Variability and Phenotypic Stability of Soybean (*Glycine max* L.) Varieties under Different Plant Densities and Locations

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Received: 01/05/2020 Accepted: 03/06/2020

Abstract

The study was carried out with the aim of testing the environmental genetic interaction for seed yield and its components and oil and protein percent's traits, estimating the broad sense heritability and stability parameters of three soybean varieties Lee74, Taqa and Aeman, which were cultivated in twelve environments resulting from the combinations of six plant densities (285714, 200000, 153846, 142875, 100000 and 76923 plants per hectare), and two locations (Bany Manqan and Kani Panaka), which belonging to Sulaymaniyah Governorate, using a randomized completely block design with three replications. Combining analysis of variance showed significant mean square of varieties for DFF, PH, HFN, NPP, SPY, 100 SW traits, locations for DFF, PH, HFN, and 100 SW traits and plant densities for PH, HFN, 100 SW, and Protein%. The interaction of varieties x environments (locations and plant densities) was highly significant for NVB, NPP, NSP, SPY and 100 SW traits. The broad sense heritability was high for DFF and PH traits (98.02 and 81.19%) respectively, moderate for HFN and 100 SW traits (26.28 and 26.91%) respectively and low for the other traits. Stability parameters results showed high stability in different environments for variety Lee74 in DFE, HFN and NSP traits, Taqa variety considered stable in PH and HFN traits, and Aeman variety for were stable in PH, SPY and Oil% traits, and the same varieties showed response to good environments only for certain traits, whereas, there was a response to inappropriate environments as shown by the two varieties Taqa in DFE and NSP and Aeman in DFE and NPP.

Key words: G X E interaction, Soybean, Stability, Plant density, Location effect.

Glycine max (L.) Merrill is one of the most important legume crops in the world because of its great importance that depends on its seeds containing a high percentage of oil (14-24%), and protein (30-50%) which is characterized by its high quality because it contains all amino acids which is necessary for humans and animals (Abbas *et al*., 2011), in addition to its cultivation to improve the soil properties and increase its fertility because it contains root nodes bacteria that stabilize the atmospheric nitrogen

in the soil and provide the plant with its needs for growth (Rizk and Ali, 1981). Soybean yield is a complex quantitative trait that is controlled by multiple genes, and is determined by the multiple interactions between genes and the environment (Li *et al*., 2008), which are greatly influenced by environmental conditions, especially the length of day from different latitudes (Bhartiya and Aditya, 2016 and Abdul Hamid *et al*., 2017). Because of the photosensitivity, the cultivation area of each soybean variety was restricted to a very small range of latitudes to achieve the highest yield (Cober and Morrison, 2010). Therefore, it is useful to identify soybean varieties that have good production performance and are more stable in a wide range of environmental conditions, though the Genotype × Environment (G × E) interaction is considered a major problem in the study of quantitative traits such as yield and yield component, because it complicated the interpretation of genetic experiments and predictions (Becker and Leon, 2010).

The stability of the genotype (whether it is a variety, pure line or hybrid) is defined as its good performance for yield and its components to a wide range of different environmental conditions, and the stability of the genotype behavior is one of its most desirable characteristics, on the basis of which it can be adopted as an appropriate variety of environmental conditions. In this case and for the purpose of identification of the phenotypic stability of genotypes, usually in crop breeding programs, genotypes are evaluated in multi-environment (years, locations and both) experiments to test their performance across environments and to choose the best in specific environments. Likewise researchers, including Singh and Chaudhary (2007) have indicated that it is possible to test the stability of genotypes in unrepeated experiments by creating different environmental conditions by applying different agricultural processes, such as the cultivation of the genotypes at different agricultural dates and distances between plants or lines, or using different fertilizer or irrigation levels ... etc. Significant (G × E) interaction of quantitative traits such as grain yield can severely limit the progression of adaptive variety selection (Luo *et al.,* 2012). Several studies have been carried out to determine the effect of (G × E) interaction on yield and other traits using several statistical modeling methods (Grüneberg *et al*., 2005; Luo et al., 2009). These methods may use linear models, such as joint regression analysis (Eberhart and Russell, 1966), or multivariate analytical methods such as AMMI analysis (Gauch, 1994), or other methods.

The aim of the current study is to evaluate three varieties of soybeans at two locations and different plant densities and to assess their stability for different environmental conditions resulting from the combinations between the locations and the levels of plant densities, as well as estimating some genetic parameters.

