

Genetic studies for selection parameters in cauliflower (*Brassica oleracea* L. var. *botrytis*)

ABSTRACT

The constant availability of high-yielding and well-adapted varieties is made possible by a vigorous breeding program and it is the first and least expensive input in improving the output of any crop. To design breeding methods for the development of a certain crop, it is essential to have a thorough understanding of genetic variations, correlations between various traits, and their direct and indirect contributions to yield. The amount of genetic variability and character outstanding from one generation to the next determine how much a crop may progress genetically. Because phenotypic selection relies on the range of genetic variability available in the population, it is necessary to separate the variability into heritable and non-heritable components. This will increase the reliability of the selection. Curd yield in cauliflower is a complicated trait that is greatly impacted by the environment since it is regulated by several genes. Some of the component qualities may be directly and favourably correlated with the marketable curd weight, making them suitable for use as selection criteria in crop improvement programs. Characters having a strong and positive/desirable correlation to one another would be used to boost yield effectively. The proper weightage for selection purposes is also determined by the proportional contribution of the component qualities to the yield. The level of genetic diversity contained in a specific crop determines the most appropriate varietal development programs.

Keywords: Cauliflower, correlation, genetic variability, phenotypic selection, yield

INTRODUCTION

Brassica oleracea L. var. *botrytis* (cauliflower), is a member of the *Brassicaceae* family and has chromosomal number $2n = 2x = 18$. The word cauliflower has been originated from the Latin words 'caulis' (stem) and 'floris' (flower). Due to its significant economic significance and high nutritional value, it is grown for its soft white curds in many nations throughout the globe (Singh et al., 2019) [1]. It is a popular vegetable for making soup, pickles, and curries.

Cauliflower is an important source of human nutrition that contains a good amount of dietary fibres, vitamins and minerals. Additionally, it contains sulforaphane, an anti-cancer substance that lowers the risk of prostate cancer (Kushwaha et al., 2013) [2]. Brassica vegetables

are also a rich source of many phytochemicals and bioactive substances. Determining the potential genotypes with high production and rising nutritional value is crucial (Ram et al., 2017) [3]. Following its arrival in the early 19th century, cauliflower has been cultivated in India for the last 200 years (Dey et al., 2019) [4]. Indian cauliflower belongs to the maturity group I and II which are developed from Cornish types, **that originated** in England whereas the temperate types i.e Erfurt or Snowball type originated in Germany and Netherlands in the 18th century (Swarup and Chatterjee 1972) [5]. Indian cauliflower is likely to inherit Cornish varieties' genes for qualities including a tall stalk, yellowish, flavorful curds, and an open growth habit. Many heat-tolerant cultivars have been created using Indian or tropical cauliflower (Dey et al., 2019) [4].

The term "cole vegetables" refers to all cultivated species of the genus Brassica with genome CC ($n = 9$) (Maggioni et al., 2018) [6]. In developing countries, productivity per unit area of cauliflower is relatively extremely low, mostly because promising cultivars with great yield potential are not readily available (Elahi et al., 2015) [7]. Making the best use of the genetic diversity existing in the desired crop, which offers a genetic pool to uncover better alleles influencing key quantitative and qualitative qualities, is one of the key strategies for creating **high-yielding** cultivars via breeding (Dey et al., 2014) [8].

The degree of genetic diversity in the germplasm is roughly equal to the crop's development potential (Singh et al., 2009) [9] and offers the chance to increase production and quality via **the planned** breeding **program**. Given that phenotypic diversity is determined by interactions between genotype and environment, the phenotype is often not an accurate predictor of its genotype. The genotype makes up the proportional percentage of the heritable component in continuous variation and decides how selection will react, while the non-heritable component is mostly caused by environmental variables and hinders the selection process. Therefore, dividing total variability into heritable and non-heritable components would be essential. With the use of heritability estimates, the genotypic and phenotypic coefficients of variation are clarified to calculate the index of character transmission and the effectiveness of selection in enhancing a given trait (Singh et al., 2013) [10]. It is clear that yield is a complicated trait, and the best technique for increasing yield is indirect selection via associated, less complex, and more readily measurable traits. The strength of the relationship between yield and the desired yield traits determines how **the indirect** selection is effective (**Espósito** et al., 2009) [11]. In general, correlation coefficients provide an evaluation of the link between characters, but they

are insufficient to explain why certain characters are associated with one another (Toker and Cagirgan, 2004) [12]. When there are more than two variables, the correlation by itself cannot provide a complete picture of the interrelationships (Fakorede and Opeke, 1985) [13].

