

**GENETIC VARIABILITY AND CORRELATION
STUDIES IN TURMERIC**

THESIS

**Submitted to
Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola
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**MASTER OF SCIENCE
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DECLARATION OF STUDENT

I hereby declare that, the experimental work and its interpretation in the thesis entitled "**GENETIC VARIABILITY AND CORRELATION STUDIES IN TURMERIC**" or part thereof has neither been submitted for any other degree or diploma of any University, nor the data have been derived from any thesis / publication of any University or scientific organization. The source of materials used and all assistance received during the course of investigation have been duly acknowledged.

Place: Akola
Date : / /2019

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CERTIFICATE

This is to certify that, the thesis entitled "**GENETIC VARIABILITY AND CORRELATION STUDIES IN TURMERIC**" submitted in partial fulfilment of the requirement for the degree of "**Master of Science in Horticulture (Vegetable Science)**" of Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola is a record of bonafide research work carried out by **Rathod Pavan Vanraj** under my guidance and supervision.

The subject of the thesis has been approved by the Student's Advisory Committee.

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(C) Abbreviations

%	-	per cent
@	-	at the rate
⁰ Brix	-	Degree Brix
⁰ C	-	Degree Celsius
⁻¹	-	per
Anon.	-	Anonymous
CD	-	Critical Difference
cm	-	Centimetre
cm ²	-	Centimeter square
CV	-	Cultivar
DAP	-	Days after planting
d.f.	-	Degree of freedom
ECV	-	Environmental coefficient of variation
<i>et al.</i>	-	et alia (And others)
etc	-	Etcetera
Fig.	-	Figure
g	-	Gram
GCV	-	Geneotypic coefficient of variation
h ²	-	Heritability estimate (broad sense)
ha.	-	Hectare
ha ⁻¹ .	-	Per hectare
i.e.	-	Id est. (that is)
kg	-	Kilogram
m	-	Meter
M.S.S	-	Mean sum of square
mg	-	Miligram
MW	-	Meteorological Week
No.	-	Number
NS	-	Non Signifiant
PCV	-	Phenotypic coefficient of variation
pH	-	puissance de hydrogen

q	-	Quintal
R	-	Correlation coefficient
R	-	Residual factor
RBD	-	Randomized Block Design
Res.	-	Research
Rs.	-	Rupees
S.S	-	Sum of square
SE(m)+	-	Standard error of mean
Sig	-	Significant
Treat.	-	Treatment
ViZ.,	-	Videlicet (Namely)
AKTL	-	Akola Turmeric Line

D) Glossary

Additive gene effect: Effect of different polygenes affecting a quantitative character being cumulative or additive in nature. It refers to straight line function of polygenes.

Additive variance: Average effect of alleles on all segregating loci. It results when there is lack of dominance.

Analysis of covariance: A statistical procedure that splits the conversation of two variables into different components.

Analysis of variance: A statistical procedure that splits the total variation into different components.

Broad sense heritability: The ratio of genotypic variance to the phenotypic variance.

Correlation: The degree of qualitative association ship among different variables of attributes.

Correlation analysis: The statistical analysis to find out the degree of relationship and the direction of relationship between two variable.

Correlation coefficient: A statistical measures of degree of the relationship between two or more series of variable.

Co-variance: The sum of the products of deviation of two or more correlated variables from their means divided by the number of degrees of freedom.

Genetic advance: A genetic parameter which depicts the improvement in performance of selected lines over the original, population, used to predict the effect of selection.

Genetic shift: The change in genetic makeup of varieties breeds for a particular environment if grown over long period in areas outside their adaptation.

Genetic variability: A measure of variation in population that is due to genotype which can be studied by using different genetic parameters like, genotypic coefficient of variation, heritability, genetic advance, etc.

Genotype: The genetic constitution i.e. gene make up of an organism.

Genotypic variance: Component of total variance due to genetic difference among the genotype.

Germplasm: A collection of genotype of an organism.

Heritability: The proportion of total phenotypic variation that is due to genotype.

Narrow sense heritability: The ratio of additive genetic variance to phenotypic i.e. total variance.

Oligogenes: Genes having large individual effect qualitative characters which show distinct classes are governed by these genes.

Partial correlation coefficient: The correlation between two series of variables independent of the accompanying variation due to other variables.

Path coefficient: Statistical analysis, which provides an effective means of entangling direct and indirect cause of association and at the same time measures the relative importance of each causal factors.

Phenotype: The observed characters of an individual without reference to its genetic nature.

Phenotypic variance: The phenotypic variation of metric traits among the genotype i.e. total variance which is ascribed due to sum total effect of genotypic variance and environmental variance.

Pleiotropic: The phenomenon of single major gene affecting more than one characters.

Polygenes: A series of multiple genes with small and cumulative effect of which produce continuous variation in the phenotypes, quantitative characters are governed by these genes.

Range: The difference between the largest and smallest item of the series.

Selection: It aims at isolating the desirable ones from the mixture of numerous genotypes in the population.

Simple correlation coefficient: The total correlation between two series of variables.

Variance: A measure of variability which is the average of the square of deviation of the observations from the mean of a sample drawn from a population.

Variation: Occurrence of difference among individual of the same species, sub species, etc. for one or more traits.

Yield component: The component or attributes which finally make up or control yield of any crop.

(F) Thesis Abstract

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- b) Full name of student : Rathod Pavan Vanraj
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ABSTRACT

The present investigations entitled “Studies on genetic variability and correlation studies in turmeric (*Curcuma longa* L.)” were carried out in a RBD with two replications at the Instructional Farm, Department of Vegetable Science, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola during Kharif season, 2018 to evaluate twenty genotypes of turmeric including two checks i.e. PDKV Waygaon and Pratibha for different traits.

The highest genotypic coefficient of variation as well as phenotypic coefficient of variation was observed for leaf area, number of primary rhizome, girth of primary rhizome, length of primary rhizome, length of mother rhizome, weight of primary rhizome and weight of mother rhizome. The highest estimates of heritability recorded for leaf area followed by length of primary rhizome, girth of primary rhizome, yield of finger rhizome per plant and weight of mother rhizome. Highest genetic advance was also observed for the characters leaf area followed by number of primary rhizome, girth of primary rhizome. However it is ranged from (2.88 to 98.61%) for all the characters.

From the genotypic and phenotypic correlation studies between yield contributing traits it is revealed that, total rhizome yield per hectare was positively and significantly associated with leaf area, number of mother rhizome, weight of mother rhizome, number of primary rhizome, weight of primary rhizome, length of primary rhizome weight of primary rhizome, yield of rhizomes per plot and yield of finger rhizome per plant. However the characters like plant height at 180 DAP, Number of leaves at 180 DAP and number of tillers had positive and non- significant correlation with rhizome yield per hectare.

Path analysis revealed that positive direct effect on rhizome yield per hectare through plant height at 180 DAP, number of leaves at 180 DAP, weight of mother rhizome, yield of finger rhizome per plant and yield of rhizome per plot.

The genotypes *viz.*, PDKV Waygaon, AKTL-13, AKTL-8, AKTL-11, AKTL-17, AKTL-19 and Gondia Haladi-1 on the basis of yield and yield contributing characters found promising for future improvement programme. Hence, these genotypes may be given consideration while formulating selection indices for the improvement of yield in turmeric.

CHAPTER I

INTRODUCTION

1.1 Background Information

Turmeric (*Curcuma longa* L.) is one of the most important spice crops in India belonging to the family Zingiberaceae and plays a vital role in the national economy. Probably, it has been originated in the slopes of hills in the tropical forests of West Coast of South India (Stahl, 1980).

Turmeric is a herbaceous perennial with a rhizome form which arises tufts of large broad, lanceolate, bridges, acute, at both ends. The plant grows up to 60-90 cm height. Leafy shoots are erect, bearing 6-10 leaves forming pseudostem having small lobes (1mm). The sheath near the ligule has ciliate margins and it is cylindrical spike, 10-55 cm long, 5-7 cm wide and terminal on leafy shoot. The flowers are yellow, born in a spike. They arise from two buds situated at axils of bracts and mature successively. Bracts are the innermost tinged with pink. The bracteoles are thin and elliptical. The calyx is short and unequally toothed down on one side. The corolla is tubular at the base and the upper half cup shaped. The lip or labellum is obovate. The ovary is inferior and trilobular with a slender style held by anther lobes between them. Fruits are seldom. The primary tubular at the base of the aerial stem is ellipsoidal, little curved, with secondary branches in two rows and further tertiary branches are present. Rhizomes have a distinctive taste and smell, brownish and scaly outside and the inside is bright orange colour fleshy, often ending in a swollen starchy tuber.

It is a tropical crop and needs a warm and humid climate with an optimum temperature, of 20° to 30°C for normal growth and satisfactory production. It thrives best on sandy, loamy and alluvial, loose, friable and fertile soil rich in organic matter status and having a pH 5 to 7.5. Alkaline soil is not suitable for its cultivation. The crop can not withstand water logging. It grows at all places ranging from sea level to an altitude at 1200 meter above the mean sea level. As a rainfed crop, turmeric needs a well distributed annual rainfall of 250 to 400 cm for successful production.

Turmeric is an exhaustive crop and responds well to fertilizer application. It requires heavy manuring for high yield (Rao and Reddy, 1977), Curcumin percentage of turmeric was found to be influenced by fertilizer application. Mulching is highly beneficial for increasing yield (Mohanty *et al.*, 1991).

Turmeric is very much identified with human civilization, religion, customs and it finds use both in developed and underdeveloped countries. It is grown for underground stem called as rhizomes, which are used to impart flavour and colour to foodstuffs after clearing, boiling, drying, polishing and powdering. It is a principal ingredient in curry powder. Turmeric oleoresin is used in brine pickles and to some extent in non-alcoholic beverages, gelatins, butter and cheese, etc. The colour curcumin extracted from turmeric is used as a colourant. Turmeric is also used as a dye in textile industry. It is used in the preparation of medicinal oils, ointments and poultice. It is stomachic carminative, tonic, blood purifier and an antiseptic. It is also used in cosmetics. The aqueous extracts have biopesticidal properties.

Turmeric occupies a dominant position due to its matchless properties accounting for 70 per cent of global production. In India turmeric having area of 238 ha and production of 1133 MT. (Anon, 2017-18). India exported 1,07,300 tonnes of turmeric valued at Rs.103.56 lakhs during 2017-18 (Spice Board). From India's total turmeric exports, 65% exported to UAE, USA, Japan, Srilanka, UK, and Malaysia. States like Andhra Pradesh, Tamil Nadu, Orissa, Karnataka, Kerala, Maharashtra and West Bengal are in the forefront in turmeric cultivation. In Maharashtra, Sangli, Hingoli, Nanded, Chandrapur, Yavatmal and Washim are the leading turmeric producing districts.

The medicinal value of turmeric has been recognised time immemorial in the Indian system of medicine. Turmeric or haldi powder, boiled in milk along with a dash of black pepper powder may be taken 2-3 times a day for sore throat, cough, cold, pharyngitis, laryngitis and other acute respiratory infections. It's most useful in the form of worm prate in spraining and bruises. In small pox and chicken pox a coating of turmeric is applied to facilitate the process of scabbing. A paste made by its flower is

used in ringworm and other parasitic skin disease. In piles an ointment made of turmeric hamp leaves, onion and warm linseed oil gives great relief when piles are painful and protruding. Its medicinal properties are also used as a stomachic tonic and blood.

The yellow-colouring matter curcumin and volatile oil (essential oil) are exclusively present in the rhizome of turmeric. The rhizome has curcumin (3-9%), essential oil (5-6%) and oleoresin (6-12%).

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 2 breeding programme can take shape in this clonally propagated crop.

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 genetic improvement of any crop depends upon its judicious exploitation of the magnitude of genetic variability in the economic characters through efficient breeding methods. In modern farming system, few high yielding varieties dominate in cultivation which often lead to genetic homogeneity. It is also well established that genetic homogeneity leads to genetic vulnerability to biotic and abiotic stresses, in any crop breeding programme, germplasm serve as the most valuable reservoir in providing variability for various traits. Proper screening and evaluation of germplasm lines would provide an estimate of their potential value as suitable genotypes for utilization in varietal developmental.

1.2 Need and importance of study

Study the extent of variability particularly important in yield and yield contributing characters is basic to plan out future improvement programme in any crop. Selection from quantitative characters is less efficient, if it is based on phenotypic expression. Hence, it is necessary to access the relative extent of genetic and non genetic variability exhibited by individual characters. This could be achieved by estimation of genetic variability using suitable parameters like genotypic coefficient of variation, heritability in broad sense and expected genetic advance for individual characters. Although genetic coefficient of variation is indicative of presence of degree of genetic variation, the amount of heritable portion of variation can only be determined with the help of estimates and genetic gain. Therefore, for development of high yielding varieties, it is necessary to study the genetic variability for yield and yield contributing characters for further exploitation in breeding programme. Similarly, it is also necessary to work out genetic association between yield and yield components which will be very effective for the improvement of crop.

The correlation coefficient gives an idea of the nature and intensity of association between two or more quantitative characters. Correlation simply measures the mutual relationship between yield and yield contributing characters. Such correlation studies are very helpful and furnish ready information as to which characters should be chosen for selection to bring about the maximum increase in yield Thus, correlation

helps in the selection of superior genotypes from diverse genetic populations.

The simple correlation coefficients do not express anything about the temporary relationship between characters. As there are number of factors involved in correlation studies, their indirect association become more complex and confusing but path coefficient analysis helps to avoid this complication by measuring the direct influence of one characters upon other as well as permits the partitioning of given correlation coefficients into its components of direct and indirect effects. The overall path coefficient analysis studies specify the causes and measures the relative importance of each temporary factors. The path coefficient analysis is an effective means of analyzing direct and indirect causes of association and permits the critical examination of specific that produces a given correlation. The path analysis provide information about magnitude and direction of direct and indirect effects of yield components, which cannot provide by correlation.

Being cross pollinated crop, turmeric exhibits considerable variation for different traits. So far only a very few attempts have been made to improve the local types and number of released varieties available for commercial cultivation are also limited. Therefore exploitation of variability and correlation involving locally adapted turmeric genotypes for commercial cultivation is priority area of research in improving the uniformity and fruit quality. In view of above facts, the present investigation was under taken with twenty genotypes to study the Genetic Variability and correlation studies in Turmeric with following objectives :

1.3 Objectives

- To investigate extent of genetic variability among available genotypes of turmeric.
- To estimate genotypic and phenotypic correlation coefficient and path coefficient of yield and yield components in turmeric.

1.4 Scope and Limitations

The results obtained from study will be useful as a guideline to turmeric breeder for selection of diverse genotypes. Genetic variability is important to select characters which are heritable. Unless and until there is large amount of variability present in the population, the breeder has little scope in breeding for high yielding varieties. Genetic association and path analysis play significant role to study interrelationship contribution of each characters and thus simultaneously for bringing crop improvement. For the improvement of rhizome yield in turmeric, it is necessary to gather information regarding association of various quantitatively inherited characters with rhizome yield.

Turmeric has received little attention in crop improvement as compared to other spice crop. The collection and procurement of genotypes from various places is very difficult in case if it is not available in country.

The close attention of all characters and narrow variability would be poorer to be limiting factor. However, on basis of weight of rhizomes, yield of rhizomes and after harvest quality characters can be thoroughly studied and better elite type can be identified for further selection.

1.5 Hypothesis

Data of genetic variability available would assist in selection of parents in crop improvement programme. Screening of these genotypes can help in identifying a better source for various characters viz. days to harvest and number of mother rhizome per plant. Thus the genotypes which show variability in morphological characteristics could be used directly in further turmeric improvement programme. The study of heritability and genetic advance would assist them in determining the scope of further selection process. Genetic improvement in any crop depends on variability present in that crop and thereafter selection of parental lines for crop improvement programme.

Study for effective selection of genetic material variability particularly improvement in yield and yield contributing characters is basic plan for future programme in crop improvement. Correlation is helpful in furnishing ready information as which characters should be chosen for selection to bring about the maximum increase in the yield. Path coefficient analysis help to avoid complications by measuring direct influence of one characters upon other as well as permits the partitioning of given correlation coefficients into its components of direct and indirect effects.

CHAPTER II

REVIEW OF LITERATURE

The information available in the literature in the pertaining to turmeric germplasm for yield and quality traits have been reviewed here under the following sub heads

2.1 Genetic variability studies

2.2 Correlation and path analysis studies

2.1 Variability studies

Mohanty and Sharma (1979) conducted an experiment on the genetic variability and heritability for 14 characters in 28 cultivars of ginger. They found a good amount of genetic variability among the cultivars. They reported that expected genetic advance and heritability estimates were high for number of secondary rhizome and total root weight. Genotypic coefficient of variation was high for weight of root tubers.

Shree Kumar *et al.* (1980) evaluated 30 ginger cultivars. The results indicated that the cultivars 'Thingpui', 'Rio-de-Janeiro' and 'China' were suitable for the production of fresh ginger. He found a considerable amount of variability among the cultivars.

Mukhopadhyay *et. al.* (1986) carried out analysis of data on yield/plant, total plot yield and five related traits from 25 germplasm types collected from southern and eastern India grown in West Bengal and revealed significant variation for shoots/clump, leaves/shoot, plant height and yield/plant. Genotypic coefficient of variation (GCV) was highest for total plot yield. Heritability estimates were moderate, being 58.7%, the highest value for shoots/clump.

Phillip and Nair (1986) conducted trails at Vellanikara, Kerala and collected data on 31 quarantine characters in *Curcuma longa* and *C. aromatica* genotypes. Considerable variation was observed for fresh by yield per 3.6 x 1.6 m plot (3.83 – 28.86 kg), curcumin content (2.33 - 6.55%), number of secondary fingers/plant (7.90 -20.9), curing percentage (14.06 -28.17) and intensity of leaf blotch infection. Heritability estimates

were highest for curing percentage (0.99), curcumin and oleoresin contents (both 0.98). Data on genetic advance indicated that selection within the existing germplasm would lead to improvements in plant height, yield, curing percentage, leaf blotch resistance, curcumin and oleoresin contents.