Materials and Methods:

Three varieties of soybeans, Lee74, Taqa and Aeman (their seeds were obtained from Faculty Agriculture, at Salahuddin University, Erbil) were used in this study, which was carried out in the Sulaymaniyah Governorate (Iraqi Kurdistan) during 2016 in two locations, the first is the Bany Manqan's Research Center (75 km west of the Governorate Center) and the second is the Kani Panaka's Research Center (35 km southwest of the Governorate Center). The seeds of the three varieties were planted in six plant densities (285714, 200,000, 153846, 142857, 100,000 and 76923 plants per hectare), calculated from three cultivation distances between lines (35, 50 and 65 cm) and two distances for cultivation between plants (10 and 20 cm). The experimental farm was plowed at a depth of 30 cm twice perpendicularly, then it was smoothed, leveled and divided. The seeds were sown on the

eighth and tenth of Mays in the two locations, respectively. Three seeds were placed in each hole at a depth of 3-5 cm, and the drip irrigation system was adopted as needed. Compound fertilizer NPK was added at a rate of 130 g per experimental unit (an area of 4 m^2) before planting during the preparation of the land, and after 45 days of planting, urea fertilizer (N 46%) was added at a rate of 80 g per experimental unit. Thinning and replanting process took place 15 days after planting, and the weeds controlled by manual cultivation three times during the growing season. Randomized complete block design was used with three replicates, whereby the combinations between the levels of the study factors (varieties and plant densities) were distributed randomly within each block (contains 18 experimental units) and each experimental unit contains three lines with a length of 5 m. On maturity, data were recorded from the average of five plants randomly chosen from each experimental unit for characteristics: number of days from planting until the first flower appeared (DFF), plant height (cm) (PH), height of the first node on the stem from the soil surface (cm) (HFN), number of vegetative branches per plant (NVB), number of pods per plant (NPP), number of seeds per pod (NSP) from the equation: [seed number per pod = (seeds number per plant) / (pods number per plant)], single plant yield (gm) (SPY), seed index (100 grams of seed weight) (100 SW) and the oil and protein percent's (calculated by the oil and protein testing device in the Peramagroon's seeds store). The combining analysis of variance was carried out across the two locations according to the experimental design method used, then the trend analysis for plant densities was performed to determine the nature of the response of the different traits to the plant densities, and the differences between the means of varieties and the combinations of the two locations with the densities levels were compared using Duncan's Multiple Range Test (Al-Zubaidy and Al-Falahy, 2016). The components of phenotypic variance (environmental and total genetics), broad sense heritability, expected genetic advance, and phenotypic, genetic and environmental coefficients of variability (PCV, GCV and ECV respectively) for all traits were estimated in the manner indicated by Al-Zubaidy and Al-Juboury (2016). For the purpose of distinguishing the stability of soybean varieties in the environmental conditions approved in this study (the number of which is 12 environments resulting from the combination between the two locations and plant densities), the following linear regression model was used: $Y_{ij} = \mu + b_i I_j + \delta_{ij} + e_{ij}$, (Eberhart and Russell, 1966), as Y_{ij}: The mean of variety (i) in the environment (j) and b_i: means the regression coefficient of variety (i) at specified environmental index, which means the response of variety to environmental change, and I_j: is the environmental index, which is defined as the mean deviation of all varieties at the specified environment from the general mean, and δ_{ij} = deviation from the regression for variety (i) at environment (j) and e_{ij} = the average experimental error.

Two parameters for stability were estimated which based on: (1) The regression coefficient, which is the regression behavior of each variety in different environments, which is estimated from the equation: $b_i=\Sigma Y_{ij}I_j / \Sigma I_j^2$ (Al-Zubaidy and Al-Juboury, 2016), where: $\Sigma Y_{ij}I_j$ is the sum of products and ΣI_j^2, sum of squares and (2) Mean deviation (S^2d_i) from linear regression: $(\Sigma\delta_{ij}^2 / s\text{-}2)] - S2e / r$, note that: $\Sigma\delta_{ij}^2 = [\Sigma Y_{ij}^2 - Y_i^2 / t] - (\Sigma Y_{ij}I_j)^2 / \Sigma I_j^2$, and S^2e is the estimation of pooled error. The significance of the regression coefficients for varieties and for each trait was tested by t - test. As the linear regression coefficient (b_i) for the relationship between each trait of the variety in each environment and the product and behavior of each trait of the environment rate is a measure of the linear response to environmental changes. The variance mean of regression deviation (S^2d_i) measures the consistency of this response, or in other words, it is a measure of heterogeneity. Depending on these two parameters,

the validity of the varieties is evaluated. In this case, when (1) S^2d_i = zero and bi > 1, the varieties respond to good environments, (2) S^2d_i = zero and b_i = 1, the varieties are less responsive to environmental changes and are highly stable, (3) S^2d_i = zero, and b_i < 1, as the varieties grow well in inappropriate environments, and (4) S^2d_i > zero, then the linear prediction is weakened.

All statistical analyzes were carried out using the available software: (SAS) Statistical Analysis System, Microsoft Office Excel 2003 and Minitab.

