GENETIC DIVERGENCE, CORRELATION AND PATH COEFFICIENTS STUDIES IN TULSI (*Ocimum spp*.)

By
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(2021A73M)

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CERTIFICATE – I

This is to certify that this thesis entitled, **"Genetic divergence, correlation and path coefficients studies in Tulsi (*Ocimum spp*.)"** submitted in partial fulfilment of the requirements for the degree of **Master of Science** in the subject of **Genetics and Plant Breeding** to the **Chaudhary Charan Singh Haryana Agricultural University**, **Hisar** is a record of bonafide research work carried out by **Mr. Vijay Kumar C. Talawade**, Admission No. **2021A73M** under my supervision and that no part of this thesis has been submitted for any other degree.

The assistance and help received during the course of investigation has been fully acknowledged.

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This is to certify that this thesis entitled, **"Genetic divergence, correlation and path coefficients studies in Tulsi (*Ocimum spp*.)"** submitted by **Mr. Vijay Kumar C. Talawade**, Admission No. **2021A73M** to the **Chaudhary Charan Singh Haryana Agricultural University, Hisar** in partial fulfilment of the requirements for the degree of **Master of Science** in the subject of **Genetics and Plant Breeding** has been approved by the Student's Advisory Committee after an oral examination on the same, in collaboration with the external examiner.

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ABBREVIATIONS

%	Per cent
ANOVA	Analysis of variance
C.D	Critical difference
C.V	Coefficient of variation
cm	Centimetre
DF	Days to 50% flowering
DHY	Dry herbage yield/plant
DM	Days to maturity
et al.	*et alia*
FHY	Fresh herbage yield/plant
FW	Number of flowers' whorls/spike
g	Gram
GCV	Genotypic coefficient of variation
H^2 (bs)	Heritability in broad sense
i.e.	*id est; that is*
NSP	Number of spikes/plant
OC	Oil content
PB	Number of primary branches/plant
PCV	Phenotypic coefficient of variation
PH	Plant height
RBD	Randomized Block Design
S.E.(m)	Standard error of mean
SDL	Seedling length
SDW	Seedling dry weight
SG	Standard germination (%)
SL	Spike length
SVI-I	Seed vigour index-I
SVI-II	Seed vigour index-II
SW	1000 seed weight
SY	Seed yield/plant
viz.	*Videlicet*

CHAPTER- I

INTRODUCTION

Tulsi is a medicinal and aromatic crop plant that belongs to the Lamiaceae family and the *Ocimum* genus. There are about 252 genera and approximately 6700 species in this family (Mabberley, 1997) and most of them have medicinal properties (Wren, 1971). The genus *Ocimum* is represented by 66 species across the world. *Ocimum* is a versatile aromatic and most important genus of the family Lamiaceae due to its immense use in traditional system of medicine, perfumery and pharmaceutical industry (Simpson & Conner, 1986). All the aromatic plants belonging to the genus *Ocimum* are collectively called Basil. The genus "*Ocimum*" gets its name from the Greek word "ozo" which means "fragrance". Similarly, the name "basil" comes from the Greek word "basilica", which means "Royal herb" because it was believed to have been used in royal baths as anointing oils. In Sanskrit, the word "*Tulsi*" means "matchless one". *Tulsi* is widely regarded as the "King of Herbs" since the plants of *Tulsi* flourish predominantly as herbs and shrubs and usually survive as annual or perennial. *Tulsi* is native to the Indian subcontinent and is widespread as a cultivated plant in the entire region of the Southeast Asian tropics. The *sanctum* species of the genus *Ocimum* is distributed in entire Indian subcontinent, as compared to other species of this genus (Nadkarni, 1976). *Ocimum tenuiflorum* is a synonymous name of *Ocimum sanctum*. Africa's tropical rain forests are home to 59 species, having the highest diversity in the genus followed by South Africa's subtropical areas (19 species), Arabia (11 species), Brazil (11 species), India (9 species), Ethiopia (8 species) and Madagascar (7 species) (Krishnamoorthy, 1989; Pushpangadan & Bradu, 1995; Verma *et al*., 1998). *Ocimum basilicum, O. kilimandscharicum, O. sanctum, O. gratissimum*, etc. are extensively cultivated species in many parts of the World (France, UK, USA, Reunion, India, etc.) (Kothari *et al*., 2001). According to the Indian Horticulture Database 2020-21 published by the National Horticulture Board, *Ocimum* is cultivated over an area of 97,300 hectares of land and with a production of 1,92,500 metric tonnes of herbage yield. Madhya Pradesh is the largest producer of *Ocimum* in India followed by Gujarat, Uttar Pradesh, Rajasthan and Bihar.

In India, so far about 9 species of *Ocimum* (*Ocimum tenuiflorum* L., *O. basilicum* L., *O. gratissimum* L., *O. kilimandscharicum* L., *O. micranthum* L., *O. campechianum* L., *O. americanum* L., *O. minimum* L. and *O. citriodorum* L.) have been reported of which the last three are exotic species (Balyan & Pushpangadan, 1988). The *Ocimum basilicum* and *O. sanctum* species are most widely distributed in India. *Ocimum americanum* and *O. canum* are two species that are primarily found in north-western India, including Jammu and Kashmir, Punjab, Himachal Pradesh, Delhi and Uttar Pradesh. *O. gratissimum* is found across North India (Krishnamoorthy, 1989). The *O. basilicum* is known by various names such as ‘Sweet Basil’, ‘Common Basil’ or ‘French Basil’. The *O. canum* species with a peculiar mint smell is known as ‘Mint Basil’. The camphor containing species *O. kilimandscharicum* is commonly called ‘Camphor Basil’. The species *O. canum* having borneol smell is known as ‘Hoasy Basil’ and the species *O. gratissimum* with high contents of eugenol is known as ‘Spice Basil’. Hindus worship the plants of *O. sanctum* hence it is popularly known as ‘Sacred Basil’ or ‘Holy Basil’. The genus *Ocimum* exhibits a range of chromosome numbers, including various haploid chromosome numbers (12, 13, 16, 20, 24, 32, 36 and 38) in addition to the basic chromosome number. According to Carovic *et al.* (2010), the basic chromosome number for *Ocimum species* is x=12. Moreover, *O. basilicum* and *O. americanum* are known to be tetraploid (2n=4x=48) and hexaploid (2n=6x=72), respectively (Sobti & Pushpangadan, 1979).

The *Ocimum species* showcase remarkable morphological diversity owing to significant variations in their leaf size, shape, colour and pubescence, which have evolved over the centuries of cultivation. They are highly branched and can grow to a height ranging from 60-150 cm. Their stems and twigs are quadrangular in shape. The leaves are simple and have petioles and appear in a range of shapes from elliptical to ovate and have either entire or serrated margins. The leaves of these plants also bear sessile glands which secrete strongly scented volatile oils with aromatic flavours. The plants have small flowers that are white or purple in colour. These flowers are hermaphrodite and zygomorphic in nature. They are arranged in whorls on racemose inflorescence. The flowers have didynamous stamens and a style with bifid stigma. After the successful process of entomophilous pollination, the corolla naturally detaches and gives way to the development of four round seeds inside the bilabiate calyx. The seed’s shape varies from elliptical to globose and becomes mucilaginous when wetted (Pushpangadan & Bradu, 1995).

Plants are the primary source of secondary metabolites and oils with therapeutic potential due to which people have relied on plant-based medicines for health care since the dawn of civilization. The therapeutic properties of *Ocimum* have been acknowledged since ancient times, not only in India but also in the ancient civilizations of China, West Asia, Europe and Africa. This recognition has elevated the status of *Ocimum spp.* to a highly valued medicinal and aromatic crop plants. *Tulsi* is a valuable natural source of various essential oils and fragrant compounds that hold great economic and medicinal significance. Its essential oils contain several notable chemicals including eugenol, methyl eugenol, thymol, linalool, methyl chavicol, camphor, citral, elimicin, sesquiterpene alcohols, linalyl acetate, geraniol, and methyl cinnamate (Gupta & Sobti, 1993; Khosla *et al.*, 2000). The medicinal herb *O. basilicum* has generally been used to cure renal problems, warts, worms, cough, diarrhoea and headaches. Its oil is directly applied to the skin for treating acne and externally it can be used as an ointment for bug bites (Javanmardi *et al*., 2002). Its seeds are used in treatment of dysentery and chronic diarrhoea (Gangrade *et al*., 2000). Oil of *O. gratissimum* has been recommended for use in biological mosquito control because of its ability to repel insects. Leaves of *O. canum* are used to cure a variety of eye conditions, bronchitis as well as parasitic skin conditions (Naithani & Kakkar, 2002).

Estimation of the genetic variability parameters provides information regarding the magnitude of phenotypic and genotypic coefficients of variation, heritability in broad sense, expected genetic advance, etc. which is helpful in the development of superior genotypes. Correlation analysis in plant breeding offers precise information about association between yield and yield contributing traits and thereby facilitate breeders to select superior genotypes from diverse genetic populations. Path coefficient analysis is designed on the assumptions of linearity and additivity and to measure the causes of association between two variables and provides information about the direct and indirect effects of independent variables on dependent variables. Genetic diversity plays an important role in plant breeding either to generate productive recombinants or to exploit heterosis. The divergence analysis can be a valuable instrument in measuring the extent of divergence between distinct germplasm lines. Thus, detailed understanding of the type and extent of genetic divergence can aid plant breeders in identifying genetically diverse plants that can be used in crop improvement programmes (Arunachalam, 1981).

Although, *Ocimum* possesses medicinal and aromatic properties of high value, it is not commonly grown on a large scale. It may become a significant crop in near future as a result of the increasing demand for aromatic compounds in the food, flavours and the pharmaceutical industries. The low cultivation area and yield of *Ocimum* can be attributed to the unavailability of genotypes that are suitable for the specific regions. When selecting *Tulsi* for cultivation, farmers consider the yield and quality of the herb and oil, as well as other related characteristics that contribute to an increased economical yield and profit. It is essential to conduct studies of different genotypes across various agro-climatic regions to identify the best-yielding genotypes with unique attributes that influence the yield. This approach will allow us to recognize promising genotypes that can be used in breeding programmes to improve the yield of sacred basil. Therefore, keeping the above points in view, the present investigation has been planned with the following objectives:

1. To study the genetic variability in *Tulsi* for seed yield and its component traits.
2. To estimate the correlation and path coefficients for seed yield and its contributing traits.
3. To determine the extent of genetic diversity for different traits to classify the *Tulsi* genotypes into different clusters.

CHAPTER- II

REVIEW OF LITERATURE

A deep understanding of the amount of genetic variation, heritability, nature and magnitude of correlation coefficients, path coefficients analysis and genetic diversity analysis studies of yield and yield attributing traits is very necessary for sound crop improvement programmes to develop the improved cultivars of different crops. Considering the objectives of present research problem entitled, "Genetic divergence, correlation and path coefficients studies in Tulsi (*Ocimum spp*.)", the literature pertaining to this investigation has been explained under the following headings and sub-headings:

2.1 To study the genetic variability in *Tulsi* for seed yield and its component traits.

2.1.1 Genetic variability parameters

2.2 To estimate the correlation and path coefficients for seed yield and its contributing traits.

2.2.1 Correlation coefficients analysis

2.2.2 Path coefficients analysis

2.3 To determine the extent of genetic diversity for different traits to classify the *Tulsi* genotypes into different clusters.

2.3.1 Genetic diversity analysis

2.1.1 Genetic variability parameters

The presence of wide range of genetic variability enables plant breeders to make the selection for the desirable traits for crop improvement. This process involves selection of desirable genotypes with high genetic variability as they may be crossed with each other to develop the new breeding material with more genetic variation. Knowledge about the morphological variation of the various plant characters enables the plant breeders to effectively utilize the available germplasm lines for the development of desired genotypes. Estimating genotypic coefficients of variation (GCV) and phenotypic coefficient of variation (PCV) is essential to understand the genetic and environmental factors affecting the variability of traits in plant populations. Thus, aiding in the selection of superior individuals for breeding programmes. Heritability is an important concept which provides a valuable information to plant breeders on how much of the variation in a trait is due to the genetic factors which is passed on to the off-springs in the next generation. Therefore, knowledge about the magnitude of heritability is very important in selecting the best performing plants for improving crop yields, quality, pest and disease resistance. Genetic advance as a percent of mean is a measure used in plant breeding to assess the effectiveness of selection for a particular trait. Studying genetic advance as a percent of mean is important because it helps plant breeders assess the rate of genetic improvement in a population. Literature related to genetic variability parameters is presented below:

Maheshwari & Singh (1989) carried out a study to evaluate 18 exotic collections of *Ocimum basilicum* L. under Delhi conditions. Assessment was carried out for 19 qualitative and quantitative characters. The results revealed that the germplasm varied in plant height, herbage yield per plant and percent oil fresh weight basis.

Verma *et al.* (1989) evaluated eight different species with a total of 12 different genotypes for their herb and oil yield under Haryana conditions. They reported that there was great variability among the different *Ocimum species* for plant height, total herbage yield per plant, percent oil (Fresh weight basis) and oil yield.

Morales *et al.* (1993) reported the high genetic variability in *O. basilicum* L. for different traits like plant height, total biomass yield (both on a fresh and dry weight basis), days to 50% flowering, leaf area and oil yield.

Panwar *et al.* (2009) carried out an experiment to study genetic variability using 20 exotic and 10 indigenous genotypes of *Ocimum* in two different environments during *Kharif* 2004 and 2005. The study revealed the presence of highly significant variations for all the traits studied. Fresh herbage yield per plant was maximum in the genotypes namely IC 333332, EC 338785, EC 128730 and EC 388788. However, high essential oil yield per plant was extracted from genotypes IC 110267 and EC 388890.

Singh & Kumar (2010) carried out heritability analysis for yield and yield attributing traits in Tulsi (*Ocimum sanctum*). Both additive and non-additive gene effects were present. In the investigation, heritability analysis showed moderate to high heritability for almost all the characters under study. The characters with high heritability were plant height, spike length, dry herbage yield and fresh herbage yield. As for as genetic advance is concerned, the traits having high heritability coupled with high genetic advance was fresh herbage yield.

Erum *et al.* (2011) conducted a study to assess the genetic variability of various species of *Ocimum* (*O. basilicum* and *O. sanctum*) which were collected from various agro-ecological zones worldwide. Qualitative and quantitative phenotypic traits as well as biochemical traits of the different species were studied. Results of the study showed significant variation in leaf area, florets per spike, spikes per plant and seed germination among the nine *Ocimum* genotypes used for the study.

Ibrahim *et al.* (2011) carried out genetic variability studies using 15 genotypes of sweet basil. Data of variability for oil yield and related characters were recorded for two seasons. The experiment was carried out in a complete randomized block design. The analysis of variance showed highly significant differences among genotypes for the traits under study. The variations in the dry herb yield (68.40-86.30g), oil content (2.30-2.90ml.) and oil yield (1.22-2.24ml.) were obtained. Overall, the maximum values of genotypic coefficients of variation (G.C.V %) were obtained for linear growth (LG), stem dry weight (SDW), herb dry weight (HDW) and leaf dry weight (LDW).

Khan *et al.* (2012) conducted a study during the *Kharif* 2008 using 25 genotypes of *Ocimum spp*. to estimate the genetic variability and heritability for 11 traits. The estimates of maximum range and coefficient of variability was recorded for six different traits including plant height, number of inflorescence per plant, days to maturity, leaf length, length of inflorescence and fresh herb yield per plant. The maximum values of genotypic and phenotypic coefficients indicated presence of wide range of variability and high heritability coupled with higher values of relative genetic advance. The highest estimates of heritability in the broad sense were observed for plant height (99.70%) followed by the length of inflorescence per plant (98.80%) and fresh herb yield per plant (98.60%). The highest values of genotypic and phenotypic coefficients indicated a wide range of variability and high heritability associated with higher values of relative genetic advance.

Chhaya *et al.* (2013) carried out assessment of the genetic variability for qualitative and quantitative characters among the 16 different genotypes of *Tulsi*. All the genotypes of *Tulsi* were grown and maintained at day temperatures of 28-33℃ and night temperatures of 20-25℃. The analysis of data showed that location had a significant effect on all 6 characters studied. The interaction between genotype and environment was also pronounced for all the characters.

Ibrahim *et al.* (2013) conducted an experiment to assess the morphological variability in three basil varieties (French, Purple and Lemon). The experiment was carried out in two seasons (2010 and 2011) over two cuts in a complete randomized block design. The statistical analysis revealed significant variations among the varieties and cuts for the studied traits. The study emphasized the significance of herb dry yield and the percentage of essential oil as crucial selection criteria for enhancing oil yield in sweet basil.

Joshi & Hoti (2014) conducted an investigation regarding the chemical composition of the essential oil derived from the flowering aerial parts of *Ocimum tenuiflorum* L., which was cultivated in North West Karnataka, India. To analyze the oil, hydro-distillation was performed, followed by its examination using gas chromatography equipped with a flame ionization detector (GC-FID) and gas chromatography coupled with mass spectrometry (GCMS). Results revealed that the oil was found to be rich in phenyl derivative compounds (83.8%). Among the twenty-six compounds identified, methyl eugenol (82.9%) emerged as the predominant compound constituting 98.9% of the total oil.

Patel *et al.* (2015) conducted a study to assess the genetic variability and heritability among five *Ocimum species*. Genotypes were evaluated from pooled data for two consecutive years (2007 to 2009) over three different locations. High genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) were observed for essential oil yield, leaf area and leaf width. The findings revealed significant variations in important economic traits among different *Ocimum* genotypes, highlighting the potential for selective breeding to enhance and further improve their characteristics. Maximum heritability estimates in the broad sense were observed for leaf area (99.20%), leaf length (98.79%) and essential oil (98.36%). High genetic advance over the mean was observed for the essential oil yield (80.59%), leaf width (74.43%), leaf length (69%) and essential oil content (64.71%).

Singh *et al.* (2015) carried out an experiment to study genetic variability seven different crosses of basil (*Ocimum basilicum*) in the F_2 segregating generations. A high range of coefficients of variation was observed for dry herb yield and fresh herb yield per plant, leaf area and the number of branches. In F_2 generation, the highest estimates of the phenotypic coefficients of variation (PCV) were observed for fresh herb yield per plant (38.07%) in cross VI, dry herb yield (37.00%) in cross VI, number of inflorescences (26.53%) in cross V, leaf area (29.21%) in cross VI and number of branches (24.85%) in cross VI. Heritability in the narrow sense was observed between 3.35% (for chlorophyll content in cross III) to 92.20% (for oil content in cross II). High narrow sense heritability was found for the traits which exhibited more than 60 percent estimates of heritability in different crosses. High values of genetic advance with high heritability were achieved in traits such as fresh herb yield per plant and dry herb yield per plant indicating the involvement of additive gene action in the inheritance of these traits.

Lal *et al*. (2017) screened the 16 accessions belonging to six species of *Ocimum* collected from three different states of India (12 accessions from Uttar Pradesh, 3 accessions from Andhra Pradesh and 1 from Maharashtra) for studying the genetic variability for ursolic acid and higher oil yields. A considerable amount of genetic variability in morphometric traits was recorded in all accessions. Variation among the pooled mean over two years of sixteen diverse genetic accessions/varieties was highly significant (p=0.01) for all ten traits. It was observed that the estimate of heritability broad sense in percent (h^2 bs %) and corresponding genetic advance (GA), both were high for herb yield (93.52 and 89.27) and oil yield (98.80 and 120.35) followed by plant height (93.54 and 52.17) and ursolic acid yield (99.99 and 78.14).

Saran *et al.* (2017) conducted an experiment for chemotypic characterization and development of morphological markers in *Ocimum basilicum* L. germplasm. The experiment was carried out at the ICAR – Directorate of Medicinal and Aromatic Plants Research (ICAR – DMAPR), Boriavi, Anand, Gujarat (India) for two harvesting stages. The experimental material consisted of eight germplasm lines. Results revealed that the colour of the leaves varied from green to purple-green with bunchy, individual and intermediate type of panicles. Maximum oil percent in leaf was observed in DOB-1 (0.70%) followed by DOB-5 (0.61%).

Edet (2018) conducted a study using six accessions of African basil (*Ocimum gratissimum*) to estimate genetic variability and heritability. The study involved analyzing eight quantitative traits, which revealed significant differences among the plant materials indicating the existence of variability. The genetic parameters analysis showed that almost all the traits assessed had considerable values of broad sense heritability, ranging from 47.37% for raceme length to 97.08% for dry matter yield, suggesting a high portion of heritable variation. While raceme length and dry weight showed moderate values of heritability and genetic advance, all other characters investigated had high values for these genetic parameters.

Gowda *et al.* (2019) studied the genetic variability for 24 characters by using six genotypes of sacred basil. The assessments of variance exhibited greater phenotypic variance than genotypic variance (PCV>GCV) because of the influence of the environment in the expression of all the studied traits. Genotypic and phenotypic coefficients of variation were high for fresh herbage yield per plant (24.04%, 24.56%), fresh leaf yield per plant (25.59%, 27.02%) and leaf oil yield (30.03%, 31.63%) indicating that these traits showed greater variation, thereby enhancing the likelihood of selection of elite genotypes. Higher heritability along with high genetic advance was observed for the total fresh weight of plant (81.87%; 66.61%), fresh weight of leaves (69.42%; 52.63%) and spikes per plant (80.78%; 75.31%). Besides seed yield per plant also exhibited GCV (52.75%), PCV (61.28%), heritability (74.09%) and genetic advance mean (93.52%) in the high range.

Kumar *et al.* (2019) conducted a detailed investigation on *Ocimum basilicum* L. (Basil), commonly known as *Bhabri*, focusing on its morphological characteristics. The research encompassed a thorough examination of various features of basil including its roots, stem, leaves, flowers, and seeds. In addition to these aspects, the study also considered quantitative measurements such as plant height, number of branches, length and width of roots, stem, and leaves. Furthermore, quantitative analysis extended to the size and length of floral components, such as the flower, calyx, corolla, androecium, gynoecium, fruit, and seed. The morphology assessment also involved the description of mature inflorescences and the determination of the average weight of 1000 seeds in grams. The results revealed presence of high variability for the traits studied.

Singh *et al*. (2020) carried out a survey on 40 genetic stocks of *Ocimum* available at the CSIR-CIMAP belonging to five species *viz*. *Ocimum basilicum* L., *Ocimum tenuiflorum* L., *Ocimum kilimandscharicum* Baker ex Gurk, *Ocimum africanum* Lour. and *Ocimum gratissimum* L. It has been observed that some selected lines of *Ocimum* produced high quantities of essential oils like *Ocimum tenuiflorum* (*O. sanctum* L.): CIM-Ayu (80% eugenol) and EOH-1 (89.75% methyl chavicol). These active ingredients have high international demand for aroma-based value additions and product development from essential oils.

Venkatesha *et al.* (2020) carried out a study to estimate the variability, nature and magnitude of association between essential oil yield and its contributing traits and to determine the direct and indirect effects of various agro-morphic traits on essential oil yield using 29 accessions of Mentha evaluated for two consecutive years (2016-2017 and 2017-2018) in a randomized complete-block design (RCBD). Data were collected on agro-morphic traits and essential oil yield. The results revealed that the herb yield per plot ranged from 1.83 kg/plot (MASP-13) to 4.36 kg/plot (MASP-12) and essential oil yield ranged between 0.118 kg/plot (MASP-1) to 0.698 kg/plot (MASP-12). Number of branches per plant, plant height and herb yield per plot can be used as a selection criterion during selection to develop high-yielding menthol mint chemotypes.

Saran *et al*. (2021) analyzed the light requirement of *Tulsi* in the non-traditional area to harvest the maximum quantity of herbage and essential oil yield. Elite germplasm 'INGR 18044 (DOS-1)' was evaluated for its quantitative and qualitative traits under green coloured shade-net of different light intensities. The fresh leaf yield, stem weight, root weight, root length, root diameter, dry leaf yield and essential oil yield from fresh leaves were found highest under controlled conditions. The poor leaf yield and oil yield were observed under different SNIs (Shade Net Intensities) but large-sized leaves stayed green and a continuous supply of fresh leaves was made possible under shade conditions and as an intercrop crop.

Yaldiz & Camlica (2021) characterized the 50 genotypes of *Ocimum* based on morphological and phenological features. A wide range of variations for traits like days to first cutting (56.92–101.6 days), plant height (13.67–71.90 cm), branch number (3.28–19.43 plant−1), fresh herb yields (12.94–274.11 g plant^{-1}) and essential oil yield (0.04–1.71%) were observed. The highest herb yield was observed in the genotypes PI 652070 and PI 296391. Overall, PI 358469 and Ames 32309 genotypes exhibited the highest essential oil content.

2.2.1 Correlation coefficients analysis

Correlation coefficients analysis measures the degree of association between two or more plant characteristics. This information is useful in identifying the component characters that have the greatest impact on crop yield. A correlation study can also help breeders to understand the relationships between different traits which is important because yield is a complex trait influenced by multiple factors. When highly heritable traits are positively and closely associated among themselves and with economically important traits like grain yield, breeders can use this information to make more effective selections for breeding programmes, ultimately leading to improved crop productivity and quality. Literature on correlation coefficients analysis concerned to *Tulsi* is presented below:

Johnson *et al.* (1955) studied that the estimates of the genotypic and phenotypic correlation among different characteristics help in planning and evaluation of breeding programmes. The correlation studies allow researchers to analyze the degree and direction of the relationship between one trait and another.

Sheen *et al.* (1991) conducted an experiment to extract oils from *Ocimum basilicum.* Various plant parts like leaves, flowers, stems and whole plant were used for the extraction of oil. The oil was further categorized into five groups by preference ranking test of their aromas. High statistical correlations were found among the volatile components of the oil.

