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Genetic Improvement of Some Quality Characteristics of Cabbage (*Brassica Oleracea* var. Capitata) through Simple Recurrent Selection.

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ABSTRACT

This investigation was conducted at El-Gemmeiza Agriculture Research Station farm, Gharbia Governorate, Horticulture Research Institute, Agriculture Research Center through the three years 2020, 2021 and 2022. Simple recurrent selection was used to improvement of some quality characteristics in Sabeiny cabbage populations. The data illustrated that the averages and ranges of characters for genotypes become greater in S_m generation than those in the S_0 and S_1 generation. Highest significant differences were recorded between all genotypes for traits. These results recorded that non - wrapper leaves number and days to harvest decreased by 27.65 and 13.57 % in the first cycle population. Meanwhile, wrapper leaves number, head weight and head diameter increased by 5.98, 28.79 and 11.78 %. Phenotypic coefficient variances were greater than the genotypic coefficient variances referring predominance of environmental actions on the expression of aforementioned traits. Highest heritability coupled with high GAM % (genetic advance as percent of mean) were recorded in all traits, especially, wrapper leaves number, head weight and days to harvest. The obtained results indicated that these characters were under the control of additive gene action and could be effectually improved during selection. Head weight had positive and significantly correlation at phenotypic and genotypic level with wrapper leaves number and head diameter. Negative and highly significant correlations were estimated with days to harvest and number of non-wrapper leaves and head length. Therefore, selection of a good cabbage in wrapper leaves number, head height, head weight and head diameter, may improving cabbage plants under this study.

Keywords: Cabbage, variance, heritability, genetic advance, correlation, selection.

INTRODUCTION

Information on selection and genetic advance of Cabbage (*Brassica oleracea* from *Cruciferae* family) genotypes is essential to maximize their use for variety development. The genetic improvement of both qualitative and quantitative traits is the main objective of plant breeders. Genetic data of different quantitative traits especially those that contribute to yield and correlated traits would be very useful in planning the breeding programs for effective selections. The value of cabbage as an important component of the human daily diet has been known for a long time because they provide all the main components of human diet, it is commonly called "protected food" because of its protective effects against degenerative diseases. Cabbage plant consumed for its nutritional values such as, carotenes, vitamins and minerals (Farnham *et al.*, 2000; Kopsell *et al.*, 2004). Cabbage plants is consumed as sauerkraut, which is cut into microchips that undergo lactic acid fermentation in brine made from its juice with salt. The improvement of vegetables has been largely limited to traditional breeding methods and such programs accreditation interspecific sexual hybridization of vegetable plants, which have favorable heritable characteristics (Chiang and Jacob 1992). Cabbage, it is the most important winter season vegetable plant of the genus *Brassica* grown in the world, which comprises fully cross-fertile groups with wide variation morphological traits. There are various genotypes of cabbage plant depends on size, color and shape. Cabbage is rich in minerals and vitamins such as A, riboflavin, thiamine and C. In addition, contains minerals such as potassium, phosphorus, calcium and iron (Samec *et al.*, 2017). Cabbage is considered one of the most famous vegetable crops around the world (Nyatuame *et al.*, 2013).

In Egypt, there are many local cultivars of cabbage, which are open pollinated populations. Populations of cabbage have been improved by farmers over mass selection. The cultivation of local cultivars, as a percentage of the entire planted area with cabbage, decreasing in comparison with commercial crosses. The local Egyptian cultivars of cabbage plants are fewer productive and their heads are lack firmness and uniformity. These genotypes are a valuable genetic source and should either be recorded and / or released as commercial hybrids after selection. Escribano *et al.*, (1998) found that estimation of variation exhibited by available genetic sources for quantitative and qualitative characteristics is important for cabbage breeding program. These characters have been used commonly for line identification and description with the International Union for the Protection of New Varieties of Plants (UPOV) (Anonymous, 1998). These characters are used to show the dissimilarity and similarity in the relationship between populations, they give the opportunity to selection of lines with better qualities for incorporating into breeding programs (Escribano *et al.*, 1991; Cartea *et al.*, 2002).

Recurrent selection is a breeding strategy in which regular selection of valuable individuals from a population is appended by recombination of the elected individuals to form a new genotype (Fehr, 1987). Hatem and Seham (2009) studied improvement of cabbage populations (*Brassica*

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oleracea L. var *capitata*) by simple recurrent selection and found that head compactness was increased in the first cycle population due to selection, depending on head length, diameter and weight, they noticed that phenotypic recurrent selection was effective in improving balady variety of cabbage for head weight, high yield, less number of non – wrapper leaves per plant, in addition to, the simple recurrent selection for studied characters was attached by loss in variability which make further advances possible. Improvement in the mean genotypic magnitude of selected populations by the parental plants is known as genetic advance.