Results and Discussion:

Table (1) shows the results of the combining analysis of variance for the traits of soybean varieties at different plant densities across the two locations of study, and it was shown that the mean square of the locations was significant at 1% probability level for the traits: DFF, PH and HFN, at 5% probability level for 100 SW and not significant for other traits. The mean square of varieties was highly significant for DFF, PH, HFN, NPP, SPY and 100 SW traits, and non-significant for the rest of the traits, these results are consistent with those of Rahman and Hossain (2011) and Seadh and Abido (2013), who found significant differences between the varieties in some soybean yield components. The mean square due to plant densities showing a high significance for PH, HFN, HFN and Protein% traits, from previous studies, significant differences were observed between plant densities for yield and its components in soybeans, among which, Güllüoğlu *et al*., (2016) from the study in which thirteen plant densities were used, found significant differences for seed yield and number of pods per plant, and Mahesh *et al*., (2017) indicated differences in the effect of plant densities on soybean traits, as the increase in density caused increase in seed yield, while the lower densities increased the number of pods per plant, number of seeds per pod and 100 seeds weight. The mean square of the interaction between the varieties and plant densities, as well as their interactions with the locations, shown significant for some traits as follows: (Varieties x Locations) for all traits except oil and protein percent's, (Densities x Locations) for NVB, NSP, 100 SW, oil% and protein%, (Varieties x Densities) for most traits except DFF, HFN and oil%, and finally (Varieties x Densities x Locations) for NVB, NPP, NSP, SPY and 100 SW traits. The significant interaction of the varieties with each of the plant densities and locations, and both of them, indicates that some varieties differ in their behavior towards the traits according to the different environmental conditions in which they grow. It is also noted that each of the locations and plant densities (which represent different environments) and the varieties and the interactions between them differed from each other in their relative importance towards the traits under study. It is clear that the variations due to the environments (locations and plant densities) were much greater than those due to each of the varieties and their interactions with the environments for the traits HFN, NVB, NPP, 100 SW and Oil%, and those due to the varieties represented twice as much as they are for the variation of the interaction of varieties with the environments for HFN, NPP and 100 SW. The variations due to varieties appeared very high for the traits DFF, PH and SPY. These results show that the highest percentage of variations in the traits: HFN, NPP, SPY and oil% were due to random environmental fluctuations, and this is confirmed by the highest values of coefficient of variability for these traits, which respectively reached 17.350%, 12.437%, 14.949 and 17.5.9 and they were much higher than that for other traits.

Table 1. Combining analysis of variance for ten traits of three varieties of soybeans in 12 environments (two locations and six plant densities).

SOV	df	Mean Square				
		DFF	PH	HFN	NVB	NPP
Location (L)	1	452.23**	6908.8**	80.601**	34.003	7340.9
Reps / Loc	2	0.351	1806.47	20.873	25.251	11192.9
Varieties (V)	2	9622.9**	14787.6**	12.67**	0.874	2476.9**
Plant density(D)	5	0.861	228.8**	3.545**	0.289	182.111
D_L	(1)	2.064	374.6**	4.965**	1.134	166.770
D_Q	(1)	0.024	582.9**	5.381**	0.004	44.092
D_C	(1)	0.079	4.153	0.131	0.008	568.68
D_{Qu}	(1)	2.032	174.31	4.686	0.005	0.909
V x L	2	93.62**	902.43**	6.876**	6.601**	2564.8**
D x L	5	0.209	62.631	1.093	2.443**	313.36
V x D	10	0.606	170.71**	1.506	1.305**	438.24*
V x D x L	10	0.365	76.130	1.475	1.357**	528.07**
Error	68	0.626	48.113	0.862	0.429	198.22
Coefficient of variability		1.016	7.882	17.350	8.279	12.437
SOV	df	NSP	SPY	100 SW	Oil %	Protein %
Location (L)	1	0.093	31.872	8.869*	0.222	4.898
Reps / Loc	2	0.224	307.36	4.928	2.142	12.781
Varieties (V)	2	0.017	54.607**	2.660**	0.004	0.107
Plant density(D)	5	0.013	2.466	0.252**	0.093	1.324**
D_L	(1)	0.006	0.029	1.046**	0.028	0.442
D_Q	(1)	0.039**	0.200	0.022	0.004	1.363**
D_C	(1)	0.0097	10.195	0.113	0.304*	2.868**
D_{Qu}	(1)	0.001	0.099	0.079	0.103	0.154
V x L	2	0.033**	63.47**	1.562**	0.066	0.016
D x L	5	0.037**	1.388	0.363**	0.564**	2.281**
V x D	10	0.016*	12.783*	0.178**	0.052	0.363**
V x D x L	10	0.018**	14.719**	0.284**	0.087	0.289
Error	68	0.007	6.045	0.065	0.057	0.153
Coefficient of variability		3.486	14.949	4.032	17.509	1.377

(**) and (*): are significant at 1% and 5% probability level respectively.

Budak (2000) indicated that the coefficient of variability was unstable in different studies, and this may be due to the variations between the varieties or the environmental conditions in which they grow. The components of phenotypic variance (genetic, environmental and their interaction) are shown in Table (2), and it is noted that the genetic variance is greater than that due to the genetic environmental interaction for DFF and PH traits, while it was lower for the other traits, and it is clear that the broad sense heritability was high for these two traits and reached 98.02% and 81.19% respectively, moderate for HFN and 100 SW traits (26.28% and 26.91%), and low for other traits (ranged from 1.17% for Protein% and 15.88% for NPP), these results show that the traits: NVB, NPP, NSP, SPY and protein% more sensitive than others to inappropriate environmental conditions, and this is explained by the presence of tension during the growth and maturity periods, which leads to a decrease in its heritability (Weibel and Pandelton, 1964). Therefore, the effect of environment on these traits is great as compared to other traits. The results also show that the expected genetic advance in the next generation as a percent of the trait mean, was high (according to the gradation proposed by Agarwal and Ahmed, 1982)

for the traits DFF and PH (36.563% and 35.116%, respectively), and low for other traits, and this confirms the greater effect of environmental variation on these last two traits, that is, the behavior of both heritability and expected genetic advance were the same for all traits.