To find desirable traits to employ as a selection criterion to increase crop output, breeders used path analysis (Ali et al., 2009) [14]. The path analysis determines the association's relative relevance and determines the magnitude of the direct and indirect impacts of causative factors on the yield (Dewey and Lu, 1959) [15]. Therefore, choosing appropriate plant types for a successful breeding program requires the evaluation of correlation and path coefficients between yield and its associated attributes. For the selection of desirable genotypes having higher productivity, the curd yield and related characteristics provide important criteria (Yanglem and Tumbare 2014) [16] which could be achieved, to analyze the genetic variability in the cauliflower genotypes, by planning an initial breeding program (Chatterjee et al. 2018a) [17].

GENETIC VARIABILITY PARAMETERS

Mean values of different genotypes indicate the variation in the performance concerning yield and its contributing traits thus showing the extent of genetic diversity among genotypes which would provide immense opportunities for genetic improvement of cauliflower. Heritability, a measure of heritable variation, is useful in forecasting the predicted level of improvement that would be attained by the selection, combined with the genotypic coefficient of variation (Burton and De Vane, 1953) [18]. The genetic connection between the parents and the progeny is explained by heritability. The heritability estimates help in designing breeding programs with the necessary level of anticipated genetic advancement and in understanding how quantitative features are inherited. Heritability in general is very important since the degree of heritability suggests consistency, which makes it easier to identify a genotype from its phenotypic expression (Lush, 1940) [19]. It is a factor that calculates projected improvement, but it has greater significance when combined with genetic advances. Johannsen (1909) [20] further emphasized that, since high heritability does not always imply high predicted genetic advance, heritability alone could not be the exclusive criterion for determining the actual impacts of selection. Predictions based on both of these estimations may thus be more beneficial in the selection process (Sharma et al., 2016) [21]. Genetic advancement is the best indicator of the population's actual gain under such circumstances. To determine the real impacts of selection, it is more useful to combine genetic advance and heritability (Johnson et al., 1955) [22]. Therefore,

genetic advance has an advantage over heritability and serves as a guiding element for breeders throughout the selection process.

Kanwar and Korla (2002) [23] examined 16 biparental offspring for several horticultural and qualitative aspects. It was discovered that the biparental progenies 13, 17, and 19 had good yield and quality traits. **Except for** net curd weight and gross plant weight, PCV was low for the bulk of variables, including leaf length, days to marketable maturity, leaf width, stalk length, leaves per plant, and harvest index. Days to marketable maturity data showed high heritability and low genetic gain, which suggested non-additive gene effects were responsible for this feature. The rest of the characteristics exhibited low genetic gain with low to moderate **heritability showing** environmental impact. Dubey et al. (2003) [24] studied 65 genotypes of cauliflower for a variety of traits including plant height, days to curd maturity (50%), leaf length, leaf width, number of leaves, curd diameter, stalk length, curd depth, net curd weight, harvest index, curd size index and gross weight. They noted that there were significant differences between all genotypes for plant weight (31.70), harvest index (25.68) and net curd weight (35.18). Plant height, days to curd maturity (50%), curd depth and leaf width exhibited low genetic advance and low GCV whereas curd weight, harvest index, and plant weight suggested high genetic advance. Gross weight, harvest index, and net curd weight were shown to be the most crucial traits for the development of cauliflower genotypes.

Sharma et al. (2006) [25] discovered high phenotypic and genotypic coefficients of variation for stalk length, net curd weight, gross plant weight, harvest index and marketable curd yield per plant, during **analyzing** genetic variability components for yield and associated parameters in 13 cauliflower cultivars. Similar to stalk length, marketable curd weight, and net curd weight, high heritability and genetic advance were seen, showing the preponderance of the additive genetic variation for these characters. Dhatt and Garg (2008) [26] evaluated 36 genotypes of November maturity cauliflower and demonstrate considerable genetic variability for marketable curd weight, net weight, and gross curd weight. High heritability in **the broad** sense coupled with low genetic advance for plant spread, leaf length, leaf width, plant height, and days to curd maturity suggested that non-additive gene action had a significant role in regulating these **characteristics**. Kumar et al. (2011) [27] studied the genetic variability in early Indian cauliflower for yield and quality parameters and found that genotypes i.e. DC-98-4, DC-98-10, and DC-124 exhibited superiority for both yield and quality traits. **The highest** heritability

