Gaziosmanpaşa Üniversitesi Ziraat Fakültesi Dergisi
Journal of Agricultural Faculty of Gaziosmanpasa University
https://dergipark.org.tr/tr/pub/gopzfd

Araştırma Makalesi/*Research Article*

JAFAG
ISSN: 1300-2910
E-ISSN: 2147-8848
(2023) 40(2) 58-65
doi:10.55507/gopzfd.1199276

Correlation, Genetic Variability, Heritability And Genetic Advance For Some Morphological Traits In Red Cabbage Lines (*Brassica oleracea* L.var. *capitata* subvar. *rubra*)

Mehtap ÖZBAKIR ÖZER[1*] Hayati KAR[1] Nur KOBAL BEKAR[1]
Şenay MURAT DOĞRU[1] Gülay BEŞİRLİ[2] İbrahim SÖNMEZ[2]

[1]Black Sea Agricultural Research Institute, Samsun
[2]Atatürk Horticultural Central Research Institute, Yalova,
***Corresponding author's email:** mehtap_ozbakir@hotmail.com

Alındığı tarih (Received): 04.11.2022 Kabul tarihi (Accepted): 30.06.2023

Abstract: Genetic variability, heritability, genetic advance, genetic gain and correlation for traits were studied in 22 lines of red cabbage. The genotypes were evaluated for seven quantitative characters such as head weight, head diameter, head length, core length, head volume, head density and head shape index. Analysis of variance showed significant variation among the genotypes for all the studied yield and yield contributing characters. Head weight of the lines was highly significant positively correlated with head length, head diameter, core length and head volume. The phenotypic coefficient of variation were observed to be higher than the corresponding genotypic coefficient of variation for all the characters studied, indicated that the traits were influenced by environment. The high phenotypic and genotypic coefficient (PCV and GCV) was observed for head density (30.61 and 20.06) followed by head volume (24.72 and 20.49), core length (15.68 and 14.99) and head weight (10.66 and 9.65). High heritability (broad sense) values were recorded for traits such as for head length (91.56%), core length (91.38%) and head diameter (82.24%). The highest genetic advance as percent of mean was shown by head volume (35.0 %) followed by core length (29.52%) and head density (27.09%). As a result, high heritability coupled with high genetic advance was observed head length, head diameter, head volume and head density which are governed by additive gene and could be effectively used as selection criteria in the breeding programme of red cabbage varieties with high yield.

Keywords: Red cabbage, genetic variability, heritability, genetic advance, correlation

Kırmızı Lahana Hatlarında Bazı Morfolojik Özelliklerin Kalıtımı, Genetik Değişkenliği, Genetik İlerlemesi ve Korelasyonu

Öz: Bu makalede 22 farklı kırmızı lahana hattında baş ağırlığı, baş çapı, baş uzunluğu, baş hacmi, baş sıkılığı, iç sap uzunluğu ve baş şekil indeksi özellikleri için genetik değişkenlik, kalıtsallık, genetik ilerleme ve korelasyon incelenmiştir. Varyans analizinde genotipler arasında verim ve verime etki eden özelliklerde önemli farklılıklar olduğu saptanmıştır. Hatların baş ağırlığı, baş uzunluğu, baş çapı, iç sap uzunluğu ve baş hacmi özelliklerinde korelasyonun pozitif yönde önemli olduğu belirlenmiştir. İncelenen tüm özelliklerde fenotipik varyasyon katsayısının genotipik varyasyon katsayısından daha yüksek olduğu ve bu özelliklerin çevreden etkilendiği tespit edilmiştir. En yüksek fenotipik ve genotipik varyasyon katsayısı baş sıkılığında (30.61 ve 20.06) belirlenmiş, onu baş hacmi (24.72 ve 20.49), iç sap uzunluğu (15.68 ve 14.99) ve baş ğırlığı (10.66 ve 9.65) özellikleri takip etmiştir. Baş uzunluğu (% 91.56), iç sap uzunluğu (%91.38) ve baş çapı (%82.24) için geniş anlamda kalıtım yüksek bulunmuştur. En yüksek genetik ilerleme baş hacmi (%35.0), iç sap uzunluğu (% 29.52) ve baş sıkığı (% 27.09) özelliklerinde belirlenmiştir. Sonuç olarak, eklemeli gen tarafından yönetilen baş uzunluğu, baş çapı, baş hacmi ve baş yoğunluğu özelliklerinde genetik ilerleme ve kalıtım derecesinin yüksek olduğu, bunun da ıslah programlarında yüksek verimli kırmızı lahana çeşitlerini geliştirmede iyi bir seleksiyon kriteri olarak kullanılabileceği saptanmıştır.