Table 2. Variance components and genetic parameters for ten traits of soybeans in 12 environments (two locations and six plant densities).

Parameters	Traits				
	DFF	**PH**	**HFN**	**NVB**	**NPP**
Genetic Variance	267.297	410.321	0.344	0.020	66.967
G x E variance	5.189	79.016	0.677	0.814	288.771
Environmental Variance	0.209	16.038	0.287	0.143	66.073
Phenotypic Variance	272.695	505.375	1.309	0.977	421.812
Heritability	0.9802	0.8119	0.2628	0.0208	0.1588
Genetic advance	28.488	32.124	0.529	0.036	5.739
Genetic advance as percent	36.563	35.116	9.888	0.457	5.069
GCV	20.983	22.143	10.960	1.799	7.228
PCV	21.194	24.574	21.382	12.488	18.140
	NSP	**SPY**	**100 SW**	**Oil %**	**Protein %**
Genetic Variance	0.001	1.461	0.073	0	0.002
G x E variance	0.008	7.428	0.178	0.013	0.080
Environmental Variance	0.002	2.015	0.022	0.019	0.051
Phenotypic Variance	0.009	10.904	0.272	0.032	0.133
Heritability	0.0424	0.1339	0.2691	0	0.0117
Genetic advance	0.007	0.779	0.247	0	0.008
Genetic advance as percent	0.309	4.734	3.920	0	0.026
GCV	0.852	7.349	4.294	0	0.139
PCV	4.137	20.077	8.278	0.755	1.282

The values of phenotypic and genotypic coefficients of variability (PCV and GCV)) are shown in the same table, and it is noted that the PCV was high for the traits DFF, PH, HFN and SPY, as it reached respectively (21.194, 20.983, 21.382 and 20.077), moderate for NVB and NPP low and low for other traits. It is noted that the values of the PCV were greater than the values of the GCV of all traits, and this is explained by high effect of environmental factors on the phenotypic expression of the traits in various degrees. It also appears that GCV following the trend of PCV in its behavior for the traits DFF and PH, and this indicates the non-significance of genetic environmental interaction, and for the same two traits were observed high values of broad sense heritability, which was also reflected on the high values of expected genetic advance, and accordingly as a result of the strong relationship among the four genetic parameters (heritability, genetic advance, PCV and GCV), genetic improvement that may occur in the next selection cycle can be expected based on the PCV for these two traits. In such cases, mass selection can achieve the desired success. This relationship among the four genetic parameters was not observed in this direction for other traits, and in such traits the expected genetic advance is not directly proportional to the values of PCV, so the last parameter is not always a true measure of genetic variability. For this reason, the values of broad sense heritability must be taken into account when conducting the selection for such cases, and these results lead to the conclusion that the expected genetic advance as a result of selection depends on both PCV and heritability. Singh and Bains (1968) obtained a similar conclusion and noted that the expected genetic advance is an outcome of both the estimated selection difference in the expression of phenotypic standard deviation, PCV and the square root of heritability.

It is observed that the results of the analysis of variance (Table 1) are reflected and documented by means of the genotypes as an average of different environments and mean of environments (combinations of plant densities and locations) as an average of the varieties and the results of which are presented in Tables (3) and (4), respectively. It was shown from Table (3) that the differences between the three varieties were insignificant for the traits NVB, NSP, Oil% and Protein%. The variety Lee 74 appeared to be more early in flowering compared to Taqa and Aeman.

Table 3. Varieties means as average of environments for ten soybean traits.

Varieties	Traits				
	DFF	**PH**	**HFN**	**NVB**	**NPP**
Lee 74	59.278 c	114.472 a	4.861 b	8.067 a	105.111 c
Taqa	84.639 b	83.761 b	6.011 a	7.928 a	121.689 a
Aeman	89.833 a	76.206 c	5.181 b	7.756 a	112.856 b
Mean	77.917	91.479	5.351	7.917	113.219
	NSP	**SPY**	**100 SW**	**Oil %**	**Protein %**
Lee 74	2.383 a	15.171 b	6.092 b	23.528 a	28.464 a
Taqa	2.382 a	17.628 a	6.210 b	23.533 a	28.372 a
Aeman	2.345 a	16.544 a	6.611 a	23.547 a	28.469 a
Mean	2.37	16.448	6.304	23.536	28.435

- **The values followed by the same letter for each trait do not differ significantly according to DMRT.**

Table 4. Means of environments as average of varieties for ten soybean traits.

