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*Original scientific paper*

## **VARIABILITY, HERITABILITY AND ASSOCIATION ANALYSIS IN PLANT TRAITS OF SWISS CHARD (*Beta vulgaris* subsp. *cicla*)**

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Plant breeders mainly interested in improvement agronomic properties of desirable trait accompanied with genetic architecture of major characters and their interrelationship. Genetic variability and character association are prime importance and provide essential contribution for successful breeding programme. In the present research genetic variability, heritability, phenotypic and genotypic correlations of several agronomic characters were studied in fifty-four swiss chard accessions and cultivars. Analysis of variance observed highly significant variations among accessions, and phenotypic coefficient of variation (PCV) was higher magnitude of genotypic coefficient of variation (GCV) for all agronomic characters. The lamina length, lamina width, petiole thickness, petiole

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width, lightness, chroma and leaf dry matter observed high magnitude broad sense heritable characters accompanied with high genetic advance. Genotypic correlation coefficient showed higher than phenotypic correlation coefficient which could be explained by low environmental effect on investigated agronomic traits. Positive correlation was revealed between petiole length, lamina length, lamina width, petiole thickness and petiole width which comprise total yield in swiss chard.

*Key words:* heritability, genetic advance, Swiss chard, variability, quantitative characters

## INTRODUCTION

Swiss chard (*Beta vulgaris* subsp. *cicla*) is member of Chenopodiaceae family and the genus *Beta* is endemic to the Old World (BARTSCH *et al.*, 1999). The plant originated from Europe and Mediterranean countries, swiss chard has been grown in Europe since classical antiquity and leaf beet has been cultivated for about 2500 years in China (TINDALL 1983; SHUN *et al.*, 2000). Petiole and stalks are edible parts of plant, the leaves may either be smooth or curly, the stalk observes white, red, yellow and orange color depending on genotype. The leaves of Swiss chard are widely use as a vegetable either in cooked or raw in salads and also stems are use chopped or cooked like celery, it is available throughout the year (PYO *et al.*, 2004).

Growing areas and consumption of leafy vegetables increase due to contribute significant nutritional sources for human diet and could be grown year around with low input. Swiss chard is not commercially great importance among leafy vegetables whereas it is nutritive demanding species (POKLUDA and KUBEN 2002), and researchers support enhance consumption to reduce mineral deficiency in diet. While nutritional variability was reported among hybrid and non-hybrid swiss chard varieties there is no comprehensive information reported on genetic variability and characters association in quantitative plant traits of swiss chard. Furthermore there is a little scientific concern available on evaluation of swiss chard accession plant properties and were not studied the information on extent and magnitude of genetic variability, heritability and genetic advance in quantitative agronomic traits. The knowledge on genetic variability and estimation of genetic parameters are useful tools to determine the selection criteria for yield and quality improvement (BOZOKALFA *et al.*, 2010). 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). Besides heritable variations are useful for permanent genetic improvement (SING 2000), heritability estimates together with genetic advance observe more effective results than heritable alone for successive selection in plant breeding (JOHNSON *et al.*, 1955). In addition the knowledge of correlations among various agronomic characters is useful for selection and further breeding. Although genetic variability and association interrelationships among agronomic characters were reported for several vegetables species, none of comprehensive

explanation available on swiss chard genetic variability, heritability and characters associations among plant traits.

Thus, the present study was conducted to estimate the magnitude of genetic variability, heritability, genetic advance, phenotypic and genotypic correlation among agronomic traits of swiss chard for further breeding and to assess quantitative plant properties and seed values of Turkish swiss chard gene pool.

#### MATERIAL AND METHODS

A total 54 swiss chard (*Beta vulgaris* subspecies *cicla*) genotypes, which has 52 accessions and two cultivars as a references, one local and one foreign cultivar gathered from Turkey and Germany. The seeds of 52 accessions which are represent whole swiss chard genetic resources collections of Turkey obtained from national public gene bank of AARI (Aegean Agricultural Research Institute), Izmir, Turkey (Table 1).