Morales *et al.* (1993) studied correlations in *O. basilicum*. Oil yield correlated positively with foliage fresh weight and plant height and negatively correlated with days to 50% flowering.

Kumar *et al.* (2012b) carried out the investigation on correlations by using 20 lines belonging to four different *Ocimum species* i.e. *O. basilicum, O. gratissimum, O. tenuiflorum,* and *O. kilimandscharicum* in randomized block design with three replications in *Kharif* 2009 to identify the traits favouring indirect selection. The genotypic correlation coefficients were higher in magnitude than corresponding phenotypic correlation coefficients in most cases indicating a strong inherent association between various characters at the genetic level. Plant height showed a significant positive association with canopy spread and exhibited a positive association with herb yield but was negatively related to oil content and oil yield. Plant height showed a significant negative correlation with a number of branches per plant indicating that tall plants have a relatively less number of branches.

Singh *et al.* (2015) conducted the field experiments during two consecutive years (2007 to 2009) to screen 13 accessions of basil for high oil content. Genotypic and phenotypic correlation coefficients analysis revealed that oil content was significantly correlated with fresh herb yield and dry herb yield. Plant height was correlated with the number of branches, leaf area, inflorescence number and inflorescence length. Fresh herb yield per plant demonstrated a positive correlation with all of the traits in all F_2 crosses including oil content, plant height in crosses II, V, and VII and number of branches in crosses IV and VII. However, fresh herb yield per plant exhibited a satisfyingly significant correlation with oil yield and its contributing traits, suggesting that high fresh herb yield per plant directly correlates with high oil content in the pertinent genotypes.

Yaseen *et al.* (2015) carried out an experiment using 11 clary sage (*Salvia sclarea* L.) accessions to estimate the relationship between agro-morphological traits, essential oil content & composition and randomly amplified polymorphic DNA (RAPD) with a known variety CIM-Chandni grown in northern Indian plains. Clary sage is used as a medicinal, flavouring agent and aromatic plant. The genotypic correlation coefficients were higher than phenotypic correlation coefficients. The research found a significant positive genotypic correlation between plant height and spike length, days to flowering and days to maturity and spike weight per plant. Furthermore, there was a positive genotypic correlation between spike length and oil content, with spike length having a high direct positive effect on oil content.

Edet (2018) conducted an experiment using six accessions of African basil (*Ocimum gratissimum*) to determine their genetic variability and correlation using agro-morphological markers. The study involved analyzing eight quantitative traits which revealed significant differences among the plant materials indicating the existence of variability. Moreover, the study observed high positive correlation coefficients for most of the traits which implies that simultaneous improvement for these traits is possible. Selecting one of the traits should result in progress for all positively correlated characters, making it easier to achieve desired outcomes.

Venkatesha *et al.* (2020) carried out a study to estimate the variability, magnitude of association between essential oil yield and its contributing traits and to determine the direct and indirect effects of various agro-morphic traits on essential oil yield using 29 accessions of Mentha evaluated for two consecutive years (2016-2017 and 2017-2018) in a randomized complete block design (RCBD). Data were collected on agro-morphic traits and essential oil yield. A significant and positive association was observed between essential oil yield and herb yield per plot (0.82) and a number of branches per plant (0.26). Among the chemical constituents of essential oil, Limonene percent was positively and significantly associated with pulegone percent.

2.2.2 Path coefficients analysis

Path coefficients analysis is a technique proposed by Wright (1921) and later described by Dewey & Lu (1959) to measure the direct influence of one variable upon another. It is a standardized partial regression coefficient that separates the correlation coefficients into direct and indirect effects. This analysis is useful when there is a cause and effect relationship among the variables. Literature related to path coefficients analysis is presented below:

Dewey & Lu (1959) demonstrated the application of path coefficients analysis in plant selection specifically in measuring wheat grass progenies. The technique provides breeders with a measurement of the direct and indirect effects of independent variables on dependent variables, making it an important tool for partitioning the correlation coefficient into components of direct and indirect effects in relation to yield.

Sharma & Tyagi (1991) conducted a study on correlation coefficients, path coefficients and heritability analysis of essential oil and quality components in Japanese mint. Their findings indicated that the oil content had the most significant direct impact on oil yield with herb yield. Furthermore, they noted that the larger indirect effects of oil yield were primarily through herb yield.

Panwar *et al.* (2009) carried out a study on path coefficients analysis using 20 exotic and 10 indigenous genotypes of *Ocimum* in two environments during *Kharif* 2004 and 2005.

The results of path analysis revealed that the fresh herbage yield per plant had the highest positive significant effect on essential oil yield per plant and the highest direct negative effect on essential oil content. The essential oil yield per plant had the highest direct positive effect at the phenotypic level on essential oil content followed by fresh herbage yield per plant whereas, the maximum negative effect was observed in the number of flower whorls per spike and days to seed maturity.

Ibrahim *et al.* (2011) carried out path coefficients analysis using 15 genotypes of sweet basil. The experiment was carried out in two seasons in a complete randomized block design. Path coefficients analysis for oil yield showed variation from one season to another and slight variation was observed among the cuts. The highest direct effects on oil yield were found for dry herb yield followed by stem dry weight and essential oil content. Hence, the study reflected the importance of dry herb yield and essential oil content as selection criteria for the improvement of oil yield in sweet basil.

Kumar *et al.* (2012b) conducted path analysis among 20 lines belonging to four different *Ocimum species* namely *Ocimum basilicum, Ocimum gratissimum, Ocimum tenuiflorum and Ocimum kilimandscharicum.* The aim of the study was to identify component traits that could favour the indirect selection. The study revealed that yield traits such as herb yield, oil content, and oil yield had a strong genetic association among them with a positive direct path of herb yield (0.729) and oil content (0.532) toward oil yield. The yield traits had high positive genetic correlations of 0.792 and 0.726, respectively.

Patel *et al.* (2015) carried out an experiment to study path analysis in 15 accessions of five *Ocimum species*. Path coefficients analysis showed maximum positive direct effects of plant canopy (4.21) and leaf width (3.80) followed by essential oil (2.49%) and fresh herb yield (0.95).

Singh *et al.* (2015) conducted the field experiments during two consecutive years (2007 to 2009) at the research farm of the Department of Genetics and Plant Breeding, Chaudhary Charan Singh University Meerut, India to screen 13 accessions of basil for high oil content. The path coefficients analysis revealed that the highest direct contribution to the oil content was made by fresh herb yield followed by leaf length, leaf area and number of inflorescence.

Lal *et al*. (2017) screened the 16 accessions belonging to six species of *Ocimum* collected from three different states of India (12 accessions from Uttar Pradesh, 3 accessions from Andhra Pradesh and 1 from Maharashtra) for studying ursolic acid and higher oil yields. The path coefficients analysis revealed that the oil content had the highest positive indirect effect (0.471) to the ursolic acid content and the maximum direct contribution to ursolic acid was made by ursolic acid content and herb yield.

Venkatesha *et al.* (2020) carried out a study to estimate the path coefficients to reveal that herb yield per plot had the highest direct effect on essential oil yield (0.8104) using

29 accessions of Mentha evaluated for two consecutive years (2016-2017 and 2017-2018) in a randomized complete-block design (RCBD). Plant height, number of branches per plant and herb yield per plot may be used as a selection criterion during selection to develop high yielding menthol mint chemotypes.

2.3.1 Genetic diversity analysis

Cluster analysis using D^2 Mahalanobis distance is an important tool for crop improvement as it helps to group genetically diverse accessions into distinct clusters based on their similarities and differences. This method aids in identifying promising parents for hybridization, detecting duplicates and selecting representative core collections for conservation purposes. It also facilitates the identification of important traits for crop improvement and can be used to develop breeding strategies for specific target environments. Literature on genetic diversity studies showing close concern to *Ocimum* is given as below:

Telci *et al.* (2006) conducted the genetic diversity studies to investigate the composition of 18 Turkish basil essential oils through the utilization of GC and GC-MS. In order to assess the variation of essential oils in the landraces, a cluster analysis was carried out, which revealed the existence of seven distinct chemotypes. These chemotypes included linalool, methyl cinnamate, a combination of methyl cinnamate and linalool, methyl eugenol, citral, methyl chavicol (estragol) and a mixture of methyl chavicol and citral.

Erum *et al.* (2011) conducted a genetic diversity study using different species of *Ocimum* (*O. basilicum* and *O. sanctum*) which were collected from various agro-ecological zones of the world and evaluated for their qualitative and quantitative phenotypic traits as well as biochemical traits. A UPGMA cluster diagram grouped the nine genotypes into two major clusters, I and II based on total seed protein and phenotypic characteristics differentiating the Siam Queen and Italian basil from other genotypes (Holy basil, Sweet basil, Hot wave basil, Garnet basil and Purple basil). Genetic distances varied from 0.11 to 1.00 based on the total seed proteins whereas, for morphological traits the Euclidian distance varied from 3.60 to 7.26.

Bompalli & Nallabilli (2013) studied eleven *Ocimum spp.* samples which were collected from the northern region of India. For the study of genetic diversity, various techniques based on the DNA and protein which includes RFLP’s, AFLP’s, RAPD’s, microsatellite DNA fingerprinting and SDS-PAGE were used according to the literature survey. Euclidean dissimilarity coefficients ranged between 0.00 and 1.00. The lowest similarity and the highest similarity were observed in the samples and the observations were represented in a dendrogram.

Malav *et al.* (2015) characterized 49 accessions of cultivated holy basil from four phyto-geographical areas of India for 18 qualitative and 14 quantitative traits using minimal descriptors developed by the National Bureau of Plant Genetic Resources (NBPGR) with slight modifications. Dendrograms were created using Ward's minimum variance method. The analysis revealed a high degree of variation among the studied accessions suggesting a rich diversity present within the populations from various phyto-geographical regions and relatedness among the morphotypes.

Chowdhury *et al*. (2017) conducted an experiment to study the diversity based on morphological, chemical and randomly amplified polymorphic DNA (RAPD) to determine the level of variation present in the genus *Ocimum.* Nine genotypes were naturally grown in the Dakshin Dinajpur district of West Bengal, India. The clusters generated from the morphological data showed two different groups *viz.* the basilicum group and the sanctum group. The results revealed that the chemical analysis did not exhibit much variation between morphologically similar species *viz. O. africanum* and *O. basilicum*. However, RAPD analyses clearly indicated that *O. africanum* and *O. basilicum* are two different species.

Singh *et al.* (2018) conducted a study to examine the genetic diversity and clustering pattern among 25 genotypes of basil. Analysis of variance revealed the presence of significant genotypic variation which was also confirmed by a wide range of D^2 values (0.074-212.97). All the accessions were grouped into seven different clusters (I–VII). It was observed that the intra-cluster divergence was maximum within cluster VII ($D^2 = 43.32$) and the inter-cluster divergence was maximum between clusters II and VI ($D^2 = 155.59$). The contribution of the character towards genetic diversity was highest for oil content (56.09%) followed by plant height (18.94%) and lowest for the number of branches (7.55%). The highly divergent accessions namely G-4, G-7, G-9, G-11, G-18 and G-25 may be exploited for further crop improvement for the development of superior genotypes with high essential oil content and better quality.

Srivastava *et al.* (2018) conducted the investigation to estimate the genetic diversity in *Ocimum basilicum* germplasm consisting of 60 accessions using Mahalanobis D^2 analysis. All the *Ocimum* accessions were grouped into seven diverse clusters and there was no parallelism observed between the genetic divergence and geographical origin. Maximum inter-cluster distance was found between clusters II and VII (200.71) and the minimum between cluster I and II (26.61). Among the nine economic traits studied during the investigation, leaf area was found to be the major contributor towards genetic divergence (16.01%) followed by oil yield (15.12%) and the lowest contributing trait was plant height (4.26%).

Saha *et al.* (2020) conducted a study to explore the genetic diversity and relationships among 24 *Ocimum* accessions from five different agro-climatic regions of West Bengal. The study was carried out using PCR-based Random Amplified Polymorphic DNA (RAPD) and Inter Simple Sequence Repeats (ISSR) markers. The RAPD primers generated 191 robust loci, of which 69.42% exhibited polymorphism while, 83 ISSR markers generated 67.46% polymorphism.

CHAPTER- III

MATERIALS AND METHODS

3.1 Experimental material

The experimental material for the present investigation, "Genetic divergence, correlation and path coefficients studies in Tulsi (*Ocimum spp*.)" comprised of 40 genotypes of Tulsi (*Ocimum spp*.) (Table 3.1). Among these, 38 genotypes were received from ICAR-National Bureau of Plant Genetic Resources (NBPGR), New Delhi and 2 genotypes from the germplasm pool maintained at the Medicinal, Aromatic and Potential Crops Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar. Hisar is located in semi-arid sub-tropical region at 29°- 10°N latitude and 75°- 46°E longitude with elevation of 215.52 m above mean sea level.

Table 3.1. List of 40 *Ocimum* genotypes studied for the present investigation

Sr. No.	Name of genotype/ accession	Sr. No.	Name of genotype/ accession
1	IC 44681	21	EC 388887
2	IC 387837	22	EC 388895
3	IC 369247	23	EC 388896
4	IC 387838	24	EC 388782
5	IC 388785	25	EC 388737
6	IC 469938	26	EC 388889
7	IC 326735	27	EC 338772
8	IC 312264	28	EC 388788
9	IC 110207	29	EC 388890
10	IC 338794	30	IC 436153
11	IC 336833	31	IC 381158
12	IC 201223	32	IC 326732
13	IC 328582	33	RDV 45
14	IC 338959	34	NSV 38
15	IC 333833	35	EC 112548
16	IC 281185	36	IC 75730
17	IC 381552	37	Local 1
18	EC 469904	38	IC 381185
19	EC 326771	39	Local 2
20	EC 388893	40	DOS 1

3.2 Field layout of experiment

To conduct the experiment, all the 40 genotypes of Tulsi (*Ocimum spp.*) were grown in the Research Area of the Medicinal, Aromatic and Potential Crops Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar during *Kharif* 2022 season.

Nursery preparation and Transplanting:

To raise the healthy plants, nursery was prepared by sowing the seeds of all the 40 different genotypes on the raised beds separately. Light irrigation was given to the young seedlings as per requirement for good growth.

Twenty days old young healthy seedlings of all the 40 different genotypes were transplanted in the Randomized Block Design (RBD) with three replications. One seedling per hill was transplanted at 10 cm spacing between the plants in two rows each of 3m length with a row to row distance of 30 cm. A light irrigation was applied immediately after transplanting. All the required cultural practices were followed to raise the good *Tulsi* crop.

Under natural field conditions, the data for the different traits were recorded on five randomly selected plants from each genotype in each replication.

3.3 Observations recorded

The observations were recorded for the following qualitative and quantitative traits.

3.3.1 Qualitative Traits: The observations for all the 40 genotypes were recorded at appropriate plant growth stage i.e. from flowering to reproductive stage of the crop for the following 10 different qualitative traits:

1. Stem colour
2. Stem pubescence
3. Leaf shape
4. Leaf colour
5. Leaf pubescence
6. Petiole colour
7. Flower colour
8. Calyx colour
9. Calyx pubescence
10. Seed colour

3.3.2 Quantitative Traits:

The observations for the following 17 quantitative traits were recorded under natural field conditions and in laboratory. The data for the quantitative traits from serial number 1 to 10 were recorded on five randomly selected competitive plants from each genotype in each replication of *Tulsi* crop grown under natural field conditions. Mean of the five plants was calculated to record the data on per plant basis. The observations for the quantitative traits from serial number 11 to 17 were recorded under laboratory conditions. The observations for 1000 seed weight (g), standard germination (%), seedling length (mm), seedling dry weight (mg), seed vigour index-I and seed vigour index-II were taken in Seed Testing Laboratory, Department of Seed Science and Technology, and for oil content (%) in the Quality Analysis

Laboratory, Medicinal, Aromatic and Potential Crops Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar.

1. Days to 50% flowering
2. Days to maturity
3. Number of primary branches/plant
4. Plant height (cm)
5. Number of spikes/plant
6. Spike length (cm)
7. Number of flowers' whorls/spike
8. Fresh herbage yield/plant (g)
9. Dry herbage yield/plant (g)
10. Seed yield/plant (g)
11. 1000 seed weight (g)
12. Oil content (%)
13. Standard germination (%)
14. Seedling length (mm)
15. Seedling dry weight (mg)
16. Seed vigour index - I
17. Seed vigour index – II

3.3.2.1 Days to 50% flowering

The observations for days to 50% flowering were recorded by counting the number of days from date of sowing to date on which at least one flower opened in 50 % plants in each genotype.

3.3.2.2 Days to maturity

Days to maturity were recorded by counting the number of days from the date of sowing to the date of physiological maturity of the plants.

3.3.2.3 Number of primary branches/plant

The data for number of primary branches per plant were recorded at physiological maturity by counting the number of branches emerging directly from the main shoot of the plant.

3.3.2.4 Plant height (cm)

The plant height was measured from the base of stem at ground level to the tip of inflorescence at physiological maturity.

3.3.2.5 Number of spikes/plant

The number of spikes per plant were counted at physiological maturity of each genotype.

3.3.2.6 Spike length (cm)

The spike length was measured in centimetre from the base to the tip of the spike (inflorescence) of primary branches emerging from the top central portion of the main stem at physiological maturity stage.

3.3.2.7 Number of flowers' whorls /spike

The data for number of flowers' whorls per spike were recorded on five randomly selected competitive plants from each genotype in each replication. The mean was calculated and expressed as number of flowers' whorls per spike.

3.3.2.8 Fresh herbage yield/plant (g)

For recording data of fresh herbage yield per plant, the single whole plant was cut individually at the bottom of the stem at green leaf and complete flowering stage and weighed in grams, immediately.

3.3.2.9 Dry herbage yield/plant (g)

After recording fresh herbage yield per plant, the same plants were kept in hot air oven for drying at a temperature of 60-62 ºC for 3 days. The dried plants were weighed and recorded as dry herbage yield per plant in grams.

3.3.2.10 Seed yield/plant (g)

Five randomly selected competitive plants of each genotype from each replication were harvested separately after physiological maturity and threshed individually after few days of sun-drying. The seeds obtained after threshing from each of the five plants were weighed on electronic balance in grams for recording data of seed yield per plant.

3.3.2.11 Oil content (%)

The essential oils of *Tulsi* was extracted by the process of hydro-distillation using Clevenger's apparatus. *Tulsi* plant at flowering stage including green stem, green leaves and immature inflorescence from each genotype was cut from the base and about 300 g plant material was placed in a round-bottomed flask and the flask was filled with water up to two-third mark on the flask. The electrical heating mantle was used to heat the water in the flask. The flask was fitted with Clevenger & condenser. The essential oil remained floated in the oil gathering area. After 3 to 4 hours of heating, when no visible essential oil was seen in the condenser area, the essential oil was collected after draining the bottom water layer and stored in a sealed glass vials (Clevenger, 1928). The oil content (%) was estimated using the following formula

$$\text{Oil content (\%)} = \frac{\text{Oil recovered (ml)}}{\text{Weight of biomass (g)}} \times 100$$

3.3.2.12 1000 seed weight (g)

The data for 1000 seed weight was taken in grams by counting the 1000 seeds randomly from each genotype in each replication and then weighed using electronic weighing balance.

3.3.2.13 Standard germination (%)

Germination test was conducted by the 'Between Paper Method' as per ISTA guidelines. To estimate standard germination (%), 50 seeds of each genotype were placed on sufficiently moistened germination papers at 25 ± 1 °C temperature and 90 ± 2 % relative humidity in the seed germinator replicated three times. At the end of the 14th day of the germination test, the number of normal, abnormal and dead seedlings for each genotype in each of three replications were counted and only normal and healthy seedlings were taken into account for recording data for standard germination (%).

$$\text{Standard germination (\%)} = \frac{\text{Number of normal seedlings}}{\text{Total number of seeds kept for germination}} \times 100$$

3.3.2.14 Seedling length (mm)

Ten seedlings were selected randomly from the normal seedlings at the time of final count of standard germination (%) of each genotype in all the three replications to measure seedling length in millimetres. Then, mean of 10 seedlings' length was calculated to record the observation for seedling length.

3.3.2.15 Seedling dry weight (mg)

Ten normal seedlings which were used for the measurement of seedling length were also used for measurement of seedling dry weight. The ten normal seedlings were kept in butter paper and dried in a hot air oven at 60 ± 1 °C temperature for 24 hours. Then seedlings were taken out from the oven and allowed to cool for 30 minutes before weighing them on an electronic weighing balance. The average weight of dried 10 seedlings of each genotype from each replication was calculated and expressed as the dry weight of seedlings in milligrams.

3.3.2.16 Seed vigour index-I (SVI-I)

Seed vigour indices were calculated according to the method suggested by Abdul-Baki & Anderson (1973).

Seed vigour index-I is calculated by multiplying the standard germination percentage by the seedling length. It indicates the seed's ability to germinate and produce a healthy seedling.

∴ Seed vigour index-I = Standard germination (%) x Average seedling length (mm)

3.3.2.17 Seed vigour index-II (SVI-II)

Seed vigour Index-II is calculated by multiplying the standard germination percentage by the seedling dry weight. This index represents the seed's potential to establish a healthy and productive plant.

∴ Seed vigour index-II = Standard germination (%) x Average seedling dry weight(mg)

3.4 Statistical Analysis

3.4.1 Analysis of variance

Analysis of variance (ANOVA) for the observations recorded on different characteristics was carried out as per the standard procedure suggested by Panse & Sukhatme (1967).

The following model was adopted for the analysis of the variance of various characters:

$$Y_{ij} = \mu + \alpha_i + \beta_j + e_{ij}$$

Where,

Y_{ij}= Observation of ith treatment and jth block.

μ = General mean

α_i = ith treatment effect

β_j = jth block effect

e_{ij} = Uncontrolled random error associated with ith treatment and jth block

Assumptions:

a) All the observations should be independent.

b) The different effects in the model should be additive.

c) Error involved in the population should be distributed normally and independently with mean zero and variance.

Table: Analysis of variance

Source of variation (SV)	**Degree of freedom (df)**	**Sum of square (SS)**	**Mean sum of square (MS)**	**Expected mean square (EMS)**	**F-calculated**
Replication	(r-1)	SSr	MSr	$\sigma^2_e + g\,\sigma^2_r$	MSr/MSe
Genotype	(g-1)	SSg	MSg	$\sigma^2_e + r\,\sigma^2_g$	MSg/MSe
Error	(r-1)(g-1)	SSe	MSe	σ^2_e	
Total	gr-1				

Where,

r = Number of replications

g = Number of genotypes

MSr, MSg and MSe stands for mean sum of squares due to replications, genotype and error, respectively.

σ^2g = Genotypic variance of character

σ^2r = Variance due to replications

σ^2e = Error variance of character

The genotypic and phenotypic variances were calculated by adopting the following formulae:

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

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

3.4.2 Genetic variability parameters

i) Mean ($\overline{X}$)

Mean was worked out by dividing total sum of all the values of observations by number of corresponding observations.

$$\overline{X} = \frac{1}{n}\sum_{i=1}^{n} X_i$$

Where,

$\overline{X}$ = Sample mean

X_i= Individual value

n = Number of observations

ii) Standard Error [SE]

Standard error of mean was calculated with the help of error mean square from the analysis of variance table as follows:

$$SE\ (m) = \sqrt{\frac{EMS}{r}}$$

Where,

EMS = Error mean square

SE (m) = Standard error of mean

r = number of replications

iii) Critical difference (CD)

Critical difference was calculated to compare the means of various genotypes. It was calculated with the help of standard error of difference and t value at error degree of freedom at 1% and 5% level of significance.

$$CD = SE_{(d)} \times t_{(1\% \text{ or } 5\%)} \text{ error degree of freedom}$$

iv) Range

Range for each character was worked out by depicting the lowest and highest values.

$$\text{Range} = H.V - L.V$$

Where,

H.V. = Highest value among the observations for any trait

L.V. = Lowest value among the observations for any trait

v) Coefficient of variation (CV)

The coefficient of variation being a standardized form of variance is useful for comparing the extent of variance between different characters with different scales (Singh & Chaudhary, 1977). According to Burton & DeVane (1953), genotypic and phenotypic coefficients of variations were estimated based on the estimates of genotypic and phenotypic variances.