Environments		**Traits**				
Locations	**Plant density (plant / ha)**	**DFF**	**PH**	**HFN**	**NVB**	**NPP**
Bany maqan	**285714**	76.222b	90.44abc	4.744 def	8.956 a	119.71 ab
	200000	75.778b	81.33 e	4.767 def	8.289 abc	120.87 ab
	153846	76.111b	82.62 e	4.33 fg	8.333 abc	131.96 a
	142857	75.889b	79.47 e	3.744 g	8.800 ab	117.44 abc
	100000	75.444b	81.62 e	4.578 efg	8.267 bc	119.27 ab
	76923	75.778b	85.40 de	4.756 def	8.222 bc	119.53 ab
Kani panka	**285714**	80.222a	104.91a	7.100 a	6.600 e	97.44 e
	200000	79.889a	101.01 a	6.444 abc	7.400 d	108.16 b-e
	153846	79.889a	98.27 ab	6.056 bc	7.267 d	101.69 de
	142857	80.222a	100.33 a	5.54 cde	7.267 d	104.18 cde
	100000	79.778a	92.38 bc	6.533 ab	7.667 cd	105.78 b-e
	76923	79.778a	99.93 a	5.611 bcd	7.933 cd	112.60 bcd
Mean		**77.917**	**91.479**	**5.351**	**7.917**	**113.219**
		NSP	**SPY**	**100 SW**	**Oil %**	**Protein %**
Bany maqan	**285714**	2.277 cd	16.83 a	6.092 cd	23.91 a	27.73 d
	200000	2.346 bcd	17.39 a	5.908 d	23.70 ab	28.27 c
	153846	2.264 d	17.32 a	5.966 cd	23.40 cde	28.27 c
	142857	2.406 ab	16.52 a	6.199 c	23.63 bc	28.40 c
	100000	2.412 ab	16.65 a	5.892 d	23.43 cde	27.80 d
	76923	2.339 bcd	17.24 a	6.049 cd	23.41 cde	28.87 b
Kani panka	**285714**	2.404 ab	15.28 a	6.850 a	23.34 de	29.32 a
	200000	2.383 ab	16.57 a	6.723 ab	23.20 e	29.17 ab
	153846	2.467 a	15.65 a	6.733 ab	23.60 bcd	28.31 c
	142857	2.423 ab	16.37 a	6.481 b	23.60 bcd	27.42 c
	100000	2.361 bc	15.39 a	6.558 b	23.63 bc	28.18 c
	76923	2.358 bc	16.16 a	6.199 c	23.57 bcd	28.49 c
Mean		**2.37**	**16.448**	**6.304**	**23.536**	**28.435**

- **The values followed by the same letter for each trait do not differ significantly according to DMRT..**

As it gave the significantly fewest number of days to flowers (59.278 days), as well as its plants were more high (114.472 cm), with a significant difference from other two varieties, and an increase of 50.214% over the variety that gave less height plants Taqa variety significantly outperformed the highest means for HFN, NPP and SPY, and by an increase in SPY (16.195%) over Lee 74 that gave the lowest yield per plant, whereas the Aeman variety showed surpassed significantly with the highest mean for 100 SW (6.611 gm). The comparison between the environments (Table 4) indicated that the plants at all plant densities in Bany maqan region were more early flowering compared to those planted in Kani panka region, and the highest mean of PH reached 104.91 cm at the highest plant density in Kani panka with non-significant difference from the same density in the Bany maqan, and this is explained by the crowding of plants to the light, which makes it tend to rise, while the lowest PH mean was at the third density in Bany maqan. It is also noted that the higher plant density in Kani panka region was outperformed by high means for the traits HFN, NSP, 100 SW and Protein%, while the top three densities in Bany maqan were outperformed by high means for NVB, NPP and Oil% traits, with a significant difference from all plant densities Kani panka. The differences between all the environments SPY did not reach to the significant limit. It is concluded from the above that the instability of SPY and other traits is due to genetic differences between the varieties and to environmental fluctuations.

A trend analysis for plant densities (as they represent levels of a quantitative factor) was conducted with the aim of identifying the nature of the response of the studied traits to it (Table 1), and it is noted that the mean squares of the second-degree relationship (quadratic) was highly significant for the PH, HFN and NSP, indicating that the second degree regression equation is the one that governs the relationship between these traits and plant densities (i.e. their response to the densities), while the relationship (the regression equation) of the third degree governs the relationship of Protein% and Oil%, since the mean squares of the third degree relationship (cubic) was significant at 1% and 5% probability levels for the two traits respectively. These relationships were graphically drawn (Figures 1-5). For other traits, the mean squares of the trend analysis degrees did not reach the significant limit, indicating that there is no appropriate regression relationship between each of them and the plant densities. Figures (1-5) were adopted in determining the best plant density giving the best response to the five traits, by drawing a vertical line on the horizontal axis (plant density levels) curvature of the curve at the best case and from it determining the best plant density, as well as a horizontal line from the same point towards the vertical axis (trait response) to determine the best mean o the trait, and it is noted from the results in the five figures and Table (5), that the best means for the traits: PH, HFN, NSP, Protein%, and Oil% reached 89.0 cm, 5.1 cm, 2.38 seeds per pod, 29 .02% and 23.59% at plant densities 140000, 130500, 235000, 230000, and 237500 plants per hectare, respectively. Table (5) also shows the appropriate regression equations for the five traits, which can be used to predict each of them at any proposed plant density.

