	0.430	0.192	0.432	0.285	0.285	0.273	0.216	-0.008	0.055	0.024	0.080	0.194	0.207
X11											1.000	0.347	0.301	0.175	0.448	0.313	0.310	0.169	0.148	0.010	0.284	-0.066	-0.092	-0.009	0.054	0.207
X12												1.000	0.642	0.622	0.349	0.830	0.602	0.414	0.426	0.466	-0.106	0.013	-0.001	-0.005	0.138	0.488
X13													1.000	0.711	0.461	0.599	0.638	0.525	0.575	0.553	-0.025	-0.004	0.002	-0.061	0.041	0.472
X14														1.000	0.358	0.547	0.619	0.643	0.695	0.704	-0.203	0.036	0.045	-0.090	0.120	0.358
X15															1.000	0.432	0.483	0.334	0.281	0.211	0.156	-0.052	0.015	-0.068	0.066	0.225
X16																1.000	0.600	0.380	0.323	0.376	-0.081	0.010	0.000	-0.009	0.156	0.413
X17																	1.000	0.678	0.553	0.521	-0.003	-0.037	0.051	-0.085	-0.043	0.405
X18																		1.000	0.620	0.617	-0.167	-0.007	0.129	-0.114	0.012	0.287
X19																			1.000	0.750	0.011	0.007	0.099	-0.154	0.058	0.357
X20																				1.000	-0.517	0.042	0.113	-0.149	0.019	0.353
X21																					1.000	-0.104	-0.087	0.054	0.021	-0.086
X22																						1.000	0.000	0.066	0.353	-0.039
X23																							1.000	0.072	0.137	-0.011
X24																								1.000	0.010	-0.075
X25																									1.000	-0.026
X26																										1.000

Significant at 5 per cent level (0.083)
Significant at 1 per cent level (0.115)

X1 Sprouting
X2 Plant height
X3 Number of leaves
X4 Length of leaf
X5 Breadth of leaf
X6 Number of tillers
X7 Days to maturity
X8 Number of mother rhizomes
X9 Weight of mother rhizomes
X10 Girth of mother rhizomes
X11 Number of Primary rhizomes
X12 Weight of Primary rhizomes
X13 Length of Primary rhizomes

X14 Girth of Primary rhizomes
X15 Number of Secondary rhizomes
X16 Weight of Secondary rhizomes
X17 Length of Secondary rhizomes
X18 Girth of Secondary rhizomes
X19 Rhizome diameter
X20 Core diameter
X21 Rhizome Core ratio
X22 Oil
X23 Oleoresin
X24 Curcumin
X25 Curing percentage
X26 Yield

Table 37. Genotypic correlation coefficients of turmeric genotypes

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17	X18	X19	X20	X21	X22	X23	X24	X25	X26
X1	1.000	0.169	0.119	0.128	0.035	0.031	0.024	-0.102	0.200	0.186	0.143	0.171	0.175	0.211	0.134	0.099	0.204	0.196	0.211	0.122	0.004	0.022	0.847	-0.032	-0.030	0.187
X2		1.000	0.692	0.880	0.869	0.618	0.315	-0.118	0.188	0.145	0.077	0.387	0.543	0.532	0.236	0.334	0.487	0.517	0.514	0.558	-0.220	0.033	0.581	-0.061	-0.050	0.513
X3			1.000	0.732	0.729	0.750	0.418	0.015	0.084	0.144	0.001	0.266	0.381	0.540	0.146	0.185	0.376	0.443	0.482	0.533	-0.289	0.091	0.460	-0.072	-0.121	0.362
X4				1.000	0.857	0.550	0.226	-0.216	0.215	0.262	0.071	0.492	0.510	0.583	0.198	0.406	0.417	0.412	0.500	0.586	-0.307	0.144	0.488	-0.085	0.096	0.497
X5					1.000	0.542	0.353	-0.145	0.161	0.284	-0.030	0.520	0.496	0.583	0.126	0.458	0.403	0.385	0.480	0.573	-0.351	0.107	0.152	-0.118	-0.015	0.455
X6						1.000	0.541	0.177	-0.121	-0.066	-0.117	-0.010	0.240	0.338	0.062	-0.058	0.246	0.374	0.354	0.476	-0.377	0.064	0.971	-0.118	-0.219	0.163
X7							1.000	0.088	-0.039	-0.127	0.004	-0.007	0.118	0.205	0.065	-0.060	0.116	0.207	0.289	0.388	-0.262	-0.201	0.349	-0.190	-0.246	0.096
X8								1.000	0.277	0.287	0.342	-0.088	0.247	0.134	0.399	-0.038	0.257	0.316	0.148	0.071	0.207	-0.045	-0.054	0.067	-0.172	-0.028
X9									1.000	0.497	0.586	0.466	0.528	0.455	0.449	0.435	0.423	0.354	0.357	0.265	0.181	0.007	0.952	-0.004	0.205	0.249
X10										1.000	0.227	0.515	0.467	0.475	0.223	0.457	0.305	0.309	0.297	0.229	-0.002	0.087	0.325	0.093	0.207	0.212
X11											1.000	0.427	0.410	0.244	0.562	0.385	0.397	0.217	0.182	0.021	0.345	-0.123	-0.869	-0.012	0.053	0.262
X12												1.000	0.696	0.652	0.379	0.844	0.621	0.430	0.449	0.480	-0.108	0.018	0.394	-0.006	0.142	0.493
X13													1.000	0.789	0.527	0.656	0.705	0.550	0.634	0.607	-0.019	-0.022	0.755	-0.064	0.034	0.526
X14														1.000	0.408	0.572	0.651	0.681	0.746	0.746	-0.217	0.067	0.189	-0.099	0.121	0.373
X15															1.000	0.470	0.528	0.365	0.318	0.238	0.169	-0.069	0.534	-0.077	0.057	0.240
X16																1.000	0.615	0.396	0.341	0.393	-0.083	0.008	0.188	-0.011	0.159	0.419
X17																	1.000	0.712	0.579	0.542	-0.007	-0.038	0.562	-0.093	-0.068	0.415
X18																		1.000	0.670	0.654	-0.172	-0.008	0.495	-0.116	0.003	0.300
X19																			1.000	0.789	-0.001	0.026	0.419	-0.178	0.056	0.374
X20																				1.000	-0.524	0.076	0.373	-0.159	0.013	0.366
X21																					1.000	-0.138	-0.849	0.071	-0.010	-0.152
X22																						1.000	0.761	0.089	0.508	-0.060
X23																							1.000	0.270	0.412	-0.464
X24																								1.000	0.013	-0.078
X25																									1.000	-0.027
X26																										1.000

Significant at 5 per cent level (0.083)   Significant at 1 per cent level (0.115)

X1 Sprouting
X2 Plant height
X3 Number of leaves
X4 Length of leaf
X5 Breadth of leaf
X6 Number of tillers
X7 Days to maturity
X8 Number of mother rhizomes
X9 Weight of mother rhizomes
X10 Girth of mother rhizomes
X11 Number of Primary rhizomes
X12 Weight of Primary rhizomes
X13 Length of Primary rhizomes
X14 Girth of Primary rhizomes
X15 Number of Secondary rhizomes
X16 Weight of Secondary rhizomes
X17 Length of Secondary rhizomes
X18 Girth of Secondary rhizomes
X19 Rhizome diameter
X20 Core diameter
X21 Rhizome Core ratio
X22 Oil
X23 Oleoresin
X24 Curcumin
X25 Curing percentage
X26 Yield

of mother rhizomes (0.233, 0.249), number of secondary rhizomes (0.225, 0.240), girth of mother rhizomes (0.207, 0.212), sprouting (0.174, 0.187), number of tillers (0.144, 0.163) and days to maturity (0.093, 0.096).

However, the rhizome yield expressed a negative correlation with oleoresin (-0.011, -0.464) followed by rhizome-core ratio, curcumin, number of mother rhizomes and curing percentage.

4.7.2. Association of plant and rhizome *inter se* (Table 36 and 37)

Sprouting: Sprouting showed significant association with girth of mother rhizomes (0.152, 0.143), rhizome diameter (0.186, 0.211), length of secondary rhizomes (0.182, 0.204), followed by plant height, number of leaves, length of leaf, weight of mother rhizomes, girth of mother rhizomes, number of primary rhizomes, weight of primary rhizomes, length of primary rhizomes, number of secondary rhizomes, weight of secondary rhizomes, girth of secondary rhizomes, core diameter and yield both at phenotypic and genotypic levels.

The oil and oleoresin were found to be significantly associated with sprouting at genotypic level. A negative correlation was noticed for number of mother rhizomes, curcumin and curing percentage (Table 36 and 37).

Plant height: Both at phenotypic and genotypic levels, plant height exhibited significant positive correlation with number of leaves, length of leaf, breadth of leaf, number of tillers, days to maturity, weight of mother rhizomes, girth of mother rhizomes, weight of primary rhizomes, length of primary rhizomes, girth of primary rhizomes, number of secondary rhizomes, length and girth of secondary rhizomes, rhizome diameter, core diameter and oil.

A negative correlation was observed for number of mother rhizomes, rhizome core ratio, curcumin and curing percentage. (Table 36 and 37).

Number of leaves: The phenotypic and genotypic correlations between number of leaves and length of leaf (0.599, 0.732), breadth of leaf (0.462, 0.729), number of tillers (0.590, 0.750), days to maturity, girth of mother rhizomes, weight of primary rhizomes, length and girth of primary rhizomes, number and weight of secondary rhizomes, length and girth of secondary rhizomes, rhizome and core diameter were positive and significant.

The negative association is reported for rhizome core ratio, curcumin and curing percentage. (Table 36 and 37).

Length of leaf: The phenotypic and genotypic levels indicated positive and significant correlation with breadth of leaf (0.462, 0.857), number of tillers, days to maturity, weight of mother rhizomes, girth of mother rhizomes, weight, length and girth of primary rhizomes, number and weight of secondary rhizomes, length and girth of secondary rhizomes, rhizome diameter, core diameter (0.428, 0.586), oleoresin (0.085, 0.488) and yield.

The negative association was linked with number of mother rhizomes, rhizome core ratio and curcumin. (Table 36 and 37).

Breadth of leaf: A positive relationship between number of tillers (0.317, 0.542), days to maturity, weight of mother rhizomes, girth of mother rhizomes, weight and length of primary rhizomes, girth of primary rhizomes (0.298, 0.583), weight, length and girth of secondary rhizomes, rhizome diameter, core diameter (0.315, 0.573,) were observed and they were found to be highly significant at both phenotypic and genotypic level.

The number of secondary rhizomes, oil and oleoresin were significantly and positively correlated with breadth of leaf at genotypic level alone. The negatively correlated characters were number of mother rhizomes, curcumin and curing percentage. (Table 36 and 37).

Number of tillers: Both at phenotypic and genotypic levels, number of tillers indicated significant positive association with days to maturity (0.485, 0.541), number of mother rhizomes, length and girth of primary rhizome, length and girth of secondary rhizomes, rhizome diameter, core diameter (0.414, 0.476) and oleoresin. The parameter showed significant and positive correlation with oil at genotypic level (0.064).

The negatively correlated characters were girth of mother rhizomes, number and weight of primary rhizomes, weight of secondary rhizomes, rhizome core ratio, curcumin and curing percentage. (Table 36 and 37).

Days to maturity: Duration associated with length and girth of primary rhizomes, length and girth of secondary rhizomes, rhizome and core diameter were significantly and positively correlated at phenotypic and genotypic levels.

Number of mother rhizomes and oleoresin were positively and significantly correlated at genotypic level alone (0.088 and 0.349 respectively). The negative correlation was observed for weight and girth of mother rhizomes, weight of primary and secondary rhizomes, rhizome core ratio, oil, curcumin and curing percentage. (Table 36 and 37).

Number of mother rhizomes: A significant and positive correlation was revealed between number of mother rhizomes and weight of mother rhizomes, girth of mother rhizomes (0.195, 0.287), number of primary rhizomes (0.259, 0.342), length and girth of primary rhizomes, number of secondary rhizomes (0.274, 0.399), length and girth of secondary rhizomes, rhizome diameter, rhizome core ratio both at phenotypic and genotypic levels.

The negative association was related with weight of primary and secondary rhizomes, oil, oleoresin, curing percentage and yield. (Table 36 and 37).

Weight of mother rhizomes: The character attributed for a significant and positive correlation with girth of mother rhizomes (0.447,0.497), number of primary rhizomes (0.445, 0.586), weight of primary rhizomes, length of primary rhizomes (0.451, 0.528), girth of primary rhizomes, number, weight, length and girth of secondary rhizomes, rhizome, diameter, core diameter and curing percentage at both phenotypic and genotypic levels. Oleoresin registered positive and significant association only at genotypic level. (Table 36 and 37).

Girth of mother rhizomes: Number of primary rhizomes, weight of primary rhizomes (0.487,0.515), length and girth of primary rhizomes, number, weight, length and girth of secondary rhizomes, rhizome diameter and curing percentage recorded significant and positive association with girth of mother rhizomes both at phenotypic and genotypic levels. However, oleoresin (0.325) and curcumin (0.093) showed significant and positive correlation at genotypic level only. The negatively associated character was rhizome core ratio. (Table 36 and 37).

Number of primary rhizomes: Number of primary rhizomes was significantly and positively associated with weight of primary rhizomes (0.347, 0.427), length of primary rhizomes (0.301, 0.410), girth of primary rhizomes, number of secondary rhizomes (0.448, 0.562), weight, length and girth of secondary rhizomes, rhizome diameter and rhizome core ratio at both phenotypic and genotypic levels. The negatively associated characters were oil, oleoresin, curcumin and curing percentage. (Table 36 and 37).

Weight of primary rhizomes: A positive relationship between weight of primary rhizomes, length of primary rhizomes (0.642, 0.696), girth of primary rhizomes (0.622, 0.652), number of secondary rhizomes, weight of secondary rhizomes (0.830, 0.844), length and girth of secondary rhizomes, rhizome and core diameter and curing percentage was observed at both phenotypic and genotypic levels. At genotypic level alone, oil and oleoresin were positively and significantly correlated. The negatively associated character was rhizome core ratio and curcumin at both the levels. (Table 36 and 37).

Length of primary rhizomes: Both at phenotypic and genotypic levels, length of primary rhizomes registered significant positive correlation with girth of primary rhizomes (0.711, 0.789), number of secondary rhizomes, weight of secondary rhizomes (0.599,0.656), length of secondary rhizomes (0.638, 0.705), girth of secondary rhizomes, rhizome and core diameter. At genotypic level alone, oleoresin (0.755) was positively and significantly correlated. The negatively associated characters were rhizome core ratio, oil and curcumin. (Table 36 and 37).

Girth of primary rhizomes: The genotypic and phenotypic correlations between girth of primary rhizomes and number of secondary rhizomes, weight, length and girth of secondary rhizomes, rhizome diameter (0.695, 0.746), core diameter (0.704, 0.746) and curing percentage. At genotypic level, oil and oleoresin were positively and significantly correlated. (Table 36 and 37).

Number of secondary rhizomes: Number of secondary rhizomes was positively and significantly correlated with weight of secondary rhizomes (0.432, 0.470), length of secondary rhizomes (0.483, 0.528), girth of secondary rhizomes, and rhizome and core diameter at both the levels. At genotypic level alone, oleoresin (0.534) was positively and significantly correlated. The negatively associated characters were oil and curcumin. (Table 36 and 37).

Weight of secondary rhizomes: The weight of secondary rhizomes was highly significant, positively associated with length (0.600, 0.615) and girth (0.380, 0.396) of secondary rhizomes, rhizome and core diameter and curing percentage at both genotypic and phenotypic levels. At genotypic level alone, oleoresin recorded significant and positive association. The negatively correlated characters are rhizome core ratio and curcumin. (Table 36 and 37).

Length of secondary rhizomes: Girth of secondary rhizomes (0.678, 0.712), rhizome diameter (0.553, 0.579), core diameter (0.521, 0.542) was significantly and positively correlated. Oleoresin (0.562) expressed a positive and significant association at genotypic level only. The rhizome core ratio, oil, curcumin and curing percentage were negatively correlated. (Table 36 and 37).

Girth of secondary rhizomes: Girth of secondary rhizomes attributed a significant and positive correlation with rhizome diameter (0.620,0.670), core diameter (0.617, 0.654), oleoresin (0.129, 0.495). The negative association was found for rhizome core ratio, oil and curcumin. (Table 36 and 37).

Rhizome diameter: Core diameter (0.750, 0.789) and oleoresin (0.099, 0.419) exhibited a positive correlation with rhizome diameter and was significant at both genotypic and phenotypic levels. Rhizome core ratio and curcumin were negatively associated. (Table 36 and 37).

Core diameter: Core diameter recorded positive and significant association with oleoresin alone at both phenotypic and genotypic levels (0.113, 0.373). At genotypic level, oil was positively and significantly correlated. The association was found to be negative for rhizome core ratio and curcumin. (Table 36 and 37).

Rhizome core ratio: This parameter did not exhibit any significant correlation. The negative association was reported for oil, oleoresin and yield. (Table 36 and 37).

Oil: Curing percentage (0.353, 0.508) recorded positive and significant correlation with oil at both phenotypic and genotypic level while oleoresin and curcumin exerted positive, significant association (0.761 and 0.089 respectively) at genotypic level. (Table 36 and 37).

Oleoresin: A trend similar to oil was observed which exhibited a positive significant correlation with curing percentage (0.137, 0.412) at both the levels while curcumin expressed positive significant correlation at genotypic level only (0.270). (Table 36 and 37).

Curcumin and curing percentage: Curcumin and curing percentage exerted no significant correlation at both the phenotypic and genotypic levels and were negatively associated with yield. (Table 36 and 37).

Simple Correlation Coefficient (Table 38)

A similar trend was noticed for simple correlations (Table 38). The rhizome yield was positively and significantly correlated with weight of primary rhizomes (0.491) followed by length of primary rhizomes (0.490), plant height (0.458), length of leaf (0.421), weight of secondary rhizomes (0.416), length of secondary rhizomes (0.410), girth of primary rhizomes (0.365), rhizome diameter (0.365), core diameter (0.359),

Table 38. Simple correlation coefficients of turmeric genotypes

	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12	X13	X14	X15	X16	X17	X18	X19	X20	X21	X22	X23	X24	X25	X26
X1	1.000	0.152	0.108	0.114	0.031	0.029	0.023	-0.088	0.183	0.168	0.119	0.165	0.165	0.201	0.130	0.095	0.193	0.184	0.198	0.114	0.004	0.020	0.094	-0.032	-0.023	0.180
X2		1.000	0.650	0.756	0.590	0.543	0.278	-0.068	0.167	0.135	0.060	0.351	0.465	0.474	0.192	0.298	0.433	0.459	0.452	0.493	-0.196	0.025	0.157	-0.060	-0.048	0.458
X3			1.000	0.651	0.537	0.660	0.385	0.031	0.062	0.127	-0.002	0.242	0.330	0.481	0.121	0.172	0.343	0.408	0.432	0.484	-0.266	0.075	0.105	-0.071	-0.112	0.328
X4				1.000	0.573	0.478	0.197	-0.168	0.185	0.208	0.035	0.419	0.407	0.499	0.146	0.348	0.359	0.351	0.416	0.492	-0.260	0.112	0.121	-0.080	0.077	0.421
X5					1.000	0.382	0.250	-0.055	0.103	0.196	-0.002	0.354	0.318	0.383	0.074	0.311	0.265	0.258	0.307	0.391	-0.245	0.065	0.141	-0.080	-0.006	0.308
X6						1.000	0.511	0.138	-0.110	-0.066	-0.097	-0.012	0.211	0.315	0.054	-0.052	0.235	0.345	0.323	0.443	-0.354	0.052	0.135	-0.117	-0.206	0.153
X7							1.000	0.061	-0.037	-0.117	0.007	-0.008	0.109	0.191	0.063	-0.058	0.114	0.199	0.278	0.375	-0.253	-0.199	0.020	-0.185	-0.241	0.094
X8								1.000	0.220	0.230	0.289	-0.071	0.181	0.121	0.321	-0.031	0.203	0.250	0.116	0.050	0.165	-0.051	-0.016	0.040	-0.108	-0.028
X9									1.000	0.471	0.505	0.449	0.486	0.431	0.418	0.419	0.399	0.332	0.335	0.253	0.172	-0.009	0.028	-0.010	0.186	0.241
X10										1.000	0.212	0.501	0.437	0.452	0.207	0.444	0.294	0.296	0.284	0.222	-0.005	0.075	0.047	0.084	0.200	0.210
X11											1.000	0.382	0.347	0.205	0.496	0.344	0.347	0.190	0.163	0.015	0.310	-0.117	-0.114	-0.012	0.056	0.231
X12												1.000	0.667	0.637	0.364	0.837	0.612	0.422	0.437	0.473	-0.107	0.017	0.009	-0.006	0.140	0.491
X13													1.000	0.751	0.491	0.626	0.670	0.537	0.603	0.579	-0.022	-0.027	0.040	-0.062	0.041	0.490
X14														1.000	0.381	0.559	0.634	0.662	0.720	0.724	-0.210	0.043	0.080	-0.095	0.125	0.365
X15															1.000	0.450	0.504	0.348	0.298	0.224	0.162	-0.073	0.022	-0.072	0.065	0.232
X16																1.000	0.607	0.388	0.332	0.384	-0.082	0.008	0.005	-0.010	0.158	0.416
X17																	1.000	0.695	0.566	0.531	-0.005	-0.054	0.069	-0.088	-0.042	0.410
X18																		1.000	0.644	0.635	-0.169	-0.016	0.200	-0.115	0.012	0.293
X19																			1.000	0.769	0.005	0.012	0.150	-0.163	0.061	0.365
X20																				1.000	-0.520	0.062	0.186	-0.154	0.020	0.359
X21																					1.000	-0.152	-0.132	0.055	0.021	-0.088
X22																						1.000	0.556	0.087	0.501	-0.060
X23																							1.000	0.108	0.183	-0.020
X24																								1.000	0.012	-0.077
X25																									1.000	-0.026
X26																										1.000

* Significant at 5 per cent level (0.083)
** Significant at 1 per cent level (0.115)

X1 Sprouting
X2 Plant height
X3 Number of leaves
X4 Length of leaf
X5 Breadth of leaf
X6 Number of tillers
X7 Days to maturity
X8 Number of mother rhizomes
X9 Weight of mother rhizomes
X10 Girth of mother rhizomes
X11 Number of Primary rhizomes
X12 Weight of Primary rhizomes
X13 Length of Primary rhizomes
X14 Girth of Primary rhizomes
X15 Number of Secondary rhizomes
X16 Weight of Secondary rhizomes
X17 Length of Secondary rhizomes
X18 Girth of Secondary rhizomes
X19 Rhizome diameter
X20 Core diameter
X21 Rhizome Core ratio
X22 Oil
X23 Oleoresin
X24 Curcumin
X25 Curing percentage
X26 Yield

number of leaves (0.328), breadth of leaf (0.308), girth of secondary rhizomes (0.293), weight of mother rhizomes (0.241), number of secondary rhizomes (0.232), number of primary rhizomes (0.231), girth of mother rhizomes (0.210), sprouting (0.180), number of tillers (0.153) and days to maturity (0.094). The negative association was found with rhizome core ratio, oil, oleoresin, curcumin and curing percentage (Table 38).