Genotypic coefficient of variation [GCV(%)] = $\frac{\sqrt{\sigma^2 g}\times 100}{\bar{X}}$

Phenotypic coefficient of variation [PCV(%)] = $\frac{\sqrt{\sigma^2 p}\times 100}{\bar{X}}$

Where,

$\bar{X}$=General mean

$\sigma^2 g$ = Genotypic variance

$\sigma^2 p$= Phenotypic variance

The genotypic and phenotypic coefficients of variations were categorized as per the method suggested by Sivasubramanjan & Menon (1973):

0-10%= Low 10-20%= Moderate >20%= High

vi) Heritability

Heritability in broad sense and genetic advance were calculated by method given by Burton & DeVane (1953). Heritability in broad sense was calculated as the ratio of genotypic variance to the phenotypic variance and expressed as percentage as given below:

Heritability in broad sense [h^2 (bs)] = $\frac{\sigma^2 g}{\sigma^2 p}\times 100$

The calculated heritability was classified into three groups as suggested by Johnson *et al.* (1955):

0-30% = Low 30-60%= Moderate >60% = High

vii) Expected genetic advance (GA)

Genetic advance was worked out by adopting the following formula given by Johnson *et al.* (1955):

$$GA = k \text{ x } h^2 \text{ x } \sigma^2 p$$

Where,

h^2 = Heritability in broad sense

k = Selection differential (= 2.06) at 5% intensity of selection

$\sigma^2 p$ = Phenotypic standard deviation

viii) Genetic advance as percent of mean (GAM)

Genetic advance as per cent of mean for each character was worked out as suggested by Johnson *et al.* (1955):

$$GAM = \frac{GA}{\bar{X}}\times 100$$

Where,

GA=Genetic advance

$\overline{X}$=General mean

The calculated genetic advance as percentage of mean was classified into three groups as suggested by Johnson *et al.* (1955):

0-10%= Low 10-20%= Moderate >20%= High

3.4.3 Correlation coefficients analysis

Analysis of Co-variance was computed by following procedure:

$$Y_{ij}= M+t_i+b_j+B(X_{ij}-X)+e_{ij}$$

Where,

Y_{ij} = Performance of i^{th} genotype in the j^{th} replication

M = General mean

t_i = True effect of i^{th} treatment

b_j = True effect of j^{th} block

B = Regression coefficient of y on x

X_{ij}-X = Covariance

e_{ij}= Random error

Table: Analysis of covariance

Source of variation (SV)	**Degree of freedom (df)**	**Sum of square (SS)**	**Mean sum of square (MS)**	**Expected mean square (EMS)**	**F-calculated**
Replication	(r-1)	SSr	MSr	$\sigma^2_e + g\,\sigma^2_r$	MSr/MSe
Genotype	(g-1)	SSg	MSg	$\sigma^2_e + r\,\sigma^2_g$	MSg/MSe
Error	(r-1)(g-1)	SSe	MSe	σ^2_e	
Total	gr-1				

Where,

df =Degrees of freedom

SS=Sum of squares

SP=Sum of products

MSS=Mean sum of squares

MSP=Mean sum of products

r=Number of replications

t=Number of genotypes

Genotypic covariance $(X_i.X_j)$ g = $\frac{(\text{MSPr - MSPe})}{r}$

Where,

$(X_i.X_j)$g = Genotypic Covariance between i^{th} and j^{th} characters

MSPr = Mean sum of products of genotypes

MSPe = Error mean sum of products

Phenotypic covariance $(X_i.X_j)$ p = $(X_i.\ X_j)$ g+ e_ie_j

Where,

e_ie_j = environmental covariance between i^{th} and j^{th} characters

Correlation coefficients:

Correlation coefficients at phenotypic and genotypic level were calculated using the variances and co-variances according to Al-Jibouri *et al*. (1958).

Genotypic correlation= r_{ij} (G) = $\frac{\sigma^2_{gij}}{\sqrt{\sigma^2_{gii}\times\sigma^2_{gjj}}}$

Where,

σ^2_{gij}= Genotypic co-variance of character x_i and x_j

σ^2_{gii}= Genotypic variance of character x_i

σ^2_{gjj}=Genotypic variance of character x_j

Phenotypic correlation= r_{ij} (P) = $\frac{\sigma^2_{pij}}{\sqrt{\sigma^2_{pii}\times\sigma^2_{pjj}}}$

Where,

σ^2_{pij}= Phenotypic co-variance of character x_i and x_j

σ^2_{pii}= Phenotypic variance of character x_i

σ^2_{pjj}=Phenotypic variance of character x_j

3.4.4 Path coefficients analysis

The phenotypic correlation coefficients were used to work out path coefficient analysis. Path coefficients were obtained according to Dewey & Lu (1959). Sets of simultaneous equations in the following form are solved.

$$r_{ny}= P_{ny}+ r_{n2}P_{2y}\ r_{n3}P_{3y} +\ldots\ldots+ r_{nx}P_{xy}$$

where,

r_{ny} = represents correlation coefficient between one character and yield

P_{ny} = represents path coefficients between the nth character and yield

r_{n2}, r_{n3},….r_{nx}=represents correlation coefficient between that character and each of other yield component in turn.

The following correlation matrices were prepared:

Matrix A Matrix B

$$\begin{bmatrix} r_{1y} \\ r_{1y} \\ \cdots \\ r_{1y} \end{bmatrix} \qquad \begin{bmatrix} 1 & r_{12} & r_{13} & \cdots & r_{1n} \\ r_{21} & 1 & r_{23} & \cdots & r_{2n} \\ \cdots & \cdots & \cdots & \cdots & \cdots \\ r_{n1} & r_{n2} & r_{n3} & \cdots & 1 \end{bmatrix}$$

Where,

$r_{12} = r_{21}$ and so on

r_{1y} = correlation coefficient between yield and one component character.

The technique given by Goulden (1952) was followed for the inversion (B^{-1}) of B matrix.

P_{ij}, the path coefficients were obtained by: $P_{ij} = B^{-1} x A$

The indirect effects for a particular character through other characters were obtained by multiplication of direct path and particular correlation coefficient between those two characters respectively.

Indirect effect = r_{ij} x P_{ij}

The residual factor i.e. the variation in yield unaccounted for those associations was calculated from the following formula:

Residual factors(X) = 1 - R^2

Where,

$R^2 = P_{ly}\ r_{ly} + P_{2y}\ r_{2y} \ldots\ldots\ldots P_{ny} r_{ny}$

R^2 is the squared multiple correlation coefficient and is the amount of variation in yield that can be accounted for by the effect of yield components on yield.

3.4.5 Genetic divergence

Procedure to compute D^2 value for measurement of genetic divergence:

D^2 analysis was done using the method suggested by Mahalanobis (1936) and elaborated by Murty & Arunachalam (1966). The variance and covariance were subjected to multivariate analysis. The original intimated variables (X's) were first transformed into set of mutually uncorrelated variable (Y's as linear function of X's) and the D^2 values were worked out. Pivotal condensation method was used to compute inverse matrix of the error dispersion matrix. The generalized distance function (D^2) between two genotypes *i.e.* ith and jth genotype is simply the sum of square of differences in Y's as followed:

$$D^2 = \sum_{k=1}^{p} \left(Y_{ik} - Y_{jk}\right)^2$$

Where,

Y_{ik} = Uncorrelated mean value of ith genotype for 'k' characters

Y_{jk} = Uncorrelated mean value of jth genotype for 'k' characters

p = Total number of characters

Clustering of genotypes using D^2 values:

All the genotypes were used to be clustered into different groups following Tocher's method (Rao, 1952). The device suggested by Tocher (Rao, 1952) was started with two closely associated populations and find a third population, which had the smallest average of D^2 from the first two. Similarly, the fourth was chosen to have a smallest average D^2 value from the first three and so on. If, at any stage increase in average D^2 value exceeded the average of already included, because of the addition of new genotypes, then that genotype was deleted. The genotypes that are included already in that group were considered as the first cluster. This procedure was repeated till D^2 valuesof the other genotypes were exhausted omitting those that were already included in the former cluster and grouping them into different cluster.

Intra- and inter-cluster average D^2 value and contribution of individual characters towards genetic divergence:

The average intra- and inter-cluster average D^2 values were calculated by the formula given by Singh & Chaudhary (1977), Nadarajan & Gunasekaran (2012).

i). Intra-cluster average D^2 value

The intra-cluster average D^2 value = $\sum D^2_i / n_i$

Where,

$\sum D^2_i$ = Sum of average D^2 value between all possible combinations within cluster

n_i = Number of all possible combinations within cluster i

ii). Inter-cluster average D^2 value

The inter-cluster average D^2 value = $\sum D^2_{ij} / (n_i \times n_j)$

Where,

D^2_{ij} = Sum of average D^2 values between all possible combinations (n_i, n_j) of the entries included in the studied two clusters.

n_i = Number of entries in cluster i

n_j = Number of entries in cluster j.

N = All possible combinations of number of genotypes considered ($N = n(n-1)/2$), where n is the total number of genotypes.

CHAPTER- IV

RESULTS

The present investigation entitled "Genetic divergence, correlation and path coefficients studies in Tulsi (*Ocimum spp*.)" comprising of 40 different genotypes of Tulsi (*Ocimum spp*.) were evaluated at research area of Medicinal, Aromatic and Potential Crops Section, Department of Genetics and Plant Breeding, CCS HAU, Hisar, during *Kharif* 2022. The 40 genotypes were characterized and evaluated based on different qualitative and quantitative traits.

Keeping in view the defined objectives of present investigation, the results obtained are explained under the following heads and sub-heads:

4.1 Genetic variability studies

4.1.1 Characterization of 40 *Tulsi* genotypes

4.1.2 Estimation of genetic variability parameters

4.2 Correlation coefficients analysis

4.3 Path coefficients analysis

4.4 Genetic divergence studies

4.1 Genetic variability studies

4.1.1 Characterization of 40 *Tulsi* genotypes based on 10 qualitative traits

The 40 genotypes of Tulsi (*Ocimum spp.*) taken for the present investigation were characterized for 10 different qualitative traits mentioned as below:

1. Stem colour
2. Stem pubescence
3. Leaf shape
4. Leaf colour
5. Leaf pubescence
6. Petiole colour
7. Flower colour
8. Calyx colour
9. Calyx pubescence
10. Seed colour

Based on the observations for each qualitative trait, the 40 genotypes were further classified into different categories which are presented in tabular, graphical and images form in the succeeding pages.

4.1.1.1 Stem colour

Based on stem colour, five different groups *viz.* dark green, green, light green, purple, and light purple (Plate 1) were observed among 40 different genotypes of *Tulsi* and all the genotypes were categorized accordingly (Table 4.1, Fig.1). Four genotypes exhibited dark green stem colour, 28 genotypes green stem colour whereas light green stem colour appeared only in one genotype. Purple stem colour was observed in five genotypes and two genotypes displayed light purple stem colour.

Table 4.1. Classification of 40 *Tulsi* genotypes on the basis of stem colour

Stem colour	No. of Genotypes	Genotypes
Dark green	4	IC 369247, IC 381552, EC 388887, EC 388895
Green	28	IC 44681, IC 387837, IC 387838, IC 388785, IC 469938, IC 326735, IC 312264, IC 110207, IC 338794, IC 201223, IC 328582, IC 338959, IC 333833, IC 281185, EC 469904, EC 326771, EC 388896, EC 388782, EC 388737, EC 388889, EC 338772, IC 436153, IC 381158, IC 326732, RDV 45, NSV 38, Local 1, Local 2
Light green	1	IC 336833
Purple	5	EC 388788, EC 388890, IC 75730, IC 381185, DOS 1
Light purple	2	EC 388893, EC 112548

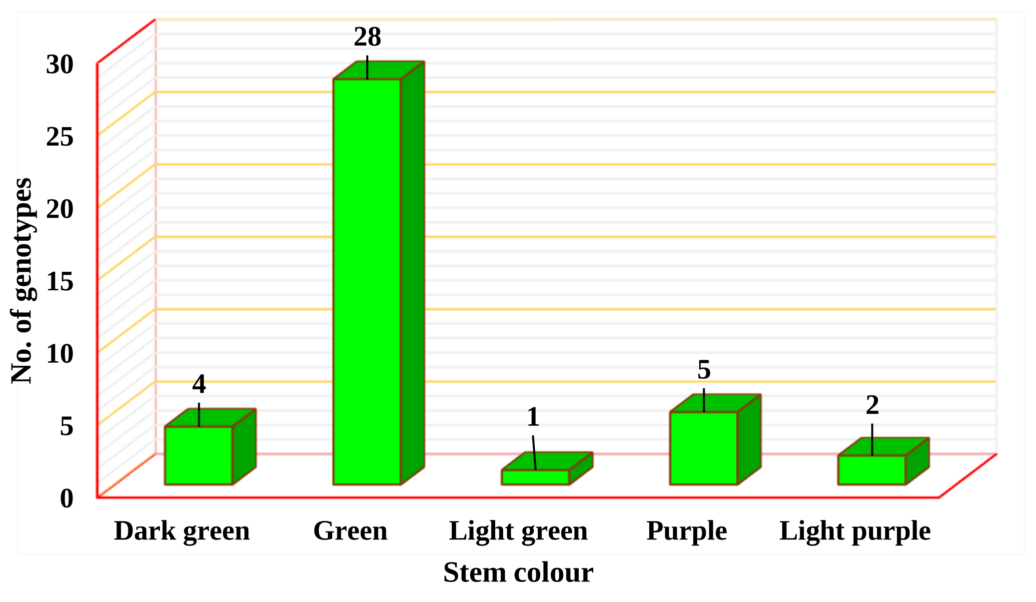


Fig. 1. Classification of 40 *Tulsi* genotypes on the basis of stem colour

4.1.1.2 Stem pubescence

On the basis of the presence or absence of the hairs on the stem, *Tulsi* genotypes were classified as sparse pubescent and non-pubescent (Plate 2). Five genotypes were observed to have sparse pubescence whereas the remaining 35 genotypes had no pubescence (Table 4.2, Fig. 2).

Table 4.2. Classification of 40 *Tulsi* genotypes on the basis of stem pubescence

Stem pubescence	No. of Genotypes	Genotypes
Sparse pubescent	5	IC 388785 , EC 469904, IC 75730, IC 381185, DOS 1
Non-pubescent	35	IC 44681, IC 387837, IC 369247, IC 387838, IC 469938, IC 326735, IC 312264, IC 110207, IC 338794, IC 336833, IC 201223, IC 328582, IC 338959, IC 333833, IC 281185, IC 381552, EC 326771, EC 388893, EC 388887, EC 388895, EC 388896, EC 388782, EC 388737, EC 388889, EC 338772, EC 388788, EC 388890, IC 436153, IC 381158, IC 326732, RDV 45, NSV 38, EC 112548, Local 1, Local 2

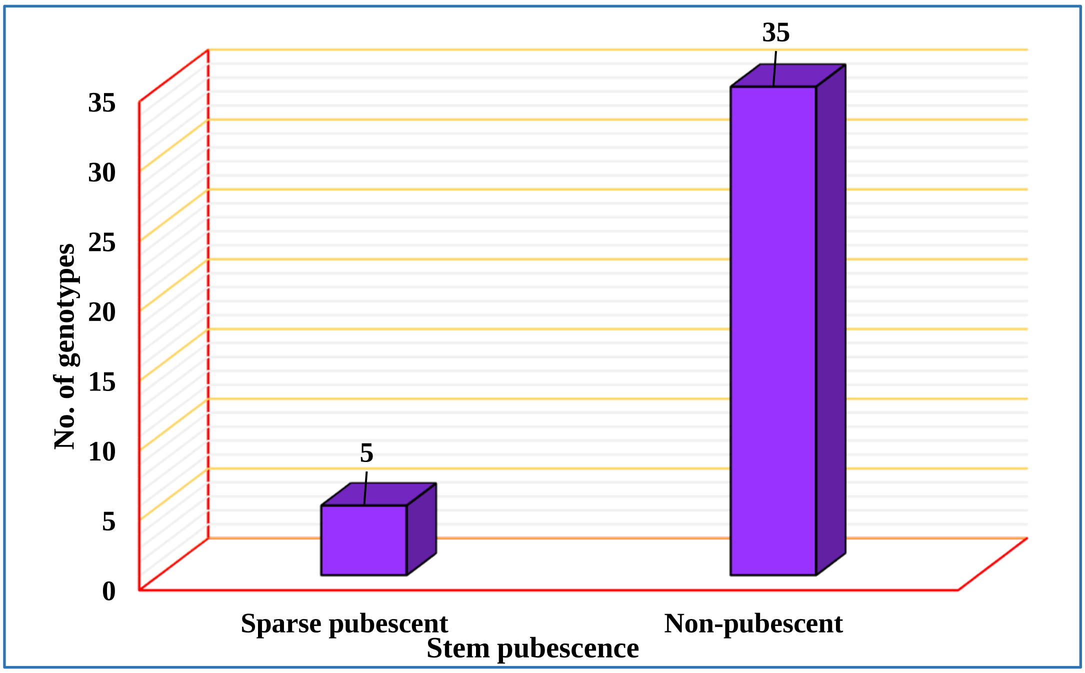


Fig. 2. Classification of 40 *Tulsi* genotypes on the basis of stem pubescence

4.1.1.3 Leaf shape

Based on the leaf shape, *Tulsi* genotypes may be characterized into three groups such as elliptical, sub-ovate and ovate. But, in the present investigation only elliptical leaf shape (Plate 3) was observed for all the 40 genotypes (Table 4.3, Fig. 3). None of the genotypes showed sub-ovate and ovate leaf shape.

Table 4.3. Classification of 40 *Tulsi* genotypes on the basis of leaf shape

Leaf shape	No. of Genotypes	Genotypes
Elliptical	40	IC 44681, IC 387837, IC 369247, IC 387838, IC 388785, IC 469938, IC 326735, IC 312264, IC 110207, IC 338794, IC 336833, IC 201223, IC 328582, IC 338959, IC 333833, IC 281185, IC 381552, IC 436153, IC 381158, IC 326732, EC 469904, EC 326771, EC 388893, EC 388887, EC 388895, EC 388896, EC 388782, EC 388737, EC 388889, EC 338772, EC 388788, EC 388890, RDV 45, NSV 38, Local 1, Local 2, DOS 1, IC 75730, IC 381185, EC 112548
Sub-ovate	0	-None-
Ovate	0	-None-

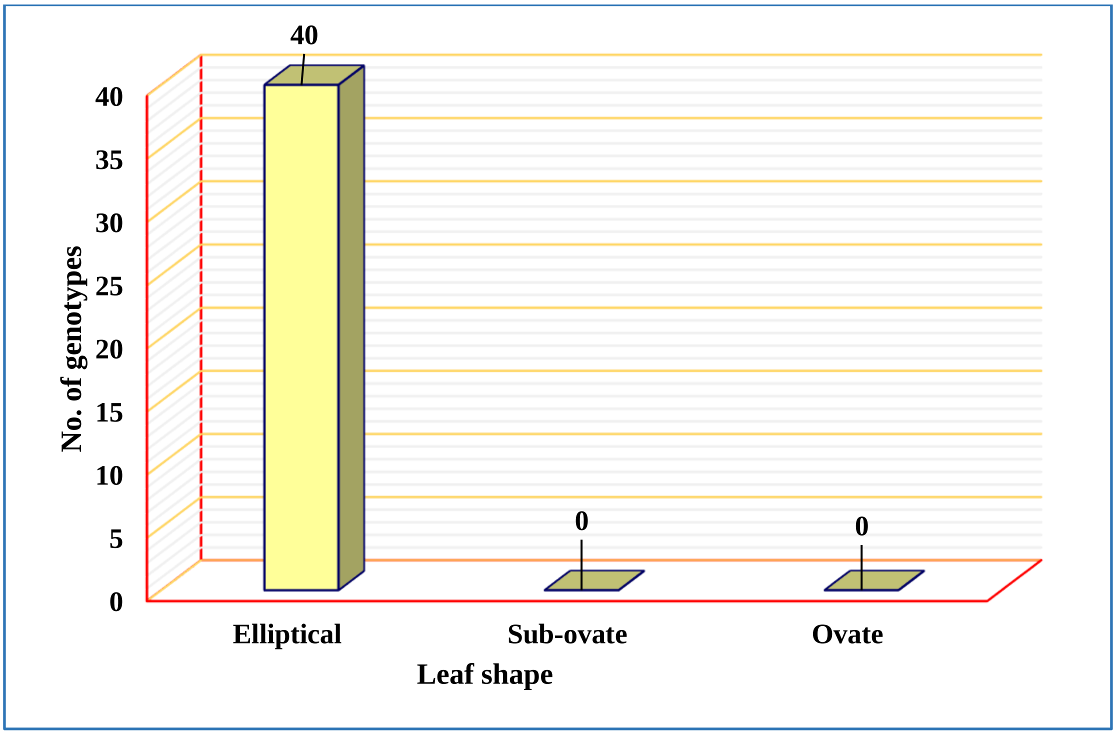


Fig. 3. Classification of 40 *Tulsi* genotypes on the basis of leaf shape

4.1.1.4 Leaf colour

All the 40 *Tulsi* genotypes were categorized into four different groups (dark green, green, light green and purple) based on the colour of their leaves (Plate 4). Dark green leaf colour was observed for 8 genotypes, green leaf colour for 25 genotypes, light green leaf colour for 6 genotypes whereas only one genotype exhibited purple leaf colour (Table 4.4, Fig. 4).

Table 4.4. Classification of 40 *Tulsi* genotypes on the basis of leaf colour

Leaf colour	No. of Genotypes	Genotypes
Dark green	8	IC 369247, IC 381552, EC 388893, EC 388887, EC 388895, IC 75730, Local 1, DOS 1
Green	25	IC 44681, IC 387837, IC 387838, IC 388785, IC 326735, IC 312264, IC 110207, IC 336833, IC 201223, IC 328582, IC 338959, IC 333833, IC 281185, EC 469904, EC 326771, EC 388896, EC 388782, EC 388737, EC 388889, EC 388788, EC 388890, IC 381158, IC 326732, NSV 38, EC 112548
Light green	6	IC 469938, IC 338794, EC 338772, IC 436153, RDV 45, Local 2
Purple	1	IC 381185

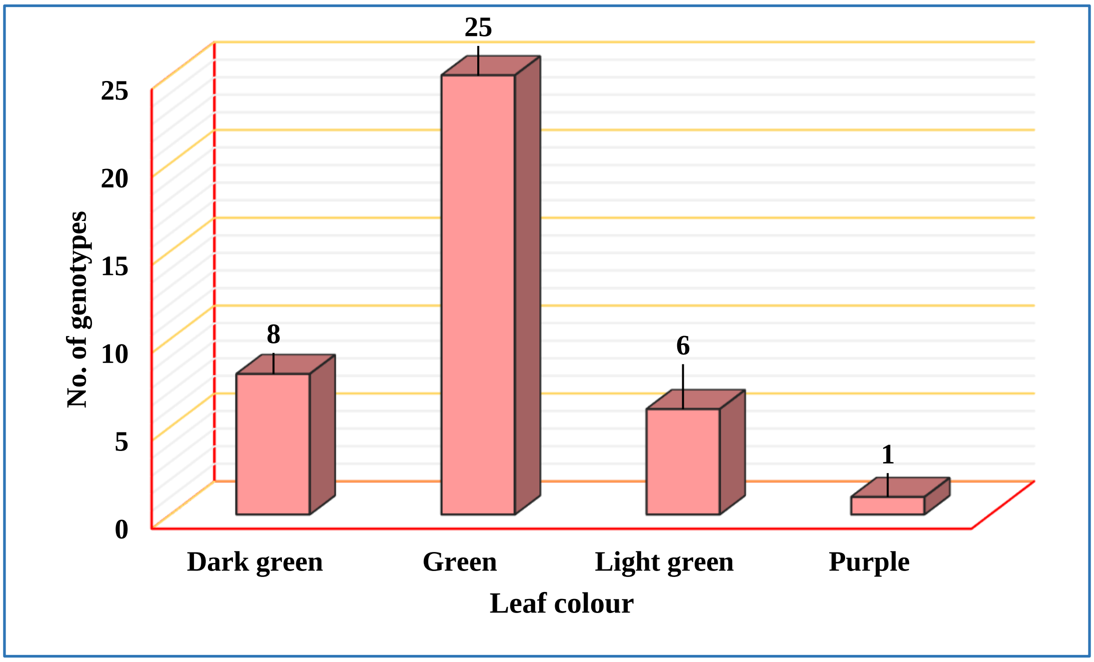


Fig. 4. Classification of 40 *Tulsi* genotypes on the basis of leaf colour

4.1.1.5 Leaf pubescence

On the basis of the presence or absence of the hairs on the leaf surface, *Tulsi* genotypes can be classified as sparse pubescent, dense pubescent and non-pubescent (Table 4.5, Fig. 5). In the present investigation, only two genotypes were observed to have sparse pubescence. Dense pubescent was not observed in any of the genotype whereas 38 genotypes showed non-pubescent characteristic for leaf pubescence (Plate 5)

Table 4.5. Classification of 40 *Tulsi* genotypes on the basis of leaf pubescence

Leaf pubescence	No. of Genotypes	Genotypes
Sparse pubescent	2	IC 388785, IC 381185
Dense pubescent	0	-None-
Non-pubescent	38	IC 44681, IC 387837, IC 369247, IC 387838, IC 469938, IC 326735, IC 312264, IC 110207, IC 338794, IC 336833, IC 201223, IC 328582, IC 338959, IC 333833, IC 281185, IC 381552, EC 469904, EC 326771, EC 388893, EC 388887, EC 388895, EC 388896, EC 388782, EC 388737, EC 388889, EC 338772, EC 388788, EC 388890, IC 436153, IC 381158, IC 326732, RDV 45, NSV 38, EC 112548, IC 75730, DOS 1, Local 1, Local 2

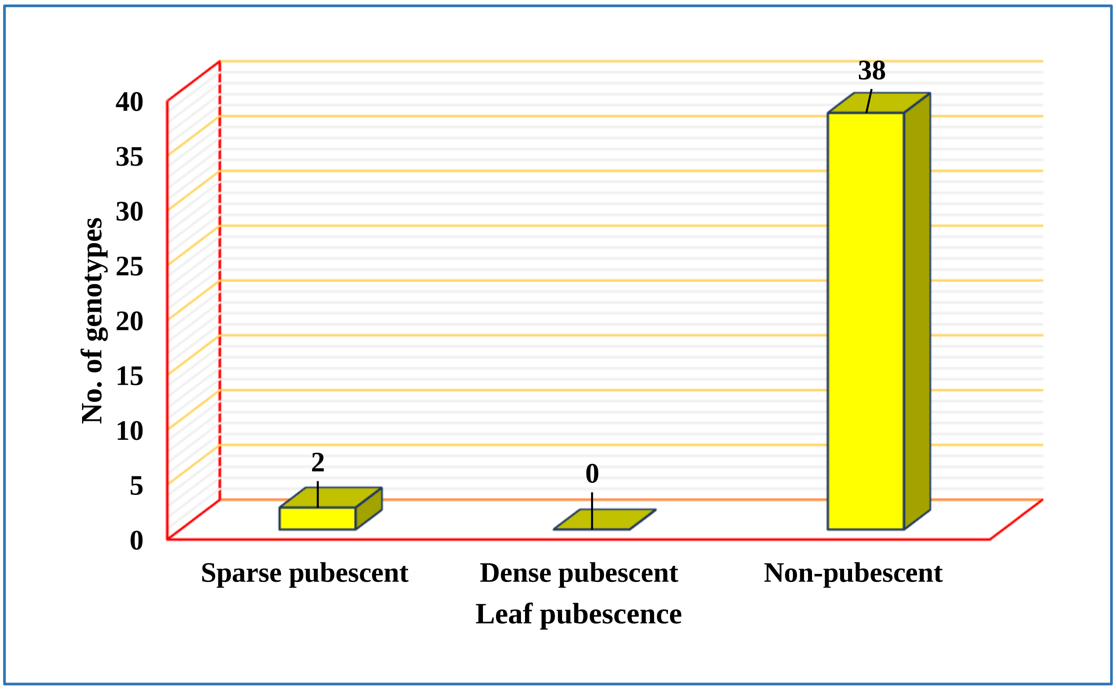


Fig. 5. Classification of 40 *Tulsi* genotypes on the basis of leaf pubescence

4.1.1.6 Petiole colour

Fourty *Tulsi* genotypes were classified into three different groups based on their petiole colour namely green, purple and purple green (Plate 6). Thirty-six genotypes exhibited green petiole colour, one purple petiole colour whereas three genotypes displayed purple green petiole colour (Table 4.6, Fig. 6).