Anahtar Kelimeler: Kırmızı lahana, genetik değişkenlik, kalıtım, genetik ilerleme, korelasyon

1. Introduction

Vegetable plays an important role in the balanced diet by providing not only energy but also supplying vital protective nutrients like, proteins, vitamins, minerals, dietary fibers, micronutrients and antioxidants. In vegetables, *Brassicaceae* are one of the most diversified families with wide range of variation in crops that supplied edible products (Kumar et al., 2020). Red cabbage belongs to the family *Brassicaceae* and is one of the most popular, nutritious vegetable crops. Red cabbage is among the winter areas with a growth potential in the Black Sea Region. Yield and quality characteristics are mostly hybrid preferences. Therefore, it is very important to develop hybrid varieties with high quality, adaptability and yield characteristics.

Development of an effective breeding program depends on the existence of genetic variability for various economic characters in the gene pool (Rauf and Rahim, 2018). Genetic variability is a measure of the tendency of individual genotypes in a population to vary from one another. Variability is different from genetic diversity, which is the amount of variation seen in a particular population. The variability of a trait describes how much that trait tends to vary in response to environmental and genetic influences (Ullah et al., 2015).

Plant breeders always use their efforts in the development of new varieties. For this, knowledge of genetic variability present in available germplasm is essential for further improvement of the crop. Variation provides useful information to the plant breeder to determine the genetic potential of the populations for developing new varieties with desirable characters in any crop species. Certain morphological parameters serve as a tool for the estimation of genetic variability (Ali et al., 2013).

The concept of correlation was first given by Galton (1987), the knowledge of the nature and magnitude of genetic association among components of economic importance can help in improving the efficiency of selection by making possible use of suitable combination of characters. Correlations are more useful, especially for indirect selection and this type of selection can be advantageous over direct selection, only when the selected trait has very high heritability and breeding value of correlation between two traits is very high (Kumar et al., 2020). Correlation of some morphological characteristics of red cabbage helps breeders for selection.

However only variation is not enough for effective selection, genetic variation, heritability and expected genetic advance in important agronomic characters are required in order to arrangement better effective breeding strategies (Jalata et al., 2011). The knowledge of inter relationships among the various components and their direct and indirect effect on yield are essential to bring genetic improvement in red cabbage. Therefore, genetic measuring diversity and understanding the inheritance pattern of qualitative and quantitative traits are important for breeding programs. The present investigation has been conducted to assess the genetic variability, heritability and genetic advance studies in 22 genotypes of red cabbage.

2. Materials and Methods

The experiment was carried out at Black Sea Agricultural Research Institute, located in Samsun during winter season during 2019-2021 growing period. The seeds of red had cabbage varieties were sown on July. Seedlings were grown in an unheated plastic greenhouse. For seedling cultivation, seed trays (45 cell) with a 5.5 x 5.5 cm pore size were used. The cultivation medium consisted of a mixture of peat + perlite in a ratio of 3: 1 placed in the seed trays and vermiculite was used as a cover material after planting.

Table 1. Some morphological traits of red cabbage lines
Çizelge 1. *Kırmızı lahana hatlarının bazı morfolojik özellikleri*

Lines	Shape of Head	Top leaf color of the head	Covering of Head	Hardness of head	Wax on the outer leaf	Days to maturity (day)
K3	Broad obovate	Dark violet	Covered	Very tight	Strong	115
K5	Elliptic	Dark violet	Partially covered	Very tight	Weak	113
K14	Broad obovate	Dakr violet	Covered	Very tight	Strong	113
K15	Elliptic	Violet	Partially covered	Very tight	Absent	113
K20	Round	Dark violet	Covered	Medium tight	Absent	78
K26	Broad obovate	Dark violet	Covered	Very tight	Medium	115
K30	Broad ovate	Dark violet	Covered	Very tight	Strong	113
K32	Broad obovate	Dark violet	Covered	Very tight	Very weak	134
K36	Broad obovate	Violet	Partially covered	Very tight	Strong	95
K41	Elliptic	Dark violet	Partially covered	Very tight	Weak	113
K42	Broad ovate	Dark violet	Covered	Very tight	Strong	113
K47	Elliptic	Dark violet	Partially covered	Medium tight	Medium	113
K62	Round	Dark violet	Covered	Very tight	Medium	95
K69	Elliptic	Dark violet	Partially covered	Very tight	Strong	113
K76	Broad obovate	Light violet	Partially covered	Very tight	Medium	134
K78	Round	Dark violet	Covered	Very tight	Very weak	113
K79	Elliptic	Dark violet	Covered	Very tight	Strong	95
K80	Round	Dark violet	Covered	Very tight	Very weak	134
K81	Broad ovate	Dark violet	Covered	Very tight	Strong	113
K83	Elliptic	Violet	Covered	Very tight	Weak	113
K85	Round	Dark violet	Covered	Very tight	Absent	134
K97	Broad ovate	Violet	Partially covered	Very tight	Strong	113

All genotypes were transplanted in Randomized Complete Block Design (RCBD) with three replications. The experiment was established with 20 plants in each replication, with 100 x 40 cm in-row and inter-row spacing and row planting distances in the second week of August. Fertilization, irrigation and weed cleaning etc were followed regularly during the study. Harvesting was done when 90% of the plant population of each plot reached to maturity. Data were recorded on 10 randomly chosen plants of each genotype in each of the three replication for different characters, such as head weight (g), head diameter (cm), head length (cm), core length (cm), head volume (g cm-3) (head weight/head density), head density (cm3) (Tanaka and Niikura, 2003), head shape index (head diameter/head length).