The aim of this investigate is genetic improvement of some quality characteristics of cabbage through simple recurrent selection to produce highly productive and quality plants of with desirable economic qualities.

MATERIALS AND METHODS

Commercial seeds (S_0) of Sabeiny cabbage cv. were sown on July 2020. Plants were transplanted on September 2020 at El-Gemmeiza Agriculture Research Station Farm, Gharbia Governorate, Horticulture Research Institute (HRI), Agriculture Research Center (ARC), Egypt. Two hundred plants were selected for high head weight, high wrapper leaves number per plant, a smaller non – wrapper leaves number per plant and fewer days to maturity. Stem steckling of selected plants were replanted after head removing on November 2020. At flowering stage, each of the selected plants was selfed using the bud pollination method.

The Selfed seeds (S_1) of the selected plants were sown and seedlings on July 2021 for cabbage production. Also, at the maturity period, plant selected procedure for aforementioned traits has conducted among the (S_1) genotypes. These plants were replanted in a separated field to produce the first cycle seeds (S_1). Original seed, first cycle seeds and improved cabbage S_m were grown on September and plants were transplanted on November 2022 in a randomized block design (RBD), with three replicates. The experimental unit was 5 m. in length and 0.90 m. in width, the cabbage plants were transplanted at 0.60 m apart. All agricultural practices were followed in accordance with adopted for cabbage commercial production in Egypt. The studied parameters have been taken at the marketable yield (full maturity stage). Observations on the plant characters namely: stem length (cm), wrapper leaves number per plant, non- wrapper leaves number per plant, head weight (kg), head length (cm), head diameter (cm) and days to harvest (days).

Phenotypic and genotypic coefficient of variation were determined according to Johnson *et al.,* (1955):

$$\textbf{PCV \% = (}\sigma^2\textbf{ph / X) x 100.}$$

$$\textbf{GCV \% = (}\sigma^2\textbf{g / X) x 100.}$$

Where,

PCV: phenotypic coefficient variation, GCV: genotypic coefficient variation, σ2ph: phenotypic variances, σ2g: genotypic variances and X: grand mean for each trait.

Heritability in broad sense ($h^2_{b.s}$) for all traits was estimated according to the method suggested by Allard, (1999) as follows: $h^2_{b.s} = \sigma^2 g / \sigma^2 ph$.

Genetic advance expected after one cycle of selection and genetic advance as percentage of the mean assuming selection of 5 % superior individuals were calculated using standard methods recorded with Johnson *et al.,* (1955) as follow:

$$\textbf{G.A.} = h^2_{b.s} \times K \times \sigma^2 ph.$$

$$\textbf{GAM. \%} = (GA / X) \times 100.$$

K: is the selection differential, which equal to 2.063 at 5 % intensity of selection.

Statistical analysis was carried out for each trait under study using CO - STAT software. The records of genetic advance classified as high (>20%), medium (10-20%) and low (<10%).

Estimation of phenotypic (r_{ph}) and genotypic (r_g) correlations coefficient among pairs of the plant traits were recorded by Singh and Chaudhary, (1985).

The significance of the r_{ph} and r_g were tested by (Cochran and Cox 1957).

RESULTS AND DISCUSSION

Analysis of variance

Analysis of variance of cv. Sabeiny and the developed genotypes was made for all studied characters and the results of mean squares are presented in Table 1.

Table 1. Analysis of variance for traits of cabbage cv Sabeiny after three cycles of selection.

S. V.	d. f.	Stem length (cm)	Wrapper leaves number / plant	Non- wrapper leaves number/ plant	Head weight (kg)	Head height (cm)	Head diameter (cm)	Days to harvest(days)
Replication	2	0.700^{ns}	8.233^{ns}	0.233^{ns}	8.333^{ns}	6.033^{ns}	1.900^{ns}	4.133^{ns}
Genotype	9	18.385**	44.741**	17.097**	808.926**	22.386**	24.000**	94.726**
Error	18	0.774	3.640	1.085	290.925	4.662	9.677	8.281

****: significant at 0.01 levels of probability.**

Analysis of variance and mean squares for all plant characters estimated in cabbage populations viz., stem length, Wrapper leaves number per plant, number of non- wrapper leaves per plant, head weight, head length, head diameter and days to harvest exhibited that the differences between the aggregate genotypes were significantly for examined traits under this study. The values of genotypic mean squares were higher than their corresponding mean squares of error. Mean squares performance of selected genotypes exhibited a remarketable change in plant traits in S_m generation comparison to S_0 and S_1 generation. Highly significant mean squares caused by three cycle selection were recorded for all studied traits, indicating the existence of sufficient variation for studied traits in the present study subsequently, there is effective scope for selection. Thus, selection of a best cabbage in wrapper leaves number/ plant, head weight, head height (cm) and head diameter(cm), may improving cabbage plants. These results are in accordance with the results recorded by Gad *et al.,* (1985), Balkaya *et al.,* (2005), El-Gendy (2012). and Kibar *et al.,* (2015 and 2016).

