GENETIC DIVERGENCE STUDIES IN CORIANDER (*Coriandrum sativum* L.)

BY
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IN
VEGETABLE SCIENCE

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2017

CERTIFICATE-I

This is to certify that this thesis entitled, **"Genetic divergence studies in coriander (*Coriandrum sativum* L.)"** submitted for the degree of **Doctor of Philosophy** in the subject of **Vegetable Science** to the **Chaudhary Charan Singh Haryana Agricultural University, Hisar** is a *bona-fide* research work carried out by **Shivaprasad, M. K. Admission No. 2013A58D** under my supervision and that no part of the 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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It is certified that the thesis submitted by Ms. **Shivaprasad, M. K.** Admn. No. **2013A58D**, a Ph.D. student of **Vegetable Science** has been checked and found as per specifications of the format circulated by Dean, PGS vide his Memo. No. PGS/A-1/09/6926-90 dated 26/8/2009.

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CHAPTER-I

INTRODUCTION

Coriander (*Coriandrum sativum* L.), also known as Kustambari in Sanskrit, Dhania in Hindi, Dhane in Bengali and Khophir in Gujarati is a cross pollinated crop originated from Mediterranean region. This annual herbaceous plant belonging to Apiaceae family with diploid chromosome number (2n) 22, is grown for its seed capsules commonly known as Dhania, which have a fragrant odour and aromatic taste used as spice in dishes and known as a medicine for over thousands of years (Mathias, 1994). With pleasant aroma, its tender shoots and leaves are also used in chutney, soups and salads. In India, its fruits are considered for medicinal benefits like carminative, diuretic, tonic, stomachic, antibilious, refrigerant, aphrodisiac and also used in preparation of pickling spices, sausages, and for flavouring pastry, cookies, buns, cakes and several alcoholic beverages, *e.g.,* gin (Jansen, 1981). It is used as condiment in the preparation of curry powder, besides this the coriander dry seeds yield contains 0.2 to 1.2 per cent essential oil on steam distillation. The seeds also contain 19 to 21 per cent of fatty oil (oleoresin), which is a base for preparation of several chemicals and also used as a flavouring agent for liquor (Tiwari and Agarwal, 2004).

Coriander is one of the earliest spices used by the man kind and extensively grown in India, Central Europe, Asia Minor and Morocco. In India, it is mainly cultivated in Rajasthan, Andhra Pradesh, Madhya Pradesh, Uttar Pradesh, Bihar, Haryana, Maharashtra, Gujarat, Karnataka and Tamil Nadu. According to the Indian national standard organization 109 spices are grown in the world and out of which 63 spices are grown in India. India contributes 48% of the total spice production of the world (Anonymous, 2009). It is cultivated as a winter or summer annual crop according to the climatic conditions. In India, during the year 2013-14 it occupied 4,47,000 ha area with production of 3,14,000 MT and 0.7 MT/ ha productivity (Anonymous, 2015).

The low production and lesser area are mainly due to the lack of good varieties with better morphological and yield attributes. This gap can be bridge by improved varities. The breeding of coriander has also long been practiced in India (Dimri *et al.,* 1976; Suthanthirapandian *et al.,* 1980; Sethi, 1981; Agrawal *et al.,* 1990; Bhandari and Gupta, 1991). Development of new varieties has progressed simultaneously along with agriculture and civilization. The continuous development of new varieties is essential cornerstone for increasing yield and productivity. The availability of germplasm is a basic requirement for the genetic improvement and characterization of germplasm for agronomic and morphological traits is necessary to facilitate for the improvement programme. Characterization is used to distinguish the genotypes on the basis of their highly heritable characters that help to select the most suitable genotypes according to the needs of user / plant breeders.

In recent IBPGR definition, characterization stands for recording those characters which are highly heritable and can be seen easily by the eyes and maybe that expressed under all climatic conditions. It is distinguished from preliminary evaluation, in the limited numbers of agronomic traits considered to be important in crop improvement programme are recorded. Characterization is carried out in précised experimental plots by spaced planting under adequate agronomic conditions and plant protection. For each accession several morpho-agronomic traits are recorded using the standard descriptors. Considering these above aspects in mind genotypes characterization work has been done by various workers on different crops like cereals, pulses, or fiber crops. Some consideration has been given in the field of vegetable crops, however very little attention has been given to the spice crops despite these being very important in day to day human life.

Efforts have been made through breeding work to contribute substantially for improving yield potential. The extent of genetic amelioration is determined by quantum of genetic variability and the extent of heritable and non-heritable variations associated with the characters. Since yield is a highly complex character and is controlled by large number of genes and greatly influenced by the environmental conditions. Thus, direct selection for yield may not be very effective because it is dependent directly or indirectly on yield contributing characters, which in turn are influenced by environment.

For any crop improvement programme, variability in working genotypes is very important. Hence, analyzing the nature and magnitude of the heritable genetic variation of population is necessary. Understanding the association of yield contributing characters towards yield forms the basic requirement for selection procedures. Correlation and path analysis methods are used to determine the extent of association between yield and its component and also bring out the relative importance of their direct and indirect effect and thus, give a clear understanding of their association with yield. Thus, correlation and path analysis provide detailed information about important characters to be considered in improvement program through selection.

Genetic diversity plays vital role in conservation and for parental selection schemes which may further be used in many breeding programmes. It helps in the development of superior recombinants. Thus, the crosses between parents with maximum genetic divergence are generally the most responsive for genetic improvement (Arunachalam 1981). Genetic diversity is estimated through D^2 analysis by evaluating the morphological traits. The D^2 technique based on multivariate analysis developed by Mahalanobis (1936) has been found to be an efficient tool for quantifying the degree of divergence in population. This estimate provides a measurement of relative contribution of different components on diversity both at intra and inter cluster level and genotypes drawn from widely divergent clusters are likely to produce heterotic combinations and wide variability in segregating generations.

In contrast to conventional variability studies, morphological and agronomic evaluation, now a days the molecular markers are widely used for analysis of genetic diversity based on DNA polymorphism. These are generally not affected by environment and are very accurate in evaluation of genotypes than traditional methods of analysis. These are the constant land marks in the genome and are best tools for determining genetic relationships. Molecular markers are regions in the genome that are heritable as simple Mendelian traits, are easy to document and can be used to detect genetic divergence quickly. The most commonly used DNA based markers are RAPD and ISSR. Random Amplified Polymorphic DNA (RAPD) can be very useful in varietal identifications, particularly when low morphological variability is present in the crop. These markers requires very small amount of DNA with no prior sequence information and is very simple, quick and inexpensive way to estimate genetic relationships. The ISSR (Inter-Simple Sequence Repeat) markers have been widely used in genetic studies because they are useful in cultivar identification, they show a high degree of polymorphism, a simplicity and do not require previous knowledge of the genome sequence.

The research work on molecular characterization in coriander is lacking for the identification of better varieties with respect to yield and its attributes. So the need of hour research based on this aspect by using different markers for the improvement of this crop may provide good genotypes for better production and productivity. Keeping the above facts explained in view, the present investigation in coriander was been carried out with the following objectives:

1. To characterize the coriander genotypes on the basis of morphological traits
2. To study the correlation and path co-efficient analysis of yield and its contributing traits
3. To study the genetic divergence using D^2 analysis and molecular markers

CHAPTER-II

REVIEW OF LITERATURE

Coriander has gained lot of importance in recent years as an herbal spice and condiment. Recent crop improvement practices of coriander have made available several new genotypes whose performance with respect to growth, yield and quality have differed greatly. The identification and selection of cultivars are important factors for successful cultivation of any crop. The knowledge regarding presence of variability for the specific economic traits enables the breeders in determining the most desirable parents. Growing importance of coriander cultivation and utilization have ultimately build up interest of many researchers towards work on various aspects of this crop including the assessment of performance of genotypes for different agro-climatic conditions.

In this chapter, the available information on performance and genetic variability, diversity and also molecular studies on coriander has been presented under various subtitles. Wherever literature on coriander crop is lacking, the related research work on other crops has also been presented in following heads;

2.1 Morphological characterization
    2.1.1 DUS characterization
    2.1.2 Genetic variability
2.2 Correlation and path coefficient
2.3 Divergence (D^2) analysis
2.4 Molecular characterization

2.1 Morphological characterization

2.1.1 DUS characterization

Complete and detailed genotype descriptions along with improved genotype identification techniques are required for the increasing number of genotypes. Coriander shows diversity with respect to growth habit and morphology, which is the fundamental requirement in any crop improvement. Here, the attempt has been made to review the work related to DUS characterization.

Seven coriander genotypes were evaluated under Jobner conditions by Jindal *et al.* (1985). The maximum plant height was recorded in cv. PCO-4 followed by PCO-2 and minimum in cv. PCO-5. Gurbuz (2001) studied 25 coriander lines. Among them higher plant height was noted in Line-20 (125.4 cm) and lowest in Line-25 (85.1 cm). To determine the morphological variation among the coriander genotypes, Bhandri and Gupta (1991) examined two hundred coriander genotypes and recorded higher genetic variation for plant height, primary and secondary branches, days to flowering and maturity, umbels and umbellets per plant, seeds per umbellet, thousand seed weight, straw yield per plant and harvest index. Rajput *et al.*, (2003) evaluated twenty genotypes of coriander under Jobner conditions. Among them, RCr-435 recorded maximum plant height (89.60 cm) followed by UD-728 (88.30 cm) whereas the genotype UD-310 recorded the minimum (44.00 cm).

Velayudham (2004) studied 11 genotypes of coriander in both kharif and rabi seasons of 2003-04 under Arabhavi conditions. In kharif season, the genotype RCr-41 recorded the highest plant height (49.03 cm) and lowest height (38.74 cm) in Guntur Local. While, in rabi season the highest plant height was recorded in CO-1 (66.97 cm) and the lowest in Ghataprabha Local (41.47 cm). Dhirender *et al.* (2006) evaluated 360 coriander genotypes for various morphological traits and seed yield. The significant variation was observed for all the traits. The range value for plant height, branches per plant, umbels per plant, umbellets per umbel, seeds per umbel, seed yield per plant were 32.99-106.49cm, 3.19-9.04, 4.36-78.26, 2.76-7.38, 8.98-61.88, 1.05-14.93g, respectively. Melo *et al.* (2009) characterized coriander varieties americano, asteca, palmeira, portugues, santo, superia, tabocas, tapacura, and verdao and line HTV-9299 on seedling, leaflets, leaves, fruits and flower characteristics. Arif *et al.* (2014) evaluated 69 coriander accessions from Pakistan, China, India and Iran for eight morphological characters i.e. number of days until start of flowering (DtFs), number of days until end of flowering (DtFe), number of days until harvesting (DtH), number of days to stem elongation (DtSE), plant height (cm), length of longest basal leaf (cm), number of basal leaves and 1000 seed weight (g).

Chauhan (2003) grouped 30 germplasm lines of fenugreek on the basis of seed morphology (seed shape, seed colour, seed weight, seedling pigmentation) and classified the germplasm lines into angular and flat oblong on the basis of seed shape and into yellow, brown, green, greenish yellow on the basis of seed colour. Dhuhan *et al.* (2005) recorded higher plant height (111.30 cm) at 140 days after sowing, in HM-232-3 while the least plant height was recorded in HM-254 (94.3 cm), among 65 genotypes of fenugreek studied at Hisar during winter season of 1997-98. Bhattacharya *et al.* (2006) among five fenugreek cultivars evaluated under Mohanpur conditions of West Bengal, local cultivar recorded higher plant height (63.44 cm) followed by EC 57752 (62.11 cm) and lowest was in J. Fenu (55.00 cm). Some seed characters like test weight, seed colour, seed luster and seed size were also found helpful in differentiating the fenugreek cultivars (Devebarta, 2011).

2.1.2 Genetic variability

Genetic variability in a population for yield attributing characters provides good opportunity for selection. Hence, thorough study of genetic variability, heritability and genetic advance are important tools for the breeders in selection of elite genotypes from mixed diverse populations.

Megeji and Korla (2002) evaluated 30 genotypes of coriander and reported the analysis of variance, which indicated significant differences in all the characters studied. Genotypic and phenotypic coefficients of variation were high for seed vigour and seed yield. Heritability was highest for 1000-seed weight followed by germination percentage. Seed vigor, leaf yield, 1000-seed weight, germination percentage and seed vigour recorded high genetic advance. Rajput *et al.* (2003) studied the genetic variability for seven characters (days to flower, plant height, branches per plant, umbels per plant, umbellets per umbel, seeds per umbel and seed yield in 20 genetically diverse genotypes of coriander. Shah *et al.* (2003) studied 20 genotypes of coriander and reported that the PCV was generally higher than GCV. High estimates of heritability were recorded for oil content, 1000-seed weight, number of days to flowering, number of days to maturity and plant height, number of umbels per plant and seed yield per plant. Oil content, 1000-seed weight, plant height and number of days to flowering were characterized by high heritability coupled with high genetic gain. Rajput *et al.,* (2003) studied variability in 20 genotypes of coriander and indicated higher estimates of genotypic coefficients of variation, PCV, heritability and genetic advance for seed yield, umbels per plant, seeds per umbel and plant height, suggesting probable role of additive gene effects on character expression.

Singh *et al.* (2006a) evaluated 35 genotypes of coriander and reported genetic variation for plant height, number of primary branches per plant, number of secondary branches per plant, number of umbels per plant, number of umbellets per umbel, number of seeds per umbellet and 1000 seed weight. Singh *et al.* (2006 a) also observed significant variability for plant height, number of primary branches per plant, number of secondary branches per plant, days to 50 percent flowering, days to maturity, number of umbels per plant, number of umbellets per umbel, number of seeds per umbellet, 1000 seed weight, essential oil content, harvest index and seeds per plant in coriander.

Singh *et al.* (2008) evaluated 70 lines of coriander and reported wide range of variability for plant height, branches per plant, umbels per plant, and seeds per umbel and seed yield. The high heritability coupled with high genetic advance and coefficients of variability was recorded for plant height, seed yield per plant, test weight and umbels per plant. Idhal *et al.* (2009) evaluated 30 genotypes of coriander and reported significant genotypic differences for all nine characters. The genotypic coefficient of variation, heritability and genetic advance were higher for branches per plant, umbels per plant and 1000-seed weight. Mengesha and Alemaw (2010) evaluated Ethiopian coriander and reported combined analysis of variance over locations, the results reveled accessions varied significantly in all traits except for basal leaf number, plant height and fatty oil contents. Highest value of GCV, broad sense heritability and genetic advance as per cent of mean was obtained for longest basal leaf length, umbels number per plant, number of umbellets per umbel, number of seeds per umbellet, number of seeds per plant and seed yield per ha. Meena *et al.* (2010) studied 30 diverse genotype of coriander and observed that PCV (%) were comparatively high for yield plot^{-1} followed by number of seed umbel^{-1}, number of secondary branches plant^{-1} and test weight (g). GCV were comparatively high for yield plot^{-1} (kg) followed by number of umbel plant^{-1}, yield plant^{-1} (g), number of seeds umbel^{-1}, test weight (g), number of umbellets umbel^{-1} and number of secondary branches plant^{-1}. The GCV was less than the corresponding PCV, indicating the role of environment in the expression of the traits under field condition, the results reveled that high genetic advance coupled with high heritability was observed for number of umbel plant^{-1} followed by yield plant^{-1} and days to maturity.

Dyulgerov and Dyulgerova (2013) recorded high genetic variability among the accessions. Traits such as seed weight per umbel, 1000 seed weight and seed weight per plant have major contribution towards genetic diversity. Meena *et al.* (2013) reported highest genotypic and phenotypic variance for number of umbels plant^{-1}, plant height and days to harvesting. High genotypic and phenotypic coefficient of variance was observed for seed yield of coriander. High heritability coupled with high genetic advance as percent of mean was recorded for test weight, plant height and number of seed umbel^{-1} indicating the importance of additive gene effects on these traits. Singh and Singh (2013) studied for genetic variability for 11 traits in nine genotypes of coriander. The maximum PCV and GCV was observed for number of umbels plant^{-1} (19.04) & (18.39) followed by primary branches (14.77) & (13.35) and number of umbellets umbel^{-1} (14.75) & (11.50). They also studied heritability and genetic advance for same traits, the maximum heritability and genetic advance values obtained for number of umbels plant^{-1} (93.5%) & (24.43%) followed by plant height (93.2%) & (16.06%), number of seeds umbel^{-1} (89.2%) & (7.26%). Meanwhile, low genetic advance was obtained for number of umbellets umbel^{-1} followed by test weight.

2.2 Correlation and path co-efficient

Correlation co-efficient analysis measures mutual relationship between various characters and determines the component characters on which selection is made for improvement of a particular character. A positive correlation between desirable characters helps in simultaneous improvement of both the characters, the relative contribution of component characters directly on the main characters or indirectly through other characters can be analyzed through path coefficient technique to increase the efficiency of selection schemes. The literature information relating these aspects is reviewed in following paragraphs.

Tripathi *et al.* (2000) studied correlations in coriander germplasm and indicated that plant height, number of secondary branches, days to flowering, days to maturity and number of umbels per plant were the major yield components. Whereas, number of primary branches, number of umbellets per umbel and number of seeds per umbel being negatively correlated with yield were less important. Gurbuz (2001) reported the highest correlation was found between single plant yield with single plant weight and number of branches in coriander. The highest direct and positive effect of single plant weight recorded on single plant yield in coriander and plant height had the highest negative effect on single plant yield.

Jain *et al.* (2003) evaluated 106 coriander accessions observed that plant height, branches per plant, umbels per plant, umbellets per umbel, seeds per umbel and test weight had positive and significant correlation with seed yield per plant. Whereas, days to 50 % flowering showed negative and significant association with seed yield per plant. Reported that total plant height exerted maximum direct effect followed by umbels per plant on seed yield. Hence, selection for plant height and umbels per plant would be highly effective for improvement of seed yield. Vijayalatha and Chezhiyan (2004) studied correlation and path analysis in coriander indicated that the plant height, number of primary branches, number of umbels, number of umbellets per umbel and essential oil exhibited positive and significant association at phenotypic and genotypic levels with yield and observed that positive direct effect of essential oil and number of umbellets was the highest on yield. Singh et al. (2006a) evaluated 360 lines of coriander reported that correlation between umbelets per plant and branches per plant were the most important traits as they recorded positive direct effect on seed yield. Singh *et al.* (2006b) observed in coriander seed yield per plant had positive and significant correlation with plant height, number of primary branches per plant, number of secondary branches per plant, number of umbels per plant, number of umbellets per umbel, number of seeds per umbellets and harvest index. In path analysis number of secondary branches per plant, harvest index, days to maturity and number of umbellets per umbel were the most important characters for selection of high yielding genotypes as they had high direct positive effects as well as positive association with seed yield per plant.

Singh *et al.* (2008) recorded that branches per plant, leaves per plant and seeds per umbel showed positive significant genotypic correlation among themselves and all were positively correlated with seed yield per plant. Seeds per umbel and umbels per plant were also noticed positive significant correlation with seed yield per plant in coriander. Idhal *et al.* (2009) reported that seed yield was highly significant and positively correlated with umbellets per umbel, seed per umbel, plant height and umbels per plant at genotypic and phenotypic level. Path coefficient analysis showed that plant height had highest positive direct effect on seed yield per plant followed by seed per umbel and 1000-seed weight in coriander. Singh *et al.* (2011) reported that seed yield was significantly and positively correlated with its component characters like the number of primary branches per plant, number of umbels per plant, number of umbellets per plant, number of seed per umbel and umbel diameter at the genotypic and phenotypic levels in coriander.

Kumar *et al.* (2012) reported seed yield was significantly and positively associated with plant height, number of secondary branches per plant and number of seeds per umbel, which indicated that the traits might be directly selected for improvement in seed yield of coriander. Miheretu (2013a) evaluated 19 coriander land races to see the correlation among yield components. The results revealed that seed yield per plant was positively correlated with all traits except the number of umbels per plant and oil content. On the other hand, the oil content showed negative correlation with all traits except days to emergence. Kassahun *et al.* (2013) evaluated coriander varieties for 15 agronomic and quality traits. The results revealed that more traits were having high correlation coefficients at genotypic level than the phenotypic level. Seeds per plant and thousand seeds weight were significantly and positively associated with seed yield per plant at phenotypic and genotypic levels. Path analysis revealed that days to 50% flowering, longest basal leaf length, plant height, days to 50% maturity and seeds per umbellet exerted positive and direct effect on seed yield per plant.

Al-Kordy *et al.* (2013) estimated the variance, broad-sense heritability, genetic advance, genotypic and phenotypic correlation coefficients for linear growth, plant height, number of primary branches per plant, number of total branches per plant and seed yield per plant in three coriander cultivars namely, russian, balady (Egyptian) and selected (variety name). Broad-sense heritability estimates were high in the three varieties ranging between 80.4 and 99.8%. Correlation coefficients were positive among all traits. The cultivar selected showed the best seed yield in both seasons (66.73 and 70.87 g/plant, respectively). El-Nasr *et al.* (2013) studied the genetic variability for seven characters in ten selected genotypes within three coriander cultivars. The analysis of variance revealed that there was highly significant ($p<0.01$) differences among and within cultivars for all the characters, except total number of branches, which showed significance ($p<0.05$) among the genotypes. Heritability and genetic advance were high for seed yield, linear growth and plant height in cultivar selected followed by russian and balady cultivar.

Tomar *et al.* (2014) did the morphological characterization of 12 different characters in 25 genotypes of coriander. The largest variation was exhibited for harvest index (36-75%), seed yield per plant (7-18 g), umbellets per plant (215-268) and seeds per umbel (20-29), while it was narrow for days to 50% flowering (27-33 days), plant height (75-80 cm), number of basal leaf (5-9) and longest basal leaf (5-7). Phenotypic coefficient of variability (PCV) was higher in magnitude than the genotypic coefficient of variability (GCV) for all the characters except number of basal leaves. Meena *et al.* (2014) evaluated twenty four genotypes of coriander and found that number of umbels per plant and test weight were associated significantly and positively with seed yield per plant. The path coefficient analysis shown for days to 50% flowering (2.08) had the highest direct effect on seed yield followed by number of seeds per umbel (1.01), number of secondary branches (0.52), number of umbels per plant (0.49), test weight (0.28) and plant height (0.23).

Dyulgerov, N. and Dyulgerova, B (2014) utilized 20 genotypes of var. *microcarpum* and 20 genotypes of var. *sativum* to investigate how yield-related traits of large-seeded (var. *sativum*) and small-seeded (var. *microcarpum* DC.). According to variance analyses, the value of the 1000-seeds weight, seed weight per umbel, seed weight per plant and number of primary branches were determined by genotype (var. *microcarpum* DC. or var. *sativum*) but other characteristics were more affected by the weather conditions of a particular year. Plant height was determined by the environment for both varieties of coriander. Number of primary branches was influenced by the genotype for var. *sativum* and by the year for var. *microcarpum*. Arif *et al.* (2014) evaluated 69 coriander accessions from Pakistan, China, India and Iran. Results revealed that co-efficient of variation (CV %) was higher for number of basal leaves (74.26), largest basal leaf length (33.89), plant height (33.24) and number of days to stem elongation (22.42). Moderate variability was recorded for days to flower start (20.62) and 1000 seed weight (13.70). Investigation was carried on 64 coriander genotypes by Singh *et al.,* (2015) to identify the traits associated with seed yield and their attributes. Results revealed that seed yield per plant exhibited a positive and significant correlation with number of fruits per umbel but negative correlation with days to 50% flowering and days to 80% maturity. Seed yield per plant exhibited a positive and significant correlation with number of fruits per umbel but was negatively correlated with days to 50% flowering and 80% maturity, whereas number of fruits per umbellet expressed a positive significant correlation with number of fruits per umbel and 1000-seed weight.

2.3 Divergence (D^2) analysis

Genetic diversity is of fundamental importance in the continuity of a species as it provides the necessary adaptation to the prevailing biotic and abiotic environmental conditions and enables changes in the genetic composition to cope up with the changes in the environment.

Genetic association and distances were assessed by Singh *et al.* (2002) in a collection of 15 Indian accessions of coriander. The study revealed genetic distance in the material was substantial with the D2 values ranging from 37.4 (between the genotypes C-2 and DH-5) to 1309 (between the genotypes C-1 and RCr-20). The genotypes clubbed into 8 clusters. The results of D^2 values and cluster means permitted rational selection of 5-33 and C-1, RCr-41 and PD-1, potent genorypes with complementary characters in morphological fitness for yield and its associated traits, for effective cross hybridization programme. Singh *et al.* (2005) evaluated seventy germplasm lines of coriander to determine the genetic divergence. The 70 genotypes were grouped into 9 clusters depending upon the genetic architecture of genotypes and characters uniformity and confirmed by canonical analysis. Seventy percent of total genotypes (49/70) were grouped in 4 clusters (V, VI, VIII and IX), while apparent diversity was noticed for 30 percent genotypes (21/70) that diverged into 5 clusters (I, II, III, IV, and VII). The maximum inter cluster distance was between I and IV (96.20) followed by III and IV (91.13) and I and VII (87.15). The cluster VI was very unique having genotypes of high mean values for most of the component traits. Pedro (2006) concluded genetic characterization of 60 coriander accessions for phenological, morphological and two chemical traits. Results described significant differences among populations for all the phenotypic traits and correlations among the phenotypic (PD), geographical (GD) and genetic distances (MD), matrices were not significant, and dendrograms obtained from PD and MD showed incongruent patterns. Phenotypic groups described in the present study differed somewhat from previous infraspecific classifications these results may be related to coriander's relatively short history as a crop plant. Pedro *et al.* (2008) examined phenotypic diversity in coriander, euclidean distances from phenotypic (PD) data were estimated. These data were subjected to cluster analyses (CA) and principal components analyses (PCA), to reveal patterns among populations and to analyses for grouping patterns from PD. The results revealed significant variation attributed among subgroups and groups was very low (4–6%), while variation among populations within groups was intermediate (24–26%), and that within populations was large (69–70%), reflecting weak differentiation among subgroups and groups, which was confirmed by values for fixation indices.