was shown for days to 50% curd formation. Mehra and Singh (2013) [28] found low GCV and PCV for days to 50% curd initiation during examining seven lines of cauliflower for genetic variability. While plant diameter demonstrated high heritability with moderate genetic advance, curd depth demonstrated low magnitude heritability and genetic advance. Nimkar and Korla (2011) [29] assessed **several** progenies of a cross between PSB1 and KT9, for different yield and quality attributes. Gross curd weight and net curd weight showed high phenotypic and genotypic coefficients of variation, but plant frame, stalk length, leaves per whorl, leaves per plant, days to harvesting, and harvest index showed low levels of both. Net curd weight, plant frame, gross plant weight, harvest index, and leaves per whorl all showed high heritability. For gross and net curd weight, **the genetic** advance was maximum, but it was little for all other characters. Maximum traits had low genetic advance and moderate heritability, which indicated the significance of environmental factors in determining how they manifested.

Singh et al. (2013) [10] studied 16 cauliflower genotypes and observed that there is a significant genetic variability for various traits (plant height, leaves per plant, leaf length, leaf width, stem diameter, days to curd initiation, days to curd maturity, gross plant height, leaves per plant, leaf length, leaf width, stem diameter, gross plant weight, curd diameter, curd weight with guard leaves, curd yield with guard leaves, average curd weight without guard leaves, and vitamin C). Vitamin C showed the highest genotypic and phenotypic coefficient of variability, while leaves/plants showed the lowest. The PCV for vitamin C was the highest, and then yield characteristics such **as curd** weight with guard leaves, overall yield, curd initiation days, and curd diameter were noted. Curd weight without guard leaves and vitamin C, curd weight demonstrated high heritability in the broad sense as well as genetic advance. Elvarasan et al. (2014) [30] examined the physical characteristics of genotypes i.e. Namdhari Seeds 60 N, Namdhari Seeds 133, Pusa Meghna, and Basant - in Kerala, India's hills and plains, and discovered significant variations in yield - between 21-26.4 kg/16 m² in the hills and 0.78-1.43 kg/16 m² in the plains. In terms of high curd yield, curd weight, and curd height, the cauliflower genotypes NS 133 performed better in hills.

Santhosha et al. (2014) [31] examined 51 cauliflower genotypes for yield and attributes associated to yield and found that gross curd weight and net curd weight followed by curd size index had high coefficients of variation, suggesting that these features should be **prioritized** during selection. Four genotypes (IIHR 263, IIHR 272, IIHR 390, and IIHR 266) were

discovered to be superior to other genotypes for a variety of horticultural traits. As a result, these genotypes may be suitable for cultivation or may be used in breeding programs due to their desirable traits for the enhancement of cauliflower curd yield and quality. Chittora and Singh (2015) [32] examined 40 early genotypes of cauliflower for genetic variability based on 23 quantitative and qualitative traits and discovered significant differences for the majority of traits among genotypes with the exception of days to curd maturity, days to curd initiation, and curd depth. Net curd weight, harvest index, gross plant weight marketable curd weight, and curd yield per hectare were all found with good magnitude for PCV, GCV, heritability, and genetic advance. On the other hand, days to curd maturity and days to curd initiation had the lowest coefficient of variation, heritability, and genetic advance. Kumar et al. (2017a) [33] studied 16 quantitative characters in 57 genotypes of mid-season cauliflower and revealed significant differences in almost all of the characters except curd length, plant spread, and curd size index. It was discovered that the genotypes INBPCF 120, PCF-93, 2013/CAUMVAR-6, PG-5, INBPCF 117 and PCF- 7 were superior and had several desired characteristics. The INBPCF 120 had the greatest curd yield, while PCF 29 had the minimum days to maturity. Stalk length, net curd weight, curd yield per hectare, gross plant weight, marketable curd weight, harvest index, and curd size index had a sufficient magnitude of PCV and GCV. Vanlalneihi et al. (2017) [34] studied genetic variability in 15 Indian cauliflower genotypes for a variety of economically important characters and found high heritability and high genetic advance for plant height, leaf width, leaf length, leaves/plant, curd diameter, curd angle, net curd weight, and marketable curd weight, indicating the presence of additive gene action. Therefore, direct selection may aid in the enhancement of these characters.