Estimation of range, means, standard error (*SE*) and coefficient of variation *C.V. (%)*:

The means of 10 selected plants of the second cycle for cabbage traits are listed in Table 2 and Figures 1 and 2. The obtained results exhibited that highly significant differences for plant traits under this study. The mean performance exhibited a clear indication of the agricultural superiority of some genotypes over others. Regarding to stem length trait, the means of stem length in the first cycle population (S_1) decreased by 17.77% comparing with that of the S_0 (original population) and 13.14 % comparing with S_m (improved local population). Stem length showed a variance varied from 8.00 -13.33 cm with a mean of 11.48 ± 0.537 stem length in S_0 population, while, it varied from 8.00 to 12.67 cm stem length with a mean of 9.44 ± 0.893 in S_1 population. Otherwise, the results showed that, the coefficient of variability (C.V.%) for S_0, S_1 and S_m were determined as 8.54, 17.26 and 10.52 %, respectively. For wrapper leaves number, data presented in Table 2 and figure 1 exhibited that significant differences between the different population under this study in wrapper leaves number. The obtained results recorded that wrapper leaves number varied in original population (S_0) from 25.00 -30.00 with a mean of 27.67 ± 1.631. It ranged from 26.00 to 33.00 in S_1 population, with a mean of 29.43 ± 1.055. Meanwhile it varied from 26.33 to 40.00 in improved local plants (S_m) with a mean of 31.33 ± 1.045. The wrapper leaves number of the S_1 population was increased by 5.98 % comparing with the original population plants (S_0) and 6.06 % comparing with the improved local (S_m) plants. In addition to the coefficient variability percentage (C.V. %) was estimated 10.759, 6.546 and 6.060 % for S_0, S_1 and S_m population, consequently. In the same manner, the average of non -wrapper leaves number in the first cycle population decreased by 27.65 % comparing with that the in original population plants and 2.90 % comparing with the improved local population. Non- wrapper leaves number exhibited a variance varied from 9.33 - 11.33 with a mean of 11.43 ± 0.478 leaves / plant in in original population plants. Meanwhile, it varied from 7.33 to 9.00 leaves / plant with a mean of 8.27 ± 0.756 in S_1 population. The coefficient of variability for S_0, S_1 and S_m were recorded as 8.369, 17.197 and 12.595 % respectively. Also, the results demonstrated that, head weight (kg) average varied in the original population plants (S_0) from 1.83 – 4.40 kg, with a mean 3.96 ± 7.356, while it varied from 2.40-5.10 kg with a mean of 3.96 ± 7.356 in S_1 population, while it ranged from 3.33-4.90 kg with a mean of 4.28 ± 9.342 in the improved local population. It is appeared that mean of head weight (kg) in the first cycle population increased that of the S_0 and S_m by28.79 and 7.48 % respectively. The coefficient of variability (C.V. (%)) for S_0, S_1 and S_m was 22.761, 10.714 and 12.602 % respectively (Table 2 and Figures 1). In the other side, the means of head length (cm) in the S_0 population varied from 17.00-24.33 cm with a mean of 21.33 ± 1.032 cm while it ranged from 26.00 to 33.00 with a mean of 21.20 ± 1.417 cm in the S_1 population. Meanwhile, it varied from 19.33 to 24.00 cm with a mean of 21.57 ± 1.183 in the S_m plants. However, the average head length of (S_1) population decreased by 0.61 % comparing with in original population plants. The C.V. % was recorded as 8.84, 12.21 and 10.01 % for S_0, S_1 and S_m populations, respectively. In addition, data of head diameter for the original, the first cycle plants and the improved local populations are presented in Table 2, it is shown that the two populations S_1 and S_m did not differ significantly in head diameter, while it is shown that the two populations differed significantly comparing with the original population plants (S_0). The head diameter of the original population plants varied from 22.67 to 30.00 cm with a mean of 26.73 ± 1.940 while, it ranged from 25.67-35.00 cm with a mean of 30.30 ± 1.426 cm in S_1 plants and varied from 28.33 to 34.67 cm with a mean of 31.00 ± 1.704 cm in the improved local population. The coefficient of variability (C.V.%) was 13.25, 8.59 and 10.04 % for S_0, S_1 and S_m populations, respectively.