Beemnet *et al.* (2011) studied the genetic divergence among 49 coriander accessions and noticed maximum genetic divergence for 1000 seed weight (15.67%) followed by basal leaf number (13.48%), plant height (10.29%), seeds per umbellet (9.81%) and umbel per plant (7.84%). Based on means of all characters, accessions in cluster III, VII and VIII could be regarded as useful sources of genes for yield and its component, and accessions from these clusters, therefore, could be used in improvement programmes to develop desirable types in coriander. Mengesha *et al.* (2011) studied the genetic divergence among 49 Ethiopian coriander (*Coriandrum sativum* L.) accessions using Mahalanobis' distance analysis based on 15 characters. The accessions were grouped into eight clusters. Cluster II and III were the largest each with 12 accessions, followed by clusters I and V each listing of seven accessions. Components, and the accessions from these clusters, therefore, could be used in improvement programmers to develop desirable types in coriander.

Miheretu (2013b) studied genetic divergence of 25 land races based on 8 characters assessed using cluster analysis and the accessions were grouped into five clusters. Cluster I was the largest consisting 19 accessions. High inter-cluster distance (47.42) was observed between cluster IV, cluster II and IV (47.33) and cluster I and IV (41.47), indicating the presence of substantial genetic diversity. Meena *et al.* (2014) studied the 24 varieties of coriander for diversity analysis. All varieties were grouped in four cluster that showed narrow genetics base of Indian varieties. Intra-cluster distance was highest in cluster III followed by cluster II, IV and I. The maximum inter-cluster distance was between clusters III and I are17.91 and 3.86 respectively. Among the 10 characters studied for genetic divergence, 50 % flowering contributed the maximum accounting for 49.64% of total divergence, followed by test weight 17.03%. The maximum divergence of these traits would be used in breeding programme for improvement in coriander.

Awas *et al.* (2016) Eighty one Ethiopian coriander genotypes were evaluated and data were collected on 21 traits. The 81 coriander genotypes were grouped in to eight clusters using Mahalanobis D^2 statistics. The largest cluster (II) and the smallest cluster (VIII), contains about 51.8% and 2.4% of studied genotypes respectively. Maximum and minimum intra cluster distance were observed in cluster II and VIII (D^2=7.48 and 1.31 respectively). Maximum inter cluster distance was observed between cluster VI and VIII (D^2=329.85) and the minimum distance was observed between cluster I and IV (D^2=19.02), suggesting the possibility of getting suitable genotypes for hybridization program among the genotypes.

2.4 Molecular characterization

To assess the genetic diversity and population structure the molecular markers are used as powerful tool, because they are independent of morphological growth and environmental effects. DNA based markers are superior to other markers because these are greater in number and are highly polymorphic to assay variation at the DNA level. The literature pertaining to this subject with respect to coriander is presented below.

Melo *et al.* (2011) evaluated the ten coriander genotypes (nine cultivars and one line) for studying genetic similarity by using 227 banded regions of ISSR molecular markers. The UBC 897 oligonucleotide generated the highest number of fragments (16), resulting in a higher polymorphism. The results indicated that the twenty-nine oligonucleotides chosen were satisfactory for detecting polymorphism. Based on the grouping analysis determined from the similarity data, there were two groups and two sub-groups. The calculated similarity for the genotypes varied from 52 to 75% (lowest similarity between Português and Verdão, at 52% and highest similarity between Português and Palmeira, at 75%). Pareek *et al.* (2011) used the random amplified polymorphic DNA markers for genetic divergence studies among 10 Indian varieties of Coriander. A total of 74 clear bands were generated, out of which 43.2% were polymorphic. The total number of markers varied from 6 to 13 with a mean of 9.25 markers per primer. The number of polymorphic markers for each primer varied from 1 to 11 with a mean of 4 polymorphic markers per primer. The amplified product size ranged from 370 to 44860 bp.

Pareek *et al.* (2012) studied the genetic variability in different genotypes of three medicinal plants, *i.e., Foeniculum vulgare*, *Coriandrum sativum* and *Verbesina encelioides* by using Random amplified polymorphic DNA (RAPD) markers. The highest polymorphism was observed in *V. encelioides* (73.66%), then in *F. vulgare* (50%) and lowest in *C. sativum*

(43.2%). The discrimination power of each locus was estimated by the PIC (Polymorphism Information Content) value. For *F. vulgare* it ranged from 0.081 to 0.281, for *C. sativum* 0.05 to 0.22 and for *V. encelioides* 0.18 to 0.416. Singh *et al.* (2013) evaluated sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) and random amplified polymorphic DNA (RAPD) separately as a tool for characterizing coriander varieties. A polymorphism of 71.4% was recorded among 20 varieties of coriander. The maximum dissimilarity value was shown by cultivar Sindhu. Twenty random primers were used for polymorphism studies of eighteen coriander varieties and these primers gave amplification and a total of 9 bands with an average of 4.5 bands per primer. The highest number of bands was generated by the primer OPC-3 and OPC-6 followed by OPC-2, OPC-7 and OPC-20 while the lowest number of band was produced by OPC-19. The variety GC-2 was highly diverse from other varieties. Al-Kordy *et al.* (2013) observed polymorphism by using five RAPD-PCR primers in three different coriander cultivars. A total of 33 fragments were delineated, 10 out of them were polymorphic. The genotype frequencies of RAPD-PCR variants were 55.56, 20, 25, 0 and 27.27 and the average of 30.30% polymorphism indicated the presence of low genetic diversity in the studied coriander cultivars. On the other hand, El-Nasr *et al.* (2013) used ISSR molecular markers for the study of genetic variability for seven characters in ten selected genotypes within three coriander cultivars. ISSR results with five primers revealed 26 amplified fragments and 12 of them were polymorphic (46%). The genetic distances of ISSR marker reveaed that the highest similarity was (71%) between the Russian and Selected cultivars. Similarity index was maximum between the Balady and Russian cultivars.

Tomar *et al.* (2014) used total 38 Randomly Amplified Polymorphic DNA (RAPD) markers, which yielded total 3721 fragments with average of 7.13 number of bands. The polymorphism with RAPD primers ranged from 38 to 100% with Jaccard’s similarity coefficient ranging from 88% to 56%. For Inter Simple Sequence Repeats (ISSR), the total 28 primers were used, which yielded 142 total fragments with average of 5.07 number of bands. The overall grouping pattern of cluster analysis clearly showed the variability among each genotype. Hora *et al.* (2016) reported polymorphism frequency of 42.91% and 55.66% in different varieties of fenugreek using RAPD and ISSR markers respectively. Based on the combined data of RAPD+ISSR marker system the maximum similarity index was observed for accessions from Mathura and RMT-143, whereas the minimum similarity index was observed for RMT-351 and RMT-303 (0.26).

CHAPTER-III

MATERIALS AND METHODS

The present investigation entitled “Genetic divergence studies in coriander (*Coriandrum sativum* L.)” was conducted at Research Farm of the Department of Vegetable Science, Chaudhary Charan Singh Haryana Agricultural University, Hisar, during winter season of 2014-15 and 2015-16 laboratory study was carried out in the Department of Molecular Biology, Biotechnology and Bioinformatics. The details of materials used and methods followed in this study are presented briefly here as under:

3.1 Experimental location

Hisar has semi-arid climate with cold winter and hot dry summer and is situated at 29°15’ North latitude, 75°72’ East longitude and at an elevation of 215.2 m above mean sea level. The rains received during July to September month is usually moderate to low and scanty.

3.2.1 Experimental material

One hundred germplasm lines of coriander evaluated during investigation were collected from different parts of the country *i.e*., Uttar Pradesh, Gujarat, Haryana and Rajasthan (Plate 1).

3.3 Experimental Details

Design : Randomized Block Design
Replications : Three
Spacing : Three meter single row & at raised a spacing of 50 cm x 20 cm

3.4 DUS characterization

During the course of experiment, the DUS characterization was done by using coriander crop standard descriptors and data was recorded for measurable traits on five plants selected randomly for every genotype in each replication. Observations were recorded for the following traits.

(i) Number of basal leaves

The number of basal leaves per plant was counted at 30 days after sowing and average recorded

(ii) Length of the longest basal leaf (cm)

Length of the longest basal leaves measured at 30 days after sowing and average recorded

(iii) Luster of longest basal leaf

The luster of longest basal leaves *viz.*, shiny and dull was recorded at 30 days after sowing.

Plate 1: GENERAL VIEW OF EXPERIMENTAL PLOT

(iv) Leaf margin of longest basal leaf

The leaf margins of longest basal leaves were recorded at 30 days after sowing as entire serrated and deeply serrated.

(v) Leaf colour of longest basal leaf

Based on visual observation of color of the longest basal leaves the genotypes were classified into dark green and green leafed at 30 days after sowing.

(vi) Stem pigmentation

The genotypes were classified for stem pigmentation into two categories as green and purple colored and recorded at 30 days after sowing

(vii) Stem pubescence

The germplasm was categorized into two groups based on visual observations recorded at 30 days after sowing for presence or absence of stem pubescence.

(viii) Streaks on stem

Based on visual observation recorded at 30 days after sowing the germplasm was categorized into two groups for presence or absence of steaks on stems.

(ix) Corolla colour

The corolla colour was recorded at 50 % flowering and germplasm lines were categorized for white, pink or purple colors.

(x) Nodal pigmentation

The germplasm was categorized into two groups based on visual observations scored at 30 days after sowing for presence or absence of nodal pigmentations.

(xi) Growth habit

The growth habit of the plants was observed visually on the basis of plant spread at matured stage and 100 germplasm lines were categorized into three groups as erect, semi-erect and spreading types.

(xii) Primary branches per plant

The number of branches that arise from the main stem was counted on five randomly selected plants at maturity and averaged.

(xiii) Secondary branches per plant

The number of branches that arise from the primary branches was counted on five randomly selected plants and average recorded.

(xiv) Plant height (cm)

Plant height in five randomly selected plants was measured in centimeters from ground level to the tip of plants at maturity and average worked out.

(xv) Umbels per plant

Total number of umbels per plant was recorded at maturity on five randomly selected plants.

(xvi) Umbellets per umbel

Five umbels from each of the selected five plants were observed and the umbellets in each umbel were counted and the average was recorded as number of umbellets per umbel.

(xvii) Seeds per umbellate

The number of seeds per umbellet was counted in umbellets collected from five randomly selected plants and averaged.

(xviii) Number of seeds per umbel

The number of seeds per umbel was counted in umbels collected from five randomly selected plants and averaged.

(xix) Test weight (g)

One thousand mature dried seeds from each plot were counted and weighed, the average weight (g) was recorded as test weight.

(xx) Seed yield per plant (g)

All the umbels from five selected plants of each genotype were harvested, dried under shade and threshed. The average weight of cleaned seeds from five plants was recorded as seed yield per plant in grams.

(xxi) Seed colour

Seed color was observed visually and recorded at fully matured stage. The germplasm was categorized for seed colour into light brown and brown.

(xxii) Seed shape

Seed shape was observed visually on dry seed and germplasm was categorized for seed shape into round, slightly round and oval.

(xxiii) Seed size

Seed size was observed visually and recorded at fully mature stage. The germplasm lines were categorized for seed size into large, medium and small.

(xxiv) Seed ridge

Seed ridges were observed visually and recorded at fully matured stage. All 100 germplasm lines were categorized for seed ridge into having prominent and non-prominent.

3.5 Statistical analysis

(i) Analysis of variance (ANOVA)

The analysis of variance was carried out as per the procedure given by Panse and Sukhatme (1967) using the mean values of random by selected plants in each replication from all treatments to find out the significance of treatment effects. The critical difference (CD) was worked out at 5% level of significance. The model of analysis of variance table adopted is given below.

Source of variation	**Degree of freedom**	**Mean sum of square (MSS)**	**F-ratio**
Replication	r –1	MSSr	MSSt / MSSe
Treatment	k – 1	MSSt	
Error	(k-1) (r-1)	MSSe	
Total	kr – 1		

(ii) Variability estimates

(a) Mean: Mean was calculated using the formula

$$\text{Mean} = \frac{\text{Total of recorded values}}{\text{Number of values}}$$

(b) Range

The range was recorded as difference between lowest and highest values of the observations.

(c) GCV and PCV

The genotypic and phenotypic coefficients of variation were computed according to the formula given by Burton and Devane (1953).

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

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

The PCV and GCV were classified into following three categories as suggested by Sivasubramanian and Menon (1973).

Low: <10%. Moderate: 10-20 %. High: > 20%.

(d) Heritability (h^2)

Heritability (h^2) in broad sense was calculated according to the method suggested by Hanson *et al*. (1956).

$$h^2 = \frac{V_G}{V_P} \times 100$$

Where,

V_G and V_P are the genotypic and phenotypic variances, respectively.

Heritability in cultivated plants could be placed in the following categories as suggested by Robinson *et al*. (1966).

Low: 0-30%. Moderate: 30-60 %. High: >60%.

(e) Genetic advance (GA)

Genetic advance refers to the expected genetic gain or improvement in the next generation by selecting superior individuals under certain amount of selection pressure. From the heritability estimates the genetic advance was estimated by the following formula given by Burton (1952).

$$GA = K.\ h^2 (b).\ \sigma_p$$

Where,

GA = Expected genetic advance
K = Selection differential, the value of which is 2.06 at 5% selection intensity
σ_p = Phenotypic standard deviation
$h^2 (b)$ = Heritability in broad sense

(f) Genetic advance as percent of mean (GAM)

The formula given by Johnson *et al*. (1955) was used to compute genetic advance.

Genetic advance = $h^2 x\ k\ x \sum p$

Where,

h^2 = Heritability
k = Standard selection differential which is 2.06 at 5% selection intensity
$\sum p$ = Phenotypic standard deviation

$$GAM = \frac{\text{Genetic advance}}{\text{Mean}} \times 100$$

The Genetic advance as per cent of mean was categorized into following groups as suggested by Johnson *et al*. (1955).

Low: <10%. Moderate: 10-20%. High: >20%.

(iii) Correlation analysis

Phenotypic 'r (p)' and genotypic 'r (g)' correlation coefficients for all possible pairs of characters were calculated from the variances and covariance according to Johnson *et al.* (1955).

The genotypic correlation was estimated as $r (g) = \sigma x y (g)/[\sigma x (g) X \sigma y (g)]$.

Where,

$\sigma x y (g)$ = Genotypic covariance between characters x and y

σ x (g) = Genotypic variance of character x

σ^2y (g) = Genotypic variance of character y

The phenotypic correlation was measured by r(p) = σ x y (p)/[σ x (p) × σ y (p)]

Where,

σ x y (p) = Phenotypic covariance between characters x and y

σ^2 x (p) = Phenotypic variance of character x

σ^2 y (p) = Phenotypic variance of character y

(iv) Path co-efficient analysis

Path co-efficient analysis suggested by Wright (1921) and Dewey and Lu (1959) was carried out to know the direct and indirect effects of the morphological traits on plant yield. The following set of simultaneous equations was formed and solved for estimating various direct and indirect effects.

r_{1y} $= a + r_{12}b + r_{13}c + \ldots\ldots\ldots\ldots\ldots\ldots\ldots + r_{1Ii}$

r_{2y} $= a + r_{21}a + b + r_{23}c + \ldots\ldots\ldots\ldots\ldots\ldots + r_{2Ii}$

r_{3y} $= r_{31}a + r_{32}b + c + \ldots\ldots\ldots\ldots\ldots\ldots\ldots + r_{3Ii}$

r_{1y} $= r_{11}a + r_{12}b + r_{13}c + \ldots\ldots\ldots\ldots\ldots\ldots + I$

Where,

r_{1y} to 1_{1y} = Co-efficient of correlation between causal factors 1 to I with dependent characters y

r_{12} to r_{II} = Co-efficient of correlation among causal factors

a, b, c…….i = Direct effects of characters 'a' to 'i' on the dependent character 'y'

Residual effect (R) was computed as follows.

$$\text{Residual effect (R)} = 1 - \sqrt{a^2 + b^2 + c^2 + \ldots\ldots\ldots i^2 + 2abr_{12} + 2acr_{13} + \ldots.}$$

(v) Estimation of genetic divergence using Mahalanobis's generalized distances (D^2)

The genetic divergence between genotypes was estimated using D^2 statistic technique of Mahalanobis (1936).

D^2 value between ith and jth genotypes for 'p' characters was calculated as:

$$D^2_{ij} = \sum_{t=1}^{P} (\overline{Y}_{it} - \overline{Y}_{jt})^2$$

Where,

Y_{it} = Uncorrelated mean values of i^{th} genotype for 't' characters

Y_{jt} = Uncorrelated mean values of j^{th} genotype for 't' characters and

D^2_{ij} = D^2 between i^{th} and j^{th} genotype

(vi) Grouping of genotypes into various clusters

Grouping of genotypes into different clusters was done using Tocher's method as described by Rao (1952). The criterion used in clustering by this method was that any two genotypes belonging to the same cluster should show at least on an average smaller D^2 value among themselves than those belonging to different clusters.

The first step in grouping the genotypes into different clusters was to arrange the genotypes in the order of their relative distance from each other. For this purpose, D^2 values of all combinations of each genotype were arranged in increasing order of their magnitude in a tabular form as described by Singh and Chaudhary (1977). To start with the two genotypes having the smallest distance from each other were considered first to which a third population having the smallest average D^2 value from the first two genotypes was added. Similarly, next nearest fourth genotype was considered and this procedure was continued till a certain stage where after adding a particular genotype, there was abrupt increase in the average D^2 value. Such population was not considered for including in that cluster. The genotypes of group of the first cluster were then omitted and the rest was treated in a similar way. This process was continued till all the genotypes were included into one or the other clusters.

(vii) Average intra cluster distance

For the measurement of intra cluster distance, the formula used was $\Sigma D^2_i / n$.

Where,

ΣD^2_i = Sum of distances between all possible combinations of the genotypes (n) included in respective clusters

n = Number of genotypes included in respective cluster

(viii) Average inter-cluster distance

Clusters were taken one by one and their distance from other clusters was calculated. The distance between two clusters was the sum of D^2 values between the members of one cluster to each of the member of other cluster divided by the product of number of genotypes in both the clusters under consideration.

The square root of the average D^2 value gave the genetic distance 'D' between the clusters. Based on D values (inter cluster distance) the scale given by Rao (1952) for rating of the distance was adopted and the cluster diagram was prepared.

$$\text{Average inter cluster distance} = \frac{D^2}{n_1 \times n_2}$$

Where,

n_1 and n_2 are the number of genotypes in cluster 1 and cluster 2, respectively.

(ix) Cluster mean

The cluster mean was calculated by summing the mean values of all the accessions belonging to a particular cluster for each trait, which was then divided by number of accessions and the value obtained thus represents the cluster mean for concerned trait.

3.6 Molecular characterization

3.6.1 Plant samples

Among the 100 coriander genotypes evaluated for morphological traits in previous season the 48 genotypes which performed best were selected for molecular characterization. The seeds of those 48 genotypes were sown in pro trays under polyhouse. Young leaves of seedlings were collected for DNA extraction. List of 48 genotypes used for molecular characterization is as follows:

1. JCR-390
2. RD-120
3. LCC-164
4. RD-391
5. RD-421
6. DH-5
7. DH-36
8. DH-228
9. RD-394
10. DH-246
11. RD-387
12. LCC-168
13. DH-318
14. DH-352
15. DH-352-1
16. NDC-38
17. NDC-31
18. JCR-380
19. DH-261
20. DH-268
21. NDC-82
22. JCR-391
23. JCR-406
24. JCR-389
25. DH-275
26. DH-276
27. DH-278
28. DH-279
29. DH-280
30. DH-281
31. RD-414
32. DH-283
33. CS-63
34. CS-60
35. CS-62
36. CS-64
37. RD-424
38. LCC-193
39. COR-38
40. COR-40
41. LCC-174
42. LCC-191
43. JCR-407
44. COR-42
45. JCR-405
46. COR-44
47. JCR-379
48. NDC-68

3.6.2 Genomic DNA isolation

Genomic DNA was isolated from young leaves of 48 coriander genotypes following CTAB (Cetyltrimethyl ammonium bromide) extraction method as given by Murray and Thompson (1980) and modified by Saghai-Maroof *et al.* (1984). The extraction method is as follows:

i. Leaf samples from 2-3 week old seedlings were taken and ground to fine powder using liquid nitrogen in a sterile pestle and mortar.

ii. Approximately two gram of the ground leaf tissue powder was transferred into a miniprep centrifuge tube in which 800 µl CTAB buffer was added earlier and dissolve by tilting it slowly.

iii. Incubation was done for 45 minutes to one hour at 65^0 C in water bath. The tubes were tilted in every 15 minutes.

iv. After incubation, samples were brought to room temperature and Chloroform :Iso amyl alcohol (24:1) was added equal to the amount of solution.

v. Mixing of the contents was done by inverting tubes.

vi. Tubes were centrifuged at 10,000 rpm for 10 minutes.

vii. Collected upper aqueous layer into fresh tubes.

viii. Chloroform: Iso-amyl alcohol (24:1) was added equal to aqueous solution and centrifuged at 8000 rpm for 10 minutes.

ix. Collected upper aqueous layer into autoclaved fresh tubes. Added equal amount of chilled Isopropanol and incubated overnight at -20^0 C.

x. Centrifugation was done at 8000 rpm for 10 minutes, which make pellets. Throwed away the remaining solution except pellet.

xi. 70 % ethanol was added for washing and centrifuged at 8000 rpm for 3 minutes and removed supernatant. Kept overnight for drying.

xii. 20-100 µl of T. E. buffer was added depending on quantity of DNA for dissolving DNA and samples were stored at -20^0 C till further use.

xiii. RNase treatment was given to DNA by adding 50 µl of RNase A.

3.6.3 Qualitative and quantitative estimation of DNA

The quality and quantity of isolated genomic DNA was estimated by UV Spectrophotometer (A260/A280 absorbance) and the DNA was also tested by submerged horizontal agarose (0.8%) gel electrophoresis.

3.6.4 Polymerase chain reaction (PCR) amplification

PCR amplification was carried out using touchdown Q-thermo cycler. For both RAPD and ISSR PCR reaction conditions followed were same and the protocol is given below. The RAPD and ISSR PCR reactions were carried out in 23.5 µl of reaction mixture containing 13.5 µl of sterile distilled water, 2.5 µl (10 x colorless buffer) reaction buffer, 2 µl dNTP (500 µl dNTP of concentation10mM + 500 µl of sterile distilled water), 2 µl of Mgcl$_2$ (25Mm), 2 µl of primer (10 µl primer + 90 µl of nuclear free water), 1 µl template DNA and 0.5 µl of Taq DNA polymerase (5U/µl). These were added into PCR tube in same sequence as above.