4.8. Path analysis (Table 39, Fig. 6)

Path coefficient analysis exhibiting direct and indirect effects of sprouting, plant height, number of leaves, length of leaf, breadth of leaf, number of tillers, days to maturity, number of mother rhizomes, weight of mother rhizomes, girth of mother rhizomes, number of primary rhizomes, weight of primary rhizomes, length of primary rhizomes, girth of primary rhizomes, number of secondary rhizomes, weight of secondary rhizomes, length and girth of secondary rhizomes, rhizome diameter, core diameter, rhizome core ratio, oil, oleoresin, curcumin, curing percentage on rhizome yield per plant is presented in Table 39.

4.8.1. Direct effect (Table 39)

The highest positive direct effect was registered for girth of secondary rhizomes (0.922) followed by breadth of leaf (0.879). The parameters sprouting (0.373), length of leaf (0.401), number of tillers (0.384), number of primary rhizomes (0.463), length of primary rhizomes (0.745), weight of primary rhizomes (0.361), number of secondary rhizomes (0.270), length of secondary rhizomes (0.104), weight of secondary rhizomes (0.575), core diameter (0.683), rhizome core ratio (0.332), curcumin (0.318) and curing percentage (0.298) exhibited positive direct effects.

The negative direct effect was the highest for oil (-0.421) followed by number of mother rhizomes (-0.679). The other parameters that showed negative effect were plant height (-0.163) and girth of mother rhizomes (-0.079), which were the least.

Table 39. Path coefficient analysis for turmeric genotypes

Characters	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26
X_1	0.373	-0.366	-0.042	0.051	0.087	0.012	-0.009	0.069	-0.018	-0.015	0.066	-0.096	0.201	-0.245	0.036	-0.057	0.021	0.180	-0.075	0.083	0.001	-0.013	-0.041	-0.010	-0.009	0.187**
X_2	0.063	-0.163	-0.245	0.353	0.133	0.237	-0.120	0.080	-0.017	-0.011	0.035	-0.217	0.623	-0.617	0.064	-0.192	0.050	0.478	-0.183	0.381	-0.073	-0.030	-0.080	-0.020	-0.015	0.513**
X_3	0.044	-0.496	-0.354	0.293	0.790	0.288	-0.159	-0.010	-0.008	-0.011	0.001	-0.149	0.436	-0.626	0.039	-0.106	0.039	0.409	-0.172	0.364	-0.096	-0.062	-0.032	-0.023	-0.036	0.362**
X_4	0.048	-0.404	-0.259	0.401	0.103	0.211	-0.086	0.147	-0.019	-0.021	0.033	-0.276	0.584	-0.677	0.054	-0.233	0.043	0.380	-0.178	0.400	-0.102	-0.097	-0.055	-0.027	0.029	0.497**
X_5	0.013	-0.295	-0.258	0.343	0.879	0.208	-0.134	0.098	-0.015	-0.023	-0.014	-0.292	0.569	-0.677	0.034	-0.263	0.042	0.355	-0.171	0.391	-0.117	-0.078	-0.092	-0.038	-0.004	0.455**
X_6	0.012	-0.337	-0.266	0.221	0.330	0.384	-0.206	-0.120	0.011	0.005	-0.054	0.005	0.275	-0.392	0.017	0.033	0.025	0.344	-0.126	0.325	-0.125	-0.052	-0.044	-0.038	-0.065	0.163**
X_7	0.009	-0.681	-0.148	0.090	0.867	0.208	-0.381	-0.059	0.004	0.010	0.002	0.004	0.135	-0.237	0.018	0.034	0.012	0.190	-0.103	0.265	-0.087	0.087	-0.008	-0.061	-0.073	0.096*
X_8	-0.038	0.256	-0.005	-0.087	-0.355	0.068	-0.033	-0.679	-0.025	-0.023	0.158	0.049	0.283	-0.156	0.108	0.022	0.027	0.291	-0.053	0.049	0.069	0.043	0.026	0.017	-0.039	-0.028
X_9	0.074	-0.406	-0.030	0.086	0.396	-0.046	0.015	-0.188	-0.091	-0.039	0.272	-0.261	0.604	-0.528	0.121	-0.250	0.044	0.326	-0.127	0.181	0.060	0.017	-0.035	-0.002	0.058	0.249**
X_{10}	0.069	-0.314	-0.051	0.105	0.706	-0.025	0.048	-0.195	-0.045	-0.079	0.105	-0.289	0.535	-0.551	0.060	-0.263	0.032	0.285	-0.106	0.157	-0.001	-0.034	-0.027	0.029	0.062	0.212**
X_{11}	0.053	-0.166	-0.0004	0.028	-0.075	-0.045	-0.002	-0.232	-0.053	-0.018	0.463	-0.240	0.470	-0.283	0.152	-0.221	0.041	0.200	-0.065	0.014	0.115	0.069	0.042	-0.005	0.018	0.262**
X_{12}	0.064	-0.838	-0.094	0.197	0.876	-0.004	0.003	0.060	-0.042	-0.041	0.198	0.361	0.797	-0.574	0.103	-0.485	0.064	-0.397	-0.160	0.328	-0.036	-0.007	-0.009	-0.002	0.042	0.493**
X_{13}	0.065	-0.176	-0.135	0.204	0.606	0.092	-0.045	-0.168	-0.048	-0.037	0.190	-0.391	0.745	-0.916	0.142	-0.377	0.073	0.507	-0.226	0.414	-0.006	0.024	-0.035	-0.020	0.013	0.526**
X_{14}	0.079	-0.543	-0.091	0.234	0.533	0.130	-0.078	-0.091	-0.041	-0.037	0.113	-0.366	0.704	-0.460	0.110	-0.329	0.067	0.428	-0.266	0.409	-0.072	-0.017	-0.043	-0.032	0.039	0.373**
X_{15}	0.050	-0.511	-0.051	0.080	0.311	0.024	-0.025	-0.271	-0.041	-0.018	0.260	-0.213	0.604	-0.473	0.270	-0.270	0.055	0.336	-0.113	0.163	0.056	0.034	-0.010	-0.024	0.019	0.240**
X_{16}	0.037	-0.722	-0.065	0.163	0.380	-0.022	0.023	0.126	-0.039	-0.036	0.278	-0.474	0.752	-0.664	0.227	0.575	0.084	-0.365	-0.122	0.268	-0.028	-0.001	-0.004	-0.004	0.048	0.419**
X_{17}	0.076	-0.924	-0.133	0.170	0.991	0.094	-0.044	-0.174	-0.038	-0.024	0.184	-0.349	0.908	-0.755	0.113	-0.354	0.104	0.656	-0.206	0.370	-0.002	0.026	-0.029	-0.029	-0.012	0.415**
X_{18}	0.073	-0.787	-0.157	0.165	0.706	0.143	-0.079	-0.214	-0.032	-0.024	0.101	-0.242	0.631	-0.791	0.099	-0.228	0.074	0.922	-0.238	0.406	-0.057	0.010	-0.095	-0.037	0.004	0.300**
X_{19}	0.079	-0.113	-0.171	0.200	0.179	0.136	-0.110	-0.100	-0.032	-0.023	0.084	-0.252	0.726	-0.866	0.086	-0.196	0.060	0.617	-0.356	0.539	-0.0003	-0.007	-0.070	-0.055	0.019	0.374**
X_{20}	0.046	-0.207	-0.189	0.235	0.408	0.183	-0.148	-0.048	-0.024	-0.018	0.010	-0.269	0.695	-0.865	0.064	-0.226	0.056	0.603	-0.281	0.683	-0.174	-0.030	-0.093	-0.050	0.006	0.366**
X_{21}	0.002	0.475	0.102	-0.123	-0.862	-0.145	0.100	-0.140	-0.016	0.0002	0.160	0.061	-0.082	0.252	0.046	0.048	-0.001	-0.159	0.0003	-0.358	0.332	0.074	0.061	0.018	0.006	-0.152
X_{22}	0.008	-0.110	-0.053	0.217	0.368	0.051	0.103	0.046	-0.002	0.002	-0.070	-0.018	-0.033	-0.055	-0.036	-0.008	-0.018	-0.009	-0.041	0.233	-0.222	-0.421	-0.223	0.029	0.153	-0.060
X_{23}	0.589	-0.746	-0.517	0.897	0.194	0.756	-0.133	0.787	-0.144	-0.097	-0.879	-0.219	0.532	-0.246	0.121	-0.103	0.136	0.565	-0.534	0.571	-0.823	-0.636	0.022	0.523	0.018	-0.464
X_{24}	-0.012	0.133	0.025	-0.034	-0.290	-0.045	0.072	-0.036	0.001	-0.007	-0.007	0.004	-0.073	0.115	-0.021	0.006	-0.009	-0.107	0.061	-0.108	0.018	-0.038	-0.050	0.318	0.004	-0.078
X_{25}	-0.011	0.108	0.043	0.038	-0.036	-0.084	0.094	0.089	-0.018	-0.016	0.028	-0.080	0.048	-0.152	0.017	-0.092	-0.004	0.011	-0.023	0.015	0.007	-0.238	-0.075	0.004	0.298	-0.027

* Significant at 5 per cent level
** Significant at 1 per cent level

X1 Sprouting
X2 Plant height
X3 Number of leaves
X4 Length of leaf
X5 Breadth of leaf
X6 Number of tillers
X7 Days to maturity
X8 Number of mother rhizomes
X9 Weight of mother rhizomes
X10 Girth of mother rhizomes
X11 Number of Primary rhizomes
X12 Weight of Primary rhizomes
X13 Length of Primary rhizomes
X14 Girth of Primary rhizomes
X15 Number of Secondary rhizomes
X16 Weight of Secondary rhizomes
X17 Length of Secondary rhizomes
X18 Girth of Secondary rhizomes
X19 Rhizome diameter
X20 Core diameter
X21 Rhizome Core ratio
X22 Oil
X23 Oleoresin
X24 Curcumin
X25 Curing percentage
X26 Yield

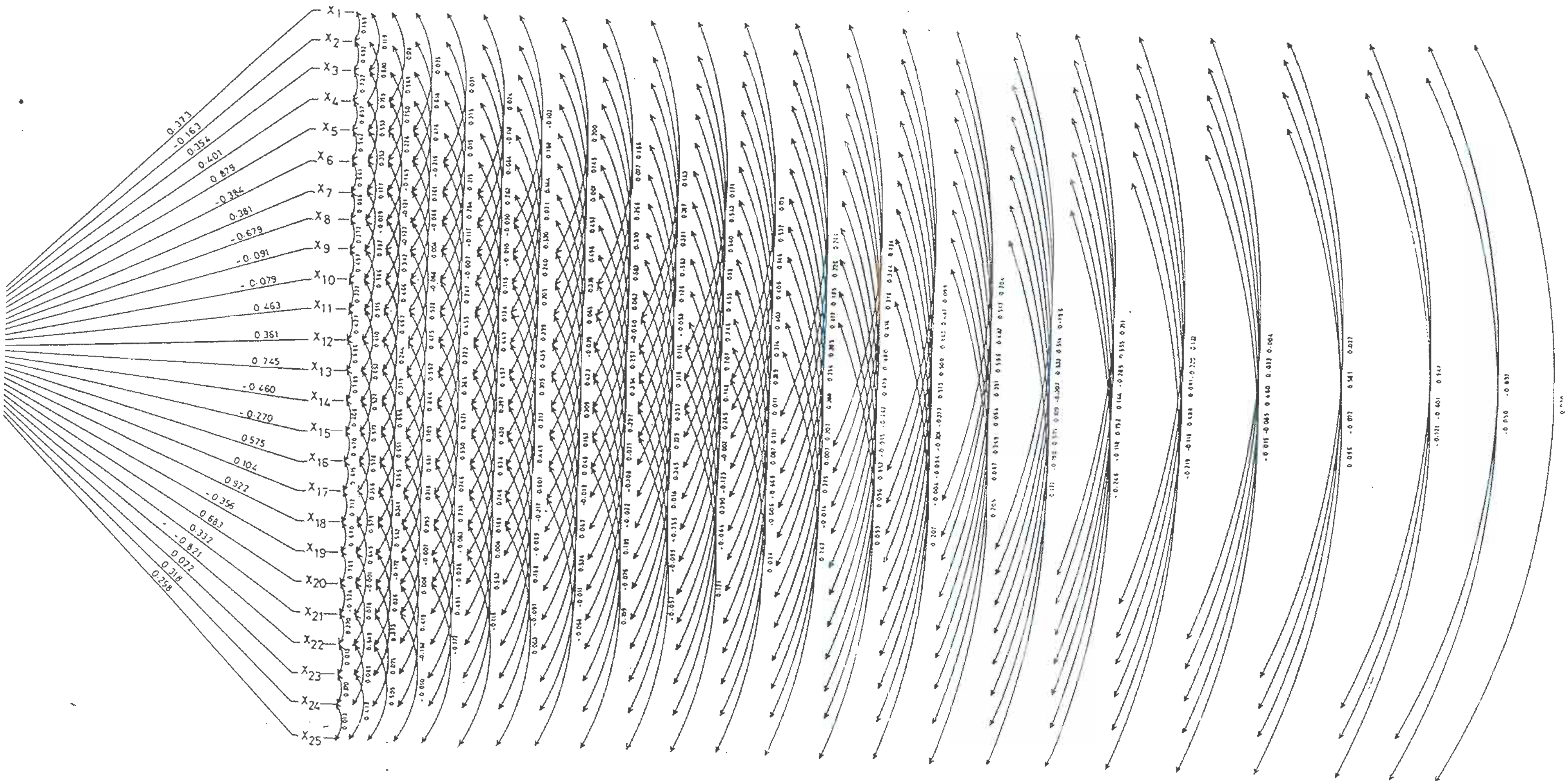


Fig.6. Path diagram

4.8.2. Indirect effect (Table 39)

Sprouting

The positive indirect effect was higher for length of primary rhizomes (0.201) followed by girth of secondary rhizomes (0.180). The positive indirect effects were also noticed for length of leaf, breadth of leaf, number of tillers, number of mother rhizomes, number of primary rhizomes, number of secondary rhizomes, length of secondary rhizomes, core diameter, rhizome core ratio and curcumin. The indirect effects observed for plant height (-0.366) was negative and the highest followed by girth of primary rhizomes (-0.245). The insignificant negative indirect effect was observed for days to maturity and curing percentage. The negative indirect effects were observed for plant height, number, number of leaves, weight of mother rhizomes, girth of mother rhizomes, weight and girth of primary rhizomes, weight of secondary rhizomes, rhizome diameter, oil, oleoresin and curcumin.

Plant height

The greatest positive indirect effect was observed for length of primary rhizomes (0.623) followed by core diameter (0.381). The indirect effect of plant height through sprouting, length of leaf, number of tillers, number of mother rhizomes, number of primary rhizomes, number of secondary rhizomes, length of secondary rhizomes, girth of secondary rhizomes were also found to be positive. The indirect effect through girth of primary rhizomes, number of leaves, weight of secondary rhizomes was negative (-0.617, -0.245 and -0.192 respectively). The other negative indirect effects were observed through days to maturity, weight of mother rhizomes, weight and girth of primary rhizomes, rhizome diameter, rhizome core ratio, oil oleoresin, curcumin and curing percentage.

Number of leaves

The highest positive indirect effect for number of leaves per plant was through breadth of leaf (0.790) followed by length of primary rhizomes (0.436). The lowest positive indirect effect was through number of primary rhizomes, sprouting, length of leaf, number of tillers, number of secondary rhizomes, length and girth of secondary rhizomes, core diameter. The negative indirect effect was the highest for girth of primary rhizomes (-0.626) followed by plant height (-0.496) and the lowest for weight of mother rhizomes. The direct negative effects were recorded for days to maturity, number and girth of mother rhizomes, weight of primary and secondary rhizomes, rhizome diameter, rhizome core ratio, oil, oleoresin, curcumin and curing percentage.

Length of leaf

This trait registered the highest positive indirect effect through breadth of leaf (0.103) followed by length of primary rhizomes (0.584), core diameter (0.400), girth of secondary rhizomes (0.380). The lowest indirect effect was noticed for curing percentage (0.029) followed by number of primary rhizomes (0.033). The positive indirect effects were also observed for sprouting, length of leaf, breadth of leaf, number of tillers, number of mother rhizomes, number of primary and secondary rhizomes and length of secondary rhizomes. The greatest indirect, negative effect was through height of the plant (-0.404) followed by girth of primary rhizomes (-0.677) and the lowest for both weight and girth of mother rhizomes (-0.019 and -0.021). Number of leaves, days to maturity, weight of primary rhizomes, weight of secondary rhizomes, rhizome diameter, rhizome core ratio, oil, oleoresin and curcumin also attributed for negative effects.

Breadth of leaf

The highest positive indirect effect was (0.569) via length of primary rhizomes followed by core diameter (0.391) and length of leaf (0.343). The least indirect effect was noticed for sprouting (0.013). The other positive effects were achieved through sprouting, number of tillers, number of mother rhizomes and secondary rhizomes, length and girth of secondary rhizomes. The highest negative indirect effects were observed for girth of primary rhizomes (-0.677) followed by plant height (-0.295). The least negative indirect effect was for curing percentage followed by weight of mother rhizomes (-0.015) and girth of mother rhizomes (-0.023). Number of leaves, days to maturity, number and weight of primary rhizomes, weight of secondary rhizomes, rhizome diameter, rhizome core ratio, oil, oleoresin, curcumin and curing percentage recorded negative indirect effects.

Number of tillers

The positive indirect effect for number of tillers was associated with girth of secondary rhizomes (0.344) followed by breadth of leaf (0.330) and core diameter (0.325). The lowest positive indirect was noticed for girth of mother rhizomes and weight of primary rhizomes. Plant height, length of leaf, weight of mother rhizomes, length of primary rhizomes, number and weight of secondary rhizomes were also positively correlated. The negative indirect effect was higher for plant height (-0.337) followed by number of leaves (-0.266). The least effect noticed was for curcumin (-0.038). The negatively correlated characters were days to maturity, number of mother rhizomes, girth of primary rhizomes, rhizome diameter, rhizome core ratio, oil, oleoresin and curing percentage.