The diameter of head in the S_1 population was increased by 11.78 % when compared with the S_0 population, meanwhile, it increased that of improved local plants (S_m) by 2.26 %. Finally, the average of days to harvest in the first cycle population decreased by 13.57 % comparing with that the original population and 2.30 % comparing with the improved local, days to harvest showed a variance ranged from 65.67 to 86.33 day with a mean of 75.47 ± 3.938 days / plant in the original population plants (S_0), while, it varied from 56.67 to 76.33 days with a mean of 65.23 ± 1.407 in S_1 population. The coefficient of variability (C.V.%) for S_0, S_1 and S_m were recorded as 9.53, 3.94 and 4.52 % respectively (Table 2 and Figures 2).

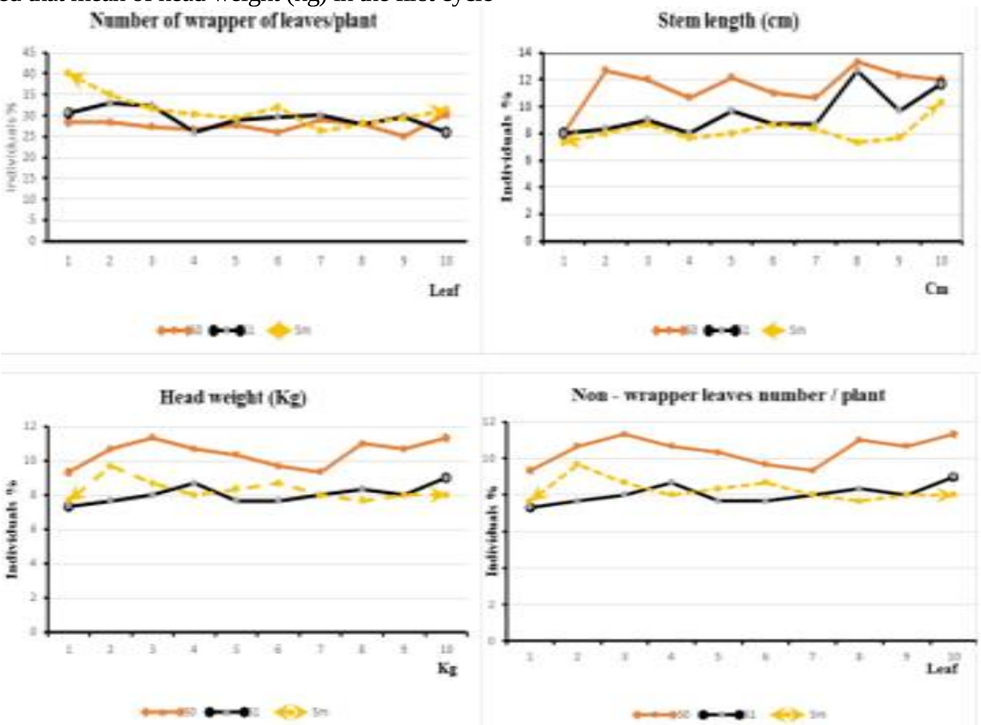

Figure 1. Distribution of stem length (cm), wrapper of leaves number / plant, non-wrapper of leaves number / plant and head weight (kg) in the original (S_0), first cycle (S_1) and improved (S_m populations of Sabeiny cabbage plant.

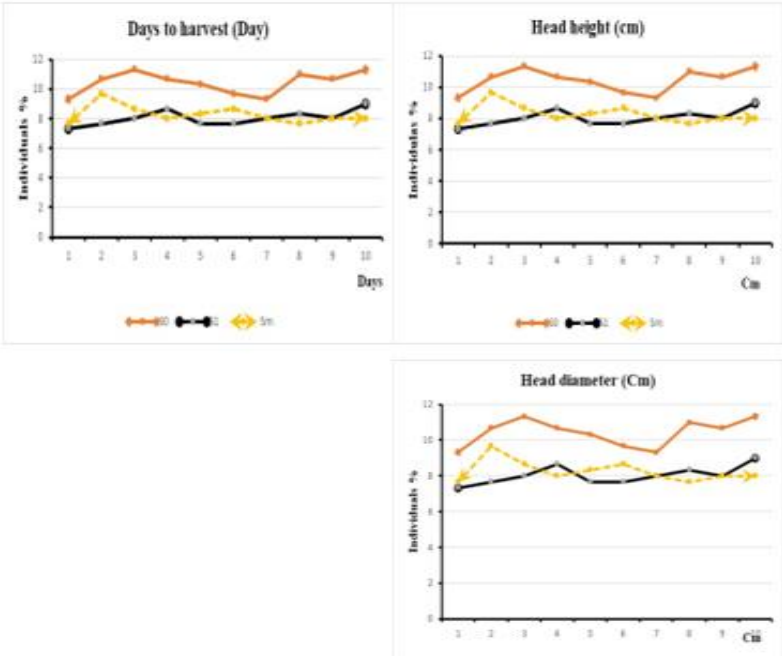

Figure 2. Distribution of head height (cm), head diameter (cm) and days to harvest in the original (S_0), first cycle (S_1) and improved (S_m) populations of Sabeiny cabbage plant.