Ratnambal (1986) carried out analysis of 120 accessions of *curcuma domestica*, 44 of *C. Aromatica* and 20 of other *Curcuma* species and showed that *C. domestica*, accessions had higher curcumin contents than those of *C. aromatica*; the content was highest in the *C. aromatica* variety. Endapalayam (10.3%).

Geetha and Prabhakaran (1987) studied association of eighteen bio-metric characters with yield in 19 turmeric varieties under Kerala condition. Their study revealed that highest genotypic coefficient of variation (GCV) was recorded for yield followed by number of nodes per mother rhizome. The yield also recorded highest phenotypic coefficient of variation (PCV). Highest heritability was noticed for girth of mother rhizome followed by plant height in which the latter recorded high genetic advance.

Reddy *et al.* (1988) studied 13 varieties and reported that the phenotypic coefficient of variation was in general higher than the genotypic coefficient of variation. The genetic coefficient of variation was very high for weight of root tubers followed by rhizomes yield, leaf area, number of primary fingers and number of tillers indicating high degree of genetic variability for these characters. A high heritability in broad sense was also observed in their study for weight of root tubers, rhizomes yield, crop duration, number of leaves and number of primary fingers

Jalgaonkar and Jamdagni (1989) carried out the experiment with yield and 11 yield related characters in 10 turmeric genotypes in the field and found that all the characters except weight of mother rhizome and yields of primary and secondary fingers per plant showed high heritability.

Rattan (1989) studied and recorded data on 10 varieties of ginger during year 1987 and 1988 on plant height, number of leaves, tillers per plant, leaf width, rhizome length, rhizome width and yield. He found

significant differences for all the characters except number of tillers per plant during both the years and number of leaves per plant during 1987.

Jalgaonkar *et al.* (1990) derived information on heritability, genetic variance and yield correlations from data on 12 yield components in 10 genotypes of turmeric and found that cured yield was significantly and positively correlated with yield of secondary fingers.

Maurya (1990) conducted a research trial with 10 lines and the control variety Dholi Local. RH-10 was superior with regard to fresh rhizome yield (41.98 t/ha) and dry rhizome yield (7.53 t/ha). RH-10 also had the shortest growth period duration (288 days).

Indiresh *et al.* (1992) found maximum genetic potentiality in rhizome yield, length of secondary and primary fingers, weight of mother rhizome and inter-nodal distance of primary fingers. Phenotypic coefficient of variation was in general higher than the genotypic coefficient of variation. Moderate values of heritability were observed in nodes, girth and number of secondary fingers, number of primary fingers, plant height and nodes in mother rhizome.

Pandey and Donbhal (1993) screened 29 collections of ginger for variability analysis. They found a wide range of variability existing among the cultivars for most of the characters, such as plant height, number of leaves per plant, number of tillers per plant, leaf area, length, girth and width of rhizomes etc.

Singh (1993) studied 103 genotypes of turmeric in 2 years for the evaluation and characterization of the genotypes. He found that considerable variability occurred in case of weight of secondary, primary and mother rhizomes, number of tillers per plant and fresh rhizome yield for girth of secondary rhizome. The magnitude of variability was of low order. While the estimates of variability were moderate for plant height, number of leaves per plant, number of primary rhizome per plant, length of mother, primary and secondary rhizomes, core diameter of mother, primary and secondary rhizomes.

Yadav and Singh (1996) grown seventeen turmeric genotypes in Manipur during the season of 1984 and evaluated for yield and yield contributing characters to study genetic variability, heritability and genetic advance. Significant differences were found among the genotypes for all the characters studied except width of leaves. Yield per plant and plant height exhibited a wide range of variation. The genotypic coefficient of variation was high for yield per plant and moderate for width and length of rhizome, number of suckers per plant and dry matter recovery. Yield per plant had high genetic advance and length and width of rhizome showed high heritability. The study indicated that selection for width and length of rhizome would be effective.

Nirmal and Yamgar (1998) studied eighteen new genotypes of turmeric and two standard varieties were evaluated at the Agricultural Research Station, K. Digraj, Sangli during 1985-88 and observed significant variability for plant height, number of leaves, length and breadth of leaf, number of tillers and fresh yield of turmeric. CLS-19, CLI- 320 and CLI-324 were identified as promising varieties.

Subramanian *et al.* (1998) conducted the variability analysis in two turmeric varieties 'BSR-T and 'CO-T for yield and other attributes and reported that the heritability in terms of percentage was found to be greater in diameter of mother rhizome followed by volume of secondary rhizome. Data on genetic advance in terms of percentage of mean revealed that diameter of mother rhizome had the highest value followed by total dry matter production and number of secondary rhizome. As such the genetic advance had the maximum value in total dry matter production followed by harvest index.

Lynrah and Chakrabarty (2000) evaluated the performance of turmeric genotypes in a field experiment conducted during 1994-1995 in Jorhat, Assam, India. Twenty five genotypes were used, including 23 of *Curcuma longa*, one of *C. aromatica* and one semi-wild genotype of *C. caesia*. The results revealed that there was significant variation with respect to growth, yield and quality parameters due to genotypes and years. Among the genotypes Black Turmeric, a semi-wild type, showed the

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 gave the lowest fresh yield.

Singh *et al.* (2003) undertaken investigation on sixty five genotypes of turmeric (*Curcuma longa* L.) with a view to assess the genetic parameters in respect of yield and yield determining characters. Characters like yield (q/ha), weight of secondary rhizome/plant (g) and number of secondary rhizomes per plant exhibited wide range of variability, maximum genotypic and phenotypic coefficient of variability, heritability and genetic gain (as per cent of mean) indicated that the individual plant selection based on these characters can effectively bring about genetic improvement in turmeric.

Hikmat *et al.* (2012) conducted an experiment to determine the extent of genetic variation and relationship among turmeric genotypes using 21 qualitative and quantitative traits. A total of 20 genotypes collected from three eco-geographical areas (Bannu, Haripur and Kasur) of turmeric cultivation in Pakistan were studied under field conditions. A considerable level of variability was displayed by various genotypes for some of the quantitative traits measured. Pattern of variation among the genotypes was different for different agro-morphological traits.

Rajyalakshmi *et al.* (2013) raised eight turmeric genotypes in a randomized block design to study the variability, heritability with genetic advance, correlation, direct and indirect effects of characters on rhizome yield for a period of four year. Variability accompanied by higher values for genetic coefficient of variation was recorded for rhizome yield. Heritability and genetic advance were high for rhizome yield and number of tillers per plant. In general, genotypic correlations were higher than phenotypic correlations for all the characters studied.

Prajapati *et al.* (2014) studied genetic variability, correlation and path analysis for rhizome yield and its component characters in 30 diverse genotype of turmeric. The analysis of variance revealed the significant differences among the genotypes for all the traits indicating presence of sufficient variability among the genotypes for various traits. On

the basis of the performance the accessions NVST 6, NVST 43, NVST 27, NVST 26 and Sugandhum found promising in rhizome yield. The high GCV and PCV were observed for weight of secondary rhizome per plant, weight of mother rhizome per plant, weight of primary rhizome per plant, dry rhizome yield per plant and initial weight of rhizome, Whereas, plant height, leaf width, leaf length and curcumin content showed low GCV and PCV.

Singh *et al.* (2014) evaluated twenty seven genotypes of turmeric (*Curcuma longa* L.) to estimate the variability and inheritance pattern, to suggest suitable breeding strategies and to identify productive genotypes.

Verma *et al.* (2014) evaluated experimental material comprised of 83 turmeric genotypes at Faizabad (U.P.), India during 2011-12. The highest magnitude for coefficient of variation at genotypic (GCV) and phenotypic levels (PCV) was observed for number of tertiary rhizomes per plant followed by number of tillers per clump and number of secondary rhizomes per plant.

Bahadur *et al.* (2015) arranged accessions in a randomized complete block design with three replications. Significant mean square of accessions for all the traits studied indicates the existence of sufficient genetic variability among the studied accessions. The rhizome yield exhibited highly significant and positive association with plant height, number of leaves plant⁻¹, number of tillers plant⁻¹, weight of rhizomes plant⁻¹, length of primary rhizome, and dry matter recovery.

Sharma *et al.* (2015) Conducted study on genetic unpredictability, heritability and correlation coefficient in turmeric (*Curcuma longa* L.) in Allahabad agro- climatic condition study including mean, genotypic and phenotypic variances, coefficient of variation, heritability and genetic advance was performed on genetically diverse nineteen genotypes of turmeric. Considerable differences were found among the genotypes for all the traits. The phenotypic coefficient of variation (PCV) was much greater than genotypic coefficient of variation (GCV) for all traits.

Hachinamani *et al.* (2016) evaluated nineteen genotypes of turmeric (*Curcuma longa* L.) to estimate the variability and inheritance pattern, to suggest suitable breeding strategies and to identify productive genotypes. Variability accompanied the PCV estimates were higher than GCV indicating the role of environment.

Neethu *et al.* (2017) carried out study to assess the genetic variability of wild turmeric in Kerala State of India in relation to growth and yield characters. Sixty two accessions of wild turmeric collected from different locations of Kerala were grown in RBD and assessed for variability in terms of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (H^2) genetic advance (GA).

Salimath *et al.* (2017) raised nineteen turmeric genotypes in randomized block design to study the Variability, Heritability and Genetic advance of growth and yield characters during the year of 2012-13. Variability accompanied the PCV estimates were higher than GCV indicating the role of environment.

Venugopal *et al.* (2017) estimated genetic variability, heritability and genetic advance for yield and quality traits in five turmeric germplasm. Wide genetic variation was observed for all genotypes like plant height, yield per plot, number of leaves per plant and curcumin content. Considering genetic parameters, high GCV was found for curcumin content (52.69%) followed by yield per plot (19.07), number of primary rhizomes per clump (14.20) and number of leaves per plant (14.02) respectively. In all cases, phenotypic variances were higher than genotypic variances except girth of primary rhizome which were found exactly same.

Aarathi *et al.* (2018) conducted study to assess variability, correlation and path analysis of 24 yield and quality characters in turmeric using 15 genotypes. Wide genetic variability was observed among the genotypes for most of the characters studied. High GCV and PCV was observed for 17 characters except for plant height, leaf length, leaf width, primary rhizome length, secondary rhizome girth, diameter of inner core of primary rhizome and diameter of primary rhizome.

Athira *et al.* (2018) conducted an experiment to assess genetic variability accessions of *Curcuma zanthorrhiza* accessions of Central Kerala, India in relation to growth and yield characters. Eighty four accessions of *Curcuma zanthorrhiza* collected from the central part of kerala were grown in RBD and assessed for variability in terms of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance in case of the characters studied indicated the presence of considerable variability in genetic resources of this important crop in range shown by characters indicates the involvement of higher number of contributing alleles and higher involvement of environmental factors in the expression of characters.

Luiram *et al.* (2018) evaluated thirty two (32) genotypes of turmeric from all the north eastern state of India along with Duggirala Red as check variety to study the genetic parameters in respect of yield and yield attributing characters. Fifty three (53) traits were analyzed for phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) and expected genetic advance at 5 per cent selection intensity.

Maurya *et al.* (2018) conducted study to determine the extent of genetic variability in turmeric genotype using 14 qualitative and quantitative characters. A total of 22 genotypes collected from four different regions were studied under field condition. A considerable level of variability for various characters was observed among different genotypes. The higher magnitude of coefficient of variation at phenotypic as well as genotypic levels were observed for number of tertiary rhizome per plant, number of secondary rhizome per plant, weight of primary rhizome per plant, number of primary rhizome per plant, number of leaves per shoot and number of tillers per clump. In general, the phenotypic coefficient of variability was higher than genotypic coefficient of variation.

Vamshi *et al.* (2018), investigated nineteen genotypes of turmeric (*Curcuma longa* L.) with a view to assess the genetic parameters in respect of yield and yield determining characters. The highest percentage of phenotypic and genotypic coefficient of variation was

observed in number of tillers, leaf area, number of secondary rhizomes, length of mother rhizome, fresh weight of rhizome per plant, dry weight of rhizome per plant, yield per plot, estimated yield per ha, curcumin content, and oleoresin content.

2.2 Correlation and path analysis studies

Muralidharan *et al.* (1980) in an analysis of correlation coefficient among the morphological characters and yield found that whatever significant positive correlations among yield and morphological characters established, were mainly due to substantial positive contribution by plant height and number of fingers either directly or indirectly. Based on this it was concluded that plant height (or pseudostem) in turmeric is a single important morphological character for which selection for yield could be made.

Rattan *et al.* (1980) reported that the number of leaves per plant has maximum direct effect to the fresh rhizome yield per plant followed by the rhizome width. They also indicated that to improve the yield per plant, an emphasis should be given to increase the number of leaves per plant and the rhizome length.

Pathania *et al.* (1981) studied on correlation and path-coefficient analysis in 23 varieties of turmeric and revealed that rhizome yield was positively correlated with number of tillers, number of leaves, plant height, leaf size and number of secondary rhizomes. Height had the most direct effect on yield.

Aoi *et al.* (1986) studied four turmeric cultivars at Tanegashima Station and classified them into two groups. One group contained two cultivars which were characterized by large plant size and a low curcuminoid content in the rhizome. The other group contained the two cultivars which were smaller and had a high curcuminoid content. A definite correlation was found between rhizome size and curcuminoid content.

Lal *et al.* (1986) carried out path coefficient analysis of 6 characters in 13 turmeric varieties and showed that rhizome length and

number of fingers per rhizome had the highest direct positive effect on rhizome yield per plant.

Mukhopadhyay and Roy (1986) evaluated 25 cultivars of turmeric and observed a high correlation between plant height and yield/plant at both the genotypic ($r=0.83$) and phenotypic ($r=0.99$) levels. Plant height had the maximum direct effect on yield, as revealed by path analysis, followed by tillers/clump. Tillers/clump, leaves/shoot and plant height are recommended as selection criteria for improving yield.

Jalgaonkar and Jamdagni (1989) conducted an experiment with yield and 11 yield related characters in 10 turmeric genotypes and found that all the characters except weight of mother rhizome and yields of primary and secondary fingers per plant showed high heritability. Secondary fingers per plant was the only character which showed a significant and positive correlation with cured turmeric yield ($r = 0.75$).

Jalgaonkar *et al.* (1990) derived information on heritability, genetic variance and yield correlations from data on 12 yield components in 10 genotypes of turmeric and found that cured yield was significantly and positively correlated with yield of secondary fingers.

Pandey and Donbhal (1993) conducted path coefficient analysis for yield and its 10 component characters in ginger cultivars. Their study revealed that weight and width of rhizome and width were the strongest forces, influencing the fresh rhizome yield per plant.

Singh (1993) conducted the path coefficient analysis with 103 genotypes of turmeric and found that only three characters viz., weight of mother, primary and secondary rhizomes per plant had a strong and positive direct effect on the fresh rhizome yield per plant during both the years. These three characters were found to be major contributing on fresh rhizome yield per plant.

Nandi *et al.*, (1994) studied fourteen cultivars of turmeric to determine whether correlations exist between rhizome characteristics and yield. It was found that the girth and weight of daughter rhizomes were

correlated with rhizome yield. It was concluded that the girth and weight of daughter rhizomes are important characteristics in the selection of high yielding plants.

Singh and Tiwari (1995) derived information on yield correlations from path analysis of data on 22 yield related characters in 103 genotypes. Weight of mother, primary and secondary rhizomes per plant had the highest positive direct effect on rhizome yield.

Shashidhar and Sulikeri (1997) carried out an experiment on turmeric to study the relationship between growth and yield attributing characters of turmeric and revealed that rhizome yield was positively correlated with plant height, number of leaves, number of tillers, leaf area, spread of rhizomes, number of mother, primary and secondary rhizomes, rhizome size and dry matter accumulation.

Lynrah *et al.* (1998) studied twenty-five genotypes of turmeric at Jorhat and found that yield and curcumin content were negatively correlated with each other.

Venkatesha *et al.* (1998) analysed multiple correlation between yield and other attributes of 10 turmeric cultivars and revealed that fresh rhizome yield had a positive and non-significant correlation with plant height, petiole length and leaf area in first year trials in 1991. In second year trial i.e.1992, yield had positive and significant correlation with plant height, leaves/clump, leaf area and petiole length. Among the yield attributes, length of primary fingers, weight of mother rhizomes and primary fingers had positive and significant correlation with yield in both years. Plant height exhibited positive and significant correlation with number of leaves/clump, leaf area, petiole length and weight of mother rhizomes.

Chandra *et al.* (1999) studied the performance of twenty-five genotypes at Barapani for three consecutive years and found that among the 19 characters studied, plant height, length of leaf and length, diameter and weight of primary finger rhizome, inter-nodal distance of primary finger rhizome and rhizome yield per hectare were significantly and positively

correlated with fresh rhizome yield per clump. A negative correlation between dry rhizome recovery and fresh rhizome yield per clump was observed.

Hazara *et al.* (2000) carried out an investigation on 22 genotypes of turmeric (*Curcuma longa*) during 1993-94, to elucidate the role of different growth characters as components of rhizome yield. Genetic variability, correlation and path coefficients were studied to assess the genetic parameters, intensity and direction of association and direct and indirect relationships in respect of growth characters and yield, leaves per clump at 180 days after planting (DAP) revealed a moderately high broad sense heritability estimate and maximum genetic gain which indicated its reliability as a selection index of the growth characters, only leaves per clump at 180 DAP exhibited significantly positive phenotypic correlation with rhizome yield. Path coefficient analysis also revealed that this growth character registered maximum direct contribution to rhizome yield. From this investigation, leaves/clump at 180 DAP emerged as an important rhizome yield component of turmeric

Jana *et al.* (2001) conducted an experiment on 11 turmeric cultivars to assess the degree of mutual associations in relation to yield and yield determining characters, at Nadia, West Bengal. Observations were recorded on fresh rhizome, yield/ha, number of primary fingers/plant, weight of secondary fingers/clump, and number of secondary fingers/plant. The fresh rhizome yield was significantly correlated to length of secondary fingers and weight of primary and secondary fingers/clump.