Days to maturity

The character breadth of leaf (0.867) recorded the highest positive indirect effect for days to maturity followed by core diameter (0.265) and number of tillers (0.208). The lowest positive indirect effect was observed for number of primary rhizomes. The positive effects were also observed for sprouting, length of leaf, weight and girth of mother rhizomes, weight and length of primary rhizomes, number, weight, length and girth of secondary rhizomes and oil. The greatest negative indirect effect was associated with plant height (-0.681) followed by girth of primary rhizome (-0.237) and the least were for number of mother rhizome. Number of leaves, days to maturity, rhizome diameter, oleoresin, curcumin and curing percentage were found to be negatively correlated.

Number of mother rhizome

The greater positive indirect effect was observed through length of primary rhizome (0.283) followed by plant height (0.256) and curcumin (0.017) registered the least. The indirect effects of number of tillers, number of primary rhizomes, number, weight, length and girth of secondary rhizomes, core diameter, rhizome core ratio, oil, oleoresin were positive. The highest negative indirect effect was noticed for breadth of leaf (-0.355) followed by girth of primary rhizomes (-0.156). The least negative indirect effect was recorded for number of leaves. The indirect effects of sprouting, length of leaf, days to maturity, number, weight and girth of mother rhizomes, rhizome diameter and curing percentage were negative.

Weight of mother rhizomes

The trait registered the highest positive indirect effect with length of primary rhizome (0.604) followed by breadth of leaf (0.396). The lowest positive indirect effect was noticed for days to maturity (0.015) followed by oil (0.017). The other positive indirect effects were noticed for sprouting, length of leaf, days to maturity, number of primary rhizomes, number, length and girth of secondary rhizomes, core diameter, oil and curing percentage. The greatest negative indirect effect was found for girth of primary rhizomes (-0.528) and the least was for curcumin. Negative indirect effects were noted for plant height, number of leaves, number of tillers, number, weight and girth of mother rhizomes, weight of primary and secondary rhizomes, rhizome diameter and oleoresin.

Girth of mother rhizomes

The positive indirect effect for girth of mother rhizomes was associated with breadth of leaf (0.706) followed by length of primary rhizomes (0.535) and the least was noticed for curcumin (0.029). The positive effects were also exhibited for sprouting, length of leaf, days to maturity, number, length and girth of secondary rhizomes, core diameter, curcumin and curing percentage. The highest negative indirect effect was recorded for weight of primary rhizomes (-0.289) followed by weight of secondary rhizomes (-0.263). The lowest effect was noticed for rhizome core ratio. The other negative effects were for plant height, number of leaves and tillers, number, weight and girth of mother rhizomes, girth of primary rhizomes, rhizome diameter, oil and oleoresin.

Number of primary rhizomes

The character, number of primary rhizomes recorded the highest positive indirect effect for length of primary rhizomes (0.470) followed by girth of secondary rhizomes (0.200). The lowest effect was observed for core diameter (0.014) followed by curing percentage (0.018). Sprouting, length of leaf, number of primary rhizomes, number of length of secondary rhizomes, rhizome core ratio, oil and oleoresin were found to be positive. The highest negative indirect effect was associated with the character girth of primary rhizomes (-0.283) and the least for number of leaves. The effects were also negative for plant height, breadth of leaf, number of tillers, days to maturity, number, weight and girth of mother rhizomes, weight of primary and secondary rhizomes, rhizome diameter and curcumin.

Weight of primary rhizomes

The highest positive indirect effect was observed for breadth of leaf (0.876) followed by length of primary rhizomes (0.797) while the lowest effect was noticed for days to maturity. The positive effects were recorded for sprouting, length of leaf, number and primary rhizomes, number, length and girth of secondary rhizomes, core diameter and curing percentage. The negative indirect effect found through plant height was the greatest (-0.838) followed by girth of primary rhizomes (-0.574). The least negative indirect effect was seen for curcumin. The other negative indirect effects were attributed for number of leaves and tillers, weight and girth of mother rhizomes, weight of secondary rhizomes, rhizome diameter, rhizome core ratio, oil and oleoresin.

Length of primary rhizomes

The greatest positive indirect effect was noticed for breadth of leaf (0.606) followed by girth of secondary rhizomes (0.507). The lowest effect was for curing percentage (0.013). The positive effects were noticed for sprouting, length of leaf, number of tillers, number of primary rhizomes, length of primary rhizomes, number of secondary rhizomes, length of secondary rhizomes, core diameter and oil. The greatest negative indirect effect was observed for girth of primary rhizomes (-0.916) followed by weight of primary rhizomes (-0.391) and the lowest was associated with rhizome core ratio. Number of leaves, days to maturity, number of mother rhizome, weight and girth of mother rhizome, weight of primary and secondary rhizomes, rhizome diameter, oleoresin and curcumin were negatively correlated.

Girth of primary rhizomes

This trait registered a positive indirect effect through length of primary rhizomes (0.704) followed by girth of secondary rhizomes (0.428). The least effect was observed for curing percentage (0.039). The highest negative indirect effect was noticed for plant height (-0.543) followed by weight of secondary rhizomes (-0.329). The least negative effects were indicated for girth of mother rhizomes (-0.037) and curcumin (-0.032). Number of leaves, days to maturity, number and weight of mother rhizomes, weight and girth of primary rhizomes, rhizome diameter, rhizome core ratio, oil and oleoresin were the parameters negatively accounted.

Number of secondary rhizomes

This character exhibited the highest positive indirect effect through length of primary rhizomes (0.604) followed by girth of secondary rhizomes (0.336) and the least effect was noticed for curing percentage (0.019). The effects were positive for sprouting, length of leaf, breadth of leaf, number of tillers, number of primary rhizomes and secondary rhizomes, length of secondary rhizomes, core diameter, rhizome core ratio and oil. The negative indirect effect through plant height (-0.511) was the greatest followed by girth of primary rhizomes (-0.473). The lowest negative indirect effect was observed for oleoresin (-0.010). The other negative effects were registered for number of leaves, days to maturity, number, weight and girth of mother rhizomes, weight of primary and secondary rhizomes, rhizome diameter and curcumin.

Weight of secondary rhizomes

The positive indirect effect was the greatest for length of primary rhizomes (0.752) followed by breadth of leaf (0.380). The least effect was noticed for days to maturity (0.023). The characters attributing for positive effects were sprouting, number of leaves, length of leaf, number of mother rhizomes and primary rhizomes, number, length and girth of secondary rhizomes, core diameter and curing percentage. The negative indirect effect was greatest for plant height (-0.722) followed by girth of primary rhizomes (-0.664) and the lowest was noticed for oil. The negative effects were accounted for number of tillers, weight and girth of mother rhizomes, weight of primary and secondary rhizomes, rhizome core ratio, oleoresin and curcumin.

Length of secondary rhizomes

The highest positive indirect effect was observed for breadth of leaf (0.991) followed by length of primary rhizomes (0.908) and the least for oil (0.026). Sprouting, length of leaf, number of tillers, number of primary rhizomes, number, length and girth of secondary rhizomes and core diameter exhibited positive effects. The negative indirect effect was noticed for plant height (-0.924) followed by girth of primary rhizomes (-0.755) and the lowest negative indirect effect was for rhizome core ratio. The indirect effects were negative for number of leaves, days to maturity, number, weight and girth of mother rhizomes, weight of primary and secondary rhizomes, rhizome diameter, oleoresin, curcumin and curing percentage.

Girth of secondary rhizomes

The indirect effect of girth of secondary rhizomes was positive and the highest for breadth of leaf (0.706) followed by length of primary rhizomes (0.631). The least effect was noticed for curing percentage. Characters accounting positive effects were sprouting, length of leaf, number of tillers, number of primary and secondary rhizomes, length and girth of secondary rhizomes, core diameter and oil. The negative indirect effects were the highest for girth of primary rhizomes (-0.791) followed by plant height (-0.787) and the least effect was noticed for girth of mother rhizomes (-0.024). Effects were negative for number of leaves, days to maturity, number and weight of mother rhizomes, weight of primary and secondary rhizomes, rhizome diameter, rhizome core ratio, oleoresin and curcumin.

Rhizome diameter

This trait registered a positive but an indirect effect with length of primary rhizomes (0.726), which was the highest, followed by girth of secondary rhizomes (0.617) and the least for curing percentage (0.019). The positive effects were noticed for sprouting, length of leaf, number of tillers, number of primary rhizomes, length and girth of secondary rhizomes and core diameter. The indirect effects were negative and highest for girth of primary rhizomes (-0.866) and the least was observed for rhizome core ratio. Negative indirect effects were also noted for number of leaves, days to maturity, number, weight and girth of mother rhizomes, weight of primary rhizomes, weight of secondary rhizomes, rhizome core ratio, oil, oleoresin and curcumin.

Core diameter

The character recorded a positive indirect effect through length of primary rhizomes (0.695) followed by girth of secondary rhizomes (0.603). The least positive indirect effect was for curing percentage. Positive effects were also revealed for sprouting, breadth of leaf, number of tillers, number of mother rhizomes, number, length and girth of secondary rhizomes and core diameter. The negative indirect effect was the highest for girth of primary rhizomes (-0.865) followed by weight of primary rhizomes (-0.269). The least effect was recorded for girth of mother rhizomes (-0.018). Effects were negative for number of leaves, days to maturity, number and weight of mother rhizomes, weight of primary and secondary rhizomes, rhizome diameter, rhizome core ratio, oil, oleoresin and curcumin.

Rhizome core ratio

The greatest positive indirect effect was observed for plant height (0.475) followed by girth of primary rhizomes (0.252). The lowest effect was recorded for girth of mother rhizomes. The indirect effects were also positive for plant height, number of leaves, days to maturity, number and weight of primary rhizomes, number and weight of secondary rhizomes, rhizome diameter, rhizome core ratio, oil, oleoresin, curcumin and curing percentage. The negative indirect effect was the highest for breadth of leaf (-0.862) followed by core diameter (-0.358) and the least was for length of secondary rhizomes. Length of leaf, number of tillers, number and weight of mother rhizomes, length of primary rhizomes and girth of secondary rhizomes exerted negative indirect effects.

Oil

The indirect effect of oil was positive and the highest for breadth of leaf (0.368) followed by core diameter (0.233) and curing percentage (0.153) and the lowest was recorded for weight of mother rhizomes. The positive effects were also accounted for sprouting, length of leaf, number of tillers, days to maturity, number of mother rhizomes, core diameter and curcumin. The indirect effect was negative and the highest for oleoresin (-0.223) followed by rhizome core ratio (-0.222). The least effect was noticed for weight of mother rhizomes. Number of leaves, girth of mother rhizomes, number, weight, length and girth of primary rhizomes, number, length and girth of secondary rhizomes, rhizome diameter, rhizome core ratio, oil. and oleoresin were found to be negatively associated.

Oleoresin

The highest positive indirect effect was registered for the character length of leaf (0.897) followed by number of mother rhizomes (0.787) and the lowest was accorded with curing percentage (0.018). The positive effects were noticed for sprouting, length of leaf, number of tillers, number of mother rhizomes, length of secondary rhizomes, core, diameter, oleoresin, curcumin and curing percentage. The highest negative indirect effect was associated with the character, rhizome core ratio (-0.823) followed by number of primary rhizomes (-0.879). The indirect effects were negative for number of leaves, days to maturity, weight of mother rhizomes, number, weight, length and girth of primary rhizomes, weight of secondary rhizomes, rhizome diameter and rhizome core ratio.

Curcumin

The effect was positive and indirect for plant height (0.133) followed by girth of primary rhizomes (0.115) and the least was observed for weight of mother rhizomes. Number of leaves, days to maturity, weight of primary and secondary rhizomes, rhizome diameter, curcumin and curing percentage too was positively associated. The negative indirect effect was the highest for breadth of leaf (-0.290) followed by girth of secondary rhizomes (-0.107) and core diameter (-0.108). The lowest effect was found for girth of mother rhizomes. The negative effects were recorded for the other characters.

Curing percentage

This trait exerted a positive indirect effect through plant height (0.108) and the lowest effect was for curcumin. The effect was positive and indirect for number of leaves, length of leaf, number of mother rhizomes and primary rhizomes, length of primary rhizomes, number and girth of secondary rhizomes, core diameter, rhizome core ratio and curing percentage. The indirect effect of curing percentage was negative and highest for oil (-0.238) followed by girth of primary rhizomes (-0.152) and the lowest was for length of secondary rhizomes. Plant height, breadth of leaf, number of tillers, weight and girth of mother rhizomes, weight of primary and secondary rhizomes, rhizome diameter and oleoresin attributed for negative effects.

4.9. Screening Studies

4.9.1. Screening of turmeric genotypes against leaf spot (*Colletotrichum curcumae*) (Table 40 and 41)

The genotypes were scored for resistance against leaf spot disease (*Colletotrichum curcumae*). Under natural conditions, all the genotypes exhibited the symptoms and rated accordingly. Most of the genotypes were found to be susceptible and none of the genotype fell into the category of resistant reaction. The per cent disease index ranged between 8.20 and 51.32. (Table 40)

The genotypes got grouped into two reactions of susceptibility (47 genotypes) and being moderately resistant (176 genotypes) (Table 41). A significant variation was noticed among the genotypes for disease reaction. The genotypes 22 (8.20), 26 (10.00), 27 (11.26), 45 (10.20), 46 (9.80), 47 (9.80), 50 (10.40), 53 (10.00), 54 (10.00) and 71 (8.90) were rated as moderately resistant and were on par and the susceptible genotypes were 9 (50.48) and 11 (51.32) which were on par.

4.9.2. Screening of turmeric genotypes against scale (*Aspidiotus hartii*) (Table 42 and 43)

The genotypes exhibited wide range of variability to the pest infestation. Under natural condition the genotypes were observed to be free from scale infestation. Hence, all the genotypes were subjected to artificial inoculation.

The per cent infestation of the genotypes varied from 4.00 % to 68.00 %. They were grouped according to their reaction. Most of the genotypes (156) fell in the category of moderately resistant. Very few genotypes (8) from Bhavanisagar and Erode were found to be resistant. (Table 43).

The genotypes exhibiting resistance to scale infestation were 116 (5.00 %), 167 (5.00 %), 170 (7.40 %), 182 (5.00 %), 214 (5.00 %), 218 (4.00 %), 219 (5.00 %) and were on par.

Table 40. Screening of turmeric genotypes for leaf spot disease (*Colletotrichum curcumae*)

Geno type	PDI Value	Geno type	PDI Value	Acc. No.	PDI Value	Geno type	PDI Value	Geno type	PDI Value
1	20.10	46	9.80	91	12.60	136	23.10	182	21.40
2	19.86	47	9.80	92	25.20	137	22.60	183	23.20
3	19.20	48	22.42	93	23.10	138	15.00	184	22.26
4	25.56	49	21.26	94	25.00	139	18.20	185	28.20
5	25.12	50	10.40	95	23.00	140	16.00	186	28.90
6	20.12	51	23.28	96	22.44	141	15.40	187	18.80
7	26.36	52	12.20	97	21.20	142	21.26	188	14.20
8	21.26	53	10.00	98	25.20	144	26.20	189	16.10
9	50.48	54	10.00	99	18.60	145	23.40	190	25.00
10	18.26	55	36.00	100	25.26	146	26.20	191	23.22
11	51.32	56	38.00	101	25.14	147	16.48	192	28.88
12	19.38	57	37.50	102	18.10	148	18.22	193	29.50
13	18.46	58	23.20	103	19.20	149	20.16	194	22.00
14	17.28	59	22.48	104	18.10	150	20.60	195	17.10
15	16.52	60	26.20	105	23.20	151	21.20	196	20.22
16	18.18	61	32.00	106	23.40	152	20.00	197	18.66
17	17.16	62	25.70	107	24.68	153	21.68	198	19.55
18	20.12	63	28.00	108	16.28	154	19.80	199	21.36
19	21.12	64	12.20	109	39.18	155	18.80	200	22.55
20	28.00	65	15.40	110	38.26	156	19.20	201	18.68
21	20.80	66	24.80	111	34.10	157	22.10	202	23.20
22	8.20	67	12.80	112	35.00	158	21.68	203	21.26
23	27.42	68	11.80	113	28.20	159	23.20	204	20.96
24	23.12	69	14.00	114	28.42	160	26.28	205	21.48
25	21.42	70	15.20	115	26.26	161	20.10	206	23.22
26	10.00	71	8.90	116	25.10	162	21.22	207	29.10
27	11.26	72	15.00	117	22.00	163	23.46	208	31.16
28	24.29	73	23.20	118	20.80	164	22.38	209	18.00
29	24.32	74	22.10	119	22.25	165	26.40	210	18.80
30	24.12	75	23.00	120	26.00	166	25.28	211	16.48
31	22.20	76	23.00	121	24.40	167	22.30	212	13.20
32	20.00	77	21.40	122	12.00	168	18.46	213	32.40
33	32.18	78	22.20	123	18.20	169	23.10	214	16.80
34	31.60	79	23.20	124	16.26	170	22.90	215	16.60
35	30.80	80	23.00	125	18.48	171	21.60	216	32.30
36	34.12	81	20.15	126	20.20	172	19.38	217	31.48
37	30.18	82	32.50	127	20.42	173	18.80	218	33.80
38	32.26	83	36.80	128	14.20	174	28.46	219	20.08
39	24.18	84	34.20	129	14.76	175	26.20	220	21.20
40	23.26	85	28.60	130	13.45	176	25.40	221	23.66
41	22.18	86	28.00	131	15.50	177	23.10	222	28.10
42	22.00	87	27.10	132	14.20	178	21.66	223	20.10
43	36.00	88	26.40	133	13.60	179	21.00	224	20.66
44	34.28	89	25.00	134	13.62	180	29.10		
45	10.20	90	26.20	135	14.20	181	22.68		
SEd 1.57		CD (.05) 3.10							

Table 41. Classification of genotypes according to its reaction to disease infection

	Susceptible genotypes	Moderately Resistant genotypes
Leaf spot (*Colletotrichum curcumae*)	7,9,11,33,34,35,36,37,38,43,44,55, 56,57,60,61,63,82,83,84,85,86,87, 88,109,110,111,112,113,114,115, 144,146,160,165,174,175,180,186, 192,193,207,208,213,216,218,222.	1,2,3,4,5,6,8,10,12,13,14,15,16,17, 18,19,20,21,22,23,24,25,26,27,28, 29,30,31,32,39,40,41,42,45,46,47, 48,49,50,51,52,53,54,58,59,62,64, 65,66,67,68,69,70,71,72,73,74,75, 77,78,79,80,81,89,90,91,92,93,94, 95,96,97,98,99,100,101,102,103, 104,105,106,107,108,116,117,118, 119,120,121,122,123,124,125,126, 127,128,129,130,131,132,133,134, 135,136,137,138,139,140,141,142, 145,147,148,149,150,151,152,153, 154,155,156,157,158,159,161,162, 163,164,166,167,168,169,170,171, 172,173,176,177,178,179,181,182, 183,184,187,188,189,190,191,194, 195,196,197,198,199,200,201,202, 203,204,205,206,207,208,209,210, 211,212,214,215,217,219,220,221, 223,224.
Total number of genotypes	47	176

Table 42. Screening of turmeric genotypes for scale (*Aspidiotus hartii*)