Highly significant differences discovered between the means of the 10 selected plants of the second cycle for cabbage traits given that there was a wide contrast of variation between genotypes for plant traits which purveys a chance for selecting desirable genotypes with best performance for the plant traits. Furthermore, the obtained results estimated that these populations of cabbage genotypes would restraint positively to selection. Same results were reported by Hatem and Seham (2009), Singh *et al.*, (2013), Hany and Ismail (2018) and Rathore *et al.*, (2018).

Table 2. The economical traits, range, mean, standard error (*SE*) and coefficient of variation of the original (S_0), first cycle (S_1) and improved local (S_m) population of cabbage cv Sabeiny.

Traits	S_0 Range Min - Max	S_0 $\bar{X} \pm SE$	S_0 C.V. %	S_1 Range Min - Max	S_1 $\bar{X} \pm SE$	S_1 C.V. %	S_m Range Min - Max	S_m $\bar{X} \pm SE$	S_m C.V. %	LSD 5 %	LSD 1 %
Stem length (cm)	8.00 - 13.33	11.48± 0.537	8.54	8.00-12.67	9.44 ± 0.893	17.26	7.33-10.33	8.20 ± 0.493	10.52	1.50	2.06
Wrapper leaves number/ plant	25.00-30.33	27.67± 1.631	10.76	26.00-33.00	29.43± 1.055	6.55	26.33-40.00	31.33 ±1.045	6.06	3.27	4.48
Non- wrapper leaves number/ plant	9.33 - 11.33	11.43± 0.478	8.37	7.33-9.00	8.27 ± 0.756	17.20	7.67-9.67	8.03 ±0.5741	12.60	1.78	2.44
Head weight (kg)	1.83 - 4.40	2.82± 11.122	22.76	20.40-5.10	3.96 ± 7.356	10.71	3.33-4.90	4.28 ± 9.342	12.60	9.25	12.67
Head height (cm)	17.00-24.33	21.33± 1.032	8.84	19.33-23.33	21.20± 1.417	12.21	19.33-24.00	21.57 ±1.183	10.01	3.70	5.07
Head diameter (cm)	22.67-30.00	26.73± 1.940	13.25	25.67-35.00	30.30± 1.426	8.59	28.33-34.67	31.00 ±1.704	10.04	5.33	7.31
Days to harvest (days)	65.67-86.33	75.47± 3.938	9.53	56.67-73.33	65.23± 1.407	3.94	56.67-72.67	63.73 ±1.576	4.52	4.93	6.76

Genetic variation:

Genetic advance is a measure of genetic gain under selection which depends on several factors, *i.e.*, genotypic coefficient of variation component (GCV), phenotypic coefficient of variation component (PCV) and heritability (Allard, (1999)). The results in Table 3 exhibited that the values of PCV (phenotypic coefficient of variation component) were higher than the corresponding the GCV (genotypic coefficient of variation component) which showed lower genetic coefficient. for all plant traits under this study, suggestion that the obvious variability is not only due to the genotypes but due to the effect of environmental. Significant differences between genotypes were noticed for plant traits. The future breeding programme may be able to benefit from the significant genetic variation in the material. Phenotypic coefficient of variation (PCV) insignificantly differs from the genotypic coefficient of variation (GCV) regarding to magnitude, the phenotypic coefficient of variation (PCV), suggesting that the existing variability was due to the combination of the genotype's inherent trait and the effect of environmental factors (Ibrahim *et al.*, (2013)). Genotypic coefficient of variation component and phenotypic coefficient of variation component values lesser than 10 % considered low, magnitudes from 10 up 20% are moderate, while magnitudes higher than 20% are regarded to be high (Sivasubramaniah and Meron, (1973)) and Manmeet *et al.*, (2018)). The Genotypic Coefficient of Variation varied from 0.76 to 30.71 % for (non - wrapper leaves number / plant) to (head weight). Moderate GCV recorded for wrapper leaves number / plant (11.81 %), while the rest of the plant traits exhibited lesser genotypic coefficient variation magnitude for stem length (8.94 %), days to maturity (8.42 %), head length (3.52 %), head diameter (2.84 %) and non - wrapper leaves number / plant (0.76 %). The genotypic variance has played a major part of total variances in all plant traits. The phenotypic coefficient of variance varied from 9.56 (days to harvest) to 50.31 % (head weight). Head weight trait show higher at phenotypic coefficient variance level (50.31 %). Moderate phenotypic coefficient variance levels were observed for stem length (13.96 %), wrapper leaves number / plant (13.29 %), non - wrapper leaves number / plant (12.62 %), head length (10.61 %), and head diameter (10.43 %) while, the lesser magnitude of phenotypic coefficient variance was recorded for days to harvest (9.56 %). The phenotypic and genotypic coefficients of variance, refers to many of genetic variation in the estimated characters. This connotes that selecting these traits can be very desirable because the effectiveness of selection is depending on the variation in genetic material. Similar results reported by Duzyaman and Vural (2002), Ahmet *et al.,* (2010), Ibrahim *et al.,* (2013).