The following protocols were used for PCR amplification:

Initial denaturation : 94^0 C for 4 minutes
Denaturation : 94^0 C for 1 minutes
Annealing : Recommended for primer
Extension : 72^0 C for 2 minutes
Final extension : 72^0 C for 8 minutes

36 cycles

Table 1: RAPD primers used in present investigation

S. No.	Primer code	Primer sequence	S. No.	Primer code	Primer sequence
1	OPA-01	CAGGCCCTTC	20	OPG-05	CTGAGACGGA
2	OPA-02	TGCCGAGCTG	21	OPH-04	GGAAGTCGCC
3	OPA-03	AGTCAGCCAC	22	OPI-02	GGAGGAGAGG
4	OPA-05	AGGGGTCTTG	23	OPJ-02	CCCGTTGGGA
5	OPA-07	GAAACGGGTG	24	OPK-02	GTCTCCGCAA
6	OPA-08	GTGACGTAGG	25	OPK-05	TCTGTCGAGG
7	OPA-10	GTGATCGCAG	26	OPK-06	CACCTTTCCC
8	OPB-05	TGCGCCCTTC	27	OPL-08	AGCAGGTGGA
9	OPB-06	TGCTCTGCCC	28	OPL-12	GGGCGGTACT
10	OPB-08	GTCCACACGG	29	OPM-02	ACAACGCCTC
11	OPD-01	ACCGCGAAGG	30	OPM-03	GGGGGATGAG
12	OPD-03	GTCGCCGTCA	31	OPM-07	CCGTGACTCA
13	OPD-05	TGAGCGGACA	32	OPN-02	ACCAGGGGCA

14	OPE-02	GGTGCGGGAA	33	OPO-03	CTGTTGCTAC
15	OPE-03	CCAGATGCAC	34	OPO-08	CCTCCAGTGT
16	OPE-05	TCAGGGAGGT	35	OPO-14	AGCATGGCTC
17	OPF-04	GGTGATCAGG	36	OPP-07	GTCCATGCCA
18	OPF-07	CCGATATCCC	37	OPR-05	GACCTAGTGG
19	OPG-02	GGCACTGAGG	38	OPR-10	CCATTCCCCA

Table 2: IISR primers used in present investigation

Sl No.	PRIMER NAME	SEQUENCE	Length
1	ISSR1	GTGTGTGTGTGTGTAT	16
2	ISSR2	GGAGAGGAGAGGAGA	15
3	ISSR3	GAGAGAGAGAGAGAGAGAAT	20
4	ISSR4	CACACACACACACACAA	17
5	ISSR5	ACACACACACACACACG	17
6	ISSR6	AGAGAGAGAGAGAGAGT	17
7	ISSR7	GAGAGAGAGAGAGAGAT	17
8	ISSR8	ATGATGATGATGATGATG	18
9	ISSR9	CACACACACACACACAA	17
10	ISSR10	CACACACACACACACAG	17
11	ISSR11	AGAGTTGGTAGCTCTTGA	18
12	ISSR12	ATATATATATATATATYC	18
13	ISSR13	ATATATATATATATATYG	18
14	ISSR14	AGAGAGAGAGAGAGAGYT	18
15	ISSR15	AGAGAGAGAGAGAGAGYC	18
16	ISSR16	AGAGAGAGAGAGAGAGYA	18
17	ISSR17	TATATATATATATATART	18
18	ISSR18	TATATATATATATATARC	18
19	ISSR19	TATATATATATATATARG	18
20	ISSR20	GAGAGAGAGAGAGAGAYT	18
21	ISSR21	GAGAGAGAGAGAGAGAYC	18
22	ISSR22	GAGAGAGAGAGAGAGAYG	18
23	ISSR23	CTCTCTCTCTCTCTCTRA	18
24	ISSR24	CTCTCTCTCTCTCTCTRC	18
25	ISSR25	CTCTCTCTCTCTCTCTRG	18
26	ISSR26	CACACACACACACACART	18
27	ISSR27	CACACACACACACACARC	18
28	ISSR28	CACACACACACACACARG	18

3.6.5 Agarose gel electrophoresis

Amplified DNA fragments were resolved by submerged horizontal agarose gel electrophoresis in 1.5 % (w/v) agarose gel (for the PCR products of RAPD and ISSR markers) and visualized by staining with ethidium bromide. Agarose solution was prepared in 1X TBE and ethidium bromide (10mg/ml) was added in the gel at a concentration of 3 µl per 100 ml of gel and then mixed gently. It was poured in gel casting tray with appropriate comb with required well number and size. PCR products were mixed with loading dye, mixed and loaded into wells. The gel was run at voltage of 100 watts for 1 hour and is seen under UV light for presence of bands. And photo was taken in gel documentation system.

3.6.6 Allele scoring

RAPD and ISSR amplification profiles were scored visually, based on presence (taken as 1) or absence (taken as 0) of bands for each genotype. Only clear and unambiguous bands were scored. The sizes of amplified bands were determined based on its migration relative to standard molecular weight markers.

3.6.7 Estimation of molecular diversity

i) Polymorphism percentage

Polymorphism percentage of each primer is calculated by using formula given below

$$\text{Polymorphism (\%)} = \frac{B_P}{B_P + B_m} \times 100$$

Where,

B_P = number of polymorphic bands scored by a primer

B_m = number of monomorphic and polymorphic bands scored by a primer

ii) Cluster analysis

The scored band data was subjected to statistical analysis using the computer programme NTSYS (version 2.02). The resultant similarity matrix was used to generate a tree by UPGMA (Unweighted Pair Group Method with Arithmetical average). Dendrogram was constructed by using distance matrix in SAHN sub-programme of NTSYS-pc software (Numerical Taxonomy and Multivariate Analysis System Programme, Rohlf, 2000) by the Unweighted Pair-Group Method with Arithmetic Average (UPGMA) algorithm.

CHAPTER-IV

RESULTS

In this chapter results of the experiment conducted on coriander genotypes are compiled in appropriate tables. The data of different parameters were analyzed statistically using randomized block design. Results of the present investigation as shown in various tables have been interpreted and presented as under:

4.1 DUS characterization

A. Plant characters

On the basis of observations recorded for various morphological characters. All the total 113 coriander lines were characterized and categorized in different classes. Based on leaf luster of the longest basal leaf recorded at 30 days after sowing the 113 genotypes were categorized as having shiny or dull leaves (Table 3). Among these 68 lines were shiny and 45 as dull. The leaf margin of longest basal leaf was also recorded at 30 days after sowing (Plate 2) and 82 coriander genotypes were categorized as having serrated and 31deeply serrated basal leaves (Table 4).

Based on visual observation regarding leaf color of the longest basal leaf, the genotypes were classified with dark green and green leaves (Plate 3). Amongst these 113 lines, 76 were marked green and remaining 37 were identified as dark green (Table 5). The genotypes were classified for stem pigmentation into two categories as green and purple as recorded at 30 days after sowing (Table 6). Among the 113 lines observed, the pigmentation was present in 31 lines and absent in remaining 82 lines (Plate 4). The germplasm was categorized into two groups based on the observation recorded at 30 days after sowing for the presence or absence of stem pubescence. Pubescence was found present in all entries investigated (Table 7).

The germplasm comprising 113 coriander genotypes was categorized into two groups based on visual observation for the presence or absence of steaks on stems (Table 8). All the 113 entries were having streaks on stem and no one was free of streaks on stems (Plate 5). The corolla colour of flowers in all entries of coriander was recorded at 50 % flowering (Plate 6). The germplasm was categorized into 93 lines with white corolla, 20 lines with pink corolla and none of the lines bear purple corolla colour (Table 9).

Based on visual observations for presence or absence of stem/leaf nodal pigmentation the germplasm was categorized into two groups and the observations recorded at 30 days after sowing revealed that 59 lines were having pigmentation and it was absent in 54 lines (Table 10). Growth habit of the plants was observed visually at matured stage and on the basis of plant structure and spread (Plate 7) 113 germplasm lines were categorized into three groups where 30 lines were erect, 60 lines semi-erect and 23 lines spreading types (Table 11).

Table 3: Characterization of coriander germplasm on the basis of leaf luster

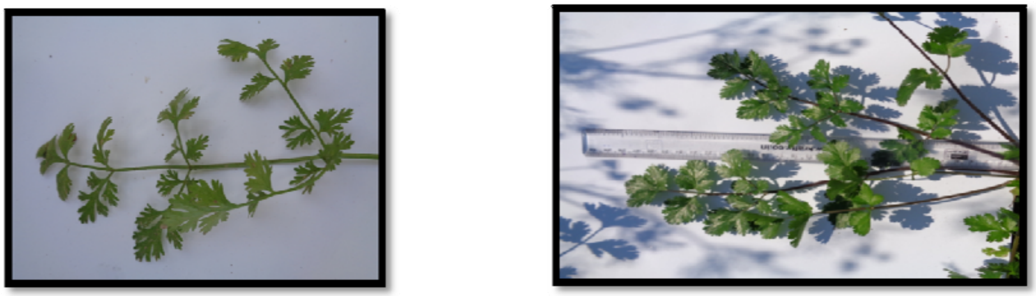
Leaf luster	Number of entries	Genotypes categorized
Dull	45	DH-36, DH-228, DH-246, DH-318, DH-352, DH-261, DH-276, DH-283, COR-36, COR-37, COR-40, COR-42, COR-43, COR-44, COR-49, COR-50, COR-54, COR-56, CS-63, CS-64, CS-65, CS-67, CS-69, JCR-401, LCC-193, LCC-197, LCC-193, LCC-197, LCC-231, LCC-232, LCC-244, LCC-250, NDC-1, NDC-3, NDC-4, NDC-10, NDC-90, NDC-100, NDC-109, NDC-111, VDVIGL-26, VDVIGL-40, VDVIGL-103, GC-1 and GC-2
Shiny	68	DH-5, DH-352-1, DH-268, DH-275, DH-278, DH-279, DH-280, DH-281, COR-53, COR-45, COR-53, COR-55, CS-60, CS-61, CS-62, CS-66, CS-70, JCR-380, JCR-389, JCR-390, JCR-391, JCR-404, JCR-405, JCR4-06, JCR-407, LCC-144, LCC-164, LCC-166, LCC-168, LCC-170, LCC-174, LCC-191, LCC-226, LCC-229, LCC-230, LCC-234, LCC-241, LCC-247, NDC-14, NDC-31, NDC-38, NDC-68, NDC-80, NDC-82, NDC-94, NDC-106, NDC-110, NDC-118, NDC-119, NDC-120, RD-120, RD-387, RD-391, RD-394, RD-400, RD-409, RD-410, RD-414, RD-422, RD-424, VDVIGL-37, VDVIGL-49, VDVIGL-50, VDVIGL-74, VDVIGL-117, VDVIGL-127, AD-1 and H. Anand

Table 4: Categorization of coriander germplasm on the basis of basal leaf margin

Leaf margin	Number of entries	Genotypes categorized
Serrated	82	DH-5, DH-228, DH-246, DH-318, DH-352, DH-261, DH-276, DH-283, COR-36, COR-37, COR-38, COR-39, COR-40, COR- 42, COR-45, COR-49, COR-50, COR-53, COR-54, COR-55, CS- 60, CS- 61, CS- 62, CS-63, CS -64, CS- 65, CS- 66, CS-67, CS- 69, CS-70, JCR-379, JCR-380, JCR-389, JCR-390, JCR-391, JCR-401, JCR-404, JCR-405, JCR-406, JCR-407, LCC-144, LCC-164, LCC-166, LCC-168, LCC-170, LCC-174, LCC-191, LCC-193, LCC-197, LCC- 244, LCC- 247, LCC-250, LCC-244, LCC-247, LCC-250, NDC-4, NDC-10, NDC-14, NDC-31, NDC-68, NDC-80, NDC-82, NDC-90, NDC-94, NDC-100, NDC-106, NDC-110, NDC-111, NDC-118, RD-391, RD- 409, RD-410, RD -414, VDVIGL-26, VDVIGL- 40, VDVIGL-49, VDVIGL-74, VDVIGL-103, VDVIGL-117, VDVIGL-127, GC-1, GC-2, AD-1and H. Anand
Deeply serrated	31	DH-36, DH-352-1, DH-268, DH-275, DH-278, DH-279, DH-280, DH-281, COR-43, COR-44, COR-56, LCC- 226, LCC-229, LCC- 230, LCC-231, LCC-232, LCC- 234, LCC-241, NDC-3, NDC-38, NDC-109, NDC-119, NDC-120, RD-120, RD-387, RD-394, RD-400, RD-422, RD-424, VDVIGL-37 and VDVIGL-50

Serrated **Deeply serrated**

Plate 2: Leaf margin



Green **Dark green**

Plate 3. Leaf color

Table 5: Categorization of coriander germplasm on the basis of basal leaf color

Leaf color	Number of entries	Genotypes categorized
Green	76	DH-5, DH-36, DH-246, DH-318, DH-352, DH-261, DH-268, DH-275, DH-261, DH-268, DH-275, COR-36, COR-38, COR-42, COR-43, COR-49, COR-50, COR-54, COR-55, COR-56, CS-61, CS-63, CS-65, CS-66, CS-67, CS-69, CS-70, JCR-379, JCR-380, JCR-389, JCR-390, JCR-401, JCR-404, JCR-406, JCR-407, LCC-144, LCC-164, LCC-166, LCC-168, LCC-170, LCC-174, LCC-191, LCC-193, LCC-197, LCC-226, LCC-229, LCC-230, LCC-231, LCC-232, LCC-234, LCC- 241, LCC-247, LCC-250, NDC-1, NDC-3, NDC-4, NDC-10, NDC-14, NDC-31, NDC-38, NDC-68, NDC-80, NDC-90, NDC-100, NDC-106, NDC-109, NDC-110, NDC-119, RD-391, RD-409, RD-410, RD-414, VDVIGL-40, VDVIGL-50, VDVIGL-103 and VDVIGL-26
Dark Green	37	DH-228, DH-352-1, DH-276, DH-281, DH-283, COR-37, COR-39, COR-40, COR-44, COR-45, COR-53, CS-60, CS-62, CS-64, JCR-391, JCR-405, LCC-244, NDC-82, NDC-94, NDC-111, NDC-118, NDC-120, RD-120, RD-387, RD-394, RD-400, RD-422, RD-424, VDVIGL-37, VDVIGL-49, VDVIGL-74, VDVIGL-117, VDVIGL-127, GC-1, GC-2, AD-1 and H. Anand

Table 6: Categorization of coriander germplasm on the basis of stem pigmentation

Stem pigmentation	Number of entries	Genotypes categorized
Absent	82	DH-5, DH-228, DH-246, DH-318, DH-352, DH-352-1, DH-261, DH-268, DH-275, DH-276, DH-278, DH-279, DH-280, DH-281, DH-283, COR-36, COR-37, COR-38, COR-39, COR-40, COR-42, COR-43, CS-62, COR-45, COR-50, COR-54, COR-55, CS-64, CS-67, CS-69, JCR-389, JCR-391, JCR-401, JCR-404, JCR-405, JCR-406, JCR-407, LCC-144, LCC-164, LCC-166, LCC-168, LCC-193, LCC-197, LCC-234, LCC-244, LCC-250, NDC-1, NDC-3, NDC-10, NDC-14, NDC-31, NDC-68, NDC-80, NDC-82, NDC-90, NDC-100, NDC-106, NDC-110, NDC-111, NDC-119, RD-120, RD-387, RD-391, RD-394, RD-400, RD-409, RD-410, RD-414, RD-422, RD-424, VDVIGL-26, VDVIGL-37, VDVIGL-40, VDVIGL-49, VDVIGL-50, VDVIGL-103, VDVIGL-117, VDVIGL-127, GC-1 and GC-2
Present	31	DH-36, AD-1, H. Anand, COR-44, COR-44, COR-49, COR-53, COR-56, CS-60, CS-61, CS-63, CS-65, CS-66, LCC-170, LCC-174, LCC-191, LCC-226, LCC-229, LCC-230, LCC-231, LCC-232, LCC-241, LCC-247, NDC-4, NDC-38, NDC-94, NDC-109, NDC-118, NDC-120 and VDVIGL-74

Table 7: Categorization of coriander germplasm on the basis of stem pubescence

Stem pubescence	Number of entries	Genotypes categorized
Absent	113	DH-5, DH-36, DH-228, DH-246, DH-318, DH-352, DH-352-1, DH-261, DH-268, DH-275, DH-276, DH-278, DH-279, DH-280, DH-281, DH-283, COR-36, COR-37, COR-38, COR-39, COR-40, COR-42, COR-43, COR-44, COR-45, COR-49, COR-50, COR-53, COR-54, COR-55, COR-56, CS-60, CS-61, CS-62, CS-63, CS-64, CS-65, CS-66, CS-67, CS-69, CS-70, JCR-379, JCR-380, JCR-389, JCR-390, JCR-391, JCR-401, JCR-404, JCR-405, JCR-406, JCR-407, LCC-144, LCC-164, LCC-166, LCC-168, LCC-170, LCC-174, LCC-191, LCC-193, LCC-197, LCC-226, LCC-229, LCC-230, LCC-231, LCC-232, LCC-234, LCC-241, LCC-244, LCC-247, LCC-250, NDC-1, NDC-3, NDC-4, NDC-10, NDC-14, NDC-31, NDC-38, NDC-68, NDC-80, NDC-82, NDC-90, NDC-94, NDC-100, NDC-106, NDC-109, NDC-110, NDC-111, NDC-118, NDC-119, NDC-120, RD-120, RD-387, RD-391, RD-394, RD-400, RD-409, RD-410, RD-414, RD-422, RD-424, VDVIGL-26, VDVIGL-37, VDVIGL-40, VDVIGL-49, VDVIGL-50, VDVIGL-74, VDVIGL-103, VDVIGL-117, VDVIGL-127, GC-1, GC-2, AD-1and H. Anand
Present	-	-

Table 8: Categorization of coriander germplasm on the basis of streaks on stem

Streaks on stem	Number of entries	Genotypes categorized
Absent	-	-
Present	113	DH-5, DH-36, DH-228, DH-246, DH-318, DH-352, DH-352-1, DH-261, DH-268, DH-275, DH-276, DH-278, DH-279, DH-280, DH-281, DH-283, COR-36, COR-37, COR-38, COR-39, COR-40, COR-42, COR-43, COR-44, COR-45, COR-49, COR-50, COR-53, COR-54, COR-55, COR-56, CS-60, CS-61, CS-62, CS-63, CS-64, CS-65, CS-66, CS-67, CS-69, CS-70, JCR-379, JCR-380, JCR-389, JCR-390, JCR-391, JCR-401, JCR-404, JCR-405, JCR-406, JCR-407, LCC-144, LCC-164, LCC-166, LCC-168, LCC-170, LCC-174, LCC-191, LCC-193, LCC-197, LCC-226, LCC-229, LCC-230, LCC-231, LCC-232, LCC-234, LCC-241, LCC-244, LCC-247, LCC-250, NDC-1, NDC-3, NDC-4, NDC-10, NDC-14, NDC-31, NDC-38, NDC-68, NDC-80, NDC-82, NDC-90, NDC-94, NDC-100, NDC-106, NDC-109, NDC-110, NDC-111, NDC-118, NDC-119, NDC-120, RD-120, RD-387, RD-391, RD-394, RD-400, RD-409, RD-410, RD-414, RD-422, RD-424, VDVIGL-26, VDVIGL-37, VDVIGL-40, VDVIGL-49, VDVIGL-50, VDVIGL-74, VDVIGL-103, VDVIGL-117, VDVIGL-127, GC-1, GC-2, AD-1and H. Anand

Present **Absent**

Plate 4. Stem pigmentation

Plate 5. Streaks on stem

Table 9: Categorization of coriander germplasm on the basis of corolla color

Corolla color	Number of entries	Genotypes categorized
White	93	DH-5, DH-36, DH-228, DH-318, DH-352, DH-352-1, DH-268, DH-275, DH-278, DH-279, COR-36, COR-37, COR-38, COR-39, COR-40, COR-43, COR-44, COR-45, COR-49, COR-50, COR-53, COR-55, COR-56, CS-60, CS-62, CS-63, CS-64, CS-67, CS-69, CS-67, CS-69, JCR-379, JCR-380, JCR-389, JCR-390, JCR-391, JCR-401, JCR-404, JCR-405, JCR-406, JCR-407, LCC-144, LCC-164, LCC-166, LCC-168, LCC-170, LCC-174, LCC-191, LCC-193, LCC-197, LCC-226, LCC-229, LCC-230, LCC-231, LCC-232, LCC-234, LCC-241, LCC-247, LCC-250, NDC-1, NDC-3, NDC-4, NDC-10, NDC-14, NDC-31, NDC-38, NDC-68, NDC-80, NDC-90, NDC-94, NDC-106, NDC-109, NDC-111, NDC-118, NDC-119, NDC-120, RD-120, RD-387, RD-391, RD-394, RD-400, RD-409, RD-410, RD-414, RD-422, RD-424, VDVIGL-26, VDVIGL-37, VDVIGL-49, VDVIGL-50, VDVIGL-74, VDVIGL-103, VDVIGL-117, AD-1and H. Anand
Pink	20	DH-246, DH-261, DH-276, DH-280, DH-281, DH-283, COR-42, COR-54, CS-61, CS-65, CS-66, CS-70, LCC-244, NDC-82, NDC-100, NDC-110, VDVIGL-40, VDVIGL-127, GC-1and GC-2

Table 10: Categorization of coriander germplasm on the basis of nodal pigmentation

Nodal pigmentation	Number of entries	Genotypes categorized
Present	59	DH-36, DH-228, DH-246, DH-261, DH-281, COR-36, COR-37, COR-39, COR-40, COR-42, COR-44, COR-49, COR-53, COR-54, COR-56, CS-61, CS-62, CS-63, CS-65, CS-66, CS-70, JCR-379, JCR-380, JCR-390, LCC-144, LCC-164, LCC-166, LCC-168, LCC-170, LCC-174, LCC-191, LCC-193, LCC-197, LCC-226, LCC-229, LCC-230, LCC-231, LCC-232, LCC-234, LCC-241, LCC-247, LCC-250, NDC-4, NDC-82, NDC-68, NDC-94, NDC-100, NDC-109, NDC-110, NDC -111, NDC-118, NDC-119, NDC-120, VDVIGL-49, VDVIGL-50, VDVIGL-74, VDVIGL-127, AD-1and H. Anand
Absent	54	DH-5, DH-318, DH-352, DH-352-1, DH-268, DH-275, DH-276, DH-278, DH-279, DH-280, DH-283, COR-38, COR-43, COR-50, COR-45, COR-55, CS-60, CS-64, CS-67, CS-69, JCR-389, JCR-391, JCR-401, JCR-404, JCR-405, JCR-406, JCR-407, LCC-244, NDC-1, NDC-3, NDC-10, NDC-14, NDC-31, NDC-38, NDC-80, NDC-90, NDC-106, RD-120, RD-387, RD-391, RD-394, RD-400, RD-409, RD-410, RD- 414, RD-422, RD-424, VDVIGL-26, VDVIGL-37, VDVIGL-40, VDVIGL-103, VDVIGL-117, GC-1and GC-2

Table 11: Categorization of coriander germplasm on the basis of growth habit

Growth habit	Number of entries	Genotypes categorized
Erect	30	DH-5, DH-228, DH-261, DH-280, COR-36, COR-38, COR-45, COR-54, COR-55, CS-62, CS-64, CS-66, CS-67, CS-69, CS-70, LCC-170, LCC-174, LCC-191, LCC-229, LCC-230, LCC-244, NDC-10, NDC-100, NDC-106, NDC-110, NDC-111, NDC-118, VDVIGL-49, GC-1and GC-2
Semi erect	60	DH-36, DH-246, DH-318, DH-352, DH-268, DH-279, DH-281, COR-37, COR-40, COR-42, COR-43, COR-44, COR-50, COR-53, COR-56, CS-61, CS-63, CS-65, JCR-389, LCC-144, LCC-164, LCC-166, LCC-168, LCC-144, LCC-164, LCC-166, LCC-168, LCC-231, LCC-232, LCC-234, LCC-241, NDC-1, NDC-14, NDC-31, NDC-82, NDC-90, NDC-94, NDC-109, NDC- 119, NDC-120, RD-120, RD-387, RD-394, RD-400, RD-422, RD-424, VDVIGL-37, VDVIGL-127, RD-391, RD-409, RD-410, RD-414, VDVIGL-26, VDVIGL-40, VDVIGL-50, VDVIGL-74, VDVIGL-103, VDVIGL-117, AD-1and H. Anand

B. Seed characters

Seed color was observed visually and recorded at fully matured stage. The 113 germplasm lines were categorized for seed colour (Plate 8) into light brown 50 lines and brown 63 lines (Table 12). Seed shape was observed visually and recorded on dry seed, germplasm lines were categorized for seed shape (Plate 9) into 56 lines slightly round, 38 lines oblong and 20 lines oval (Table 13). Based on visual observation seed size (Plate 10) was recorded at fully matured stage germplasm lines were categorized as 18 lines large, 32 lines medium and 63 lines were small (Table 14). Seed ridge was observed visually at fully matured stage and germplasm were categorized and recorded as seed ridge (Plate 11) having 78 lines prominent and 35 lines are non-prominent ridged (Table 15).