Geno type	Percent	Geno type	Percent	Geno type	Percent	Geno type	Percent	Geno type	Percent
1	10.00	46	12.00	91	14.00	136	62.00	182	5.00
2	13.30	47	12.00	92	66.00	137	10.00	183	5.00
3	14.00	48	13.00	93	10.00	138	15.00	184	19.80
4	11.00	49	60.00	94	10.00	139	10.00	185	12.00
5	10.00	50	12.00	95	10.00	140	15.00	186	13.00
6	10.00	51	13.00	96	56.00	141	13.00	187	15.00
7	13.00	52	12.00	97	12.00	142	15.00	188	20.00
8	17.00	53	15.00	98	13.00	144	13.00	189	28.00
9	10.00	54	12.00	99	12.00	145	15.00	190	10.00
10	11.00	55	40.00	100	14.80	146	15.00	191	10.00
11	38.00	56	12.00	101	19.60	147	12.00	192	18.00
12	22.20	57	13.00	102	14.00	148	10.00	193	42.00
13	16.20	58	12.00	103	12.00	149	14.00	194	5.00
14	13.60	59	14.00	104	13.00	150	13.00	195	14.00
15	11.80	60	12.00	105	48.00	151	25.00	196	16.00
16	33.00	61	20.00	106	14.00	152	15.00	197	19.00
17	12.00	62	50.00	107	68.00	153	10.00	198	17.00
18	11.00	63	25.00	108	10.00	154	10.00	199	13.00
19	11.00	64	25.00	109	12.00	155	13.00	200	64.00
20	11.00	65	15.00	110	14.00	156	22.00	201	15.00
21	13.00	66	13.00	111	12.00	157	10.00	202	12.00
22	12.00	67	20.00	112	12.00	158	12.00	203	15.40
23	12.00	68	12.00	113	26.80	159	12.00	204	21.00
24	16.00	69	11.00	114	17.80	160	19.80	205	23.00
25	62.00	70	12.00	115	10.00	161	10.00	206	15.00
26	14.00	71	15.00	116	5.00	162	15.00	207	10.00
27	12.00	72	40.00	117	20.00	163	15.00	208	21.00
28	21.40	73	17.00	118	10.00	164	14.00	209	30.00
29	11.00	74	12.00	119	12.00	165	14.00	210	20.00
30	11.20	75	13.00	120	12.00	166	12.00	211	16.00
31	15.00	76	14.00	121	16.00	167	14.00	212	15.00
32	27.00	77	14.00	122	37.00	168	15.00	213	20.00
33	11.00	78	15.00	123	20.00	169	15.00	214	12.00
34	12.00	79	12.00	124	10.00	170	7.40	215	10.00
35	10.00	80	15.00	125	20.00	171	13.00	216	5.00
36	12.00	81	30.00	126	10.00	172	15.00	217	13.00
37	13.00	82	10.20	127	10.00	173	13.00	218	4.00
38	12.00	83	11.00	128	52.00	174	13.40	219	5.00
39	13.00	84	12.00	129	10.00	175	5.00	220	10.00
40	12.00	85	12.00	130	10.00	176	13.00	221	10.00
41	30.00	86	14.00	131	30.00	177	12.00	222	15.00
42	13.00	87	17.80	132	13.00	178	15.00	223	20.00
43	14.00	88	11.00	133	12.00	179	14.00	224	25.00
44	13.00	89	50.00	134	13.00	180	15.00		
45	30.00	90	25.00	135	30.00	181	14.00		
SEd 3.55		CD (.05) 7.01							

Table 43. Classification of genotypes according to its reaction to pest infestation

	Resistant	Moderately resistant	Susceptible	Highly susceptible
Scale (Aspidiotus hartii)	116,175, 182,183, 194,216, 218,219	1,2,3,4,5,6,7,9,10,14,15,17,18, 19,20,21,22,23,24,26,27,29,30, 31,33,34,35,36,37,38,39,40,42, 43,44,46,47,48,50,51,52,53,54, 55,56,57,58,59,60,65,66,68,69, 70,71,74,75,76,77,78,79,80,82, 83,84,85,86,88,91,93,94,95,97, 98,99,100,101,102,103,104,105, 106,108,109,110,111,112,115, 118,119,120,124,126,127,129, 130,132,133,134,137,142,144, 145,146,147,148,149,150,152, 153,154,155,157,158,159,161, 162,163,164,165,166,167,168, 169,171,172,173,174,175,176, 177,178,179,180,181,185,186, 187,190,191,194,195,199,201, 203,206,207,212,214,215,217, 220,221,222	8,12,13,28,32,61, 63,64,67,73,87, 90,113,114,117, 121,123,125,151, 156,160,184,188, 189,192,196,197, 198,204,205,208, 210,211,213,223, 224	11,16,25,41,45, 49,55,62,72,81, 89,92,96,105, 107,122,128, 131,135,136, 193,200,209
Total number of genotypes	8	156	36	23

The following genotypes 25 (62.00 %), 92 (66.00 %), 136 (62.00 %) and 200 (64.00 %) were susceptible and were on par. (Table 43).

4.9.3. Correlation with yield and curcumin (Table 44)

The incidence of disease and pest infestation correlated with yield and curcumin content indicated non significant correlation.

4.10. Phase II

4.10.1. D^2 analysis

Mahalonobis D^2 statistic was performed for the two twenty three genotypes based on 22 quantitative traits and they were grouped into two clusters. The two clusters exhibited wide variations for 8 characters among the 22 characters analyzed. Between the two clusters, cluster 1 was the largest, grouping 144 genotypes and cluster 2 accommodating 79 genotypes. The D^2 values varied from 547.202 to 660.031. (Table 45).

4.10.2. Cluster mean of turmeric genotypes for twenty-two characters

For the 8 characters that showed variability in their mean values, D^2 statistic was repeated for all the genotypes. The 8 characters that were subjected to the analysis were plant height, number of leaves, number of tillers, days to maturity, weight of primary rhizomes, weight of secondary rhizomes, girth of secondary rhizomes and yield. (Table 46).

4.10.3. Cluster composition of turmeric genotypes based on eight characters

The genotypes were clustered into 5 groups. The cluster 1 was the largest accommodating 143 genotypes followed by cluster 5 grouping 74 genotypes. While the clusters 2, 3 and 4 comprised two genotypes each. (Table 47).

4.10.4. Inter and Intra cluster values (Table 48, Fig.7)

The values for the 5 clusters indicated that the range of D^2 values were between 3.832 and 447.012. The intra cluster D^2 value was the highest for cluster 5 (447.012) followed by cluster 1 (307.484) while it was the least for cluster 2 (3.832). The D^2 values

Table 44. Correlation of yield and curcumin to leaf spot and scale

Character	Leaf spot	Scale	Curcumin	Yield
Leaf spot	1.000			
Scale	0.00154	1.000		
Curcumin	-0.11941	0.08079	1.000	
Yield	-0.04985	-0.09048	-0.07658	1.000

Table 45. Cluster composition of turmeric genotypes based on D^2 statistic (Phase II)

Cluster	Number of genotypes	Cluster members
1	144	1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26, 27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,4 9,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71, 72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95 ,96,97,98,99,100,101,102,103,104,105,106,107,108,109,110,111,112,113, 114,115,116,117,118,119,120,121,122,123,124,125,126,127,128,129,130, 131,132,133,134,135,136,137,138,139,140,141,142,164,208
2	79	144,145,146,147,148,149,150,151,152,153,154,155,156,157,158,159, 160,161,162,163,165,166,167,168,169,170,171,172,173,174,175,176, 177,178,179,180,181,182,183,184,185,186,187,188,189,190,191,192, 193,194,195,196,197,198,199,200,201,202,203,204,205,206,207,209, 210,211,212,213,214,215,216,217,218,219,220,221,222,223,224.

Table 46. Cluster means of twenty two characters for turmeric genotypes (Phase II)

Cluster	1	2
Sprouting (%)	90.94	91.17
Plant height (cm)	**37.29**	**34.06**
Number of leaves	**14.97**	**12.83**
Length of leaf (cm)	38.39	37.81
Breadth of leaf (cm)	12.74	11.92
Number of tillers	**3.66**	**1.76**
Days to maturity	**248.67**	**235.81**
Number of Mother rhizomess	2.87	2.67
Weight of Mother rhizomes (g)	8.64	8.93
Girth of Mother rhizomes (cm)	62.20	62.03
Number of Primary rhizomes	5.84	3.35
Weight of Primary rhizomes (g)	**100.21**	**107.48**
Length of Primary rhizomes (cm)	7.60	7.13
Girth of Primary rhizomes (cm)	6.89	6.02
Number of Secondary rhizomes	6.88	6.91
Weight of Secondary rhizomes (g)	**67.31**	**71.51**
Length of Secondary rhizomes(cm)	5.96	5.43
Girth of Secondary rhizomes (cm)	**5.08**	**4.24**
Rhizome diameter (cm)	1.91	1.64
Core diameter (cm)	1.06	0.75
Rhizome Core ratio (cm)	1.85	3.76
Yield (Kg/plot)	**2.31**	**3.61**

Table 47. Cluster composition of turmeric genotypes based on D^2 statistic (Phase II) (eight character basis)

Cluster	Number of genotypes	Cluster members
1	143	1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25, 26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46, 47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67, 68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88, 89,90,91,92,93,94,95,96,97,98,99,100,101,102,103,104,105,106, 107,108,109,110,111,112,113,114,115,116,117,118,119,120,121, 122,123,124,125,126,127,128,129,130,131,132,133,134,135,136, 137,138,139,140,141,142,187
2	2	159,175
3	2	182,209
4	2	184,204
5	74	144,145,146,147,148,149,150,151,152,153,154,155,156,157,158, 160,161,162,163,164,165,166,167,168,169,170,171,172,173,174, 176,177,178,179,180,181,183,185,186,188,189,190,191,192,193, 194,195,196,197,198,199,200,201,201,203,205,206,207,208,210, 211,212,213,214,215,216,217,218,219,220,221,222,223,224

Table 48. Inter and Intra Cluster D^2 values (Phase II)

Cluster	1	2	3	4	5
1	307.484	214.999	210.062	192.332	418.545
	17.535	(14.663)	(14.494)	(13.868)	(20.458)
2		3.832	68.641	65.118	231.996
		1.958	(8.267)	(8.070)	(15.237)
3			4.830	84.167	253.190
			2.198	(9.174)	(15.912)
4				5.056	283.472
				2.249	(16.837)
5					447.012
					21.143

Values in paranthesis indicate inter cluster distances
Values in bold are intra cluster distances
Other values are inter cluster values

Table 49. Cluster mean values of eight characters for turmeric genotypes (Phase II)

Cluster / character	1	2	3	4	5	% contribution
Plant height (cm)	37.36	34.07	32.61	32.46	34.06	0.08
Number of leaves	15.03	12.04	11.38	11.75	12.84	0.22
Number of tillers	3.68	1.67	1.75	1.71	1.74	0.60
Days to maturity	248.71	233.25	242.75	251.50	235.38	0.63
Weight of primary rhizomes (cm)	100.89	92.50	127.08	87.09	106.51	8.57
Weight of secondary rhizomes (cm)	67.44	71.67	75.00	61.25	71.38	7.77
Girth of secondary rhizomes (cm)	5.11	4.42	4.46	4.21	4.19	10.46
Yield (kg/plot)	3.77	2.96	2.78	2.70	3.65	65.65

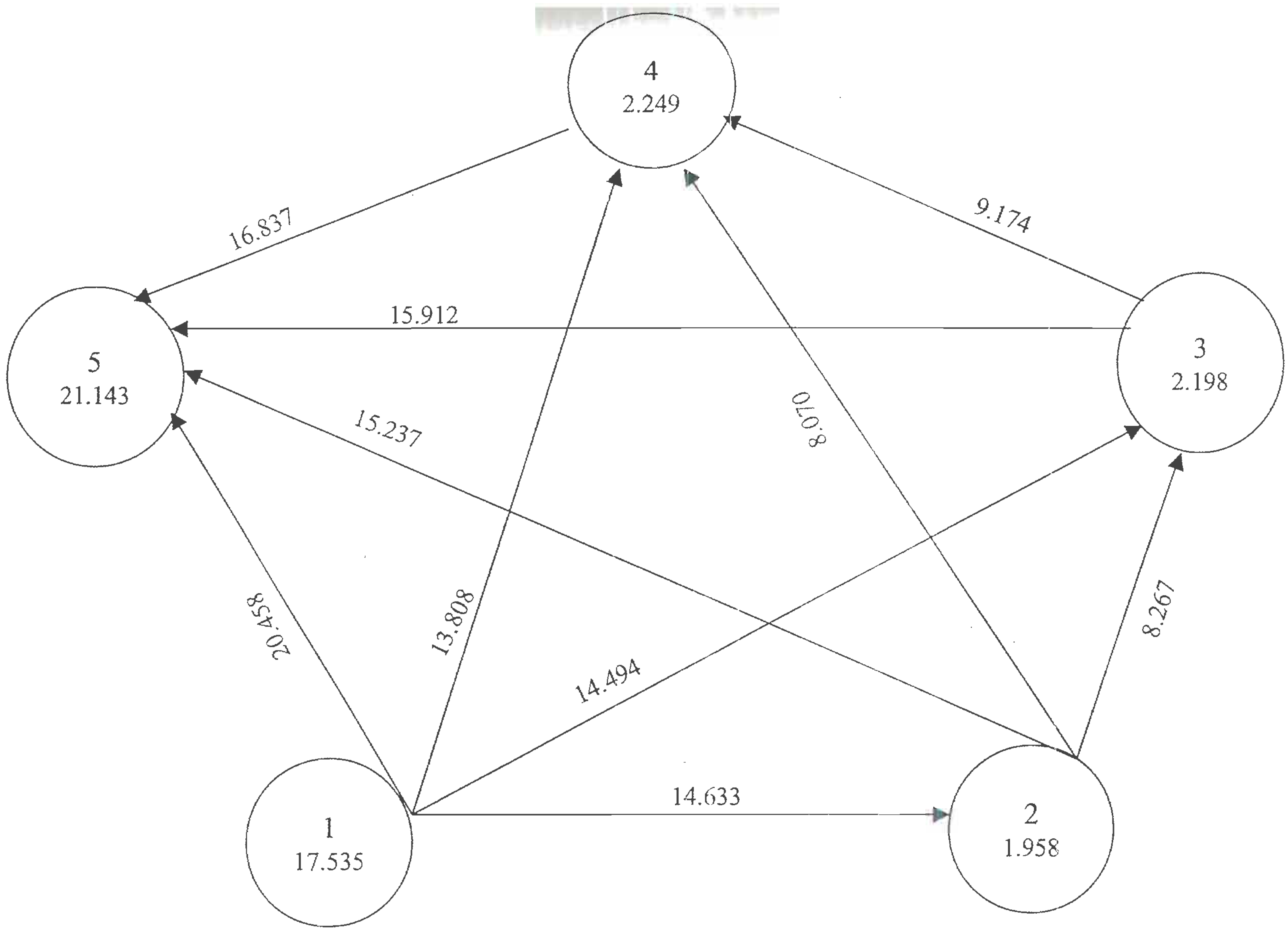


Fig.7. Cluster diagram showing inter and intra cluster distance
(not to scale)

1.

between the clusters 1 and 5 were the highest (418.545) followed by 4 and 5 (283.472) and the least for clusters 2 and 4 (65.118).

The clusters 1 and 5 were separated at a distance of 20.458 followed by 4 and 5 (16.837), which were found to be the highest. The closest clusters were linked together at a distance of 8.070 for 2 and 4. Intra cluster distance was large for the cluster 5.

4.10.5.Cluster mean values for the characters (Table 49)

The genotypes of the cluster 1 registered the highest mean for plant height (37.359 cm) followed by cluster 2 (34.07 cm) and the lowest mean for the cluster 4 (32.463 cm). The number of leaves was high for the cluster 1 (15.027) followed by cluster 5 (12.838) and the least for cluster 3 (11.375). Number of tillers was found to be more for the cluster 1 (3.683) and the other clusters did not reveal much variation in their mean value. The days to maturity exhibited variation among the clusters. The longer duration genotypes were accommodated in the cluster 4 (251.500) and short duration ones in the cluster 2 (233.250).

The weight of primary rhizomes too indicated significant variation with genotypes of cluster 3 producing heavier rhizomes (127.083 g) followed by cluster 5 (106.507 g) and the least in the cluster 4 (87.085 g). The weight of secondary rhizomes was found to be the highest for cluster 3 (75.020 g) and the least mean values for cluster 4 (61.250 g). The girth of secondary rhizomes did not show appreciable variation in their mean values. However, the cluster 1 recorded the highest girth (5.106 cm).

Yield values were high for cluster 1 and 5 (3.772 and 3.645) while cluster 2, 3 and 4 did not exhibit marked differences.

4.10.6. Selection of genotypes

On ranking the characters, the relative contribution of yield (65.65 %) followed by girth of secondary rhizomes (10.46 %), weight of primary and secondary rhizomes (8.57 % and 7.77 % respectively) and days to maturity (6.63 %) were the highest contributing to total divergence while plant height, number of leaves and number of tillers contributed the least for divergence. (Fig. 8)

Taking into account, the characters contributing for total divergence, the genotypes were selected from each cluster based on its performance. The genotypes were selected to represent each cluster and as well as at both the extremities facilitating a mode of comparison of genotypes both at morphological and molecular levels.

Thus thirty genotypes were chosen representing all the clusters. They were selected based on their performance to growth, yield and resistance to leaf spot and scale. The source of the genotypes is provided in Appendix II.

Hence, seventeen genotypes of cluster 1, ten genotypes of cluster 5 and single genotype from cluster 2, 3 and 4 comprised the experimental material for phase II. (Table 50).

4.11. Genetic diversity studies

4.11.1. Based on Quantitative data using D^2 statistic

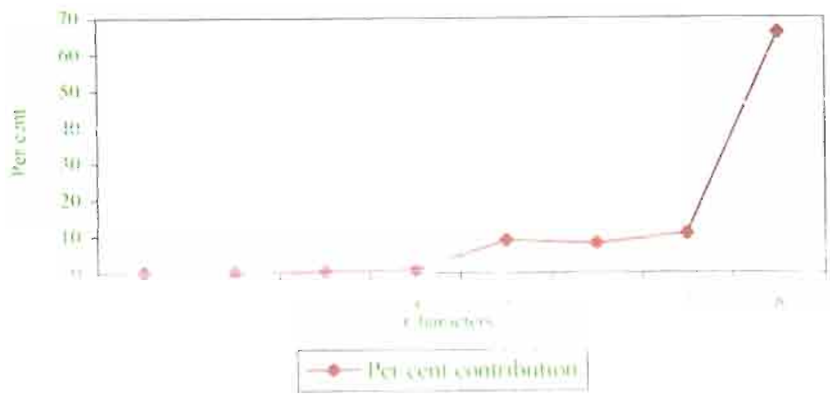
The genotypes were grouped into five clusters based on D^2 statistic for 22 quantitative traits. The clustering pattern revealed that except BS 2 and BS 76, other genotypes from Bhavanisagar were clustered together. Among the genotypes from Erode, ER 169 was found to be distinct. The genotypes having same geographical origin *viz*. Sudarshana, Suguna from Andhra Pradesh; VK 5, Prabha and Prathibha from Kerala were clustered together while PTS 55 was distinct from the genotypes of Orissa. (Table 51).

The D^2 values indicated that genotypes BS 90 and BS 115 from Bhavanisagar, Sudarshana and Suguna from Andhra Pradesh, ER 175 and ER 184 from Erode exhibited similar values and were grouped in the same cluster.

4.11.2. Using K means

A cluster tree was constructed involving 22 quantitative traits using K means clustering based on Euclidean distance. The K means grouped the genotypes into five

Fig 8. Relative contribution of characters towards genetic divergence



1 Plant height
2 Number of leaves
3 Number of tillers
4 Days to maturity
5 Weight of Primary rhizomes
6 Weight of Secondary rhizomes
7 Girth of Secondary rhizomes
8 Yield

Table 50. Genotypes selected by D^2 statistic (Phase II)

S.No.	Genotype Number	Genotypes	Cluster number
1	2	BS - 2	1
2	15	BS - 16	1
3	22	BS -23	1
4	47	BS - 48	1
5	52	BS - 53	1
6	75	BS - 76	1
7	88	BS - 89	1
8	89	BS - 90	1
9	114	BS - 115	1
10	120	Kanthi	1
11	121	Shoba	1
12	122	VK 5	1
13	130	Sudarshana	1
14	131	Suguna	1
15	132	Suvarna	1
16	133	Roma	1
17	134	Kalimpong	1
18	146	Allepey	5
19	148	PTS 12	5
20	151	Prabha	5
21	152	Prathibha	5
22	156	PTS 2	5
23	169	Erode local	5
24	175	Erode local	2
25	184	Erode local	4
26	189	CO 1	5
27	194	JTS 2	5
28	195	Rajendra Sonia	5
29	198	PTS 55	5
30	209	Erode local	3

Table 51. Cluster composition of turmeric genotypes based on different cluster analysis

Cluster No.	Cluster members based on D^2 statistic	Cluster members based on K means
1	BS 2, BS 76, Kalimpong	BS 2, BS 16, BS 23, BS 53, BS 89, BS 90, Prathibha, PTS 2, JTS 2, ER 209
2	CO1, JTS 2	BS 76, Shoba, VK 5, Prabha, ER 175, ER 184, CO1, Salem local
3	Bs 16, BS 23, BS 53, BS 89, BS 90, BS 115, Kanthi, Shoba, Roma, Salem local	Sudarshana, Suguna, Rajendrasonia
4	VK 5, Sudarshana, Suguna, Suvarna, Allepey, PTS 12, Prabha, Prathibha, PTS 2, ER 169	BS 115, Kanthi, Allepey
5	ER 175, ER 184, Rajendrasonia, PTS 55, ER 209	Suvarna, Roma, Kalimpong, PTS 12, ER 169, PTS 55

Cluster No.	Cluster members based on UPGMA	Cluster members based on RAPD
1	BS 2, PTS 2, BS 89, BS 23, BS 76, BS 115, BS 16, VK 5, Suvarna, PTS 12, PTS 55, Sudarshana	BS 2, BS 76, PTS 12, Prabha, PTS 2
2	BS 53, ER 175, ER 184	BS 16, BS 23, BS 53, BS 90, BS 115, Sudarshana, Suguna, Kanthi, Roma
3	ER 169, JTS 2	JTS 2, Rajendrasonia
4	BS 90, Roma, Kanthi, Allepey, Suguna, Prabha, Prathibha, ER 209, Salem local, CO1, Shoba	Shoba, VK 5, Suvarna, Prathibha, ER 175, ER 184, CO1, PTS 55, Allepey, Salem local, ER 209
5	Rajendrasonia	ER 169
6	Kalimpong	Kalimpong

clusters (Table 51). The pattern of clustering revealed that the genotypes from Bhavanisgar were clustered together except BS 76, BS 89 and BS 115. Among the genotypes from Erode, ER 209 and ER 175 were clustered together while ER 184 was clustered with CO 1. The genotypes from same geographical origin, Sudarshana and Suguna, VK 5, Prabha and Shoba were similar while Prathibha and Suvarna were distinct from the other Kerala genotypes. Among the genotypes from Orissa, PTS 2 was distinct from the others and clustered with Bhavanisagar genoytpes. The genotype Rajendrasonia was distinct from rest of the genotypes. (Fig. 9)

4.11.3. Using UPGMA

A dendrogram was constructed involving 22 quantitative traits using UPGMA on the basis of squared Euclidean distance of standardized data. The pattern of clustering indicated two distinct groups among the genotypes. All the genotypes except Kalimpong formed a single cluster. The remaining 29 genotypes formed two subgroups, one with 17 genotypes and the other with 12 genotypes.