Manjunathgoud *et al.* (2001) determined the morphological yield in correlation with rhizome yield of turmeric and found that fresh rhizome yield was positively correlated with plant height, whereas it was positively and not significantly correlated with leaf area, length of primary and secondary fingers, number of leaves, tillers, primary and secondary fingers. On the other hand, it was negatively correlated with number of mother rhizomes. Plant height was positively and significantly correlated with length of primary fingers, leaf area, number of leaves, tillers, primary

and secondary fingers and dry weight of aerial parts as well as rhizome. Similarly, the leaf area, number of leaves, tillers, mother rhizomes and secondary fingers, length of secondary fingers, dry weight of aerial parts, roots and rhizomes showed a positive and significant correlation among these characters.

Raveendra *et al.* (2001) conducted an experiment at Arabhavi, Karnataka to evaluate the correlation among 14 growth and yield related traits in 16 cultivars of turmeric and revealed that all traits were positively correlated with yield but such correlations were either significant or non-significant.

Shanmugasundaram *et al.* (2001) reported that partitioning of the correlation coefficient value into direct and indirect effects of yields. Associated characters in the path analysis showed the weight of primary, secondary and mother rhizomes as the major yield components of turmeric due to their high direct effect on yield.

Hazra *et al.* (2002) carried out an investigation on 22 genotypes of turmeric to elucidate the role of different growth characters as components of rhizome yield. Path coefficient analysis revealed that these growth characters registered maximum direct contribution to rhizome yield. From this investigation, leaves/clump at 180 days after planting emerged as an important rhizome yield component of turmeric.

Pandey *et al.* (2002) studies on correlation in different quality characters and reported that weight of fresh rhizome per plant was positive and significantly correlated with dry matter per cent while oleoresin per cent was negatively correlated with weight of fresh rhizome per plant. In path coefficient plant height, weight of primary rhizome, weight of secondary rhizome per plant had direct positive effect on rhizome yield.

Panja *et al.* (2002) studied nineteen characters of eight turmeric genotypes and found that plant height, number of leaves and primary fingers, number and weight of secondary fingers had positive genotypic correlation while length of primary fingers, internode length and

ratio of outer and inner core of primary fingers had significant negative association with rhizome yield. The number and weight of secondary rhizomes exhibited higher positive correlation with yield than other characters.

Chattopadhyay *et al.* (2004) evaluated ten promising genotypes of turmeric in Nadia, West Bengal for 17 growth and yield parameters at genotypic and phenotypic levels along with their interactions with the environment. Path analysis indicated that leaf length, leaf breadth, weight of primary finger had substantial positive effect on yield at genotypic level but weight of primary and secondary fingers had positive direct effect on yield at phenotypic level.

Prasad *et al.* (2004) studied correlation between growth, yield and quality parameters of intercropped turmeric at Pusa, Bihar. Data were recorded for rhizome yield, plant height, number of leaves per plant, number of tillers per plant, leaf area index, weight of mother rhizomes, weight of finger rhizomes and total curing percentage. The study revealed that all characters, except for plant height, had positive and significant correlation with rhizome yield.

Rao *et al.* (2004) evaluated fifty-four turmeric cultivars at Jagtial, Andhra Pradesh for growth, yield and quality characters. Correlation studies revealed that all the growth and yield characters showed significant positive correlation with cured yield, whereas the quality characters curcumin content, essential oils and oleoresins had negative correlation with cured yield.

Tomar *et al.* (2005) studied correlation between 11 characters of 22 genotypes of turmeric in Chhattisgarh. Plant height, leaf length, thickness of primary and secondary rhizomes and number of secondary rhizomes revealed significant positive associations with rhizome yield.

Datta *et al.* (2006) carried out the correlation studies in 11 turmeric germplasm in West Bengal. The data was recorded for 19 yield

attributes. The significant correlation of number of primary and secondary fingers with number of mother rhizome and plant height indicates the scope for obtaining a good response through direct and indirect selection.

Kumar *et al.* (2006) carried out the experiment with twenty six turmeric genotypes of diverse origin and correlation was studied on rhizome yield. The correlation study comprising sixteen traits revealed that biometrical traits viz., girth of mother rhizomes (0.565), weight of mother rhizomes (0.456), weight of primary rhizomes (0.753), length of primary rhizomes (0.777), girth of primary rhizome (0.713), number of secondary rhizomes per clump (0.618), weight of secondary rhizomes (0.597), length of secondary rhizome (0.605), rhizome diameter (0.546), core diameter (0.566) and rhizome to core ratio (0.577) exerted significant positive correlation with yield.

Yadav *et al.* (2006) carried out path-coefficient analysis on forty-one turmeric genotypes in Meghalaya for 12 characters, i.e. yield per plant, plant height, clumps per plant, leaves per plant, primary and secondary rhizomes per plant, length of mother, primary and secondary rhizomes, and weight of mother, primary and secondary rhizomes. Weight of mother, primary and secondary rhizomes had the highest positive direct effects on yield.

Kumar *et al.* (2007) conducted an experiment in Tamil Nadu on 26 turmeric genotypes of diverse origin to determine the correlation between component traits and path coefficient analysis on rhizome yield. The study revealed that plant height (0.870), number of leaves (0.859), length of leaf (0.938), breadth of leaf (0.418) and number of tillers (0.632) expressed significant positive correlation with yield which was highly amenable for simultaneous improvement. Path analysis projected the number of leaves (0.650), length of leaf (0.679) and number of tillers (0.123) as dominating contributors towards yield.

Velmurugan *et al.* (2008) conducted studies on correlation and association analyses for yield and its components in Coimbatore. The association analysis revealed that plant height, leaf area index, length of

primary rhizome, number of tillers, number of leaves, total dry matter production, mother rhizome yield, primary rhizome yield and diameter of primary rhizome had positive and significant effects on rhizome yield. Path analysis showed that the total dry matter production and mother rhizome yield had the greatest effect on rhizome yield.

Sharon *et al.* (2011) evaluated ten varieties of turmeric at the Department of Spices & Plantation Crops, Coimbatore. The data recorded on yield and yield attributing characters revealed that the characters viz., number of tillers, number of leaves, leaf breadth, weight of mother rhizomes, weight of primary rhizomes, length of mother rhizomes, leaf length and plant height had significant and positive correlations with that of yield which indicates that these components are amendable for simultaneous improvement with that of yield. Path coefficient analysis revealed positive and direct effect on rhizome yield was maximum for weight of primary rhizomes (0.666) followed by leaf length (0.405), number of leaves (0.3828) and weight of mother rhizomes (0.292). Since the correlation of these characters with yield was positive and the indirect effect was positive and high, direct selection of these traits can be practised for improving the yield.

Singh *et al.* (2012) conducted the studies on the associated character of the turmeric at different site and estimated the curcumin and oleoresin content. Rhizome yield had positive and significant correlation with plant height, number of 15 leaves on main shoot, plant girth, length and width of mother rhizome, number and weight of primary rhizome per plant, number of secondary rhizome per plant and weight of fresh rhizome per plant at phenotypic and genotypic levels, while only one character viz. number of tillers per clump showed positive and significant association at genotypic level only. The estimates of genetic parameters revealed scope for further improvement of rhizome yield by selection.

Rajyalakshmi *et al.* (2013) raised eight turmeric genotypes in a randomized block design to study the variability, heritability with genetic advance, correlation, direct and indirect effects of characters on rhizome

yield for a period of four year. Variability accompanied by higher values for genetic coefficient of variation was recorded for rhizome yield. Heritability and genetic advance were high for rhizome yield and number of tillers per plant. In general, genotypic correlations were higher than phenotypic correlations for all the characters studied.

Bahadur *et al.* (2015) arranged accessions in a randomized complete block design with three replications. Significant mean square of accessions for all the traits studied indicates the existence of sufficient genetic variability among the studied accessions. The rhizome yield exhibited highly significant and positive association with plant height, number of leaves plant⁻¹, number of tillers plant⁻¹, weight of rhizomes plant⁻¹, length of primary rhizome, and dry matter recovery.

Kallur *et al.* (2017) collected twenty-two turmeric genotypes from different parts of the country there were evaluated for growth, yield and quality at College of Horticulture, Sirsi, Karnataka, India. The data recorded on different characters were subjected to work out correlation and path analysis to investigate the association, direct and indirect contribution of various characters on fresh rhizome yield per plant, Internode length and ratio of outer and inner core of primary fingers had significant negative association with rhizome yield. The number and weight of secondary rhizomes exhibited higher positive correlation with yield than other characters.

CHAPTER III

MATERIALS AND METHODS

The present investigations entitled “Studies on Genetic Variability and Correlation Studies in Turmeric (*Curcuma longa* L.)” were carried out at the Instructional Farm of the Department of Vegetable Science, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola, during the Kharif season of 2018. The details of material used and methodologies employed have been described as under:

3.1 GENERAL

3.1.1 Experimental Site

The investigation “Genetic Variability and Correlation Studies in turmeric was carried out at Instructional Farm, Department of Vegetable Science, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola during kharif season 2018-2019

3.1.2 Climate and weather situation

Akola is situated in the sub-tropical zone at latitude of 22.42°N and longitude of 77.02°E. The altitude of the place is 307.42 m from mean sea level. The mean annual precipitation on the basis of last fifteen years average is 802 mm, which is received almost from the South-West monsoon from June to October. The mean annual maximum and minimum and minimum temperature are 35° C and 19° C, respectively. The relative humidity ranges from 22.25 per cent in summer to 64.1 per cent in rainy season. Akola. Thus has hot dry summer and moderate cold winter. The hail storms are not common in this area.

The meteorological data in respect of maximum and minimum temperature, rainfall and relative humidity was recorded at University campus during the course of study for the period from June 2018 to March 2019 and is furnished in Appendix I.

3.1.3 Soil

The experiment farm was having black cotton soil with uniform texture, colour and good drainage capacity. The experiment plot was developed into fine tilth by ploughing and harrowing.

3.2 Materials

3.2.1 Details of Experimental Site

The soil of experimental plot was medium black soil with moderate fertility and having good drainage. It was free from weeds and disease infection. In order to understand the physical and chemical properties of soil, a representative soil sample from 3 spots were taken from whole experimental field. The soil samples were collected after scrapping the surface litter, a uniform layer or a thin slice of soil from the surface to a plough depth i.e. 15-22 cm (Seetharaman *et al.*, 1994).

3.2.2 Nutrient status of Experimental Plot

The chemical analysis of the soil from experimental plot was carried out before the experiment and the details of the soil analysis (NPK status) are given as under.

Nutrient	Quantity (kg ha ⁻¹)	Method adopted
Available N (kg ha ⁻¹)	230.16	Alkaline permanganate method (Subbaih and Assija, 1956)
Available P (kg ha ⁻¹)	20.16	Olsen's method (Jackson, 1967)
Available K (kg ha ⁻¹)	380.41	Neutral normal ammonium acetate method (Jackson, 1967)
pH (1 : 2.5)	-	Potentiometry, Jackson (1973)
E.C. (dSm ⁻¹)	-	Conductometry, Jackson (1973)
CaCO ₃ (%)	-	Acid neutralization, Jackson (1967)
Organic carbon (%)	-	Wet oxidation, Nelson and Sommers (1982)

3.2.3 Experimental details :-

1.	Name of the crop	Turmeric (<i>Curcuma longa</i> L.)
2.	Family	Zingiberaceae
3.	Year of study	2018-2019
4.	Number of Genotypes	17 (Seventeen)
5.	Checks	3 (Three)
6.	Replications	2
7.	Design	RBD (Randomized Block Design)
8.	Spacing	45 x 30 cm
9.	Plot size	Net Plot Size= 3.3 m ² Gross plot Size = 6.96 m ²
10.	Planting Method	Ridges and furrows
11.	Planting Time	7 th August, 2018
12.	Harvesting Time	16 th March, 2019
13.	Season	Kharif season
14.	Place of Research Work	Instructional Farm, Department of Vegetable Science, Dr. P. D. K. V. Akola

3.2.4 EXPERIMENTAL MATERIAL

Twenty diverse genotypes of turmeric collected, including two recommended varieties as checks viz. PDKV Waygaon and Pratibha were used for the present investigations. The sources of genotypes are presented in Table 3.1.

Table 1 : List of turmeric genotypes studied

Sr. No.	Genotypes	Sr. No.	Genotypes
1	AKTL- 3	12	AKTL – 15
2	AKTL- 4	13	AKTL – 16
3	AKTL- 5	14	AKTL-17
4	AKTL -6	15	AKTL-18
5	AKTL – 8	16	AKTL-19
6	AKTL – 9	17	AKTL-20
7	AKTL -10	18	Gondia Haladi -1
8	AKTL-11	Sr. No	Checks
9	AKTL-12	1	PDKV Waygaon
10	AKTL-13	2	Pratibha
11	AKTL-14		

3.2.5 SOURCE OF MATERIAL :-

1. Genotypes AKTL-3 to AKTL-20 and Gondia Haladi-1 were collected by Department of Vegetable Science, Dr. P.D.K.V. Akola.
2. Pratibha used as check variety is released by IISR, Calicut
3. PDKV Waygaon used as check variety is released by Dr. P.D.K.V.Akola.

3.2.6 EXPERIMENTAL LAYOUT

Rhizomes were directly sown in the field at 7th august, 2018 at a spacing of 45 x 30 cm in a ridges and furrows plot of 3 x 1 m size. Drainage channels were also made between plots. The collections were planted in a Randomized Block Design with two replications.

3.3 Methods

3.3.1. Preparatory tillage

The experimental field was prepared by two ploughing and two criss cross harrowing. Clod crushing was done for obtaining fine texture of soil. Prior to last harrowing, well decomposed farm yard manure was incorporated into the field at the rate of 20 tones ha⁻¹ and mixed thoroughly in the soil. Later the plot were laid out as per plan. Stubbles and

weeds were cleaned from the experimental area and smoothed with wooden plank to prepare fine flat bed.

3.3.2 Planting

The rhizomes were planted at the spacing of 45 cm × 30 cm and 30 cm deep on ridges and furrows method of planting. The planted rhizomes were then covered gently with the soil and slightly pressed. After planting, light irrigation was given. The planting was carried out on 7th August 2018.

3.3.3 Fertilizer application

The recommended dose of fertilizer i.e. 200:100:100 Kg N:P:K ha⁻¹ were applied. The half dose of Phosphorus and Potassium i.e. 50 kg ha⁻¹ in the form of Single super phosphate and Murate of potash was applied at the time of planting, respectively and remaining half dose of Phosphorus and Potassium i.e. 50 kg ha⁻¹ were applied after 60 days of planting. While, first half dose of Nitrogen i.e. 100 kg ha⁻¹ in the form of Urea was applied 30 days after planting and second half dose of Nitrogen was applied after 30 days after first dose.

3.3.4. Irrigation

The experimental plot, was regularly irrigated as and when required in kharif season whereas during winter season at an interval of 10-12 days and 7-8 days during summer season. Crop received 18 irrigations during entire life period. Irrigation was stopped when the plants begin to show yellowing of leaves, around 50 per cent of the total leaves showing bending towards soil surface of the crop approaching maturity.

3.3.5 Intercultural Operations

In order to keep the plots free from weeds and have good aeration to the roots, five hand weeding and earthing up were given.

3.3.6. Plant protection measures

The incidence of leaf blotch was observed during the growing period of crop. Accordingly it was controlled by an application of Mancozeb @ 2-2.5 g/litre. Similarly, application of Carbandenzium @ 1-1.5 g/litre

alternately was made at an interval of 8 days to prevent the infection of fungal diseases. Total 8 sprays were given.

3.3.7. Harvesting

Every genotypes were harvested independently when it became ready to harvest. It become ready for harvesting when plant leaves start yellowing, get dried and bended towards the ground. Harvesting were done on dated 16th and 24th March of 2019

3.4 OBSERVATIONS RECORDED

The observations were recorded from five randomly selected plants from each plot in each replication for different morphological and rhizome characters. The characters studied were

Biometric Characters:	Frequency	Stages
Sprouting (%)	1	30 DAP
Height of plant(cm)	2	120 and 180 DAP
No. of leaves(no/plant)	2	120 And 180 DAP
No. of tillers(no/plant)	1	120 DAP
Leaf area (cm ²)	1	
Rhizome characters :-		
No. of mother rhizome(g/plant)	1	At harvest
Weight of mother rhizome(g)	1	At harvest
Girth of mother rhizomes(cm)	1	At harvest
No. of primary rhizomes(no/clump)	1	At harvest
Weight of primary rhizomes(g/clump)	1	At harvest
Length of primary rhizomes(cm)	1	At harvest
Girth of primary rhizome (cm)	1	At harvest
Core diameter(cm)	1	At harvest
Yield of finger rhizome per plant (gm)	1	At harvest
Yield of rhizomes per plot (kg)	1	At harvest
Total yield of rhizomes per ha (t)	1	At harvest

3.4.1 Growth parameters

3.4.1.1 Sprouting (%)

Number of plants sprouted after 30 days of planting were counted and emergence percentage was calculated as:

$$\text{Sprouting (\%)} = \frac{\text{Number of plants emerged per plot}}{\text{Total number of rhizomes sown per plot}} \times 100$$

3.4.1.2 Number of tillers per plant

Number of tillers (pseudo stem) per plant were counted from the selected plants and averaged.

3.4.1.3 Number of leaves per plant

Number of leaves per plant were counted from the selected plants and averaged.

3.4.1.4 Plant height (cm)

Height of plant was measured in centimeters from the base of the clump up to the tip of the longest leaf of the tallest tiller.

3.4.1.5 Leaf Area

The leaf area was measured with LI 3100 Leaf Area Meter (LICOR INC.Linocolin, Nebraska,USA). Leaves were cut and were fed to Leaf Area Meter.