Chatterjee et al. (2018a) [35] evaluated 20 mid-late and late groups of cauliflower genotypes in order to determine the nature and magnitude of genetic variability, heritability, and genetic gain for the characters viz., leaves per plant, stalk length, days to marketable curd maturity from the date of transplanting, gross plant weight, plant height, curd depth, curd size index, leaf size index, curd solidity and marketable plant yield. The Curd size index showed high heritability and high genetic gain, while leaves/plant, curd depth, leaf size index, gross plant weight, and marketable plant yield showed high heritability and moderate genetic gain. The research found that the germplasm had enough variation, that additive gene action predominated, and that the traits were highly transmissible indicating that direct selection would be rewarding

depending upon these characteristics. Gariya et al. (2019) [36] assessed 22 genotypes of cauliflower in order to study the genetic variability for different yields and their associated characteristics. For the attributes viz., stalk weight, leaves weight, curd weight with guard leaves, and curd weight, higher PCV and GCV values were observed, suggesting the presence of a broad range of genetic variability in the germplasm for these characters. Additionally, research showed that these features have a broad genetic base, little environmental effect, and are governed by additive genes, indicating that there is considerable potential for further developing these traits via selection. Shree et al. (2019) [37] studied 13 genotypes of cauliflower for a variety of horticultural traits. For marketable curd, net curd weight, and curd compactness, PCV and GCV were high. For marketable curd weight, plant height, curd compactness, and leaf length, high heritability and moderate genetic advance were identified, indicating the existence of additive gene action for which phenotypic selection would be more successful for their improvement.

Lakshmi et al. (2022) [38] examined cauliflower (*Brassica oleracea* var. *botrytis*) genotypes for genetic variability studies. For all of the traits under study, the analysis of variance indicated significant genotype differences, suggesting a high degree of variability. High PCV and GCV were found for yield per plot, gross curd weight, curd size, yield per hectare, net curd weight, curd compactness and number of leaves per plant. For number of leaves per hectare, plant spread, curd diameter, plant height, curd size, curd compactness, gross curd weight, net curd weight, yield per hectare and yield per plot; high heritability and genetic advance as a percentage of mean were noted. As a result, selection for these features may result in the accumulation of more additive genes, which will improve their performance in the cauliflower breeding programme.

Vanlalneihi et al. (2020) [39] assess the agromorphological features, bioactive substances, and antioxidant activity of 16 early Indian cauliflower genotypes. The genotype with the highest marketable curd weight was CC 12 (450 g). The maximum amount of curd sinigrin (3.29 to 16.37 mol 100g⁻¹ FW) was found in DC 41-5. For all the traits, the phenotypic coefficient of variation (PCV) was greater than the genotypic coefficient of variation (GCV).

Biswal (2022) [40] studied the range, mean, phenotypic and genotypic coefficients of variation, and correlation coefficient in mid-season cauliflower. Five randomly selected plants from each replication were observed with regard to yield and growth parameters. In terms of marketable curd yield per plot, genotypes 2020/CAUMHYB-1 and 2020/CAUMHYB-2 both perform

statistically best, but when other important traits that are directly related to yield are calculated, genotype 2020/CAUMHYB-1 clearly outperforms genotype 2020/CAUMHYB-2.

CORRELATION AND PATH COEFFICIENT ANALYSIS

The association among the characters may be used to choose those traits whose genotypic values are affected by environmental factors and are thus difficult to monitor. Additionally, it provides details on the nature and extent of direction and selection pressure on various characters. When two opposing desired traits impacting the main character are to be chosen, genotypic and phenotypic correlations assist to base the selection process by revealing the degree of relationship with various characters. Additionally, it helps to improve different characteristics simultaneously (Falconer, 1981) [41]. Thus, it would be imperative to examine the magnitude and direction of **the correlation** of different attributes with marketable curd weight and to identify the traits of interest to obtain **a high** yield. Yield is a complicated attribute that is impacted by environmental conditions and is driven by **several** processes like **phenology**, canopy growth, biomass production, etc. Correlation analysis demonstrates interdependence by revealing the relationship pattern between component characters and yield. Instead of demonstrating a **cause-and-effect** relationship, it only illustrates the total impact of a certain character on yield. Path coefficient analysis is used to evaluate the **cause-and-effect** relationship as well as efficient selection. It enables the division of correlation coefficients into the direct and indirect impacts of different qualities toward the dependent variable and is crucial in establishing the degree of relationship between yield and its component effects. **To** enhance curd production, breeders might choose the best selection criteria with the use of path coefficient analysis.