The experiment was carried out in 2007-2008 autumn and winter season at the experimental field of Ege University, Agriculture Faculty, Department of Horticulture, Izmir, Turkey. The experimental field is located 38° 28' N latitude, 27° 15' E longitude and altitude of 25 m above sea level. Randomized block design were applied with three replications, the plot of each replication was 4.5 m<sup>2</sup> and consists of 20 plants.

Seeds were sown in October by hand and usual cultural practices were followed, furrow irrigation method provided regularly every week until the beginning of rainfall season. No chemical fertilizer, fungicide and insecticide were applied during cultivation, and weeds were controlled mechanically by hand until the plant reached harvest maturity. Fifteen plant samples of each replication were harvested by hand at leaves fully matured and ready for edible use. In the experiment thirteen agro-morphological traits were evaluated based on Descriptors for Beta (IBPGR 1991).

1. Leaf weight (g): a total weight of harvested leaf divided into number of harvested leaf
2. Plant height (cm): height of main shoot from soil level to the top at flowering period
3. Plant canopy (cm): average of plant width measured across the two way at flowering period
4. Petiole length (cm): petiole width across the widest portion of petiole
5. Lamina length (cm): lamina length across the largest portion of leaf
6. Lamina width (cm): lamina width across the widest portion of leaf
7. Petiole thickness (cm): thickest point of petiole
8. Petiole width (cm): petiole width across the widest portion of petiole
9. Lightness (L\*): Fruit lightness measured in 10 leaf lamina using a Minolta CR-300 (Osaka, Japan) colorimeter CIE L\*a\*b
10. Hue (<sup>0</sup>H): Leaf colour was measured with a Minolta CR-300 colorimeter (Osaka, Japan) CIE L\*a\*b were calculated using the formula  $^{\circ}H = \tan^{-1}(b/a)$

11. Chroma (C\*): Leaf colour measured with a Minolta CR-300 (Osaka, Japan) colorimeter CIE L\*a\*b and chroma were calculated using the formula  $C^* = \sqrt{a^2 + b^2}$
12. 1000 Seed weight (g): 100 seed was weighed and multiple by ten.
13. Leaf dry matter (%): Leaf lamina and petiole dried in an oven at 65°C until weight loss between measurements was <0.05 g. The percentage difference between the fresh and dry weights was used to calculate the dry matter content of the leaf.

*Table 1. Accessions number / cultivar names, collection locale, origin and collected altitude of 54 swiss chard accessions and genotypes.*

No	Accession number / cultivar names	Collection locale	Country of Origin	Altitude (m)
1	TR 30741	Gaziantep	Turkey	--
2	TR 35012	Çanakkale	Turkey	--
3	TR 35065	Bursa	Turkey	300
4	TR 35137	Tokat	Turkey	630
5	TR 35164	Kayseri	Turkey	1050
6	TR 35180	Sivas	Turkey	--
7	TR 35278	Şanlıurfa	Turkey	--
8	TR 35821	Mardin	Turkey	550
9	TR 35289	Mardin	Turkey	550
10	TR 35316	Hakkari	Turkey	1550
11	TR 35331	Kahramanmaraş	Turkey	--
12	TR 35354	Muğla	Turkey	600
13	TR 35355	Muğla	Turkey	120
14	TR 35393	Hatay	Turkey	155
15	TR 40459	Siirt	Turkey	1320
16	TR 43621	Sakarya	Turkey	30
17	TR 46354	Kayseri	Turkey	1260
18	TR 51154	Hatay	Turkey	140
19	TR 51160	Adana	Turkey	15
20	TR 51169	Mersin	Turkey	10
21	TR 51170	Mersin	Turkey	20
22	TR 51194	Muğla	Turkey	--
23	TR 51199	İzmir	Turkey	--
24	TR 52424	Erzurum	Turkey	1400
25	TR 52488	Artvin	Turkey	410
26	TR 55632	Giresun	Turkey	1100
27	TR 55633	Giresun	Turkey	1200
28	TR 55664	Giresun	Turkey	150
29	TR 55689	Trabzon	Turkey	350
30	TR 55756	Rize	Turkey	50
31	TR 55767	Rize	Turkey	250