Table 12: Categorization of coriander germplasm on the basis of seed color

Seed color	Number of entries	Genotypes categorized
Light Brown	50	DH-5, DH-36, DH-228, DH-246, DH-318, DH-275, DH-276, DH-280, DH-281, DH-283, COR-45, COR-56, CS-60, CS-61, CS-63, CS-66, CS-67, CS-69, CS-70, JCR-379, JCR-389, JCR-390, JCR-391, JCR-401, JCR-404, LCC-191, LCC-193, LCC-197, LCC-226, LCC-229, LCC-230, LCC-231, LCC-232, LCC-234, LCC-241, LCC-244, LCC-247, LCC-250, NDC-1, NDC-3, NDC-14, NDC-31, NDC-106, RD-394, RD-410, VDVIGL-26, VDVIGL-40, VDVIGL-74, VDVIGL-103 and AD-1
Brown	63	DH-352, DH-352-1, DH-261, DH-268, DH-278, DH-279, COR-36, COR-37, COR-38, COR-39, COR-40, COR-42, COR-43, COR-44, COR-49, COR-50, COR-53, COR-54, COR-55, CS-62, CS-64, CS-65, JCR-380, JCR-405, JCR-406, JCR-407, LCC-144, LCC-164, LCC-166, LCC-168, LCC-170, LCC-174, NDC-4, NDC-10, NDC-38, NDC-68, NDC-80, NDC-82, NDC-90, NDC-94, NDC-100, NDC-109, NDC-110, NDC- 111, NDC-118, NDC-119, NDC-120, RD-120, RD-387, RD-391, RD-400, RD-409, RD-414, RD- 422, RD-424, VDVIGL-37, VDVIGL-49, VDVIGL-50, VDVIGL-117, VDVIGL-127, GC-1and GC-2

White Pink

Plate 6. Corolla color

Erect Semi-erect Spreading

Plate 7. Growth habit

Table 13: Categorization of coriander germplasm on the basis of seed shape

Seed shape	Number of entries	Genotypes categorized
Slightly Round	56	DH-246, DH-318, DH-352, DH-268, DH-275, DH-276, DH-278, DH-280, DH-281, DH-283, COR-36, COR-39, COR-40, COR-42, COR-43, COR-44, COR-49, COR-50, COR-54, COR-56, CS-63, CS-64, CS-65, JCR-379, JCR-390, JCR-404, JCR-406, JCR-407, LCC-226, LCC-229, LCC-231, LCC-232, LCC-234, NDC-1, NDC-3, NDC-4, NDC-10, NDC-14, NDC-31, NDC-38, NDC-82, NDC-90, NDC-94, NDC-100, NDC-109, NDC-111, RD-391, RD-394, RD- 400, VDVIGL-49, VDVIGL-50, VDVIGL-74, VDVIGL-117, VDVIGL-127, GC-1 and GC-2
Oblong	38	DH-5, DH-352-1, COR-45, COR-37, COR-38, COR-45, COR-53, COR-55, CS-61, CS-62, CS-67, CS-69, CS-70, JCR-405, LCC-164, LCC-144, LCC-164, LCC-168, LCC-170, LCC-174, LCC-191, LCC-193, LCC-197, LCC-230, LCC-241, LCC-244, RD-120, RD-409, RD-414, RD-422, RD-424, VDVIGL-40, VDVIGL-103, AD-1 and H. Anand
Oval	20	DH-261, DH-279, CS-60, CS-66, JCR-380, JCR-389, JCR-391, LCC-166, LCC-247, NDC-68, NDC-80, NDC-106, NDC-110, NDC-118, NDC-119, NDC-120, RD-387, RD-410, VDVIGL-26 and VDVIGL-37

Table 14: Categorization of coriander germplasm on the basis of seed size

Seed size	Number of entries	Genotypes categorized
Large	18	DH-5, DH-36, DH-352-1, DH-261, AD-1, H. ANAND, CS-60, CS-61, LCC-164, LCC-170, LCC-226, LCC-230, LCC-231, LCC-232, LCC-234, LCC-241, LCC-244 and LCC-247
Medium	32	DH-352, DH-268, DH-283, COR-37, COR-38, COR-45, COR-55, COR-56, CS-62, CS-63, CS-64, CS-65, CS-66, CS-67, CS-69, CS-70, JCR-380, JCR-401, JCR-404, JCR-406, LCC-144, LCC-166, LCC-168, LCC-174, LCC-191, LCC-193, LCC-197, LCC-229, LCC-250, NDC-1, NDC-4 and RD-414
Small	63	DH-228, DH-246, DH-318, DH-275, DH-276, DH-278, DH-279, DH-280, DH-281, COR-36, COR-39, COR-40, COR-42, COR-43, COR-44, COR-49, COR-50, COR-53, COR-54, JCR-379, JCR-389, JCR-390, JCR-391, JCR-405, JCR-407, NDC-3, NDC-10, NDC-14, NDC-31, NDC-38, NDC-68, NDC-80, NDC-82, NDC-90, NDC-94, NDC-100, NDC-106, NDC-109, NDC-110, NDC-111, NDC-118, NDC-119, NDC-120, RD-120, RD-387, RD-391, RD-394, RD-400, RD-409, RD-410, RD-422, RD-424, VDVIGL-26, VDVIGL-37, VDVIGL-40, VDVIGL-49, VDVIGL-50, VDVIGL-74, VDVIGL-103, VDVIGL-117, VDVIGL-127, GC-1 and GC-2

Table 15: Categorization of coriander germplasm on the basis of seed ridges

Seed ridges	Number of entries	Genotypes categorized
Prominent	78	DH-5, DH-36, DH-228, DH-318, DH-352, DH-268, DH-275, DH-276, DH-278, DH-280, DH-281, DH-283, COR-37, COR-38, COR-40, COR-42, COR-43, COR-45, COR-49, COR-50, COR-53, COR-55, CS-60, CS- 61, CS-62, CS-63, CS-64, CS-70, JCR-380, JCR-389, JCR-390, JCR-404, JCR 405, LCC-144, LCC-164, LCC-166, LCC-168, LCC-170, LCC-174, LCC-191, LCC-193, LCC-197, LCC-229, LCC-230, LCC-231, LCC-232, LCC-234, LCC-241, LCC-244, LCC-247, LCC-250, NDC-1, NDC-3, NDC-4, NDC-31, NDC-82, NDC-90, NDC-94, NDC-100, NDC-106, NDC-109, NDC-110, NDC-111, NDC-118, NDC-119, NDC-120, RD-120, RD-387, RD-391, RD-394, RD-400, RD-409, RD-410, RD-422, RD- 424, VDVIGL-37, AD-1 and H. Anand
Non-prominent	35	DH-246, DH-352-1, DH-261, DH-279, COR-36, COR-39, COR-44, COR- 54, COR-56, CS-65, CS-66, CS-67, CS-69, JCR-379, JCR-391, JCR-401, JCR-406, JCR-407, LCC-226, NDC-10, NDC-14, NDC-38, NDC-68, NDC-80, RD-414, VDVIGL-26, VDVIGL-40, VDVIGL-49, VDVIGL-50, VDVIGL-74, VDVIGL-103, VDVIGL-117, VDVIGL-127, GC-1 and GC-2

4.2 Variability studies

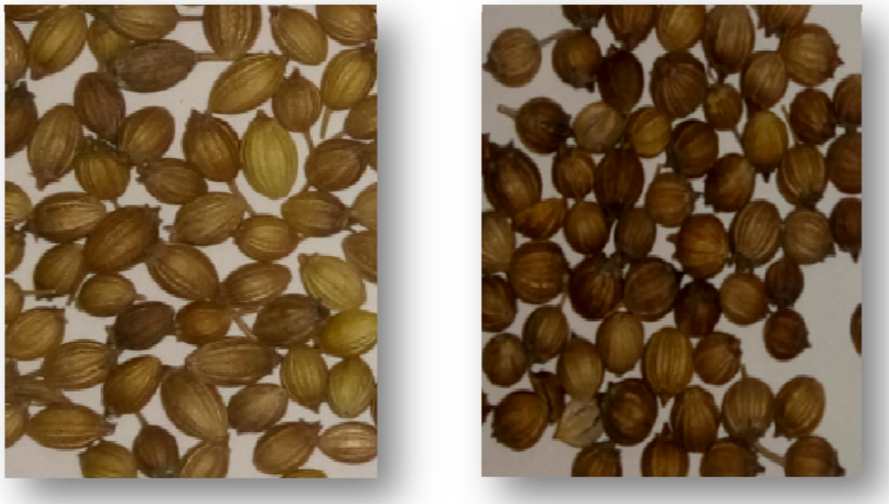
4.2.1 Analysis of variance

The results of the analysis of variance for different quantitative characters for 113 genotypes of coriander are presented in Table 16**.** The results indicated that there were highly significant (P=0.01) differences among genotypes for the eleven growth and yield parameters recorded at different stages of crop growth. This sufficient genetic variation in the genotypes helps the breeders in selection process.

Table 16: Analysis of variance for different characters observed in coriander germplasm

Sr. No.	Source of variation	Replications	Treatments	Error
		d. f.		
		2	112	224
1.	Plant height (cm)	23.12	464.44**	20.11
2.	Number of basal leaves	0.02	1.50**	0.05
3.	Length of basal leaves (cm)	0.09	5.35**	0.12
4.	Primary branches	0.10	6.14**	0.13
5.	Secondary branches	2.45	39.81**	4.19
6.	Umbels per plant	54.64	569.27**	31.61
7.	Umbellets per umbel	0.08	0.92**	0.05
8.	Number of seeds per umbellet	0.03	1.61**	0.05
9.	Number of seeds per umbel	3.05	95.10**	3.21
10.	Test weight (g)	1.69	28.36**	1.52
11.	Seed yield per plant (g)	0.15	18.22**	0.37

** Significant at 1%



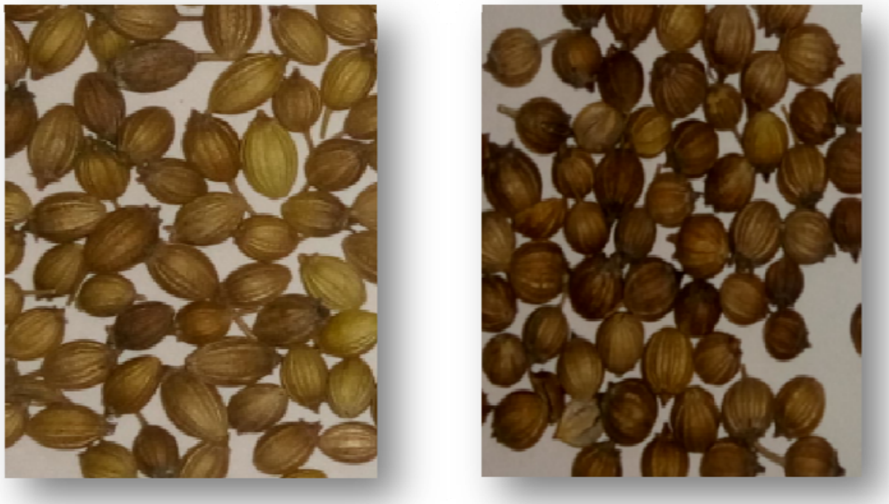
Light brown **Brown**

Plate 8. Seed color

Oblong **Oval**

Slightly round

Plate 9. Seed shape



Light brown **Brown**

Plate 8. Seed color

Oblong **Oval**

Slightly round

Plate 9. Seed shape

Large **Medium**

Small

Plate 10. Seed size

Prominent **Non-prominent**

Plate 11. Seed ridge

4.2.2 Genetic components of variation

Improvement of any crop mainly depends on the magnitude of variability present in the genotypes. The polygenic variation present in a plant population is of three types, *viz.*, phenotypic, genotypic and environmental. Phenotypic variability is observable, it includes both genotypic and environmental variations and therefore, is also called total variation. It changes under environmental conditions and is measured in term of phenotypic variance. Genotypic variation refers to genetic or inherent variability which remains unaltered by environmental conditions. This type of variability is more useful to a plant breeder for exploitation in selection or hybridization. It is measured in terms of genotypic variance and consists of additive, dominance and epistatic components. With a view to understand these observed variations, the range, mean, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability (h^2) and genetic advance as per cent mean (GAM) were worked out and presented in Table 17 and 18.

The data revealed the existence of large amount of variability in most of the characters studied. Phenotypic coefficient of variation ranged from 11.03 (Umbellets per umbel) to 30.60 (Umbels per plant). Genotypic coefficient of variation ranged from 10.23 (Umbelletes per umbel) to 28.21 (Umbels per plant). Genetic advance as percent mean ranged from 19.54 (Umbelletes per umbel) to 53.59 (Umbels per plant). The estimates of heritability ranged from 80.62 per cent (Secondary branches) to 94.12 per cent (Seed yield per plant).

Plant height was recorded at matured stage and data was presented in Table 17. There was a significant difference observed among the 113 genotypes which varied from 53.80 cm (DH-352) to 109.49 cm (VDVIGL-103). The maximum plant height was recorded in VDVIGL-103, while minimum plant height was recorded by DH-352. Plant height had moderate phenotypic and genotypic coefficients of variation, with high heritability and genetic advance as percent of mean. Phenotypic and genotypic coefficients of variation were 16.89 and 15.85%, respectively. The heritability was 88.05% and genetic advance as percent of mean was 30.64% with an overall mean of plant height is 76.78 cm (Table 18).

The number of basal leaves ranged between 2.23 (DH-352) to 5.26 (VDVIGL-117) with mean of 3.57 (Table 17). The estimate of phenotypic and genotypic coefficients of variation were high with 20.50 and moderate 19.46%. High heritability (90.11%) was observed along with high genetic advance as per cent of mean (38.05%) presented in Table 18. Length of basal leaves recorded at 30 days of plant growth and data presented in Table 17. It is ranged from 3.54 (DH-352) to 9.31 (VDVIGL-117). The maximum length was recorded in the VDVIGL-117 genotype where it was minimum in the DH-352 genotype. This character showed high phenotypic and genotypic coefficients of variation with 21.88 and 21.19%, respectively. Heritability estimate was recorded high 93.77%, with high genetic advance as per cent of mean (42.27%). Over all mean is 6.23 presented in Table 18.

Table 17: Mean performance of coriander genotypes for different plant growth and seed yield parameters

Genotypes	Plant height (cm)	Number of basal leaves	Length of basal leaves (cm)	Primary branches	Secondary branches	Umbel / plant	Umbellets/ umbel	Seeds/ umbellet	Number of seeds/umbel	Test weight (g)	Seed yield/ Plant (g)
DH-5	58.16	2.50	3.94	3.86	19.65	44.28	5.22	4.12	36.23	8.32	12.80
DH-36	57.29	2.42	3.80	3.84	16.07	30.54	4.53	4.00	36.04	8.22	12.68
DH-228	55.88	2.40	3.73	3.73	13.92	20.60	4.00	3.96	33.74	8.11	13.81
DH-246	55.30	2.38	3.70	3.61	13.11	18.10	3.69	3.95	29.38	7.95	15.96
DH-318	54.58	2.33	3.64	3.47	22.66	34.67	4.31	3.94	29.05	7.85	15.67
DH-352	53.80	2.23	3.54	3.25	15.10	70.73	6.24	3.79	30.91	7.73	15.63
DH-352-1	55.01	2.31	3.61	3.44	14.70	69.82	6.22	3.71	31.75	7.52	15.54
DH-261	60.28	2.59	4.01	4.14	14.43	68.35	6.20	3.54	32.21	6.87	15.41
DH-268	59.14	2.53	4.00	5.49	19.37	66.85	6.13	5.40	33.21	13.59	15.21
DH-275	82.35	3.91	6.66	8.27	26.54	65.70	6.02	6.26	39.49	17.08	15.02
DH-276	93.84	4.60	7.94	8.16	26.40	64.69	6.01	6.22	39.32	16.85	14.98
DH-278	93.43	4.60	7.90	8.14	26.35	64.10	6.00	6.16	38.85	11.48	14.95
DH-279	93.14	4.57	7.90	8.00	26.14	63.40	6.00	6.06	38.62	11.40	14.72
DH-280	92.07	4.46	7.88	7.94	25.69	62.93	5.99	6.01	38.39	16.49	14.63
DH-281	91.12	4.40	7.82	7.92	27.12	73.34	6.14	6.00	38.02	16.35	14.59
DH-283	90.65	4.40	7.74	7.91	26.90	71.50	6.07	5.98	37.98	16.23	14.57
COR-36	90.39	4.40	7.68	7.78	25.22	61.62	5.88	5.90	37.95	16.07	14.56
COR-37	90.22	4.38	7.65	7.68	24.80	61.28	5.87	5.86	37.72	15.83	14.45
COR-38	89.56	4.33	7.59	7.59	24.73	60.49	5.82	5.85	37.27	15.70	14.37
COR-39	89.10	4.30	7.53	7.44	24.64	59.82	5.80	5.85	36.90	15.69	14.33
COR-40	88.74	4.24	7.50	7.44	24.57	59.56	5.80	5.80	36.88	15.62	14.28
COR-42	88.21	4.20	7.46	7.44	24.48	59.07	5.80	5.79	36.70	15.59	14.20
COR-43	87.45	4.20	7.43	7.33	24.44	58.67	5.80	5.70	36.60	15.45	14.06
COR-44	86.88	4.20	7.38	7.21	24.36	58.12	5.79	5.67	36.35	15.39	13.99
COR-45	86.38	4.20	7.33	7.20	24.01	57.81	5.77	5.66	35.19	15.32	13.98
COR-49	85.97	4.20	7.31	7.11	23.92	57.08	5.74	5.66	38.31	15.19	13.98
COR-50	85.52	4.20	7.25	7.00	23.78	56.61	5.71	5.64	41.08	15.06	13.97
COR-53	84.85	4.20	7.19	6.99	23.64	56.16	5.67	5.60	35.79	14.99	13.91
COR-54	84.44	4.20	7.11	6.96	23.45	55.74	5.64	5.60	35.53	14.92	13.73
COR-55	84.25	4.20	7.10	6.90	23.40	55.39	5.64	5.60	35.22	14.80	13.61

COR-56	83.96	4.11	7.09	6.83	23.09	55.09	5.64	5.59	41.52	14.73	13.57
CS -60	83.55	4.10	7.04	6.80	22.83	54.63	5.60	5.56	47.38	14.60	13.55
CS -61	83.19	4.01	7.00	6.79	22.71	54.02	5.60	5.56	38.20	14.50	13.54
CS -62	83.01	4.00	6.98	6.72	22.63	53.77	5.60	5.49	34.76	14.41	13.50
CS -63	82.22	4.00	6.97	6.72	22.62	53.29	5.60	5.47	34.49	14.27	13.45
CS -64	81.62	4.00	6.97	6.71	22.59	52.81	5.56	5.47	34.29	13.76	13.30
CS -65	81.21	3.99	6.92	6.68	22.57	52.55	5.53	5.45	34.20	13.51	13.23
CS -66	80.75	3.98	6.90	6.60	22.55	52.33	5.48	5.40	34.10	13.38	13.17
CS -67	80.31	3.90	6.90	6.60	22.54	52.08	5.47	5.40	33.85	13.21	13.07
CS -69	79.95	3.89	6.88	6.49	22.48	51.62	5.46	5.40	33.63	13.10	13.00
CS -70	79.75	3.80	6.84	6.48	22.43	51.35	5.46	5.38	33.48	13.01	13.00
JCR -379	79.48	3.80	6.81	6.48	22.36	51.14	5.46	5.38	32.63	12.90	19.49
JCR -380	79.21	3.80	6.80	6.45	22.30	50.67	5.46	5.38	30.92	12.83	18.02
JCR -389	78.85	3.80	6.79	6.40	22.10	50.16	5.45	5.31	33.05	12.76	16.49
JCR -390	78.54	3.80	6.77	6.35	22.00	49.84	5.41	5.29	32.80	12.63	12.61
JCR -391	78.04	3.79	6.74	6.31	21.81	49.59	5.40	5.29	32.72	12.57	12.60
JCR -401	77.49	3.76	6.71	6.30	21.60	49.30	5.40	5.29	32.59	12.51	12.56
JCR -404	77.28	3.71	6.64	6.24	21.44	49.05	5.40	5.27	32.58	12.39	12.56
JCR -405	77.18	3.70	6.58	6.20	21.29	48.80	5.40	5.24	32.46	12.27	12.53
JCR -406	77.06	3.70	6.50	6.20	21.11	48.62	5.40	5.24	32.39	12.17	12.44
JCR -407	76.64	3.62	6.46	6.20	21.06	48.48	5.36	5.21	32.32	12.06	12.40
LCC-144	76.25	3.60	6.45	6.20	21.02	48.08	5.34	5.20	32.18	12.04	12.31
LCC-164	75.97	3.60	6.40	6.12	20.87	47.86	5.34	5.20	32.01	11.91	12.21
LCC-166	75.83	3.60	6.34	6.10	20.60	47.50	5.32	5.20	38.03	11.77	12.03
LCC-168	75.61	3.60	6.32	6.00	20.58	47.28	5.30	5.20	40.43	11.70	12.01
LCC-170	75.42	3.60	6.27	6.00	20.53	46.94	5.28	5.11	37.38	11.62	12.00
LCC-174	75.22	3.60	6.21	6.00	20.45	46.74	5.28	5.10	31.50	11.57	12.00
LCC-191	74.80	3.55	6.16	6.00	20.26	46.55	5.28	5.10	31.33	11.46	11.98
LCC-193	74.61	3.52	6.13	6.00	20.17	46.37	5.27	5.05	31.29	11.37	11.90
LCC-197	74.26	3.50	6.12	6.00	20.09	46.11	5.25	5.02	31.12	11.31	11.77
LCC-226	73.93	3.50	6.10	5.93	19.98	45.90	5.24	5.02	39.93	11.21	11.64
LCC-229	73.82	3.49	6.09	5.90	19.80	45.22	5.24	5.02	33.57	11.13	11.64
LCC-230	73.77	3.43	6.04	5.89	19.77	44.63	5.24	5.01	30.49	11.09	11.61
LCC-231	73.61	3.40	6.00	5.85	26.27	63.93	5.81	5.01	30.44	11.04	11.56

LCC-232	73.41	3.40	5.99	5.80	31.90	97.73	6.67	5.00	30.42	10.99	11.53
LCC-234	73.07	3.40	5.98	5.80	19.62	43.84	5.20	4.99	30.40	10.92	11.40
LCC-241	72.66	3.40	5.97	5.79	19.60	43.64	5.20	4.98	30.25	10.80	11.32
LCC-244	72.42	3.39	5.93	5.74	19.59	43.39	5.20	4.91	30.24	10.73	11.21
LCC-247	71.93	3.33	5.90	5.71	19.58	43.05	5.13	4.91	30.20	10.70	11.10
LCC-250	71.53	3.28	5.88	5.70	19.56	42.65	5.10	4.91	30.11	10.66	11.05
NDC-1	71.13	3.25	5.83	5.62	19.54	42.07	5.10	4.90	30.00	10.59	11.01
NDC-3	70.72	3.23	5.80	5.60	19.53	41.93	5.07	4.84	29.93	10.49	11.00
NDC-4	70.31	3.20	5.76	5.58	19.47	41.57	5.01	4.84	29.85	10.43	11.00
NDC-10	70.10	3.20	5.71	5.54	19.35	41.20	5.01	4.80	29.67	10.36	10.82
NDC-14	69.88	3.20	5.68	5.52	19.07	40.72	5.01	4.80	42.92	10.27	10.68
NDC-31	69.67	3.20	5.63	5.52	18.91	40.43	5.01	4.80	42.35	10.16	10.67
NDC-38	69.35	3.16	5.60	5.40	18.72	40.13	5.01	4.72	37.35	10.09	10.67
NDC-68	69.27	3.11	5.57	5.40	18.65	39.99	5.01	4.72	28.92	9.99	10.56
NDC-80	69.14	3.10	5.53	5.40	18.62	39.71	5.00	4.68	28.81	9.98	10.45
NDC-82	69.00	3.09	5.49	5.39	18.60	39.29	5.00	4.66	28.76	9.89	10.39
NDC-90	68.86	3.06	5.47	5.34	18.55	39.13	4.98	4.66	28.67	9.83	10.26
NDC-94	68.49	3.01	5.39	5.29	18.53	38.60	4.98	4.66	28.47	9.76	10.24
NDC-100	68.23	3.00	5.35	5.23	18.49	38.32	4.98	4.62	28.17	9.68	10.13
NDC-106	67.87	3.00	5.33	5.21	18.44	37.95	4.97	4.60	28.02	9.62	10.00
NDC-109	67.57	3.00	5.31	5.21	18.40	37.74	4.93	4.60	27.88	9.60	9.99
NDC-110	66.94	2.99	5.23	5.17	18.29	37.49	4.91	4.55	27.79	9.52	9.88
NDC-111	66.67	2.94	5.20	5.05	18.20	37.32	4.91	4.53	27.47	9.44	9.85
NDC-118	66.53	2.91	5.19	5.04	18.13	36.86	4.91	4.53	27.22	9.41	9.70
NDC-119	66.28	2.90	5.13	5.03	18.01	36.27	4.90	4.48	27.10	9.34	9.70
NDC-120	65.89	2.90	5.09	5.00	17.89	35.90	4.85	4.48	27.04	9.31	9.63
RD-120	65.71	2.88	5.02	5.00	17.70	35.58	4.80	4.46	26.85	9.29	9.60
RD-387	65.34	2.83	5.00	4.95	17.59	35.39	4.80	4.40	26.72	9.24	9.57
RD-391	65.22	2.80	4.92	4.82	17.55	35.16	4.78	4.38	26.63	9.15	9.54
RD-394	65.02	2.80	4.89	4.80	17.47	34.89	4.75	4.34	26.54	9.08	9.45
RD-400	64.85	2.80	4.86	4.70	17.40	34.40	4.73	4.34	26.41	8.98	9.40
RD-409	64.54	2.80	4.81	4.63	17.25	33.57	4.73	4.33	25.99	8.93	9.34
RD-410	64.21	2.77	4.77	4.60	17.09	33.19	4.70	4.30	25.74	11.51	9.31
RD-414	63.89	2.72	4.64	4.55	16.79	31.76	4.68	4.30	25.49	16.61	9.23

RD-422	63.66	2.67	4.51	4.54	16.58	30.88	4.67	4.27	25.08	8.78	9.17
RD-424	63.46	2.62	4.43	4.49	16.47	30.17	4.62	4.20	24.82	8.69	9.12
VDVIGL-26	63.18	2.60	4.36	4.39	16.36	29.81	4.59	4.18	24.60	8.62	9.00
VDVIGL-37	62.51	2.60	4.25	4.29	16.27	29.07	4.55	4.15	24.45	8.57	8.92
VDVIGL-40	61.68	3.93	5.59	4.20	16.23	28.60	4.55	4.14	24.06	8.48	8.81
VDVIGL-49	90.16	5.27	8.43	4.13	19.87	28.23	4.47	4.12	23.85	8.43	8.62
VDVIGL-50	100.87	4.61	8.17	6.93	19.22	28.03	4.40	5.08	23.42	13.18	8.49
VDVIGL-74	96.13	3.27	8.07	8.38	15.38	27.72	4.38	6.95	23.02	21.45	8.40
VDVIGL-103	109.50	3.28	9.09	9.66	24.16	26.99	4.37	6.80	22.41	19.72	8.16
VDVIGL-117	96.84	5.27	9.32	10.16	28.16	26.49	4.36	6.42	22.09	18.58	7.99
VDVIGL-127	97.55	5.10	9.03	9.68	27.50	26.04	4.29	6.64	21.89	18.27	7.76
GC-1	101.21	4.95	8.85	9.45	16.88	37.82	4.83	6.60	21.30	17.86	7.48
GC-2	108.15	4.82	8.63	9.17	28.30	79.13	6.26	6.53	19.89	17.63	7.23
AD -1	109.24	4.80	4.06	8.93	29.24	78.52	6.38	6.57	19.37	17.52	6.86
H. ANAND	106.40	4.77	8.21	8.53	28.68	74.06	6.24	6.67	16.84	17.33	6.37
SEm±	2.59	0.13	0.20	0.21	1.18	3.25	0.13	0.13	1.03	0.71	0.35
C.D@ 5%	7.22	0.37	0.55	0.58	3.29	9.05	0.35	0.37	2.88	1.98	0.98
C.V (%)	5.84	6.45	5.46	5.92	9.76	11.85	4.13	4.46	5.66	10.07	5.11

Table 18: Genetic parameters for different characters of coriander genotypes

Characters	Mean	Range	Heritability BS (%)	GCV (%)	PCV (%)	GA value % mean
Plant height (cm)	76.78	53.80-109.49	88.05	15.85	16.89	30.64
Number of basal leaves	3.57	2.23-5.26	90.11	19.46	20.50	38.05
Length of basal leaves (cm)	6.23	3.54-9.31	93.77	21.19	21.88	42.27
Primary branches	6.14	3.24-10.16	93.82	23.06	23.80	46.00
Secondary branches	20.99	13.11-31.9	80.62	17.14	19.09	31.71
Umbels per plant	47.45	18.09-97.73	85.01	28.21	30.60	53.59
Umbellets per umbel	5.28	3.68-6.66	85.98	10.23	11.03	19.54
Number seeds per umbellet	5.13	4.12-6.67	90.81	14.02	14.71	27.52
Number of seeds per umbel	31.68	16.83-47.37	90.51	17.47	18.36	34.23
Test weight (g)	12.24	6.87-21.45	85.49	24.44	26.44	46.56
Seed yield per plant (g)	11.93	6.37-19.49	94.12	20.44	21.07	40.86

Where, GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation, GA= Genetic Advance

The number of primary branches ranged between 3.24 (DH-352) and 10.16 (VDVIGL-117) with mean of 6.14 (Table 17). High phenotypic (23.80 %) and genotypic coefficients of variation (23.06%) were recorded. High heritability (93.82%) was observed along with high genetic advance as per cent of mean (46.00) presented in Table 18. Secondary branches ranged from minimum 13.11 (DH-246) to maximum 31.90 (LCL-232) data presented in Table 17. Secondary branches had moderate phenotypic and genotypic coefficients of variation 19.09 and 17.14%, respectively. High heritability 80.62% and genetic advance as percent of mean 31.71%, with an overall mean of secondary branches was 20.99 cm (Table 18).