Kanwar and Korla (2002) [23] revealed that net curd weight was found to be significantly and positively associated with leaf length, leaf width, gross plant weight, and harvest index. Gross plant weight and harvest index provided the maximum direct and indirect contributions to the total association, according to the path analysis. Garg and Lal (2004) [42] observed a positive and significant association of net curd weight with equatorial curd diameter, curd size index, plant spread, polar curd diameter, and curd compactness index, after evaluating 36 genotypes of cauliflower. Early maturity was associated with fewer leaves per plant, short stalk length and less plant height. According to **the path-coefficient** study, characteristics including the curd compactness index, curd size index, and equatorial curd diameter had the most positive direct influence on net curd weight. Liu et al. (2004) [43] investigated the connection between plant

growth traits and curd yield in cauliflower, following path analysis. The path analysis revealed that plant mass and curd diameter contributed directly towards curd mass whereas leaf mass, leaf area, and curd stem diameter made appreciable **contributions** indirectly. Sharma et al. (2006) [25] revealed a positive association of marketable curd yield with leaves per plant, curd length, curd size index, net curd weight, gross plant weight and curd width (at both genotypic and phenotypic levels). Selection based on these characteristics may thus aid in locating promising genotypes with high marketable curd yield. Gross plant weight had the greatest direct impact on marketable curd yield, according to path coefficient analyses. Kumar et al. (2011) [27] found that the harvest index and net curd weight were positively and significantly correlated with total yield, but the duration of curd availability and the days to curd formation were negatively correlated with yield. According to path analysis, curd compactness and net curd weight had the highest positive magnitude **toward** the total yield. Sheemar et al. (2012) [44] observed that there is a significant and positive association between net curd weight and total plant weight. The plant weight also significantly correlates with the leaf width, stem length, leaf length, curd compactness index, and leaves per plant. The net curd weight of cauliflower may thus be efficiently increased by selection for these features. Path analysis showed that the total plant weight had the most direct and positive impact on net curd weight. Singh and Dogra (2013) [45] revealed that there is a significant and positive correlation between net curd weight and gross curd weight, as well as among days to curd maturity, plant width, and leaf area, after evaluating 23 cauliflower genotypes. High net curd weight and gross weight per plant might be crucial factors in the selection process for improving cauliflower genotypes.

Ansari et al. (2017) [46] found a positive and significant correlation **between** curd yield with leaves per plant, curd diameter, marketable curd weight, gross plant weight, and net curd weight. According to path coefficient analysis, net curd weight had a significant direct positive impact on the total yield, but harvest index had a significant direct negative impact on curd yield. Chittora and Singh (2017) [47] revealed that curd yield had a positive correlation with marketable curd weight, gross plant weight, net curd weight, leaves per plant, curd diameter, curd size index, curd depth and harvest index. The selection method for the development of cauliflower genotypes would heavily **emphasize** parameters like gross weight per plant, marketable curd weight, net curd weight, number of leaves, curd diameter, harvest index, and curd size index. Manaware et al. (2017) [48] demonstrated that for all the traits, including days to harvest, leaves

per plant, curd length, curd width, total plant weight, curd weight, net curd weight, curd circumference, **the core** length, days to curd initiation, days to curd formation, the magnitude of genotypic correlation was higher than that of phenotypic correlation. Days to curd initiation, days to curd formation and leaves per plant, all exhibited a negative and significant correlation with stalk length. Days to curd initiation, curd circumference, total plant weight, curd width, curd length, curd weight, days to curd formation, days to harvest, and core length are all significantly and positively correlated with leaves/plant. Shree et al. (2019) [37] revealed that the magnitude of phenotypic correlation was lower than that of genotypic for all the characters which showed the inherent association between various traits. Path coefficient analysis at both phenotypic and genotypic levels revealed that the marketable curd weight had maximum positive and direct contribution towards net curd weight followed by leaf length. At **the phenotypic** level, marketable curd weight had maximum positive and direct contribution on net curd weight followed by the curd compactness. They suggested that for the improvement of net curd weight direct selection for marketable curd weight and curd compactness would be beneficial. **Lakshmi et al. (2022)** [38] studied correlation and path coefficient analysis in cauliflower (*Brassica oleracea* var. botrytis) genotypes, and showed that yield per hectare significantly correlated with plant height, plant spread, gross curd weight, net curd weight, curd diameter, curd size, yield per plot and curd compactness. Therefore, selecting for these traits aids in increasing yield. The results of the path analysis revealed that plant spread, number of leaves per plant, yield per plot, net curd weight, curd compactness and curd diameter exerting a positive direct influence on yield per hectare.