Table (6) shows the results of the analysis of variance for stability by Eberhart and Russel method (1966), and it is clear that the mean square of environments (linear) did not reach the significant limit for all traits, indicating that the response to different environments is under genetic control (Dawod, 2008). It appears that the mean square of the linear component of of varieties x environments interaction when tested against pooled deviation was significant for all traits except NVB, Oil% and Protein%, while the test pooled deviation against pooled experimental error indicates that its mean square was not significant for traits. It is also evident that the mean squares of each of the three

varieties reached the significant limits in variety Lee 74 for NVB, NPP, SPY, 100 SW and Protein%, Taqa variety for NVB, SPY and 100 SW, and Aeman variety for NVB, NSP, 100 SW, and Protein%.

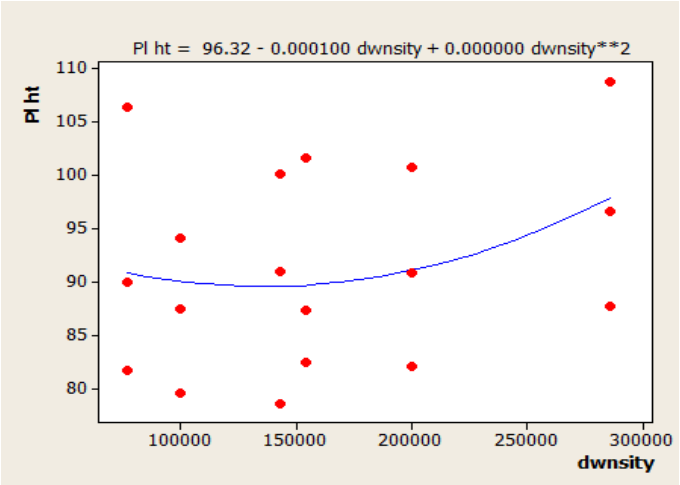

Fig. 1. Response of plant height to plant density

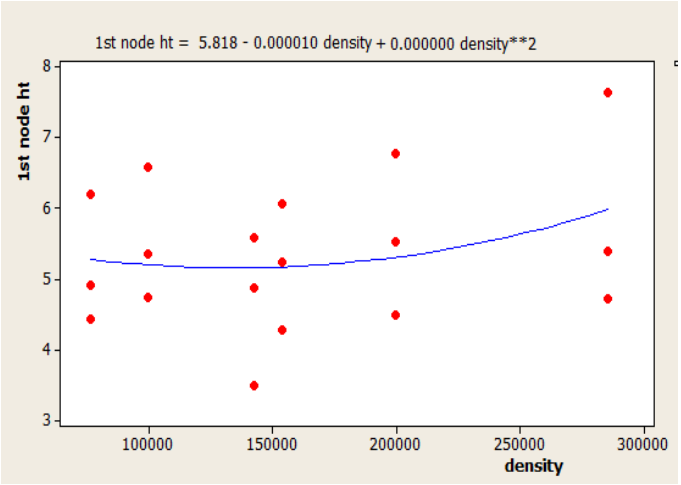

Fig. 2. Response of first node height to plant density

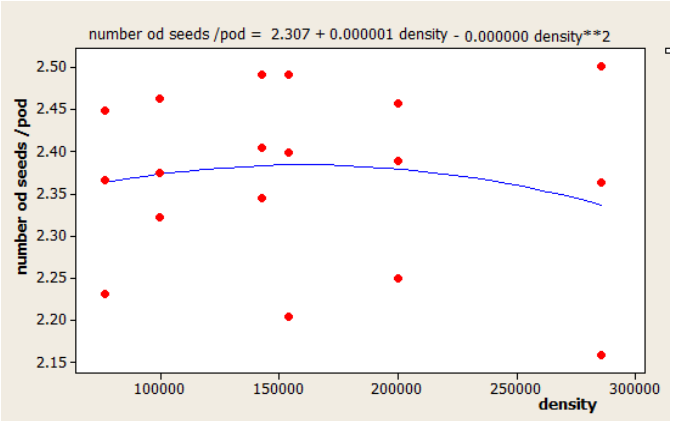

Fig.3. Response of number of seeds/pod to plant density

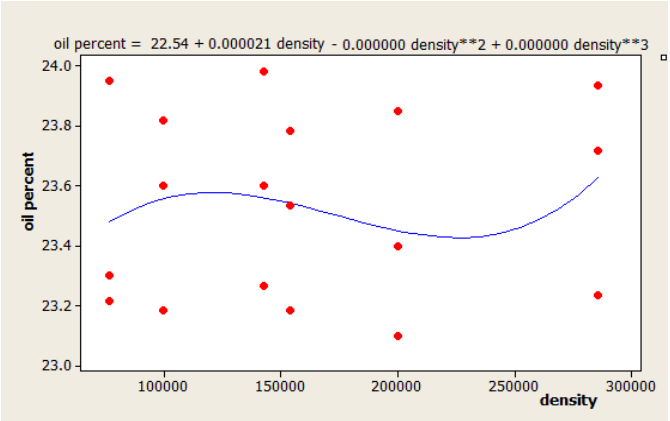

Fig 4. Response of oil percent to plant density

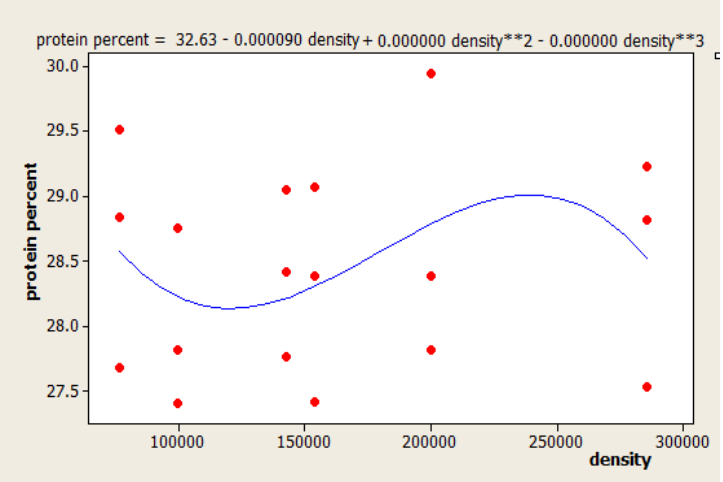

Fig 5. Response of protein percent to plant density

Table 5. The best regression equation between plant density and five traits in soybeans.

Traits	Degree of equation	Surpassed response value	Best density	The prediction equation
PH	Quadratic	89.0	140000	Plant height = 96.32 - 0.000100 density + 0.000000 density^2
HFN	Quadratic	5.1	130500	1st node height = 5.818 - 0.00001 density + 0.0000001 density^2
NSP	Quadratic	2.38	235000	Number seeds/pod = 2.307+ 0.000001density - 0.0000001 density^2
Oil %	Cubic	23.59	237500	oil percent = 22.54 + 0.000021 density - 0.0000001 density^2 + 0.0000001 density^3
Protein %	Cubic	29.02	230000	protein percent = 32.63 - 0.000090 density + 0.0000001 density^2 - 0.0000001 density^3

Table 6. The results of combining analysis for stability of three varieties of soybean.

SOV	df	Mean Square				
		DFF	**PH**	**HFN**	**NVB**	**NPP**
Varieties (V)	(2)	3207.3**	4929.24**	4.211**	0.291	825.715*
E+(V x E)	(33)	6.611	298.74	1.488	0.884	248.595
Environment (E) (linear)	1	152.56	2788.45	34.603	15.894	3272.81
VxE (linear)	2	30.276**	376.52**	2.177*	1.046	798.284*
Pooled deviation	30	0.169	22.383	0.339	0.373	111.142
Lee 74	(10)	0.250	25.712	0.273	0.505**	150.723*