32	TR 55773	Rize	Turkey	350
33	TR 55778	Rize	Turkey	350
34	TR 55787	Rize	Turkey	50
35	TR 55800	Rize	Turkey	10
36	TR 55821	Rize	Turkey	400
37	TR 55832	Artvin	Turkey	20
38	TR 55848	Artvin	Turkey	4
39	TR 55866	Artvin	Turkey	75
40	TR 55879	Artvin	Turkey	200
41	TR 55889	Artvin	Turkey	20
42	TR 55931	Rize	Turkey	10
43	TR 55936	Rize	Turkey	4
44	TR 55983	Trabzon	Turkey	500
45	TR 55993	Trabzon	Turkey	750
46	TR 55999	Trabzon	Turkey	100
47	TR 56010	Trabzon	Turkey	700
48	TR 56017	Giresun	Turkey	10
49	TR 56046	Ordu	Turkey	20
50	TR 71077	Kayseri	Turkey	1463
51	TR 73437	Turkey	Turkey	--
52	TR 73438	Turkey	Turkey	--
53	Local cultivar	Pinaper seed	Turkey	--
54	Foreign cultivar	Freya	Germany	--

To estimate the extent of magnitude of variation among examined traits, all data were subjected to analysis of variance. Mean, standard error, range were analyzed according to SINGH and CHAUNHARY (1985). Components of variance  $\sigma^2 g$  = genotypic variance,  $\sigma^2 p$  = phenotypic variance and  $\sigma^2 e$  = error variance were estimated using the following formula (WRICKE and WEBER, 1986);

$$GCV = \frac{\sqrt{\sigma^2 g}}{\bar{X}} \times 100$$

$$PCV = \frac{\sqrt{\sigma^2 p}}{\bar{X}} \times 100$$

where,  $\sigma_p$ ,  $\sigma_g$ , and  $X$  are the phenotypic, genotypic standard deviation and grand mean of the traits respectively. Heritability in the broad sense ( $h^2$ ) was estimates on genotypic mean described by ALLARD (1999) as:

$$\text{Heritability } (h^2) = \frac{\sigma^2 g}{\sigma^2 p}$$

Expected genetic advance (GA) and GA as percent of the mean calculated according to SHUKLA *et al.* (2006).

Expected genetic advance ( $GA$ ) =  $i\sigma p h^2$

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

where,  $i$ : standardized selection differential, a constant (2.06),  $\sigma p$ : phenotypic standard deviation.

Genotypic ( $r_g$ ) and phenotypic ( $r_F$ ) correlation coefficient between x and y traits were calculated based on the procedure described by KEMPTHORE (1973)

$$r_g(x, y) = \frac{COV_g(x, y)}{\sqrt{\sigma_g^2(x)}\sqrt{\sigma_g^2(y)}}$$

$$r_F(x, y) = \frac{COV_F(x, y)}{\sqrt{\sigma_F^2(x)}\sqrt{\sigma_F^2(y)}}$$

where,  $Cov_{xy}(g)$  and  $Cov_{xy}(p)$  are genotypic and phenotypic covariance between x and y characters,  $\sigma_g^2$  = genotypic variance,  $\sigma_p^2$  = phenotypic variance

## RESULTS AND DISCUSSION

The analysis of variance observed highly significant variations among accessions for all the examined traits. Estimation of mean squares of accessions year and error for thirteen traits of 54 swiss chard accessions are shown in Table 2. The plant weight ranged from 7.98-53.77 g, plant height 63.65- 165.55 cm, plant canopy 39.29-145.73 cm, petiole length 5.46-18.28 cm, lamina length 11.88-27.56 cm, lamina width 9.29-23.21 cm, petiole thickness 4.55-13.91 mm, petiole width 6.08-23.46 mm, L\* 35.21-51.76,  $h^0$  15.37-38.75, C\* 115.89-140.26, 1000 seed weight 9.78-35.80 g, leaf dry weight 8.72-19.21%.