Table 4.6. Classification of 40 *Tulsi* genotypes on the basis of petiole colour

Petiole colour	No. of genotypes	Genotypes
Green	36	IC 44681, IC 387837, IC 369247, IC 387838, IC 388785, IC 469938, IC 326735, IC 312264, IC 110207, IC 338794, IC 336833, IC 201223, IC 328582, IC 338959, IC 333833, IC 281185, IC 381552, EC 469904, EC 326771, EC 388887, EC 388895, EC 388896, EC 388782, EC 388737, EC 388889, EC 338772, EC 388788, EC 388890, IC 436153, IC 381158, IC 326732, RDV 45, NSV 38, EC 112548, Local 1, Local 2
Purple	1	IC 381185
Purple green	3	EC 388893, IC 75730, DOS 1

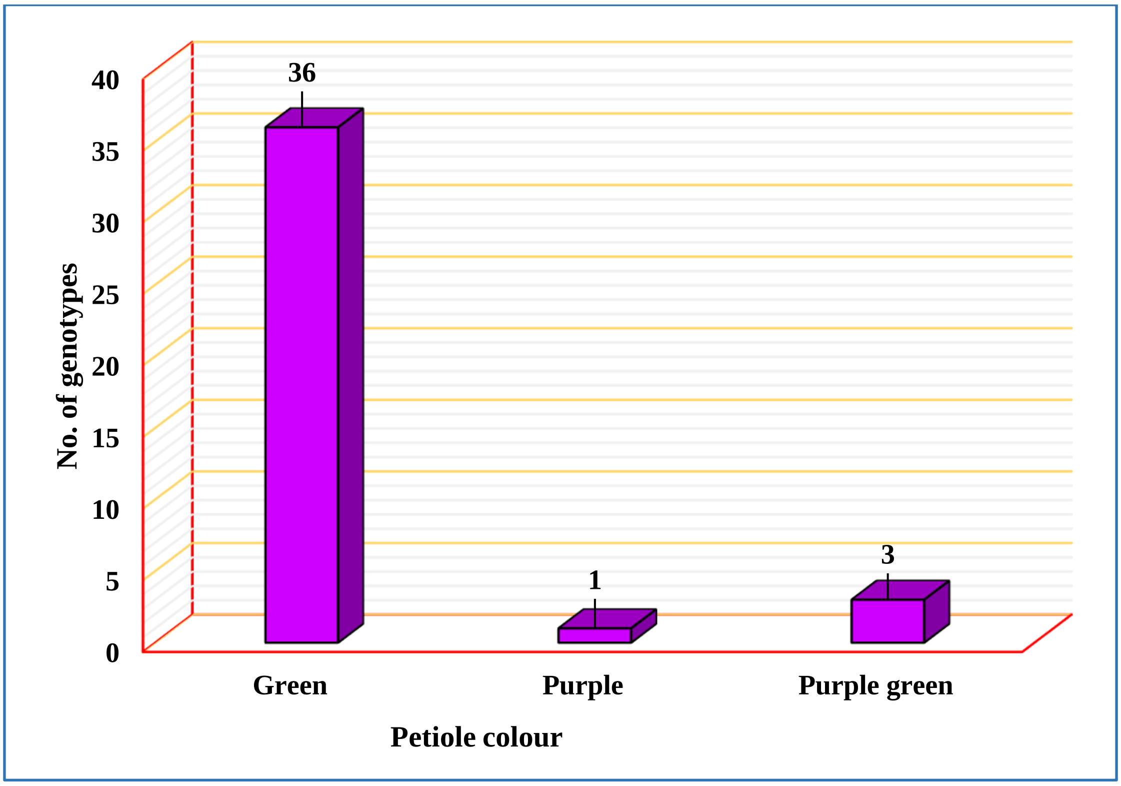


Fig. 6. Classification of *Tulsi* genotypes on the basis of petiole colour

4.1.1.7 Flower colour

On the basis of flower colour, *Tulsi* genotypes were classified into three categories which included white, light purple and purple (Plate 7). Among the 40 genotypes, 27 genotypes exhibited white flower colour, 8 genotypes light purple flower colour and purple flower colour expressed in the remaining 5 genotypes (Table 4.7, Fig. 7).

Table 4.7. Classification of 40 *Tulsi* genotypes on the basis of flower colour

Flower colour	No. of genotypes	Genotypes
White	27	IC 44681, IC 387837, IC 387838, IC 388785, IC 312264, IC 110207, IC 338794, IC 201223, IC 328582, IC 338959, IC 333833, IC 281185, EC 469904, EC 326771, EC 388887, EC 388895, EC 388782, EC 388737, EC 388889, EC 338772, IC 381158, IC 326732, RDV 45, NSV 38, EC 112548, Local 1, Local 2
Light purple	8	IC 369247, IC 469938, IC 326735, IC 381552, EC 388896, EC 388788, EC 388890, IC 436153
Purple	5	IC 336833, EC 388893, IC 75730, IC 381185, DOS 1

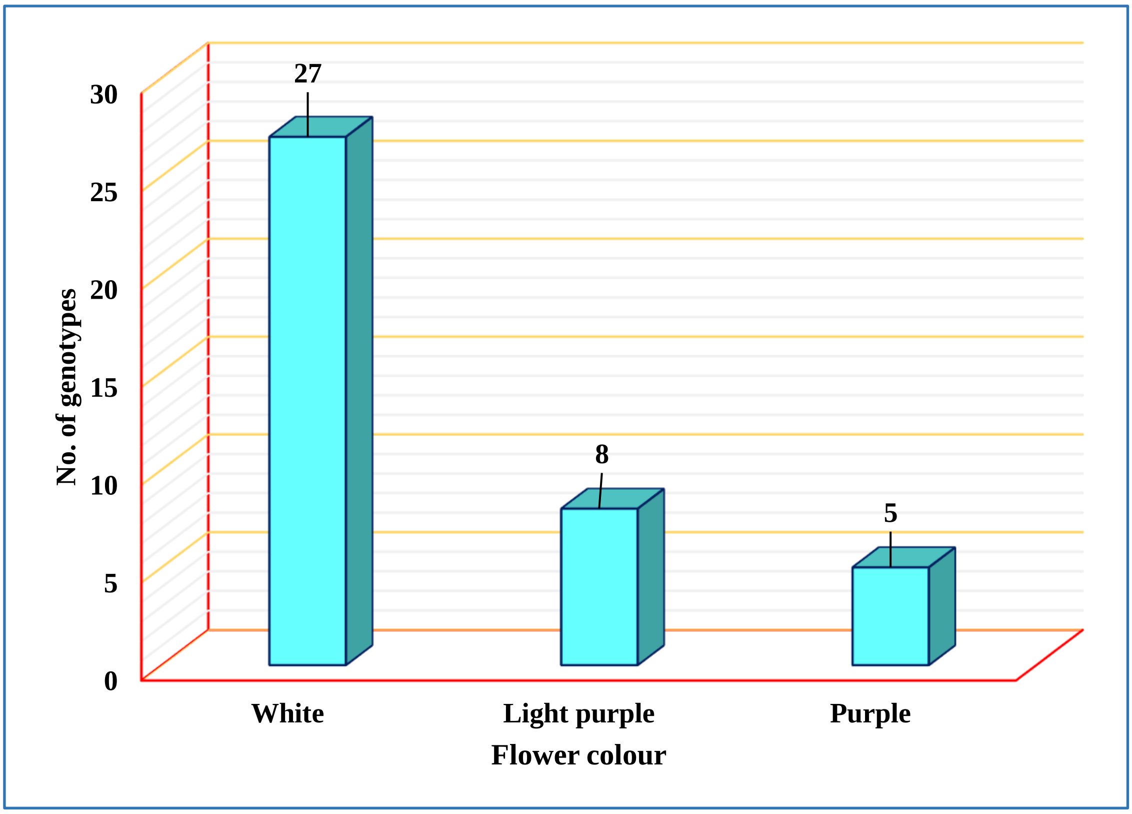


Fig. 7. Classification of 40 *Tulsi* genotypes on the basis of flower colour

4.1.1.8 Calyx colour

Five categories of calyx colour (Plate 8) *viz.* green (25 genotypes), light green (2 genotypes), purple (6 genotypes), light purple (6 genotypes) and dark purple (1 genotype) were observed for the 40 *Tulsi* genotypes studied for the present investigation (Table 4.8, Fig. 8).

Table 4.8. Classification of 40 *Tulsi* genotypes on the basis of calyx colour

Calyx colour	No. of genotypes	Genotypes
Green	25	IC 387838, IC 388785, IC 312264, IC 110207, IC 338794, IC 201223, IC 328582, IC 338959, IC 333833, IC 281185, EC 469904, EC 326771, EC 388887, EC 388895, EC 388782, EC 388737, EC 388889, EC 338772, IC 381158, IC 326732, RDV 45, NSV 38, EC 112548, Local 1, Local 2
Light green	2	IC 44681, IC 387837
Purple	6	EC 388893, EC 388788, EC 388890, IC 436153, IC 75730, DOS 1
Light purple	6	IC 369247, IC 469938, IC 326735, IC 336833, IC 381552, EC 388896
Dark purple	1	IC 381185

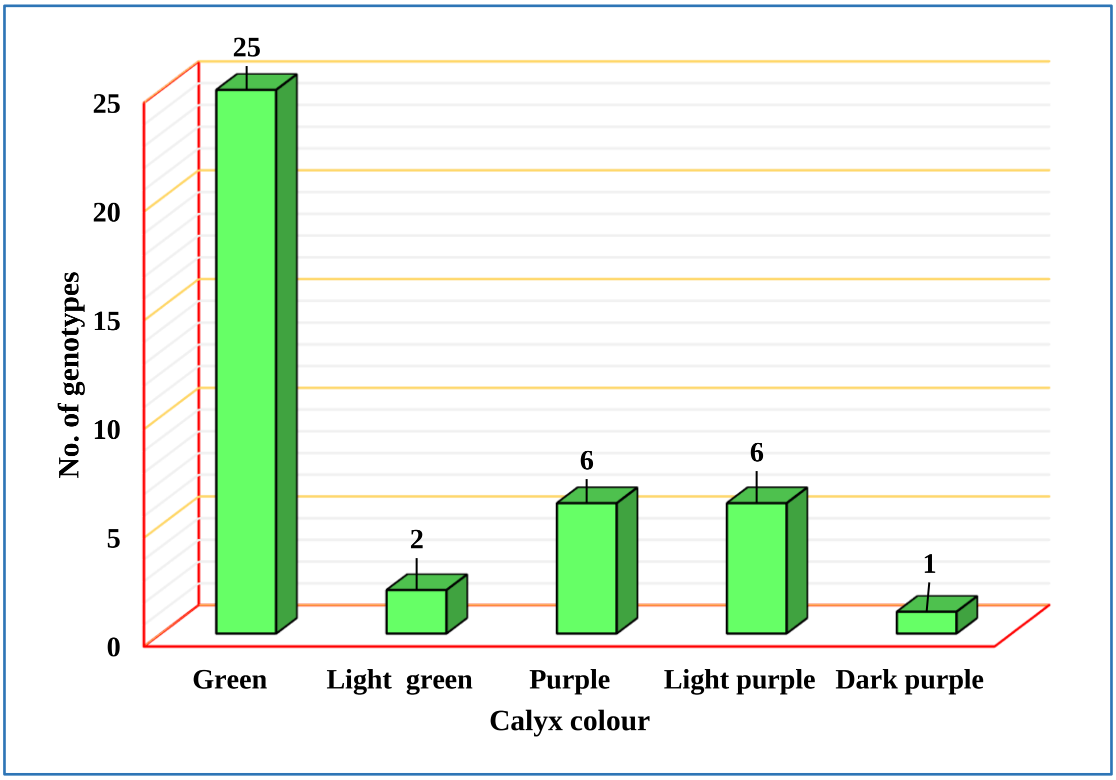


Fig. 8. Classification of 40 *Tulsi* genotypes on the basis of calyx colour

4.1.1.9 Calyx pubescence

Tulsi genotypes can be classified as sparse pubescent, dense pubescent and non-pubescent based on the presence or absence of the hairs on the calyx. In the present investigation, 13 genotypes were observed to have sparse pubescence, whereas 27 genotypes showed non-pubescent characteristic for calyx pubescence (Plate 9). None of the genotypes exhibited dense pubescence on calyx (Table 4.9, Fig. 9).

Table 4.9. Classification of 40 *Tulsi* genotypes on the basis of calyx pubescence

Calyx Pubescence	No. of genotypes	Genotypes
Sparse pubescent	13	IC 44681, IC 369247, IC 388785, IC 469938, IC 312264, IC 338794, IC 381552, IC 75730, IC 381185, EC 469904, EC 388893, EC 338772, DOS 1
Dense pubescent	0	-None-
Non-pubescent	27	IC 387837, IC 387838, IC 326735, IC 110207, IC 336833, IC 201223, IC 328582, IC 338959, IC 333833, IC 281185, IC 436153, IC 381158, IC 326732, EC 326771, EC 388887, EC 388895, EC 388896, EC 388782, EC 388737, EC 388889, EC 388788, EC 388890, RDV 45, NSV 38, EC 112548, Local 1, Local 2

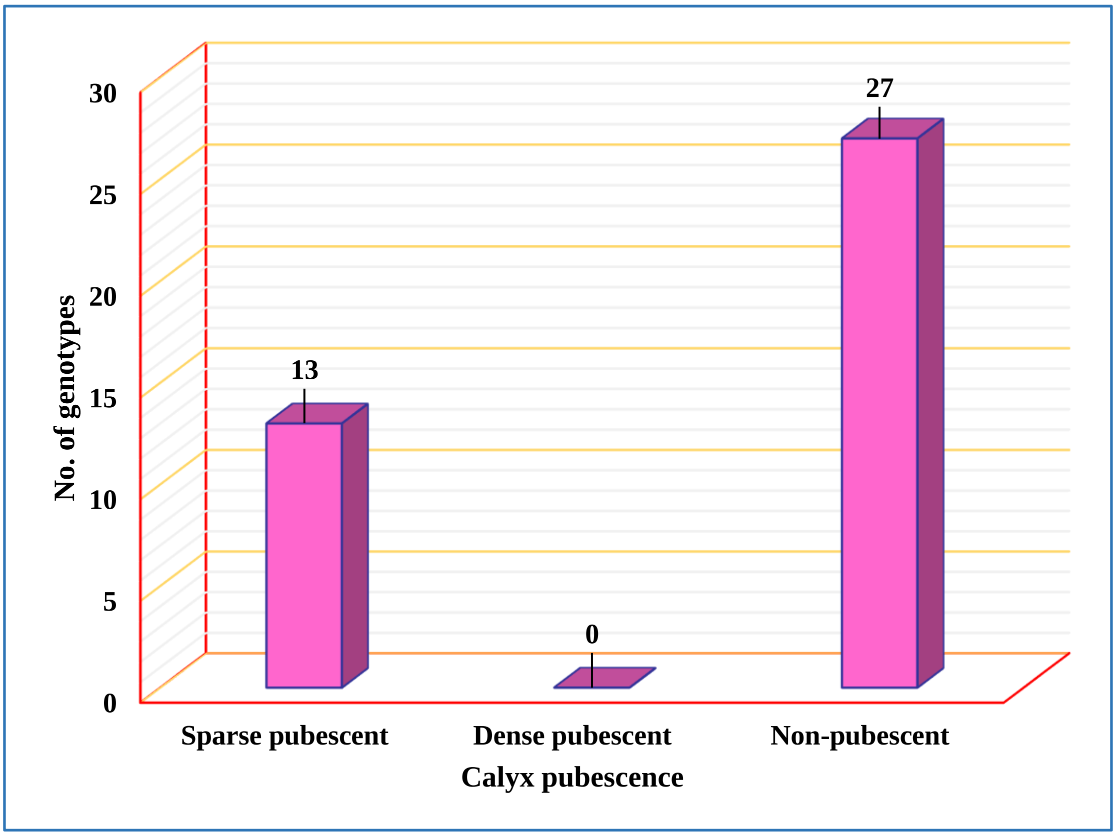


Fig. 9. Classification of 40 *Tulsi* genotypes on the basis of calyx pubescence

4.1.1.10 Seed colour

Four categories of seed colour (Plate 10) *viz.* black (1 genotype), dull black (35 genotypes), brownish black (1 genotype) and brown (3 genotypes) were observed for the 40 *Tulsi* genotypes studied in the present investigation (Table 4.10, Fig. 10).

Table 4.10. Classification of 40 *Tulsi* genotypes on the basis of seed colour

Seed colour	No. of genotypes	Genotypes
Black	1	IC 44681
Dull black	35	IC 387837, IC 369247, IC 387838, IC 388785, IC 469938, IC 326735, IC 312264, IC 110207, IC 338794, IC 201223, IC 328582, IC 338959, IC 333833, IC 281185, IC 381552, EC 469904, EC 326771, EC 388893, EC 388887, EC 388895, EC 388896, EC 388782, EC 388737, EC 388889, EC 338772, EC 388788, EC 388890, IC 436153, IC 381158, IC 326732, RDV 45, NSV 38, EC 112548, Local 1, DOS 1
Brownish black	1	IC 336833
Brown	3	IC 75730, IC 381185, Local 2

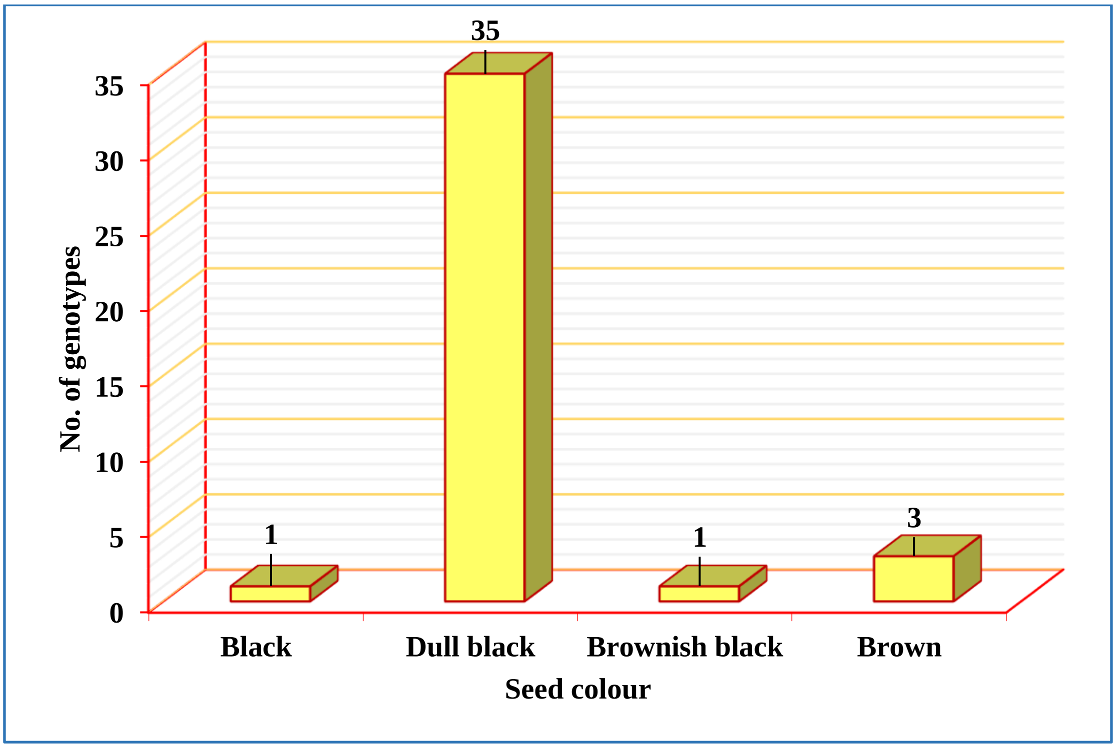


Fig. 10. Classification of 40 *Tulsi* genotypes on the basis of seed colour

4.1.2 Estimation of genetic variability parameters

4.1.2.1 Analysis of variance (ANOVA)

The analysis of variance for seed yield and its contributing traits are presented in Table 4.11. From the analysis of variance Table 4.11, it was found that mean sum of squares due to genotypes were highly significant for all the 17 quantitative traits namely days to 50% flowering, days to maturity, number of primary branches per plant, plant height (cm), number of spikes per plant, spike length (cm), number of flowers' whorls per spike, fresh herbage yield per plant (g), dry herbage yield per plant (g), seed yield per plant (g), 1000 seed weight (g), oil content (%), standard germination (%), seedling length (cm), seedling dry weight (mg), seed vigour index-I and seed vigour index-II. It indicated that sufficient amount of genetic variability was present for these 17 characters in the 40 genotypes studied which can be used for genetic improvement of Tulsi (*Ocimum spp.*) genotypes.

4.1.2.2 Mean performance of genotypes

The mean performances for all the 17 quantitative traits in 40 genotypes of *Tulsi* are presented in Table 4.12. The particular genotypes with maximum and minimum mean values recorded for 17 different quantitative traits among 40 *Tulsi* genotypes have been presented in Table 4.13. The mean performance of the various traits is explained as below:

i). Days to 50% flowering

The days to 50% flowering varied from 41 to 81 days with mean value of 58.5 days (Table 4.12). The maximum days (81) for 50% flowering were taken by the genotype EC 112548 and the minimum days (41) by the genotypes DOS 1 (Table 4.13).

ii). Days to maturity

The days to maturity varied from 140 to 177.7 days with mean value of 163.6 days (Table 4.12). The maximum days (177.7) for maturity was taken by the genotype EC 388893 whereas, minimum days (140) by the genotype DOS 1 (Table 4.13).

iii). Number of primary branches/plant

The number of primary branches per plant ranged from 10.6 to 21.7 with mean value of 16.0 (Table 4.12). The number of primary branches per plant were recorded maximum (21.7) for genotype EC 338772 while, the minimum number of primary branches per plant (10.6) were observed for the genotype IC 326732 (Table 4.13).

iv). Plant height (cm)

The plant height ranged from 70.9 cm to 114.5 cm with mean value of 86.4 cm (Table 4.12). Maximum plant height (114.5 cm) was observed for the genotype IC 381185 while, the minimum by the genotype EC 388895 (70.9 cm) (Table 4.13).

Dark green **Green** **Light green** **Purple** **Light purple**

Plate 1. Different categories of stem colours observed in 40 genotypes of Tulsi (*Ocimum spp*.)

Sparse pubescent **Non-pubescent**

Plate 2. Different categories of stem pubescence observed in 40 genotypes of Tulsi (*Ocimum spp*.)

Elliptical leaf shape

Plate 3. Leaf shape observed in 40 genotypes of Tulsi (*Ocimum spp*.)

Dark green Green Light green Purple

Plate 4. Different categories of leaf colours observed in 40 genotypes of Tulsi (*Ocimum spp*.)

Sparse pubescent Non-pubescent

Plate 5. Different categories of leaf pubescence observed in 40 genotypes of Tulsi (*Ocimum spp*.)

Green Purple Purple green

Plate 6. Different categories of petiole colours observed in 40 genotypes of Tulsi (*Ocimum spp*.)

White **Light purple** **Purple**

Plate 7. Different categories of flower colours observed in 40 genotypes of Tulsi (*Ocimum spp*.)