Taqa	(10)	0.166	13.956	0.454	0.298*	115.090
Aeman	(10)	0.089	27.482	0.289	0.316*	67.612
Pooled Error	72	0.157	17.469	0.336	0.159	69.497
SOV	**df**	**NSP**	**SPY**	**100 SW**	**Oil %**	**Protein %**
Varieties (V)	(2)	0.006	18.202*	0.887**	0.00095	0.0355
E+(V x E)	(33)	0.0075	4.577	0.199	0.05086	0.2978
Environment (E) (linear)	1	0.1140	17.047	3.982	1.16951	7.6449
VxE (linear)	2	0.0155*	15.459*	0.497**	0.03452	0.0217
Pooled deviation	30	0.0034	3.436	0.053	0.01466	0.0713
Lee 74	(10)	0.0029	4.703*	0.047*	0.01634	0.085**
Taqa	(10)	0.0034	4.966*	0.065**	0.00962	0.0171
Aeman	(10)	0.0039*	0.637	0.047*	0.01803	0.112**
Pooled Error	72	0.0019	2.295	0.022	0.01249	0.0302

(**) and (*): are significant at 1% and 5% probability level respectively.

Table (7) shows the traits means, the regression coefficient values bi (which determines the response of the varieties to the different environments, which are measured by the linear regression of the variety mean over the average of varieties in each environment) and the mean deviation from the regression (S^2di) for each variety. It is noted for the traits DFE, NVP, NPP, NSP and Protein% that the regression coefficient reached in variety Lee74, 0.394, 0.487, 0.018, 0.382 and 0.917, respectively, and was not significant from one, and given that the deviation from the regression was not significant for DFE and NSP traits, then the variety Lee74 has a good response to different environments and highly stable environments for these two traits, and at the same time it was surpassed NSP mean over the other two

varieties. For PH and 100 SW traits, the regression coefficient was insignificant in Taqa and Aeman varieties, and the deviation from the regression was highly significant for the trait in both varieties, therefore, they respond well to different environments with high stability for PH trait. The two varieties, Lee74 and Taqa were distinguished by a non-significant regression coefficient and deviation from regression for HFN trait, indicating high performance and stability for this trait for different environments, especially Taqa variety that exceeded the two varieties with highest mean for the trait. Finally, it is noted that the regression coefficient and the deviation from the regression were not significant in Aeman variety for SPY and oil% traits, indicating the quality of its performance (gave the highest means) and its high stability to the varying environmental conditions for these two traits.