2.1. Statistical analysis

The mean values of each genotype were computed for statistical analysis. Relationships among the examined traits were examined by a correlation analysis. Analysis of variance was performed for each character to determine whether there were differences between and within the populations. All statistical analyses were carried out to the data obtained after characterization using JMP 7.0.

Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability, genetic advance and genetic gain were computed as per standard formulas. The formula of genotypic correlation coefficients were estimated by Al-Jibouri et al. (1958). Phenotypic and genotypic coefficient of variation, heritability (broad sense) and genetic advance as percent of mean were estimated by the formula al suggested by Burton (1952), Lush (1949) and Johnson et al. (1955).

$$\text{Genetic variance (Vg)}=\frac{\text{Genotype Mean Square (GMS)-Error Mean Square (EMS)}}{\text{Number of Replications (r)}} \quad (1)$$

Environmental Variance=Error Mean Suare (EMS)

Phenotypic Variance (Vp)=Vg+Ve/r

Genotypic phenotypic and environmental coefficient of Variation was calculated as

$$\text{GCV\%}=\sqrt{\frac{\text{Vg}}{\text{x}}}\times 100 \quad (2)$$

$$\text{PCV\%}=\sqrt{\frac{\text{Vp}}{\text{x}}}\times 100 \quad (3)$$

$$\text{ECV\%}=\sqrt{\frac{\text{Ve}}{\text{x}}}\times 100 \quad (4)$$

GCV% : Genotypic coefficient of variation
Vg : Genotypic variance
PCV % : Phenotypic coefficient of variation
Vp : Phenotypic variance
ECV % : Environmental coefficient of variation
Ve : Environmental variance

$$\text{Broad Sense Heritability } (h^2B) = \frac{Vp}{Vg}\times 100 \quad (5)$$

$$\text{Genetic Advance (GA)}= GA = K\sqrt{Vp}H^2 \quad (6)$$

Where, K = 1.40 at 20% selection intensity for trait;
Vp : Phenotypic variance for trait

Genetic advance as percentage of mean is calculated as,

$$\text{GA\%}=\frac{\text{GA}}{\text{X}}\times 100 \quad (7)$$

Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability, genetic advance and genetic gain were computed as per standard formulas. The formula of genotypic correlation coefficients were estimated by Al-Jibouri et al. (1958). Phenotypic and genotypic coefficient of variation, heritability (broad sense) and genetic advance as percent of mean were estimated by the formula al suggested by Burton (1952), Lush (1949) and Johanson et al. (1955).

3. Result and discussion

Analysis of variance showed that there were significant differences among genotypes for all traits studied. Estimation of mean squares of accessions year and error for seven traits of 22 red cabbege lines are shown in Table 2. This is an indication of existence of sufficient amount of variability exist for in red cabbage. Similar results were determined by researchers examining different morphological traits in different Brassica species (Kibar et al., 2014; Thakur & Vidyasagar, 2016; Chatterjee et al., 2018; Aktar et al., 2019). Variability is the most important characteristic feature of any population is of remarkable importance in breeding programme. Estimation of genetic variability is an important precondition for realizing response to selection as the progress in breeding depends upon its amount, nature and magnitude of genetic variability (Nandhini at al., 2020). These results are important for the further red of material on the selection of promising genotypes in red cabbage breeding.

The mean performance of genotypes for various characters is presented in Table 3. The mean values of genotypes were recorded for head weight (755.57–1244.11 g), head length (12.54-18.79 cm), head diameter (9.86-13.79 cm), core length (5.46-10.89 cm), head volume (719.49-1650.34 cm3), head density (2.18-3.64 g cm-3), head shape index (0.73-1.95) (Table 3). Different results were obtained for the properties studied under different environmental conditions in cabbage (Kaygısız Ascıogul, 2009; Sharma, 2010; Cervenski et al., 2011; Kibar et al., 2014; Özbakır Özer 2014; Singh et al., 2019; Sharma et al., 2019a).

Table 2. Analysis of variance for seven morphological traits of red cabbage lines.