3.4.2 Yield parameters

3.4.2.1 Length of mother rhizome (cm)

The length of mother rhizomes was measured in centimeters longitudinally from one end of the rhizome to the other end and the average was taken.

3.4.2.2 Girth of mother rhizome (cm)

The girth of mother rhizomes was measured in centimeters with the help of a thread from three different places and the average was taken.

3.4.2.3 Weight of mother rhizome (g)

The weight of the mother rhizomes was measured in grams and the average was taken.

3.4.2.4 Number of primary rhizomes per plant

Number of primary rhizomes per plant were counted from the selected plants and averaged.

3.4.2.5 Length of primary rhizome (cm)

The length of primary rhizomes of the selected plants was measured in centimeters longitudinally from one end of the rhizome to the other end and the average was taken.

3.4.2.6 Girth of primary rhizome (cm)

The girth of primary rhizomes of the selected plants was measured in centimeters with the help of a thread from five different places and the average was taken.

3.4.2.7 Core diameter of primary rhizome (cm)

The core diameter of primary rhizomes was measured in centimeters with the help of Digital Vernier Caliper from three different places and the average was taken.

3.4.2.8 Weight of primary rhizome (g)

The weight of primary rhizomes was measured in grams and the average was taken.

3.4.2.9 Yield of finger rhizome per plant (g)

The yield of finger rhizomes of the selected plants was recorded in grams and the average was taken.

3.4.2.10 Yield of rhizomes per plot (Kg)

The yield of rhizomes (mother, primary and secondary) was recorded in kilograms for each plot.

3.4.2.11 Total yield of rhizomes per hectare (t)

The yield of mother rhizome per plot in kilograms was converted into yield per hectare (t)

3.5 Statistical and biometrical analysis

The data obtained in respect of all the characters have been subjected to the following statistical analysis.

3.5.1 Analysis of variance

Analysis of variance was carried out in order to partition the total variation showed by different characters under study into its components *viz.* blocks, treatments, and error. This was carried out as per the standard method suggested by Panse and Sukhatme (1954). The details are given in the Table

Analysis of variance

Sr. No.	Source of variation	D.F.	S.S.	M.S.S. of variance
1)	Replications	(r-1)	R-SS	M ₁
2)	Treatments (genotypes)	(n-1)	Tr-SS	M ₂
3)	Error	(r-1) (n-1)	E-SS	M ₃
	Total	(rn-1)		M₁ + M₂ + M₃

Where,

r = Number of replications

n = Number of genotypes

$$M_2 - M_3$$

$$\text{Genotypic variance} = \frac{\text{-----}}{R}$$

$$M_2 - M_3$$

$$\text{Phenotypic variance} = \frac{\text{-----}}{r} + M_3$$

$$\text{Genotypic variance} = M_3$$

3.5.2 Genetic parameters

The genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense and genetic advance for different characters were worked out for all the genotypes under study following the standard procedures.

3.5.2.1 Genotypic and phenotypic coefficient of variation

Genotypic and phenotypic coefficients of variation were estimated by the formulae as suggested by Burton (1952).

$$\text{GCV} = \frac{\sqrt{\text{Genotypic variance}}}{\bar{X}} \times 100$$

Where,

\bar{X} = The mean of character

$$\text{PCV} = \frac{\sqrt{\text{Phenotypic variance}}}{\bar{X}} \times 100$$

Where,

\bar{X} = The mean of character

To categories the magnitude the scale used was explained by Shivasubramanyam and Menon, (1973) which was as follows:

> 20%	high
10-20 %	moderate
< 10 %	low

3.5.2.2 Heritability estimates (h^2)

Heritability of a character on the other hand is an index of its transmissibility. In broad sense, it may be defined as the proportion of genotypic variance to phenotypic variance and heritability percentage in

broad sense is calculated by the formulae as suggested by Johnson *et al.* (1995^{a,b}).

$$h^2 = \frac{VG}{VP} \times 100$$

Where,

h^2 = Heritability estimates in broad sense

VG = Genotypic variance

VP = Phenotypic variance

To categories the magnitude the scale used as explained by Robinson *et al.* (1951) was as follows:

> 60 % high

30-60 % moderate

< 30 % low

3.5.2.3 Expected genetic advance (EGA)

$$EGA = \frac{VG}{\sqrt{VP}} \times K$$

Where,

VG = Genotypic variance

\sqrt{VP} = Phenotypic standard deviation

K = Selection differential at 5% selection intensity

Value of K = 2.06 at 5% level, Lush (1949)

Value of K = 2.64 at 1%

Expected genetic advance is expressed in percentage over mean.

$$EGA \text{ in \% of mean} = \frac{EGA}{\bar{X}} \times 100$$

Where,

\bar{X} = The mean of treatment

To categories the magnitude the scale used as explained by Johnson *et al.* (1955a) was as follows:

> 20%	high
10-20 %	moderate
< 10%	low

3.5.3 Correlation studies

The relationship between two or more quantitative characters is of great interest and carries much practical significance. Correlation is a measure of the degree to which various characters are associated with yield or among themselves (Burton, 1952).

3.5.3.1 Partitioning of variance

Variance is partitioned into genotypic, phenotypic and in environmental components. In order to form a reliable basis for selection, it is necessary to break up the observed variance and covariance into its heritable (genetic) and non-heritable (non-genetic) components. This was done as per the method suggested by Fisher (1954).

$$\text{Genotypic variance} = \frac{\text{Treatment variance} - \text{Error variance}}{\text{No. of replications}}$$

$$\text{Phenotypic variance} = \text{Genotypic variance} + \text{Error variance}$$

$$\text{Environmental variance} = \text{Error variance}$$

3.5.3.2 Calculation of genotypic and phenotypic correlation coefficients

To study the extent of association between different traits under study the simple genotypic, phenotypic and environmental correlation coefficients were worked out from the respective variances and co-variances as per the formulae suggested by Hays *et al.* (1955^{a,b})

$$\text{Genotypic } r_{1,2} = \frac{\text{Genotypic covariance 1, 2}}{\sqrt{\text{Genotypic variance 1} \times \text{genotypic variance of 2}}}$$

$$\text{Phenotypic } r_{1,2} = \frac{\text{Phenotypic covariance 1, 2}}{\sqrt{\text{Phenotypic variance 1} \times \text{phenotypic variance of 2}}}$$

$$\text{Environmental } r_{1,2} = \frac{\text{Environmental covariance 1, 2}}{\sqrt{\text{Environmental variance 1} \times \text{Environmental variance of 2}}}$$

3.5.4 Path coefficient analysis

Path coefficient analysis was suggested by Wright (1921), and illustrated and carried out separately by Dewey and Lu (1957) to know the direct and indirect effects of the important component traits on total yield per plant. Standard path coefficients, which are the standardised partial regression coefficients were obtained by solving the following set of 'P' simultaneous equations through 'Doolittle technique' as given by Goulden (1959).

$$P_{01} + P_{02} r_{12} + \dots + P_{0p} r_{1p} = r_{01}$$

$$P_{01} r_{12} + P_{02} + \dots + P_{0p} r_{2p} = r_{02}$$

$$P_{01} r_{1p} + P_{02} r_{2p} + \dots + P_{0p} = r_{0p}$$

Where, $P_{01}, P_{02} \dots P_{0p}$ are the direct path effects of 1, 2, ..., P variable on zero variables and $r_{12}, r_{13}, \dots, r_{1p} r_p (P-1)$ are the possible coefficients between dependent variable and independent variables and $r_{01}, r_{02}, \dots, r_{0p}$ are the correlation coefficients between dependent variables and independent variables. The indirect effect of i^{th} variable on dependent character through j^{th} variable was worked out ($P_{0j} \times r_{ij}$).

The contribution of the remaining unknown was measured as the residual factor and calculated as given below:

$$P_{ox}^2 = 1 - (P_{01}^2 + 2P_{01} P_{02} r_{12} + 2P_{01} P_{03} r_{13} + \dots + P_{02}^2 + 2P_{02} P_{03} r_{23} + \dots + P_{0p}^2)$$

$$\text{Residual factor (R)} = \sqrt{P_{ox}^2}$$

CHAPTER IV

RESULT AND DISCUSSION

The present investigations were carried out on twenty genotypes of turmeric including two recommended checks viz. PDKV Waygaon and Pratibha for yield and yield contributing traits during Kharif season 2018 with following objectives.

- To investigate extent of genetic variability among available genotypes of turmeric.
- To estimate genotypic and phenotypic correlation coefficient and path coefficient of yield and yield components in turmeric.

The experimental results obtained from the present investigation have been presented and discussed under the following subheadings.

4.1 Analysis of variance

4.2 Genetic Variability Studies

4.3 Correlation Studies

4.4 Path Coefficient Analysis

4.5 Discussion

The observations were recorded on five randomly selected competitive plants from each genotype in each replication. The characters studied were Sprouting (%), Plant height (cm) at 120 and 180 DAP, Number of leaves at 120 and 180 DAP, Number of tillers per plant, Leaf area (cm²), Number of primary rhizome, Girth of primary rhizome (cm), Length of primary rhizome(cm), Weight of primary rhizome(g), Number of mother rhizome, Length of mother rhizome(cm), Girth of mother rhizome (cm), Weight of mother rhizome(g), Core diameter (cm), Yield of finger rhizome per plant (g), Yield of rhizomes per plot (kg), Total yield of rhizomes per hectare (tonnes). Results obtained during the present investigation are presented here under following headings.

4.1 Analysis of variance

The analysis of variance was carried out for all the characters under study to know whether the genotypes included differed significantly among themselves. Analysis of variance for all the characters presented in the Table 3.

From Table 3, it is revealed that the mean sum of square for plant height (cm) at 120 and 180 DAP, number of leaves at 120 and 180 DAP, number of tillers, leaf area (cm²), no of primary rhizome, girth of primary rhizome (cm), length of primary rhizome(cm), weight of primary rhizome(g), no of mother rhizome, length of mother rhizome(cm), girth of mother rhizome (cm), weight of mother rhizome(g), core diameter (cm), Yield of finger rhizome per plant (g), yield of rhizomes per plot (kg), Total yield of rhizomes per hectare (tonnes) were significant at one percent therefore indicated that, genotypes studied were differed from each other. This indicated presence of substantial amount of genetic variability among the different turmeric genotypes.

4.2 Genetic variability studies

With a view to understand the extent to which the observed variation is due to genetic factors, the mean, range, genotypic coefficient of variance (GCV), phenotypic coefficient of variance (PCV), environmental coefficient of variance (ECV), expected genetic advance as per cent over mean (EGA), heritability (h^2), were worked out for 20 genotypes traits.

4.2.1 Range of mean performance

Mean performance of the genotypes for twenty characters under study has been presented in Table 4.

Range for the character sprouting in percent recorded was 78.70 to 95.26%. The genotype AKTL-9 had highest sprouting percent (95.26%) followed by AKTL-3 (93.63%), AKTL-15 (93.34%), AKTL-11 (91.42%), and AKTL-18 (90.76%). The genotype AKTL-12 had lowest sprouting in percent (78.70%). While sprouting percent for twenty genotypes was (85.43%).



Plate 1. Variability among rhizome of the turmeric genotypes



Plate 2. Variability among mother rhizomes of turmeric genotypes



Plate 3. Variability among primary rhizomes of turmeric genotypes

For the character plant height at 120 DAP the range recorded was 87 -133.69 cm. The maximum plant height (133.69 cm) was recorded in AKTL- 8 , which was found at par with AKTL-20 (129.36 cm), AKTL-4 (124.88 cm) AKTL-13 (126.64 cm) and AKTL-15 (121.54 cm) while, genotype AKTL-11 showed minimum plant height at 120 (87 cm). The mean plant height at 120 DAP of twenty genotypes was (107.27 cm).

Plant height recorded at 180 DAP was in between 100.13 cm to 143.19 cm. The genotype AKTL- 8 had the maximum plant height (143.19 cm) which was found at par with AKTL-4 (132.88 cm), AKTL-13 (131.54 cm) and AKTL-3 (130.69 cm), whereas, genotype AKTL-14 had shortest plant height (100.13 cm). The mean plant height of twenty genotypes recorded at 180 DAP was (120.66 cm).

Number of leaves recorded at 120 DAP was in between 6.92 to 10.09. The genotype AKTL- 12 had the highest number of leaves (9.91) which was found at par with AKTL- 15 (9.94), AKTL-12 (9.91), Pratibha (9.72), PDKV Waygaon (9.60) and AKTL-16 (9.26), and AKTL-5 (9.01). The genotype AKP-20 had the lowest number of branches (6.92). The mean number of leaves for twenty genotypes was (8.53).

Number of leaves was in between 8.45 to 13.26 recorded at 180 DAP. The genotype AKTL-6 had the highest number of leaves (13.26) amongst all the genotypes studied which was found at par with AKTL-15 (13.11), Gondia Haladi-1 (12.65), Pratibha (12.25), AKTL-8 (12.17), AKP-11 (11.62), PDKV Waygaon (11.25), AKTL-4 (10.26), AKTL-9 (10.18), AKTL-12 (10.16). While, genotype AKTL-20 had the lowest number of leaves (8.45). The mean number of leaves 180 DAP of twenty genotypes was (10.38).

Table 2: Analysis of variance for yield and yield attributing characters in turmeric

Source	DF	Sprouting (%)	Plant Height at 120 DAP (cm)	Plant Height at 180 DAP (cm)	Number of leaves At 120 DAP	Number of leaves At 180 DAP	Leaf area (cm ²)	No of tillers (no/plant)	Number of mother rhizomes (no/plant)	Weight of mother rhizomes (g)	Length of mother rhizomes (cm)	Girth of mother rhizome (cm)
Replication	1	106.668	0.388	21.506	0.2117	0.3478	217.0	0.021	0.0087	62.250	0.4601	0.801
Treatment	19	198.761	448.69**	289.98**	2.102**	5.130**	46879.8**	0.179**	0.495**	915.1**	7.683**	16.79**
Error	19	166.395	51.517	95.646	0.2861	0.416	580.7	0.058	0.101	72.3	0.315	0.776

Source	DF	No of primary rhizomes (no/clump)	Weight of primary rhizomes (g/clump)	Length of primary rhizomes (cm)	Girth of primary rhizomes (cm)	Core Diameter (cm)	Yield of finger rhizome per plant (gm)	Yield of rhizome per plot (Kg)	Total yield of rhizomes per ha (t)
Replication	1	0.067	85.5	0.228	0.408	0.047	16.180	0.213	3.534
Treatment	19	20.712**	1008.5**	10.407**	5.586**	0.178**	1966.5**	0.993**	17.712**
Error	19	0.455	76.4	0.190	0.118	0.049	74.2	0.058	0.957

Significant at 5% level - *

Significant at 1% level - **

For the trait leaf area (cm²) was observed between 138.47 to 522.72 cm². The genotype AKTL-6 had the highest leaf area (522.72) which was found at par with AKTL-9 (520.16), Pratibha (507.80), AKTL-16 (503.32), AKTL-10 (495.60), Gondia Haladi-1 (482.10) and PDKV Waygaon (471.04), Whereas the genotype AKTL-15 had the lowest leaf area (138.47). The mean value for leaf area for twenty genotypes was (313.92).

Range for the character number of mother rhizome recorded was 1.93 to 4.01. The genotype AKTL-17 had the significant highest no of mother rhizome (4.01) which was at par with Gondia Haladi-1 (3.91), AKTL-4 (3.43), Pratibha (3.40), AKTL-15(3.23), AKTL-12 (3.20), AKTL-13 (3.14), PDKV Waygaon (3.03) and AKTL-10(3.00) while the genotype AKTL-14 had the lowest number of mother rhizome (1.93). The mean no of mother rhizome for twenty genotypes was (3.00).

Weight of mother rhizome was recorded in between 67.74 to 138.01 g. The highest weight of mother rhizome (138.01 g) was recorded in the genotype Gondia Haladi -1 followed by AKTL-10 (136.11 g), PDKV Waygaon (135.77 g), AKTL-5 (133.62 g), AKTL-17 (132.12 g), AKTL-19 (129.80 g) and Pratibha (126.80 g) whereas the lowest weight of mother rhizome (138.01 g) was recorded in variety AKTL-15. The mean Weight of mother rhizome for twenty genotypes was (67.74 g).

For the trait length of mother rhizome the range recorded was in between 3.84 to 9.93 cm. The genotype AKTL-9 had the lowest length of mother rhizome (3.84 cm) followed by AKTL- 19 (9.62 cm), AKTL-10 (8.28 cm), AKTL-13 (8.24 cm), PDKV Waygaon (8.21 cm), AKTL-17 (8.12 cm), Pratibha (8.11 cm) and AKTL-8 (8.10 cm). AKTL-11 having the highest node length of mother rhizome (9.93) and while the mean of length of mother rhizome for twenty genotypes was (6.63 cm).

The girth of mother rhizome was in the range between 3.25 to 11.39 cm. The genotype AKTL-6 had the lowest girth of mother rhizome (3.25 cm) followed by Gondia Haladi-1 (11.65 cm), PDKV Waygaon (11.39 cm), AKTL-8 (11.16 cm), AKTL-11 (11.13 cm), AKTL-19 (11.01 cm), AKTL-18 (10.64 cm), AKTL-16 (10.28 cm). Whereas, the genotype PDKV

Waygaon had the highest girth of mother rhizome (11.39 cm). The mean of girth of mother rhizome for twenty genotype was (8.79 cm).

Number of primary rhizome was recorded in between 3.06 to 12.80. The genotype AKTL-4 had highest no of primary rhizome (12.80) followed by AKTL-8 (12.36), PDKV Waygaon (12.34), Pratibha (12), Gondia Haladi-1 (11.31), AKTL-10 (11.17), AKTL-17 (10.54), AKTL-19 (8.26) and AKTL-3 (7.62). The genotype AKTL-13 had lowest no of primary rhizome (3.06). While the mean of no of primary rhizome of twenty genotypes was (8.14).