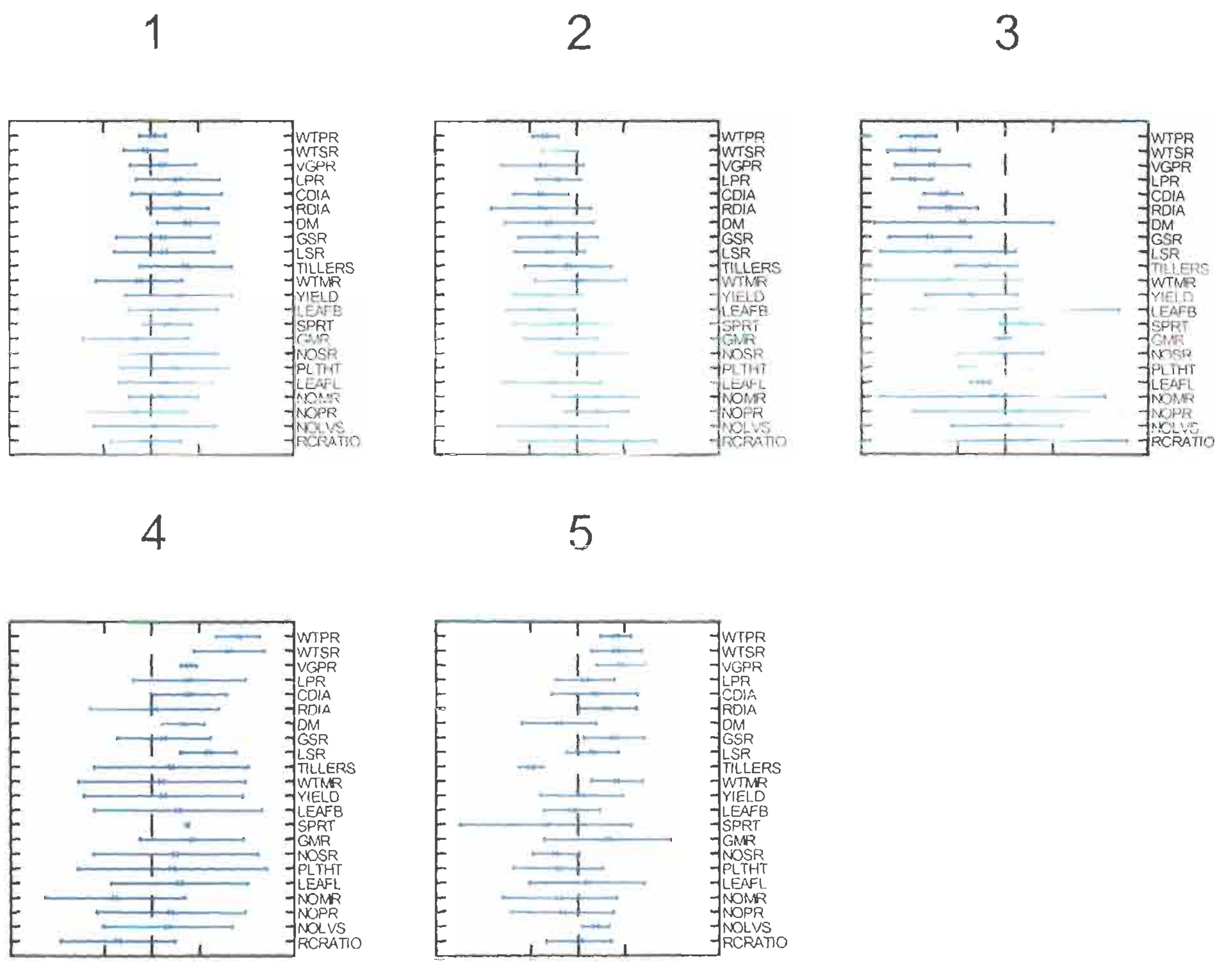
The genotypes from Bhavanisagar and Erode locations exhibited similarity between them except BS 90 and ER 209 which were distinct. Among the genotypes, BS 76, and BS 115 from Bhavanisagar; PTS 12 and PTS 55 from Orissa exhibited higher level of similarity between them. The genotypes Sudarshana and Suguna from Andhra Pradesh and Prabha and Prathibha from Kerala were very distinct between them though they were from the same geographical areas. (Table 51 and Fig.10)

However, genotypes of diverse geographical origin like the PTS 2 and Roma (Orissa) and VK 5 and Suvarna (Kerala) got clustered together with the genotypes of Bhavanisagar (Tamil Nadu).

4.11.4. RAPD polymorphism

RAPD profiles among thirty genotypes were generated for genetic diversity analysis. Of the seventy-decamer primers used for RAPD analysis, 21 primers yielded scorable, unambiguous markers and 14 primers failed to amplify any fragment.

Fig. 9. Cluster profile plots of 30 genotypes based on K means



The PCR amplification of the template DNA produced a total of 89 markers, of which 61 markers were found to be polymorphic (68.5%) and the rest monomorphic (Table 52).

The number of markers produced per primer varied from two (OPB 11, OPB 14, OPC 01, OPC 16, OPC 18, OPE 03 and OPE 04) to 10 (OPG 19). Maximum number of polymorphic markers (10) was obtained with the primer OPG 19 and the primer OPC 18 produced monomorphic markers. Based on the level of polymorphism detected by individual primers, four primers (OPB 08, OPC 20, OPE 09 and OPG 19) revealed more than 90 per cent polymorphism. (Table 53 , Plate 8 and 9)

The similarity indices estimated from the RAPD marker data set of 21 primers ranged between 0.43 and 0.97. The genotypes BS 16 and BS 23 were closely related (0.97) among the Bhavanisagar genotypes, like wise genotypes Sudarshana and Suguna (Andhra Pradesh) were more similar (0.94) and among the genotypes from Erode, ER 175 and ER 184 were similar (0.93). Kalimpong (West Bengal) was found to be distinct from other genotypes. The genotype ER 169 exhibited low level of similarity with Sudarshana (0.43) and BS 53 (0.43). (Table 54).

Cluster analysis was performed based on Jaccard's similarity coefficient and dendrogram was constructed (Fig. 11) involving all the genotypes. The dendrogram on RAPD profiles reflected considerable level of genetic similarity based on the geographical distribution. The genotypes were classified into two major groups. The first group was further subgrouped into three (1A, 1B, 1C) clusters. This group consisted the genotypes from Bhavanisagar viz, BS 16, BS 23, BS 53, BS 89, BS 90 and BS 115 with higher level of similarity among them. The other genotypes grouped along with the genotypes of Bhavanisagar include PTS 12, Prabha, Roma, JTS 2 and Rajendrasonia.

The genotypes viz, ER 175, ER 184 were grouped with CO1. Certain genotypes having same geographical origin and higher level of similarity based on the quantitative data were found to be in different clusters. Prabha, Pathibha, VK 5 and Kanthi from

Table 52. Level of polymorphic loci detected by RAPD analysis

Number of Primers	21
Total number of markers produced	89
Range of markers	2 – 10
Average number of markers	4
Number of monomorphic markers	27
Number of polymorphic markers	62
Per cent polymorphism	68.50

Table 53. Details of random primers used for RAPD analysis

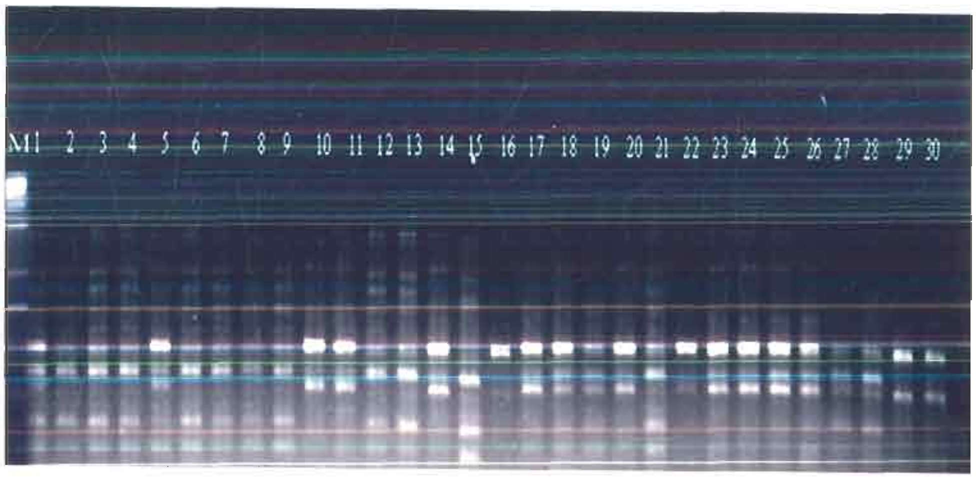
Random Primer	5 ' to 3' sequence	GC CONTENT (%)	Total markers	Polymorphic markers	Polymorphism (%)
OPB - 08	GTCCACACGG	70	4	4	100.00
OPB - 09	TGGGGGACTC	70	7	6	85.71
OPB - 11	GTAGACCCGT	80	2	1	50.00
OPB - 14	TCGGCTCTGG	70	2	1	50.00
OPB - 15	GGAGGGTGTT	60	5	3	60.00
OPC - 01	TTCGAGCCAG	70	2	1	50.00
OPC - 16	CACACTCCAG	60	2	1	50.00
OPC - 18	TGAGTGGGTG	60	2	0	0.00
OPC - 20	ACTTCGCCAC	60	3	3	100.00
OPE - 03	CCAGATGCAC	60	2	1	50.00
OPE - 09	CTTCACCCGA	60	4	4	100.00
OPF - 03	CCTGATCACC	60	5	3	60.00
OPF - 04	GGTGATCAGG	60	2	1	50.00
OPF - 09	CCAAGCTTCC	60	9	8	88.89
OPF - 13	GGCTGCAGAA	60	9	5	55.55
OPG - 10	AGGGCCGTCT	70	6	2	33.33
OPG - 13	CTCTCCGCCA	70	3	1	33.33
OPG - 14	GGATGAGACC	60	3	2	66.67
OPG - 17	ACGACCGACA	60	4	3	75.00
OPG - 19	GTCAGGGCAA	60	10	9	90.00
OPG - 20	TCTCCCTCAG	60	3	2	66.67
Total			**89**	**61**	**68.50**
Average marker / primer			**4.23**	**2.90**	

Plate. 8. RAPD profiles of 30 genotypes for primer OPB 09 and OPB 08

Lane			
M	Marker		
1	BS - 2	16	Roma
2	BS - 16	17	Kalimpong
3	BS -23	18	Allepey
4	BS - 48	19	PTS 12
5	BS - 53	20	Prabha
6	BS - 76	21	Prathibha
7	BS - 89	22	PTS 2
8	BS - 90	23	ER 169
9	BS - 115	24	ER 175
10	Kanthi	25	ER 189
11	Shoba	26	CO 1
12	VK 5	27	JTS 2
13	Sudarshana	28	Rajendra Sonia
14	Suguna	29	PTS 55
15	Suvarna	30	ER 209

Plate 8. RAPD marker profiles of 30 genotypes

1. Primer OPB 09



2. Primer OPB 08

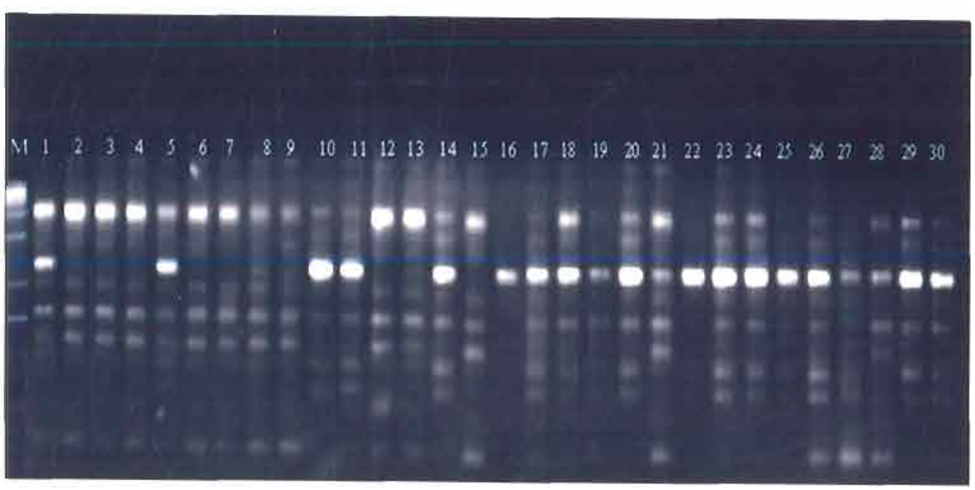


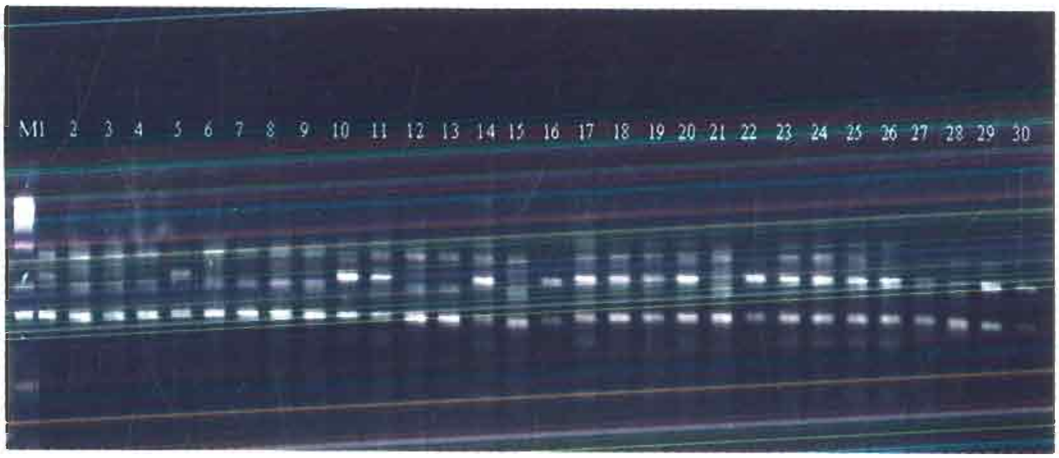
Plate. 9. RAPD profiles of 30 genotypes for primer OPG 17 and OPF 09

Lane

M	Marker		
1	BS - 2	16	Roma
2	BS - 16	17	Kalimpong
3	BS -23	18	Allepey
4	BS - 48	19	PTS 12
5	BS - 53	20	Prabha
6	BS - 76	21	Prathibha
7	BS - 89	22	PTS 2
8	BS - 90	23	ER 169
9	BS - 115	24	ER 175
10	Kanthi	25	ER 189
11	Shoba	26	CO 1
12	VK 5	27	JTS 2
13	Sudarshana	28	Rajendra Sonia
14	Suguna	29	PTS 55
15	Suvarna	30	ER 209

Plate 9. RAPD marker profiles of 30 genotypes

1. Primer OPG 17



2. Primer OPF 09

Table 54. Similarity coefficient indices based on Jaccard's similarity coefficient

Genotypes	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
BSR 2	1.00																													
BS 16	0.87	1.00																												
BS 23	0.87	0.97	1.00																											
BS 53	0.86	0.93	0.96	1.00																										
BS 76	0.88	0.81	0.81	0.82	1.00																									
BS 89	0.85	0.95	0.95	0.96	0.81	1.00																								
BS90	0.84	0.96	0.93	0.95	0.82	0.96	1.00																							
BS115	0.83	0.89	0.92	0.93	0.78	0.92	0.91	1.00																						
KANTHI	0.75	0.84	0.84	0.85	0.75	0.86	0.85	0.89	1.00																					
SHOBA	0.60	0.55	0.54	0.52	0.62	0.51	0.54	0.55	0.57	1.00																				
VK 5	0.70	0.63	0.63	0.62	0.68	0.61	0.61	0.61	0.59	0.82	1.00																			
SUDARSHANA	0.78	0.90	0.90	0.92	0.77	0.93	0.94	0.90	0.82	0.51	0.57	1.00																		
SUGUNA	0.78	0.90	0.88	0.89	0.79	0.90	0.94	0.90	0.87	0.54	0.57	0.94	1.00																	
SUVARNA	0.66	0.60	0.60	0.58	0.68	0.57	0.58	0.59	0.59	0.77	0.89	0.53	0.55	1.00																
ROMA	0.71	0.78	0.80	0.84	0.71	0.80	0.81	0.85	0.84	0.53	0.58	0.80	0.83	0.58	1.00															
KALIMPONG	0.63	0.58	0.58	0.59	0.69	0.59	0.58	0.59	0.62	0.66	0.70	0.57	0.57	0.68	0.60	1.00														
ALLEPEY	0.71	0.69	0.69	0.67	0.71	0.66	0.65	0.66	0.69	0.78	0.85	0.60	0.62	0.80	0.63	0.72	1.00													
PTS 12	0.80	0.80	0.78	0.77	0.78	0.75	0.76	0.75	0.74	0.69	0.71	0.71	0.73	0.67	0.71	0.64	0.82	1.00												
PRABHA	0.81	0.79	0.79	0.78	0.79	0.76	0.75	0.76	0.78	0.66	0.72	0.70	0.72	0.68	0.74	0.71	0.83	0.91	1.00											
PRATHIBHA	0.62	0.59	0.57	0.58	0.64	0.57	0.59	0.57	0.59	0.81	0.85	0.54	0.56	0.77	0.59	0.66	0.84	0.74	0.73	1.00										
PTS 2	0.83	0.85	0.85	0.86	0.79	0.85	0.83	0.85	0.79	0.59	0.63	0.78	0.78	0.61	0.80	0.60	0.71	0.85	0.83	0.63	1.00									
ERODE 169	0.49	0.44	0.44	0.43	0.50	0.44	0.44	0.47	0.49	0.72	0.69	0.43	0.47	0.67	0.47	0.65	0.66	0.55	0.56	0.67	0.50	1.00								
ERODE 175	0.62	0.58	0.58	0.57	0.64	0.55	0.56	0.55	0.58	0.84	0.91	0.51	0.53	0.83	0.58	0.69	0.87	0.72	0.73	0.93	0.64	0.73	1.00							
ERODE 184	0.62	0.58	0.60	0.59	0.64	0.55	0.56	0.59	0.60	0.81	0.88	0.55	0.55	0.80	0.60	0.71	0.87	0.70	0.71	0.87	0.62	0.70	0.93	1.00						
CO 1	0.65	0.60	0.62	0.61	0.63	0.58	0.57	0.60	0.60	0.76	0.85	0.54	0.54	0.78	0.61	0.67	0.87	0.72	0.73	0.84	0.64	0.68	0.90	0.90	1.00					
SALEM LOCAL	0.65	0.64	0.64	0.61	0.63	0.62	0.60	0.62	0.64	0.73	0.82	0.56	0.58	0.78	0.61	0.64	0.87	0.77	0.76	0.78	0.68	0.68	0.82	0.79	0.82	1.00				
JTS 2	0.71	0.66	0.68	0.69	0.69	0.66	0.65	0.68	0.69	0.61	0.65	0.62	0.62	0.59	0.67	0.67	0.74	0.75	0.81	0.66	0.73	0.58	0.66	0.64	0.69	0.71	1.00			
RAJENDRA SONIA	0.79	0.76	0.74	0.75	0.77	0.74	0.75	0.76	0.75	0.68	0.67	0.70	0.74	0.63	0.69	0.64	0.78	0.83	0.84	0.70	0.81	0.56	0.68	0.66	0.66	0.68	0.83	1.00		
PTS 55	0.57	0.53	0.55	0.54	0.59	0.51	0.51	0.52	0.53	0.77	0.82	0.50	0.50	0.74	0.53	0.65	0.81	0.67	0.68	0.83	0.59	0.72	0.90	0.90	0.84	0.73	0.63	0.65	1.00	
ERODE 209	0.68	0.63	0.61	0.60	0.66	0.59	0.60	0.59	0.58	0.75	0.79	0.55	0.57	0.72	0.56	0.66	0.86	0.76	0.75	0.80	0.65	0.67	0.83	0.80	0.81	0.78	0.70	0.77	0.80	1.00

Kerala were found to be in different clusters. At the same time, genotypes of diverse geographical origin such as PTS 12 (Orissa) and Prabha (Kerala) and Suvarna (Andhra Pradesh) and VK 5 (Kerala) formed separate clusters.