The range, mean, standards errors, phenotypic, genotypic and error variance, phenotypic (PCV) and genotypic coefficient of variability (GCV), broad sense heritability ( $h^2B$ ), genetic advance in a percentage mean (GA) are given Table 3. The phenotypic coefficient of variation was higher than genotypic coefficient of variation for all agronomic traits. In addition high (>87%) broad sense heritability recorded for all plant trait except chroma values. The lamina length (77.52%), lamina width (91.39%), petiole thickness (124.19%), petiole width (79.33%), L\* (86.09%), C\* (87.69%) and leaf dry matter (139.15%) observed high heritability (>79%) with high genetic advance in percentage mean, petiole length (63.51%),  $h^0$  (65.85%) accompanied with high heritability (>99%) and moderate (>65%) genetic advantage in percentage mean, remaining agronomic traits showed high heritability (>87%) with low genetic advance (<63%) except seed weight which is resulted low heritability (42.09%) and low genetic advance (37.92%).

Table 2. Analysis of variance for thirteen agronomic trait of swiss chard

Traits	Mean Squares		
	Genotypes (df 53)	Replications (df 2)	Error (df 107)
Leaf weight (g)	172.52**	12.67	0.60
Plant height (cm)	1472.922**	982.63	28.77
Plant canopy (cm)	1564.12**	237.95	10.60
Petiole length (cm)	31.56**	10.34	0.17
Lamina length (cm)	21.184**	24.23	0.89
Lamina width (cm)	15.241**	13.19	0.38
Petiole thickness (cm)	8.254**	0.18	0.03
Petiole width (cm)	20.227**	9.38	0.36
Lightness	17.176**	40.98	1.72
Hue	29.357**	1.38	0.21
Chroma	16.554**	163.40	8.15
Seed weight (g)	89.935**	8.14	0.25
Leaf dry matter (%)	6.574**	2.87	0.12

Table 3. Range, mean, standard error, variance components ( $\sigma^2_g$ ,  $\sigma^2_p$ ,  $\sigma^2_e$ ), phenotypic (PCV) and genotypic (GCV) coefficients of variation, broad sense heritability ( $h^2_B$ ) and genetic advance (GA) (%) for various agronomic traits in swiss chard.

Traits	Range	Mean	SE	$\sigma^2_p$	$\sigma^2_g$	$\sigma^2_e$	PCV (%)	GCV (%)	$h^2_B$	GA	GA (%)
Leaf weight	7.98 ± 53.77	22.91	0.59	57.51	57.27	0.24	13.24	13.21	99.59	15.56	27.17
Plant height	63.65 ± 165.55	120.65	1.77	490.97	478.44	12.53	4.34	4.29	97.45	44.48	9.30
Plant canopy	39.29 ± 145.73	99.28	1.80	521.37	517.14	4.23	4.36	4.34	99.19	46.66	9.02
Petiole length	5.46 ± 18.28	12.29	0.26	10.52	10.43	0.09	30.69	30.56	99.15	6.63	63.51
Lamina length	11.88 ± 27.56	19.01	0.22	7.06	6.69	0.37	34.43	33.52	94.76	5.19	77.52
Lamina width	9.29 ± 23.21	13.98	0.18	5.08	4.91	0.17	42.10	41.41	96.71	4.49	91.39
Petiole thickness	4.55 ± 13.91	8.19	0.13	2.75	2.74	0.01	60.60	60.49	99.64	3.40	124.19
Petiole width	6.08 ± 23.46	11.83	0.21	6.74	6.60	0.15	37.34	36.93	97.82	5.23	79.33
Lightness	35.21 ± 51.76	41.20	0.21	5.73	5.03	0.70	33.92	31.79	87.85	4.33	86.09
Hue	15.37 ± 38.75	22.73	0.25	9.79	9.71	0.08	31.87	31.75	99.23	6.39	65.85
Chroma	115.89 ± 140.26	123.41	0.27	5.52	2.32	3.20	19.77	12.83	42.09	2.04	87.69
Seed weight	9.78 ± 35.80	18.30	0.43	29.98	29.87	0.11	18.36	18.32	99.64	11.24	37.62
Leaf dry matter	8.72 ± 19.21	10.89	0.12	2.19	2.14	0.05	65.40	64.66	97.75	2.98	139.15