Heritability coefficient is a helpful quantitative trait that estimates how environment and genetics interaction to estimate a trait's manifestation. Broad sense heritability evaluates alone do not provide reliable data about the gene action controlling the expression of a particular trait and also this does not provide the data of the magnitude of genetic progression resulting from the selection of the good individuals. The estimates of heritability in broad sense for all studied traits of cabbage population were found significant and listed in Table 3 and indicated existence of heritable genetic variability between genotypes for various aforementioned traits of cabbage population. The results presented in Table 3 showed that the broad sense heritability it was generally high for studied traits expect for head length and head diameter, respectively. The estimated magnitudes of broad sense heritability varied from (0.37%) for non - wrapper leaves number/ plant trait to (79.01%) for wrapper leaves number /plant. High broad sense heritability was recorded wrapper leaves number per plant (79.01%), days to maturity (77.68 %), stem length (cm) (41.22%), head weight (kg) (37.28%) whereas, moderate heritability broad sense were recorded for head length (cm) (11.07%). In addition, the lower magnitude of broad sense heritability was reported for non - wrapper leaves number per plant trait (0.37 %). the lower magnitude of heritability broad sense for non - wrapper leaves number / plant suggested that direct selection in the proceeding generations would not be effective for this trait.

Expectable genetic advance estimates the level of stability of the traits under selection and reflects the expected genetic advance for that trait during selection cycles. The high genetic advance was noted for days to harvest (93.66 %), wrapper leaves number / plant (90.20 %) and head weight (82.71 %). Moderate genetic advance was recorded stem length (13.54 %) and non - wrapper leaves number / plant (10.04 %). The lesser genetic advance was noticed in only two traits namely head length (5.52 %) and head diameter (4.87 %). The high heritability coefficient was showed due to affected of desirable environment instead of genotype and selection for such character may not be reward. Generally, selection should be done very carefully as heritability is calculated in a broad sense and which may be effective. High broad sense heritability does not mean high genetic advance as percent of mean for a particular quantitative trait. Johnson *et al.,* (1955) had pointed out that the heritability coefficient assessments along with genetic advance genetic advance as percent of mean were more useful in predicting the influence of selecting the better individual. However, from the obtained results, genetic advance was calculated as percentage of the mean. Where days to harvest and wrapper leaves number / plant traits exhibited high heritability along with high genetic advance as percent of the mean (GAM %); suggest that effective selection depends on wrapper leaves number / plant might be effective to increase head weight (kg) and days to maturity (harvest). As a result, these characters are mainly controlled by additive gene actions respectively, selection would be effective to improvement these characters. High the percentage of genotypic coefficient of variance combined with high heritability in broad sense and genetic advance provides major data than other criterions alone (Akanda *et al.,* 1997). In this study, wrapper leaves number/plant and head weight exhibited high heritability in broad sense along with high genetic advance as percent of the mean and the percentage of genotypic coefficient of variance. That is, its generality significant different quantitative characters to consider for superior cabbage selection and deserve greatest interest in future breeding programme for developing distinctive cabbage, and it is mooted that pedigree phenotypic selection procedure is a beneficial breeding program for improve studied traits under this study.

Table 3. Estimation of genotypic variance, phenotypic variance, the percentage of phenotypic and genotypic coefficient of variation, heritability in broad sense and genetic advance for different quantitative traits of cabbage cv. Sabeiny.

Traits Parameters	Genetic parameters						
	σ^2g	σ^2ph	Coefficient of variation		$h^2_{b.s}$ %	GA	GAM %
			PCV%	GCV %			
Stem length(cm)	0.54	1.31	13.96	8.94	41.22	1.11	13.54
Wrapper leaves number/plant	13.70	17.34	13.29	11.81	79.01	28.26	90.20
Non - wrapper leaves number/plant	0.004	1.09	12.62	0.76	0.37	0.83	10.04
Head weight (kg)	1.73	4.64	50.31	30.71	37.28	3.54	82.71
Head length (cm)	0.58	5.24	10.61	3.52	11.07	1.19	5.52
Head diameter (cm)	0.77	10.45	10.43	2.84	7.37	1.51	4.87
Days to harvest (days)	28.82	37.10	9.56	8.42	77.68	59.69	93.66