Green **Light green**

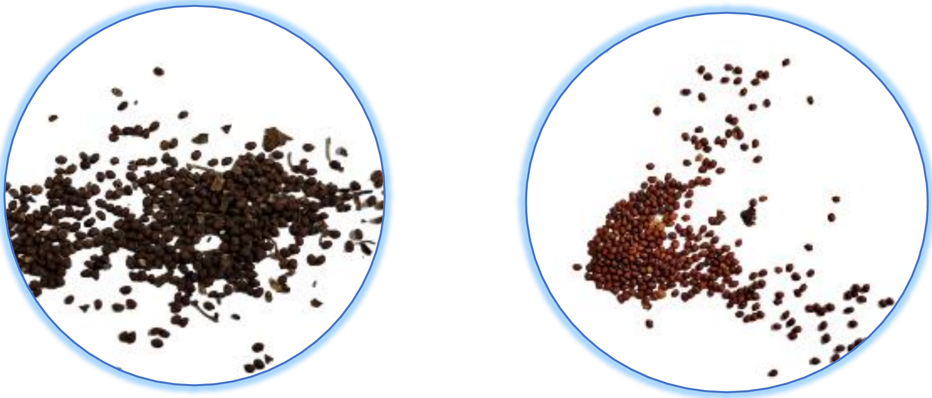
Purple **Light purple** **Dark purple**

Plate 8. Different categories of calyx colours observed in 40 genotypes of Tulsi (*Ocimum spp*.)

Sparse pubescent **Non pubescent**

Plate 9. Different categories of calyx pubescence observed in 40 genotypes of Tulsi (*Ocimum spp*.)

Black **Dull black**



Brownish black **Brown**

Plate 10. Different categories of seed colours observed in 40 genotypes of Tulsi (*Ocimum spp*.)

Table 4.11. Analysis of variance (ANOVA) for seed yield and its component traits in 40 *Tulsi* genotypes

Source of Variation	DF	Mean sum of squares								
		DF	DM	PB	PH	NSP	SL	FW	FHY	DHY
Replication	2	4.01	5.73	1.70	25.80	17.79	0.31	0.06	486.91	385.20
Genotype	39	504.77**	371.32**	19.35**	275.33**	876.71**	37.54**	11.58**	163239.79**	21752.76**
Error	78	4.85	4.96	1.10	11.85	21.03	0.86	0.83	804.67	130.25

Contd.

Table 4.11. Contd. …

Source of Variation	DF	Mean sum of squares							
		SY	SW	OC	SG	SDL	SDW	SVI-I	SVI-II
Replication	2	5.59	0.002	0.000302	12.10	1.58	0.29	79664.43	2124.72
Genotype	39	561.88**	0.482**	0.022271**	453.80**	692.94**	16.36**	8615014.11**	119627.79**
Error	78	7.58	0.001	0.000098	6.19	37.05	0.11	224980.60	1203.10

** Significant at 1% level of significance, *Significant at 5 % level of significance, DF: Degree of freedom

DF: Days to 50% flowering, DM: Days to maturity, PB: Number of primary branches/plant, PH: Plant height (cm), NSP: Number of spikes/plant, SL: Spike length (cm), FW: Number of flowers' whorls/spike, FHY: Fresh herbage yield/plant (g), DHY: Dry herbage yield/plant (g), SY: Seed yield/plant (g), SW: 1000 seed weight (g), OC: Oil content (%), SG: Standard germination (%), SDL: Seedling length (mm), SDW: Seedling dry weight (mg), SVI-I: Seed vigour index-I, SVI-II: Seed vigour index-II

Table 4.12. Mean performance of 17 quantitative traits of 40 *Tulsi* genotypes evaluated during *Kharif* 2022 at CCSHAU, Hisar

Genotype	DF	DM	PB	PH	NSP	SL	FW	FHY	DHY	SY	SW	OC	SG	SDL	SDW	SVI-I	SVI-II
IC 44681	73.3	168.0	17.7	88.7	66.0	23.3	15.1	713.3	215.8	33.7	1.590	0.263	66.0	104.0	11.5	6861.3	761.1
IC 387837	78.3	170.3	17.3	101.9	**56.7**	22.4	11.9	671.7	292.2	22.3	1.176	0.133	75.3	95.0	10.5	7158.0	788.9
IC 369247	74.0	153.3	17.1	82.4	102.8	20.7	13.6	409.6	118.4	38.1	1.375	0.149	**86.7**	93.0	8.4	8056.0	727.5
IC 387838	75.0	173.7	16.0	73.1	58.0	22.3	10.5	331.9	102.6	13.0	1.158	0.108	54.0	85.0	9.4	4589.3	507.9
IC 388785	79.3	156.7	10.7	103.1	146.6	22.5	**17.8**	1026.3	382.9	38.2	1.379	0.331	54.0	110.0	9.5	5941.3	511.7
IC 469938	57.3	159.3	14.3	84.9	81.0	17.8	14.6	1087.8	382.1	16.1	0.628	0.401	44.7	81.3	9.4	3628.0	421.7
IC 326735	43.3	142.7	15.6	71.1	117.7	14.5	12.3	474.2	123.3	23.9	0.734	0.177	46.0	85.0	10.3	3908.7	475.7
IC 312264	69.0	147.0	19.3	97.3	108.6	16.0	12.9	454.5	113.7	22.3	0.783	0.265	56.0	94.7	13.0	5299.3	728.1
IC 110207	50.7	162.3	12.8	84.4	97.3	15.4	15.3	349.5	110.2	39.9	1.545	0.115	52.7	**128.7**	11.4	6836.0	600.5
IC 338794	48.7	142.7	18.7	85.6	114.7	13.9	11.8	424.6	118.7	21.1	0.665	0.288	74.7	104.0	9.8	7768.0	734.1
IC 336833	42.7	160.0	17.3	91.7	125.2	17.2	14.9	476.3	128.2	32.2	0.938	0.164	80.7	94.7	10.3	7636.7	833.4
IC 201223	80.3	166.7	14.6	104.6	120.0	16.9	16.4	458.9	123.8	20.8	**1.862**	0.206	70.7	94.0	10.2	6644.0	723.3
IC 328582	78.3	160.0	15.6	104.0	89.8	17.2	16.1	1003.4	319.3	48.7	1.538	0.153	68.0	93.7	11.6	6365.3	790.9
IC 338959	69.3	153.7	18.9	92.4	62.0	11.7	10.5	721.2	198.5	14.4	0.608	0.228	50.0	95.0	9.7	4752.0	483.5
IC 333833	52.3	174.0	13.8	76.6	74.9	12.8	12.1	359.5	116.9	27.1	0.932	0.255	76.7	106.3	9.2	8151.3	707.5
IC 281185	52.3	176.3	13.1	80.7	63.1	13.6	10.7	640.0	220.2	14.6	0.824	0.250	66.7	108.3	9.4	7216.0	629.0
IC 381552	46.3	175.3	13.7	83.0	82.6	19.3	12.9	442.9	134.9	22.0	1.354	0.264	56.7	105.3	8.9	5964.0	502.7
EC 469904	45.0	173.7	14.1	80.9	71.7	**24.1**	13.5	492.8	158.6	31.0	1.202	0.325	62.7	103.3	9.4	6470.7	591.2
EC 326771	72.7	175.7	15.2	75.5	61.8	14.4	11.1	436.4	164.4	15.0	1.213	0.262	76.0	102.0	9.6	7746.7	732.9
EC 388893	55.7	**177.7**	17.9	88.2	145.7	17.5	16.2	350.1	104.2	28.1	1.411	0.155	64.7	101.7	10.6	6580.7	688.5
EC 388887	49.0	170.7	16.1	82.5	83.8	17.6	14.1	476.4	150.6	15.4	0.632	0.157	67.3	97.3	9.9	6562.0	662.9
EC 388895	50.3	172.7	15.3	**70.9**	95.6	14.9	13.4	750.0	203.2	24.9	0.912	0.172	75.3	96.0	9.8	7236.7	735.2
EC 388896	54.0	166.0	14.9	90.9	84.0	18.5	14.3	481.7	115.9	26.3	0.965	0.315	78.0	88.7	7.9	6914.7	615.7
EC 388782	62.0	167.7	17.1	81.1	111.2	17.8	14.2	782.1	222.2	30.2	1.134	0.225	65.3	85.0	8.9	5556.0	581.6
EC 388737	62.0	153.0	14.9	76.7	124.2	15.7	13.7	**329.7**	104.7	27.2	0.762	**0.092**	77.3	114.7	10.5	8859.3	812.3

Contd.

Table 4.12. Contd. …

Genotype	DF	DM	PB	PH	NSP	SL	FW	FHY	DHY	SY	SW	OC	SG	SDL	SDW	SVI-I	SVI-II
EC 388889	80.7	159.3	15.8	81.2	121.8	11.6	**9.7**	507.0	118.6	26.6	0.992	0.136	67.3	110.7	**13.8**	7461.3	931.1
EC 338772	55.3	175.3	**21.7**	73.9	189.0	15.5	13.1	573.8	144.8	**61.5**	1.546	0.234	65.3	104.7	10.1	6845.3	661.9
EC 388788	44.3	166.7	15.7	88.8	172.7	17.4	15.6	601.8	142.8	46.3	1.015	0.219	81.3	98.0	9.9	7973.3	805.4
EC 388890	46.0	168.0	19.1	87.1	195.2	16.7	12.7	**1250.0**	**414.9**	57.1	0.815	**0.493**	70.7	97.3	10.0	6878.0	709.2
IC 436153	50.7	161.7	13.1	87.7	150.1	12.3	15.5	362.1	104.4	40.8	0.996	0.159	46.7	92.7	9.7	4317.3	450.9
IC 381158	45.0	172.0	18.5	88.9	95.9	16.3	13.3	1014.2	318.5	53.2	0.862	0.334	60.0	107.7	9.1	6456.7	548.2
IC 326732	53.3	162.0	**10.6**	83.2	127.8	16.4	13.2	646.4	218.6	31.2	1.006	0.266	74.7	124.0	13.0	**9269.3**	**968.6**
RDV 45	49.3	160.3	14.9	86.0	232.0	17.1	16.6	382.5	117.7	60.9	1.606	0.220	52.7	86.0	7.9	4537.3	416.9
NSV 38	53.3	170.0	12.2	88.0	85.5	15.3	10.9	339.9	**97.9**	13.5	0.696	0.103	61.3	99.7	8.5	6120.0	521.9
EC 112548	**81.0**	173.7	17.2	83.4	69.4	17.1	13.7	544.4	125.6	15.9	0.716	0.229	85.3	96.3	9.5	8220.0	813.8
IC 75730	59.7	143.7	21.1	85.2	99.1	**9.9**	10.5	582.3	165.0	**10.2**	0.247	0.285	**41.3**	**56.7**	**3.1**	**2350.0**	**127.0**
Local 1	66.3	175.3	18.8	92.7	102.0	12.3	11.9	656.4	193.6	27.2	1.550	0.170	64.7	104.3	10.6	6742.7	683.1
IC 381185	44.3	142.7	17.8	**114.5**	186.1	10.6	15.3	834.8	243.2	14.8	**0.221**	0.308	42.0	61.7	3.2	2594.0	135.9
Local 2	47.0	175.3	14.6	81.6	78.2	15.9	15.3	632.8	139.9	15.5	0.615	0.325	48.0	65.3	4.2	3138.7	199.7
DOS 1	**41.0**	**140.0**	17.1	81.0	**326.4**	10.4	14.3	825.2	206.8	30.5	0.237	0.242	62.7	63.3	3.8	3969.3	236.5
Mean	58.5	163.6	16.0	86.4	114.4	16.3	13.5	597.5	179.4	28.8	1.011	0.229	64.3	95.9	9.4	6239.4	613.9
SE (m±)	1.27	1.29	0.60	1.98	2.45	0.62	0.61	16.18	6.52	1.61	0.02	0.006	1.44	3.51	0.20	273.85	20.03
CD (p=0.05)	3.58	3.62	1.70	5.58	6.88	1.75	1.72	45.53	18.34	4.53	0.05	0.017	4.04	9.89	0.55	771.02	56.38
CV (%)	3.77	1.36	6.54	3.98	3.73	5.99	6.96	4.79	6.37	9.28	2.78	4.47	3.87	6.35	3.59	7.60	5.65

DF: Days to 50% flowering, DM: Days to maturity, PB: Number of primary branches/plant, PH: Plant height (cm), NSP: Number of spikes/plant, SL: Spike length (cm), FW: Number of flowers' whorls/spike, FHY: Fresh herbage yield/plant (g), DHY: Dry herbage yield/plant (g), SY: Seed yield/plant (g), SW: 1000 seed weight (g), OC: Oil content (%), SG: Standard germination (%), SDL: Seedling length (mm), SDW: Seedling dry weight (mg), SVI-I: Seed vigour index-I, SVI-II: Seed vigour index-II

Note: The maximum and minimum mean values for each of the quantitative traits have been highlighted with bold digits.

Table 4.13. The genotypes with maximum and minimum mean values recorded for each of the 17 different quantitative traits among 40 *Tulsi* genotypes

Sr. No.	Trait	Genotype with maximum mean value		Genotype with minimum mean value	
		Genotype	Maximum mean value	Genotype	Minimum mean value
1	Days to 50% flowering	EC 112548	81.0	DOS 1	41.0
2	Days to maturity	EC 388893	177.7	DOS 1	140.0
3	Number of primary branches/plant	EC 338772	21.7	IC 326732	10.6
4	Plant height (cm)	IC 381185	114.5	EC 388895	70.9
5	Number of spikes/plant	DOS 1	326.4	IC 387837	56.7
6	Spike length (cm)	EC 469904	24.1	IC 75730	9.9
7	Number of flowers' whorls/spike	IC 388785	17.8	EC 388889	9.7
8	Fresh herbage yield/plant (g)	EC 388890	1250.0	EC 388737	329.7
9	Dry herbage yield/plant (g)	EC 388890	414.9	NSV 38	97.9
10	Seed yield/plant (g)	EC 338772	61.5	IC 75730	10.2
11	1000 seed weight (g)	IC 201223	1.862	IC 381185	0.221
12	Oil content (%)	EC 388890	0.493	EC 388737	0.092
13	Standard germination (%)	IC 369247	86.7	IC 75730	41.3
14	Seedling length (mm)	IC 110207	128.7	IC 75730	56.7
15	Seedling dry weight (mg)	EC 388889	13.8	IC 75730	3.1
16	Seed vigour index-I	IC 326732	9269.3	IC 75730	2350.0
17	Seed vigour index-II	IC 326732	968.6	IC 75730	127.0

v). Number of spikes per plant

The Number of spikes per plant ranged between 56.7 to 326.4 with mean value of 114.4 (Table 4.12). The number of spikes per plant were observed maximum (326.4) for the genotype DOS 1 whereas, the minimum number of spikes per plant (56.7) for the genotype IC 387837 (Table 4.13).

vi). Spike length (cm)

The spike length ranged from 9.9 cm to 24.1 cm with mean value of 16.3 cm (Table 4.12). Spike length was observed maximum (24.1 cm) for genotype EC 469904 while, the minimum spike length (9.9 cm) expressed in the genotype IC 75730 (Table 4.13).

vii). Number of flowers’ whorls/spike

The Number of flowers’ whorls per spike ranged from 9.7 to 17.8 with mean value of 13.5 (Table 4.12). The number of flowers’ whorls per spike were observed maximum (17.8) for genotype IC 388785 whereas, the minimum number of flowers’ whorls per spike (9.7) were recorded for the genotype EC 388889 (Table 4.13).

viii). Fresh herbage yield/plant (g)

The fresh herbage yield per plant ranged from 329.7 g to 1250.0 g with the mean value of 597.5 g (Table 4.12). Maximum Fresh herbage yield per plant (1250.0 g) was observed for genotype EC 388890 while, the minimum for the genotype EC 388737 (329.7 g) (Table 4.13).

ix). Dry herbage yield/plant (g)

The dry herbage yield per plant varied between 97.9 g to 414.9 g with the mean value of 179.4 g (Table 4.12). Dry herbage yield per plant was observed maximum (414.9 g) for genotype EC 388890 while, the minimum dry herbage yield per plant (97.9 g) was recorded in the genotype NSV 38 (Table 4.13).

x). Seed yield/plant (g)

The seed yield per plant ranged from 10.2 g to 61.5 g, with the mean value of 28.8 g (Table 4.12). Highest seed yield per plant (61.5 g) was observed for the genotype EC 338772 whereas, the lowest seed yield per plant (10.2 g) was shown by the genotype IC 75730 (Table 4.13).

xi). 1000 seed weight (g)

1000 seed weight ranged from 0.221 g to 1.862 g with the mean value of 1.011 g (Table 4.12). 1000 seed weight was recorded maximum (1.862 g) for the genotype IC 201223 while, the minimum 1000 seed weight (0.221 g) by the genotype IC 381185 (Table 4.13).

xii). Oil content (%)

The oil content ranged between 0.092% to 0.493% with the mean value of 0.229% (Table 4.12). Oil content was observed maximum (0.493%) for the genotype EC 388890 while, the minimum oil content (0.092%) by the genotype EC 388737 (Table 4.13).

xiii). Standard germination (%)

The standard germination (%) ranged from 41.3% to 86.7% with mean value of 64.3% (Table 4.12). Standard germination was observed maximum (86.7%) for the genotype IC 369247 whereas, the minimum standard germination (41.3%) was exhibited by the genotype IC 75730 (Table 4.13).

xiv). Seedling length (mm)

The seedling length ranged from 56.7 mm to 128.77 mm with the mean value of 95.9 mm (Table 4.12). Maximum seedling length (128.77 mm) was recorded for the genotype IC 110207 while, the minimum seedling length (56.7 mm) was observed for the genotype IC 75730 (Table 4.13).

xv). Seedling dry weight (mg)

The seedling dry weight ranged between 3.1 mg to 13.8 mg with the mean value of 9.4 mg (Table 4.12). Seedling dry weight was observed maximum (13.8 mg) for the genotype EC 388889 while, the minimum seedling dry weight (3.1 mg) was recorded for the genotype IC 75730 (Table 4.13).

xvi). Seed vigour index-I (SVI-I)

The seed vigour index-I ranged from 2350.0 to 9269.3 with the mean value of 6239.4 (Table 4.12). Maximum seed vigour index-I (9269.3) was recorded for the genotype IC 326732 whereas, the seed vigour index-I (2350) was minimum for the genotype IC 75730 (Table 4.13).

xvii). Seed vigour index–II (SVI-II)

The seed vigour index-II ranged from 127.0 to 968.6 with the mean value of 613.9 (Table 4.12). Seed vigour index-II was observed maximum (968.6) for the genotype IC 326732 while, the minimum seed vigour index-II (127.0) was recorded for the genotype IC 75730 (Table 4.13).

4.1.2.3 Genetic variability parameters

The estimates of genetic variability parameters such as mean, range, genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), heritability in broad sense (%) and genetic advance as percent of mean for all the 17 quantitative traits studied were worked out which are presented in the Table 4.14. Two of the genetic variability parameters i.e. mean and range has already been explained whereas, rest of the three genetic variability parameters i.e. coefficients of variability (GCV% and PCV%), heritability in broad sense (%) and genetic advance as percent of mean are being explained in the following way.

Further, the classification of all the traits based on different categories (high, moderate and low) of genetic variability parameters namely GCV (%), PCV (%), heritability in broad sense (%) and genetic advance as percent of mean has also been presented in the Table 4.15.

i). Genotypic coefficients of variation (%)

The estimates of genotypic coefficients of variation (GCV) were lower than their corresponding phenotypic coefficients of variation (PCV) for all the 17 quantitative traits (Table 4.14). The highest GCV was observed for dry herbage yield per plant (47.31%) followed by seed yield per plant (47.21%), number of spikes per plant (47.18%), 1000 seed weight (39.63%), fresh herbage yield per plant (38.95%), oil content (37.47%), seed vigour index-II (32.36%), seed vigour index-I (26.80%), seedling dry weight (24.78%), days to 50% flowering (22.08%) and spike length (21.43%) (Table 4.14). Thus, high GCV (>20%) was found for these 11 traits. Moderate GCV (10-20%) was observed for standard germination (19.01%), seedling length (15.42%), number of primary branches per plant (15.41%), number of flowers' whorls per spike (13.98%) and plant height (10.85%). Low GCV (0-10%) was observed for days to maturity (6.75%) (Table 4.15).

ii). Phenotypic coefficients of variation (%)

The estimates of phenotypic coefficients of variation (PCV) were found highest for seed yield per plant (48.17%) followed by dry herbage yield per plant (47.74%), number of spikes per plant (47.35%), 1000 seed weight (39.73%), fresh herbage yield per plant (39.24%), oil content (37.74%), seed vigour index-II (32.85%), seed vigour index-I (27.86%), seedling dry weight (25.04%), days to 50% flowering (22.40%) and spike length (22.17%) (Table 4.14). Thus, these 11 traits showed high PCV (>20%). Moderate PCV (10-20%) was observed for standard germination (19.40%), number of primary branches per plant (16.74%), seedling length (16.68%), number of flowers' whorls per spike (15.52%) and plant height (11.56%). Low PCV (%) was found for days to maturity (6.89%) (Table 4.15).

iii). Heritability in broad sense (%)

The estimates of heritability in broad sense were found highest for 1000 seed weight (99.51%) followed by number of spikes per plant (99.28%), oil content (98.60%), fresh herbage yield per plant (98.54%), dry herbage yield per plant (98.23%), seedling dry weight (97.94%), days to 50% flowering (97.17%), seed vigour index-II (97.04%), days to maturity (96.09%), seed yield per plant (96.06%), standard germination (96.02%), spike length (93.44%), seed vigour index-I (92.55%), plant height (88.12%), seedling length (85.51%), number of primary branches per plant (84.75%) and number of flowers' whorls per spike (81.21%) (Table 4.14). Hence, heritability in broad sense was observed high (>60%) for all the 17 quantitative traits studied (Table 4.15).

iv). Genetic advance as percent of mean

Genetic advance as percent of mean were found high (>20) for all the traits except days to maturity (Table 4.15). The estimates of genetic advance as percent of mean was found highest for number of spikes per plant (96.84) followed by dry herbage yield per plant (96.59), seed yield per plant (95.32), 1000 seed weight (81.44), fresh herbage yield per plant (79.64), oil content (76.65), seed vigour index-II (65.67), seed vigour index-I (53.12), seedling dry weight (50.51), days to 50% flowering (44.84), spike length (42.66), standard germination (38.38), seedling length (29.38), number of primary branches per plant (29.23), number of flowers' whorls per spike (25.96), plant height (20.98) (Table 4.14). For days to maturity, the estimate of genetic advance as percent of mean existed in moderate (10-20) category (Table 4.15).

Table 4.14. Estimates of genetic variability parameters for 17 quantitative traits among 40 *Tulsi* genotypes

Sr. No.	Trait	Mean	Range		Coefficients of Variability		h^2 (bs) (%)	GA (% of mean)
			Min.	Max.	GCV (%)	PCV (%)		
1.	Days to 50% flowering	58.5	41.0	81.0	22.08	22.40	97.17	44.84
2.	Days to maturity	163.6	140.0	177.7	6.75	6.89	96.09	13.64
3.	Number of primary branches/plant	16.0	10.6	21.7	15.41	16.74	84.75	29.23
4.	Plant height (cm)	86.4	70.9	114.5	10.85	11.56	88.12	20.98
5.	Number of spikes/plant	114.4	56.7	326.4	47.18	47.35	99.28	96.84
6.	Spike length (cm)	16.3	9.9	24.1	21.43	22.17	93.44	42.66
7.	Number of flowers' whorls/spike	13.5	9.7	17.8	13.98	15.52	81.21	25.96
8.	Fresh herbage yield/plant (g)	597.5	329.7	1250	38.95	39.24	98.54	79.64
9.	Dry herbage yield/plant (g)	179.4	97.9	414.9	47.31	47.74	98.23	96.59
10.	Seed yield/ plant (g)	28.8	10.2	61.5	47.21	48.17	96.06	95.32
11.	1000 seed weight (g)	1.011	0.221	1.862	39.63	39.73	99.51	81.44
12.	Oil content (%)	0.229	0.092	0.493	37.47	37.74	98.60	76.65
13.	Standard germination (%)	64.3	41.3	86.7	19.01	19.40	96.02	38.38
14.	Seedling length (mm)	95.9	56.7	128.7	15.42	16.68	85.51	29.38
15.	Seedling dry weight (mg)	9.4	3.1	13.8	24.78	25.04	97.94	50.51
16.	Seed vigour index-I	6239.4	2350.0	9269.3	26.80	27.86	92.55	53.12
17.	Seed vigour index-II	613.9	127.0	968.6	32.36	32.85	97.04	65.67

GCV (%) : Genotypic coefficients of variation (%)
PCV (%) : Phenotypic coefficients of variation (%)
h^2 (bs) : Heritability in broad sense (%)
GA (% of mean) : Genetic advance as percent of mean

Table 4.15. Classification of 17 quantitative traits on the basis of different categories of GCV (%), PCV (%), heritability in broad sense (%) and genetic advance as percent of mean of 40 *Tulsi* genotypes

Genetic variability parameters	Categories	Traits (estimates)
1	2	3
Genotypic coefficients of variation (GCV) (%)	High (>20%)	• Dry herbage yield/plant (47.31) • Seed yield/plant (47.21) • Number of spikes/plant (47.18) • 1000 seed weight (39.63) • Fresh herbage yield/plant (38.95) • Oil content (37.47) • Seed vigour index – II (32.36) • Seed vigour index - I (26.80) • Seedling dry weight (24.78) • Days to 50% flowering (22.08) • Spike length (21.43)
	Moderate (10-20%)	• Standard germination (19.01) • Seedling length (15.42) • Number of primary branches/plant (15.41) • Number of flowers’ whorls/spike (13.98) • Plant height (10.85)
	Low (0-10%)	• Days to maturity (6.75)
Phenotypic coefficients of variation (PCV) (%)	High (>20%)	• Seed yield/plant (48.17) • Dry herbage yield/plant (47.74) • Number of spikes/plant (47.35) • 1000 seed weight (39.73) • Fresh herbage yield/plant (39.24) • Oil content (37.74) • Seed vigour index – II (32.85) • Seed vigour index - I (27.86) • Seedling dry weight (25.04) • Days to 50% flowering (22.40) • Spike length (22.17)
	Moderate (10-20%)	• Standard germination (19.40) • Seedling length (16.68) • Number of primary branches/plant (16.74) • Number of flowers’ whorls/spike (15.52) • Plant height (11.56)
	Low (0-10%)	• Days to maturity (6.89)

Contd.