Simple correlations among examined plant traits are given Table 4. In swiss chard yield estimation is mainly related with leaf weight which is highly ( $p < 0.01$ ) positively correlated with petiole length, lamina length, lamina width, petiole thickness and petiole width as expected, it is interesting that lightness and  $h^0$  values is negatively correlated with leaf weight at  $p < 0.05$ , and  $p < 0.01$  level respectively. This result informed that high leaf weighed accessions observed low  $h^0$  values which mean dark green leaf color accessions produce low amount of leaf weight. This suggested that leaf weight could be improved through direct selection of leaf color.

Phenotypic and genotypic correlation was given Table 5. In general the genotypic correlation coefficient values were higher than corresponding phenotypic values. The utilize selection based on genotypic correlation is an effective instrument for examining degree of relationships among plant traits due to phenotypic correlation obtain from genotype and environment interaction.

Fruit and vegetables are providing a primary feed source for human diet and recent studies informed that need to encourage the consumption of fruit and vegetables in order to reduce mineral deficiency and malnutrition particularly in developing countries. In this respects leafy vegetables are contain high amount of nutritive elements and provides health promoting compound and also grown year around with low input. Thus, growing areas and production are to continue all around the world and plant breeder's effort to develop new cultivar with desirable quality traits. Plant genetic resources are primary source for plant breeders and supply large genetic base in order to succeed breeding. Genetic diversity of germplasm determinates the limit of selection in crop improvement (BHARGAVA *et al.*, 2007). Furthermore knowledge of genetic associations among agronomic traits is regarded to support considerable help to maintain genetic improved to breeding programme (BOZOKALFA *et al.*, 2010). Crop improvement with heritable characters, estimation of genetic parameters and their association is prime importance in breeding (AJMAL *et al.*, 2009).

In the present study significant differences were found among swiss chard plant collection for investigated agronomic plant and seed traits indicating existence of genetic differences among the genotypes. The identified high variability basis on leaf properties and quantitative agronomic traits demonstrates that examined germplasm have a high potential for effective swiss chard selection and breeding. POKLUDA and KUBEN (2002) pointed out significant differences agronomic properties among twelve swiss chard cultivars and underlined that variety as an important factor influencing all growth characteristics, and showed variety selection for assurance of optimum stalk quality. Genetic variability were not only reported for agronomic trait in swiss chard but also underlined for mineral concentration and nutritive value. ROZYCKI *et al.*, (1997) informed that the variability's found in nutrient composition among cultivars, non-hybrid and wild forms of swiss chard, and varieties difference was reported for vitamin C concentration in swiss chard (GIL *et al.*, 1998). In addition antioxidant activity and phenolic compound differentiation was reported between white and red stem swiss chard cultivar (PYO *et al.*, 2004).







The presented results revealed that phenotypic coefficient of variability (PCV) were higher for all examined traits than corresponding genotypic coefficient of variability (GCV) among fifty-four swiss chard accessions. Variability and association studies were carried out several vegetables such as onion (*Allium cepa* L.) (HOSAMANI *et al.*, 2010), pea (*Pisum sativum* L.) (SARDANA *et al.*, 2007), green chili (*Capsicum annuum* L.) (UKKUND *et al.*, 2007), okra (*Abelmoschus esculentus* L. Moench) (BELLO *et al.*, 2006), eggplant (*Solanum melongena*) (PARBHU *et al.*, 2009) and researchers reported higher the magnitude of phenotypic coefficient of variability than genotypic coefficient of variability which is good scope for improvement special agronomic traits through phenotypic selection (JALATA *et al.*, 2011). In addition estimation of genotypic coefficient of variability provides information on genetic potential in crop improvement through selection in breeding program (JOHNSON *et al.*, 1955).