Number of umbels per plant at maturity varied from 18.09 (DH-246) to 97.73 (LCL-232) with grand mean of 47.45 (Table 17). The estimates of phenotypic (30.60) and genotypic coefficients of variations (28.21) recorded high for this trait. The trait had high heritability (85.01%) coupled with very high genetic advance as per cent of mean (53.59) presented in Table 18. The number of umbellets per umbel varied from 3.68 (DH-246) to 6.66 (LCL-232) with mean of 5.28 (Table 17). The maximum number recorded in genotype LCL-232 and minimum in DH-246 genotype. Umbelletes per umbel had moderate phenotypic and genotypic coefficients of variation, with high heritability and moderate genetic advance as percent of mean. Phenotypic and genotypic coefficients of variation were 11.03 and 10.23%, respectively. The heritability was 85.98% and genetic advance as percent of mean was 19.54% (Table 18).

Number of seeds per umbellet in present genotypes varied from 3.54 (DH-261) to 6.95 (VDVIGL-74) with mean of 5.13 (Table 17). The estimates of phenotypic coefficients of variation (14.71) and genotypic coefficients of variation (14.02) were moderate for this character. The trait had high heritability (90.81%) coupled with high genetic advance as per cent of mean (27.52) presented in Table 18. The number of seeds per umbel ranged from 16.83 (H. Anand) to 47.37 (CS-60). Maximum number of seeds per umbel recorded in CS-60 genotype and minimum number in H. Anand genotype. Number of seeds per umbel exhibited moderate phenotypic and genotypic coefficients of variation, with high heritability and genetic advance as percent of mean. Phenotypic and genotypic coefficients of variation were 18.36 and 17.47 %, respectively. The heritability was 90.51 % and genetic advance as percent of mean was 34.23 % with an overall mean of number of seeds per umbel 31.68 (Table 18).

The test weight ranged from 6.87 g (DH-261) to 21.45g (VDVIGL-74) with an overall average mean of 12.24g (Table 17). The Phenotypic coefficients of variation (26.44 %) and genotypic coefficients of variation (24.44 %) were high for this character. High heritability (85.49 %) was associated with high genetic advance as per cent of mean (46.56 %) presented in Table 18. The coriander genotypes showed variation for seed yield (Table 17). Seed yield ranged from 6.37 g (H. Anand) to 19.49 g (JCR-79). The Maximum yield per plant obtained from JCR-79 genotype and minimum yield in H. Anand genotype. Seed yield per plant had high phenotypic and genotypic coefficients of variation, with high heritability and genetic advance as percent of mean. Phenotypic and genotypic coefficients of variation were 21.07 and 20.44%, respectively. The heritability was 94.12% and genetic advance as percent of mean was 40.86% with an overall mean of 11.93g seed yield per plant (Table 18).

4.3 Correlation studies

The genotypic and phenotypic correlation studies were carried out to know the nature of relationship existing between seed yield and its attributing traits. The values of all possible correlation coefficients among the characters were calculated at genotypic level and phenotypic level presented in the Table 19. The genotypic correlation coefficient has same association pattern with seed yield and other morphological traits inter se like phenotypic correlation coefficient. In general, the estimates of genotypic correlation coefficient were higher than their respective phenotypic correlation coefficients for most of the traits. The difference between genotypic and phenotypic correlation coefficients was negligible.

Genotypic correlation analysis showed that, the seed yield per plant had significant and positive association with number of seeds per umbel (0.740), umbelletes per umbel (0.508), umbels per plant (0.487) and secondary branches (0.239). The character plant height (-0.034) showed negative non-significant correlation and number of basal leaves (0.091), length of basal leaves (0.073), primary branches (0.025) and seeds per umbellet (0.085) showed non-significant positive correlation with the seed yield per plant. At phenotypic level the seed yield per plant had significant and positive association with number of seeds per umbel

(0.677), umbelletes per umbel (0.457), umbels per plant (0.435) and secondary branches (0.199). The character plant height (-0.033) showed negative non-significant correlation and number of basal leaves (0.083), length of basal leaves (0.068), primary branches (0.023) and seeds per umbellet (0.078) showed non-significant positive correlation with the seed yield per plant.

At genotypic level, plant height was significantly positively correlated with number of basal leaves (0.920), length of basal leaves (0.913), primary branches (0.968), secondary branches (0.802), umbels per plant (0.425), umbellets per umbel (0.412), seeds per umbellet (0.958) and test weight (0.908). Whereas, number of seeds per umbel (0.043) had non-significant positive association. Plant height had significant positive phenotypic correlation with number of basal leaves (0.865), length of basal leaves (0.862), primary branches (0.884), secondary branches (0.688), umbels per plant (0.372), umbellets per umbel (0.358), seeds per umbellet (0.849) and test weight (0.781).Whereas, number of seeds per umbel (0.038) had non-significant positive correlation.

In genotypic correlation, number of basal leaves was significantly and positively correlated with length of basal leaves (0.904), primary branches (0.864), secondary branches (0.820), umbels per plant (0.444), umbellets per umbel (0.446), seeds per umbellet (0.839), number of seeds per umbel (0.181) and test weight (0.775).Whereas, seed yield (0.091) had non-significant positive association. Significant and positive results recorded at phenotypic level with length of basal leaves (0.874), primary branches (0.800), secondary branches (0.691), umbels per plant (0.386), umbellets per umbel (0.389), seeds per umbellet (0.758), number of seeds per umbel (0.164) and test weight (0.679).Whereas, seed yield (0.083) had non-significant positive association.

Genotypic correlation analysis reveals that length of basal leaves was significantly and positively correlated with primary branches (0.889), secondary branches (0.734), umbels per plant (0.302), umbellets per umbel (0.309), seeds per umbellet (0.872), number of seeds per umbel (0.176) and test weight (0.820).Whereas, seed yield (0.073) had non-significant positive association. At phenotypic level significant and positive correlation results recorded with primary branches (0.838), secondary branches (0.623), umbels per plant (0.267), umbellets per umbel (0.276), seeds per umbellet (0.803), number of seeds per umbel (0.163) and test weight (0.731).Whereas, seed yield (0.068) had non-significant positive association.

At genotypic level, primary branches were significantly and positively correlated with number of secondary branches (0.827), umbels per plant (0.430), umbellets per umbel (0.422), seeds per umbellet (0.993), number of seeds per umbel (0.111) and test weight (0.932).Whereas, seed yield per plant (0.025) had non-significant positive association.

Table 19: Genotypic (below diagonal) and phenotypic (above diagonal) correlation coefficients for yield attributing traits in coriander genotypes

Characters	Plant height (cm)	Number of basal leaves	Length of basal leaves (cm)	Primary branches	Secondary branches	Umbel/ plant	Umbellets/ umbel	Number seeds/ umbellet	Number of seeds/umbel	Test weight (g)	Seed yield/plant (g)
Plant height (cm)	1.000	0.865^{**}	0.862^{**}	0.884^{**}	0.688^{**}	0.372^{**}	0.358^{**}	0.849^{**}	0.038	0.781^{**}	-0.033
Number of basal Leaves	0.920^{**}	1.000	0.874^{**}	0.800^{**}	0.691^{**}	0.386^{**}	0.389^{**}	0.758^{**}	0.164^{**}	0.679^{**}	0.083
Length of basal leaves (cm)	0.913^{**}	0.904^{**}	1.000	0.838^{**}	0.623^{**}	0.267^{**}	0.276^{**}	0.803^{**}	0.163^{**}	0.731^{**}	0.068
Primary branches	0.968^{**}	0.864^{**}	0.889^{**}	1.000	0.702^{**}	0.379^{**}	0.375^{**}	0.951^{**}	0.102	0.869^{**}	0.023
Secondary branches	0.802^{**}	0.820^{**}	0.734^{**}	0.827^{**}	1.000	0.613^{**}	0.551^{**}	0.683^{**}	0.232^{**}	0.590^{**}	0.199^{**}
Umbel / plant	0.425^{**}	0.444^{**}	0.302^{**}	0.430^{**}	0.727^{**}	1.000	0.976^{**}	0.414^{**}	0.374^{**}	0.347^{**}	0.435^{**}
Umbellets /umbel	0.412^{**}	0.446^{**}	0.309^{**}	0.422^{**}	0.693^{**}	0.985^{**}	1.000	0.410^{**}	0.423^{**}	0.339^{**}	0.457^{**}
Seeds /umbellet	0.958^{**}	0.839^{**}	0.872^{**}	0.993^{**}	0.835^{**}	0.474^{**}	0.466^{**}	1.000	0.148^{**}	0.913^{**}	0.078
Number of seeds/umbel	0.043	0.181^{**}	0.176^{**}	0.111^{*}	0.281^{**}	0.427^{**}	0.480^{**}	0.163^{**}	1.000	0.110^{*}	0.677^{**}
Test weight (g)	0.908^{**}	0.775^{**}	0.820^{**}	0.932^{**}	0.753^{**}	0.410^{**}	0.399^{**}	0.934^{**}	0.125^{*}	1.000	0.071
Seed Yield/Plant (g)	-0.034	0.091	0.073	0.025	0.239^{**}	0.487^{**}	0.508^{**}	0.085	0.740^{**}	0.079	1.000

Primary branches had significant positive phenotypic correlation with secondary branches (0.702), umbels per plant (0.379), umbellets per umbel (0.375), seeds per umbellet (0.951) and test weight (0.869).Whereas, number of seeds per umbel (0.102) had non-significant positive correlation.

Genotypic correlation analysis, revealed that secondary branches receded significant and positive correlation with umbels per plant (0.727), umbellets per umbel (0.693), seeds per umbellet (0.835), number of seeds per umbel (0.281), test weight (0.753) and seed yield (239).Whereas, at phenotypic level significant and positive correlation results recorded with umbels per plant (0.613), umbellets per umbel (0.551), seeds per umbellet (0.683), number of seeds per umbel (0.232) and test weight (0.590).

In genotypic correlation studies, umbels per plant recorded significant and positive correlation with umbellets per umbel (0.985), seeds per umbellet (0.474), number of seeds per umbel (0.427) and test weight (0.410). At phenotypic level significant and positive correlation results recorded with umbellets per umbel (0.976), seeds per umbellet (0.414), number of seeds per umbel (0.374) and test weight (0.347).

In genotypic correlation analysis, umbellets per umbel receded significant and positive correlation with seeds per umbellet (0.466), number of seeds per umbel (0.480) and test weight (0.399). At phenotypic level significant and positive correlation results recorded with seeds per umbellet (0.410), number of seeds per umbel (0.423) and test weight (0.339). In both genotypic and phenotypic level, seeds per umbellet showed the significant and positive correlation with number of seeds per umbel (0.163 & 0.148) and test weight (0.934 & 0.913). Number of seeds per umbel was positively and significantly correlated with test weight (0.125 & 0.110 respectively) in both conditions.

4.4 Path coefficient analysis

In a breeding programme, we are often concerned with the improvement in yield which is an overall product depends on a number of morpho-physiological attributes. Such characters are often interrelated. Hence, their effect on yield is also modified by other. Path coefficient analysis was used to partition correlation coefficient of the characters studied for yield per plant into direct and indirect effects. All 11 characters were subjected to phenotypic path coefficient analysis by considering seed yield per plant as dependent variable and others as independent variables viz., plant height, number of basal leaves, length of basal leaves, primary branches, secondary branches, umbels per plant, umbellets per umbel, seed per umbellet, number of seeds per umbel and test weight (Table 20).

Direct and indirect effects of component characters on yield per plant

The low (0.4697) residual effect indicated high contribution of independent characters toward the dependent character i.e. seed yield per plant. The data presented in Table 20 shows that plant height exerted moderate negative direct effect (-0.28478) on seed yield per plant, its indirect effects were moderate negative *via* number of basal leaves (-0.24624), length of basal leaves (-0.24553), primary branches (-0.25176), secondary branches (-0.19588), umbels per plant (-0.10601), umbellets per umbel (-0.10198), seed per umbellet (-0.24183), number of seeds per umbel (-0.01089) and test weight (-0.22239). Number of basal leaves showed moderate positive direct effect (0.0169) for seed yield per plant. Moderate positive indirect effects were exerted *via* plant height (0.0146), length of basal leaves (0.01478), primary branches (0.01353), secondary branches (0.01168), seed per umbellet (0.01281) and test weight (0.01148). Positive negligible indirect effect was shown by umbels per plant (0.00652), umbellets per umbel (0.00658) and number of seeds per umbel (0.00278).

The data presented in Table 20 shows that length of basal leaves exerted moderate positive direct effect (0.17264) on seed yield per plant, its indirect effects were moderate positive via plant height (0.14885), number of basal leaves (0.15087), primary branches (0.14469), secondary branches (0.10763), seed per umbellet (0.13864) and test weight (0.12626). Positive negligible indirect effect was shown by umbels per plant (0.04615), umbellets per umbel (0.04757) and number of seeds per umbel (0.02809). The path coefficient data shows that primary branches exerted moderate negative direct effect (-0.18840) on seed yield per plant, its indirect effects were moderate negative via plant height (-0.16657), number of basal leaves (-0.15073), length of basal leaves (-0.15791), secondary branches (-0.13225), seed per umbellet (-0.17912) and test weight (-0.16366). Low negative indirect effect was exerted by umbels per plant (-0.07149), umbellets per umbel (-0.07064) and number of seeds per umbel (-0.01916).

Secondary branches showed negligible positive direct effect (0.00521) on seed yield per plant, its indirect effects were low positive via plant height (0.00358), number of basal leaves (0.00360), length of basal leaves (0.00325), primary branches (0.00366), secondary branches (0.00319), umbels per plant (0.00319), umbellets per umbel (0.00287), seed per umbellet (0.00355), number of seeds per umbel (0.00121) and test weight (0.00307). Path coefficient analysis, shows that umbels per plant exerted moderate high positive direct effect (0.34534) on seed yield per plant, its indirect effects were moderate high positive via plant height (0.12856), number of basal leaves (0.13322), primary branches (0.13103), secondary branches (0.21178), umbellets per umbel (0.33690), seed per umbellet (0.14295), number of seeds per umbel (0.12919) and test weight (0.11989). Negligible positive indirect effect exerted by length of basal leaves (0.09231).

The path coefficient data shows that umbelletes per umbel exerted negative direct effect (-0.04880) on seed yield per plant, its indirect effects were also negligible negative via plant height (-0.01746), number of basal leaves (-0.01898), length of basal leaves (-0.01343), primary branches (-0.01828), secondary branches (-0.02686), umbels per plant (-0.04756), seed per umbellet (-0.01999), number of seeds per umbel (-0.02063) and test weight (-0.01655). Seeds per umbellet showed negligible positive direct effect (0.00508) on seed yield per plant, its indirect effects were also negligible positive via plant height (0.00432), number of basal leaves (0.00385), length of basal leaves (0.00408), primary branches (0.00483), secondary branches (0.00347), umbels per plant (0.00210), umbellets per umbel (0.00208), number of seeds per umbel (0.00075) and test weight (0.00464).

High positive direct effect exerted for the character number of seeds per umbel (0.54978) on seed yield. Its indirect effects were also moderate positive for secondary branches (0.12748), umbels per plant (0.20568) and umbellets per umbel (0.23261) and low positive for plant height (0.02102), number of basal leaves (0.09027), length of basal leaves (0.08946), primary branches (0.05590), number of seeds per umbel (0.08134) and test weight (0.06051). Path coefficient analysis, shows that test weight exerted moderate high positive direct effect (0.14754) on seed yield per plant, its indirect effects were moderate positive via plant height (0.11522), number of basal leaves (0.10021), length of basal leaves (0.10790), seed per umbellet (0.13477) and primary branches (0.12815). Negligible positive effects were observed for secondary branches (0.08699), umbels per plant (0.05122), umbellets per umbel (0.05008) and number of seeds per umbel (0.01624).

Table 20: Direct (diagonal) and indirect (off-diagonal) phenotypic path coefficients of different characters for yield per plant in 113 genotypes of coriander

Characters	Plant height (cm)	Number of basal leaves	Length of basal leaves (cm)	Primary branches	Secondary branches	Umbel/ plant	Umbellets/ umbel	Number seeds/ umbellet	Number of seeds/umbel	Test weight (g)	Correlation with yield
Plant height (cm)	**-0.28480**	0.01462	0.14885	-0.16657	0.00358	0.12856	-0.01746	0.00432	0.02102	0.11522	-0.034
Number of basal Leaves	-0.24624	**0.01691**	0.15087	-0.15073	0.00360	0.13322	-0.01898	0.00385	0.09027	0.10021	0.091
Length of basal leaves (cm)	-0.24553	0.01478	**0.17264**	-0.15791	0.00325	0.09231	-0.01343	0.00408	0.08946	0.10790	0.073
Primary branches	-0.25176	0.01353	0.14469	**-0.18840**	0.00366	0.13103	-0.01828	0.00483	0.05590	0.12815	0.025
Secondary branches	-0.19588	0.01168	0.10763	-0.13225	**0.00521**	0.21178	-0.02686	0.00347	0.12748	0.08699	0.239
Umbel / plant	-0.10601	0.00652	0.04615	-0.07149	0.00319	**0.34534**	-0.04756	0.00210	0.20568	0.05122	0.487
Umbellets /umbel	-0.10198	0.00658	0.04757	-0.07064	0.00287	0.33690	**-0.04880**	0.00208	0.23261	0.05008	0.508
Seeds /umbellet	-0.24183	0.01281	0.13864	-0.17912	0.00355	0.14295	-0.01999	**0.00508**	0.08134	0.13477	0.085
Number of seeds/umbel	-0.01089	0.00278	0.02809	-0.01916	0.00121	0.12919	-0.02063	0.00075	**0.54978**	0.01624	0.740
Test weight (g)	-0.22239	0.01148	0.12626	-0.16366	0.00307	0.11989	-0.01655	0.00464	0.06051	**0.14754**	0.079

Residual effect 0.46978

4.5 Genetic divergence

4.5.1. Genetic diversity of the genotypes

D^2 method as suggested by Mahalanobis (1936) is most common method used for clustering of genotypes, however this method is applicable, when genotypes are evaluated in a standard replicated designs such as RBD, strip plot or lattice designs. The data on clustering pattern have been presented in Table 21. Analysis of variance revealed that genotypes varied significantly for all the characters under study. Based on the D^2 value, the 113 genotypes were grouped into 10 clusters (Fig 1). The largest cluster (II) accommodated about 26 (23.00%) of the genotypes followed by cluster VII 23 (20.35%), cluster V 22 (19.46%) and IV 21 (18.58%). On the other hand cluster VIII accommodated the smallest number of genotypes (0.88%) followed by cluster VI (1.77%), X (2.65%) and cluster III (3.54%) respectively.

The intra and inter-cluster distances (D^2) values are presented in Table 22. The intra-cluster distance was lower than the inter-cluster distances, which suggested heterogeneous and homogenous nature between and within groups, respectively. The highest intra-cluster distance (3.42) was observed in cluster IX, followed by cluster VI (3.1), X (2.78), I (2.74) and III (2.67). Minimum intra cluster distance was observed in cluster VIII (0.00) contained only one accession and, hence, the intra cluster distance was zero. This is followed by cluster II (1.36) and V (1.4) Table 22.

The magnitude of inter- cluster distance (D^2) were generally high and were indicators for the presence of genetic divergence in genotypes. The highest inter-cluster distance (11.17) was observed between cluster I and X, followed by cluster III and cluster IX (10.63) and cluster III and X (10) suggesting wide diversity among the genotypes included in these clusters and crossing between these clusters will result in high heterotic response and thereby better segregants. Cluster VII, VIII, IX and X were most divergent with cluster I, this indicates wide relationship between the clusters. The lowest inter-cluster distance (D2) was observed between cluster IV and V (2.33) followed by cluster II and V (2.67) and cluster IV and VII (2.72) which indicates that, genotypes involved in these clusters have low genetic diversity and they are closely related (Fig 2).