Table 4.15. Contd. …

1	2	3
Heritability in broad sense (%)	High (>60%)	• 1000 seed weight (99.51) • Number of spikes/plant (99.28) • Oil content (98.60) • Fresh herbage yield/plant (98.54) • Dry herbage yield/plant (98.23) • Seedling dry weight (97.94) • Days to 50% flowering (97.17) • Seed vigour index – II (97.04) • Days to maturity (96.09) • Seed yield/plant (96.06) • Standard germination (96.02) • Spike length (93.44) • Seed vigour index – I (92.55) • Plant height (88.12) • Seedling length (85.51) • Number of primary branches/plant (84.75) • Number of flowers' whorls/spike (81.21)
	Moderate (30-60%)	-Nil-
	Low (0-30%)	-Nil-
Genetic advance as percent of mean	High (>20)	• Number of spikes/plant (96.84) • Dry herbage yield/plant (96.59) • Seed yield/plant (95.32) • 1000 seed weight (81.44) • Fresh herbage yield/plant (79.64) • Oil content (76.65) • Seed vigour index – II (65.67) • Seed vigour index - I (53.12) • Seedling dry weight (50.51) • Days to 50% flowering (44.84) • Spike length (42.66) • Standard germination (38.38) • Seedling length (29.38) • Number of primary branches/plant (29.23) • Number of flowers' whorls/spike (25.96) • Plant height (20.98)
	Moderate (10-20)	• Days to maturity (13.64)
	Low (0-10)	-Nil-

4.2 Correlation coefficients analysis

The knowledge regarding nature and magnitude of association of various yield contributing traits with the seed yield plays a significant role for effective selection of desirable genotypes in breeding programmes. For computing the nature and magnitude of association of various yield contributing traits with seed yield, correlation coefficients analysis was carried out at both genotypic as well as phenotypic level and the estimates of correlation coefficients were compared for their significance against tabulated value at 5% and 1% levels of significance. The phenotypic correlation coefficients and genotypic correlation coefficients computed in the present investigation among 17 yield and yield attributing traits in 40 *Tulsi* genotypes has been presented in Table 4.16.

4.2.1 Seed yield per plant

Seed yield per plant exhibited positive and highly significant association with number of spikes per plant (0.507** and 0.501**), 1000 seed weight (0.471** and 0.459**), number of flowers' whorls per spike (0.455** and 0.396**), seedling length (0.291** and 0.264**), fresh herbage yield per plant (0.262** and 0.257**) at both genotypic as well as phenotypic level, respectively. Seed yield per plant showed positive and highly significant association with dry herbage yield per plant (0.240**) at genotypic level and positive and significant association (0.233*) at phenotypic level. Seed yield per plant exhibited positive and significant association with seedling dry weight (0.234* and 0.225*), seed vigour index-I (0.217* and 0.209*) and seed vigour index-II (0.211* and 0.205*) at both genotypic as well as phenotypic level, respectively. Seed yield per plant showed negative and significant association with days to 50% flowering (-0.180*) at genotypic level only (Table 4.16).

4.2.2 Seed vigour index-II

Seed vigour index-II exhibited positive and highly significant association with seed vigour index-I (0.915** and 0.891**), seedling dry weight (0.850** and 0.847**), standard germination (0.791** and 0.789**), seedling length (0.762** and 0.704**), 1000 seed weight (0.447** and 0.438**), days to 50% flowering (0.368** and 0.355**), days to maturity (0.318** and 0.307**) and spike length (0.303** and 0.285**) at both genotypic as well as phenotypic level, respectively. Seed vigour index-II showed negative and highly significant association with number of spikes per plant (-0.257** and -0.254**) and oil content (-0.288** and -0.284**) at both genotypic as well as phenotypic level, respectively (Table 4.16).

4.2.3 Seed vigour index-I

Seed vigour index-I exhibited positive and highly significant association with standard germination (0.890** and 0.875**), seedling length (0.788** and 0.790**), seedling dry weight (0.649** and 0.620**), 1000 seed weight (0.389** and 0.372**), days to maturity (0.384** and 0.368**) and spike length (0.269** and 0.244**) at both genotypic as well as

Table 4.16. Phenotypic correlation coefficients (above diagonal values) and genotypic correlation coefficients (below diagonal values) among 17 yield and yield attributing traits in 40 *Tulsi* genotypes

Traits	DF	DM	PB	PH	NSP	SL	FW	FHY	DHY	SW	OC	SG	SDL	SDW	SVI-I	SVI-II	SY
DF	1	0.087	0.036	0.243**	-0.376**	0.258**	-0.095	0.001	0.077	0.391**	-0.264**	0.197*	0.140	0.359**	0.197*	0.355**	-0.175
DM	0.077	1	-0.186*	-0.228*	-0.411**	0.374**	-0.022	-0.082	-0.017	0.457**	-0.038	0.294**	0.361**	0.243**	0.368**	0.307**	0.069
PB	0.053	-0.192*	1	0.055	0.146	-0.211*	-0.235**	0.140	0.018	-0.163	0.109	0.017	-0.326**	-0.150	-0.156	-0.072	0.094
PH	0.261**	-0.247**	0.059	1	0.082	0.054	0.378**	0.320**	0.340**	0.093	0.134	-0.131	-0.142	-0.066	-0.167	-0.086	0.029
NSP	-0.384**	-0.422**	0.155	0.090	1	-0.305**	0.347**	0.187*	0.076	-0.115	0.130	-0.098	-0.257**	-0.295**	-0.207*	-0.254**	0.501**
SL	0.267**	0.380**	-0.229*	0.057	-0.318**	1	0.299**	0.029	0.159	0.498**	0.038	0.235**	0.229*	0.284**	0.244**	0.285**	0.173
FW	-0.111	-0.037	-0.261**	0.435**	0.393**	0.324**	1	0.166	0.150	0.322**	0.091	-0.051	-0.044	-0.081	-0.079	-0.093	0.396**
FHY	0.003	-0.085	0.156	0.337**	0.188*	0.022	0.191*	1	0.944**	-0.174	0.621**	-0.150	-0.179	-0.118	-0.199*	-0.148	0.257**
DHY	0.081	-0.018	0.023	0.368**	0.077	0.160	0.163	0.947**	1	-0.071	0.575**	-0.135	-0.043	-0.021	-0.116	-0.078	0.233*
SW	0.398**	0.469**	-0.177	0.094	-0.115	0.521**	0.354**	-0.176	-0.071	1	-0.258**	0.231*	0.483**	0.511**	0.372**	0.438**	0.459**
OC	-0.269**	-0.041	0.113	0.134	0.131	0.032	0.110	0.623**	0.580**	-0.260**	1	-0.187*	-0.211*	-0.285**	-0.222*	-0.284**	0.125
SG	0.204*	0.302**	-0.003	-0.141	-0.099	0.250**	-0.042	-0.154	-0.136	0.239**	-0.189*	1	0.409**	0.366**	0.875**	0.789**	0.142
SDL	0.159	0.391**	-0.370**	-0.148	-0.279**	0.263**	-0.079	-0.196*	-0.058	0.524**	-0.221*	0.433**	1	0.750**	0.790**	0.704**	0.264**
SDW	0.372**	0.253**	-0.161	-0.066	-0.299**	0.298**	-0.084	-0.124	-0.025	0.518**	-0.289**	0.374**	0.820**	1	0.620**	0.847**	0.225*
SVI-I	0.209*	0.384**	-0.184*	-0.175	-0.215*	0.269**	-0.092	-0.208*	-0.125	0.389**	-0.226*	0.890**	0.788**	0.649**	1	0.891**	0.209*
SVI-II	0.368**	0.318**	-0.088	-0.085	-0.257**	0.303**	-0.088	-0.154	-0.081	0.447**	-0.288**	0.791**	0.762**	0.850**	0.915**	1	0.205*
SY	-0.180*	0.072	0.100	0.032	0.507**	0.178	0.455**	0.262**	0.240**	0.471**	0.125	0.144	0.291**	0.234*	0.217*	0.211*	1

** Significant at 1% level of significance, *Significant at 5 % level of significance

DF: Days to 50% flowering, DM: Days to maturity, PB: Number of primary branches/plant, PH: Plant height (cm), NSP: Number of spikes/plant, SL: Spike length (cm), FW: Number of flowers' whorls per spike, FHY: Fresh herbage yield/plant (g). DHY: Dry herbage yield/plant (g), SY: Seed yield/plant (g), SW: 1000 seed weight (g), OC: Oil content (%), SG: Standard germination (%), SDL: Seedling length (mm), SDW: Seedling dry weight (mg), SVI-I: Seed vigour index-I, SVI-II: Seed vigour index-II phenotypic level, respectively. Seed vigour index-I showed positive and significant association with days to 50% flowering (0.209* and 0.197*) at both genotypic as well as phenotypic level, respectively. Seed vigour index-I exhibited negative and significant association with fresh herbage yield per plant (-0.208* and -0.199*), number of spikes per plant (-0.215* and -0.207*) and oil content (-0.226* and -0.222*) at both genotypic as well as phenotypic level, respectively. Seed vigour index-I showed negative and significant association with number of primary branches per plant (-0.184*) at genotypic level only (Table 4.16).

4.2.4 Seedling dry weight

Seedling dry weight exhibited positive and highly significant association with seedling length (0.820** and 0.750**), 1000 seed weight (0.518** and 0.511**), standard germination (0.374** and 0.366**), days to 50% flowering (0.372** and 0.359**), spike length (0.298** and 0.284**) and days to maturity (0.253** and 0.243**) at both genotypic as well as phenotypic level, respectively. Seedling dry weight showed negative and highly significant association with oil content (-0.289** and -0.285**) and number of spikes per plant (-0.299** and -0.295**) at both genotypic as well as phenotypic level, respectively (Table 4.16).

4.2.5 Seedling length

Seedling length exhibited positive and highly significant association with 1000 seed weight (0.524** and 0.483**), standard germination (0.433** and 0.409**) and days to maturity (0.391** and 0.361**) at both genotypic as well as phenotypic level, respectively. Seedling length showed positive and highly significant association at genotypic level (0.263**) but at phenotypic level, the association was positive and significant (0.229*) only with spike length. Seedling length exhibited negative and highly significant association with number of primary branches per plant (-0.370** and -0.326**) and number of spikes per plant (-0.279** and -0.257**) at both genotypic as well as phenotypic level, respectively. Seedling length exhibited negative significant association with oil content (-0.221* and -0.211*) at both genotypic as well as phenotypic level, respectively. Seedling length showed negative and significant association with fresh herbage yield per plant at genotypic level (-0.196*) only (Table 4.16).

4.2.6 Standard germination

Standard germination exhibited positive and highly significant association with days to maturity (0.302** and 0.294**) and spike length (0.250** and 0.235**) at both genotypic as well as phenotypic level, respectively. Standard germination exhibited positive and highly significant association with 1000 seed weight (0.239**) at genotypic level but at phenotypic level, only positive and significant association (0.231*). Standard germination showed positive and significant association with days to 50% flowering (0.204* and 0.197*) at both genotypic as well as phenotypic level, respectively. Standard germination exhibited negative and significant association with oil content (-0.189* and -0.187*) at both genotypic as well as phenotypic level, respectively (Table 4.16).

4.2.7 Oil content

Oil content showed positive and highly significant association with fresh herbage yield per plant (0.623** and 0.621**) and dry herbage yield per plant (0.580** and 0.575**) but negative and highly significant association with 1000 seed weight (-0.260** and -0.258**) and days to 50% flowering (-0.269** and -0.264**) at both genotypic as well as phenotypic level, respectively (Table 4.16).

4.2.8 1000 seed weight

The 1000 seed weight exhibited positive and highly significant association with spike length (0.521** and 0.498**), days to maturity (0.469** and 0.457**), days to 50% flowering (0.398** and 0.391**) and number of flowers' whorls per spike (0.354** and 0.322**) at both genotypic as well as phenotypic level, respectively (Table 4.16).

4.2.9 Dry herbage yield per plant

Dry herbage yield per plant exhibited positive and highly significant association with fresh herbage yield per plant (0.947** and 0.944**) and plant height (0.368** and 0.340**) at both genotypic as well as phenotypic level, respectively (Table 4.16).

4.2.10 Fresh herbage yield per plant

Fresh herbage yield per plant showed positive and highly significant association with plant height (0.337** and 0.320**) whereas, positive and only significant association with number of spikes per plant (0.188* and 0.187*) at both genotypic as well as phenotypic level, respectively. Fresh herbage yield per plant exhibited positive significant association with number of flowers' whorls per spike (0.191*) at genotypic level only (Table 4.16).

4.2.11 Number of flowers' whorls per spike

Number of flowers' whorls per spike exhibited positive and highly significant association with plant height (0.435** and 0.378**), number of spikes per plant (0.393** and 0.347**) and spike length (0.324** and 0.299**) while, negative and highly significant association with number of primary branches per plant (-0.261** and -0.235**) at both genotypic as well as phenotypic level, respectively (Table 4.16).

4.2.12 Spike length

Spike length exhibited positive and highly significant association with days to maturity (0.380** and 0.374**) and days to 50% flowering (0.267** and 0.258**) at both genotypic as well as phenotypic level, respectively. Spike length showed negative and highly significant association with number of spikes per plant (-0.318** and -0.305**) whereas, negative and only significant association with number of primary branches per plant (-0.229* and -0.211*) at both genotypic as well as phenotypic level, respectively (Table 4.16).

4.2.13 Number of spikes per plant

Number of spikes per plant exhibited negative and highly significant association with days to 50% flowering (-0.384* and -0.376*) and days to maturity (-0.422** and -0.411) at both genotypic as well as phenotypic level, respectively (Table 4.16).

4.2.14 Plant height

Plant height exhibited positive and highly significant association with days to 50% flowering (0.261** and 0.243**) and negative and highly significant association with days to maturity (-0.247** and -0.228**) at both genotypic as well as phenotypic level, respectively (Table 4.16).

4.2.15 Number of primary branches per plant

Number of primary branches per plant exhibited negative and significant association with days to maturity (-0.192* and -0.186*) at both genotypic as well as phenotypic level, respectively (Table 4.16).

4.3 Path coefficients analysis

The path coefficients analysis was carried out to estimate the direct as well as indirect effects taking seed yield per plant as a dependent variable and yield contributing traits studied in the present investigation as independent variables. For computing this, the correlation coefficients recorded at genotypic level were taken into consideration. The results have been presented in tabular form in Table 4.17 and diagrammatically as genotypical path diagram for seed yield per plant in Fig.11.

4.3.1 Direct effects

The diagonal values given in the path coefficients analysis Table 4.17 represent the direct effect of that particular trait on seed yield per plant. The maximum direct positive effect on seed yield per plant was observed for seedling length (0.582) followed by 1000 seed weight (0.487), number of spikes per plant (0.371), number of primary branches per plant (0.292), fresh herbage yield per plant (0.292), seed vigour index-II (0.232), number of flowers' whorls per spike (0.209), standard germination (0.117), spike length (0.049) and dry herbage yield per plant (0.044) whereas, seed vigour index-I (-0.349), days to 50 % flowering (-0.242), seedling dry weight (-0.217), plant height (-0.185), days to maturity (-0.105) and oil content (-0.031) showed direct negative effects on seed yield per plant (Table 4.17).

4.3.2 Indirect effects

4.3.2.1 Days to 50% flowering

Days to 50% flowering exhibited maximum positive indirect effect on seed yield per plant via number of spikes per plant (0.093) followed by oil content (0.065) and number of flowers' whorls per spike (0.027) whereas, negative indirect effect via 1000 seed weight (-0.096), seedling dry weight (-0.090) and seed vigour index-II (-0.089) (Table 4.17).

Table 4.17. Direct (diagonal values) and indirect effects of various yield contributing traits on seed yield of 40 *Tulsi* genotypes

Traits	DF	DM	PB	PH	NSP	SL	FW	FHY	DHY	SW	OC	SG	SDL	SDW	SVI-I	SVI-II	r_g (SY)
DF	**-0.242**	-0.008	0.015	-0.048	-0.142	0.013	-0.023	0.001	0.004	0.194	0.008	0.024	0.092	-0.081	-0.073	0.085	-0.180*
DM	-0.019	**-0.105**	-0.056	0.046	-0.156	0.019	-0.008	-0.025	-0.001	0.228	0.001	0.035	0.227	-0.055	-0.134	0.074	0.072
PB	-0.013	0.020	**0.292**	-0.011	0.057	-0.011	-0.054	0.046	0.001	-0.086	-0.004	0.001	-0.215	0.035	0.064	-0.020	0.100
PH	-0.063	0.026	0.017	**-0.185**	0.034	0.003	0.091	0.099	0.016	0.046	-0.004	-0.017	-0.086	0.014	0.061	-0.020	0.032
NSP	0.093	0.044	0.045	-0.017	**0.371**	-0.016	0.082	0.055	0.003	-0.056	-0.004	-0.012	-0.162	0.065	0.075	-0.060	0.507**
SL	-0.064	-0.040	-0.067	-0.011	-0.118	**0.049**	0.068	0.006	0.007	0.254	-0.001	0.029	0.153	-0.065	-0.094	0.070	0.178
FW	0.027	0.004	-0.076	-0.080	0.146	0.016	**0.209**	0.056	0.007	0.172	-0.003	-0.005	-0.046	0.018	0.032	-0.020	0.455**
FHY	-0.001	0.009	0.045	-0.062	0.070	0.001	0.040	**0.292**	0.041	-0.086	-0.020	-0.018	-0.114	0.027	0.072	-0.036	0.262**
DHY	-0.020	0.002	0.007	-0.068	0.029	0.008	0.034	0.277	**0.044**	-0.035	-0.018	-0.016	-0.034	0.005	0.043	-0.019	0.240**
SW	-0.096	-0.049	-0.052	-0.017	-0.043	0.026	0.074	-0.051	-0.003	**0.487**	0.008	0.028	0.305	-0.112	-0.136	0.104	0.471**
OC	0.065	0.004	0.033	-0.025	0.048	0.002	0.023	0.182	0.025	-0.127	**-0.031**	-0.022	-0.129	0.063	0.079	-0.067	0.125
SG	-0.049	-0.032	-0.001	0.026	-0.037	0.012	-0.009	-0.045	-0.006	0.116	0.006	**0.117**	0.252	-0.081	-0.310	0.183	0.144
SDL	-0.038	-0.041	-0.108	0.027	-0.103	0.013	-0.017	-0.057	-0.003	0.255	0.007	0.051	**0.582**	-0.178	-0.275	0.176	0.291**
SDW	-0.090	-0.026	-0.047	0.012	-0.111	0.015	-0.017	-0.036	-0.001	0.252	0.009	0.044	0.477	**-0.217**	-0.226	0.197	0.234*
SVI-I	-0.051	-0.040	-0.054	0.032	-0.080	0.013	-0.019	-0.061	-0.005	0.190	0.007	0.104	0.458	-0.141	**-0.349**	0.212	0.217*
SVI-II	-0.089	-0.033	-0.026	0.016	-0.095	0.015	-0.018	-0.045	-0.004	0.218	0.009	0.093	0.443	-0.185	-0.319	**0.232**	0.211*

Residual Effect = 0.22764

** Significant at 1% level of significance, *Significant at 5 % level of significance

DF: Days to 50% flowering, DM: Days to maturity, PB: Number of primary branches/plant, PH: Plant height (cm), NSP: Number of spikes/plant, SL: Spike length (cm), FW: Number of flowers' whorls/spike, FHY: Fresh herbage yield/plant (g). DHY: Dry herbage yield/plant (g), SY: Seed yield/plant(g/plant), SW: 1000 seed weight (g), OC: Oil content (%), SG: Standard germination (%), SDL: Seedling length (mm), SDW: Seedling dry weight (mg), SVI-I: Seed vigour index-I, SVI-II: Seed vigour index-I

4.3.2.2 Days to maturity

Days to maturity showed positive indirect effect via number of spikes per plant (0.044) followed by plant height (0.026) and number of primary branches per plant (0.020) whereas, negative indirect effect via 1000 seed weight (-0.049) followed by seedling length (-0.041) and seed vigour index-I (-0.040) on seed yield per plant (Table 4.17).

4.3.2.3 Number of primary branches per plant

Number of primary branches per plant exhibited positive indirect effect on seed yield per plant via fresh herbage yield per plant (0.045) and number of spikes per plant (0.045) followed by oil content (0.033) and plant height (0.017) whereas, negative indirect effect via seedling length (-0.108) followed by number of flowers’ whorls per spike (-0.076) and spike length (-0.067) (Table 4.17).

4.3.2.4 Plant height

Plant height showed positive indirect effect on seed yield per plant via days to maturity (0.046) followed by seed vigour index-I (0.032), seedling length (0.027) and standard germination (0.026) while, negative indirect effect via number of flowers’ whorls per spike (-0.080) followed by dry herbage yield per plant (-0.068) and fresh herbage yield per plant (-0.062) (Table 4.17).

4.3.2.5 Number of spikes per plant

Number of spikes per plant exhibited positive indirect effect on seed yield per plant via number of flowers’ whorls per spike (0.146) followed by fresh herbage yield per plant (0.070) and number of primary branches per plant (0.057) whereas, negative indirect effect on seed yield per plant via days to maturity (-0.156) followed by days to 50% flowering (-0.142) and spike length (-0.118) (Table 4.17).

4.3.2.6 Spike length

Spike length had positive indirect effect on seed yield per plant via 1000 seed weight (0.026) followed by days to maturity (0.019) and number of flowers’ whorls per spike (0.016). Spike length had negative indirect effect on seed yield per plant via number of spikes per plant (-0.016) and number of primary branches per plant (-0.011) (Table 4.17).

4.3.2.7 Number of flowers’ whorls per spike

Number of flowers’ whorls per spike showed positive indirect effect on seed yield per plant via plant height (0.091) followed by number of spikes per plant (0.082) and 1000 seed weight (0.074) whereas, negative indirect effect on seed yield per plant via number of primary branches per plant (-0.054) followed by days to 50% flowering (-0.023) and seed vigour index-I (-0.019) (Table 4.17).

4.3.2.8 Fresh herbage yield per plant

Fresh herbage yield per plant had positive indirect effect on seed yield per plant via dry herbage yield per plant (0.277) followed by oil content (0.182) and plant height (0.099) while, negative indirect effect via seed vigour index-I (-0.061) followed by seedling length (-0.057) and 1000 seed weight (-0.051) (Table 4.17).

4.3.2.9 Dry herbage yield per plant

Dry herbage yield per plant exhibited positive indirect effect on seed yield per plant via fresh herbage yield per plant (0.041) followed by oil content (0.025) and plant height (0.016) whereas, negative indirect effect via standard germination (-0.006) followed by seed vigour index-I (-0.005) and seed vigour index-II (-0.004) (Table 4.17).

4.3.2.10 1000 seed weight

1000 seed weight had positive indirect effect on seed yield per plant via seedling length (0.255) followed by spike length (0.254) and seedling dry weight (0.252). The 1000 seed weight had negative indirect effect on seed yield per plant via oil content (-0.127) followed by number of primary branches per plant (-0.086) and fresh herbage yield per plant (-0.086) (Table 4.17).

4.3.2.11 Oil content

Oil content exhibited positive indirect effect on seed yield per plant via seedling dry weight (0.009) followed by seed vigour index-II (0.009) and days to 50% flowering (0.008). Oil content had negative indirect effect on seed yield per plant via fresh herbage yield per plant (-0.020) followed by dry herbage yield per plant (-0.018) and plant height (-0.004) (Table 4.17).

4.3.2.12 Standard germination

Standard germination had positive indirect effect on seed yield per plant via seed vigour index-I (0.104) followed by seed vigour index-II (0.093) and seedling length (0.051) while, negative indirect effect via oil content (-0.022) followed by fresh herbage yield per plant (-0.018) and plant height (-0.017) (Table 4.17).

4.3.2.13 Seedling length

Seedling length showed positive indirect effect on seed yield per plant via seedling dry weight (0.477) followed by seed vigour index-I (0.458) and seed vigour index-II (0.443). Seedling length had negative indirect effect on seed yield per plant via number of primary branches per plant (-0.215) followed by number of spikes per plant (-0.162) and oil content (-0.129) (Table 4.17).

4.3.2.14 Seedling dry weight

Seedling dry weight had positive indirect effect on seed yield per plant via number of spikes per plant (0.065) followed by oil content (0.063) and number of primary branches per plant (0.035). Seedling dry weight had negative indirect effect on seed yield per plant via seed vigour index-II (-0.185) followed by seedling length (-0.178) and seed vigour index-I (-0.141) (Table 4.17).

4.3.2.15 Seed vigour index-I

Seed vigour index-I exhibited positive indirect effect on seed yield per plant via oil content (0.079) followed by number of spikes per plant (0.075) and fresh herbage yield per plant (0.072) whereas, negative indirect effect via seed vigour index-II (-0.319) followed by standard germination (-0.310) and seedling length (-0.275) (Table 4.17).

4.3.2.16 Seed vigour index-II

Seed vigour index-II showed positive indirect effect on seed yield per plant via seed vigour index-I (0.212) followed by seedling dry weight (0.197) and standard germination (0.183) while, seed vigour index-II had negative indirect effect on seed yield per plant via oil content (-0.067) followed by number of spikes per plant (-0.060) and fresh herbage yield per plant (-0.036) (Table 4.17).