The clustering pattern revealed a poor level of congruence between the quantitative data and RAPD marker data. However, the clustering of Bhavanisagar genotypes, Sudarshana and Suguna, ER 175 and ER 184 were similar both at morphological and molecular level.

4.12. Screening studies under artificial conditions

4.12.1. Against leaf spot (*Colletotrichum curcumae*) (Table 55)

The genotypes were scored against leaf spot (*Colletotrichum curcumae*) under inoculated conditions. All the genotypes were found susceptible and the per cent disease index ranged between 10.19 and 41.64. The genotypes 2, 15, 22, 53, 88, 89, 120, 121, 122, 131, 133, 134, 146, 148, 151, 153, 156, 175, 184, 189, 195, 198 were moderately resistant. The genotypes 114, 130, 132 and 209 were susceptible to the disease. (Table 55).

4.12.2. Against scale (*Aspidiotus hartii*) (Table 55)

The genotypes exhibited wide range of variability to the pest infestation when artificially inoculated. The per cent infestation ranged between 10.90 and 47.30. The genotypes 114 (43.40) and 209 (47.30) were highly susceptible. The other genotypes were classified into susceptible and moderately resistant types. (Table 55).

Table 55. Screening of thirty genotypes for resistance to leaf spot and scale

Genotypes	PDI (leaf spot)	% infestation (scale)
2	14.48	16.75
15	12.67	13.70
22	13.32	11.30
53	11.22	14.70
75	15.28	13.00
88	14.48	14.80
89	11.79	12.55
114	41.64	43.40
120	16.57	20.45
121	13.11	14.60
122	14.77	17.86
130	38.41	24.10
131	10.88	11.96
132	31.29	27.40
133	14.50	15.00
134	11.32	13.64
146	13.15	14.56
148	14.78	15.73
151	11.24	10.90
152	24.19	24.05
153	14.29	17.68
156	10.19	12.25
169	22.8	22.95
175	14.18	14.50
184	15.05	16.63
189	20.96	19.70
192	28.26	25.21
195	13.38	13.92
198	18.94	17.65
209	31.61	47.30
CD(.05)	12.49	13.75

Discussion

CHAPTER V
DISCUSSION

The current study focused on the turmeric germplasm (223 genotypes) that was assembled with the genotypes from principal turmeric producing states in India, in critically evaluating the extent of variability, association of characters, degree of divergence among them at morphological and molecular level and screening the genotypes for resistance to leaf spot disease and scale insect using appropriate genetic tools.

Development of cultivars with high yield levels coupled with good quality attributes requires information on the nature and extent of variability available in germplasm collections. Germplasm characterization is an important link between conservation and utilization of the plant genetic resources. For any breeding programme, genetic diversity is the raw material to a breeder since genetic variation determines the potential for making gains from selection and in resolving their phylogenetic relationships. In this regard, studies providing information about the diversity in germplasm would play an important role in crop improvement. For years, farmers have been the major contributors to crop genetic diversity. Locally cultivated varieties well adapted to environmental conditions were the major criteria for long-term biodiversity conservation. Many of these attributes of local varieties are very desired genetic sources for plant breeding.

Breeding is regarded as accelerated and targeted evolution. Just as evolution is based on genetic variation, so is breeding. Genetic variation through yield attributes is the major concern. Yield is a complex trait influenced by genetic and environmental factors. Complexity of yield and its components can be understood by employing various techniques available to plant breeders.

Evaluation of genetic variation among the germplasm particularly of landraces is crucial in harnessing the genetic potential of these genotypes for improvement of traits needed for adaptation to various stress conditions. However, evaluation of genetic variability is inundated with a variety of problems arising out of interaction between genes and environment, heterozygosity at many loci as a consequence of open pollination resulting in instability of genome.

A variety of tools and techniques have been developed based on the principle of genetics and statistics through which the environmental effects can be largely nullified and real genetic effects defined. Biometrical genetics, analyses the variation into various heritable and non-heritable components. This has the power to trace the causation and in interpretation of results to plan the strategies for plant breeding programmes. Next is the multivariate analysis, which includes D^2 statistic, K-means clustering, principal component analysis etc. and these tools give quantitative measurement of divergence among the genotypes and define the relative contribution of characters for differentiation of genotypes.

Turmeric breeding is beset with numerous obstacles, which poses multivarious problems to synthesize high yielding varieties with high curcumin content assuming prime importance for export promotion. Concerted efforts on varietal improvement in the past have given dividends to release as many as 20 varieties till recently (Johny and Ravindran, 2002). The study was contemplated to elucidate appropriate breeding strategies for crop improvement by exploring the existing variability and genetic diversity.

A significant variation in growth was observed among the genotypes with regard to sprouting, number of tillers and number of leaves per plant and leaf area. This is in confirmity with Cholke (1993) and Venkatesha (1994). The genotypes from Bhavanisagar were better in growth with respect to plant height, number of leaves, length and breadth of leaf and number of tillers. The cv. BSR 2 was outstanding in its performance to growth characters, which explains for better adaptability of the genotype to Coimbatore conditions than other genotypes. The genotypes from Kerala (VK 146, VK 112, Prabha) too exhibited good vigour. This probably attributes for the optimum or higher synthesis of carbohydrates due to increased photosynthetic efficiency resulting in better partitioning of reserved food. This is in concordance with the reports of Indiresh *et al.* (1990), Venkatesha (1994) and Kurian and Nair (1996) in turmeric.

Crop duration determines the cropping sequence to be adopted in a region. All the genotypes invariably were early in maturity. The short duration genotypes (upto 7 months) exhibited moderate growth and yield while the medium duration (upto 8 months) excelled in plant and rhizome characteristics as in line with the work of Shanmugasundaram (1998) in turmeric. Considerable variation in duration of turmeric genotypes was reported by several workers *viz.,* Reddy *et al.* (1988), Cholke (1993) and Sasikumar *et al.* (1994). The growth and development of genotypes highly depend on the climatic conditions and soil factors under which they were grown and also that most of the genotypes were region specific.

The variation in rhizome characteristics like the number, weight, length and girth of mother, primary and secondary rhizomes were noticed and acknowledged, with earlier studies by Indiresh *et al.* (1990), Hegde (1992), Cholke (1993) and Venkatesha (1994) in turmeric. The genotypes from Bhavanisagar were high yielding as a result of vigorous growth, which were highly correlated, with yield. The results also reveal that genotypes Sudarshana, Prathibha, PTS 2, PTS 55 produced better rhizome characteristics. Higher production of mother, primary and secondary rhizomes may be due to better growth and vigour in these genotypes, as a result, they were highly correlated with yield. The rhizome growth is also attributed for better absorption of nutrients from soil.

Yield is governed by genetic and environmental factors and it varied with the genotypes in corroboration to the findings of Rajeshkumar and Jain (1998) and MutyalaNaidu *et al.* (2000). Yield of any crop by and large depends on the vigour of the plant as indicated by various growth parameters like plant height, number of leaves, and rhizome characters. Best growth normally results in high yield and is influenced by genetic and environmental factors too, under which the crop is grown.

The average fresh yield in the released varieties ranged between 9.2 to 31.3 t / ha (Edison *et al.*,1991). Significant variation among the genotypes for yield was noticed in the present study which were in agreement with the works of Indiresh *et al.* (1990), Radhakrishnan *et al.* (1995), Maurya *et al.* (1998c) and Rajeshkumar and Jain (1998).

Average fresh yield was higher for Bhavanisagar genotypes and PTS 2 owing to positive relationship with growth components like better leaf growth, number of tillers and rhizome characters. This is attributed for active photosynthesis favouring accumulation and assimilation, in enhancing yield. The characters that exhibited negative association with yield have also contributed indirectly for yield through other characters.

The curing per cent was higher in Bhavanisagar genotypes grouped under short and medium duration classes and significantly low in longer duration genotypes. This is in conformity with the works of Reddy *et al.* (1989) and Cholke (1993).

The variation in curing per cent among the genotypes is mainly due to genetic factors than the environment and the process of curing. Higher curing percentage is due to the production of slender rhizomes, perhaps due to low moisture retention at harvest. (Philip, 1983).

The variation in oil, oleoresin and curcumin content might be due to the genetic potential, method of curing and method of extraction, which corroborate with the findings of Krishnamurthy *et al.* (1975) and Ratnambal (1986). However, the present study showed no significant variation among the genotypes for essential oil and oleoresin content.

Curcumin, chemically dicinnamoyl methane is an odourless yellow crystalline powder. Curcumin levels were found to vary from 1.73 to 5.94 per cent in the present

Ratnambal (1986) (2.30 to 10.90 %) and Edison *et al.* (1991) (2.80 to 9.30 %). Quality variation in relation to agroclimatic condition is confirmed with respect to curcumin content in turmeric (Satheesan and Ramadasan, 1987). Curcumin has also been found to vary depending upon soil organic carbon, available nitrogen and manganese (Vijaykumar *et al.,* 1992). Venkatesha (1994) and Kurian and Nair (1996) reported similar distinct differences.

The use of turmeric oleoresin is gaining importance in the processed food industry. It is a highly a viscous orange brown product containing 30-35 per cent curcumin, 15-20 per cent volatile oil and has a characteristic turmeric aroma (Zachariah and Babu, 1992). It is prepared by solvent extraction and subsequent disolventisation to meet the specifications. (Sampathu *et al.,* 1990). In the present study, the oleoresin content was found to vary from 2.90 to 5.55 per cent. Similar variation among the genotypes was documented by Ratnambal (1986) and Shanmugasundaram (1998).

Turmeric oil is usually obtained by the steam distillation of ground spice. It is light yellow with harsh odour and is obtained as a byproduct from oleoresin industry. The odour of turmeric is mainly due to turmerones (Sampathu *et al.,*1990). The oil content was found to vary from 4.00 to 9.50 per cent (Ratnambal, 1986). The oil content was considerably low from 1.00 to 1.48 per cent, contrary to the earlier reports.

It is evident from the study that genotypes showing promise under Kerala conditions were not able to succeed at Coimbatore condition in comparison to the genotypes from Bhavanisagar and Erode. This might be due to the acclimatization of those genotypes to that particular region. Similar trend was noticed with the genotypes of Orissa, Bihar, Sikkim etc. However, certain genotypes from Kerala (Prabha Prathibha, VK 146) expressed a fair degree of repetitive performance under Coimbatore conditions.

In turmeric, the genotypes should excel not only in plant morphological characters but also in rhizome characteristics to gain higher yield. The yield should be in compensation with good quality to meet the export standards. As the crop is vegetatively propagated, any new variability can be fixed immediately. Systematic screening of genotypes may yield lines with desired quality and agronomic traits.

The success in obtaining highly variable genotypes and creating greater variability for efficient selection in a breeding programme depends to a larger measure in the degree of divergence. One such tool is the D^2 statistic that has found favour for estimating genetic divergence. The importance of the choice of characters has been stressed since they reflect the usefulness of D^2 analysis.

The D^2 statistic measures the forces of differentiation at two levels namely, intra cluster and inter cluster levels and thus helps in the selection of genetically divergent genotypes for exploitation in breeding programmes.

In the present study, as many as twenty-two characters of developmental and economic importance were considered. The pooled values were significant, an indication of wide spectrum of variability among the genotypes. Conventionally, the selection of genotypes was purely empirical, based on geographic divergence. However, experimental evidences have proven that geographic diversity need not necessarily be related to genetic diversity.

Among the characters that contributed towards genetic divergence, yield recorded the highest rank emphasizing the character to be the contributing factor. This was in corroboration with the findings of Singh *et al.* (2000) in ginger.

The other characters weight of primary rhizomes, secondary rhizomes, rhizome-core ratio, dimensions of secondary rhizome contributed to divergence underlying the importance of these characters as selection traits in further crop improvement. The leaf characters exhibited negligible effect on divergence.

The cluster means for 22 characters revealed that cluster 1 registered higher mean values for morphological and rhizome characters. Cluster 2 and 3 were indicative of the rhizome characteristics. Cluster 5 projected better biometric traits than the cluster 4, 6 and 7.

Though cluster 1 was found to be superior in plant morphology, cluster 2 gained importance contributing higher yield in significance to the rhizome components. This implies the usefulness of cluster 1 and 2 for selection of genotypes to excel both in plant architecture and yield.

D^2 statistic identified eight clusters, of which, cluster 1 and 8 were the largest representing the fact that rest of the clusters was the transitional form between them. The genotypes of Bhavanisagar and Erode clustered into different categories owing to similarity within the cluster and their ancesstors sharing a common origin. The clustering pattern in 5^{th} group included genotypes from Bhavanisagar, Kerala and Orissa that pointed out that geographic diversity did not have significant impact on genetic diversity. This was in agreement with earlier findings of Kumaran *et al.* (2000) in coconut. This could also be due to the genetic drift and natural selection forces within a region, which could have a considerable effect on genetic diversity (Murthy and Arunachalam, 1966).

The diversity within the cluster was reflected in the intra cluster distance, which was high for the cluster 5 that accommodated genotypes from different origins. Genotypes grouped in this cluster have similarity for few traits like plant height and leaf dimensions. The least intra cluster distance was for cluster 3, though the cluster contained two different genotypes, they were closely related. Under constant selection, such similar types were expected to be established. Another possibility is that these accessions might have been introduced into these regions from a common origin (Kumaran *et al.*, 2000).

The inter cluster distance expresses the diversification among the clusters, being the highest for clusters 3 and 5 as well as 5 and 8. These clusters were genetically divergent. The closely related genotypes were found in 2, 4 and 6 reflecting low inter cluster distances. This is supported by investigation of Chandra *et al.* (1997) that variation among the clusters resulted as a course of differential genetic make up.

K means clustering referred as non-hierarchical clustering reduces the size of matrix by joining most similar pairs. A cluster centroid is selected which combines all objects within a specified distance. This divergent analysis could bring to focus the possibilities of utilizing the suitable genotypes thus widening the operational base for breeding. The K means clustered the genotypes into 8 groups. The clusters 2 and 6 were the largest and clusters 3, 5 and 7 were least and characterized by poor rhizome characters while the former exhibited superior plant traits.

The traits that exhibited greater variability for the clusters were rhizome yield per plant, weight of primary rhizomes and secondary rhizomes, days to maturity, girth of mother rhizomes and sprouting. Of the clusters, cluster 6 documented wide variability for most of the traits.

The clusters 1, 2, 6 and 8 grouped genotypes of distant origin like Roma (Orissa), Sudarshana and Suguna (Andhra Pradesh) with the genotypes of Kerala and Bhavanisagar. This clustering pattern too indicated that geographical diversity did not have any impact on genetic diversity. This may be because turmeric is inherently propagated through rhizomes and the chances for genetic variability are restricted unless and otherwise if there is any natural mutation.

The clusters showing variation among the groups might be due to differential genetic make up. Though genetic make up of each genotype was different in a cluster, the expression of these genotypes to rhizome characteristics and yield potential made them cluster together within.

Genotypes selected from different clusters based on genetic difference will help for further evaluation of the genetic architecture of the quantitative traits, in view of the greater spectrum of variability encountered in subsequent populations.

Comparing the clustering pattern observed in case of D^2 analysis and K means clustering, the results have indicated that differential grouping of genotypes were based on variance in biometric traits. In Euclidean distance, the axes are at right angles to each other and find the structure within the bounds, to be explicitly stated for (K means), while

Mahalonobis D^2 between two axes is inversely proportional to correlation between two attributes.

Quantitative characterization of phenotypic traits has been used in various germplasm descriptions. Such studies are important because they provide information on germplasm classification and facilitate the utilization of genetic resources among the genotypes and identified the traits that could be utilized for germplasm grouping.

The parameters like weight of secondary rhizomes, primary rhizomes and yield were the major contributing factors towards divergence and need to be emphasized during selection programme.

Though a minor discrepancy existed between the two clustering techniques, it illustrated the fact that the outward expression of genotypes were modified and grouped similar, though the genotypes were brought from different locations. The morphological descriptions reflect not only the genetic constitution of the cultivars but also the interaction of the genotypes with the environment (G x E) within which it is expressed (Lin and Bins, 1984). These clustering techniques have defined clearly that geographic diversity need not necessarily be related to genetic diversity. The cluster distances that separated the genotypes attributed for the reason that the genotypes were distinct of their genetic background among the clusters and more likely within the cluster.

Hence, studies on genetic divergence are an important pre-requisite before embarking on genetic improvement of any crop. Since turmeric is a vegetatively propagated crop, it offers very little or no scope for heterotic breeding to achieve high yield and quality. So genotypes selected from divergent clusters ensuring genetic variability when subjected to artificial induction prove for better results (Singh *et al.*, 2000).

For any selection programme, it is useful to have information as causative factors of genetic diversity. A series of univariate analysis made on each character ignores the possible interrelations among sets of variables and lead to misinterpretation of data.

Multicollinearility in regression analysis give rise to biased and illogical estimates. One method of overcoming this difficulty is to express the extent of variability in a multivariate system by a fewer number of statistically independent linear combinations.

Identification of factors help in reducing the dimensionality of the data and in building up a rigorous basis for the choice of traits in crop improvement programmes (Tikka and Asawa, 1978).

Principal component analysis is a multivariate statistical tool, which attempts to describe total variation in a sample with fewer variables than in the original data set. It is done by successively selecting linear combinations on the principal components of the attributes, which retain the highest proportion of unexplained variability between the units and attributes. It differs from the regression analysis that PCA chooses a line with minimum sum of squared perpendicular distances to the data sets.

In the current study, three factors were found to contribute for more than 80 per cent of total variability. The first component was dominated by weight of primary and secondary rhizomes and their dimensions. The other two factors were dominated by weight of primary and secondary rhizomes. This attributes for the reason that these characters were major contributors to total variance with a share towards genetic divergence. The genotypes that exhibited higher mean values for these two characters would form the basis for selection. The phenotypic effects produced interpret for the existing variability among the genotypes, which is interpreted by the positive and negative scores. This indicates that this variability could be exploited in turmeric breeding. These characters are likely to be linked together and behave alike during inheritance and another possibility of being governed by independent set of alleles.

The emphasis was laid for length – girth dimensions of secondary fingers and length of mother and primary rhizome characters which was in conjunction with the earlier work by Prabhakaran (1991).

Similar findings for cultivars and trait discrimination were obtained using PCA by Julian *et al.* (1997) in banana, Kumaran *et al.* (2000) in coconut and Rekha *et al.* (2002) in banana.

Genetic variability is the prime concern for the breeder for exercising selection and isolation of superior types. A very good response to selection is possible only when divergent genotypes are pooled in the breeding stock. The sample measure for the assessment of variability is the coefficient of variation (Singh and Narayanan, 1993).

It is evident from the study that analysis of variance indicated significant differences among the genotypes for most of the traits. Estimates of PCV was greater than GCV for all the traits and the apparent variation is not only due to genotypes but also due to the influence of environment as normally expected.