GENETIC DIVERGENCE STUDIES

The D^2 statistic is a useful tool for examining the genetic diversity across various genotypes and locating the diverse parents who should participate in hybridization to produce transgressive recombinants. It is important to note that when determining cluster means, genotypes that are present in the same cluster but are inferior or intermediate for the specific trait in question may dilute the superiority of a given genotype **concerning** that characteristic. As a result, for a hybridization **program**, one can consider choosing parents based on the degree of divergence with respect to a characteristic of interest, in addition to genotypes from clusters with larger inter-cluster **distances**. Because genotypes with the same geographic distribution were divided into various clusters, the genetic makeup of the genotypes had an impact on the

clustering patterns. Thus, it suggests that genetic diversity and geographical diversity are not necessarily linked (Dey et al., 2010 [49]; Santhosha et al., 2011 [50]; Kumar et al., 2017b [51] and Chatterjee et al. 2018b [52]).

Quamruzzaman et al. (2007) [53] studied 20 genotypes of cauliflower, divided into five clusters, for the genetic diversity studies. The largest cluster, Cluster III, included nine genotypes, whereas Cluster II was monogenotypic (single genotype). Cluster IV (0.93), had the maximum intra-cluster distance, whereas cluster II had the lowest. The highest inter-cluster distance (24.07) was recorded between Cluster I and IV. The inter-cluster distance was found to be greater than the intra-cluster distance. As a result, it indicated that the genotypes of different groups of cauliflower were genetically quite diverse. To get suitable segregants, hybridization between the genotypes of the most divergent cluster should be carried out. Days to curd initiation, curd height, and curd weight in cluster I, and curd diameter, leaves/plant in cluster V, had the highest cluster mean values. Dey et al. (2010) [49] examined the genetic diversity for 12 distinct traits in 52 cauliflower genotypes, including three CMS lines (Ogu 3A, Ogu 1A, and Ogu 2A). Ten clusters were created using all of the genotypes. While cluster VII was monogenotypic, cluster IX accommodated maximum genotypes (13). Cluster V (899.0) showed the highest intra-cluster distance while cluster VII (0.0) was monogenotypic. The inter-cluster distance was lowest between cluster I and cluster VIII (554.3) and highest between cluster VI and cluster VII (12654.1) indicating sufficient genetic diversity in the population. Therefore, the formation of excellent breeding lines would result from hybridization between the most diverged parents. Furthermore, based on the cluster mean values, clusters I, II, and VIII revealed the characteristics that were most desired.

Varalakshmi et al. (2010) [54] investigated the genetic diversity in 77 genotypes of cauliflower that were divided into 13 clusters, with a maximum of 30 genotypes in cluster I and 22 genotypes in cluster IV. The other clusters each had just two or three genotypes. The clustering pattern demonstrated that there was no linkage between the genetic divergence and the geographic distance, suggesting that the genetic diversity was caused by causes such as spontaneous variation, genetic stock and artificial or natural selection. Selection for a hybridization program should be based on genetic diversity (instead of geographic divergence). Cluster VII and cluster XI had the maximum intra-cluster distance (16.08). Crossing between genotypes that belong to clusters VII and XII was said to take advantage of the heterosis.