Çizelge 2. *Kırmızı lahana hatlarının bazı morfolojik özelliği için varyans analizi.*

Lines	df	Head Weight (g)	Head length (cm)	Head diameter (cm)	Core length (cm)	Head volüme (g cm^{-3})	Head density (cm^{3})	Head shape index
Replication	2	0.68	3.20	1.31	3.35	9.18	5.16	0.73
Genotypes	21	38955.50**	5.97**	3.48**	4.25**	241131.00**	0.30**	0.02**
Error	42	7067.30	0.50	0.62	0.37	75437.00	0.17	0.01

***, **:** Significant at 5 and 1 per cent levels, respectively

Table 3. Mean performance of 22 red cabbage lines for different morphological traits

Çizelge 3. *22 kırmızı lahana hattının farklı morfolojik özellikler için ortalama performansı*

Lines	Head weight	Head length	Head diameter	Core length	Head density	Head volume	Head shape index
K3	755.57	12.54	10.99	7.52	2.71	719.49	1.13
K5	1059.00	14.91	12.93	6.47	2.67	1139.48	0.97
K14	1040.99	15.52	12.24	6.10	2.56	937.47	1.23
K15	944.34	14.77	12.19	5.93	2.30	1240.29	0.82
K20	1055.23	14.13	13.12	6.72	2.77	1217.78	0.87
K26	1048.34	16.09	10.81	8.61	2.82	857.19	1.24
K30	1244,11	18.79	13.38	10.89	3.36	1650.34	0.78
K32	1191.34	15.73	10.81	8.80	3.16	1157.85	1.09
K36	1166.68	15.66	14.02	9.43	3.23	1562.96	0.73
K41	1133.57	15.80	13.23	7.57	2.94	1142.84	1.06
K42	1156.12	15.57	11.32	7.66	2.71	946.34	1.43
K47	1138.57	17.64	12.72	8.60	2.84	1376.09	0.78
K62	940.57	13.51	12.8	7.93	3.64	1145.75	0.87
K69	1184.10	16.10	9.86	8.03	2.22	874.56	1.42
K76	962.78	15.67	12.10	5.46	2.51	793.75	1.95
K78	1143.79	15.18	13.79	6.50	2.62	1447.58	0.80
K79	1073.46	14.88	11.88	7.26	2.18	1125.94	0.99
K80	1227.78	17.88	13.78	7.54	3.12	1522.29	0.87
K81	1025.46	15.90	11.10	7.89	2.94	988.26	1.02
K83	943.34	15.44	12.49	7.77	3.23	1201.79	0.84
K85	945.27	13.08	11.77	6.77	3.07	892.80	1.18
K97	1128.66	16.37	12.38	7.57	2.98	1288.20	0.89

The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all traits (Table 4). Thus indicated the influences of environmental factor on these traits. Variability and association studies were carried out several Brassica species such as cauliflower (Chittora & Singh, 2015; Dey et al., 2015; Chıttora et al., 2016); Chatterjee et al., 2018; Kumar et al., 2018), knolkhol (Dolkar et al., 2018), cabbage (Sharma et al., 2019a, Sharma et al., 2019b), broccoli (Nandhini et al., 2020), kale (Wudneh, 2020; Gorka et al., 2021) and researchers reported higher the magnitude of phenotypic coefficient of variability than genotypic coefficient of variability.

The respective PCV and GCV was high for head weight (10.66, 9.65), head length (9.09, 8.70), head diameter (8.78, 7.96), core length (15.68, 14.99), head volume (24.72, 20.49), head density (30.61, 20.06) and head shape index (9.64, 7.45). Moderate PCV was recorded for core length, head volüme and head density. However, it was found low for head head diameter, head weight, head length and head weight. Similar type results are in with earlier findings of various researchers for net head weight (Atter et al., 2009, Meena et al., 2009, Thakur & Vidyasagar, 2016). Conversely, Kaur et al., 2018 reported high PCV for gross head weight

Table 4. Phenotypic (PCV) and genotypic (GCV) coefficients of variation, broad sense heritability (h^2B) and genetic advance (GA) (%) for various morphological traits in red cabbage

Çizelge 4. *Kırmızı lahana hatlarında bazı morfolojik özellikler için fenotipik (PCV) ve genotipik (GCV) varyasyon katsayıları, geniş anlamda kalıtım derecesi (h^2B) ve genetik ilerleme (GA) (%)*

Traits	GCV(%)	PCV(%)	h^2B(%)	GA	GA (%)
Head weight	9.65	10.66	81.86	192.16	17.98
Head length	8.70	9.09	91.56	2.66	17.15
Head diameter	7.96	8.78	82.24	1.82	14.87
Core length	14.99	15.68	91.38	2.24	29.52
Head volume	20.49	24.72	68.72	401.32	35.00
Head density	20.06	30.61	42.97	0.28	27.09
Head shape index	7.45	9.64	59.77	0.09	11.87

Variability is the most important characteristic feature of any population (Nandhini et al., 2020). In a population observed variation is due to both factors i.e. genetics and environmental where as genetic variability is the only heritable from generation to the next generation so the heritability alone does not give an idea about the expected gain in the next generation but it has to be considered in conjunction with the genetic advance (Ahsan et al., 2015). Genetic advance is also important due to observe of the expected genetic gain in the selection (Eşiyok et al., 2011).