According to the gradation shown by Eberhart and Russell (1966) and as shown in Table (8), it was concluded from the above that there is a high stability in the different environments in variety Lee74 for DFE, HFN and NSP traits, Taqa variety for PH and HFN traits, and Aeman variety for PH, SPY and oil%, as well as response to good environments only in variety Lee74 for PH and oil%, Taqa variety for NPP, oil% and protein%, and Aeman for HFN. Whereas there was a response to inappropriate environments in Taqa variety for DFE and NSP and Aeman variety for DFE and NPP traits,

Conclusion:

The results provide the possibility of using this information in crop breeding programs by hybridization techniques.

References

Abbas, J.M.; I.A. Sarhan; and N.A. Mutlaq (2011). The effect of foliar feeding with iron and manganese on the yield and quality of three varieties of soybeans. Diyala J. of Agric. Sci., 3 (1): 218-227.

AbdulHamid, M.I.E.; N. Qabil; and F.M.A. El-Saadony (2017). Genetic variability, correlation and path analyses for yield and yield components of some bread wheat genotypes. J. Plant Prod., 8: 845–852.

Agarwal, V.; and Z. Ahmad (1982). Heritability and genetic advance in triticale. Indian J. Agric. Res., 16:19-23.

Al-Zubaidy, K.M.D.; and M.A.H. Al-Falahy (2016). Principle and procedures of statistics and experimental design. Duhok University Press, Iraq.

Al-Zubaidy, K.M.D.; and Kh. Kh. A. Al-Jubory (2016). Design and analysis of genetically experiments. Dar Al Wadah for Publishing, Jordan, Amman, Dijla Bookshop for Printing, Publishing and Distribution, Iraq – Baghdad. (In Arabic).

Becker, H.C.; and J. Leon (2010). Stability analysis in plant breeding. Plant Breed. 101:1–23.

Bhartiya, A.; and J. P. Aditya (2016). Genetic variability, character association and path analysis for yield and component traits in black seeded soybean lines under rain fed condition of Uttarakhand hills of India. Legume Res., 39: 31–34.

Budak, N. (2000). Heritability, correlation and genotype x year interaction of grain yield, test weight and protein content in durum wheat. Society of Field Crop Sci., 5(2): 1301-1311.

Cober, E.R.; and M.J. Morrison (2010). Regulation of seed yield and agronomic characters by photoperiod sensitivity and growth habit genes in soybean. Theor. Appl. Genet., 120: 1005–1012.

Dawod, Kh.M. (2008). Genetic stability in some cotton varieties (*Gossypium hirsutum* L.). Proceedings of the Fourth Agricultural Scientific Conference, College of Agriculture, Tikrit University, for the period 29-30 / 4/2008.

Eberhart, S.A.; and W.A. Russell (1966). Stability parameters for comparing varieties. Crop Sci., 6: 36–40.

Gauch, H.G. (1994). Statistical analysis of regional yield trials AMMI analysis of factorial designs. Agric. Ecosyst. Environ., 48, 307–308.

Grüneberg, W. J.; K. Manrique; D. Zhang; and M. Hermann (2005). Genotype × environment interactions for a diverse set of sweet potato clones evaluated across varying ecogeographic conditions in Peru. Crop Sci., 45: 2160.

Li, Y.C.; D.Y. Yu; R. Xu; and J.Y. Gai (2008). Effects of natural selection of several quantitative traits of soybean RIL populations derived from the combinations of Peking ×7605 and RN-9×7605 under two ecological sites. Sci. Agric. Sin., 41: 1917–1926.

Luo, J.; H. Zhang; Z.H. Deng; and Y.X. Que (2012). Trait stability and test site representativeness of sugarcane varieties based on GGE-biplot analysis. Ying Yong Sheng Tai Xue Bao., 23: 1319–1325.

Luo, J.; Z. Yuan; Z. Hua; Y.A. Chen; and R. Chen (2009). Stability analysis on yield characters of sugarcane. Chin. J. Appl. Environ. Biol., 15: 488–494.

Rahman, M.M.; and M. M. Hossain (2011). Plant densıty effects on growth, yield and yield components of two soybean varieties under equidistant planting arrangement .Asian Journal of Plant Sciences. 10(5): 278–286.

Rizk, T.Y.; and H.A. Ali (1981). Oil and sugar crops. Ministry of Higher Education and Scientific Research. Iraq, University of Mosul, p. 592.

Seadh, S.E.; and W.A.E. Abido (2013). How soybean cultivars canopy affect yield and quality. Journal of Agronomy. 12(1): 46-52.

Singh, J.H.; and S.S. Bains (1968). Genetic divergence for ginning outturn and its components in upland cotton. Indian Journal of Genetics and Plant Breeding, New Delhi. 28: 262-267.

Singh, R.K.; and B.D. Chaudhary (2007). Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi. 304p.

Weibel, R.O.; and J.W. Pendleton (1964). Effect of artificial lodging on winter grain yield and quality. Agron. J., 56: 487-488.