Correlation coefficient:

Association among two or more characters in terms of direction and degree can be defined by correlation coefficient. In the present study correlation between different traits were studied and presented in Table 4. Genotypic and phenotypic association coefficients among important plant traits were determined. Data in Table 4 were exhibited that significant positive or negative and non – significant magnitudes. Environment plays a major role in association among traits. So, the possibility of high yield over yield attributes, such as primary insert in cabbage improvement. Hence, requires understanding the values of magnitudes of association between different yield traits. The obtained results illustrated that the phenotypic correlation was lower as compared to genotypic correlation. Head weight had highly significant and positive correlation at phenotypic and genotypic level with wrapper leaves number / plant, head diameter and days to harvest trait. Days to harvest exhibited that significant and negative correlation with non- wrapper leaves number / plant and head length. Head diameter was highly significant and positively correlated with wrapper leaves number per plant, head weight, head length and days to harvest. On the other side, it had highly significant and negative correlation with days to harvest at phenotypic and genotypic level. Positive and significant correlation was noticed among head length and wrapper leaves number / plant trait at genotypic and phenotypic level.

These estimates are an important aspect which should be used to plan a better selection program. The relationship between the characters may be the result of either a pleiotropic effects of a gene on different parts of plant of the plants or the linkage. The evaluated phenotypic and genotypic correlation coefficients values of the all studied traits. It is observed that the genotypic correlation coefficients (r_g) of all studied plant traits were generally higher than their corresponding phenotypic correlation coefficients (r_{ph}) which pointed that the apparent correlation might be the results of genetic reason. Also, determination of phenotypic and genotypic correlation between traits is essential in cabbage breeding program. Positive association among desirable traits is valuable to the vegetable breeder because it helps in estimating the extent of improvement that could be made in the traits and also in selecting favorable genotypes. Obtained results indicated that for improving cabbage yield, recurrent selection program was used to maintain additive portion in the population of cabbage. So, recurrent selection program is a helpful to improve the yield and its components traits and to select opposite the trait that has negative association with cabbage yield. Significant and desirable positive correlations were found for traits by many researchers and among them were Davik, (2008), Hatem and Seham (2009); Singh *et al.*, (2013); Kibar *et al.*, (2016) and Hany and Ismail (2018). Where: σ^2g = genotypic variance; σ^2ph= phenotypic variance; *PCV %*= the percentage of phenotypic coefficient of variation; *GCV %*= the percentage of genotypic coefficient of variation; $h^2_{b.s}$ = broad sense heritability, *GA* = genetic advance at 5% and GAM % = genetic advance as % of mean at 5%.

The obtained results reveal that magnitudes of phenotypic correlations were lower than those of their respective genotypic correlations in the majority of cases suggesting that genotypic correlations were stronger reliable and free of the environmental factors. Also, this study inferred that most importantly positive traits contribution towards yield / plant at genotypic level were all plant traits, indicating that selection procedure applied to increase aforementioned traits ultimately help to increasing the yield.

Table 4. Estimation of genotypic and phenotypic correlation among different quantitative traits of cabbage cv. Sabeiny.

Traits		Wrapper leaves number / plant	Non- wrapper leaves number/ plant	Head weight (kg)	Head length (cm)	Head diameter (cm)	Days to harvest (days)
Stem length (cm)	r_g	-0.74**	0.56**	-0.67**	-0.39*	-0.31	0.78**
	r_{ph}	-0.26	0.07	0.34	0.06	-0.31	0.59**
Wrapper leaves number / plant	r_g		0.16	0.74**	-0.04	0.91**	0.60**
	r_{ph}		0.13	0.66**	-0.02	0.88**	0.50**
Non- wrapper leaves number / plant	r_g			0.16	0.83**	0.17	-0.51*
	r_{ph}			0.16	0.74**	0.13	-0.71**
Head weight (kg)	r_g				0.27	0.81**	0.80**
	r_{ph}				0.24	0.79**	0.72**
Head length (cm)	r_g					0.53**	-0.40
	r_{ph}					0.52**	-0.66**
Head diameter (cm)	r_g						0.83**
	r_{ph}						0.53**

***, **: significant at 0.05 and 0.01 levels of probability, respectively.**

CONCLUSION

The obtained results demonstrated that the simple recurrent selection for one cycle for the studied traits was attached by slight loss in variability. This obtained results is an accordance to Hatem and Seham (2009); Singh *et al.,* (2013); Kibar *et al.,* (2016) and Hany and Ismail (2018). The results of the study reported that the simple recurrent selection was effective on the genes responsible for increase of wrapper leaves number/ plant, less non- wrapper leaves number / plant, shortness of stem length, high diameter and weight and compactness of the head. consequently, it could be inferred that worthwhile improvement could be acheived in cabbage crop by selection programs.