Burton (1952) and Panse (1957) viewed that if a character is governed by non-additive gene action, it may have high heritability but low genetic advance, whereas, if it is governed by additive gene action, heritability and genetic advance both would be high. The broad sense heritability and genetic advance as percent of mean of the traits are presented in Table 4. Heritability estimates were classified as low (<50%), moderate (50-80%) and high (>80%) as suggested by Sharma (1994). Accordingly, we recorded high heritability for head length (91.56%), core length (91.38%), head diameter (82.24%) and head weight (81.86%). In the research, high heritability accompanied with a high genetic advance for head weight, head dimater and head length revealed the role of additive gene action and thus, a high genetic gain is expected from selection for these traits. Panse and Sukhatme (1978), stated that ıf a trait is governed by additive gene action, both heritability and genetic progression will be high. The result is in accordance with the findings for ascorbic acid content in cabbage (Singh et al., 2013), for days to first flowering in rapeseed (Hasan et al., 2014), for mineral content (Fe, Zn, Cu, Ca, Mn, K) in cabbage head, for total yield in cauliflower (Chittora & Singh, 2015), for minerals contents (Ca, Fe, Mg, Zn) in Chinese cabbage (Xie et al., 2018), for head weight and ascorbic acid in cabbage (Kaur et al., 218), for yield and its component traits in ethiopian kale (Wudneh, 2020).

The highest genetic advance as percent of mean was shown by head volume (35.0 %) followed by core length (29.52%) and head density (27.09%) (Table 4). Chittora and Singh (2015), reported highest genetic advance as per cent of mean was observed for net curd weight (39.54 %) followed by marketable curd weight (32.82 %), curd yield per hectare (32.81 %), harvest index (27.08%) and gross plant weight (27.30 %). Thakur and Vidyasagar (2016) also reported high genetic advance for gross weight and total yield per plot. High heritability coupled with moderate genetic advance for gross head weight, net head weight, number of non-wrapper leaves, head shape index and TSS (^{0}Brix) were reported by Sharma et al. (2019a). However, on the contrary to present findings Gorka et al.(2021) also observed high heritability with low genetic advance as percentage of mean was marked for all the three biochemical traits.

Knowledge of relationships between yield and its components is essential as this may help in constructing suitable selection criteria for yield (Kibar et al., 2014). For this purpose, correlation coefficients were calculated to determine the relationships between red cabbage traits. Significant differences were observed among all the genotypes for all the traits in table 5. Head weight of the lines was highly positively correlated with head length, head diameter, wcore length and head volume.

Cervenski et al. (1998) and Kibar et al. (2014) also reported that head weight significant and positive correlation with head diameter and head length. The results of our present analysis are in agreement with these. Owing to the high positive correlation between head weight and head diameter and head length; the selection of genotypes with desired head size and head weight will be effective to obtain high yielding cultivars/genotypes (Kibar et al. 2014). Meena et al. (2014), also reported that whole plant weight significant and positive correlation with curd length, curd breadth, total number of leaf, days to curd formation and days to 50% maturity in cabbage. While positive and significant correlation in curd weight with curd length, total number of leaf, leaves per plant, days to curd formation and days to 50 percent maturity in cauliflower by Dutta et al. (1992), Kanwar et al. (2010), Kumar et al. (2011), Sheemar et al. (2012), Nimkar (2013), (Nimkar and Soniya 2013).

Table 5. Correlation coefficients for morphological traits in red cabbage lines
Çizelge 5. *Kırmızı lahana hatlarında bazı morfolojik özelliklerinkorelasyon katsayıları*

Traits	**Head weight**	**Head length**	**Head diameter**	**Core length**	**Head volume**	**Head density**	**Head shape index**
Head weight	1.000	0.0661**	0.2725**	0.4067*	0.5693**	-0.1520	-0.1858
Head length		1.000	0.2336**	0.4783**	0.5176**	-0.19,31**	-0.4617**
Head diameter			1.000	0.0617	0.7071**	-0.4129*	0.5190**
Core length				1.000	0.3945*	-0.2930**	-0.2619*
Head volume					1.000	-0.7317**	0.2852*
Head density						1.000	-0.2756*
Head shape index							1.000

***, **:** Significant at the 0.05 and 0.01 probability level, respectively

Some negative correlations were also observed among the red cabbage traits. Head weight was highly negatively correlated with head density and head shape index (Table 5). As can be seen from the table 5, head length, head diameter, core length, head volume and head density was highly negatively correlated observed head density and head shape index. Dey et al (2005) explained the knowledge of correlation among yield and its contributing traits may be helpful to a plant breeder to determine the degree of association between them and help to improve the efficiency of selection by the use of favourable combination of characters and to minimize the retarding effect of those characters which are negatively correlated.