Range for the character weight of primary rhizome recorded was 44.26 to 146.82 g. The genotype PDKV Waygaon had highest weight of primary rhizome (146.82 g) followed by Gondia haladi-1 (141.21 g), AKTL-13 (134.21 g), AKTL-17 (132.67 g), AKTL-19 (130.77 g), Pratibha (128.00 g), AKTL-4 (126.17 g), AKTL-10 (123.44 g) and AKTL-16 (122.55 g). The genotype AKTL-14 had lowest weight of primary rhizome (44.26 g). While the weight of primary rhizome for twenty genotypes was (112.96 g).

Length of primary rhizome was recorded between 4.11 to 10.05 cm. AKTL-13 had highest Length of primary rhizome (10.05 cm) which was found at par with AKTL-19 (10.03 cm), Gondia Haladi-1(9.93), AKTL-14 (9.79 cm), PDKV Waygaon (9.35 cm), AKTL-10 (9.17 cm), AKTL-11 (9.0 cm), AKTL-5 (8.94), Pratibha (8.56), AKTL-20 and (8.20) whereas, the genotype AKTL-4 had lowest length of primary rhizome (4.11 cm). The average Length of primary rhizome for twenty genotypes was (7.31 cm).

Girth of primary rhizome was recorded between 1.52 to 7.03 cm. PDKV Waygaon had highest girth of primary rhizome (7.03 cm) which was found at par with AKTL-8 (6.73cm), Gondia Haladi-1 (6.65 cm), AKTL-19 (6.42 cm), AKTL-13 (6.15), Pratibha (6.12), AKTL-16 (5.68 cm) and AKTL-17 (5.57 cm) whereas, the genotype AKTL-9 had lowest length of primary rhizome (1.52 cm). The average girth of primary rhizome for twenty genotypes was (4.69 cm).

The range of core diameter was in between 1.64 to 2.78. The genotype Gondia Haladi-1 had the highest core diameter (2.78 cm) which was found at par with AKTL-9 (2.52 cm), PDKV Waygaon (2.38 cm), AKTL-13 (2.32 cm), AKTL-3 (2.25 cm), AKTL-17 (2.19 cm), AKTL-16 (2.16 cm), AKTL-11 (2.07 cm), AKTL-19 (2.03 cm), AKTL-15 (1.99 cm), Pratibha (1.86 cm) and AKTL-18 (1.845 cm), while genotype AKTL-5 had the lowest core diameter (1.64 cm). The average core diameter for twenty genotypes was (2.04 cm).

Yield of finger rhizome per plant in the range of 115.67 to 217.12. The genotype PDKV Waygaon produced maximum yield of finger rhizome per plant (217.12 g) which was found at par with Gondia Haladi-1 (214.46 g), Pratibha (197.57 g), and the genotype AKTL-5 produced minimum yield of finger rhizome per plant (115.67 g), while the average yield of finger rhizome per plant was (168.6 g).

Yield of rhizomes per plot in the range of 3.57 to 5.90 kg. The genotypes PDKV Waygaon produced maximum Yield of mother rhizome per plot (5.90 kg) which was found at par with Gondia Haladi-1 (5.85 kg), AKTL-10 (5.52 kg), AKTL-17 (5.36 kg), AKTL-19 (5.35 kg) AKTL-13 (5.13 kg), and the genotype AKTL-12 produced minimum Yield of rhizomes per plot (1.22 kg), while the average yield of mother rhizome per plot was (4.68).

Total yield of rhizomes per hectare was in the range of 14.73 to 24.31. The genotypes PDKV Waygaon produced maximum total yield of rhizome per hectare (24.31 t) which was found at par with Gondia Haladi (24.12 t), AKTL-19 (22.87 t), AKTL-10 (22.75 t), AKTL-17 (22.08 t), AKTL-19 (19.61 t), AKTL-8 (21.71 t), AKTL-13 (21.13 t), pratibha (21.12 t), and the genotype AKTL-12 produced minimum yield of mother rhizome per hectare (14.72 t), while the average total yield of rhizomes per hectare was (19.44 t).

Number of tillers was in between 1.67 to 2.78 recorded. The genotype Gondia Haladi-1 had the highest number of leaves (2.78) amongst all the genotypes studied which was found at par with AKTL-9 (2.52), AKTL-13 (2.32), AKTL-17 (2.19), AKTL-16 (2.16), AKTL-17 (2.16), AKTL-11 (2.10), AKTL-3 (2.07), While, genotype AKTL-14 had the lowest number of leaves (1.67). The mean number of tillers of twenty genotypes was (2.03).

Table 3. Mean performance of turmeric genotypes based on different parameters

Sl. No	Genotypes	Sprouting (%)	Plant Height at 120 DAP (cm)	Plant Height at 180 DAP (cm)	Number of leaves At 120 DAP	Number of leaves At 180 DAP	Leaf area (cm ²)	Number of mother rhizomes (no/plant)	Weight of mother rhizomes (g)	Length of mother rhizomes (cm)	Girth of mother rhizome (cm)
1	AKTL-3	93.63	114.1	130.695	7.08	9.025	290.76	2.73	113.965	5.08	5.98
2	AKTL-4	88.96	124.885	132.885	8.405	10.265	166.03	3.435	110.645	4.155	2.265
3	AKTL-5	79.93	94.045	115.495	9.015	9.335	187.995	2.945	133.62	5.245	4.435
4	AKTL-6	86.39	90.835	107.775	10.09	13.26	522.72	2.965	87.71	4.03	3.25
5	AKTL-8	85.45	133.69	143.19	7.74	12.17	176.285	2.34	121.62	8.1	11.165
6	AKTL-9	95.26	106.655	116.155	7.07	10.185	520.16	2.555	99.765	3.845	9.645
7	AKTL-10	82.52	97.055	103.255	9.09	9.24	495.6	3	136.11	8.28	9.435
8	AKTL-11	91.42	87.835	123.835	8.625	11.625	154.28	2.685	125.655	9.93	11.13
9	AKTL-12	78.705	87	109.035	9.915	10.165	262.29	3.2	83.205	4.18	8.39
10	AKTL-13	86.52	121.545	131.545	8.025	9.185	164.155	3.145	107.025	8.24	9.78
11	AKTL-14	88.79	90.3	100.13	7.565	8.555	143.97	1.93	117.085	4.705	5.095
12	AKTL-15	93.34	123.08	126.59	9.94	13.11	138.47	3.235	67.74	6.145	9.885
13	AKTL-16	82.65	97.705	108.75	9.265	9.265	503.32	2.59	101.265	7.815	10.285

Sl. No	Genotypes	Sprouting (%)	Plant Height at 120 DAP (cm)	Plant Height at 180 DAP (cm)	Number of leaves At 120 DAP	Number of leaves At 180 DAP	Leaf area (cm ²)	Number of mother rhizomes (no/plant)	Weight of mother rhizomes (g)	Length of mother rhizomes (cm)	Girth of mother rhizome (cm)
14	AKTL-17	90.53	91.25	116.39	8.275	8.775	246.23	4.01	132.125	8.12	10.205
15	AKTL-18	90.76	111.145	120.145	7.645	9.96	339.86	2.775	116.355	6.255	10.64
16	AKTL-19	86.39	98.74	108.74	7.905	8.96	351.535	2.835	129.805	9.625	11.015
17	AKTL-20	83.58	129.36	138.34	6.92	8.455	153.745	2.545	73.69	5.235	10.025
18	PDKV WAYGAON	47.56	113.96	126.96	9.605	11.255	471.045	3.03	135.77	8.215	11.395
19	GONDIA HALADI-1	87.815	116.575	122.575	8.765	12.65	482.105	3.915	138.01	7.205	11.65
20	PRATIBHA	88.56	115.78	130.78	9.725	12.255	507.805	3.4	126.805	8.11	10.22
	Range	78.70 -95.26	87 - 133.69	100.13 -143.19	6.92 – 10.09	8.45 – 13.26	138.47 – 522.72	1.93 – 4.01	67.74 - 138.01	3.84 - 9.93	3.25 – 11.395
	Mean	85.43	107.27	120.66	8.53	10.38	313.92	3.00	112.89	6.63	8.79
	SE(m)	3.06	5.61	7.43	0.38	0.46	17.04	0.22	6.01	0.40	0.62
	CV	4.94	7.39	8.63	6.27	6.21	7.68	10.71	7.53	8.47	10.01
	CD (5%)	9.05	16.62	22	1.12	1.35	68.94	0.66	17.79	1.17	1.84

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Sl. No.	Genotypes	No of primary rhizomes (no/clump)	Weight of primary rhizomes (g/clump)	Length of primary rhizomes (cm)	Girth of primary rhizomes (cm)	Core Diameter (cm)	Yield of finger rhizome per plant (gm)	Yield of rhizome per plot (Kg)	Total Yield of rhizome per ha (t)	No of tillers (no/plant)
1	AKTL-3	7.625	117.365	5.28	3.555	2.25	163.305	4.85	19.975	2.07
2	AKTL-4	3.06	126.175	4.11	2.85	1.70	177.035	4.79	19.725	1.675
3	AKTL-5	4.875	74.92	8.94	2.72	1.64	115.67	4.295	17.685	1.775
4	AKTL-6	10.415	108.74	3.365	4.755	1.93	159.85	4.135	17.03	1.93
5	AKTL-8	12.36	81.855	6.365	6.73	1.96	191.04	4.945	21.71	1.975
6	AKTL-9	6.09	80.975	5.62	1.525	2.52	117.865	3.925	16.165	2.52
7	AKTL-10	11.175	123.04	9.17	4.44	1.845	179.04	5.525	22.75	1.745
8	AKTL-11	3.945	78.55	9.005	5.32	2.075	127.175	4.29	17.67	2.105
9	AKTL-12	5.435	88.715	7.555	4.54	1.925	134.27	3.575	14.735	1.94
10	AKTL-13	12.805	134.215	10.055	6.15	2.325	193.885	5.13	21.13	2.325
11	AKTL-14	3.315	44.26	9.79	3.76	1.72	128	4.175	17.18	1.67
12	AKTL-15	5.07	111.62	4.54	1.755	1.995	176.565	3.805	15.685	2.02
13	AKTL-16	7.145	122.555	6.855	5.685	2.165	185.22	4.67	19.245	2.165
14	AKTL-17	10.54	132.67	4.59	5.575	2.195	192.68	5.365	22.085	2.195
15	AKTL-18	7.05	94.47	4.79	4.91	1.845	151.265	4.33	18.335	1.805
16	AKTL-19	8.265	130.775	10.035	6.42	2.035	194.315	5.35	22.875	2.035
17	AKTL-20	5.01	101.285	8.2	3.275	1.70	156.03	3.74	15.405	1.75
18	PDKV WAYGAON	12.345	146.825	9.355	7.035	2.385	217.12	5.90	24.31	2.385
19	GONDIA HALADI-1	11.31	141.21	9.93	6.655	2.78	214.46	5.855	24.125	2.78
20	PRATIBHA	12.005	128.005	8.56	6.125	1.865	197.57	5.13	21.125	1.755
	Range	3.06 – 12.80	44.26 – 146.82	4.11 – 10.05	1.52 – 6.73	1.64 – 2.78	115.67 – 217.12	3.57 – 5.90	14.73 -24.31	1.67 – 2.78
	Mean	8.14	112.96	7.31	4.69	2.04	168.6	4.689	19.44	2.03
	SE(m)	0.48	6.18	0.31	0.24	0.16	6.09	0.17	0.69	0.24
	CV	8.28	7.74	5.97	7.31	10.78	5.11	5.15	5.03	11.84
	CD (5%)	1.41	18.29	0.91	0.72	0.46	18.03	0.51	2.05	0.50

4.2.2 Genotypic coefficient of variation (GCV)

It is revealed from Table 4. That, the genotypic coefficient of variation (GCV) ranged from 4.708 (sprouting) per cent to 48.46 per cent (leaf area) for different characters under studied. The high value of genotypic coefficient of variation was observed for leaf area (48.46%). Whereas, genotypic coefficient of variation was of low order for the characters, sprouting (%) plant height at 180 (8.16). while moderate values for characters yield of finger rhizome per plant (18.24%), weight of mother rhizome (18.23%), no of mother rhizome(14.98%), total yield of rhizomes per hectare (14.88%) number of leaves at 180 (14.78), yield of rhizomes per plot (14.57%), plant height at 120 (13.13%), core diameter(12.49), no of tillers (12.09%), number of leaves at 120 (11.33), plant height at 180 (8.61), sprouting (3.21), While the moderate to high values of GCV were recorded for weight of primary rhizome (20.79), length of mother rhizome (28.96%) length of primary rhizome (30.93), girth of mother rhizome (32.17), girth of primary rhizome (35.26), no of primary rhizome (40.37).

4.2.3 Phenotypic coefficient of variation (PCV)

The phenotypic coefficient of variation ranged from 11.50 (plant height at 180) per cent to 49.07 (leaf area) per cent for the various characters studied (Table 4).

Highest phenotypic coefficient of variation was recorded for the character leaf area (49.07%). While, high to moderate values of PCV were observed for characters, no of primary rhizome (43.26%), girth of primary rhizome (36.01%), girth of mother rhizome (33.70%), and length of primary rhizome (31.50%), length of mother rhizome (30.18) weight of primary rhizome (28.23), weight of mother rhizome (18.95%), yield of finger rhizome per plant (18.94%), number of mother rhizome (18.42%), Number of tillers(16.92%), core diameter(16.49%), number of leaves 180 (16.03), sprouting (15.81%), total yield of rhizomes per hectare (15.71%), yield of rhizomes per plot (15.46%), plant height at 120 (14.74%), Number of leaves at 120(14.74%), Number of leaves at 120 (13.27%) and plant height at 180 (11.50%).

Table 4. Estimates of variability, heritability, expected genetic advances per cent of mean.

Sr. No.	Character	Range	Mean	PCV (%)	GCV (%)	Heritability (h²) %	Expected genetic advance as % over mean
1	Sprouting (%)	78.70-95.26	85.43	15.815	4.708	8.864	2.888
2	Height of plant (cm) at 120 DAP	87-133.69	107.27	14.742	13.136	79.402	24.113
3	Height of plant (cm) at 180 DAP	100.13-143.19	120.66	11.508	8.169	50.395	11.947
4	No. of Leaves (no/plant) at 120 DAP	6.92-10.09	8.53	13.273	11.333	72.902	19.933
5	No. of Leaves (no/plant) at 180 DAP	8.45-13.26	10.38	16.036	14.784	84.995	28.077
6	No. of tillers (no/plant)	1.67-2.78	2.03	16.926	12.097	51.078	17.81
7	Leaf area (cm)	138.47-522.72	313.92	49.072	48.468	97.553	98.615
8	No. of mother rhizome	1.93-4.01	3.00	18.422	14.987	66.181	25.115
9	Weight of mother rhizome(g)	67.74-138.01	112.89	33.701	32.179	91.171	63.294
10	Girth of mother rhizomes(cm)	3.25-11.39	8.79	30.181	28.968	92.127	57.277

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Sr. No.	Character	Range	Mean	PCV (%)	GCV (%)	Heritability (h²) %	Expected genetic advance as % over mean
15	Length of mother rhizomes(cm)	3.84-9.93	6.63	18.956	18.231	92.495	36.119
16	No. of primary rhizomes(no/clump)	3.06-12.80	8.14	43.268	40.372	87.063	77.6
17	Weight of primary rhizomes(g/clump)	44.26-146.82	112.96	36.014	35.264	95.879	71.132
18	Length of primary rhizomes(cm)	4.11-10.05	7.31	31.508	30.938	96.412	62.577
19	Girth of primary rhizome (cm)	1.52-6.73	4.69	28.238	20.791	54.209	31.534
20	Core diameter(mm)	1.64-2.78	2.04	16.496	12.49	57.329	19.481
21	Yield of finger rhizome per plant (gm)	115.67-217.12	168.6	18.944	18.242	92.726	36.187
22	Yield of rhizome per plot (kg)	3.57-5.90	4.68	15.461	14.577	88.894	28.312
23	Total yield of rhizome per ha (t)	14.73-24.31	19.44	15.71	14.883	89.75	29.046

4.2.5 Heritability estimates in broad sense (h^2)

Result presented in the Table 4, it is revealed that the heritability estimates in broad sense were of lower magnitude except the character leaf area (97%), length of primary rhizomes (96%), girth of primary rhizomes (95%), yield of finger rhizomes per plant (92%), weight of mother rhizomes (92%), length of mother rhizomes (92%), girth of mother rhizomes (91%), total yield of rhizomes per hectare (89%), yield of rhizomes per plot (88%), number of primary rhizomes (87%), number of leaves at 180 DAP (84%), plant height at 120 DAP (79%), number of leaves at 120 DAP (72%) and number of mother rhizome (66%).

The moderate heritability character core diameter (57%), weight of primary rhizomes (54%), no of tillers (51%) and plant height at 180 DAP (50%), Low heritability character sprouting (8%).

4.2.6 Expected genetic advance (EGA)

Expected genetic advance over mean was estimated for different characters and results are presented in Table 4. The results indicated that the expected genetic advance over mean observed was in the range of 2.88 per cent to 98.61 per cent for different characters. The highest per cent of expected genetic advance to the extent of 98.61% was noted for the character leaf area followed by number of primary rhizomes (77.6%), girth of primary rhizomes (71.13%), girth of mother rhizomes (63.29%), length of primary rhizomes (62.57%), length of mother rhizomes (57.27%), yield of finger rhizomes per plant (36.18%), weight of mother rhizomes (36.11%), weight of primary rhizomes (31.53%), total rhizome yield per hectare (29.04%), yield of rhizomes per plot (28.31%), number of leaves at 180 DAP (28.07%), plant height at 120 DAP (27.07%) and number of mother rhizomes (25.11%), The moderate values were recorded in the character number of leaves at 120 DAP (19.93) core diameter (19.48%), number of tillers (67.73%), plant height at 180 DAP (11.94%).

Low values of expected genetic advance were observed for the character sprouting (2.88%).