Santhosha et al. (2011) [50] examined the genetic diversity of 51 genotypes of cauliflower that was divided into 14 clusters, with the XIV cluster having the maximum number of genotypes (14 genotypes). Cluster VIII had the maximum intra-cluster value (10.13), while Cluster II had the lowest (2.84). Cluster VIII and cluster X had the maximum inter-cluster distance (14.10). The genotypes in cluster X had the greatest potential to be used as parents in hybridization programs to increase the yield of cauliflower, as evidenced by the highest mean values for leaves/plant, curd size, curd diameter, plant weight, net curd weight, marketable curd weight, yield/hectare, and net plot yield in cluster X. Kumar et al. (2017b) [51] evaluated the genetic diversity among 57 mid-season cauliflower genotypes, divided into eight clusters. Cluster I (17) had the maximum genotypes, followed by cluster VI (14) and cluster V (10) whereas cluster II and VII were monogenotypic. Cluster VIII had the maximum intra-cluster distance (22.290), whereas clusters II, IV, and VII had the minimum (0.000) intra-cluster distance. Cluster IV and cluster VII had the maximum inter-cluster distance (240,078), whereas cluster VI and cluster III had the minimum inter-cluster distance (17.670). Leaf length and leaf width in cluster II, petiole length and harvest index in cluster VII, plant height, plant spread, leaves per plant, gross plant weight, the marketable plant weight, and net curd weight in cluster IV, stalk length in cluster VIII, days to maturity in cluster VIII (early), and curd length and curd size index in cluster V, all had the highest cluster mean values. Therefore, according to the results of the cluster analysis, hybridization programs should be carried out in accordance with the clusters that have the greatest intra- and inter-cluster distances as well as the highest cluster mean values.

Chatterjee et al. (2018b) [52] examined 20 genotypes of cauliflower to determine the extent of genetic diversity. All of the genotypes were grouped into four clusters, with cluster II having the maximum genotypes (8), followed by cluster IV (6), and clusters I and III having three genotypes apiece. Cluster IV was more heterogeneous than cluster I, as shown by the fact that cluster IV had the maximum intra-cluster distance (2.091), while cluster I had the minimum (1.086). Cluster I and cluster IV (6.496) had the maximum inter-cluster distance, indicating that they were more divergent and may have greater odds of producing excellent segregants in F₂ and subsequent generations than clusters II and III, which had the lowest inter-cluster distance (3.191). The mean values for leaf size index in cluster I, curd solidity in cluster II, leaves per plant and stalk length in cluster III, gross plant weight, the curd depth, marketable plant weight, days to marketable curd maturity, and curd size index in cluster IV, were the highest. Kumar et

al. (2018) [55] studied the genetic diversity in tropical cauliflower genotypes which were grouped into four clusters with the largest in cluster I (14) followed by cluster II while cluster III and cluster IV were monogenotypic. Cluster I and IV had the maximum inter-cluster distance (580.42), whereas clusters I and III had the minimum inter-cluster distance (438.36). Additionally, cluster IV had the lowest number of days to curd initiation and curd maturity. Furthermore, Cluster IV had the highest net curd weight (304.08 g). These findings suggested that in order to get a high amount of heterosis, clusters IV and I should be crossed. Sharma and Singh (2018) [56] examined the genetic diversity in 25 genotypes of cauliflower for 17 quantitative traits. Three clusters were created out of all the genotypes. Cluster II indicated the minimum intra-cluster distance (3.314), whereas Cluster I displayed the maximum intra-cluster distance (3.454). The inter-cluster distance was maximum between Clusters I and II (5.138), whereas Clusters II and III exhibited the minimum (3.515). It suggested that in order to produce better segregants in F_2 and subsequent generations, hybridization should be performed using genotypes from the divergent clusters I and II. Vanlalneihi et al. (2020) [39] studied 16 early Indian cauliflower genotypes for agromorphological features, bioactive substances, and antioxidant activity. The genotypes were divided into three clusters by D2 statistics, with genotypes in cluster I having high sinigrin levels in both the curd and the leaf. The PCA showed that the first principle component (PC1) and the second principal component (PC2) each contributed 47.86% and 35.14%, respectively, to the total variation. The genotypes CC 13, Pusa Deepali, and Selection 71 may be utilised in breeding programmes to produce plants with higher yields and bioactive compounds.

CONCLUSION

The selection of superior/desirable genotypes often relies on how they manifest themselves phenotypically, which results from interactions between the genotype and the environment. Therefore, the phenotypic superiority of the plants over the original population is related to both the genotype of the plant and favorable environmental circumstances. Because most economic traits are correlated with one another and the degree to which one trait increases or decreases in frequency depends on the other correlated trait, a thorough understanding of the nature and extent of association between characters is crucial for changing the mean population under study in the desired direction. Path coefficient enables rigorous analysis of certain elements for a given correlation and aids in establishing the degree of association between yield and its component

impacts. By identifying the best recombinants, the D^2 statistic aids in the removal of genetically identical/duplicate breeding lines from the germplasm as well as the provision of diverse parents for use in hybridization programs that provide a range of broad genetic variability.

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