Heritability provides information only on magnitude of interference of quantitative traits. However, estimation of heritability is of little significance in coherent selection breeding programs unless accompanied by sufficient genetic gain (TEFERA *et al.*, 2003). In addition high heritability estimates along with high genotypic coefficient of variation and genetic advance is more effective in predicting the response of any selection than using heritability alone (JOHNSON *et al.*, 1955). Genetic advance is also important due to observe of the expected genetic gain in the selection. In the present study high (>87%) broad sense heritability recorded for all plant trait except chroma values, high genetic advance accompanied with high heritability was obtained from lamina length, lamina width, petiole thickness, petiole width, lightness, chroma, and leaf dry matter which traits were informed that these agronomic traits are under genotypic control could be explained by additive gene effects (BELLO *et al.*, 2006). Moreover high heritability also indicated phenotype is strongly reflected genotypes (PARBHU *et al.*, 2009). High heritability coupled with high genetic advance was also reported for leaf length and leaf width in spinach (SRIVASTAVA *et al.*, 1977). The variation among genotypes for all examined traits showed promise for their improvements in agronomic traits through selection. Lamina length, lamina width, petiole thickness, petiole width, lightness, chroma, and leaf dry matter observed high heritability with high genetic advance in a percent mean and these characters can be improved efficiently by individual selection or breeding strategies in the examined population.

The magnitude of genotypic and phenotypic correlation of coefficient observed similar trends and for most of the characters showed higher genotypic correlation coefficient than phenotypic correlation which could be explained by low environmental effect on investigated agronomic traits. Moreover genotypic correlation is more effective examining the degree of relationships between agronomic traits and correlation studies provide information in order to visualize simultaneously improvement of single character may cause changes in other character in breeding programme (DIVAKARA *et al.*, 2010)

Positive correlation was revealed between petiole length, lamina length, lamina width, petiole thickness and petiole width which comprise total yield in swiss

chard. In this respects its possible to simultaneous improvement yield with these characters. Furthermore lamina length, lamina width, petiole thickness, petiole width showed high genetic advance accompanied with high heritability. Similar findings reported among leaf properties of rocket plant (*Eruca sativa* L.) and high correlation coefficient reported for leaf width, petiole length, petiole thick, and plant weight among accessions (BOZOKALFA *et al.*, 2010).

As a conclusion swiss chard is not only consuming as vegetables but also use in folk medicine (NINFALI *et al.*, 2007) also its potential donors of traits lacking in sugar beet breeding programmes (BARANSKI *et al.*, 2001). In recent years economic value of swiss chard increase and researchers have more attention the plants due to containing high nutritive elements, dietary properties, and potential value for beet breeding (BARANSKI *et al.*, 2001). Thus, examined research reported provides the knowledge of genetic variability and character association and contributes necessities information the knowledge of swiss chard breeding. Additionally the results revealed that Turkish swiss chard gene pool showed great diversity among examined plant traits and accessions maintain large variability.

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## VARIJABILNOST, NASLEDNOST I ANALIZA ASOCIJACIJE OSOBINA BILJAKA KOD SWISS CHARD (*Beta vulgaris*, subsp. *cicla*)

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### I z v o d

Oplemenjivači biljaka su velikim delom zainteresovani za poboljšanje željene osobine vezane za genetičku strukturu glavnih osobina i njihovu međuzavisnost. Genetička varijabilnost i asocijacija osobina su od primarnog značaja i obezbeđuju ključni doprinos uspešnom programu oplemenjivanja. U radu su prikazana istraživanja genetičke varijabilnosti, fenotipska i genotipska korelacija više agronomskih osobina kod 54 genotipa šećerne repe. Analizom varijanse utvrđeno je značajno variranje, a fenotipski koeficijent variranja (PCV) je imao veći raspon od genotipskog koeficijenta variranja (GCV) za sve agronomske osobine. Za dužinu i širinu lamine, debljinu i širinu petiole, boju i sadržaj suve materije u listu su utvrđene šire magnitude variranja naslednih osobina sa visokom genetičkom prednošću. Utvrđen viši genotipski koeficijent u odnosu na fenotipski ukazuje na nizak efekat spoljne sredine na ispitivane osobine. Utvrđena je pozitivna korelacija između dužine petiole, dužine i širine lamine, debljine i širine petiole što doprinosi ukupnom prinosu ispitivanog genotipa šećerne repe

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