4.3 Correlation studies

In order to find out the degree of association between yield contribution traits, genotypic and phenotypic correlation coefficient were estimated are presented in Table 6.

4.3.1 Genotypic correlation

4.3.1.1 Association between yield contributing characters and among themselves

a) Plant height at 180

Plant height at 180 showed positive and significant genotypic correlations with number of leaves at 180 ($r=0.321$), Number of tillers ($r=0.338$) weight of primary rhizome ($r=0.413$) and yield of finger rhizomes per plant ($r=0.378$), While, it showed positive and non –significant correlation with number of mother rhizome ($r=0.094$), number of primary rhizome ($r=0.241$), yield of rhizomes per plot ($r=0.138$) and yield of rhizomes per hectare ($r=0.165$). However it showed negative and non-significant genotypic correlation with weight of mother rhizome ($r=-0.091$) and length of primary rhizome (-0.160) while negative and significant genotypic correlation with leaf area ($r=-0.423$).

b) Number of leaves at 180

Number of leaves at 180 showed positive and significant genotypic correlations with number of tillers ($r=0.333$), number of primary rhizome ($r=0.323$). However it showed positive and non-significant genotypic correlation with leaf area ($r=0.252$), number of mother rhizome ($r=0.304$), weight of primary rhizome ($r=0.100$), yield of finger rhizomes per plant ($r=0.240$), Total yield of rhizomes per hectare ($r=0.008$) While, it showed negative and non-significant genotypic correlations were seen with weight of mother rhizome($r=-0.081$), length of primary rhizome ($r=-0.241$) and yield of rhizomes per plot ($r=-0.005$).

c) Number of tillers

Number of tillers showed positive and significant genotypic correlations with leaf area ($r=0.459$), weight of primary rhizome ($r=0.611$),

yield of mother rhizome per plant (0.499). yield of rhizomes per plot ($r=0.495$), yield of finger rhizomes per plant ($r=0.461$) and total yield of rhizome per hectare ($r=0.474$). However it shows positive and non-significant correlation with weight of mother rhizome ($r=0.139$) and length of primary rhizome ($r=0.187$).

d) Leaf area

Leaf area showed positive and significant genotypic correlations with number of primary rhizome ($r=0.502$), weight of primary rhizome ($r=0.493$), yield of rhizome per plot ($r=0.384$) and total yield of rhizomes per hectare ($r=0.358$) However, it showed positive and non-significant genotypic correlations with number of mother rhizome ($r=0.187$), weight of mother rhizome ($r=0.221$), length of primary rhizome ($r=0.003$) and yield of finger rhizomes per plot ($r=0.306$).

h) Number of mother rhizome

Number of mother rhizome showed positive and significant genotypic correlations with number of primary rhizome ($r=0.379$), weight of primary rhizome ($r=0.898$), yield of finger rhizome per plant ($r=0.532$), yield of rhizomes per plot ($r=0.477$) and total yield per hectare ($r=0.417$) However, it showed positive and non-significant genotypic correlations with, weight of mother rhizome ($r=0.143$). While, it showed negative and non-significant genotypic correlation with length of primary rhizome ($r=-0.140$).

k) Weight of mother rhizome (g)

Weight of mother rhizome showed positive and significant genotypic correlations with number of primary rhizome ($r=0.431$), length of primary rhizome ($r=0.451$), total yield of rhizome per hectare ($r=0.778$) and yield of rhizomes per plot ($r=0.771$), While it showed positive and non-significant genotypic correlation with weight of primary rhizome ($r=0.200$) and yield of finger rhizomes per plant ($r=0.292$).

Table 5 :- Estimates of Genotypic and Phenotypic correlation coefficient for various characters (above diagonal genotypic correlation coefficient and below diagonal phenotypic correlation coefficient)

Characters	PH 180	NOL 180	NOT	LA	NMR	WMR	NPR	LPR	WPR	YF	YRP	TRY
PH 180	1.000	0.321*	0.338*	-0.423**	0.094 ^{NS}	-0.091 ^{NS}	0.241 ^{NS}	-0.160 ^{NS}	0.413**	0.378*	0.138 ^{NS}	0.165 ^{NS}
NOL 180	0.215 ^{NS}	1.000	0.333*	0.252 ^{NS}	0.304 ^{NS}	-0.081 ^{NS}	0.323*	-0.241 ^{NS}	0.100 ^{NS}	0.240 ^{NS}	-0.005 ^{NS}	0.008 ^{NS}
NOT	-0.046 ^{NS}	0.184 ^{NS}	1.000	0.459**	0.579**	0.139 ^{NS}	0.499**	0.187 ^{NS}	0.611**	0.461**	0.495**	0.474**
LA	-0.311 ^{NS}	0.236 ^{NS}	0.299 ^{NS}	1.000	0.187 ^{NS}	0.221 ^{NS}	0.502**	0.003 ^{NS}	0.493**	0.306 ^{NS}	0.384*	0.358*
NMR	0.122 ^{NS}	0.242 ^{NS}	0.186 ^{NS}	0.163 ^{NS}	1.000	0.143 ^{NS}	0.379*	-0.140 ^{NS}	0.898**	0.532**	0.477**	0.417**
WMR	-0.074 ^{NS}	-0.065 ^{NS}	0.069 ^{NS}	0.205 ^{NS}	0.128 ^{NS}	1.000	0.431**	0.451**	0.200 ^{NS}	0.292 ^{NS}	0.771**	0.778**
NPR	0.144 ^{NS}	0.227 ^{NS}	0.336*	0.473**	0.325*	0.389*	1.000	0.179 ^{NS}	0.743**	0.762**	0.757**	0.764**
LPR	-0.106 ^{NS}	-0.229 ^{NS}	0.127 ^{NS}	-0.010 ^{NS}	-0.114 ^{NS}	0.429**	0.175 ^{NS}	1.000	0.040 ^{NS}	0.124 ^{NS}	0.383*	0.369*
WPR	0.117 ^{NS}	0.145 ^{NS}	0.285 ^{NS}	0.364*	0.570**	0.149 ^{NS}	0.512**	0.003 ^{NS}	1.000	0.982**	0.786**	0.759**
YF	0.283 ^{NS}	0.252 ^{NS}	0.272 ^{NS}	0.290 ^{NS}	0.484**	0.274 ^{NS}	0.710**	0.125 ^{NS}	0.730**	1.000	0.819**	0.818**
YRP	0.072 ^{NS}	0.047 ^{NS}	0.315*	0.360*	0.404**	0.748**	0.683**	0.342*	0.660**	0.779**	1.000	0.994**
TRY	0.100 ^{NS}	0.057 ^{NS}	0.296 ^{NS}	0.336*	0.366*	0.759**	0.699**	0.334*	0.623**	0.789**	0.992**	1.000

Significant at 5% level - *

RESIDUAL EFFECT = 0.00552

Significant at 1% level - **

1. PH 180 :- Plant height at 180

2. NOL 180 :- Number of leaves at 180

3. NOT :- Number of tillers

4. LA :- Leaf Area

5. NMR :- Number of mother rhizome

6. WMR :- Weight of mother rhizome

7. NPR :- Number of primary rhizome

8. LPR :- Length of primary rhizome

9. WPR :- Weight of primary rhizome

10. YF :- Yield of finger rhizome per plant

11. TRY :- Total yield of rhizomes per hectare

12. YRP :- Yield of rhizomes per plot

l) Number of primary rhizome

Number of primary rhizome showed positive and significant genotypic correlation with weight of primary rhizome ($r=0.743$), yield of finger rhizomes per plant ($r=0.762$), yield of rhizomes per plot ($r=0.757$) and yield of rhizome per hectare ($r=0.764$). However it showed positive and non-significant genotypic correlation with length of primary rhizome ($r=0.179$).

n) Length of primary rhizome

Length of primary rhizome showed positive and significant genotypic correlation with yield of rhizomes per plot ($r=0.383$) and yield of rhizomes per hectare ($r=0.369$). However it showed positive and non-significant genotypic correlation with weight of primary rhizome ($r=0.040$), yield of finger rhizomes per plant ($r=0.124$).

n) Weight of primary rhizome

Weight of primary rhizome showed positive and significant genotypic correlation with yield of finger rhizomes per plant ($r=0.982$) and yield of rhizomes per plot ($r=0.786$), total yield of rhizomes per hectare ($r=0.759$).

q) Yield of finger rhizomes per plant

Yield of finger rhizomes per plant However it showed positive and significant genotypic correlation with total yield of rhizomes per hectare ($r=0.818$), and yield of rhizomes per plot ($r=0.819$).

q) Yield of rhizomes per plot

Yield of rhizomes per plot However it showed positive and significant genotypic correlation with yield of rhizomes per hectare ($r=0.994$).

4.3.2 Phenotypic correlations

4.3.2.1 Association between yield contributing characters and among themselves

a) Plant height at 180 DAP (cm)

Plant height at 180 DAP showed positive and non-significant phenotypic correlation with number of leaves at 180 ($r=0.215$), number of primary rhizomes ($r=0.144$), number of mother rhizomes ($r=0.122$), weight of primary rhizomes ($r=0.117$), yield of finger rhizomes per plant ($r=0.283$) and yield of rhizomes per plot ($r=0.072$), total yield of rhizomes per hectare ($r=0.100$). However it showed negative and non-significant phenotypic correlation with number of tillers ($r=-0.046$), leaf area ($r=-0.311$), weight of mother rhizomes ($r=-0.074$), length of primary rhizomes ($r=-0.106$).

b) Number of leaves at 180 DAP (cm)

Number of leaves at 180 DAP showed positive and non-significant phenotypic correlation with number of tillers ($r=0.184$), leaf area ($r=0.236$), number of mother rhizomes ($r=0.242$), number of primary rhizomes ($r=0.227$), weight of primary rhizomes ($r=0.145$), yield of finger rhizomes per plant ($r=0.252$), yield of rhizomes per plot ($r=0.047$) and total yield of rhizomes per hectare ($r=0.057$). while, it has negative and non-significant correlation with weight of mother rhizomes ($r=-0.065$) and length of primary rhizomes ($r=-0.229$).

c) Number of tillers

Number of tillers showed positive and significant phenotypic correlations with number of primary rhizomes ($r=0.336$), yield of rhizomes per plot ($r=0.315$). While, it showed positive and non-significant phenotypic correlations with leaf area ($r=0.299$), number of mother rhizomes ($r=0.186$), length of primary rhizomes ($r=0.127$), weight of mother rhizomes ($r=0.069$), weight of primary rhizomes ($r=0.285$), yield of finger rhizomes per plant ($r=0.272$) and total rhizomes yield per hectare ($r=0.296$).

d) Leaf area

Leaf area showed positive and significant phenotypic correlations with number of primary rhizome ($r=0.473$), weight of primary rhizome ($r=0.364$), yield of rhizomes per plot ($r=0.360$), total rhizome yield per hectare ($r=0.336$). However, it showed positive and non-significant phenotypic correlations with number of mother rhizome ($r=0.163$), weight of mother rhizome ($r=0.205$), yield of finger rhizomes per plant ($r=0.290$). However, it showed negative and non-significant phenotypic correlations with length of primary rhizome ($r=-0.010$).

e) Number of mother rhizome

Number of mother rhizome showed positive and significant phenotypic correlations with number of primary rhizome ($r=0.325$), weight of primary rhizome ($r=0.570$) and yield of finger rhizomes per plant ($r=0.484$) and yield of rhizomes per plot ($r=0.404$) and total yield of rhizomes per hectare ($r=0.366$). However, it showed positive and non-significant phenotypic correlations with weight of mother rhizome ($r=0.075$). While, it showed negative and non-significant phenotypic correlation with length of mother rhizome ($r=-0.114$).

f) Weight of mother rhizome

Weight of mother rhizome showed positive and significant phenotypic correlations with number of primary rhizome ($r=0.389$), length of primary rhizome ($r=0.429$), total yield of rhizome per hectare ($r=0.759$), yield of rhizomes per plot ($r=0.748$). While it showed positive and non-significant phenotypic correlation with weight of primary rhizome ($r=0.149$), yield of finger rhizome per plant ($r=0.274$).

g) Number of primary rhizome

Number of primary rhizome showed positive and significant phenotypic correlation with weight of primary rhizome ($r=0.512$), yield of finger rhizomes per plant ($r=0.710$), yield of rhizomes per plot ($r=0.683$), yield of rhizome per hectare ($r=0.699$). However it showed positive and non-significant phenotypic correlation with length of primary rhizome ($r=0.175$).

h) Length of primary rhizome

Length of primary rhizome showed positive and significant phenotypic correlation with yield of rhizomes per plot ($r=0.342$) and total yield of rhizome per hectare ($r=0.334$). However it showed positive and non-significant phenotypic correlation with yield of finger rhizomes per plant ($r=0.125$), weight of primary rhizome ($r=0.003$).

i) Weight of primary rhizome

Weight of primary rhizome showed positive and significant phenotypic correlation with yield of finger rhizomes per plant ($r=0.730$), yield of rhizomes per plot ($r=0.660$) and total yield of rhizomes per hectare ($r=0.623$).

j) Yield of finger rhizomes per plant

Yield of finger rhizomes per plant However it showed positive and significant phenotypic correlation with yield of rhizomes per plot ($r=0.779$), total yield of rhizomes per hectare ($r=0.789$).

k) Yield of rhizomes per plot

Yield of rhizomes per plot showed positive and significant phenotypic correlation with total yield of rhizome per hectare ($r=0.992$).

4.4 Path coefficient analysis studies

In order to find out direct and indirect influence of each yield contributing character studied on rhizome yield, path analysis was carried out and results obtained are presented in Table 7 and 8.

4.4.1 Plant height at 180 DAP (cm)

The direct effect of character plant height at 180 DAP on yield per hectare in turmeric is (0.05076) and the maximum indirect effect is via yield of rhizomes per plot (0.12037) followed by yield of finger rhizomes per plant (0.06055). The correlation between yield per hectare ($r=0.165$) and plant height at 180 showed positive and non-significant.

4.4.2 Number of leaves at 180 DAP

The direct effect of character number of leaves at 180 DAP on yield per hectare in turmeric is (0.01807) and the maximum indirect effect is via yield of finger rhizomes per plant (0.03841) followed by plant height at 180 DAP (0.0163). Positive and significant correlation was recorded between yield per hectare ($r=-0.008$) and number of leaves at 180 DAP.

4.4.3 Number of tillers

This trait had high positive direct effect on yield per hectare (-0.19259) and the maximum indirect effect is via yield of rhizomes per plot (0.43288) followed by yield of finger rhizomes per plant (0.07394). The correlation between yield per hectare ($r=0.474$) and number of tillers showing positive and significant.

4.4.4 Leaf area (cm²)

This trait had direct effect on yield per hectare in turmeric (-0.04824) and the maximum indirect effect is via yield of rhizomes per plot (0.33577) followed by weight of mother rhizomes (0.02666). Positive and significant correlation was recorded between yield per hectare ($r=0.358$) and leaf area.

4.4.5 Number of mother rhizomes

The direct effect of character number of mother rhizomes on yield per hectare in turmeric is (-0.05436) and the maximum indirect effect is via yield of rhizomes per plot (0.41679) followed by yield of finger rhizomes per plot (0.0853). The correlation between yield per hectare ($r=-0.417$) and number of mother rhizomes recorded positive and significant.

4.4.6 Weight of mother rhizomes (g)

This character had direct effect on yield per hectare in turmeric (0.12057) and the maximum indirect effect is via yield of rhizomes per plot (0.67369) followed by yield of finger rhizomes per plant (0.04683). Positive and significant correlation was recorded between yield per hectare ($r=0.778$) and weight of mother rhizomes.

Table 6. Path coefficient showing direct (under lined) and indirect effects of various traits on mother rhizome yield per hectare

Characters	PH 180	NOL 180	NOT	LA	NMR	WMR	NPR	LPR	WPR	YF	YRP	TRY
	1	2	3	4	5	6	7	8	9	10	11	12
PH 180	<u>0.05076</u>	0.0163	0.01715	-0.02145	0.00477	-0.00464	0.01222	-0.00811	0.02094	0.01917	0.00699	-0.091
NOL 180	0.0058	<u>0.01807</u>	0.00602	0.00456	0.00549	-0.00147	0.00584	-0.00436	0.0018	0.00433	-0.00008	-0.120
NOT	-0.06508	-0.06418	<u>-0.19259</u>	-0.08831	-0.11148	-0.02686	-0.09617	-0.0361	-0.1177	-0.0888	-0.09542	0.490
LA	0.02039	-0.01218	-0.02212	<u>-0.04824</u>	-0.00903	-0.01067	-0.02424	-0.00016	-0.02378	-0.01474	-0.01854	0.255
NMR	-0.00511	-0.01651	-0.03147	-0.01018	<u>-0.05436</u>	-0.00779	-0.02062	0.00763	-0.04883	-0.02892	-0.02593	0.228
WMR	-0.01102	-0.00978	0.01682	0.02666	0.01727	<u>0.12057</u>	0.0519	0.05439	0.02411	0.03521	0.09296	1.000
NPR	0.00466	0.00626	0.00967	0.00973	0.00734	0.00834	<u>0.01936</u>	0.00346	0.01438	0.01476	0.01465	0.438
LPR	0.00289	0.00436	-0.00339	-0.00006	0.00254	-0.00815	-0.00323	<u>-0.01807</u>	-0.00073	-0.00224	-0.00692	0.473
WPR	-0.00582	-0.00141	-0.00863	-0.00696	-0.01268	-0.00282	-0.01048	-0.00057	<u>-0.01411</u>	-0.01477	-0.01109	0.234
YF	0.06055	0.03841	0.07394	0.049	0.0853	0.04683	0.12224	0.01983	0.16786	<u>0.16037</u>	0.13128	0.991
YRP	0.12037	-0.00397	0.43288	0.33577	0.41679	0.67369	0.66113	0.33465	0.6867	0.71521	<u>0.87371</u>	0.327

Significance at 5% level - *

Significance at 1% level - **

Residual Effect = 0.1676

1. PH 180 :- Plant height at 180

2. NOL 180 :- Number of leaves at 180

3. NOT :- Number of tillers

4. LA :-Leaf Area

5. NMR :- Number of mother rhizome

6. WMR :- Weight of mother rhizome

7. NPR :- Number of primary rhizome

8 LPR :- Length of primary rhizome

9. WPR :- Weight of primary rhizome

10. YF :- Yield of finger rhizome per plant

11. YRP :- Yield of rhizomes per plot

12. TRY :- Total rhizomes yield per hectare

4.4.7 Number of primary rhizome

The direct effect of character number of primary rhizome on yield per hectare in turmeric was (0.01936) and the maximum indirect effect is via yield of rhizome per plot (0.66113) followed by yield of finger rhizomes per plot (0.12224). Positive and significant correlation was recorded between yield per hectare ($r=0.764$) and number of primary rhizome.