4. Conclusion

The PCV was higher than the GCV for all the characters studied, which indicated that the envıronment ıs effectıve on the herıtage of the characters. High heritability in percentage of mean was observed for head length, head weight, head diameter and core length. On the other hand, the GA was determined the most in head volume, core length and head density characteristics. High positive correlation was observed in the same characteristics. These features need to be taken into account in the development of high yielding cabbage varieties.

Acknowledgements

The study was supported by The Scientific and Technological Research Council of Turkey (TUBITAK) Project No. 117G002 (Line and/or Variety Development Project in Winter Vegetable Growing)..

References

Ahsan, M.Z, Majidano, M.S., Bhutto, H., Soomro, A.W., Panhwar, F.H., Channa, A.R. & Sial, K.B. (2015). Genetic Variability, Coefficient of Variance, Heritability and Genetic Advance of Some Gossypium hirsutum L. Accessions. *Journal of Agricultural Science*, 7(2): 147-151 doi: 10.5539/jas.v7n2p147

Aktar, T., Nuruzzaman, M., Rana, M.S., Huda, M.M., Hossain, M.A & Hassan, L. (2019). Genetic parameters and diversity studies of yield and yield contributing characters in Brassica genotypes. *Journal of Bangladesh Agricultural University*, 17(3): 295–300. doi: 10.3329/jbau.v17i3.43200

Ali, Y., Rahman, H., Nasim, A., Azam, S. & Khan, A. (2013). Heritability and Correlation Analysis for Morphological and Biochemical Traits in *Brassica carinata* L. *Sarhad Journal of Agriculture*, 29 (3): 45-58

Al-Jibouri, H.A, Millar, P.A & Robinson, H.F. (1958). Genotypic and environmental variance and co-variances in cauliflower. *Agronomy Journal* 50: 633-637.

Allard, R.W. (1999). Principles of plant breeding. 2nd edn. New York, John Wiley & Sons. ISBN 10: 0471023094 ISBN 13: 9780471023098

Atter, R.S., Sharma, K.C. & Sundouri, A.S. (2009). Genetic variability, heritability and genetic advance studies in cabbage. *Indian Society of Plant Genetic Resources* 22: 62-65

Burton, G.W. (1952). Quantitative inheritance in grasses, Proceedings of 6th İnternational Grassland Congress, 1:227- 283.

Cervenski, J., Gvozdenovıc, D.J, Takac, A. & Bugarskı, D. (1998). Correlation between some of the yield components of cabbage (*Brassica oleracae* var. *capitata* L.). Proceedings of 2nd Balkan Symposium of Field Crops 1: 509-513.

Cervenski, J, Gvozdanovic-Varga, J., & Glogovac, S. (2011). Local cabbage (*Brassica oleracea* var. *capitata* L.) populations from Serbian Province of Vojvodina. *African Journal of Biotechnology*, 10, 5281–5285 doi: 10.13140/RG.2.2.20319.15528

Chatterjee, S., Aralikatti, O., Sharma, S., Mukherjee, D., Patil, S., Kanwar, H.S. & Choudhur, P. (2018). Studies of Genetic Variability, Heritability and Genetic Gain for Some Important Horticultural Traits in Cauliflower (*Brassica oleracea* var. *botrytis* L.). ***International Journal of Current Microbiology and Applied Sciences***,7(4):82-92. doi: 10.20546/ijcmas.2018.704.010

Chittora, A & Singh, D.K. (2015). Genetic variability studies in early cauliflower (*Brassica oleracea* var. *botrytis* L.). *Electronic Journal of Plant Breeding*, 6(3): 842-847.

Chıttora, A., Sıngh, D.K. & Kaushal, A. (2016). Genetıc varıabılıty, herıtabılıty and genetıc advance ın early maturıng caulıflower. *Annals of Plant and Soil Research* 18(3): 251-256

Dey, S.S., Behera, T.K., Pal, A & Munshi, A.D. (2005). Correlation and path coefficient analysis in bitter gourd (*Momordica charantia* L.). *Vegetable Science*, 32(2):173-176

Dey, S.S, Bhatia, R, Sharma, S., Sharma, K., Kumar, R, Sharma, V.K. & Parkash, C. (2015). Genetic divergence and interaction among CUPRAC, FRAP and total phenolics content in cauliflower (*Brassica oleracea* var. *botrytis* L.). Indian. *Journal of Genetics and Plant Breeding*. 75:79-85. doi: 10.5958/0975-6906.2015.00010.3

Dolkar, R, Samnotra, R.K., Kumar, S., Gupta, R.K & Vijayakumar (2018). Variability for Ascorbic Acid, Beta Carotene and Minerals Content (Phosphorous, Potassium and Calcium) in Knolkhol (*Brassica oleracea* var. *gongylodes* L.) Genotypes. *International Journal of Current Microbiology and Applied Sciences*. 7(6): 1020-1025 doi: 10.20546/ijcmas.2018.706.120

Dutta, S.K, Korla. B.N & Sharma, P.P. (1992). Path coefficient analysis in late cauliflower. *Indian Journal of Agricultural Sciences* 76(1): 37-40.