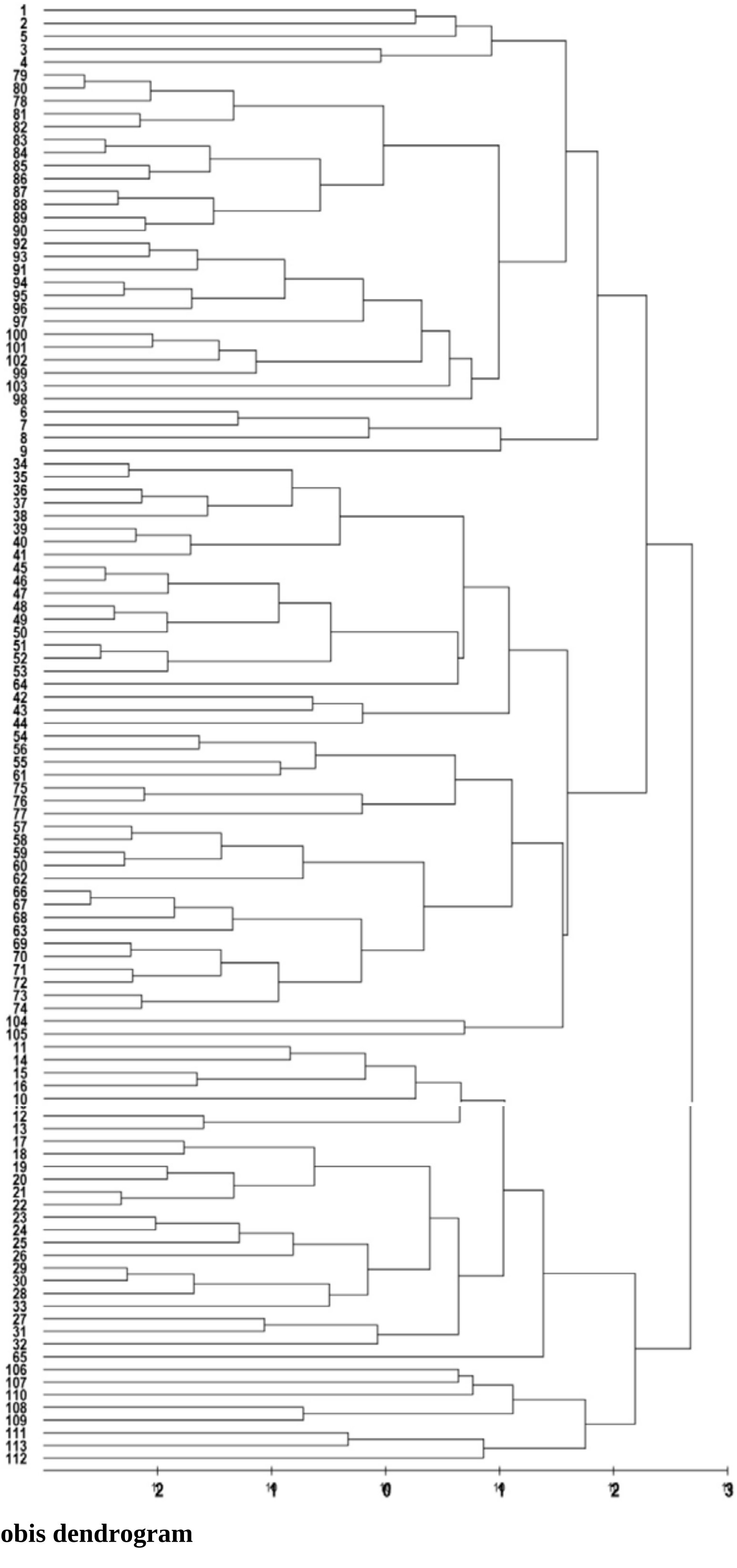


Fig 1: Mahalanobis dendrogram

Table 21: Clustering of genotypes based on Mahalanobies D^2 analysis

Clusters	Number of genotypes with % share		Genotypes
I	5	4.42%	DH-5, DH-36, DH-228, DH-246, DH-318
II	26	23.00%	NDC-68, NDC-80, NDC-82, NDC-90, NDC-94, NDC-100, NDC-106, NDC-109, NDC-110, NDC-111, NDC-118, NDC-119, NDC-120, RD-120, RD-387, RD-391, RD-394, RD-400, RD-409, RD-410, RD-414, RD-422, RD-424, VDVIGL-26, VDVIGL-37, VDVIGL-40,
III	4	3.54%	DH-352, DH-352-1, DH-261, DH-268
IV	21	18.58%	LCC-231, CS -62 , CS -63, CS -64, CS -65, CS -66, CS -67, CS -69, CS -70, JCR -379, JCR -380, JCR -389, JCR -390, JCR -391, JCR -401, JCR -404, JCR -405, JCR -406, JCR -407, LCC-144, LCC-164
V	22	19.46%	LCC-166, LCC-168, LCC-170, LCC-174, LCC-191, LCC-193, LCC-197, LCC-226, LCC-229, LCC-230, LCC-234, LCC-241, LCC-244, LCC-247, LCC-250, NDC-1, NDC-3, NDC-4, NDC-10, NDC-14, NDC-31, NDC-38
VI	2	1.77%	VDVIGL-49, VDVIGL-50
VII	23	20.35%	DH-276, DH-278, DH-279, DH-280, DH-281, DH-283, COR-36, COR-37, COR-38, COR-39, COR-40, COR-42, COR-43, COR-44, COR-45, COR-49, COR-50, COR-53, COR-54, COR-55, COR-56, CS -60, CS -61
VIII	1	0.88%	LCC-232
IX	5	4.42%	VDVIGL-74, VDVIGL-103, VDVIGL-117, VDVIGL-127, GC-1
X	3	2.65%	GC-2, AD -1, H. Anand

Table 22: Average intra and inter-cluster distance (D^2) values in 113 coriander genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	7.51 (2.74)	12.74 (3.57)	25.50 (5.05)	33.87 (5.82)	20.25 (4.50)	51.27 (7.16)	60.84 (7.80)	74.48 (8.63)	97.42 (9.87)	124.77 (11.17)
II		1.85 (1.36)	24.80 (4.98)	17.47 (4.18)	7.13 (2.67)	25.00 (5.00)	39.69 (6.30)	51.27 (7.16)	58.22 (7.63)	75.69 (8.70)
III			7.13 (2.67)	29.38 (5.42)	23.62 (4.86)	70.56 (8.4)	47.61 (6.90)	39.44 (6.28)	113.00 (10.63)	100.00 (10.00)
IV				2.25 (1.50)	5.43 (2.33)	24.6 (4.96)	7.40 (2.72)	26.63 (5.16)	39.06 (6.25)	42.38 (6.51)
V					1.96 (1.40)	22.28 (4.72)	17.56 (4.19)	34.81 (5.90)	45.97 (6.78)	56.55 (7.52)
VI						9.61 (3.10)	37.58 (6.13)	69.72 (8.35)	31.92 (5.65)	56.25 (7.50)
VII							2.37 (1.54)	26.32 (5.13)	39.31 (6.27)	33.99 (5.83)
VIII								0.00 (0.00)	86.86 (9.32)	39.94 (6.32)
IX									11.70 (3.42)	37.45 (6.12)
X										7.73 (2.78)

Value in parenthesis: Square root value of D^2

Table 23: Cluster means of coriander genotypes

Clusters	Plant height (cm)	Number of basal leaves	Length of basal leaves (cm)	Primary branches	Secondary branches	Umbel / plant	Umbellets /umbel	Seeds /umbellet	Number of seeds/umbel	Test weight (g)	Seed yield/plant (g)
I	56.24	2.41	3.76	3.70	17.08	29.64	4.35	3.99	32.89	8.09	14.18
II	65.92	2.92	5.05	4.91	17.67	35.27	4.82	4.44	26.84	9.67	9.66
III	57.06	2.42	3.79	4.08	15.90	68.94	6.20	4.11	32.02	8.93	15.45
IV	78.78	3.79	6.72	6.40	22.18	51.21	5.47	5.32	32.95	12.80	13.50
V	72.73	3.39	5.98	5.79	19.76	43.99	5.17	4.97	33.56	10.93	11.39
VI	95.51	4.94	8.30	5.53	19.54	28.13	4.44	4.60	23.64	10.80	8.56
VII	87.89	4.27	7.44	7.45	24.72	60.29	5.83	5.82	38.14	15.22	14.23
VIII	73.41	3.40	5.99	5.80	31.90	97.73	6.67	5.00	30.42	10.99	11.53
IX	100.25	4.37	8.87	9.47	22.42	29.01	4.45	6.68	22.14	19.17	7.96
X	107.93	4.80	6.97	8.88	28.74	77.24	6.29	6.59	18.70	17.49	6.82

4.5.2 Cluster mean analysis

There were considerable differences between cluster means for most of the characters, Table 23. On the basis of cluster analysis the cluster means indicated that mean seed yield per plant was highest in cluster III (15.45 g) followed by cluster VII (14.23g). Cluster X followed by cluster IX had the lowest mean seed yield per plant. Thus diversity for seed yield per plant was observed among the clusters. Perusal of the cluster means for other traits also indicated diversity for most of the traits. Some trends were also observed. Cluster X had highest mean for plant height, primary branches and seeds per umbellet. This cluster also had lower number of seeds per umbel. Cluster VII containing single genotype recorded highest mean values for secondary branches, umbels per plant and umbellates per umbel. Seeds per umbellate cluster IX and number of seeds per umbel in cluster VII showed highest values. For particular characters, these, clusters may be useful in crop improvement programme.

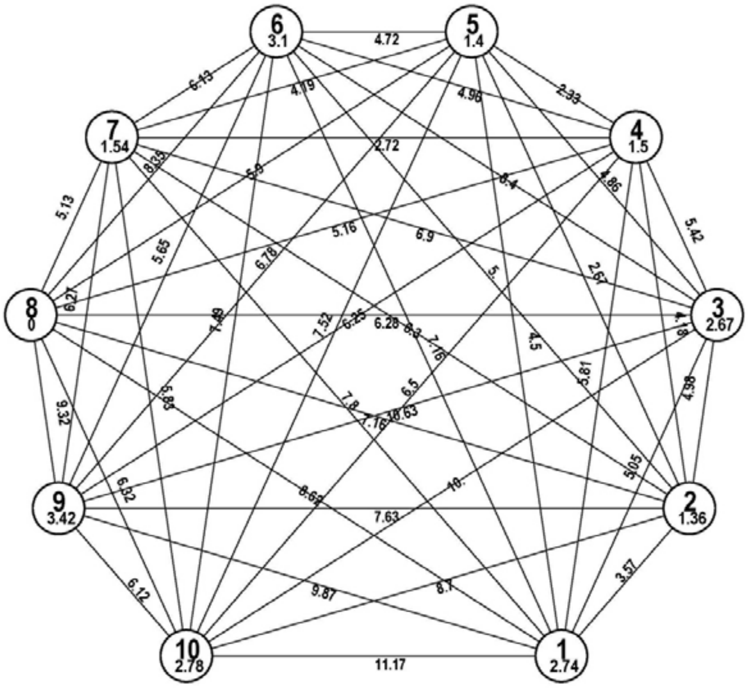


Fig 2: D^2 cluster distance dendrogram

4.6 Molecular characterization

The RAPD and ISSR markers were used for screening of 48 genotypes of coriander and the results have been presented under the following headings:

DNA isolation

The DNA was isolated using CTAB method and tested for its quantity and quality using agarose gel (0.8%) electrophoresis.

A. RAPD analysis

Primer selection and polymorphism exhibited

Thirty eight RAPD primers were initially screened out of which eighteen primers amplified unambiguous, readable and reproducible polymorphic bands. A total of 146 alleles were produced from the selected 18 primers out of which 113 alleles were polymorphic. The number of bands varied from 3 to 12 and the size ranged from 80 to 1200 bp. The highest number of bands (12) was obtained for primer OPD-01, while the lowest number alleles (3) was observed for primer OPO-08 with an average of 8.11 bands per primer. Highest number of polymorphic bands were observed for primer OPN-02 and the lowest number of polymorphic bands were observed for primer OPO-08 and OPO-14. The percentage of polymorphism ranged from 50.00 to 100.00 per cent with an average of 77.39 % polymorphism per primer. Primer OPA-02, OPA-08 and OPM-02 revealed the highest polymorphism (100.00%), whereas the primer OPO-14 and OPP-07 exhibited the lowest polymorphism (50.00%). All these details are presented in Table 24. The gel pictures of primers OPA-02 and OPM-02 are presented in plates 12 &13.

Table: 24: Polymorphism exhibited by RAPD primers in coriander genotypes

Sl. No.	Primer series	Sequence	Total number of band	No. PB	No. MB	% of PM	Mol. wt range (bp)
1	OPA-02	TGCCGAGCTG	9	9	0	100	150- 1200
2	OPA-05	AGGGGTCTTG	10	8	2	80	150- 1200
3	OPA-08	GTGACGTAGG	7	7	0	100	200-800
4	OPA-10	GTGATCGCAG	4	3	1	75	200-960
5	OPB-05	TGCGCCCTTC	10	6	4	60	150-1200
6	OPD-01	ACCGCGAAGG	12	9	3	75	150-1100
7	OPD-03	GTCGCCGTCA	7	7	0	100	300-950
8	OPE-02	GGTGCGGGAA	7	5	2	71.42	150-1100
9	OPF-04	GGTGATCAGG	9	5	4	55.55	170-900
10	OPF-07	CCGATATCCC	8	5	3	62.5	200-950
11	OPG-05	CTGAGACGGA	11	9	2	81.8	310-1100
12	OPK-05	TCTGTCGAGG	7	5	2	71.42	150-850
13	OPL-08	AGCAGGTGGA	9	8	1	88.88	250-1050
14	OPM-02	ACAACGCCTC	8	8	0	100	150-900
15	OPN-02	ACCAGGGGCA	11	10	1	90.9	210-1050
16	OPO-08	CCTCCAGTGT	3	2	1	66.66	350-700
17	OPO-14	AGCATGGCTC	4	2	2	50	80-1080
18	OPP-07	GTCCATGCCA	10	5	5	50	220-1200
Total			**146**	**113**	**33**		
Average			**8.11**	**6.27**	**1.88**	**77.39**	

PB : Polymorphic band, MB: Monomorphic band, PM: Polymorphism, Mol. Wt: Molecular weight

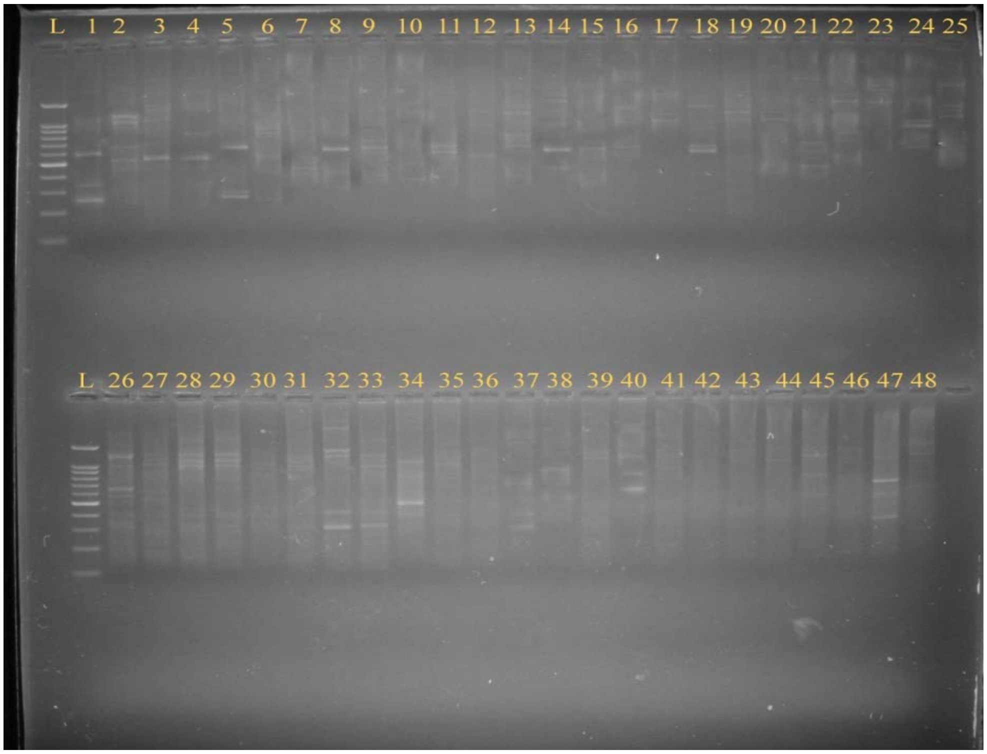


Plate 12. Gel picture of 48 coriander genotypes produced using RAPD primer OPA-02

1. JCR-390
2. RD-120
3. LCC-164
4. RD-391
5. RD-421
6. DH-5
7. DH-36
8. DH-228
9. RD-394
10. DH-246
11. RD-387
12. LCC-168
13. DH-318
14. DH-352
15. DH-352-1
16. NDC-38
17. NDC-31
18. JCR-380
19. DH-261
20. DH-268
21. NDC-82
22. JCR-391
23. JCR-406
24. JCR-389
25. DH-275
26. DH-276
27. DH-278
28. DH-279
29. DH-280
30. DH-281
31. RD-414
32. DH-283
33. CS-63
34. CS-60
35. CS-62
36. CS-64
37. RD-424
38. LCC-193
39. COR-38
40. COR-40
41. LCC-174
42. LCC-191
43. JCR-407
44. COR-42
45. JCR-405
46. COR-44
47. JCR-379
48. NDC-68

Note: This applies for all gel pictures

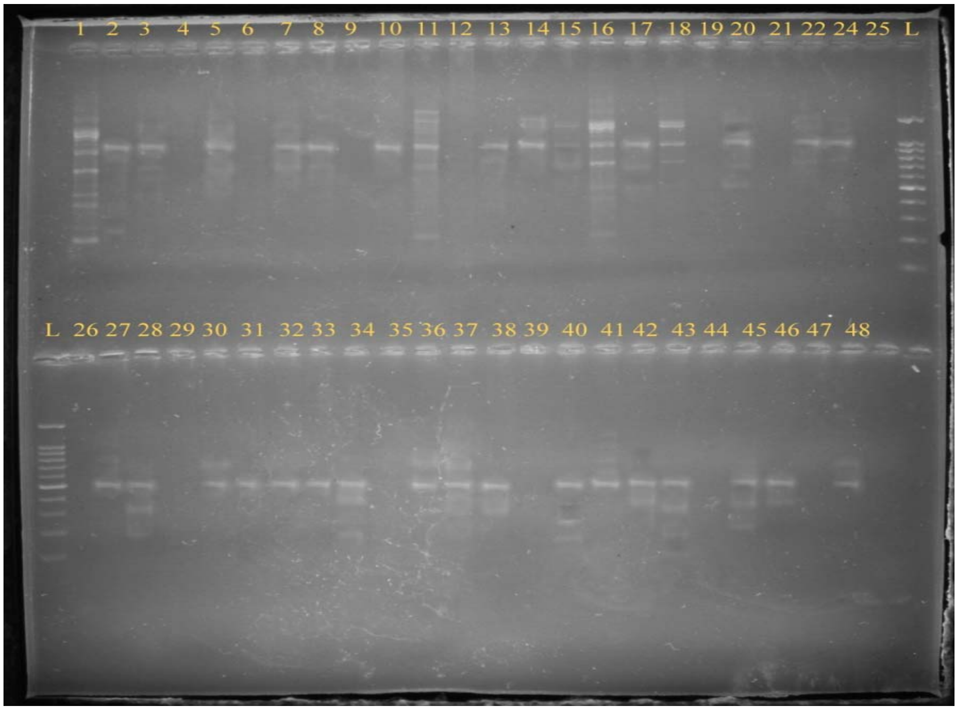


Plate 13. Gel picture of 48 coriander genotypes produced using RAPD primer OPM- 02

Cluster analysis

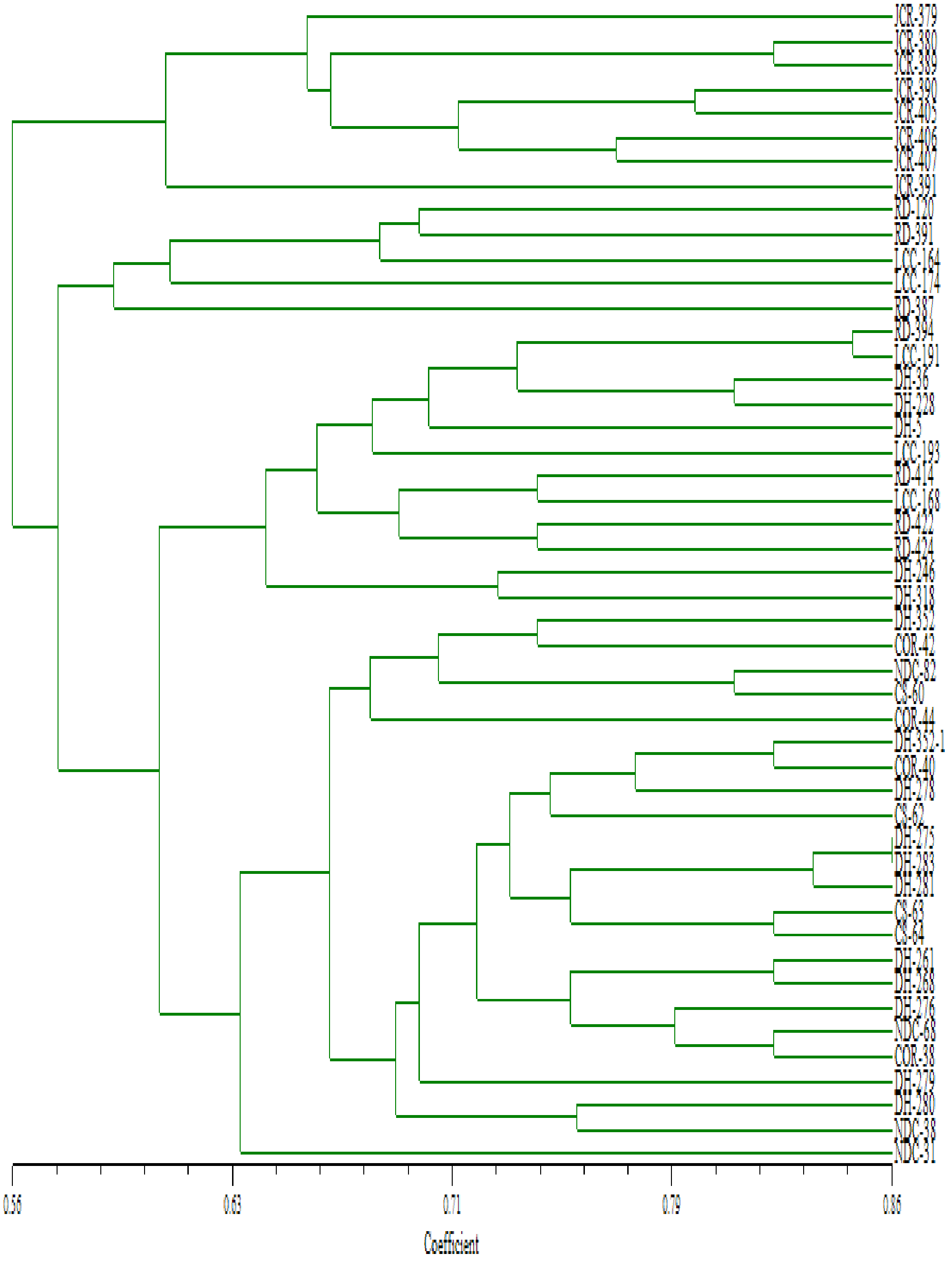
Molecular data obtained using 18 RAPD primers was used to construct dendrogram which, divided the coriander genotypes into 13 clusters (Table 25) at 0.67 similarity coefficient (Fig 3).

Table 25: Grouping of 48 coriander genotypes based on RAPD assay at 0.67% similarity coefficient

Cluster	Number of genotypes	Cluster members
I	1	JCR 379
II	2	JCR 380, JCR389
III	4	JCR 390, JCR 405, JCR 406, JCR 407
IV	1	JCR 391
V	3	RD120, RD391, LCC 164
VI	1	LCC 174
VII	1	RD 387
VIII	6	RD 394,LCC 191, DH36, DH228, DH 5,LCC 193
IX	4	RD 414, LCC 168, RD 422, RD424
X	2	DH 246, DH 318,
XI	5	DH 352,COR 42, NDC 82, CS 60, COR 44
XII	17	DH 352-1, COR 40, DH 278, CS 62, DH 275, DH 283, DH 281, CS 63, CS 64, DH 261, DH 268, DH 278, NDC 68, COR 38, DH 279, DH 280, NDC 38
XIII	1	NDC 31

The similarity co-efficient ranged from 0.56 to 0.86. In this group I, IV, VI, VII and XIII consists of only one genotype which shows that these genotype are entirely different from all other group members. Group II and X includes two genotypes (JCR- 380 and JCR-389, DH - 246 and DH-318) which belong to same geographical area i.e. Rajasthan and Haryana respectively. Group -III and IX consisted of four genotypes each (JCR 390, JCR 405, JCR 406, JCR 407 and RD 414, LCC 168, RD 422, RD424) which were from Rajasthan. Three genotypes which were collected from Rajasthan and Lam region Andra Pradesh, grouped in cluster V which includes RD120, RD391 and LCC 164. Group-VIII included six genotypes which were from Hisar and Andra Pradesh and include RD 394,LCC 191, DH36, DH228, DH 5 and LCC 193. The genotypes DH 352,COR 42, NDC 82, CS 60 and COR 44, which were collected from Hisar, Uttar Pradesh and Tamil Nadu formed group which fall under cluster number XI. Group-XII includes large number of genotypes (17), which includes genotypes collected from three geographical regions among which three genotypes was from Tamil Nadu, (CS-62, CS 63, CS 64), 2 genotypes from Utttar Pradesh NDC-38 and NDC-68 and twelve genotypes from Hisar, HR (DH 352-1, COR 40, DH 278, DH 275, DH 283, DH 281, DH 261, DH 268, DH 278, COR 38, DH 279 and DH 280).