4.4.8 Length of primary rhizome (cm)

This trait had direct effect on yield per hectare in turmeric (-0.01807) and the maximum indirect effect is yield of rhizomes per plot (0.33465) followed by weight of mother rhizome (0.05439). The correlation between yield per hectare ($r=-0.369$) and length of primary rhizome recorded positive and significant.

4.4.9 weight of primary rhizome (g)

This trait had direct effect on yield per hectare in turmeric (0.011411) and the maximum indirect effect is yield of rhizomes per plot (0.6867) followed by yield of finger rhizomes per plant (0.16786). The correlation between yield per hectare ($r=0.59$) and weight of primary rhizome recorded positive and significant.

4.4.10 Yield of finger rhizome per plant (g)

This trait had direct effect on yield per hectare in turmeric (0.16037) and the maximum indirect effect is yield of rhizome per plot (0.71521) followed by weight of mother rhizome (0.03521) The correlation between yield per hectare ($r=0.818$) and yield of finger rhizome per plant recorded positive and significant

4.4.11 Yield of rhizomes per plot (g)

This trait had direct effect on yield per hectare in turmeric (0.87371) and the maximum indirect effect is yield of finger rhizome per plant (0.13128) followed by weight of mother rhizome (0.09296) The correlation between yield per hectare ($r=0.994$) and yield of finger rhizome per plant recorded positive and significant

4.5 Discussion

The present investigation "Genetic Variability and Correlation Studies in Turmeric" was carried out on twenty genotypes of turmeric during kharif season 2018 with the following objectives.

1. To investigate the extent of genetic variability among the available germplasm of turmeric.
2. To assess the extent of genotypic, phenotypic and environmental coefficient of variation, expected genetic advance and heritability for yield and yield contributing characters in turmeric.

In a crop improvement programme the success of selection depends on genetic variability and correlation studies between the characters in the population. The genetic variability estimated in terms of genotypic coefficient of variation and phenotypic coefficient of variation is not adequate for the estimation of heritable variation. The heritability values, in broad sense are also helpful in selections on the basis of phenotypic performance of the quantitative characters. However, heritability estimates alone are not of any use in predicting the result of selection unless, it is accompanied by genetic advance (Johnson *et al.*, 1955^{a&b}). The heritable variation among genotypes can be ascertained with greater degree of accuracy when heritability along with genetic advance is studied.

The correlation studies which indicate degree of relationship between yield and its components, among the components themselves is of great interest to plant and carries much practical significance.

The correlation studies provided information on nature, extent and direction of selection, but still it becomes difficult to find out the direct and indirect effect on the components. Thus, direct and indirect effects of yield components on yield assessed through the use of path analysis.

Considering these and ultimate aim exploiting all the possibilities for the improvement of the various characters studied, the results obtained in the present investigation are discussed here under.

4.5.1 Analysis of Variance

Perusal of data presented in Table 3, revealed significant differences among genotypes for all the traits, suggesting presence of wide range of variation among all the genotypes for all the characters under study. The variation amongst the genotypes as regards to characters might be due to genetic variability, inherent characters and climatic adaptability in a region, which might prove an important diagnostic character for selection of genotypes for local conditions. The findings are in consonance with Neethu *et.al.* (2017), Aarthi *et al.* (2018), Athira *et al.* (2018), Luiram *et al.* (2018), Maurya *et al.* (2018)

4.5.2 Genetic Variability Studies

The study of genetic variability present in the existing genetic stock, the extent to which desirable characters are in heritable and the method and mode of selection is of prime importance in making any breeding programme success. The observed phenotypic variability is the resultant of genotypic and environmental factors. Mostly economic characters are quantities in heritance, which are influenced by genotypic and environmental interactions. Therefore, it is required to disintegrate the phenotypic variance in to genetic and environmental components. Simultaneously, the estimate of heritability that indicates the degree of transmissibility of a trait into the off springs and genetic advance, a measure of expected genetic gain in the next generation through selection is of paramount importance. Therefore, genetic parameters *viz*, genotypic and phenotypic coefficients of variation, heritability (in broad sense) genetic advance and expected genetic advance (as per cent of mean) to explore the possibilities of improvement of various traits were estimated.

Estimates of GCV, PCV, and EGA as percent of means and heritability (h^2) are given in Table 5.

4.5.2.1. Range

The assessment of available germplasm for its nature and magnitude of genetic variability is a pre-requisite for developing any variety with high potential and the desired morphological and bio-chemical

characters. This helps the breeder to assess and identify superior genotypes before initiating the breeding programme for improvement of any crop. In the present study involving twenty turmeric genotypes, a wide range of variability observed for all the characters.

The yield of any crop is an important trait. Besides inherent genetic potential of genotypes, the yield is also influenced by environment. In turmeric, plant height (cm) 180 DAP, number of leaves 180 DAP, number of tillers per plant, leaf area (cm²), no of primary rhizome, girth of primary rhizome (cm), length of primary rhizome(cm), weight of primary rhizome(g), no of mother rhizome, length of mother rhizome(cm), girth of mother rhizome (cm), weight of mother rhizome(g), core diameter (cm), Yield of finger rhizome per plant (g), yield of rhizomes per plot (kg), total yield of rhizome per hectare (tonnes) were the yield contributing characters. The plant height (cm) at 180 DAP ranged from 100.13 to 143.19 (cm), number of leaves 180 DAP ranging from 8.45 to 13.26, number of tillers per plant ranged from 1.67 to 2.78, leaf area (cm²) range from 138.47 to 522.72, no of primary rhizome ranged from 3.06 to 12.80, girth of primary rhizome (cm) range from 1.52 to 6.73, weight of primary rhizome(g) ranging from 44.26 to 146.82, no of mother rhizome ranged from 1.93 to 4.01 , length of mother rhizome(cm) ranged from 3.84 to 9.93 , girth of mother rhizome ranged from 3.25 to 11.395 (cm), weight of mother rhizome ranged from 67.74 to 138.01 (g), core diameter ranging from 106.1.64 to 2.78 (cm), Yield of finger rhizome per plant ranging from 115.67 to 217.12 (g), yield of rhizome per plot ranging from 3.57 to 5.90 (kg), total yield of rhizome per hectare ranging from 14.73 to 24.31 (tonnes). Hence wide range of variability for these traits was observed in the present investigation. This result is encouraging because the presence of high variability, among the traits has been an indication of better chance for improvement. Significant variability for various characters in turmeric have been reported by various workers viz. Singh *et al.*, (2003), Singh *et al.*, (2012), Rajyalaxmi *et al.* (2013), Prajapati *et al.*(2014), Kallur *et al* (2017), Athira *et al.*(2018). The above findings were in broad conformity with the reports of these workers.

4.5.2.2. Genotypic and phenotypic coefficient of variation

It is essential to assess the genetic components of variability in the total variation before the variability can be utilized for further genetic improvement. The additive genetic variance will be the constant heritance portion of the total variation.

In the present investigation the phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all the characters (Table 5), indicating the substantial modifying effect of environment in the expression of all traits studied. These results corroborate the view of Rajyalakshmi *et al.*, (2013), Neethu *et al.* (2017), Athira *et al.*, (2018).

The highest genotypic coefficient of variation was observed for leaf area, no of primary rhizome, girth of primary rhizome, length of primary rhizome, length of mother rhizome, girth of mother rhizome. High GCV is an indication of greater range of variability among the population and the scope of improvement of these characters through simple selection.

Similar findings pertaining to different traits including the characters, number of tillers, number of primary rhizome Singh *et al.*, (2012), leaf area Singh *et al.*, (2014), number of primary rhizome, in turmeric, Aarathi *et al.*, (2018), number of mother rhizome, Maurya *et al.*, (2018), number of primary rhizome, Luiram *et al.* (2018)

Whereas the highest phenotypic coefficient of variation was observed for leaf area, no of primary rhizome, girth of primary rhizome, girth of mother rhizome , and length of primary rhizome, length of mother rhizome ,weight of primary rhizome, High PCV is an indication of the existence of wide scope of selection for the improvement of the traits from a considerable amount of variability present. Thus, a greater potential is expected in the selection for these characters. The above findings stood parallel with length of primary rhizome Singh *et al.*, (2003), length of primary rhizome, length of mother rhizome, weight of primary rhizome, Aarathi *et al.*, (2018)

Wide difference between PCV and GCV for yield implies it's susceptibility to environmental fluctuation, whereas narrow difference suggested their relative resistance to environmental alteration. This suggests the need for generation of variability either by introduction, exploration or by hybridization to get substantial gain in their improvement.

4.5.2.3. Heritability and Expected genetic advance (EGA)

The genotypic coefficient of variation is not sufficient to determine the amount of variation which is heritable. Burton (1952) also made clear that the heritable variation cannot be estimated through genetic coefficient of variation and as such the genotypic coefficient of variation together with heritability would furnish the most reliable information on the magnitude of genetic advance to be expected from selection.

In the light of this explanation, heritability was calculated to assist the breeder in choosing the characters that can be relief upon for selection.

The present study revealed high percentage of heritability in broad sense for the yield of finger rhizome per plant, leaf area, length of primary rhizome, girth of primary rhizome, length of mother rhizome, girth of mother rhizome, number of primary rhizome, weight of mother rhizome, total yield of rhizomes per hectare, yield of rhizomes per plot, number of leaves at 180 DAP, plant height at 120 DAP, number of leaves at 120 DAP and number of mother rhizome.

Medium heritability noticed in case of core diameter, weight of primary rhizome, plant height at 180 DAP and number of tillers. Low percentage of heritability was recorded for sprouting

High heritability indicated the effectiveness of selection based on phenotypic performance but does not necessarily mean a high genetic advance for the particular trait. The characters with high heritability when associated with high genetic gain may be attributed to the additive gene effects (Panse, 1957), which can be effectively be improved by selection. On the other hand, high heritability and low genetic advance may be attributed to low phenotypic variability. These characters may be improved

through hybridization, while low heritability estimates suggested that the selection for the character under consideration will not be effective.

The expected genetic advance (EGA) expressed as percentage over mean ranged from 2.88 (sprouting) to 98.61 percent (leaf area). In the present study high value EGA was observed for the characters leaf area (98.61%) followed by followed by number of primary rhizome (77.6%), girth of primary rhizome (71.13%), girth of mother rhizome (63.29%), length of primary rhizome (62.57%), length of mother rhizome (57.27%), yield of finger rhizome per plant (36.18%), weight of mother rhizome (36.11%), weight of primary rhizome (31.53%) total rhizome yield per hectare (29.04%), yield of rhizomes per plot (28.31%), number of leaves at 180 (28.07%), plant height at 120 (27.07%), number of mother rhizome (25.11%), The moderate values were recorded in the character number of leaves at 120 (19.93) core diameter (19.48%), number of tillers (67.73%), plant height at 180 (11.94%),

Low values of expected genetic advance were observed for the character sprouting (2.88%).

Similar findings with high EGA were pertaining to different traits reported for the character weight of mother rhizome, length of mother rhizome Prajapati *et al.*, (2014), weight of primary rhizome , weight of mother rhizome, number of primary rhizome , yield of finger rhizome per plant Luiram *et al.*, (2018), Number tillers per plant, , Number of primary rhizome, weight of mother rhizome, Hachinamani *et al.*, (2016), Number of primary rhizome, Weight of mother rhizome, Weight of primary rhizome, Length of primary rhizome Salimath *et al.*, (2017).

Similar findings with moderate EGA were pertaining to different traits reported for the character number of leaves at 120, number of leaves at 180, Singh *et al.*, (2012), plant height at 120 Aarthi *et al.* (2018). The low EGA was reported for the character core diameter Neethu *et al.* (2017).

Generally high heritability accompanied with high genetic advance in a characters suggest that the inheritance of such character was

governed mainly by additive gene effects and therefore improvement in these traits would be more effective by selection in the present material. During present study characters like yield of finger rhizome per plant, leaf area, length of primary rhizome, girth of primary rhizome, length of primary rhizome, girth of mother rhizome, number of primary rhizome, weight of mother rhizome, yield of mother rhizome per hectare and yield of mother rhizome per plot had high heritability values along with the high genetic advance. Although, estimates of high heritability are useful to breeder as they provide basis of transmissible genes from parent to progeny. More reliable conclusion can be drawn when heritability is considered along with the genetic advance. Thus, the expressions of these traits were predominantly governed by additive gene effects and therefore selection based on phenotypic performance will be useful to improve these characters in future. More, over it was seen that these traits had less influence of the environment. These results are in consonance with the character number of primary rhizome, length of primary rhizome, girth of mother rhizome, weight of mother rhizome, Prajapati *et al.*, (2014), Number of mother rhizome, Number of primary rhizome, Weight of mother rhizome Hachinamani *et al.*, (2016), Number of mother rhizome, Number of primary rhizome, Weight of mother rhizome, Weight of primary rhizome, Length of primary rhizome, Salimath *et al.*, (2017), number of leaves per plant, number of primary rhizome Luiram *et al.*, (2018).

During present study estimates of high heritability along with moderate genetic advance were observed for the characters The moderate values were recorded in the character number of leaves at 120, plant height at 120, core diameter

These characters can be partially improved by selection. The results corroborate with the view of .when heritability is predominantly due to non-additive gene effects (dominance and epistasis) then the genetic gain by selection would be low, as observed in present study for these fifteen characters. Recurrent selection may be employed to carry out further improvement for these characters. The high heritability is being exhibited due to favorable influence of environment rather than genotype. The

improvement in these traits would be more effective by selecting specific combinations.

4.5.3 Correlation

The interrelationship between two characters can be directly observed by the phenotypic correlations. The genotypic correlation may be interpreted as the correlation of breeding value. When two characters are invariably and linearly associated, the underlined, genetic mechanism causing such association may be due to complete linkage between the two traits or pleiotropy, some gene may increase both the traits (positive association), while other may increase one and reduces the other (negative association). The present discussion is mostly concentrated on genotypic correlation because they provide an idea of association at genotypic level of inherent association between two traits and that help in carry out reliable selection in situation where phenotypic and genotypic association is closer one.

In the present investigation, the estimates of genotypic correlation were slightly higher than the corresponding phenotypic correlation (Table 6) indicates that genotypic was superior but their expression was reduced under the influence of environment.

In the present investigation, the characters exhibiting significant positive phenotypic correlation with total rhizome yields per hectare were found to be length of mother rhizome and weight of mother rhizome. These characters were also positively interlinked with among themselves. Thus, it indicated the importance of these character while selection.

The character plant height at 180 DAP showed positive and significant correlation with number of leaves at 180, weight of primary rhizome, yield of finger rhizome per plant at genotypic level. However it showed negative and non-significant genotypic and phenotypic correlation with leaf area, weight of mother rhizome and length of primary rhizome.

Number of leaves at 180 DAP showed positive and significant correlation with number of tillers and number of primary rhizome at both

genotypic and phenotypic level. While, it exhibit negative and non-significant correlation with weight of mother rhizome, length of primary rhizome, yield of finger rhizome per plant at genotypic level.

The character leaf area showed positive and significant correlation with number of primary rhizome and weight of primary rhizomewhile, positive and non-significant genotypic correlation with, Number of mother rhizome, weight of mother rhizome.

Number of tillers showed positive and significant genotypic correlation with leaf area, number of mother rhizome, number of primary rhizome, weight of primary rhizome, yield of rhizomes per plot, yield of fingers per plant and total yield of rhizomes per hectare

Number of mother rhizome showed positive and significant correlation with number of primary rhizome. Weight of primary rhizome, yield of finger rhizome per plant and yield of rhizomes per hectare.

The character weight of mother rhizomes showed positive and significant genotypic and phenotypic correlation for number of primary rhizome. length of primary rhizomes However it showed positive genotypic correlation with number of primary rhizomes and length of primary rhizomes. Similar findings reported by Hazra *et al.* (2002), Raveendra *et al.* (2001), Yadav *et al.* (2006). Prajapati *et al.*, (2014) and Verma *et al.*, (2014) and Kallur *et al.*, (2017)

The character number of primary rhizome showed positive and significant genotypic and phenotypic correlation weight of primary rhizomes and yield of rhizomes per plot and total yield of rhizomes per hectare. Kallur *et al.*, (2017), Prajapati *et al.*,(2014) and Verma *et al.*, (2014)

The character length of primary rhizomes showed positive and significant genotypic correlation with yield of mother rhizomes per plot and yield of mother rhizomes per hectare.

The character weight of primary rhizomes showed positive and significant genotypic correlation with yield of finger rhizomes per plant and total yield of rhizomes per hectare diameter. Hazra *et al.* (2002),

Raveendra (2001), Yadav *et al.* (2006) Panja *et al.*, (2002), Prajapati *et al.*, (2014), Verma *et al.*, (2014), and Kallur *et al.*, (2017).

The character yield of rhizome per plot showed positive and significant genotypic correlation with yield of finger rhizome per plant and total yield of rhizome per hectare.