4.3.3 Residual effect

The value of computed residual effect is 0.2276 (Table 4.17). It indicated that besides the studied traits, there are some other factors or traits which were having effects on seed yield per plant.

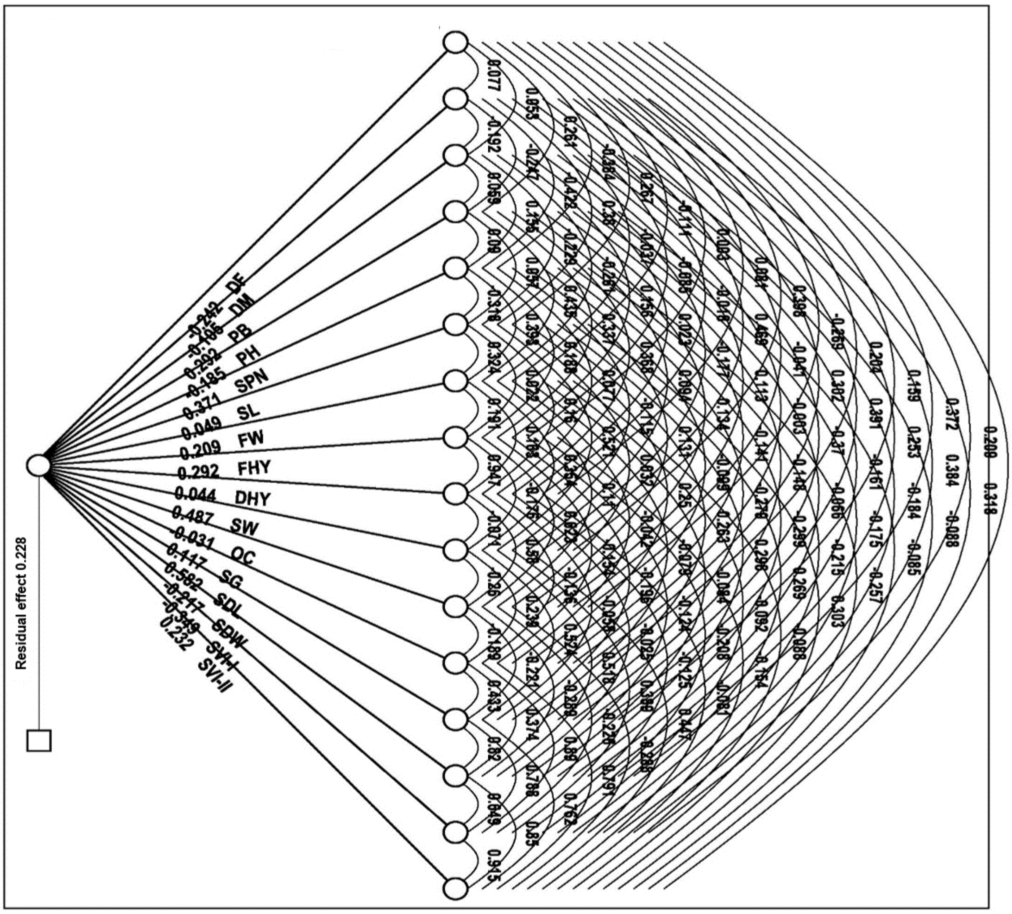


Fig.11. Genotypical path diagram for seed yield per plant

4.4 Genetic divergence analysis

Mahalanobis (1936) D^2 distance matrix elaborated by Murthy and Arunachalam (1966) was used to study the genetic divergence among the 40 *Tulsi* genotypes taken for the present investigation. The 40 *Tulsi* genotypes were grouped into 10 clusters by Tocher's method as described by Rao (1952) after computing D^2 statistical analysis. It revealed that a considerable amount of genetic diversity existed among the 40 *Tulsi* genotypes. The genotypes grouped within same cluster are considered to be more closely related to each other. Maximum number of genotypes (29) were grouped in cluster 1 followed by cluster 7 (3 genotypes) and one each genotype in cluster 2, cluster 3, cluster 4, cluster 5, cluster 6, cluster 8, cluster 9 and cluster 10 as shown in Table 4.18 and Fig.12. Intra and inter cluster distances are presented in Table 4.19. The maximum intra-cluster distance was observed for the cluster 7 (35.57) followed by cluster 1 (31.73) whereas, intra-cluster distance was zero for cluster 2, cluster 3, cluster 4, cluster 5, cluster 6, cluster 8, cluster 9 and cluster 10. The maximum inter-cluster distance was observed between cluster 2 and cluster 10 (105.80) followed by between cluster 4 and cluster 10 (99.80), cluster 3 and cluster 10 (98.65), cluster 1 and cluster 10 (83.26), cluster 8 and cluster 10 (83.08), cluster 3 and cluster 7 (77.76), cluster 2 and cluster 7 (77.11), cluster 4 and cluster 7 (76.30), cluster 6 and cluster 10 (76.18), cluster 5 and cluster 10 (75.90), cluster 5 and cluster 7 (68.68), cluster 9 and cluster 10 (62.76) and cluster 4 and cluster 9 (59.63).

Table 4.18. Clustering of 40 *Tulsi* genotypes on the basis of D^2 statistic by Tocher method

Cluster	No. of genotypes	Name of genotypes
1	29	EC 388887, NSV 38, IC 281185, EC 388895, IC 333833, IC 336833, EC 388737, IC 436153, IC 326735, EC 388782, EC 388896, EC 112548, IC 326732, IC 338794, EC 388788, EC 388889, IC 312264, EC 326771, IC 381552, EC 469904, EC 388893, IC 381158, IC 338959, IC 387838, Local 1, IC 369247, IC 110207, EC 338772, IC 387837
2	1	IC 44681
3	1	IC 201223
4	1	IC 328582
5	1	RDV 45
6	1	IC 469938
7	3	IC 75730, Local 2, IC 381185
8	1	IC 388785
9	1	EC 388890
10	1	DOS 1

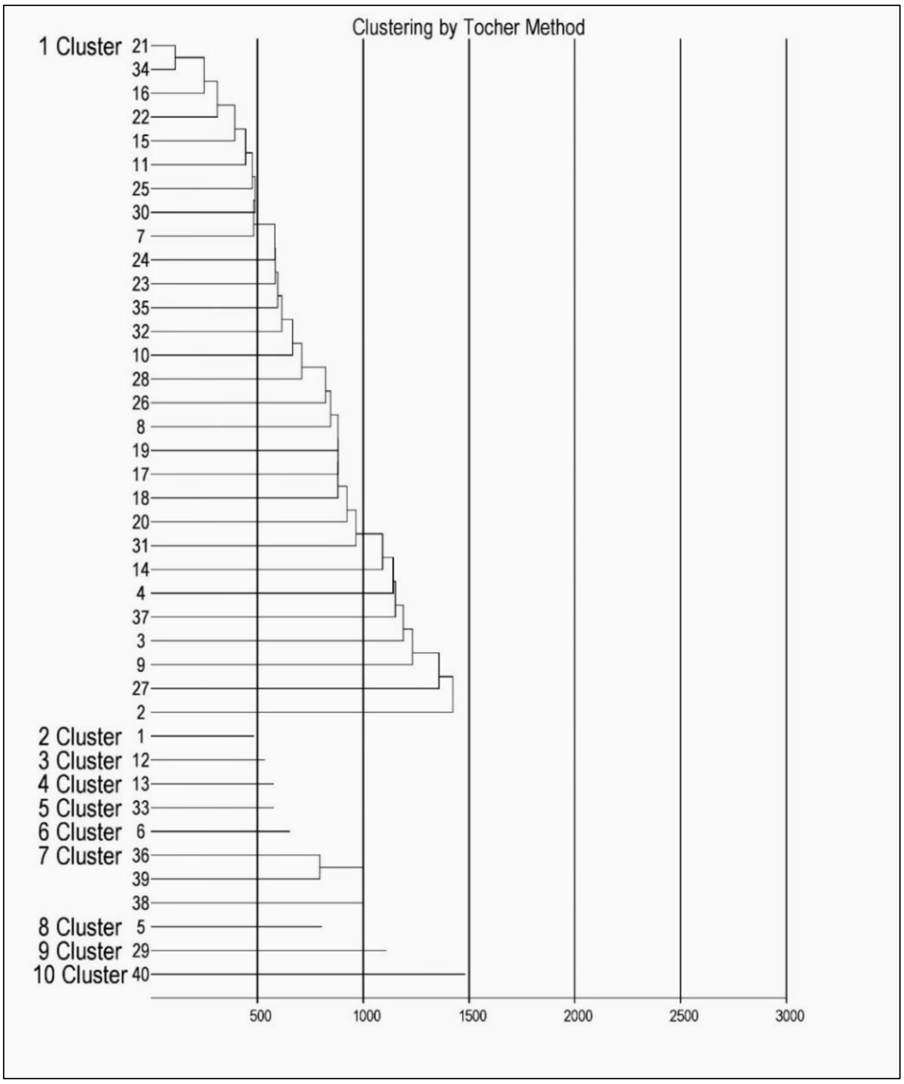


Fig. 12. Dendrogram representing the clustering pattern for 40 genotypes of *Tulsi*

Table 4.19. Intra and Inter Cluster distances (D^2) among Ten clusters of *Tulsi* genotypes

Clusters	**C 1**	**C 2**	**C 3**	**C 4**	**C 5**	**C 6**	**C 7**	**C 8**	**C 9**	**C 10**
C 1	31.73	38.53	41.39	43.81	45.80	40.57	57.51	40.25	48.21	83.26
C 2		0.00	23.47	26.99	49.15	51.68	77.11	33.57	59.16	105.80
C 3			0.00	33.16	36.29	60.03	77.76	32.34	60.18	98.65
C 4				0.00	51.17	54.59	76.30	32.08	59.63	99.80
C 5					0.00	62.53	68.68	39.94	50.34	75.90
C 6						0.00	45.85	41.28	33.71	76.18
C 7							35.57	65.27	52.13	58.04
C 8								0.00	36.69	83.08
C 9									0.00	62.76
C 10										0.00

C 1: Cluster 1
C 2: Cluster 2
C 3: Cluster 3
C 4: Cluster 4
C 5: Cluster 5
C 6: Cluster 6
C 7: Cluster 7
C 8: Cluster 8
C 9: Cluster 9
C 10: Cluster 10

4.4.1 Cluster means for different quantitative traits of *Tulsi* genotypes

The genetic divergence among 40 genotypes of *Tulsi* was also supported by cluster means computed for 17 different quantitative traits (Table 4.20). The results revealed that cluster 2 showed the maximum cluster mean for spike length (23.30), cluster 3 for days to 50% flowering (80.33), plant height (104.60) and 1000 seed weight (1.86), cluster 4 for seedling dry weight (11.63) and seed vigour index-II (790.93), cluster 5 for seed yield (60.90), cluster 8 for number of flowers' whorls per spike (17.80) and seedling length (110.00), cluster 9 for days to maturity (168.13), number of primary branches per plant (19.13), fresh herbage yield per plant (1249.97), dry herbage yield per plant (414.87), oil content (0.49), standard germination (70.87) and seed vigour index-I (6878.00) and cluster 10 for number of spikes per plant (326.40). From this, it is clear that cluster 9 exhibited the highest cluster means for maximum (i.e. 7) number of characters. Whereas, the minimum cluster mean was shown by cluster 2 for number of spikes per plant (66.00), cluster 4 for oil content (0.15), cluster 5 for fresh herbage yield per plant (382.50) and dry herbage yield per plant (117.67), cluster 7 for seed yield per plant (13.52), standard germination (43.78), seedling length (61.22), seedling dry weight (3.49), seed vigour index-I (2694.22) and seed vigour index-II (154.22), cluster 8 for number of primary branches per plant (10.67), cluster 9 for number of flowers' whorls per spike (12.73) and cluster 10 for days to 50% flowering (41.00), days to maturity (140.00), plant height (81.00), spike length (10.43) and 1000 seed weight (0.24).

4.4.2 Relative contribution of different traits towards genetic diversity

The relative contribution of the 17 yield and yield attributing traits towards genetic divergence in 40 *Tulsi* genotypes is presented in Table 4.21 and Fig.13. It was observed that 1000 seed weight (41.41%) contributed maximum towards genetic divergence followed by number of spikes per plant (17.31%), fresh herbage yield per plant (13.46%), oil content (10.77%), seedling dry weight (5.00%), standard germination (3.59%), days to 50% flowering (2.69%), days to maturity (2.05%), seed vigour index-II (1.54%), dry herbage yield per plant (1.15%), seed yield per plant (0.64) and spike length (0.38%).

Table 4.20 Cluster means for 17 different quantitative traits of 40 *Tulsi* genotypes

Traits	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8	Cluster 9	Cluster 10
DF	58.02	73.33	80.33	78.33	49.33	57.33	50.33	79.33	46.00	41.00
DM	165.67	168.00	166.67	160.00	160.33	159.33	153.89	156.67	168.13	140.00
PB	15.96	17.67	14.60	15.60	14.87	14.27	17.83	10.67	19.13	17.13
PH	83.96	88.70	104.60	104.03	85.97	84.90	93.77	103.13	87.13	81.00
NSP	101.92	66.00	120.00	89.80	232.03	81.00	121.12	146.60	195.23	326.40
SL	16.36	23.30	16.87	17.23	17.10	17.77	12.12	22.47	16.73	10.43
NFW	12.99	15.13	16.40	16.07	16.60	14.60	13.71	17.80	12.73	14.27
FHY	520.72	713.27	458.87	1003.43	382.50	1087.77	683.29	1026.33	1249.97	825.23
DHY	154.02	215.77	123.77	319.30	117.67	382.10	182.71	382.87	414.87	206.77
SY	27.76	33.73	20.80	48.70	60.90	16.13	13.52	38.17	57.07	30.47
SW	1.02	1.59	1.86	1.54	1.61	0.63	0.36	1.38	0.81	0.24
OC	0.21	0.26	0.21	0.15	0.22	0.40	0.31	0.33	0.49	0.24
SG	67.22	66.00	70.67	68.00	52.67	44.67	43.78	54.00	70.87	62.67
SDL	100.75	104.00	94.00	93.67	86.00	81.33	61.22	110.00	97.33	63.33
SDW	10.04	11.53	10.23	11.63	7.90	9.43	3.49	9.47	10.03	3.77
SVI-I	6781.65	6861.33	6644.00	6365.33	4537.33	3628.00	2694.22	5941.33	6878.00	3969.33
SVI-II	673.24	761.07	723.33	790.93	416.87	421.73	154.22	511.67	709.20	236.47

DF: Days to 50% flowering, DM: Days to maturity, PB: Number of primary branches/plant, PH: Plant height (cm), NSP: Number of spikes/plant, SL: Spike length (cm), FW: Number of flowers' whorls/spike, FHY: Fresh herbage yield/plant (g). DHY: Dry herbage yield/plant (g), SY: Seed yield/plant (g), SW: 1000 seed weight (g), OC: Oil content (%), SG: Standard germination (%), SDL: Seedling length (mm), SDW: Seedling dry weight (mg), SVI-I: Seed vigour index-I, SVI-II: Seed vigour index-II

Table 4.21. Relative contribution of yield and yield attributing traits towards genetic diversity in 40 *Tulsi* genotypes

S. No.	Traits	Contribution (%)
1.	Days to 50% flowering	2.69
2.	Days to maturity	2.05
3.	Number of primary branches/plant	0.00
4.	Plant height (cm)	0.00
5.	Number of spikes/plant	17.31
6.	Spike length (cm)	0.38
7.	Number of flowers' whorls/spike	0.00
8.	Fresh herbage yield/plant (g)	13.46
9.	Dry herbage yield/plant (g)	1.15
10.	Seed yield/plant (g)	0.64
11.	1000 seed weight (g)	41.41
12.	Oil content (%)	10.77
13.	Standard germination (%)	3.59
14.	Seedling length (mm)	0.00
15.	Seedling dry weight (mg)	5.00
16.	Seed vigour index-I	0.00
17.	Seed vigour index-II	1.54

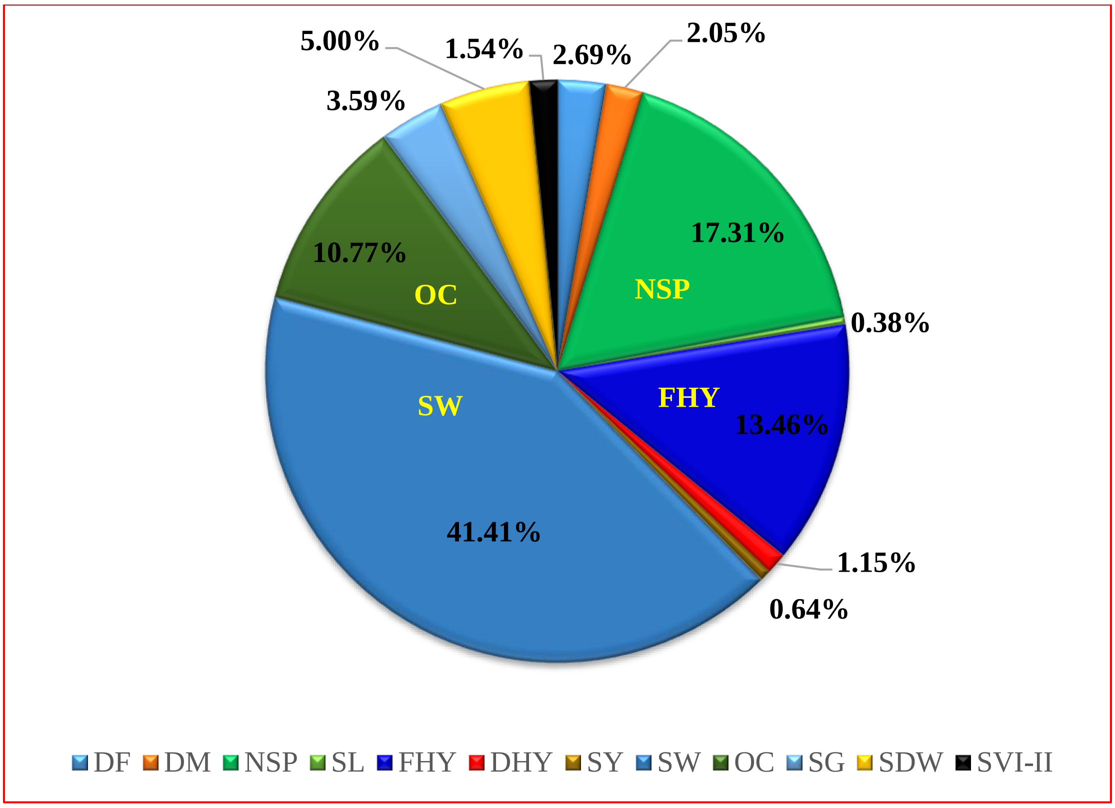


Fig. 13. **Relative contribution of yield and yield attributing traits towards genetic diversity in 40 *Tulsi* genotypes**

DF : Days to 50% flowering
DM : Days to maturity
PB : Number of primary branches/plant
PH : Plant height (cm)
NSP : Number of spikes/plant
SPL : Spike length (cm)
NFW : Number of flowers’ whorls/spike
FHY : Fresh herbage yield (g/plant)
DHY : Dry herbage yield (g/plant)

SY : Seed yield (g/plant)
SW : 1000 seed weight (g)
OC : Oil content (%)
SG : Standard germination (%)
SDL : Seedling length (mm)
SDW : Seedling dry weight (mg)
SVI-I : Seed vigour index-I
SVI-II : Seed vigour index-II

CHAPTER- V

DISCUSSION

Tulsi (*Ocimum spp.*) is one of the most important medicinal and aromatic crop plant that has been traditionally used in *Ayurvedic* medicine for its therapeutic properties. It is a versatile crop that can be grown by farmers with limited resources. Despite the numerous benefits and uses of *Tulsi,* cultivation of this crop at commercial scale in India is relatively less due to lack of awareness and demand, lack of organized marketing channels, limited research and development. *Tulsi* accounts for greater variability in the germplasm because of its highly cross-pollinated nature which is a prerequisite for any successful breeding programme.

Genetic variability studies help in the conservation and utilization of genetic resources by providing the base germplasm to develop the improved genotypes (cultivars) for higher yield, disease resistance and high essential oil content which are important for commercial cultivation. These studies also help towards understanding the molecular basis of the plant's biochemical and physiological processes leading to the discovery of new pharmaceutical drugs and other beneficial compounds. In the crop improvement programmes, understanding the genetic makeup of any advance breeding line in precise manner is utmost important that requires categorizing total genetic variability into heritable and non-heritable components such as genotypic and phenotypic coefficients of variation, heritability and genetic advance.

Yield is a complex trait that is influenced by various factors. In order to select the best genotypes for a particular environment, it is important to understand the relationship between yield and its attributing traits. By examining the correlation between yield and yield attributing traits, we can gain information about the nature and magnitude of association of traits which are most important for achieving high yield. Path coefficient analysis is a useful tool for investigating the direct and indirect effects of these traits on yield. This analysis helps to identify which components have a substantial effect on yield, and to what extent they contribute to the correlation. Keeping the above points in view, the experiment comprising of 40 different genotypes of Tulsi (*Ocimum spp.*) was carried out during *Kharif* 2022 at Chaudhary Charan Singh Haryana Agricultural University, Hisar with the following objectives:

1. To study the genetic variability in *Tulsi* for seed yield and its component traits.
2. To estimate the correlation and path coefficients for seed yield and its contributing traits.
3. To determine the extent of genetic diversity for different traits to classify the *Tulsi* genotypes into different clusters.

The results obtained in the present investigation are discussed in this chapter in the light of previous research findings under the following subheadings:

5.1 Genetic variability studies

5.1.1 Characterization of 40 *Tulsi* genotypes

5.1.2 Estimation of genetic variability parameters

5.2 Correlation coefficients analysis

5.3 Path coefficients analysis

5.4 Genetic divergence studies

5.1 Genetic variability studies

5.1.1 Characterization of 40 *Tulsi* genotypes

Knowledge about the genetic variation of the various plant characters enables the plant breeders to effectively utilize the available germplasm lines for the development of elite genotypes. Morphological and cytological studies have helped in resolving the identity issues in many genera (Paton & Putievsky, 1996). The experimental material of the present investigation comprising of 40 genotypes of Tulsi (*Ocimum spp*.) were characterized for 10 qualitative traits *viz.* stem colour, stem pubescence, leaf shape, leaf colour, leaf pubescence, petiole colour, flower colour, calyx colour, calyx pubescence and seed colour.

On the basis of stem colour, all the 40 *Tulsi* genotypes were categorized into five groups: green (28 genotypes), purple (5), dark green (4), light purple (2) and light green stem colour (1). Based on presence or absence of minute hairs on the surface of the stem, two categories were formed: sparse pubescence (5 genotypes) and non-pubescent (35). Regarding leaf shape, elliptical leaf shape was observed in all the 40 genotypes of *Tulsi*. Based on leaf colour, all the *Tulsi* genotypes were classified into four group: green (25 genotypes), dark green (8), light green (6) and purple leaf colour (1). On the basis of leaf pubescence, two categories were observed: sparse pubescent (2 genotypes) and non-pubescent (38). Genotypes were classified into three groups on the basis of petiole colour: green (36 genotypes), purple green (3) and purple petiole colour (1). Based on flower colour, three categories were formed *viz.* white (27 genotypes), light purple (8) and purple (5). Based on the colour of the calyx, the genotypes were classified into five groups: green (25 genotypes), purple (6), light purple (6), light green (2) and dark purple calyx colour (1). On the basis of presence or absence of minute hairs on the calyx surface, two categories were observed such as non-pubescent (27) and sparsely pubescent (13). Genotypes were classified into four groups based on seed colour *viz.* dull black (35), black (3), brownish black (1) and brown seed colour (1). The characterization of *Tulsi* genotypes based on qualitative traits has also been reported by Maheshwari & Singh (1989), Prabhu *et al.* (2009), Kumar *et al.* (2012a), Nassar *et al.* (2013), Malav *et al.* (2015) and Kumar *et al.* (2019).

5.1.2 Estimation of genetic variability parameters

5.1.2.1 Analysis of variance

Analysis of Variance (ANOVA) is a statistical procedure which splits the total variation into different components. In plant breeding experiments, analysis of variance divides the total variation into two parts, *viz.* variation between genotypes and variation within genotypes. The mean sum of squares due to genotypes for all the 17 quantitative traits studied in the present investigation were found highly significant indicating the presence of sufficient amount of genetic variability for all the traits which agree with Panwar *et al.* (2009), Erum *et al*. (2011) and Ibrahim *et al.* (2013).

5.1.2.2 Genetic variability parameters

Success of any breeding programme depends on the proper management of genetic variability present in the material (Ober & Luterbacher, 2002). The degree of variability within a population helps in the improvement of desirable traits in a variety. The genetic worth of any genotype and the potential for improving a specific trait in a population can be determined using the genetic variability parameters *viz.* genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance as a percent of mean.

i). Genotypic and phenotypic coefficients of variation

In the present study, the estimates of phenotypic coefficients of variation (PCV) were found higher than that of the corresponding genotypic coefficients of variation (GCV) for all the 17 quantitative traits studied indicating the influence of environmental factors on the expression of traits to some extent. Higher values of GCV and PCV for several traits may indicate a high degree of genetic diversity or variation within the population. This could be due to several reasons including differences in the genetic makeup of the genotypes, environmental factors, or a combination of both. Sivasubramanjan & Menon (1973) categorized GCV and PCV into three groups i.e. high (more than 20%), moderate (10-20%) and low (less than 10%). In the present study, the GCV and PCV values were found high for 11 traits, moderate for five traits and low for one trait. High GCV and PCV estimates were observed for dry herbage yield (47.31% and 47.74%), seed yield (47.21% and 48.17%), number of spikes per plant (47.18% and 47.35%), fresh herbage yield per plant (38.95% and 39.24%), 1000 seed weight (39.63% and 39.73%), seed vigour index-II (32.36% and 32.85%), seed vigour index-I (26.80% and 27.86%), seedling dry weight (24.78% and 25.04%), days to 50% flowering (22.08% and 22.40%) and spike length (21.43% and 22.17%). Moderate GCV and PCV estimates were observed for standard germination (19.01% and 19.40%), seedling length (15.42% and 16.68%), number of primary branches per plant (15.41% and 16.74%), number of flowers' whorls per spike (13.98% and 15.52%), and plant height (10.85% and 11.56%), respectively.