The characters yield, number of tillers and weight of primary and secondary rhizomes recorded high GCV and PCV emphasizing these characters to be potentially variable. Hence, selection will be more effective with respect to these characters. These findings are in corroboration with the earlier works of Indiresh *et al.* (1992), NirmalBabu *et al.* (1993), Radhakrishnan *et al.* (1995), Yadav and Singh (1996), Maurya *et al.* (1998b) and Shanmugasundaram (1998).

Although GCV and PCV reveal the extent of genetic variability present, they do not indicate the extent of heritable variation, so that the selection can be effective and repeatable. The practical implications in breeding programmes are based on magnitude of heritable variations of the character concerned. Out of the 26 characters evaluated, days to maturity, weight of primary rhizomes, girth of primary rhizomes, weight of secondary rhizomes, length of secondary rhizomes, girth of secondary rhizomes, rhizome core ratio, curing percentage and yield showed high heritability estimate. This indicates that these characters are promising in crop improvement. This is in confirmation with earlier works by Reddy (1987) and Indiresh *et al.* (1992). However, a contradictory report is established by Jalgaonkar *et al.* (1990) for weight of mother and primary rhizomes. This may be due to the fact that character expression might have been affected by a difference in environment conditions and background of the material used.

Estimates of heritability appreciate the proportion of variation. High heritability (> 90 %) recorded for yield and rhizome characters indicate that selection of such characters is easy because of the close correspondence between the genotype and phenotype due to relatively smaller contribution of the environment to phenotype. But the estimates of heritability was low (< 50 %) for leaf characters, number of mother rhizomes for which, selection may be considerably difficult or virtually impractical due to the masking effect of the environment on genotypic effects.

Heritability along with genetic advance is more helpful in predicting the gains under selection than heritability estimates alone (Johnson *et al.*, 1955). High heritability coupled with genetic advance was observed for yield, weight of primary and secondary rhizomes and number of tillers. High heritability coupled with genetic advance is governed by additive genes and pave the way for improvement of those characters in individual plant selection (Panse, 1957). Similar findings are reported in ginger by Maity *et al.* (1989), Pandey and Dobhal (1993) and Yadav (1999). So the predominance of additive genetic variance in expression of these traits is the most reliable indices for effective selection. This is in agreement with Yadav and Singh (1996) and Shanmugasundaram *et al.* (2000) in turmeric.

The ultimate goal of crop improvement in turmeric is to achieve a higher level of rhizome yield. Being a complex trait, the rhizome yield is largely influenced by many component characters. So information on strength and direction of correlation of these component characters on rhizome yield and *interse* association among them would be useful in designing breeding programmes for yield improvement.

The relationship between yield and its component characters is likely to vary according to the genetic material used, environment under which the material is evaluated as well as due to interaction of these factors. Therefore it is worth while to study the heritable association between variables (genotypic correlation) for identification of important yield components so that due weightage can be given to the characters of importance in further breeding programmes (Johnson *et al.,*1955).

In the present investigation, genotypic correlation coefficient was higher than the phenotypic correlation coefficient thus revealing a strong association at genotypic level between the characters. This is in corroboration with the previous findings of Reddy (1987), Maurya *et al.* (1998a) and Shanmugasundaram (1998).

Among the 26 characters studied, the positive association was noticed for all the biometric traits except number of mother rhizomes and quality characters (oil, oleoresin and curcumin) and curing percentage indicating the possibility of simultaneous improvement of component characters and yield. This is in agreement with the findings of Geetha and Prabhakaran (1987) and Shanmugasundaram (1998) with respect to number of mother rhizomes.

This apparent negative association at genetic level would have arisen from repulsion linkage of gene(s) controlling the direct and indirect effects. Conversely the positive correlation is due to the coupling phase of linkage.

Correlation coefficients between the characters revealed that those characters that had positive association among others are prone for improvement underlined the fact that one component character leads to the concurrent improvement of the other component characters. The findings are concurrent with Shanmugasumdaram (1998).

The simple correlation coefficients showed that yield was significantly associated with all characters studied except for number of mother rhizomes, rhizome core ratio, oil, oleoresin, curcumin and curing percentage. Sarma and Krishnamurthy (1965) and Shanmugasumdaram (1998) projected that high yielding genotypes of turmeric are low in curing per cent. The reason attributed is that curing of rhizomes appear plumpy with more water content, as a result, the curing yield is low.

Information on the direct and indirect effects on yield is important which is explicable by path analysis proposed by Wright (1921) and illustrated by Dewey and Lu (1959).The inter relationships of the component characters on yield provides the likely consequences of their selection for simultaneous improvement of desirable characters with yield.

In the present study, positive and direct effects on rhizome yield were high for girth of secondary rhizome followed by breadth of leaf. The dimension of primary rhizome and weight of primary and secondary rhizome exhibited direct positive effects. Since the correlation of these characters with yield is positive, direct selection of these traits can be practiced for improving the yield.

The direct effect was negative and comparatively high for plant height. Direct effect on yield is negative but exhibit a positive association phenoytpically. This apparent conflict between the correlation and path coefficient analysis arises largely from the fact that correlation simply measures the mutual association without regard to causation while path specifies the relative importance of each causal factor. However, the correlation for this character with yield is positive and, it becomes clear that plant height contributes to yield via girth of secondary rhizomes, core diameter, leaf dimensions due to high value of indirect effects. Similar negative direct effect was recorded by Lal *et al.* (1986) and Shanmugasundaram (1998).

On the contrary, Pathania *et al.* (1981) and Geetha and Prabhakaran, (1987) reported a maximum direct contribution of plant height to rhizome yield, which might be due to the variation in the environment in which it was grown.

It is also evident from the study that direct selection can be made on girth of secondary rhizomes weight of rhizomes and leaf dimensions, as they are true components relating to yield and selection on these will be rewarding. This is supported by the earlier works of Nandi *et al.* (1992), Maurya *et al.* (1998a) and Shanmugasundaram (1998).

Screening the genotypes to leaf spot disease (*Colletotrichum curcumae*) categorized them into two. The critical period for the disease incidence was during the peak vegetative phase (140-180 days). The genotypes varied in degree of tolerance to the disease. The medium duration types were more susceptible to leaf spot than short duration types as they complete their vegetative period simultaneously. Similar line of work was established by Sarma and Krishnamurthy (1962), Philip and Nair (1981) for leaf spot and Upadhyay and Pavgi (1967), Patil and Patil (1983) for leaf blotch.

The correlation between incidence of leaf spot and curcumin content was negative. So screening for resistance is a reliable measure reflecting direct effects on quality. The yield was also considerably reduced emphasizing the importance and need for resistance genotypes.

The 30 genotypes were also screened for resistance to leaf spot under artificial conditions (inoculated with the culture). All the genotypes were susceptible and moderately resistant genotypes were identified (BS 48, BS 89, Sudarshana and PTS-12).

Similarly, screening of the genotypes for resistance to rhizomatous scale was done. There was discrimination observed for duration and degree of tolerance. Under natural conditions, genotypes were tolerant to the pest and on artificial induction, identified 8 resistant genotypes (BS 116, Erode 175, 182, 183, 216, 218, 219 and JTS 2).

Incidentally, BS 43, which was found to be resistant and promising under Bhavanisagar condition (Tirumurthy *et al.*, 1993), was found to be moderately resistant under Coimbatore conditions. This implies the necessity for the uniformity of the material and screening methodology for resistance.

The correlation of pest infestation with yield and quality indicated that the quality was not hampered; however, reduction in yield was noticeable. Hence, periodical screening of genotypes for resistance to this pest and disease is essential to improve yield. Screening studies under artificial condition, indicated that the genotypes exhibited the symptoms for the pest and disease. As in case of phase I, the genotypes 114 (Bhavanisagar) and 209 (Erode) were susceptible to scale and in phase II also. The genotypes were found to vary in their degree of tolerance for leaf spot disease, comparing both the phases.

Evaluation of the genotypes is the basic approach to detect the possible genetic variation among them. This requires clear-cut information on the observable differences at morphological and molecular level to assess the level of genetic diversity in the germplasm. The extent of genetic diversity has been estimated based on morphological characters over the years. Recently, variations in profiles of molecular markers such as RFLP, RAPD, AFLP and SSR are also employed to assess the level of genetic diversity in plants.

In the present study, the attempt made to estimate the genetic diversity among the 30 genotypes involving both quantitative traits and RAPD markers exhibited only considerable level of congruence between them. The probable reason might be due to inherent variation in the nature of algorithms involved. The genetic diversity assessed involving 22 quantitative traits among the 30 genotypes was not consistent with all the methods used. This inconsistency may be due to the efficiency of the algorithm to eliminate the bias in the quantitative data, which is always under the influence of environment. The discrepancy among the three tools studied indicates that morphological traits solely are not sufficient in discriminating the genotypes as turmeric lacks defined morphological descriptors coupled with cultivar specific characters.

Recently, the use of molecular markers assumed greater significance in germplasm characterization and assessment of genetic diversity. Several reports have claimed the use of these markers in germplasm characterization of several crops (Al-Jibouri and Adham, 1990; Bhat *et al.*, 1992; dosSantos *et al.*, 1994; Rout *et al.*, 1998; Boehm *et al.*, 1999; Rekha *et al.*, 2002). However their reliability and accuracy is questionable as evident from the limited number of isozymes and influence of environment on phenotypic expression. Moreover, they pose problems of producing artifacts during electrophoresis (Shamina *et al.*, 1998).

Considering the problems associated with morphological and isozyme markers, alternative molecular tools were identified for genetic diversity analysis. Among the molecular tools, RAPD markers are known for their technical simplicity and high throughput were employed as one of the methods for effective germplasm management, estimating diversity, monitoring genetic erosion and removing duplicates from germplasm collections (Virk *et al.,* 1995).

The present study on the germplasm characterization using 22 quantitative traits detected low levels of polymorhism among the genotypes of same geographical location morphologically. However, there was considerable variation noticed at the molecular level. This reinforces on the belief that genotypes collected from same area may not be genetically distinct. This signifies for the role played by environment in modifying the phenotypic expression. This meager morphological diversity exhibited among the genotypes might be due to their related pedigrees, which make discrimination of genotypes rather cumbersome.

The study focused to assess the genetic diversity using molecular markers (RAPD) revealed the advantage of GC rich primers in producing amplification. The GC content in the range of 60-70 per cent tended to increase the number of amplification products. An average of 4.23 fragments per primer was generated. The high level of polymorphism supports the fact that RAPD is capable of detecting single base pair changes in genomic DNA (Williams *et al.*, 1990). RAPD polymorphisms are caused by differences in nucleotide sequences at the primary sites or by structural rearrangement within the amplified sequence. It also indicated sufficient level of diversity among the genotypes.

The clustering pattern of quantitative traits and RAPD markers reflected a genetic similarity based on geographical location. The credibility of genetic diversity analysis involving 22 quantitative traits and 89 RAPD markers could not be established beyond doubt since the genotypes involved do not have their pedigree details though the genotypes are known for their geographical origin, which could not be used as criterion to establish the relationship between the genotypes.

Though RAPD markers are widely used for genetic analysis, the inherent problems with RAPD technique do not make the markers as a reliable system which can be sorted out by repeated experiments. However, the technical simplicity and high throughput in the technique (Williams *et al.*, 1990) helps to engage the RAPD markers for large scale survey. Using marker systems such as SSR may help to establish the differences among the genotypes with more accuracy when compared to RAPD markers. Further, use of molecular markers should be combined with reliable morphological descriptors of qualitative nature and pedigree details of the genotype to get strength to the diversity analysis and inturn germplasm management. The present study is an attempt to employ the possibility of using new tools such as molecular markers to assess genetic diversity in vegetatively propagated crops. This will help to maintain the integrity of the germplasm by identifying duplicates.

Thus, the crop improvement should focus on the selection and improvement of genotypes from the available germplasm by exploiting and utilizing the already existing variability and creating variability. Turmeric being an asexually propagated crop, is highly heterozygous, causative of inbreeding depression. Reduced flowering seriously handicaps the breeding of turmeric and seed set is a rare phenomenon, as a result, hybridization is implausible.

The already existing variability can be exploited through genetic divergence among the genotypes. As with the current study, the surveys failed to confirm similar patterns of diversity based on morphological characters and RAPD marker. Several multivariate statistical tools are potent in identification of traits contributing towards divergence and selection of genotypes for further improvement by clonal selection. It is easy to produce large number of clones as it is propagated through rhizomes. The selection of the best genotype to produce superior clone form the basis for variability (Clonal selection). Genetic variability within clones may be created due to somatic mutation under *invivo* and *invitro* conditions. Induced mutagenesis using single cell cultures to isolate chimera free mutants for yield and quality parameters are a potential avenue and various degree of success is reported by KaruvinaShetty *et al.* (1980).

From the foregoing, it is clear that, genetic diversity is a ubiquitous property of all species in nature. The distribution and organization of genetic variation within and among the populations of a species are the consequences of its evolution. Further, the various multivariate tools used viz., D^2 statistic, K means on phenotypic data as well as RAPD marker data elucidated the same results on genetic divergence, though there were minor differences.

Summary

CHAPTER VI

SUMMARY

The two twenty three genotypes of turmeric (*Curcuma longa* L.) were evaluated in two phases for yield, quality and screened for resistance to pest (scale) and disease (leaf spot); assessing the extent of variability, heritability, genetic advance, character association and path analysis besides analyzing the extent of genetic diversity among them. The salient findings are summarised hereunder.

1. All the biometric characters except the quality parameters exhibited significant variations among the 223 genotypes evaluated for their mean performance.
2. The study on morphological characters indicated that performance of genotypes from Bhavanisagar were superior than other genotypes. Among them, BSR 2 produced the tallest plant (48.56 cm) coupled with more number of tillers (5.09) and higher leaf dimensions (51.00 cm long and 14.16 cm wide).
3. As regard to crop duration, the genotypes of Bhavanisagar (9, 10, 14, 15, 16 and 17) exhibited longer duration (> 260 days) and early genotypes (218 – 240 days) were Prabha, PTS 15, Rajendrasonia, 170 (from Erode). The other genotypes were with medium duration (240 – 260 days).
4. The genotypes Prathibha, Sudarshana, PTS 2, PTS 55 were better in rhizome dimensions and yield of mother, primary and secondary rhizomes. The rhizome yield was the highest (12.82 kg/plot) in genotype 101 from Bhavanisagar. Genotypes 110 and 123 from Bhavanisagar were found to be poor in rhizome characteristics.
5. The curing percentage was high for the genotype from Erode, ER 157 (23.35), BS 7 (22.92), Allepey (22.70) and PTS 12 (23.11). The lowest out turn was obtained for 187 (12.23) and Sudarshana (12.43).

6. Among the quality characters, oil and oleoresin showed no significant variation. Curcumin was found to be the highest in Allepey (5.94%) and lowest in BS 26 (1.73%).
7. The D^2 statistic for 22 quantitative traits revealed significant contribution of the characters towards variability. The genotypes were clustered into 8 groups. The clustering technique grouped Bhavanisagar genotypes together (cluster 1) and Erode genotypes together in cluster 8 and other genotypes were transitional to the two clusters.
8. The genetically diversed clusters were 3, 5 and 8 accommodating the genotypes from Bhavanisagar, Erode, Kerala and Orissa. The divergence within the cluster was high for cluster 5 (1021.742) and 1 (682.244).
9. The cluster mean for the characters indicated that genotypes of cluster 1 excelled in morphological traits and cluster 1 and 2 documented the highest values for rhizome characteristics.
10. The relative contribution of characters towards genetic divergence identified yield to be the major factor (61.62 %) followed by weight of primary rhizomes (5.95 %).
11. A non-hierarchial clustering technique (K-means) was performed on 223 genotypes and grouped them into 8 clusters. The clusters 1, 2, 6 and 8 grouped genotypes of diverse geographical origin (Kerala, Orissa, Andhra Pradesh and Tamil Nadu). The cluster 8 exhibited greater variability for the rhizome yield (1-13 Kg / plot), weight of primary and secondary rhizomes (74-139 and 52-115 kg / plot respectively).
12. Both the clustering techniques defined clearly the contributing parameters towards divergence (weight of primary, secondary rhizomes and yield). They also implied that geographical location did not have much impact on genetic diversity.
13. The PCA executed for 223 genotypes for 22 characters revealed the first three components contributing more than 80 per cent of total variability. All the three principal components were dominated by weight of primary and secondary rhizomes

attributing for total variation. The PC 1 accounted for more variability (76.30%) than PC 2 and PC 3 (8.59 and 5.57% respectively).

14. The highest GCV estimates were observed for yield (67.39), number of tillers (38.76) and lowest for oil and oleoresin.

15. A higher heritability estimate followed by higher genetic gain were obtained for yield (98.89, 138.05 respectively), weight of primary (97.99 h^2) and secondary rhizomes (98.16 h^2) suggesting additive gene action.

16. The rhizome yield was positively and significantly correlated with weight of primary rhizomes (0.491) followed by length of primary rhizomes (0.490), plant height (0.458), length of leaf (0.421), weight of secondary rhizomes (0.416), length of secondary rhizomes (0.410), girth of primary rhizomes (0.365), rhizome diameter (0.365), core diameter (0.359), number of leaves (0.328), breadth of leaf (0.308), girth of secondary rhizomes (0.293), weight of mother rhizomes (0.241), number of secondary rhizomes (0.232), number of primary rhizomes (0.231), girth of mother rhizomes (0.210), sprouting (0.180), number of tillers (0.153) and days to maturity (0.094). A negative correlation was exhibited for oil, oleoresin, rhizome core ratio, curcumin, number of mother rhizomes and curing percentage.

17. Path coefficient analysis projected girth of secondary rhizomes (0.922), breadth of leaf (0.879), length of primary rhizomes (0.745), core diameter (0.683), weight of secondary rhizomes (0.575), number of primary rhizomes (0.463), weight of primary rhizomes (0.361) as the major contributors towards yield due to high positive direct effects.

18. The genotypes screened for resistance to leaf spot indicated a significant variation among genotypes. They were rated into susceptible and moderately resistant types. Under artificial conditions, all the genotypes were susceptible. The incidence exhibited non-significant correlation with yield.

19. The genotypes screened for resistance to scale on artificial inoculation resulted in 4.00- 68.00 % infestation. The genotypes from Bhavanisagar and Erode were resistant to this pest. The infestation exerted non-significant correlation with yield.
20. The genetic diversity was assessed for 30 genotypes at the molecular level and compared with the morphological traits for degree of divergence.
21. The pattern of clustering of the quantitative data based on D^2, K means and UPGMA revealed discrepancy among them. The cluster profile based on quantitative data and RAPD marker exhibited considerable level of congruence between them.
22. The genotypes studied for degree of divergence by RAPD profiles revealed 68.50% polymorphism for 21 primers and other 14 primers have failed to produce any amplified fragments.
23. The highest number of fragments (10) was obtained for primer OPG 19 and OPC 18 was completely monomorphic. The primers OPB 08, OPC 20, OPE 09 and OPG 19 detected high level of polymorphism (> 90%).
24. The Jaccard's similarity coefficient found BS 16 and BS 23 to be closely related (0.97) and similarity between the genotypes from Erode (172 and 184) with CO1, Suguna and Sudarshana of Andhra Pradesh, while Prabha and Prathibha of IISR were genotypically different.
25. There was minor discrepancy noticed at both the morphological and molecular levels for the genotypes emphasizing specific morphological and molecular markers for discriminating the genotypes.

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* Originals not seen

Annexure 1

Sources of turmeric genotypes maintained in the germplasm

S.No.	Genotype Number	Genotypes	Source
1	1	BS 1	Agricultural Research Station, Bhavanisagar
2	2	BS 2	ARS, Bhavanisagar
3	3	BS 3	ARS, Bhavanisagar
4	4	BS 5	ARS, Bhavanisagar
5	5	BS 6	ARS, Bhavanisagar
6	6	BS 7	ARS, Bhavanisagar
7	7	BS 8	ARS, Bhavanisagar
8	8	BS 9	ARS, Bhavanisagar
9	9	BS 10	ARS, Bhavanisagar
10	10	BS 11	ARS, Bhavanisagar
11	11	BS 12	ARS, Bhavanisagar
12	12	BS 13	ARS, Bhavanisagar
13	13	BS 14	ARS, Bhavanisagar
14	14	BS 15	ARS, Bhavanisagar
15	15	BS 16	ARS, Bhavanisagar
16	16	BS 17	ARS, Bhavanisagar
17	17	BS 18	ARS, Bhavanisagar
18	18	BS 19	ARS, Bhavanisagar
19	19	BS 20	ARS, Bhavanisagar
20	20	BS 21	ARS, Bhavanisagar
21	21	BS 22	ARS, Bhavanisagar
22	22	BS 23	ARS, Bhavanisagar
23	23	BS 24	ARS, Bhavanisagar
24	24	BS 25	ARS, Bhavanisagar
25	25	BS 26	ARS, Bhavanisagar
26	26	BS 27	ARS, Bhavanisagar
27	27	BS 28	ARS, Bhavanisagar
28	28	BS 29	ARS, Bhavanisagar
29	29	BS 30	ARS, Bhavanisagar
30	30	BS 31	ARS, Bhavanisagar
31	31	BS 32	ARS, Bhavanisagar
32	32	BS 33	ARS, Bhavanisagar
33	33	BS 34	ARS, Bhavanisagar
34	34	BS 35	ARS, Bhavanisagar
35	35	BS 36	ARS, Bhavanisagar
36	36	BS 37	ARS, Bhavanisagar
37	37	BS 38	ARS, Bhavanisagar
38	38	BS 39	ARS, Bhavanisagar
39	39	BS 40	ARS, Bhavanisagar
40	40	BS 41	ARS, Bhavanisagar
41	41	BS 42	ARS, Bhavanisagar
42	42	BS 43	ARS, Bhavanisagar
43	43	BS 44	ARS, Bhavanisagar
44	44	BS 45	ARS, Bhavanisagar
45	45	BS 46	ARS, Bhavanisagar

Contd.