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التحسين الوراثى لبعض الصفات فى الكرنب بالإنتخاب المتكرر البسيط.

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الملخص

يهدف هذا البحث الى التحسين الوراثى لمحصول الكرنب صنف السبعينى بما يتوافق مع الظروف المحلية عن طريق الإنتخاب المتكرر البسيط لذلك أجرى هذا البحث بمزرعة محطة البحوث الزراعية بالجميزة - معهد بحوث البساتين – مركز البحوث الزراعية فى أعوام 2020 ، 2021 ،2022 وأجريت الدراسة على دورة واحدة من الإنتخاب. حيث زراعت نباتات الصنف السبعينى كعشيرة أصلية عام 2020 م وعند الحصاد أنتخب منها 200 نبات تميزت بالساق القصيرة وزيادة أعداد الأوراق الداخلية الملتفة والعدد القليل من الأوراق الخارجية الغير ملتفة وقطر ووزن الرأس الكبير وقلة عدد الأيام اللازمة للنضج (الحصاد)، وأعيدت زراعة السيقان وتركت حتى مرحلة الإزهار ثم أجرى فيها التلقيح الذاتى البرعمى لكل نبات على حدة وفى يوليو 2021 زرعت تقاوى النباتات الذاتية وكانت كل سلالة على حدة وعند الحصاد تم إنتخاب 200 نبات منها وزرعت السيقان معزولة عن زراعات الكرنب الأخرى وتركت للتلقيح المفتوح لإنتاج بذور دورة الإنتخاب الأولى. وفى نوفمبر 2022 زرعت نباتات العشيرة الأصلية مع نباتات دورة الإنتخاب الأولى وبذور الكرنب المحسن المحلى للمقارنة فى تجربة مصممة بطريقة قطاعات كاملة العشوائية فى ثلاث مكررات وقد تم أخذ القياسات التالية طول الساق (سم)، عدد الأوراق الداخلية الملتفة، عدد الوراق الخارجية الغير ملتفة، وزن الرأس (كجم)، طول الرأس (سم)، قطر الرأس(سم) و الأيام حتى الحصاد(الأيام). وقد أظهرت النتائج وجود اختلافات عالية المعنوية بين التراكيب الوراثية فى الصفات محل الدراسة مما يمكن معه إجراء الإنتخاب و الحصول علي تباينات في الصفات المختلفة. أجري برنامج الإنتخاب لثلاث دورات متتالية و كان الإنتخاب لصفات عدد الأوراق الداخلية الملتفة للنبات ووزن وقطر الرأس و عدد الأيام حتى النضج (الحصاد). وكانت التباينات المظهرية أكبر من نظيرتها الوراثية وتشكل الجزء الأكبرمن التباين الكلى مما يدل على أهمية التباين البيئى وتأثيره على التعبير على إظهار هذه الصفات. وتباينت قيم معاملات التباين الوراثي من صفة إلى أخرى. وكانت القيم المقدرة لمعامل التوريث فى المدى الواسع قد تراوحت بين 0.37٪ إلى 79.01٪ لصفة عدد الأوراق الخارجية الغير ملتفة للنبات وصفة عدد الأوراق الداخلية الملتفة للنبات على التوالي، وقد لوحظت نسبة توريث عالية بالمعنى الواسع مع تقدم وراثي عالي كنسبة مئوية من المتوسط وخاصة صفات عدد الأوراق الداخلية الملتفة للنبات ووزن الرأس و عدد الأيام حتى النضج (الحصاد). أشارت النتائج إلى الدور الكبير للتباين الإضافي في وراثة تلك الصفات والتى يمكن تحسينها بشكل فعال من خلال الإنتخاب. أظهر معامل الإرتباط بين كل زوج من الصفات قيماً موجبة وعالية المعنوية لبعض الصفات خاصة وزن الرأس (كجم) مع كلا من عدد الأوراق الداخلية الملتفة للنبات وقطر الراس على التوالى. ، مما يشير الى أن الإنتخاب لصفة واحدة من تلك الصفات سيكون مرتبطاً بتحسين الصفات الأخرى ،كذلك يدل علي أهمية هذه الصفات أثناء عملية الإنتخاب حيث يمكن الإنتخاب الموجهه لهذه الصفات وإنتاج أصناف عالية الإنتاجية. لذلك، فإن إختيار كرنب جيد من حيث عدد الأوراق الداخلية الملتفة للنبات، ووزن الرأس، وإرتفاع الرأس وقطر الرأس قد يؤدي إلى تحسين فى إنتاجية نباتات الكرنب.