Eşiyok, D., Bozokalfa, M.K. & Aşçıoğul, T.K. (2011). Variability, heritability and assocıatıon analysis in plant traits of swıss chard (*Beta vulgaris* subsp. *cicla*). *Genetika*, 43 (2): 239-252. Doi.10.2298/GENSR1102239E

Galton, F. (1987). Nature Inheritance. Mac Million London.

Gorka, S., Samnotra, R.K., Kumar, S. & Gupta, M. (2021). Variability studies for vitamin C, beta carotene and total phenol content in kale (*Brassica oleracea* L. var. *acephala*) genotypes. *Journal of Pharmacognosy and Phytochemistry*, 10(2): 1221-1227.

Hasan, E.U, Mustafa, H.S.B., Bibi, T., & Mahmood, T. (2014). Genetic variability, correlation and path analysis in advanced lines of rapeseed (*Brassica napus* L.) for yield components. *Cercetări Agronomice în Moldova*, 47(1): 157-159.

Jalata, Z., Ayana, A, & Zeleke, H. (2011). Variability, heritability and genetic advance for some yield and yield related traits in Ethiopian barley (*Hordeum vulgare* L.). *İnternational Journal of Plant Breeding and Genetics*. 5(1), 44-52 doi:10.3923/ijpbg.2011.44.52

Johnson, H.W., Robinson, H.F, & Comstock, R.E. (1955). Estimation of genetic and environmental variability in soybeans. *Agronomy Journal*, 47: 314–318.

Kanwar, H.S, Sharma, A., Kanwar, M.S., & Anand V (2010) Evaluation of cauliflower (*Brassica oleracea* var. *bortrytis* L.) genotypes for quantitative traits, their resistance against diamond back moth and cabbage white butterfly. *Journal of Research* 9(2): 156-163.

Kaur, M., Chadha, S., Kumar, N., Sehgal, N. & Kanwar, S. (2018). Characters association and path analysis among CMS and SI based cabbage hybrids under mid hill conditions of Himachal Pradesh, India. *International Journal of Current Microbiology and Applied Sciences*. 7(1): 424-430. doi:10.20546/ijcmas.2018.701.049

Kaygısız Aşçıoğul, T. (2009).Researches on the determınatıon of morphologıcal and molecular characterızatıon of some cabbage genotypes. Ege University. (MSc Thesis, Printed, İzmir).

Kibar, B., Karaağaç, O. & Kar, H. (2014). Correlation and path coefficient analysis of yield and yield components in cabbage. *Acta Scientiarum Polonorum HortorumCultus* 13(6): 87-97

Kumar, M., Sharma, S.R., Kalia, P. & Saha, P. (2011). Genetic variability and character association for yield and quality traits in early maturing Indian cauliflowers. *Indian Journal of Horticulture* 68(2): 206-211.

Kumar, A., Roy, C., Kumar, R., Kumar, R., Singh, V.K. & Sinha, S.K. (2018). Estimation of existing genetic variability, heritability and genetic advance in tropical cauliflower (*Brassica oleracea* var. *botrytis* L.). *Journal of Pharmacognosy and Phytochemistry*, 7(2): 2048-2050

Kumar, M., Rana, D.K., Choudhary, G.R., Kumar, H. & Kumar, M. (2020). Correlation coefficient studies in Knol-Khol (*Brassica oleracea* var. *gongylodes*) cv. White Vienna under Srinagar Garhwal Valley. *International Journal of Chemical Studies*, 8(4): 1244-1247

Lush, J.L. (1949). Heritability of quantitative characters in farm animals. Proceedings of 8th Congress of Genetics and Hereditas. 35: 356-375

Meena, M.L., Ram, R.B. & Rubee, L. (2009). Genetic variability and correlation studies for some quantitative traits in cabbage (*Brassica oleracea* var. *capitata* L.) under Lucknow conditions. *Progressive Horticulture*, 41, 89–93.

Meena, M.L., Ram, R.B., Lata, R. & Shastra, S.R. (2014). Determining yield components in cabbage (*Brassica oleraceae* var. *capitata* L.) through correlation and path analysis. *International Journal of Science and Nature* 1(1): 27-30.