Low GCV (6.75%) and PCV (6.89%) estimates was observed for days to maturity. Similar results were reported by Sharma & Tyagi (1991), Khan *et al.* (2012), Patel *et al.* (2015), Singh *et al.* (2015), Smita & Kishori (2018) and Gowda *et al.* (2019).

ii). Heritability

Heritability is a measure of the proportion of phenotypic variation in a trait that is due to genetic factors. It represents the degree of similarity between parents and offspring for a given trait and is expressed in percentage. The estimates of heritability in broad sense along with genetic coefficients of variation provide clear picture on the efficiency of the selection (Burton & DeVane, 1953). The association between heritability in the broad sense and genetic advance plays an important role in yield performance which helps the plant breeders in identifying key variables for effective selection. Here in the current study, highest estimates of heritability in broad sense was observed for 1000 seed weight (99.51%) followed by number of spikes per plant (99.28%), oil content (98.60%), fresh herbage yield per plant (98.54%), dry herbage yield per plant (98.23%), seedling dry weight (97.94%), days to 50% flowering (97.17%), seed vigour index-II (97.04%), days to maturity (96.09%), seed yield per plant (96.06%), standard germination (96.02%), spike length (93.44%), seed vigour index-I (92.55%), plant height (88.12%), seedling length (85.51%), number of primary branches per plant (84.75%) and number of flowers' whorls per spike (81.21%). These results are in agreement with the earlier studies reported by Singh & Kumar (2010), Ibrahim *et al.* (2011), Khan *et al.* (2012), Patel *et al.* (2015), Edet (2018) and Smita & Kishori (2018).

iii). Genetic Advance as percent of mean

Genetic advance as a percent of mean is a measure used in plant breeding to assess the effectiveness of selection for a particular trait. It is the increase in the mean value of a trait achieved through selection, expressed as a percentage of the original mean value. The highest genetic advance as percent of mean were observed for the traits namely number of spikes per plant (96.84%) followed by dry herbage yield per plant (96.59%), seed yield per plant (95.32%), 1000 seed weight (81.44%), fresh herbage yield per plant (79.64%), oil content (76.65%), seed vigour index-II (65.67%), seed vigour index-I (53.12%), seedling dry weight (50.51%), days to 50% flowering (44.84%), spike length (42.66%), standard germination (38.38%), seedling length (29.38%), number of primary branches per plant (29.23%), number of flowers' whorls per spike (25.96%) and plant height (20.98%). The high value of genetic advance as percent of mean (>20%) indicates that during selection, there is a large gain for that particular trait. It suggests that the trait is under strong genetic control and has a high heritability. High heritability coupled with high genetic advance as percent of mean was observed for the traits number of spikes per plant (99.28% and 96.84%), 1000 seed weight (99.51% and 81.44%), fresh herbage yield per plant (98.54% and 79.64%), dry herbage yield per plant (98.23% and 96.59%) and oil content (98.60% and 76.65%), respectively. It may be due to effect of additive gene action for these characters and hence, simple selection might be practiced (Singh *et al*., 2013) for improvement of these traits in *Tulsi*. Higher estimates of heritability coupled with high genetic advance increase the efficacy of selection (Shukla *et al.*, 2006). High heritability in broad sense (96.09%) coupled with moderate genetic advance (13.64%) was observed for days to maturity which indicated the presence of non-additive gene action. Similar findings were reported by Verma *et al*. (1989), Singh & Kumar (2010), Khan *et al.* (2012), Singh *et al.* (2013), Singh *et al.* (2015) and Patel *et al.* (2018).

5.2 Correlation coefficients analysis

Correlation is the measure of association between two or more traits indicating how much they are related to each other in terms of inheritance and environmental factors. Understanding the relationship between yield and its contributing traits is very helpful to decide about the selection procedure for the targeted crop improvement programme. In the correlation coefficients analysis studies, generally, the estimates of genotypic correlation coefficients are more than the corresponding phenotypic correlation coefficients indicating the dominance of genetic factors over environmental factors for the association between traits.

In the present investigation, it was observed that the seed yield per plant had positive and highly significant correlation with number of spikes per plant (0.507** and 0.501**), 1000 seed weight (0.471** and 0.459**), number of flowers' whorls per spike (0.455** and 0.396**), seedling length (0.291** and 0.264**) and fresh herbage yield per plant (0.262** and 0.257**) at both genotypic as well as phenotypic level, respectively. Whereas, seed yield per plant showed positive and highly significant association with dry herbage yield per plant at genotypic level (0.240**) and positive and significant association at phenotypic level (0.233*) only. Seed yield per plant exhibited positive and significant association at both genotypic as well as phenotypic level, respectively, with seedling dry weight (0.234* and 0.225*), seed vigour index-I (0.217* and 0.209*) and seed vigour index-II (0.211* and 0.205*). In addition to seed yield per plant, it was observed that the oil content showed positive and highly significant correlation with fresh herbage yield per plant (0.623** and 0.621**) and dry herbage yield per plant (0.580** and 0.575**) at both genotypic as well as phenotypic level, respectively. Similar results for the correlation studies were also reported by Morales *et al.* (1993), Kumar *et al.* (2012b), Singh *et al.* (2015), Yaseen *et al.* (2015), Edet (2018) and Venkatesha *et al.* (2020).

5.3 Path coefficients analysis

Path coefficients analysis is a statistical technique used to evaluate the direct and indirect effects of various characters on a specific character of interest. It helps us to understand the complex interrelationships among multiple variables and determine the relative contributions of these variables towards the expression of the trait. Positive and negative associations among different traits and their relationship with seed yield may be revealed with the help of nature and magnitude of estimates of correlation coefficients. However, path coefficients analysis offers a more effective approach to distinguish the direct and indirect causes of these associations. Partitioning the genotypic correlations between seed yield per plant and its component traits revealed that, for the majority of traits, the direct effects tended to have a greater magnitude than the indirect effects. Therefore, combining correlation studies with path coefficients analysis can lead to a better understanding of trait associations and facilitate better planning of crop improvement programmes.

In the present investigation, positive direct effect on seed yield per plant was observed maximum for seedling length (0.582) followed by 1000 seed weight (0.487), number of spikes per plant (0.371), number of primary branches per plant (0.292), fresh herbage yield per plant (0.292), seed vigour index-II (0.232), number of flowers' whorls per spike (0.209), standard germination (0.117), spike length (0.049) and dry herbage yield per plant (0.044). These traits can be used as selection indices for seed yield improvement in *Tulsi*. Thus, direct selection for these traits would be helpful to choose the genotype for higher yield. Similar suggestions were given by Baslma (2008) and Mijic *et al.* (2009). The highest indirect positive effects on seed yield per plant were exhibited by seedling length via seedling dry weight (0.477), seedling length via seed vigour index-I (0.458), seedling length via seed vigour index-II (0.443), fresh herbage yield per plant via dry herbage yield per plant (0.277) and 1000 seed weight via spike length (0.254). Similar results were achieved by Sharma & Tyagi (1991) in Japanese mint, Ibrahim *et al.* (2011) and Kumar *et al.* (2012b) in *Ocimum*.

5.4 Genetic divergence studies

Genetic diversity analysis in plant breeding refers to the assessment of genetic variation within a population, which helps in selecting diverse parents for improvement of traits and enhance the overall adaptability. Genetic diversity studies are also essential to ensure resilience and adaptability of crop plants to changing environmental conditions, pests, and diseases. These studies help to identify and conserve diverse genetic resources, enabling breeders to develop new varieties with improved traits, higher productivity and enhanced resistance to biotic and abiotic stresses.

Genetic divergence analysis (D^2 analysis) was done using the method suggested by Mahalanobis (1936) and elaborated by Murty and Arunachalam (1966). The level of genetic divergence between two genotypes enhances with increase in range of D^2 values between them. The grouping of genotypes into different clusters was done following the Tochers' method as described by Rao (1952). Dendrogram was also plotted for genetic divergence studies of 40 *Tulsi* genotypes which offered a visual representation that simplifies the understanding of genetic divergence. The D^2 analysis grouped the 40 *Tulsi* genotypes into 10 different clusters which supports the existence of substantial amount of genetic diversity among them.

Genotypes falling within the same cluster exhibited low genetic variability as compared to those falling in different clusters. Cluster 1 was the largest cluster grouping 29 genotypes followed by cluster 7 with 3 genotypes and remaining clusters each with one genotype. The intra-cluster distance provides information about the level of variation within distinct individual clusters. The maximum intra-cluster distance was observed for the cluster 7 (35.57) and cluster 1 (31.73). The intra-cluster distances for cluster 2, cluster 3, cluster 4, cluster 5, cluster 6, cluster 8, cluster 9 and cluster 10 were observed zero because of the presence of single genotype within these clusters which indicated the absence of genetic variability within these clusters.

The maximum inter-cluster distance was observed between cluster 2 and cluster 10 (105.80) followed by between cluster 4 and cluster 10 (99.80), cluster 3 and cluster 10 (98.65), cluster 1 and cluster 10 (83.26) & cluster 8 and cluster 10 (83.08). The maximum inter-cluster distance indicates the presence of sufficient genetic diversity among genotypes of these clusters. This finding suggested that these specific clusters can serve as valuable parental sources for the development of superior improved varieties.

After clustering of 40 *Tulsi* genotypes involving 17 different quantitative traits into 10 different clusters, the cluster means unveiled the presence of sufficient genetic variation among 10 clusters in terms of these traits. In cluster 9, the highest cluster means were observed for maximum number of characters *viz*. days to maturity (168.13), number of primary branches per plant (19.13), fresh herbage yield per plant (1249.97), dry herbage yield per plant (414.87), oil content (0.49), standard germination (70.87) and seed vigour index-I (6878.00). Therefore, the genotype (EC 388890) of cluster 9 can be used extensively for further *Tulsi* crop improvement programmes. Relative contribution of different traits towards genetic diversity revealed that 1000 seed weight (41.41%) contributed maximum towards genetic divergence followed by number of spikes per plant (17.31%), fresh herbage yield per plant (13.46%) and oil content (10.77%). Similar results for genetic diversity analysis were reported by Erum *et al.* (2011), Singh *et al.* (2018) and Srivastava *et al.* (2018).

CHAPTER- VI

SUMMARY AND CONCLUSION

The present investigation entitled, "Genetic divergence, correlation and path coefficients studies in Tulsi (*Ocimum spp*.)" comprising of 40 different *Tulsi* genotypes were evaluated based on different qualitative and quantitative traits at Research Area of Medicinal, Aromatic and Potential Crops Section, Department of Genetics and Plant Breeding, Chaudhary Charan Singh Haryana Agricultural University, Hisar during *Kharif* 2022. The present investigation was carried out with following objectives:

1. To study the genetic variability in *Tulsi* for seed yield and its component traits.
2. To estimate the correlation and path coefficients for seed yield and its contributing traits.
3. To determine the extent of genetic diversity for different traits to classify the *Tulsi* genotypes into different clusters.

The experimental material consisting of 40 *Tulsi* genotypes were grown in Randomized Block Design (RBD) with three replications. The observations were recorded on 10 qualitative traits *viz.* stem colour, stem pubescence, leaf shape, leaf colour, leaf pubescence, petiole colour, flower colour, calyx colour, calyx pubescence & seed colour, and 17 quantitative traits namely days to 50% flowering, days to maturity, number of primary branches per plant, plant height (cm), number of spikes per plant, spike length (cm), number of flowers' whorls per spike, fresh herbage yield per plant (g), dry herbage yield per plant (g), seed yield per plant (g), 1000 seed weight (g), oil content (%), standard germination (%), seedling length (mm), seedling dry weight (mg), seed vigour index-I & seed vigour index-II. Genetic variability parameters like phenotypic and genotypic coefficients of variance, heritability in broad sense and genetic advance as percent of mean were calculated following the formulae suggested by Burton & DeVane (1953), Burton (1952) and Johnson *et al*. (1955), and correlation and path coefficients according to Dewey and Lu (1959). D^2 analysis was done using the method suggested by Mahalanobis (1936) and elaborated by Murty and Arunachalam (1966). The grouping of genotypes into different clusters was done following the Tocher's method as described by Rao (1952).

The summary of results and the conclusion drawn from the present investigation are given as below:

❖ **Summary:**

- On the basis of stem colour, all the 40 *Tulsi* genotypes were categorized into five groups. Twenty-eight genotypes were having green stem colour, five genotypes purple, four genotypes dark green, two genotypes light purple and one genotype with light green stem colour.

- Based on presence or absence of minute hairs on the surface of the stem, two categories were formed. Five genotypes were having sparse pubescence and the rest thirty five genotypes were non-pubescent.
- Elliptical leaf shape was observed in all the 40 genotypes of *Tulsi*.
- Based on leaf colour, all the *Tulsi* genotypes were classified into four groups. Twenty five genotypes were found having green leaf colour, eight genotypes with dark green, six genotypes with light green and one with purple leaf colour.
- On the basis of leaf pubescence, two categories were observed. Two genotypes were found to have sparse pubescence and the remaining 38 genotypes were non pubescent.
- Genotypes were classified into three groups on the basis of petiole colour. Thirty six genotypes had green petiole colour, three genotypes with purple green and only single genotype with purple petiole colour.
- Based on flower colour, three categories were formed *viz.* white, light purple and purple. White flower colour was observed in twenty seven genotypes, light purple flower colour in eight genotypes and purple flower colour in five genotypes.
- Based on the colour of the calyx, the genotypes were classified into five groups. It was observed that twenty five genotypes were having green calyx colour, six genotypes with purple, six genotypes with light purple, two genotypes with light green and one genotype with dark purple calyx colour.
- On the basis of presence or absence of minute hairs on the calyx surface, two categories were formed. Twenty seven genotypes were non-pubescent and the remaining thirteen genotypes were sparsely pubescent.
- Genotypes were classified into four groups based on seed colour. Thirty five genotypes were observed to have dull black seed colour, three genotypes with brownish black, one genotype with brownish black and one genotype with brown seed colour.
- Analysis of variance (ANOVA) revealed that the mean sum of squares due to genotypes for all the 17 quantitative traits studied were highly significant.
- On the basis of mean performance of individual genotypes, the highest seed yield per plant was recorded for the genotype EC 338772 (61.5g) followed by RDV 45 (60.9g), EC 388890 (57.1g) and IC 381158 (53.2g).
- The estimates of phenotypic coefficients of variation (PCV) were slightly more than the corresponding genotypic coefficients of variation (GCV) for all the traits indicating the role of environment on the expression of traits.
- High GCV and PCV (>20%) estimates were observed for 11 quantitative traits such as dry herbage yield (47.31.21% and 47.74%), seed yield (47.21% and 48.17%) and number of spikes per plant (47.18% and 47.35%), respectively.

- In general, high heritability in broad sense coupled with high genetic advance as percent of mean were observed for most of the traits like 1000 seed weight (99.51% and 81.44%), seed yield (96.02% and 95.32%), dry herbage yield (98.23% and 96.59%), fresh herbage yield (98.54% and 79.64%), number of spikes per plant (99.28% and 96.84%), oil content (98.60% and 76.65%), seed vigour index-II (97.04% and 65.67%) and seed vigour index-I (92.55% and 53.12%), respectively.
- Positive and highly significant genotypic correlation coefficients of seed yield per plant were observed with number of spikes per plant (0.507**), 1000 seed weight (0.471**), number of flowers' whorls per spike (0.455**), seedling length (0.291**), fresh herbage yield per plant (0.262**), dry herbage yield per plant (0.240**), seedling dry weight (0.234**) whereas, positive and significant at 5% level of significance with seed vigour index-I (0.217*) and seed vigour index-II (0.211*).
- Path coefficient analysis revealed that the maximum direct positive effect on seed yield per plant was observed for seedling length (0.582) followed by 1000 seed weight (0.487), number of spikes per plant (0.371), number of primary branches per plant (0.292), fresh herbage yield per plant (0.292), seed vigour index-II (0.232), number of flowers' whorls per spike (0.209), standard germination (0.117), spike length (0.049) and dry herbage yield per plant (0.044) whereas, the highest indirect positive effects on seed yield per plant were shown by seedling length via seedling dry weight (0.477), seedling length via seed vigour index-I (0.458), seedling length via seed vigour index-II (0.443), fresh herbage yield per plant via dry herbage yield per plant (0.277) and 1000 seed weight via spike length (0.254).
- The maximum intra-cluster distance was observed for the cluster 7 (35.57) and cluster 1 (31.73).
- The maximum inter-cluster distance was observed between cluster 2 and cluster 10 (105.80) followed by between cluster 4 and cluster 10 (99.80), cluster 3 and cluster 10 (98.65), cluster 1 and cluster 10 (83.26), cluster 8 and cluster 10 (83.08), cluster 3 and cluster 7 (77.76), cluster 2 and cluster 7 (77.11), cluster 4 and cluster 7 (76.30), cluster 6 and cluster 10 (76.18) & cluster 5 and cluster 10 (75.90).
- The highest cluster means were observed in cluster 9 for maximum number of characters *viz*. days to maturity (168.13), number of primary branches per plant (19.13), fresh herbage yield per plant (1249.97), dry herbage yield per plant (414.87), oil content (0.49), standard germination (70.87) and seed vigour index-I (6878.00).
- Relative contribution of different traits towards genetic diversity revealed that 1000 seed weight (41.41%) contributed maximum towards genetic divergence followed by number of spikes per plant (17.31%), fresh herbage yield per plant (13.46%) and oil content (10.77%).

❖ Conclusion:

From the findings of the present study, it may be concluded that the sufficient amount of genetic variability was present for all the 17 quantitative traits studied in the 40 Tulsi (*Ocimum spp.*) genotypes because the mean sum of squares due to genotypes for all the traits studied were highly significant. In general, high heritability in broad sense coupled with high genetic advance as percent of mean were observed for most of the traits like 1000 seed weight, seed yield per plant, dry herbage yield per plant, fresh herbage yield per plant, number of spikes per plant, oil content, seed vigour index-II and seed vigour index-I which indicates the effect of additive gene action in the expression of these traits. Hence, simple selection procedure may be very effective for further improvement of these traits. Seed yield per plant exhibited positive and significant genotypic and phenotypic association with number of spikes per plant, 1000 seed weight, number of flowers' whorls per spike, seedling length, fresh herbage yield per plant, dry herbage yield per plant, seedling dry weight, seed vigour index-I and seed vigour index-II. Path coefficient analysis revealed that the maximum direct positive effect on seed yield per plant was observed for seedling length followed by 1000 seed weight, number of spikes per plant, number of primary branches per plant, fresh herbage yield per plant, seed vigour index-II, number of flowers' whorls per spike, standard germination, spike length and dry herbage yield per plant whereas, the highest indirect positive effects on seed yield per plant were shown by seedling length via seedling dry weight, seedling length via seed vigour index-I seedling length via seed vigour index-II, fresh herbage yield per plant via dry herbage yield per plant and 1000 seed weight via spike length. Through genetic diversity analysis, the 40 *Tulsi* genotypes were grouped into 10 different clusters which revealed that a lot of genetic diversity was present among all the *Tulsi* genotypes. The maximum intra-cluster distance was observed for the cluster 7 and cluster 1 whereas, the maximum inter-cluster distance was observed between cluster 2 and cluster 10 followed by between cluster 4 and cluster 10 & cluster 3 and cluster 10. The highest cluster means were observed in cluster 9 for maximum number of characters *viz*. days to maturity, number of primary branches per plant, fresh herbage yield per plant, dry herbage yield per plant, oil content, standard germination and seed vigour index-I. Relative contribution of different traits towards genetic diversity revealed that 1000 seed weight contributed maximum towards genetic divergence followed by number of spikes per plant, fresh herbage yield per plant and oil content.

The maximum seed yield per plant and number of primary branches per plant were observed for the genotype EC 338772, maximum fresh as well as dry herbage yield per plant and maximum oil content were recorded for EC 388890, and seed vigour index-I and II were found maximum for the genotype IC 326732. Hence, the genotypes EC 338772, EC 388890 and IC 326732 can further be exploited in the breeding programmes to develop the improved cultivars of *Tulsi* for seed yield, oil content and other economically important traits.

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ABSTRACT

Title of thesis : **Genetic divergence, correlation and path coefficients studies in Tulsi (*Ocimum spp.*)**
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The present investigation comprising of 40 Tulsi (*Ocimum spp.*) genotypes received from ICAR- National Bureau of Plant Genetic Resources, New Delhi were grown in Randomized Block Design (RBD) with three replications in the Research Area of Medicinal, Aromatic and Potential Crops Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar during *Kharif* 2022. The observations were recorded for 10 qualitative and 17 quantitative traits. The 40 *Tulsi* genotypes were characterized into different categories for each of the qualitative trait. Analysis of variance revealed the presence of sufficient amount of genetic variability for all the 17 quantitative traits studied. The GCV and PCV estimates were high for dry herbage yield (47.31% and 47.74%), seed yield (47.21% and 48.17%) and number of spikes per plant (47.18% and 47.35%), respectively. High heritability coupled with high genetic advance was observed for number of spikes per plant, 1000 seed weight, fresh herbage yield, dry herbage yield and oil content. Seed yield per plant showed highly significant and positive correlation with number of spikes per plant (0.507** and 0.501**), 1000 seed weight (0.471** and 0.459**), number of flowers' whorls per spike (0.455** and 0.396**), seedling length (0.291** and 0.264**) and fresh herbage yield per plant (0.262** and 0.257**) at both genotypic as well as phenotypic level, respectively. Path coefficients analysis revealed that the maximum positive direct effect was exhibited by seedling length (0.582) followed by 1000 seed weight (0.487), number of spikes per plant (0.371), number of primary branches per plant (0.292), fresh herbage yield per plant (0.292), seed vigour index-II (0.232) and number of flowers' whorls per spike (0.209). The 40 *Tulsi* genotypes were grouped into 10 different clusters indicating the presence of genetic divergence among different genotypes. The maximum intra-cluster distance was recorded for cluster 7 and maximum inter-cluster distance was recorded between cluster 2 and cluster 10. Relative contribution of different traits towards genetic diversity revealed that 1000 seed weight (41.41%) contributed maximum towards genetic divergence followed by number of spikes per plant (17.31%), fresh herbage yield per plant (13.46%) and oil content (10.77%). Based on the maximum mean performance for seed yield, number of primary branches, fresh as well as dry herbage yield, oil content and seed vigour index-I & II, the genotypes EC 338772, EC 388890 and IC 326732 may be exploited in the breeding programmes to develop the improved cultivars of *Tulsi* for higher seed yield, oil content and other economically important traits.

MAJOR ADVISOR **SIGNATURE OF STUDENT**

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Co-curricular activities: I was actively involved in the following co-curricular activities.

- Languages known: Kannada, English, Hindi and Telugu.
- Participated and successfully completed six days ***"Special Course of Mountaineering"*** organized by Nehru Institute of Mountaineering, Uttarkashi (Uttarakhand) during April 12-17, 2013 and displayed good team work, discipline and determination.
- Awarded as ***"Best Outgoing Student in Academics"*** for having secured highest OGPA (8.926/10.0) at the completion of B.Sc. (Hons.) Agri. Programme from 2017-2021 in College of Agriculture, Kalaburagi, University of Agricultural Sciences, Raichur (Karnataka).
- Participated in the ***"NSS State level Suvarna Mahothsva Youth Festival-2019"*** held at Vidyanagari Sports Residential School, Bangalore from 10th to 14th September, 2019 as NSS Volunteer of College of Agriculture, Kalaburagi, University of Agricultural Sciences, Raichur.
- Partcipated in the ***"South Zone Inter University Tournaments"*** held at Vellore Institute of Technology, Vellore, Tamilnadu from December 09-12, 2019 as a member of Football (Men) Team of University of Agricultural Sciences, Raichur.
- Received **ICAR-PG Scholarship (JRF)** from Indian Council of Agricultural Research, New Delhi during my Post Graduation [M.Sc. (Genetics and Plant Breeding) Agri.] Programme from 2021-2023.
- Participated in ***"International Conference on Climate Resilient Agriculture for Food Security and Sustainability"*** held during February 17-19, 2023 at CCS Haryana Agricultural University, Hisar (Haryana) and presented Poster on the topic, "Morphological Characterization of Different Tulsi (*Ocimum spp.*) Germlasm Lines".

I, hereby, declare that all the information given in the resume is true to the best of my knowledge.

Place: Hisar
Dated: 09.06.2023 **(Vijay Kumar C. Talawade)**

UNDERTAKING OF THE COPYRIGHT

I**, Vijay Kumar C. Talawade,** Admission. No. **2021A73M,** undertakes that I give copyright to the CCS Haryana Agricultural University**,** Hisar (Haryana) of my thesis entitled, **"Genetic divergence, correlation and path coefficients studies in Tulsi (*Ocimum spp*.)".** I also undertake that, patent, if any, arising out of the research work conducted during the programme shall be filed by me only with due permission of the competent authority of CCS Haryana Agricultural University, Hisar (Haryana).

Vijay Kumar C. Talawade