Fig. 3: Dendrogram generated using RAPD markers in 48 coriander genotypes



B. ISSR analysis

Primer selection and polymorphism exhibited

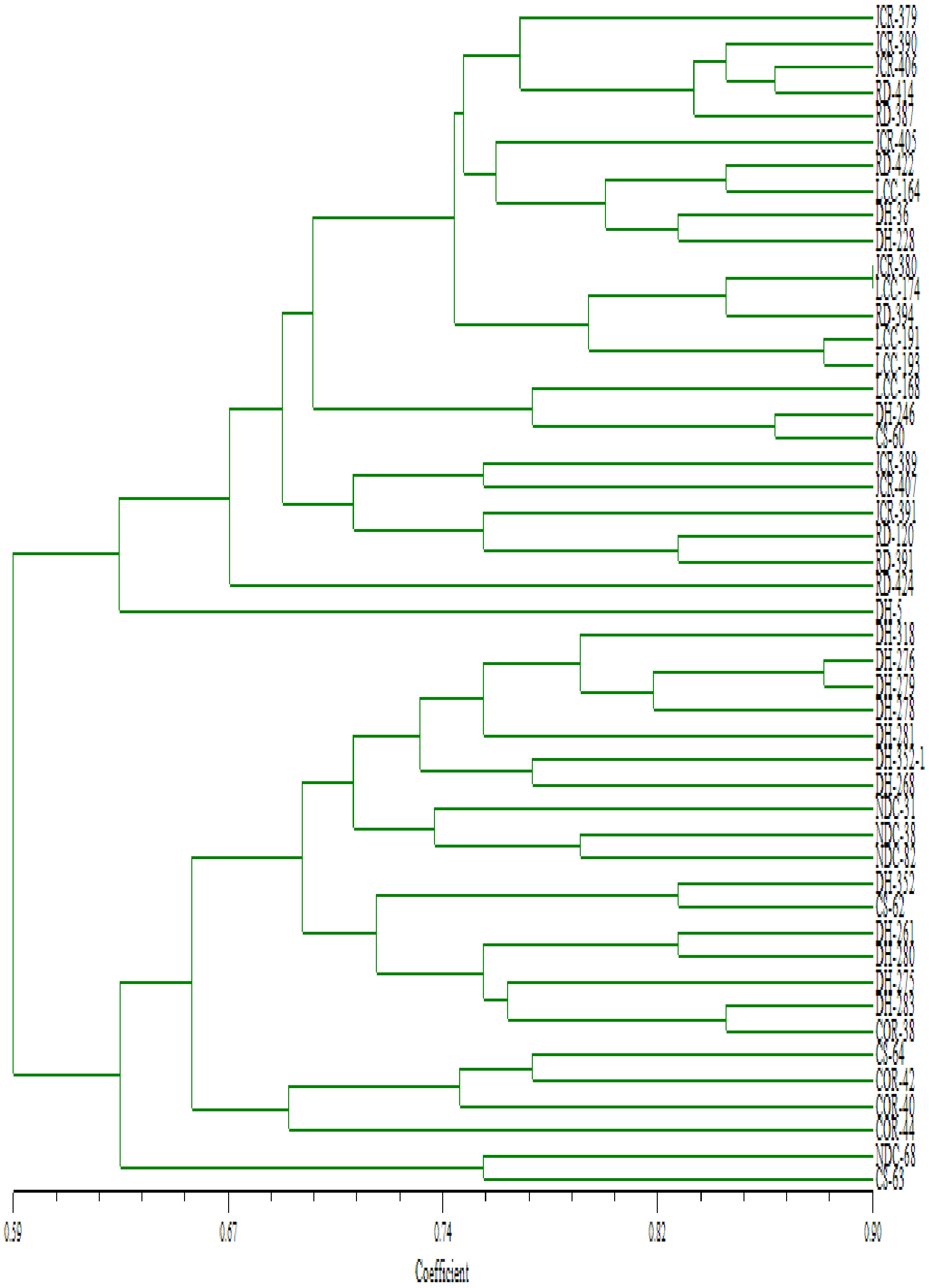
Initially twenty eight ISSR primers were screened among which eight primers amplified unambiguous, readable and reproducible polymorphic bands. A total of 60 amplification products were produced from the selected 8 primers out of which 50 bands were polymorphic. The number of bands varied from 5 to 10 and the size ranged from 150 to 1200 bp. The highest number of bands (10) was obtained for primer ISSR 27, while the lowest number of bands (5) was observed with primer ISSR 10 with an average of 7.5 bands per primer. Highest number of polymorphic bands (9) were observed in primer ISSR 27 and the lowest number of polymorphic bands (3) were observed in primer ISSR 10. The percentage of polymorphism ranged from 60.00 to 100 per cent with an average of 83.33 % polymorphism per primer. Primer ISSR 4 revealed the highest polymorphism (100 %), whereas the primer ISSR 10 exhibited the lowest polymorphism (60.00 %). The details are presented in Table 26. The gel pictures of primers ISSR 4, ISSR 6, ISSR 9 and ISSR 27 are presented in plates 14-17.

Table: 26: Polymorphism exhibited by ISSR primers in coriander genotypes

Sl. No.	Primer series	Sequence	Total number of band	No. PB	No. MB	% of PM	Mol. wt range (bp)
1	ISSR2	GGAGAGGAGAGGAGA	8	7	1	87.5	150-850
2	ISSR4	CACACACACACACACAA	8	8	0	100	350-750
3	ISSR6	AGAGAGAGAGAGAGAGT	7	6	1	85.71	200-850
4	ISSR7	GAGAGAGAGAGAGAGAT	7	6	1	85.71	150-1150
5	ISSR9	CACACACACACACACAA	9	7	2	77.77	150-950
6	ISSR10	CACACACACACACACAG	5	3	2	60	310-1200
7	ISSR25	CTCTCTCTCTCTCTCTRG	6	4	2	66.66	210-900
8	ISSR27	CACACACACACACACARC	10	9	1	90	180-950
Total			60	50	10		
Average			7.5	6.25	1.25	83.33	

PB : Polymorphic band, MB: Monomorphic band, PM: Polymorphism, Mol. Wt: Molecular weight

Fig. 4: Dendrogram generated using ISSR markers in 48 coriander genotypes



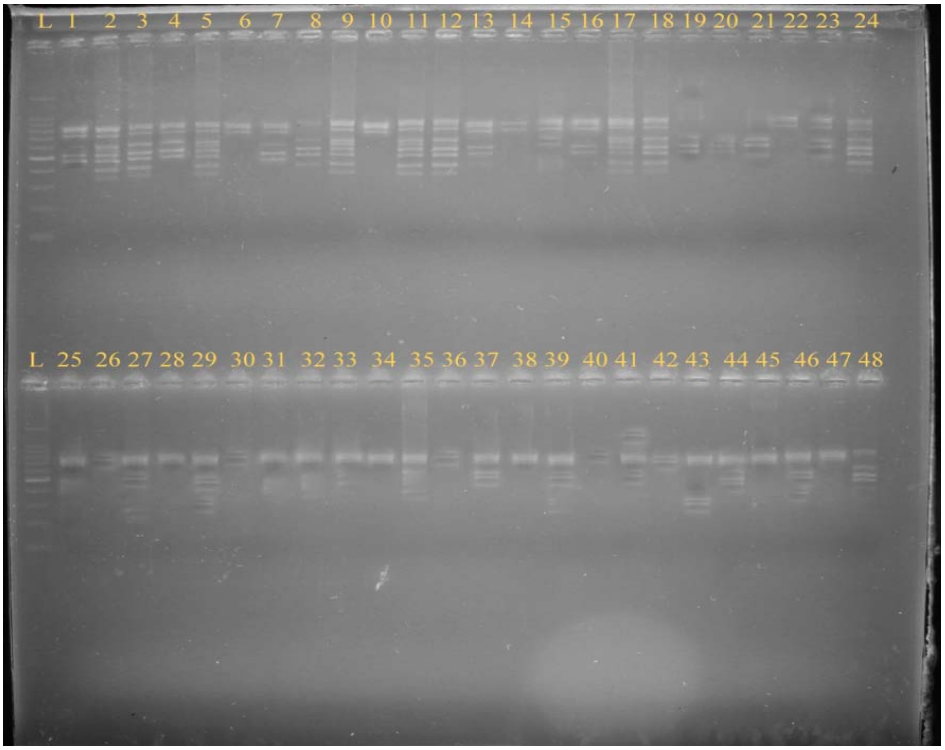


Plate 14. Gel picture of 48 coriander genotypes produced using primer ISSR-4

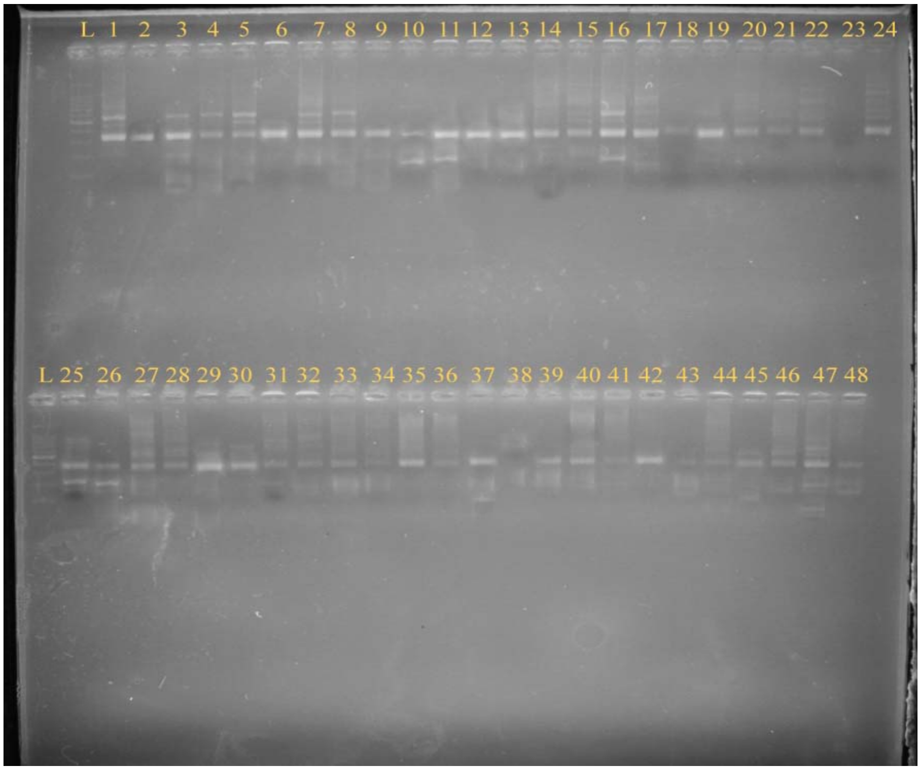


Plate 15. Gel picture of 48 coriander genotypes produced using primer ISSR-06

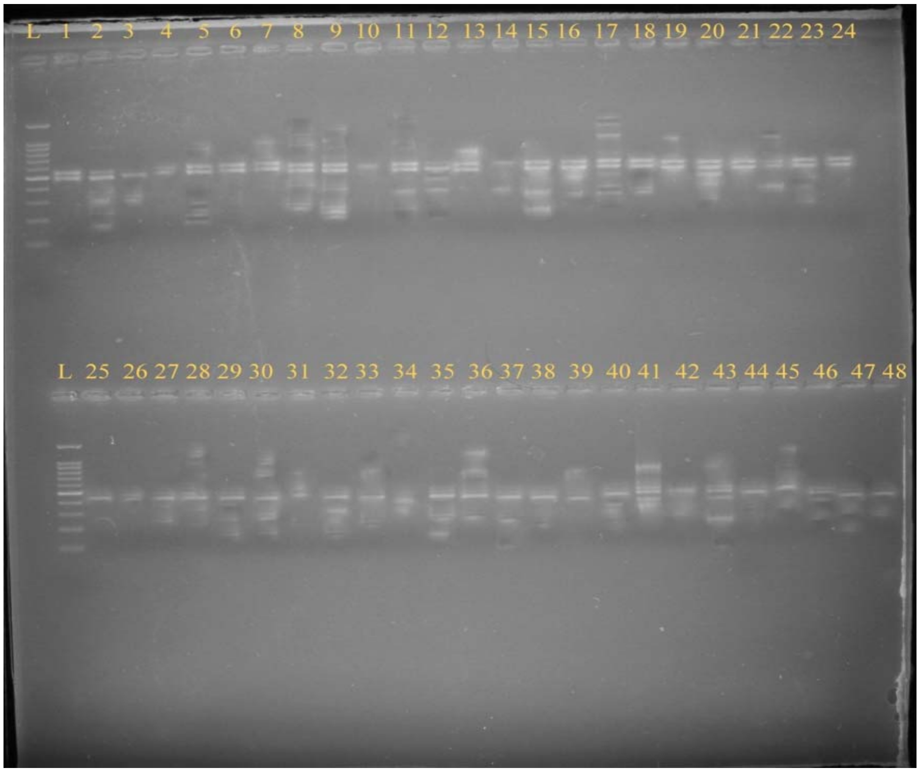


Plate 16. Gel picture of 48 coriander genotypes produced using primer ISSR-09

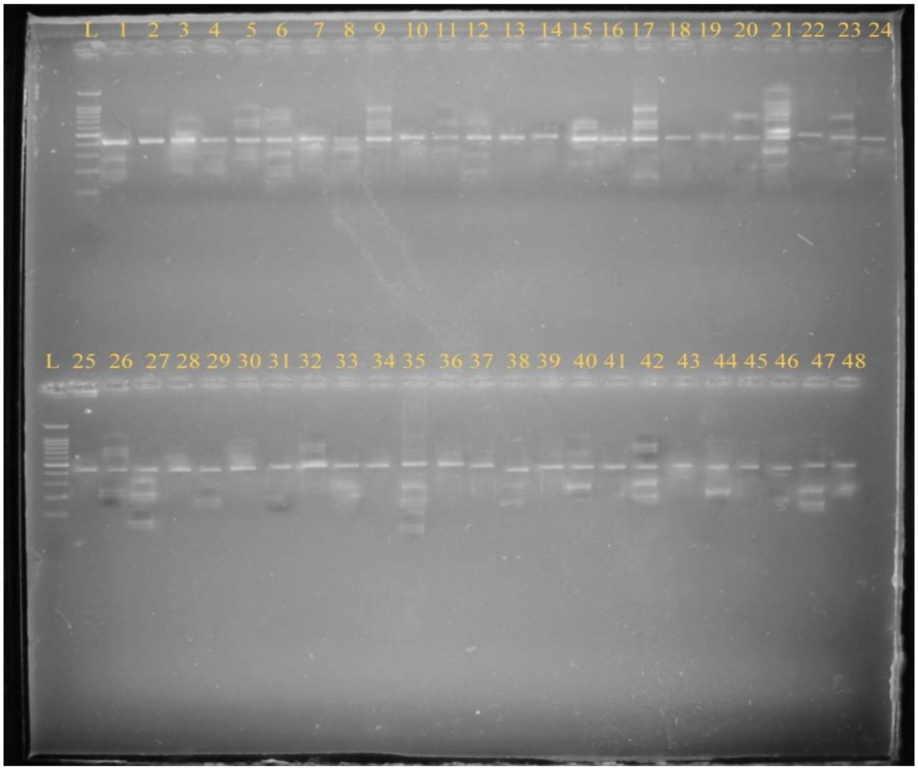


Plate 17. Gel picture of 48 coriander genotypes produced using primer ISSR-27

Cluster analysis

Molecular data obtained using 8 ISSR primers was used to construct dendrogram which divided the coriander genotypes into 13 clusters (Table 27) at 0.72 similarity coefficient (Fig. 4). The similarity co-efficient ranged from 0.59 to 0.90. At 0.75 similarity co-efficient group I accommodated maximum number (15) of genotypes (collected from Hisar, Rajasthan and Andhra Pradesh) which shows that, these genotypes are genetically similar. Groups II, VI, VIII and XI consisted 3 genotypes each i.e. (LCC 68, DH 246, and CS 60), (JCR 391, RD 120 and RD 391), (NDC 31, NDC 38 and NDC 82) and (CS 64, COR 42 and COR 40) respectively, which were collected from Rajasthan, Uttar Pradesh, Andra Pradesh and Tamil Nadu respectively. The groups V, VI and XII consisted one genotype (RD- 424 DH-5 and COR-44) which include genotypes from Hisar and Rajasthan. Group-VII included seven genotypes which were from Hisar region alone it included DH 318, DH 276, DH 279, DH 278, DH 281, DH 352-1 and DH 268. Group XI and XII included two genotypes each which were collected from Hisar Uttar Pradesh and Tamil Nadu. Group X included 5 genotypes DH 261, DH 280, DH 275, DH 283 and COR 38 all were from Hisar region.

Table 27: Grouping of 48 coriander genotypes based on IISR assay at 0.72 % similarity coefficient

Cluster	Number of genotypes	Cluster members
I	15	JCR 379, JCR 390, JCR 406, RD 414, RD 387, JCR 405, RD 422, LCC 164, DH 36, DH 228, JCR 380, LCC 174, RD 394, LCC 191, LCC 193
II	3	LCC 68, DH 246, CS 60
III	2	JCR 389, JCR 407
IV	3	JCR 391, RD 120, RD 391
V	1	RD 424
VI	1	DH 5
VII	7	DH 318, DH 276, DH 279, DH 278, DH 281, DH 352-1, DH 268,
VIII	3	NDC 31, NDC 38, NDC 82
IX	2	DH 352, CS 62
X	5	DH 261, DH 280, DH 275, DH 283, COR38
XI	3	CS 64, COR 42, COR 40
XII	1	COR 44
XIII	2	NDC 68, CS 63

Comparison between RAPD and ISSR results

Results from clustering of 48 coriander genotypes using RAPD and ISSR formed thirteen groups each at 0.67 and 0.72 similarity coefficient. Similarity coefficient ranged from 0.56 to 0.85 in RAPD and 0.59 to 0.90 in ISSR. Average polymorphism exhibited by RAPD is 77.39 %, by ISSR is 83.33% and combined average polymorphism of both markers is 80.36 %.

Average number of bands per primer in RAPD 8.11, in ISSR 7.50 and combined (RAPD and ISSR) 7.80 (Table 28).

Table 28: Comparison of DNA marker systems (RAPD and ISSR) in coriander

Marker system	Number of primers	Total number of bands	Average number of bands per primer	% polymorphism
RAPD	18	146	8.11	77.39
ISSR	8	60	7.50	83.33
RAPD+ISSR	26	103	7.80	80.36

There is no much difference between the polymorphism exhibited by these two primers. But, with respect to assessment of diversity both markers proved best. Clustering pattern obtained from both the markers found different. But, some members of the clusters showed similarity between the members in both the cases like (RD-120 and RD-391), (DH-275 and DH-283), (DH-279 and DH-278), (JCR-390, JCR-405 and JCR-406) and (DH-36, DH-228 and LCC-193). The results indicated that both the marker systems RAPD and ISSR, individually or combined can be effectively used in determination of genetic relationship among coriander genotypes.

CHAPTER-V

DISCUSSION

The present investigation entiteled “Genetic divergence studies on coriander (*Corianadrum sativum* L.)”, an attempt has been made to evaluate the available germplasm collected around the country. The information on extent and nature of variability present in the germplasm collection and the degree of association of different morphological attributes among themselves and seed yield is necessary not only in finding the suitability of material for breeding programme, but also in devising suitable selection criteria. So, the experiment was, therefore, undertaken to estimate the some of these parameters include genotypic (GCV) and phenotypic (PCV) coefficient of variation, broad sense heritability and genetic advance, genotypic and phenotypic correlations, path coefficient and D^2 statistics. These helps in base selection procedure to a required balance when, two opposite desirable characters affecting the principle characters are also being selected. It also helps in simultaneous improvement of different characters (Falconer, 1981).

5.1 DUS characterization

The basic objective of germplasm characterization is to test the occurrence of traits that helps in identifying a particular variety. Characterization of the cultivars developed on the ideotype concept to establish their distinctiveness is of crucial importance to fulfill the conditions of Distinctness, Uniformity and Stability (DUS) as laid down by the International Union for Protection Plant Varieties (UPOV, 1994) and Seed Act 1996, Government of India. The characters used to distinguish cultivars must be capable of precise description and recognition and are considered important only when they are unduly subjected to environmental influence.

A. Plant characters

Growth habit of the plant shows a great divergence. All the 113 genotypes of coriander were categorised in to erect (30 genotypes), semi erect (60 genotypes) and spreading (23 genotypes). Similar results was reported by Rana (2006) thirty two genotypes of cluster bean and grouped the genotypes into erect (8 genotypes) and bushy (24 genotypes). In the present research work, it was noticed that there was a less variation in the 113 genotypes on the basis of stem pigmentation, stem pubescence and streaks on stem. Based on stem pigmentation genotypes observed and recorded as absent and present (82 and 31 genotypes). Stem pubescence is non variable in this study and it was absent in all 113 genotypes. Final observation on the streaks on stem showed 100 percent presence and it is also considered as non-variable character.

Nodal pigmentation showed much variation recorded as present (59 genotypes) and absent (54 genotypes). Similar, results were observed by Sengupta (2011) in fenugreek. On the basis of leaf margin the genotypes were classified into serrated (82 genotypes) and deeply serrated (31 genotypes). However, wide range of variation was found in 113 genotypes on the basis of leaf luster and leaf colour. They were classified as shiny (68 genotypes) and dull (45 genotypes) and variation in leaf colour was observed as dark green (37 genotypes) and green (76 genotypes). Corolla color showed the considerable variation as recorded as white (93 genotypes) and pink (20 genotypes). Similar results were reported by Dahiya et al. (1993) in chickpea, Kahre et al. (1998) in soybean, Singh (2001) in kabuli and Chauhan (2003) and Sengupta (2011) in fenugreek.

B. Seed characters

Seed colour had shown variation in the genotypes differentiated into two groups namely, Light brown (50 genotypes) and Brown (63 genotypes). Chauhan (2003) studied on thirty genotypes of fenugreek on the basis of seed colour and found wide range of diversity in seed colour. Seed ridge and seed shape were also a valuable character for varietal identification as both showed a wide variation. On the basis of seed ridge genotypes were classified into prominent (78 genotypes) and non-prominent (35 genotypes). While on the basis of seed shape the 113 genotypes were classified into slightly round (56 genotypes) oblong (38 genotypes) and oval (20 genotypes). Seed size varied from small (18 genotypes), medium (32 genotypes) and large (63 genotypes). Similar study on shape, size, and colour in rice was found helpful in characterizing the cultivars (Subramaniam and Ramakrishnan, 1978) and other researchers also characterized different crops using morphological characters such as sunflower (Jagadeesh et al., 1994), fenugreek (Chauhan, 2003) and lentil (Kahre et al., 2006).

5.2 Variability studies

The magnitude of heritable variability is the most important component in any breeding material as it has a close bearing on response to selection. Therefore, occurrence of adequate genetic variability is an essential pre requisite for all crop improvement programmes. Knowledge of the amount of variability and heritability aids the crop breeder for effecting improvement in any crop by choosing suitable breeding technique. The source material for genetical improvement would be identified by studying the amount of variability available in the gene pool or germplasm. This necessitates the evaluation of the assemblage for various requirements in the single environment. Accordingly, coriander germplasm evaluated for their genetic potential in respect of yield and yield attributes, so as to identify source material to enhance productivity.

The results of the analysis of variance for different quantitative characters in 113 genotypes of coriander indicated that there was highly significant difference among genotypes yield and yield attributing parameters through plant height (cm), number of basal leaves , length of basal leaves (cm), primary branches, secondary branches, umbels per plant, umblets per plant, seeds per umblet, number of seeds per umbel, test weight (g) and seed yield per plant (g). Similarly, highly significant variations for all characters studied and reported by Sharma and Sharma (1989), Sridhar *et al.* (1990 b), Ali *et al.* (1993), Bhandari and Gupta (1991), Idhal *et al*. (2009) and Beemnet *et al.* (2011), Mengesha and Alemaw (2010) in coriander.

5.2.1 Genetic components of variation

Plant height was recorded at matured stage showed that there was a significant difference among the genotypes which varied from 53.80 cm (DH-352) to 109.49 cm (VDVIGL-103). Plant height had moderate phenotypic and genotypic coefficients of variation, indicating that there was a broad genetic variability for this character. The plant height exhibited high heritability coupled with high genetic advance as percent of mean, indicating that selection of genotype for plant height in early generations would be effective. Similar results were obtained by Rajput and Singh (2003), Patel *et al.* (2008) in coriander and ajowan.

The number of basal leaves ranged between 2.23 (DH-352) to 5.26 (VDVIGL-117) with mean of 3.57. The estimate of phenotypic and genotypic coefficients of variation were high and moderate. High heritability and high genetic advance as percent mean was observed for number of basal leaves and similar results reported by Beemnet *et al.* (2011), Mengesh and Alemaw (2010), Singh *et al.* (2006) and Rajput and Singh (2003), indicating that these characters are less influenced by environmental factors and are under the control of additive gene effect for improvement for such character would be rewarding. Length of basal leaves recorded at 30 days of plant growth ranged from 3.54 (DH-352) to 9.31 (VDVIGL-117). This character showed high phenotypic and genotypic coefficients of variation. Heritability estimate was recorded high with high genetic advance as per cent of mean indicating that these characters are less influenced by environmental factors and are under the control of additive gene effect for improvement for such character selection would be rewarding and similar results reported by (Beemnet *et al.* 2011, Mengesh and Alemaw 2010; Singh *et al*., 2006: Rajput and Singh 2003).

The number of primary branches ranged between 3.24 (DH-352) and 10.16 (VDVIGL-117) with mean of 6.14. High phenotypic and genotypic coefficients of variation were recorded. High heritability was observed along with high genetic advance as per cent of mean, which indicated that maximum amount of variability is present in genotypes. These results are in conformity with Singh et al. (2005) in coriander. High heritability coupled with high genetic advance as percent of mean suggested additive gene action for this trait, thus, for improving this trait, the selection could be effective in early generations. Similar results have also been reported by Pushpa et al. (2010), Singh et al. (2012) and Jain et al. (2013) in fenugreek. Secondary branches ranged from 13.11(DH-246) to 31.90(LCL-232). Secondary branches had moderate phenotypic and genotypic coefficients of variation, indicating that there was a broad genetic variability for this character. High heritability coupled with high genetic advance as percent of mean suggested additive gene action for this character, thus, for improving this trait, the selection could be effective in early generations. Similar results have also been reported by Pushpa et al. (2010), Singh et al. (2012), Jain et al. (2013) and Verma et al. (2016) in fenugreek.