S.No.	Genotype Number	Genotypes	Source
46	46	BS 47	ARS, Bhavanisagar
47	47	BS 48	ARS, Bhavanisagar
48	48	BS 49	ARS, Bhavanisagar
49	49	BS 50	ARS, Bhavanisagar
50	50	BS 51	ARS, Bhavanisagar
51	51	BS 52	ARS, Bhavanisagar
52	52	BS 53	ARS, Bhavanisagar
53	53	BS 54	ARS, Bhavanisagar
54	54	BS 55	ARS, Bhavanisagar
55	55	BS 56	ARS, Bhavanisagar
56	56	BS 57	ARS, Bhavanisagar
57	57	BS 58	ARS, Bhavanisagar
58	58	BS 59	ARS, Bhavanisagar
59	59	BS 60	ARS, Bhavanisagar
60	60	BS 61	ARS, Bhavanisagar
61	61	BS 62	ARS, Bhavanisagar
62	62	BS 63	ARS, Bhavanisagar
63	63	BS 64	ARS, Bhavanisagar
64	64	BS 65	ARS, Bhavanisagar
65	65	BS 66	ARS, Bhavanisagar
66	66	BS 67	ARS, Bhavanisagar
67	67	BS 68	ARS, Bhavanisagar
68	68	BS 69	ARS, Bhavanisagar
69	69	BS 70	ARS, Bhavanisagar
70	70	BS 71	ARS, Bhavanisagar
71	71	BS 72	ARS, Bhavanisagar
72	72	BS 73	ARS, Bhavanisagar
73	73	BS 74	ARS, Bhavanisagar
74	74	BS 75	ARS, Bhavanisagar
75	75	BS 76	ARS, Bhavanisagar
76	76	BS 77	ARS, Bhavanisagar
77	77	BS 78	ARS, Bhavanisagar
78	78	BS 79	ARS, Bhavanisagar
79	79	BS 80	ARS, Bhavanisagar
80	80	BS 81	ARS, Bhavanisagar
81	81	BS 82	ARS, Bhavanisagar
82	82	BS 83	ARS, Bhavanisagar
83	83	BS 84	ARS, Bhavanisagar
84	84	BS 85	ARS, Bhavanisagar
85	85	BS 86	ARS, Bhavanisagar
86	86	BS 87	ARS, Bhavanisagar
87	87	BS 88	ARS, Bhavanisagar
88	88	BS 89	ARS, Bhavanisagar
89	89	BS 90	ARS, Bhavanisagar
90	90	BS 91	ARS, Bhavanisagar

Contd.

S.No.	Genotype Number	Genotypes	Source
91	91	BS 92	ARS, Bhavanisagar
92	92	BS 93	ARS, Bhavanisagar
93	93	BS 94	ARS, Bhavanisagar
94	94	BS 95	ARS, Bhavanisagar
95	95	BS 96	ARS, Bhavanisagar
96	96	BS 97	ARS, Bhavanisagar
97	97	BS 98	ARS, Bhavanisagar
98	98	BS 99	ARS, Bhavanisagar
99	99	BS 100	ARS, Bhavanisagar
100	100	BS 101	ARS, Bhavanisagar
101	101	BS 102	ARS, Bhavanisagar
102	102	BS 103	ARS, Bhavanisagar
103	103	BS 104	ARS, Bhavanisagar
102	102	BS 105	ARS, Bhavanisagar
105	105	BS 106	ARS, Bhavanisagar
106	106	BS 107	ARS, Bhavanisagar
107	107	BS 108	ARS, Bhavanisagar
108	108	BS 109	ARS, Bhavanisagar
109	109	BS 110	ARS, Bhavanisagar
110	110	BS 111	ARS, Bhavanisagar
111	111	BS 112	ARS, Bhavanisagar
112	112	BS 113	ARS, Bhavanisagar
113	113	BS 114	ARS, Bhavanisagar
114	114	BS 115	ARS, Bhavanisagar
115	115	BS 116	ARS, Bhavanisagar
116	116	BS 117	ARS, Bhavanisagar
117	117	BS 118	ARS, Bhavanisagar
118	118	BS 119	ARS, Bhavanisagar
119	119	BS 120	ARS, Bhavanisagar
120	120	Kanthi	Kerala Agricultural University, Vellanikara
121	121	Shoba	KAU, Vellanikara
122	122	VK 5	KAU, Vellanikara
123	123	VK 112	KAU, Vellanikara
124	124	VK 116	KAU, Vellanikara
125	125	VK 111	KAU, Vellanikara
126	126	VK 73	KAU, Vellanikara
127	127	VK 76	KAU, Vellanikara
128	128	VK 96	KAU, Vellanikara
129	129	VK 146	KAU, Vellanikara
130	130	Sudarshana	Andhra Pradesh
131	131	Suguna	Andhra Pradesh
132	132	Suvarna	IISR, Kerala
133	133	Roma	Orissa
134	134	Kalimpong	West Bengal
135	135	Sikkim local	Orissa

Contd.

S.No.	Genotype Number	Genotypes	Source
136	136	Koraput local	Orissa
137	137	Sunduk local	Orissa
138	138	Prathibha	Kerala
139	139	PTS 10	Pottangi, Orissa
140	140	JTS 2	Jagital
141	141	Rajendra Sonia	Bihar
142	142	XYP patti	Andhra Pradesh
144	144	Salem local	Salem
145	145	PTS 62	Pottangi, Orissa
146	146	Allepey	Spice Board, Kerala
147	147	PTS 43	Pottangi, Orissa
148	148	PTS 12	Pottangi, Orissa
149	149	PTS 38	Pottangi, Orissa
150	150	Sonali	Orissa
151	151	Prabha	IISR, Kerala
152	152	Prathibha	IISR, Kerala
153	153	JTS 1	Jagital
154	154	PTS 2	Pottangi, Orissa
155	155	PTS 2	Pottangi, Orissa
156	156	PTS 2	Pottangi, Orissa
157	157	ER 157	Erode
158	158	ER 158	Erode
159	159	ER 159	Erode
160	160	ER 160	Erode
161	161	PTS 10	Pottangi, Orissa
162	162	ER 162	Erode
163	163	ER 163	Erode
164	164	PTS164	Pottangi, Orissa
165	165	ER 165	Erode
166	166	ER 166	Erode
167	167	ER 167	Erode
168	168	PTS168	Pottangi, Orissa
169	169	ER 169	Erode
170	170	ER 170	Erode
171	171	ER 171	Erode
172	172	PTS 172	Pottangi, Orissa
173	173	ER 173	Erode
174	174	ER 174	Erode
175	175	ER 175	Erode
176	176	ER 176	Erode
177	177	ER 177	Erode
178	178	ER 178	Erode
179	179	ER 179	Erode
180	180	ER 180	Erode

Contd.

S.No.	Genotype Number	Genotypes	Source
181	181	ER 181	Erode
182	182	ER 182	Erode
183	183	ER 183	Erode
184	184	ER 184	Erode
185	185	ER 185	Erode
186	186	ER 186	Erode
187	187	N 187	North India
188	188	BD JR –1250	UHF- Solan
189	189	CO 1	TNAU, Coimbatore
190	190	BS 4	Erode
191	191	RH 5	RAU, Bihar
192	192	Salem local	Salem
193	193	Prabha	Kerala
194	194	JTS 2	Jagital
195	195	Rajendra Sonia	Bihar
196	196	JTS 2	Jagital
197	197	PTS 12	Pottangi, Orissa
198	198	PTS 55	Pottangi, Orissa
199	199	PTS 15	Pottangi, Orissa
200	200	PTS 17	Pottangi, Orissa
201	201	Sonali	Orissa
202	202	Anaikatti	Anaikatti
203	203	ER 203	Erode
204	204	ER 204	Erode
205	205	ER 205	Erode
206	206	ER 206	Erode
207	207	ER 207	Erode
208	208	ER 208	Erode
209	209	ER 209	Erode
210	210	ER 210	Erode
211	211	ER 211	Erode
212	212	ER 212	Erode
213	213	ER 213	Erode
214	214	ER 214	Erode
215	215	ER 215	Erode
216	216	ER 216	Erode
217	217	ER 217	Erode
218	218	ER 218	Erode
219	219	ER 219	Erode
220	220	ER 220	Erode
221	221	ER 221	Erode
222	222	ER 222	Erode
223	223	Indonesia	Indonesia
224	224	Rallis Research centre	Rallis Research centre, Banglore

Annexure II

Sources of thirty genotypes studied in Phase II

S.No.	Genotype Number	Genotypes	Source
1	2	BS 2	ARS, Bhavanisagar
2	15	BS 16	ARS, Bhavanisagar
3	22	BS 23	ARS, Bhavanisagar
4	52	BS 53	ARS, Bhavanisagar
5	75	BS 76	ARS, Bhavanisagar
6	88	BS 89	ARS, Bhavanisagar
7	89	BS 90	ARS, Bhavanisagar
8	114	BS 115	ARS, Bhavanisagar
9	120	Kanthi	KAU, Vellanikara
10	121	Shoba	KAU, Vellanikara
11	122	VK 5	KAU, Vellanikara
12	130	Sudarshana	Andhra Pradesh
13	131	Suguna	Andhra Pradesh
14	132	Suvarna	IISR, Kerala
15	133	Roma	Orissa
16	134	Kalimpong	West Bengal
17	146	Allepey	Spice Board, Kerala
18	148	PTS 12	Pottangi, Orissa
19	151	Prabha	IISR, Kerala
20	152	Prathibha	IISR, Kerala
21	156	PTS 2	Pottangi, Orissa
22	169	ER 169	Erode
23	175	ER 175	Erode
24	184	ER 184	Erode
25	189	CO 1	TNAU, Coimbatore
26	192	Salem local	Salem
27	194	JTS 2	Jagital
28	195	Rajendra Sonia	Bihar
29	198	PTS 55	Pottangi, Orissa
30	209	ER 209	Erode

Appendix III

Mean data for quantitative and qualitative traits

Genotypes	Sprouting (%)	Plant height (cm)	Number of leaves	Leaf Length (cm)	Leaf breadth (cm)	Number of tillers	Days to maturity	Number Of mother rhizomes (g)	Girth of mother rhizomes (cm)	Weight of mother rhizomes (g)	Number of primary rhizomes
2	100.00	48.56	15.34	51.00	14.16	5.09	240.50	3.00	9.30	51.67	5.50
15	96.00	45.53	17.00	45.15	14.22	4.25	261.00	3.16	7.09	51.84	5.84
22	100.00	44.30	16.75	40.42	13.18	5.09	253.50	2.50	8.79	57.50	5.00
52	96.00	42.14	15.92	40.34	13.66	4.34	255.00	2.84	9.54	71.67	6.67
75	88.00	45.70	16.34	48.64	13.26	4.42	228.00	3.00	8.60	95.00	6.00
88	95.50	44.59	15.92	50.13	13.85	4.25	254.00	3.17	8.63	79.17	7.34
89	96.00	42.61	16.17	48.10	14.46	4.84	256.00	2.83	9.02	59.17	6.50
114	100.00	44.70	15.09	50.90	14.27	4.59	252.00	2.17	9.08	47.50	8.00
120	100.00	45.99	17.17	48.05	14.56	4.25	254.00	2.17	10.45	77.50	6.00
121	73.50	37.60	14.42	41.49	13.13	4.00	228.00	3.50	7.90	80.00	6.50
122	100.00	35.52	14.25	41.78	12.44	3.09	241.00	3.17	8.85	75.00	6.33
130	94.00	35.27	14.59	40.84	12.75	3.09	230.50	2.50	9.20	60.84	5.17
131	94.00	40.94	16.34	39.14	15.15	2.75	251.50	3.50	9.00	60.00	6.17
132	96.00	32.64	15.67	38.14	13.82	1.84	241.00	3.17	9.00	83.33	5.17
133	100.00	33.79	15.67	39.64	13.39	1.59	251.00	2.00	9.70	85.84	4.83
134	94.00	34.00	14.59	41.87	12.77	1.59	246.00	2.84	8.00	92.33	6.50
146	100.00	31.80	13.50	39.16	12.19	1.84	247.00	3.00	10.20	95.00	6.00
148	62.50	34.64	15.75	40.77	12.64	2.34	235.50	3.00	10.35	94.17	7.50
151	100.00	35.70	14.42	45.69	12.68	3.25	245.50	2.50	9.25	79.17	6.50
152	100.00	41.37	10.75	45.70	14.43	2.84	250.50	2.50	10.55	100.50	4.83
153	91.00	39.27	15.00	47.49	13.54	4.00	252.50	2.50	8.37	59.25	6.00
156	66.50	39.19	15.34	48.79	13.04	1.92	234.50	2.50	10.49	79.83	5.84
169	91.50	36.52	11.42	34.41	11.53	1.67	230.00	2.50	9.85	79.17	6.84
175	77.50	33.32	12.25	34.84	11.59	1.67	234.00	3.17	8.25	57.50	6.17
184	89.00	33.46	11.25	34.15	12.04	2.00	251.00	3.00	8.75	54.17	7.67
189	95.50	35.18	15.84	36.90	12.60	2.59	246.00	2.67	9.49	47.00	7.50
192	85.00	31.44	13.59	42.44	12.24	3.25	256.00	3.17	8.22	53.34	4.67
195	100.00	36.19	13.25	39.54	12.19	1.92	223.00	2.00	9.15	24.17	8.34
198	95.00	44.24	15.00	53.99	12.44	2.00	232.00	2.17	10.78	70.00	5.94
209	100.00	31.73	11.50	33.63	12.08	1.59	242.00	3.17	9.35	66.67	7.27

Contd.

Mean data for quantitative and qualitative traits

Genotypes	Weight of primary rhizomes (g)	Length of primary rhizomes (cm)	Girth of primary rhizomes (cm)	Number of secondary rhizomes	Weigh of secondary rhizomes (g)	Length of secondary rhizomes (cm)	Girth of secondary rhizomes (cm)	Rhizome diameter (cm)	Core diameter (cm)	Rhizome core ratio	Yield (Kg/plot)
2	137.50	9.82	7.27	8.50	81.67	7.40	6.40	2.55	1.62	1.58	7.25
15	117.50	8.79	7.10	8.17	103.17	8.28	6.79	2.49	1.47	1.70	6.50
22	130.00	9.38	8.98	6.17	74.17	7.10	8.08	2.78	1.75	1.76	8.77
52	135.00	9.00	7.98	9.77	96.50	6.34	6.55	2.29	1.30	1.76	4.27
75	108.33	8.64	6.60	7.00	75.84	7.10	6.90	2.23	1.04	2.15	4.52
88	155.00	10.77	9.05	6.67	80.00	7.28	6.73	2.20	1.10	2.01	9.00
89	122.50	8.45	7.35	6.50	82.50	7.27	5.95	2.22	1.49	1.50	8.08
114	205.83	10.07	8.70	7.67	115.00	7.37	5.42	2.37	1.45	1.63	8.16
120	219.50	9.85	8.50	8.84	144.00	8.15	4.75	1.20	1.59	0.76	4.18
121	118.34	7.79	7.20	7.34	86.67	6.10	4.70	0.50	0.70	0.73	1.68
122	110.50	7.10	6.89	6.17	74.34	4.65	6.10	0.65	1.00	0.65	1.37
130	58.34	5.25	5.15	5.43	38.34	5.45	3.90	0.90	0.65	1.07	0.57
131	62.50	5.70	3.35	7.50	40.84	5.10	2.95	1.45	0.50	2.90	3.71
132	149.50	8.45	8.69	5.84	104.17	6.30	6.95	2.50	1.60	1.57	4.75
133	184.50	8.64	9.25	6.10	96.67	6.35	6.25	2.55	1.50	1.66	4.16
134	167.84	7.42	8.10	6.95	108.67	6.15	7.35	2.55	1.42	1.80	2.36
146	190.00	7.69	8.27	5.93	122.67	7.05	7.00	2.15	1.10	1.96	2.17
148	156.00	7.13	7.50	6.33	92.34	6.02	6.70	1.87	1.05	1.79	2.55
151	95.00	8.14	7.47	7.27	76.67	4.67	3.40	1.99	0.95	2.10	1.63
152	137.50	8.55	7.60	6.95	75.00	5.22	3.89	1.82	0.95	1.92	3.04
153	122.50	9.74	7.12	6.11	78.33	5.02	3.68	2.17	1.45	1.46	3.81
156	163.34	8.99	9.10	7.05	129.17	5.97	4.85	1.85	0.85	2.19	7.39
169	105.00	7.19	6.10	6.44	85.00	4.92	4.67	1.50	0.60	2.51	5.42
175	92.50	6.97	4.20	7.90	72.50	4.85	4.25	1.59	0.62	2.58	1.93
184	90.00	7.09	4.15	8.67	61.67	5.30	4.25	1.45	0.56	2.59	4.30
189	92.50	6.87	4.50	7.13	60.84	4.67	3.55	1.45	0.45	3.26	1.75
192	119.17	6.14	8.30	6.17	62.67	4.55	4.90	2.15	1.22	1.77	2.64
195	40.00	4.77	5.08	4.60	20.84	2.95	1.89	1.16	0.40	2.89	3.38
198	156.84	9.10	9.70	6.17	104.00	7.65	7.05	2.20	0.82	2.70	5.32
209	130.00	8.22	5.07	6.59	74.17	5.30	4.42	1.45	0.47	3.13	3.15

ANNEXURE IV

Weather data during the cropping period (June 2000 to February 2002)

Month	Temp. °C (Max.)	Temp. °C (Min.)	RH (%)	Daily evaporation	Sunshine hours	Rainfall (mm)
June 2000	31.8	22.7	81.0	6.5	4.5	27.4
July	31.5	22.7	78.0	7.2	6.0	15.7
August	30.4	22.5	78.0	5.4	4.6	163.6
September	31.6	22.2	82.0	4.8	6.5	210.4
October	30.9	21.2	89.0	4.0	5.6	36.8
November	29.9	20.8	91.0	3.7	7.9	75.3
December	31.0	18.0	90.0	3.8	6.2	22.6
January 2001	30.3	19.7	88.0	4.3	7.2	-
February	33.5	20.0	87.0	4.5	6.7	-
March	35.3	22.1	80.0	6.8	7.4	-
April	34.7	23.6	82.0	5.6	8.6	96.0
May	35.0	23.5	78.0	6.8	4.9	6.5
June	31.2	22.1	80.0	6.9	5.6	52.6
July	31.2	22.7	85.0	6.8	6.7	19.9
August	31.4	22.3	89.0	6.0	6.8	22.8
September	32.7	22.1	90.0	5.1	6.3	96.6
October	31.0	21.6	92.0	4.3	6.4	286.7
November	29.5	18.7	90.0	3.8	6.2	136.6
December	28.2	19.2	88.0	3.6	7.5	16.1
January 2002	30.3	19.8	86.0	3.9	7.1	-
February	31.6	21.3	84.0	4.9	9.4	-

ANNEXURE V

LIST OF ABBREVIATIONS

DNA	-	Deoxy ribonucleic acid
RAPD	-	Randomly Amplified Polymorphic DNA
PCR	-	Polymerase Chain Reaction
SAHN	-	Sequential Agglomerative Non-over lapping clustering
UPGMA	-	Unweighted Pair Group method with Arithmetic Average method
PDA	-	Potato Dextrose Agar
PDI	-	Per cent Disease Index
GCV	-	Genotypic Coefficient of Variation
PCV	-	Phenotypic Coefficient of Variation
ECV	-	Environment Coefficient of Variation
PCA	-	Principal Component Analysis
PC	-	Principal Component