Nandhini, D., Arumugam, T., Ganesan, K.N., Subramanian, K.S. & Keisar Lourdusamy, D. (2020). Assessment of variability in Broccoli (*Brassica oleracea* var. italica L.) genotypes. The Pharma Innovation Journal, 9(1): 338-340

Nimkar, S.A. (2013). Correlation and path coefficient studies in biparental progenies in cauliflower (Brassica oleracea var. botrytis L.).. *Research Journal of Agricultural Sciences*, 4(5/6):667-669.

Nimkar, S.A. & Soniya, A. (2013). Correlation and path coefficient studies in biparental progenies in cauliflower (*Brassica oleracea* var. *botrytis* L.). Research Journal of Agricultural Sciences 4(5/6): 667 669.

Özbakır Özer, M. (2014). The breedıng of a resıstant hybrıd cultıvar agaınst root-knot nematodes ın whıte head cabbage (brassica oleraceae var. capitata subvar. alba) genotypes. Ondokuz Mayıs University (Doctoral dissertation, PhD Thesis (Printed), Samsun)

Panse, V.G. (1957). Genetics of quantitative characters in relation to plant breeding. *Indian Journal of Genetics and Plant Breeding*, 47: 318-325

Panse, V.G. & Sukhatme, P.V. (1978). Statistical methods for Agricultural Workers. ICAR, New Delhi, 1978. 235-246.

Rauf, M.A. & Md Abdur Rahim, M.A. (2018). Genetic Variability Studies among Yield and Its Contributing Traits in Mustard (*Brassica napus* L.). *Advances in Zoology and Botany* 6(4): 101-108 doi: 10.13189/azb.2018.06040

Sharma, P. (1994). Genetic variability and path coefficient analysis in cabbage (*Brassica oleracea* var. *capitata*). Dr YS Parmar University of Horticulture and Forestry (M.Sc. Thesis, Printed, India).

Sharma, K.C. (2010). Genetic variability, characters association and path analysis in exotic lines of cabbage under mid hill, sub-humid conditions of Himachal Pradesh. *Journal of Hill Agriculture*, 1, 146–150.

Sharma, S., Chadha, S., Sharma, N. & Singh, P. (2019a). Genetic Evaluation of CMS Lines and their Maintainers for Yield and Horticultural Traits in Cabbage (*Brassica oleracea* var.*capitata* L.). *International Journal of Current Microbiology and Applied Sciences* 8(8): 2398-2408. Doi: 10.20546/ijcmas.2019.808.279

Sharma, S., Chadha, S., Sharma, N. & Singh, P. (2019b). Correlation and path analysis among CMS lines and their maintainers for yield and quality attributes in cabbage (*Brassica oleracea* var. *capitata* L.) *International Journal of Chemical Studies*, 7(5): 2731-2737.

Sheemar, G., Singh, D., Malik, A. & Kumar, A. (2012). Correlation and path analysis studies of economic traits in cauliflower (*Brassica oleracea* var. *botrytis* L). *Journal of Agriculture Technology* 8(5): 1791-1799.

Singh, S., Dey, S.S., Bhatia, R., Kumar, R., Sharma, K. & Behera, T.K. (2019). Heterosis and combining ability in cytoplasmic male sterile and doubled haploid based *Brassica* *oleracea* progenies and prediction of heterosis using microsatellites. PLoS ONE 14(8): e0210772. doi: 10.1371/journal.pone.0210772.

Singh, B.K, Sharma, S.R. & Singh, B. (2013). Genetic variability inheritance and correlation for mineral contents in cabbage (*Brassica oleracea* var. *capitata* L.), Journal of *Horticultural Research*, 21(1): 91-97.

Tanaka, N. & Nikura, S. (2003). Characterization of early maturing F1 hybrid varieties in cabbage (*Brassica oleracea* L.). *Breeding Science* 53: 325-333.

Thakur, H. & Vidyasagar (2016). Estimates of genetic variability, heritability and genetic advances for yield and horticultural traits in cabbage (*Brassica oleracea* var. *capitata* L.). *Journal of Environment and Bio-Sciences.* 30:155-157.

Ullah, N., Farhatullah, N.A., Rahman, H.U., Fayyaz, L. & Amin, N.U. (2015). Genetic Variability Among Advanced Lines of Brassica. *Pakistan Journal of Botany* 47(2): 623-628.

Wudneh, A.Y. (2020). Genetıc varıabılıty, herıtabılıty and genetıc advance for vegetable yıeld and ıts component traıts ın ethıopıan kale (*Brassica carinata* A.). International *Journal of Plant Breeding and Crop Science*. 7(3): 946-952.

Xie, F., Zha, J., Tang, H., Xu, Y., Liu, X. & Wan, Z. (2018). Combining ability and heterosis analysis for mineral elements by using cytoplasmic male-sterile systems in non-heading Chinese cabbage (*Brassica rapa*). C*rop and Pasture Science*69: 296–302. doi: /10.1071/CP17357