Number of umbels per plant varied from 18.09 (DH-246) to 97.73 (LCL-232) with grand mean of 47.45. The estimates of phenotypic and genotypic coefficients of variation were high for this trait. The trait had high heritability coupled with very high genetic advance as per cent of mean. Similar, results have been reported by Beemnet *et al.* (2011), Mengesh and Alemaw (2010), Singh *et al.* (2006) and Rajput and Singh (2003), indicating that these characters are less influenced by environmental factors and are under the control of additive gene effect for improvement for such character selection would be rewarding. The number of umbellets per umbel varied from 3.68 (DH-246) to 6.66 (LCL-232). Umbelletes per umbel had moderate phenotypic and genotypic coefficients of variation, indicating that there was a broad genetic variability for this character. High heritability and high genetic advance as percent mean was observed for number of umbellets per umbel. Similar results were reported Beemnet *et al.* (2011), Mengesh and Alemaw (2010), Singh *et al.* (2006) and Rajput and Singh (2003), indicating that these characters are less influenced by environmental factors and are under the control of additive gene effect.

Seeds per umbellet in present genotypes varied from 3.54 (DH-261) to 6.95 (VDVIGL-74). Moderate Phenotypic coefficients of variation and genotypic coefficients of variation was recorded for number of seeds per umbellet. The trait had high heritability coupled with high genetic advance as per cent of mean. Indicates variability existing in the genotypes for these characters and offers good scope for improvement by simple selection through these characters. Similar results were obtained by Rajput and Singh (2003), Patel *et al.* (2008), in coriander and ajowan. The number of seeds per umbel ranged from 16.83 (H. Anand) to 47.37 (CS-60). Number of seeds per umbel moderate phenotypic and genotypic coefficients of variation. High heritability and high genetic advance as percent mean was observed for number of seeds per umbel and similar results reported by Beemnet *et al.* (2011), Mengesh and Alemaw (2010), Singh *et al.* (2006) and Rajput and Singh (2003), indicating that these characters are less influenced by environmental factors and are under the control of additive gene effect.

The test weight ranged from 6.87 g (DH-261) to 21.45 g (VDVIGL-74) with an overall average mean of 12.24 g. The Phenotypic coefficients of variation and genotypic coefficients of variation were high for this character. High heritability was associated with high genetic advance as per cent of mean indicates maximum variability existing in the genotypes for these characters and offers good scope for improvement by simple selection through these characters. Similar results were obtained by Rajput and Singh (2003), Patel *et al.* (2008), in coriander and ajowan. The seed yield ranged from 6.37 g (H. Anand) to 19.49 g (JCR-79). Seed yield per plant had high phenotypic and genotypic coefficients of variation, with high heritability and genetic advance as percent of mean indicates maximum variability existing in the genotypes for these characters and offers good scope for improvement by simple selection through these characters. Similar results were obtained by Rajput and Singh (2003), Patel *et al.* (2008), in coriander and ajowan.

In conclusion, heritability estimates along with genetic gain (genetic advance as per cent of mean) is more useful than heritability alone in predicting the resultant effect for selecting the best individuals (Johnson *et al.*, 1955). Genetic advance is the measure of improvement that can be achieved by practicing selection in a population. High heritability with low genetic advance indicates the importance of non-additive gene action, while high heritability with high genetic advance indicates the additive gene effects. In the present study, high genetic advance as per cent of mean coupled with high heritability was observed in all the characters like plant height, number of basal leaves, length of basal leaves, primary branches, secondary branches and most of yield attributing traits like umbels per plant, number of umbellets per umbel, number of seeds per umbel and seed yield per plant. Thus, these characters were under additive gene effect and could be improved by simple selection procedure. The high heritability is being exhibited due to favorable influence of environment rather than genotype and selection for such trait may not be rewarding. The findings are in accordance with results reported by Singh *et al* (2008), Rajput and Singh (2003), Kailashchandra *et al.* (2000), Singh *et al.* (2006), Beemnet *et al.* (2011), Mengesh and Alemaw (2010) in coriander and fenugreek.

5.3 Correlation analysis

In any crop improvement programme, it becomes necessary to have simultaneous progress of more than one character, especially in the complex character like yield, which is influenced by many other traits. This is due to the physiological and linkage relationship of genes governing various characters. Hence, knowledge of correlations among different economical characters is important in selection programmes. Positive correlation makes simultaneous improvement in two or more attributes possible, whereas, negative association indicates the need to compromise between desirable characters. In the present investigation, the genotypic correlation coefficient was higher than phenotypic correlations for all the characters, indicating little influence of environment and the presence of inherent association between various characters. Similar results were reported by Singh *et al.* (2005), Abhay *et al.* (2011) in coriander and fenugreek.

The seed yield per plant had significant and positive association with number of seeds per umbel, umbelletes per umbel, umbels per plant and secondary branches at both genotypic and phenotypic levels. Since, these associations or characters are in the desirable direction, selection for these traits may improve the yield per plant. Similar results were reported by Singh *et al.* (2006), Kole and Mishra (2006). At genotypic and phenotypic level, plant height was significantly positively correlated with number of basal leaves, length of basal leaves, primary branches, secondary branches, umbels per plant, umbellets per umbel, seeds per umbellet and test weight. Whereas, number of seeds per umbel had non-significant positive association. Similar results are reported by Singh et al. (2008) in coriander.

All genotypic and phenotypic level, number of basal leaves was significantly positively correlated with length of basal leaves, primary branches, secondary branches, umbels per plant, umbellets per umbel, seeds per umbellet, number of seeds per umbel and test weight. Whereas, seed yield had non-significant positive association. Similar results obtained for length of basal leaves by Singh *et al.* (2006), Ali *et al.* (1993) in coriander. At genotypic and phenotypic level, primary branches and secondary branches were significantly and positively correlated with number of secondary branches, umbels per plant, umbellets per umbel, seeds per umbellet, number of seeds per umbel and test weight. Similar results are reported by Singh *et al.* (2006), Ali *et al.* (1993) in coriander.

In phenotypic and genotypic correlation studies, umbels per plant receded significant and positive correlation with umbellets per umbel, seeds per umbellet, number of seeds per umbel and test weight and umbellets per umbel recorded significant and positive correlation with seeds per umbellet, number of seeds per umbel and test weight. Similar results were reported by Shridhar *et al.* (1990 b) Singh *et al.* (2006), Kailashchandra *et al.,* (2000) in coriander and fenugreek. If both genotypic and phenotypic level, seeds per umbellet showed the significant and positive correlation with number of seeds per umbel and test weight. Similarly, number of seeds per umbel were positively and significantly correlated with test weight in both conditions. Similar results are reported by Shridhar *et al.* (1990 b) Singh *et al.* (2006), Kailashchandra *et al.,* (2000) in coriander and fenugreek.

5.4 Path coefficient analysis

Though correlation analysis indicated the association pattern of component traits with yield, they simply represent the overall influence of particular trait on yield rather than proving cause and effect relationship. The technique of path analysis developed by Wright (1921) and demonstrated by Dewey and Lu (1959) facilitates in portioning the correlation coefficients into direct and indirect contribution of various characters to the yield. As such, it measures the direct influence of one variable upon others. Such information would be of great value in enabling the breeder to specifically identify important component traits of yield and utilize the genetic stock for improvement in a planned way. In the present study, path coefficient analysis was worked out using yield per plant as a dependent character and other ten selected characters as independent variables. It measures the direct as well as indirect effects of independent variables (characters) on one variable through other traits.

Among 11 characters chosen for path analysis, the results reveals that high positive direct effects were exerted by traits like number of basal leaves, length of basal leaves, secondary branches, umbels per plant, seeds per umbellet, number of seeds per umbel and test weight on seed yield per plant. Similar, results were obtained by Singh et al. (2006), Prajapati *et al.* (2010), Kole (2004) and Jain *et al.* (2013) in coriander and fenugreek. Other characters viz., plant height, primary branches and umbellets per umbel showed moderate negative direct effect on seed yield per plant. These results are in accordance with findings of, Singh *et al.* (2008), Singh *et al.* (2006), Prajapati *et al.* (2010) in coriander and fenugreek.

5.5 Genetic divergence

Based on the D^2 values, the 113 genotypes were grouped into 10 clusters. The largest cluster (II) accommodated maximum number of genotypes followed by cluster VII, cluster V and IV. On the other hand cluster VIII accommodated the less number of genotypes followed by cluster VI, X and cluster III. This is in agreement with Singh et al. (2005) in coriander. Likewise, Sirohi and Dar (2009) reported that changing of genetic material, genetic drift, natural variation and artificial selection other than ecological and geographical diversifications are the causes of genetic divergence. The intra-cluster distance was lower than the inter-cluster distances, which suggested heterogeneous and homogenous nature between and within groups, respectively. The highest intra-cluster distance was observed in cluster IX, followed by cluster VI, X, I and III. Minimum intra cluster distance was observed in cluster VIII followed by cluster II and V. Similar results were reported by Singh *et al* (2005) and Agedew (2006). Hence, intensive selection for agronomically important characters and similarity in parentage might cause narrow genetic diversity, and uniformity between clusters of low intra cluster distances.

The magnitude of inter- cluster distance (D^2) were generally high and were indicators for the presence of genetic divergence in genotypes. The highest inter-cluster distance was observed between cluster I and X, followed by cluster III and cluster IX and cluster III and X suggesting wide diversity among the genotypes included in these clusters and crossing between these clusters will result in high heterotic response and thereby better segregants. The lowest inter-cluster distance (D^2) was observed between cluster IV and V followed by cluster II and V and cluster IV and VII which indicates that, genotypes involved in these clusters have low genetic diversity. Similar results were obtained by Singh *et al.* (2005) and comparable to the values (7.67 to 663.93) reported by Wassihun (2006).

There were considerable differences between cluster means for most of the characters. On the basis of cluster analysis, the cluster means indicated that mean seed yield per plant was highest in cluster III followed by cluster VII. Cluster X followed by cluster IX had the lowest mean seed yield per plant. Thus diversity for seed yield per plant was observed among the clusters. These results on cluster means for other traits also indicated diversity for most of the traits. Some trends were also observed. Cluster X had highest mean for plant height, primary branches and seeds per umbellet. This cluster also had lower number of seeds per umbel. Cluster VII containing single genotype recorded highest mean values for secondary branches, umbels per plant and umbellates per umbel. Seeds per umbellate cluster IX and number of seeds per umbel cluster VII showed highest values. For particular characters, these, clusters may be useful in crop improvement programme. Similar results were reported by Singh *et al.* (2005).

5.6 Molecular characterization

A. RAPD analysis

In total thirty eight RAPD primers were initially screened out of which, eighteen primers amplified unambiguous, readable and reproducible polymorphic products. A total of 146 amplification bands were produced from the selected 18 primers out of which 113 bands were polymorphic. The number of bands varied from 3 to 12 and the size ranged from 80 to 1200 bp. The highest number of bands (12) was obtained with primer OPD-01, while the lowest number of bands (3) was observed with primer OPO-08 with an average of 8.11 bands per primer. Highest number of polymorphic bands as observed with primer OPN-02 and the lowest number of polymorphic bands with primer OPO-08 and OPO-14. The percentage of polymorphism ranged from 50.00 to 100.00 per cent with an average of 77.39 % per primer. Primer OPA-02, OPA-08 and OPM-02 revealed the highest polymorphism (100.00%), whereas the primer OPO-14 and OPP-07 exhibited the lowest polymorphism (50.00%). So, the primers OPA-02, OPA-08, OPM-02, OPN-02, and OPL-08 proved best to assess the diversity in Coriander. Similar results were reported by Pareek *et al.* (2012), Melo *et al.* (2011), El-Nasr *et* *al.* (2013), and Tomar *et al.* (2014) in coriander and Dangi *et al*. (2004), Sundaram and Purwar (2011) and Choudhary *et al.* (2013) in fenugreek.

B. ISSR analysis

Initially twenty eight ISSR primers were screened among which, eight primers amplified unambiguous, readable and reproducible polymorphic bands. A total of 60 amplification products were produced from the selected 8 primers out of which 50 bands were polymorphic. The number of bands varied from 5 to 10 and the size ranged from 150 to 1200 bp. The highest number of bands (10) was obtained with primer ISSR 27, while the lowest number of bands (5) was observed with primer ISSR 10 with an average of 7.5 bands per primer. Highest number of polymorphic bands (9) were observed in primer ISSR 27 and the lowest number of polymorphic bands (3) were observed in primer ISSR 10. The percentage of polymorphism ranged from 60.00 to 100 per cent with an average of 83.33 % polymorphism per primer. Primer ISSR 4 revealed the highest polymorphism (100 %), whereas the primer ISSR 10 exhibited the lowest polymorphism (60.00 %). So, the primers ISSR 4, ISSR 6, ISSR 9 and ISSR 27 among eight primers proved best to assess the diversity in coriander. Similar results were reported by Pareek *et al.* (2012), Melo *et al.* (2011), El-Nasr *et al.* (2013), and Tomar *et al.* (2014) in coriander and Dangi *et al*. (2004), Sundaram and Purwar (2011) and Choudhary *et al.* (2013) in fenugreek.

C. Clustering based on molecular data

Molecular data obtained using 18 RAPD primers and 8 ISSR primers were used to construct dendrograms which, divided the coriander genotypes into 13 clusters at 0.67 and 0.72 similarity co-efficient. The similarity co-efficient ranged from 0.56 to 0.86 in RAPD and in ISSR ranged from 0.59 to 0.90.

With respect to RAPD clustering, group II and X includes two genotypes which belong to same geographical area i.e. Rajasthan and Haryana respectively. Group III and IX consisted of four genotypes each of which was from Rajasthan. Three genotypes which were collected from Rajasthan and Lam region Andra Pradesh, grouped in cluster V. Group-VIII included six genotypes which were from Hisar and Andra Pradesh regions. The genotypes collected from Hisar, Uttar Pradesh and Tamil Nadu formed group which fall under cluster number XI. Group XII includes large number of genotypes collected from three geographical regions among which three genotypes from Tamil Nadu, 2 genotypes from Utttar Pradesh, twelve genotypes from Hisar, HR. While, in ISSR clustering group I accommodated maximum number (15) of genotypes (collected from Hisar, Rajasthan, Andra Pradesh) which shows that, these genotypes are genetically similar. Groups II, VI, VIII and XI consisted of 3 genotypes each, which were collected from Rajasthan, Uttar Pradesh, Andra Pradesh and Tamil Nadu respectively. Group-VII included seven genotypes and group X includes 5 genotypes which were from Hisar region alone. Group XI and XII includes two genotypes each which were collected from Hisar Uttar Pradesh and Tamil Nadu. The genotypes from one region were grouped together in some cases while they were placed in different clusters in certain cases. The clusters containing genotypes from same region maybe due to their pedigree relationship or they may be selected from same breeding population and the genotypes which are falling in different groups indicate the presence of genetic diversity between the members of different clusters. Crossing can be made between the members of different clusters as they are genetically diverse. Similar results were reported by Pareek *et al.* (2012), Melo *et al.* (2011), El-Nasr *et al.* (2013), and Tomar *et al.* (2014) in coriander.

Comparison between RAPD and ISSR results

Results from clustering of 48 coriander genotypes using RAPD and ISSR formed thirteen groups each at 0.67 and 0.72 similarity coefficient. Similarity coefficient ranged from 0.56 to 0.85 in RAPD and 0.59 to 0.90 in ISSR. Average polymorphism exhibited by RAPD was 77.39 % and by ISSR was 83.33%. Average number of bands per primer in RAPD was 8.11 and in ISSR was 7.50. There was not much difference between the polymorphism exhibited by these two primers. But, with respect to assessment of diversity both markers were equally good. Clustering pattern obtained from both the markers found different. But, some members of the clusters shown similarity between the members in both the cases like (RD-120 and RD-391), (DH-275 and DH-283), (DH-279 and DH-278), (JCR-390, JCR-405 and JCR-406) and (DH-36, DH-228 and LCC-193). The results obtained indicated that both the marker systems RAPD and ISSR, individually or combined can be effectively used in determination of genetic relationship among coriander genotypes. Similar results were reported by Pareek *et al.* (2012), Melo *et al.* (2011), El-Nasr *et al.* (2013), and Tomar *et al.* (2014) in coriander and in fenugreek by Dangi *et al*. (2004), Gupta *et al*. (2011), and Hora *et al*. (2016).

CHAPTER-VI

SUMMARY AND CONCLUSION

The present investigation entitled "Genetic divergence studies in coriander (*Coriandrum sativum* L.)" was conducted at Research Farm of the Department of Vegetable Science, Chaudhary Charan Singh Haryana Agricultural University, Hisar, during winter season of 2014-15 and the laboratory study was carried out in the Department of Molecular Biology, Biotechnology and Bioinformatics during 2015-16.

For morphological characterization 113 coriander genotypes collected from different regions were sown in field, with randomized block design with three replications. To study DUS characters genotypes were observed visually and were categorized into different classes based on different morphological traits with the help of crop descriptors. For variability studies, observations were recorded in three replications for quantitative traits like number of basal leaves, length of the longest basal leaf, primary branches, secondary branches, plant height (cm), umbels per plant, umbellates per umbel, seed per umbellate, number of seeds per umbel, test weight (g) and seed yield per plant (g). These were also used in estimating the heritability, genetic advance, correlation and path coefficients for yield and its attributing traits. The best performing 48 coriander genotypes among 113 evaluated genotypes were selected and sown in succeeding *rabi* season of 2015-16 for molecular characterization. RAPD and ISSR markers were used for this purpose. Results of present investigation are summarized as below:

- DUS characterization resulted in categorization of coriander genotypes into distinct groups for the traits like leaf luster of longest basal leaf, leaf margin of longest basal leaf, leaf colour of longest basal leaf, stem pigmentation, corolla colour, nodal pigmentation, growth habit, seed colour, seed shape, seed size and seed ridge. These traits showed genetic divergence and proved best for identification purpose of 113 coriander genotypes evaluated.
- A limited genetic divergence was observed for stem pubescence and streaks on stem categorization of genotypes based on these traits proved unsuccessful. Hence, these traits were very poor for identification purpose.
- Analysis of variance indicated high significant differences among the genotypes for all 11 traits evaluated. This revealed prevalence of sufficient variation in genotypes evaluated.
- Mean and range values indicated ample variability for most of the characters evaluated.
- Moderate to high PCV and GCV as well as moderate to high heritability and genetic advance as per cent of mean were observed for traits like number of basal leaves, length of

the longest basal leaf, primary branches, secondary branches, plant height (cm), umbels per plant, seed per umbellate, number of seeds per umbel, test weight (g) and seed yield per plant (g). This indicates the presence of moderate to high range of genetic variability for yield and its attributing traits among the genotypes evaluated and can be improved by simple selection.

- Low PCV, GCV and high heritability coupled with low genetic advance as per cent of mean was recorded for umbellates per umbel. This indicates the existence of very low genetic variation in present population and this trait can be improved through heterosis breeding, as direct selection would not be effective.
- The analysis of genotypic as well as phenotypic correlations showed that, the seed yield per plant had positive association with number of seeds per umbel, umbelletes per umbel, umbels per plant and secondary branches. Thus selection for these traits should be employed to improve the yield.
- Path analysis revealed that high positive direct effects were exerted by traits like number of seeds per umbel and umbel per plant. Length of longest basal leaves and test weight exerted moderate positive direct effect on seed yield per plant. This suggests that these traits directly contribute towards yield per plant. So, importance should be given for these traits during crop improvement programme to increase yield per plant.
- Divergence study concluded that genotypes of cluster III and VI showed highest mean values for seed yield per plant. Hybridization between these clusters and other with highest mean for yield contributing traits can give promising results in coriander improvement.
- Totally 38 RAPD primers were used for PCR amplification, among which, only 18 primers gave good amplification. While, among 28 ISSR primers used for PCR amplification, only 8 primers gave good amplification.
- RAPD primers OPA-02, OPA-08, OPM-02, OPN-02, and OPL-08 gave highest polymorphism. So, these primers can be used for diversity studies as they are effective among others.
- At 0.67 similarity coefficient the genotypes were grouped in thirteen clusters, showing that they are genetically diverse between the clusters and we can go for hybridization between the members of different clusters for crop improvement.
- Among ISSR primers, primers ISSR 4, ISSR 6, ISSR 9 and ISSR 27 exhibited highest polymorphism.
- At 0.72 similarity coefficient genotypes were grouped in ten clusters, showing that they are genetically diverse and we can go for hybridization between the members of different clusters.

- Results from clustering of 48 coriander genotypes using RAPD and ISSR formed 13 groups each at 0.67 and 0.72 similarity coefficient. Similarity coefficient ranged from 0.56 to 0.85 in RAPD and 0.59 to 0.90 in ISSR.
- Average polymorphism exhibited by RAPD was 77.39 %, by ISSR was 83.33% and combined average polymorphism of both markers was 80.36 %. Average number of bands per primer in RAPD was 8.11, in ISSR was 7.50 and combined (RAPD and ISSR) was 7.80. There is not much difference between the polymorphism exhibited by these two primers. But, with respect to assessment of diversity both markers proved best. Clustering pattern obtained from both the markers were found different. Similar results were observed regarding clustering of genotypes.
- The molecular marker analysis of 48 coriander genotypes by RAPD and ISSR revealed ample genetic diversity among the genotypes which otherwise was not possible by morphological analysis of these genotypes.
- RAPD and ISSR markers were found efficient in diversity study individually or in combination.

Conclusion

From the present study it was concluded that the morphological traits like leaf luster of longest basal leaf, leaf margin of longest basal leaf, leaf colour of longest basal leaf, stem pigmentation, corolla colour, nodal pigmentation, growth habit, seed colour, seed shape, seed size and seed ridge in coriander genotypes were best for identification purpose. Variability studies revealed wide range of genetic diversity for yield and its attributing traits in 113 coriander genotypes evaluated under field conditions. The correlation studies showed that yield per plant had positive association with number of seeds per umbel, umbelletes per umbel, umbels per plant and secondary branches. Path analysis revealed that traits like number of seeds per umbel, umbel per plant, length of longest basal leaves and test weight are important for crop improvement programme as they directly contributed towards yield per plant. Diversity analysis indicated that there is wide range of genetic diversity in the tested germplasm for most of the characters studied. Hybridization among accessions from different clusters identified in this study could lead to considerable genetic improvement by following appropriate selection strategies in the segregating generations. The best performing 48 genotypes selected among 113 genotypes were characterized by using RAPD and ISSR markers. This gave the clear picture of existence of diversity in genotypes at genetic level as DNA markers are not influenced by environmental effects or plant growth stages whereas morphological markers does. Both RAPD as well as ISSR markers proved best for assessing genetic diversity in coriander germplasm. This showed that the genotypes used in the present study can be utilized in further crop improvement programme.

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ABSTRACT

Title of Thesis	: **“Genetic divergence studies in coriander (*Coriandrum sativum* L.)”**
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The present investigation entitled “Genetic divergence studies in coriander (*Coriandrum sativum* L.)” was conducted at Research Farm of the Department of Vegetable Science, Chaudhary Charan Singh Haryana Agricultural University, Hisar, during winter season of 2014-15 and the laboratory study was carried out in the Department of Molecular Biology, Biotechnology and Bioinformatics during 2015-16. 113 coriander genotypes collected from different regions were sown in field following randomized block design with three replications. To study DUS characters, the genotypes were observed visually and categorized into different classes based on different morphological traits with the help of crop descriptors. It is concluded that the morphological traits like leaf luster of longest basal leaf, leaf margin of longest basal leaf, leaf colour of longest basal leaf, stem pigmentation, corolla colour, nodal pigmentation, growth habit, seed colour, seed shape, seed size and seed ridge proved best for identification purpose, and from this, it is also evident that there was a sufficient diversity for these traits in genotypes under study. Variability studies reveal that there was a wide range of genetic diversity for yield and its attributing traits in 113 coriander genotypes, which were evaluated under field conditions. The genotypic as well as phenotypic correlations showed that the seed yield per plant had significant and positive association with number of seeds per umbel, umbelletes per umbel, umbels per plant and secondary branches. Path analysis revealed that high positive direct effects were exerted by traits like number of seeds per umbel, umbel per plant, length of longest basal leaves and test weight on seed yield per plant, these are importance in crop improvement, as they directly contribute towards seed yield per plant and in divergence study genotypes of cluster III and VI showed highest mean values for seed yield per plant. Hybridization between these clusters and other with highest mean for yield contributing traits can give promising results. However, for more precise and accurate identification, the modern biotechnological tool like molecular markers could be utilized. RAPD and ISSR were employed to assess the genetic diversity in best performing 48 coriander genotypes, which were selected among 113 genotypes evaluated, which gave the clear picture of diversity existence in genotypes at genetic level as DNA markers are not influenced by environmental effects or plant growth stages, and both RAPD and ISSR markers proved best for assessing genetic diversity.

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1. **Shivaprasad M.K.,** Tehlan, S.K., Mukesh Kumar., Batra, V.K. and Shikha Yashveer. (2017). Correlation and path coefficient studies in coriander for yield and yield attributing traits. *Int.J.Curr.Microbilo.App.Sci* 6(9):3593-3599.

Signature of student

UNDERTAKING OF COPY RIGHT

I, **Shivaprasad M. K., Admission No. 2013A58D** undertake that I give copy right to the CCS Haryana Agricultural University, Hisar of my thesis entitled **"Genetic divergence studies in coriander (*Coriandrum sativum* L.)".** I also undertake the patent if any, arising out of the research work conducted during the programme shall be filed by only with due permission of the competent authority of CCS Haryana Agricultural University, Hisar.

SIGNATURE OF THE STUDENT