The character yield of finger rhizome per plant showed positive and significant genotypic correlation with total yield of rhizome per hectare

4.5.4 Path coefficient analysis

The genotypic path diagram (Fig. 4) shows the nature of cause and effect system. It consist of eighteen characters The characters studied were 1) Sprouting (%), 2) Plant height (cm) 120 3) Plant height (cm) at 180 DAP, 4) Number of leaves 120 5) Number of leaves at 180 DAP, 6) Number of tillers per plant, 7) Leaf area (cm²), 8) Number of primary rhizomes, 9) Girth of primary rhizomes (cm), 10) length of primary rhizomes (cm), 11) Weight of primary rhizomes (g), 12) Number of mother rhizomes, 13) Length of mother rhizomes (cm), 14) Girth of mother rhizomes (cm), 15) Weight of mother rhizomes (g), 16) Core diameter (cm), 17) Yield of finger rhizomes per plant (g), 18) Yield of rhizomes per plot (kg), 19) Total yield of rhizomes per hectare (tonnes) residual factor (represented by 'x'). All the components were related directly or indirectly with yield and inter-related among themselves except residual factor.

The result of path coefficient analysis presented in Table 7 and Table 8 are discussed as under.

Plant height at 180 DAP showed positive indirect effect with number of leaves at 180 DAP, leaf area, number of primary rhizome and length of primary rhizome and negative indirect effects with number of tillers. The above findings stood parallel with Rajyalakshmi *et al.*, (2013).

Number of leaves at 180 DAP showed positive and non-significant correlation with rhizome yield per hectare and path analysis revealed it had positive direct effect on rhizome yield per hectare and indirect positive effects via number of primary rhizome, length of primary

rhizome and total rhizome yield per hectare. Path analysis revealed that the correlation was due to direct effects of these characters' through another component traits, will be effective in carry out yield improvement. The above findings stood parallel with Rajyalakshmi et al. (2013)

Number of tillers showed negative and non-significant correlation with total rhizome yield per hectare and path analysis revealed it had negative direct effect on rhizome yield per hectare and indirect positive effects via plant height at 180 DAP and number of leaves at 180 DAP. Hence, path analysis studies confirmed the effectiveness of number of tillers influencing the high rhizome yield per hectare in turmeric. Rajyalakshmi *et al.* (2013)

The correlation between leaf area and total rhizome yield per hectare showed positive and significant. It had exhibited negative direct effect on rhizome yield per hectare and indirect positive effects via number of primary rhizome and weight of mother rhizome. Path analysis revealed that the correlation is due to indirect effects of these characters' through another component traits, hence indirect through this will be effective in carrying out yield improvement.

Number of mother rhizome showed high positive and significant correlation with total rhizome yield per hectare and path analysis revealed it has positive direct effect on total rhizome yield per hectare and indirect positive effect via weight of mother rhizome, number of primary rhizome and length of primary rhizome.

The character weight of mother rhizome showed positive and significant correlation with total rhizome yield per hectare. Weight of mother rhizome exhibited high positive direct effect on total rhizome yield per hectare. Thus path analyses showed the significant role of weight of mother rhizome in breeding for high yield in turmeric. The above findings stood parallel with, Singh and Tiwari (1995), Tomar *et al.* (2005) and Yadav *et al.* (2006), Velmurugan *et al.* (2008), Sharon *et al.* (2011), Prajapati *et al.* (2014), Kallur *et al.*, (2017) and Aarthi *et al.*, (2018).

Number of primary rhizome showed positive and significant correlation with rhizome yield per hectare. Path analysis indicated that positive direct effect on rhizome yield per hectare, and indirect positive effects via weight of mother rhizome and number of primary rhizome. Number of primary rhizome showed positive indirect effect on rhizome yield per hectare. Path analysis revealed that the correlation is due to indirect effects of these characters' through another component traits, hence indirect through this will be effective in carrying out yield improvement. These findings also agree with the findings of Kallur et al., (2017)

The character length of primary rhizome showed positive and significant correlation with total rhizome yield per hectare. From path analysis revealed, it had negative direct effect on total rhizome yield per hectare and indirect positive effects via number of mother rhizome, number of primary rhizome and weight of mother rhizome. Hence path analysis revealed true relationship between these characters and this trait will be rewarding for yield improvement. Similar findings were reported by Hazra *et al.* (2000), Tomar *et al.* (2005) and Yadav *et al.* (2006).

The character weight of primary rhizome showed positive and significant correlation with rhizome total rhizome yield per hectare. Path analysis revealed it had high positive direct effect and positive indirect effect on rhizome yield per hectare and indirect positive effects via weight of mother rhizome and number of primary rhizome. Hence path analysis revealed true relationship between these characters and this trait will be rewarding for yield improvement. Similar findings were reported by Singh and Tiwari (1995), Jana *et al.* (2001), Chatopadhyay *et al.* (2004), Sharon *et al.* (2011), Prajapati *et al.* (2014), Kallur *et al.*, (2017), Aarthi *et al.*, (2018).

The character yield of rhizome per plot showed positive and significant correlation with rhizome yield per hectare. Path analysis revealed that yield of mother rhizome per plot had positive direct and positive indirect effect on rhizome yield per hectare. The path analysis thus

pinpointed the significant role of yield of mother rhizome per plot in turmeric breeding for yield improvement.

The character yield of finger rhizome per plant showed positive and non-significant correlation with rhizome yield per hectare. Path analysis revealed that yield of finger rhizome per plant had negative direct and positive indirect effect on rhizome yield per hectare. The path analysis thus pinpointed the insignificant role of yield of finger rhizome per plant in turmeric breeding for yield improvement

Path coefficient analysis indicated that utility of the character viz., leaf area, n number of mother rhizome, weight of mother rhizome, number of primary rhizome, length of primary rhizome, yield of rhizomes per plot because of their strong genotypic correlation with rhizome yield per hectare. The path analysis further suggested that the yield of finger rhizome per plant, weight of mother rhizome which showed highest positive direct effects as the major yield contributing traits for enhancing the yield, they are most reliable and effective character for selection when high yield is objective.

CHAPTER V

SUMMARY AND CONCLUSION

The present study on "Genetic variability and correlation studies in Turmeric" was undertaken on twenty genotypes of turmeric. The statistical design adopted was Randomized Block Design with two replication. This experiment was carried out during *kharif* season of 2018 at Instructional Farm and analytical work was done at Analytical Laboratory, Department of Vegetable Science, Faculty of Horticulture, Dr. Panjabrao Deshmukh Krishi Vidyapeeth, Akola with the following objectives:

- 1) To investigate the extent of genetic variability among the available germplasm of turmeric.
- 2) To estimate the genotypic and phenotypic correlation coefficient and path coefficient of yield and yield components in turmeric.

Salient findings of the present investigation are being summarized below:

A wide range of variability was observed for all the characters. The estimates of genotypic coefficients of variation were lower than that of phenotypic coefficient of variation for all the characters indicating the substantial modifying effect of environment in the expression of all traits under study.

The highest genotypic and phenotypic coefficient of variation was observed for the character leaf area 48.46% (G), leaf area (49.07%), (P). followed by number of primary rhizomes 40.37% (G), 43.26% (P), girth of primary rhizomes (35.26% (G), 36.01% (P), girth of mother rhizomes (32.17%) (G), 33.70% (P) indicating predominance of additive gene action in the inheritance of this character revealing like hood of favorable response to selection by this character. In respect of other characters studied presence of low genotypic coefficient of variation as well as phenotypic coefficient of variation indicated predominance of non-additive type of gene action in the inheritance of these characters.

The heritability estimates (broad sense) for the characters studied showed wide range from high degree leaf area (97%) to sprouting (8.86%). This has extended the hope for reliability of selection in the present material studied. Since, it is broad sense heritability a caution has to be exercised for its direct application while making the selection.

The genetic advance in the present study showed wide range sprouting (2.88) to leaf area (98.61). These results observed with high values for expected genetic advance accompanied with high heritability estimates are indicative of fact that the improvement could be effectively realized through selection in these characters on phenotypic values.

High heritability coupled with high genetic advanced observed for leaf area, girth of primary rhizomes, length of primary rhizomes, girth of mother rhizomes, length of mother rhizomes, weight of mother rhizomes and weight of primary rhizomes indicated that these characters were governed largely through the additive gene effect and improvement of these characters may be achieved through phenotypic selection.

The correlations amongst the yield attributes indicate that leaf area, number of mother rhizomes, weight of mother rhizomes, number of primary rhizomes, weight of primary rhizomes, length of primary rhizomes, weight of primary rhizomes, yield of rhizomes per plot and yield of finger rhizomes per plant showed positive and significant direction and they are helpful and advantageous for improvement in yield.

Path analysis indicated the importance of yield contributing characters like leaf area, number of mother rhizomes, weight of mother rhizomes, number of primary rhizomes, length of primary rhizomes, weight of primary rhizomes, yield of rhizomes per plot and yield of finger rhizomes per plant which have directly and indirectly influenced all the correlations of yield with its components.

Conclusion:

On the basis of findings reported in present investigation the following conclusions could be drawn.

The mean sum of squares for all the characters studied was found to be significant, indicating the variation for the characters under study.

Phenotypic coefficient of variation in general were greater in magnitude than the corresponding genotypic ones. The differences between PCV and GCV for many characters such as height of plant at 120 DAP, No. of leaves at 120 DAP, leaf area, weight of mother rhizomes, yield of finger rhizomes per plant were found minimum indicating less environmental effect. High values of GCV and heritability estimates supplemented with greater genetic gains are also indicative of additive gene effects regulating the inheritance of such traits therefore, these characters reflect greater selective value and offer ample scope for selection and phenotypic coefficient of variation was lessened under the influence of environment.

The total yield of rhizomes per hectare recorded significant correlation with leaf area, number of mother rhizome, weight of mother rhizomes, number of primary rhizomes, length of primary rhizomes, weight of primary rhizomes, yield of finger rhizomes per plant and yield of rhizomes per hectare indicating that the superior yielding ability was associated with these yield contributing characters.

Based on direct and indirect effects of different yield components on yield it appears that it would be rewarding to lay stress on leaf area, number of mother rhizomes, weight of mother rhizomes, number of primary rhizomes, length of primary rhizomes, weight of primary rhizomes and yield of finger rhizomes per plant will be useful in identifying the genotypes as parents for further improvement in turmeric.

The genotypes *viz.*, PDKV Waygaon, AKTL-13, AKTL-8, AKTL-11, AKTL-17, AKTL-19 and Gondia Haladi-1 on the basis of yield and yield contributing characters are found promising for future improvement programme. Hence, these genotypes may be given consideration while formulating selection indices for the improvement of yield in turmeric.

CHAPTER VI

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(Rathod Pavan Vanraj)

Appendix																					
Weekly Weather data for the year 2018 recorded at Meteorological Observatory Department of Agronomy Dr. PDKV., Akola																					
Weeks	Dates	Actual				2018				Normal				1971-2000							
		T MAX (oC)		T MIN (oC)		BSH (hrs)		WS (km/hr)		RH I (%)		RH II (%)		Evap (mm)		RF (mm)		CRF (mm)	Rainy Days		
		N	A	N	A	N	A	N	A	N	A	N	A	N	A	N	A		N	A	
19	7-13	42.6	43.7	26.5	29.3	10.1	9.4	12.7	6.3	43	30	17	11	16.4	14.9	0.3	0.5	4.9	0.1	0.0	
20	14-20	42.6	43.5	27.3	31.1	9.7	8.0	14.6	6.9	48	34	18	14	17.3	14.9	1.8	0.0	4.9	0.2	0.0	
21	21-27	42.4	44.3	27.4	31.1	9.8	7.6	15.7	8.8	50	41	20	18	17.0	15.0	4.1	0.0	4.9	0.5	0.0	
22	28-3 Jun	41.9	43.1	27.6	29.5	9.7	8.0	16.2	8.8	56	50	23	23	16.3	14.5	5.7	8.5	13.4	0.5	1.0	
31	30-5 Aug	31.1	32.2	23.1	24.2	3.6	5.8	11.7	8.1	88	81	66	56	4.6	6.0	49.3	3.2	561.6	2.5	1.0	
32	6-12	30.2	30.8	22.9	24.3	3.5	1.4	11.6	9.4	87	84	69	65	4.2	5.2	59.9	4.8	566.4	2.9	1.0	
33	13-19	30.5	29.4	22.8	24.0	4.4	1.2	11.7	8.5	86	89	66	74	4.5	4.1	40.6	97.8	664.2	2.2	3.0	
34	20-26	30.5	27.6	22.6	22.6	4.3	1.8	11.0	9.2	88	91	66	77	4.3	4.0	46.7	106.4	770.6	2.0	3.0	
35	27-2 Sep	30.4	28.5	22.7	23.4	4.4	0.1	10.6	6.6	86	88	64	70	4.2	2.9	47.1	1.0	771.6	2.4	0.0	
36	3-9	31.1	29.8	22.5	21.9	5.7	3.8	9.1	8.1	85	84	61	56	4.7	4.5	28.5	1.0	772.6	1.5	0.0	
37	10-16	32.2	32.6	22.4	24.0	7.1	8.6	9.0	2.6	85	81	56	48	5.1	5.6	18.9	0.0	772.6	1.1	0.0	
38	17-23	33.4	33.3	22.3	23.1	7.2	4.4	8.5	3.3	83	85	53	52	5.3	4.9	24.6	62.4	835.0	1.4	2.0	
39	24-30	33.7	33.6	21.9	22.7	7.6	8.5	5.4	0.6	83	85	50	49	4.9	4.5	24.4	0.0	835.0	1.5	0.0	
40	1-7 Oct	33.9	35.1	20.2	21.3	8.1	8.6	7.5	0.6	81	78	45	38	5.5	4.9	21.8	0.0	835.0	1.1	0.0	
41	8-14	34.1	35.4	18.7	18.6	4.2	8.6	4.1	0.8	76	77	40	29	5.3	5.1	16.0	0.0	835.0	0.9	0.0	
42	15-21	33.9	34.8	18.1	19.3	8.4	8.5	4.4	0.5	74	72	36	30	5.5	5.1	3.1	0.0	835.0	0.4	0.0	
43	22-28	33.1	35.3	18.5	17.1	8.4	8.9	4.1	0.4	73	68	36	22	5.3	5.2	10.0	0.0	835.0	0.6	0.0	
44	29-4 Nov	33.0	33.4	15.8	18.1	8.7	8.9	4.7	1.3	72	68	31	32	5.3	5.9	2.3	0.0	835.0	0.3	0.0	
45	5-11	32.4	33.6	14.8	16.5	8.6	7.0	4.5	0.5	70	76	30	28	5.2	4.2	3.7	0.0	835.0	0.3	0.0	
46	12-18	31.7	33.3	13.7	14.0	8.6	8.9	4.6	0.4	70	66	30	20	4.9	5.0	1.1	0.0	835.0	0.2	0.0	
47	19-25	31.0	32.8	13.1	17.2	8.6	7.8	4.4	0.6	71	78	30	34	4.6	4.8	10.1	4.5	839.5	0.3	1.0	
48	26-2 Dec	30.3	31.0	12.4	12.3	8.8	8.0	4.6	0.5	71	74	31	27	4.3	4.3	6.8	0.0	839.5	0.3	0.0	
49	3-9	29.8	29.8	11.2	15.9	8.7	5.2	4.7	0.9	70	76	29	41	4.3	4.0	1.3	0.0	839.5	0.2	0.0	
50	10-16	29.4	28.9	10.3	12.3	8.8	6.6	4.5	1.1	70	83	27	31	4.2	4.1	1.3	0.0	839.5	0.2	0.0	
51	17-23	29.5	26.5	10.6	10.2	8.7	7.5	4.7	1.1	69	116	29	34	4.3	4.2	0.9	0.0	839.5	0.1	0.0	
52	24-31	29.2	27.5	10.7	9.6	8.6	8.4	4.8	1.5	70	59	31	23	4.3	5.0	2.6	0.0	839.5	0.2	0.0	

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1	1-7 Jan	29.0	29.8	10.3	9.4	8.7	8.4	4.9	0.7	78	68	30	22	4.2	4.0	1.7	0.0	0.0	0.2	0.0
2	8-14	29.2	28.1	11.3	10.0	8.6	7.8	6.3	1.2	71	72	30	30	4.5	5.4	3.4	0.0	0.0	0.2	0.0
3	15-21	29.9	29.4	11.6	10.4	8.9	7.6	5.4	1.2	69	66	28	24	4.8	5.2	0.9	0.0	0.0	0.1	0.0
4	22-28	30.8	28.1	11.8	14.0	9.1	6.1	5.5	1.7	67	75	27	36	5.2	5.0	1.1	0.0	0.0	0.2	0.0
5	29-4 Feb	31.1	28.1	12.1	10.7	9.3	7.9	5.8	1.5	61	61	25	22	5.6	5.3	2.8	0.0	0.0	0.2	0.0
6	5-11	31.3	29.6	11.9	13.3	9.1	8.2	5.6	3.6	59	49	23	20	5.9	6.3	4.9	0.0	0.0	0.4	0.0
7	12-18	32.5	32.2	13.4	15.9	9.4	7.9	6.1	2.3	56	54	22	24	6.6	5.9	0.1	0.0	0.0	0.0	0.0
8	19-25	33.0	35.5	13.8	18.6	9.5	8.6	6.5	2.4	57	55	22	21	7.3	6.1	3.3	1.9	1.9	0.5	0.0

9	26-4 Mar	34.7	33.2	14.8	17.7	9.6	8.9	7.0	4.0	50	47	17	23	8.1	7.8	3.4	0.0	1.9	0.3	0.0
10	5-11	36.1	33.7	16.7	16.2	9.6	9.1	6.8	3.2	44	48	18	21	9.0	7.5	2.1	0.0	1.9	0.3	0.0
11	12-18	37.3	36.8	17.5	16.9	9.6	8.5	6.9	3.1	42	43	17	21	9.5	8.1	2.5	0.0	1.9	0.3	0.0
12	19-25	38.5	37.9	18.3	15.9	9.6	8.9	6.9	2.2	37	47	13	18	10.5	8.4	0.3	0.0	1.9	0.1	0.0