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Original scientific article

FORAGE YIELD COMPONENTS OF SOME TOLERANT AND SENSITIVE GRASS PEA GENOTYPE SEEDLINGS AFFECTED BY THE SALINITY STRESS

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Grass pea (*Lathyrus sativus* L.) is relatively tolerant to several abiotic stresses such as salinity. Twenty-five grass pea genotypes provided by the Dryland Agricultural Research Institute, Maragheh, Iran, were exposed to four salinity levels (0, 40, 80, 120 mM). Based on the primary screen, 8 tolerant genotypes and 17 sensitive genotypes were selected. Principal components analysis for the sensitive and tolerant genotypes showed that the first four components explained approximately 71-80% of variance. In PCA, the coefficients associated with leaf showed that, in tolerant genotypes, leaf length and leaf number increased but, leaf width decreased. In other words, salinity stress makes the leaves grow larger and longer, but the width of the leaves decreases and angle of the leaf becomes tighter. So, these traits may be used as an index of salinity tolerance in grass pea selection programs. Cluster analysis based on Ward's algorithm and Euclidean distance measure effectively separated the tolerant and sensitive genotypes. Cut off dendrogram located tolerant genotypes (except one genotype) in the same subgroup. This fact shows that cluster analysis efficiently divided and/or separated semi-tolerant tolerant genotypes. Shoot dry weight had significant negative correlation with *pH*, plumule length and plantlet length. Path analysis on tolerant genotypes, revealed the direct effects of leaf number and pod number with shoot dry weight. In stepwise regression, two traits including leaf

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number and pod number were entered into the model. The results showed that leaf number and pod number had the most direct and positive effect on the shoot dry weight, and the plant height had the highest indirect effect through leaf number on the shoot dry weight. About sensitive genotypes, the results showed that leaf number and fruit fresh weight had the most direct and positive effect on the shoot dry weight, and the plant height had the highest indirect effect through leaf number on the shoot dry weight. Several characteristics were identified to explain shoot dry weight during path analysis. The selections based on the identified characters would be more effective in improving yield in the breeding programs of grass pea.

Keywords: Cluster Analysis, Grass pea, PCA, Tolerance to Salinity

INTRODUCTION

Grass pea (*Lathyrus sativus* L.), an annual pulse crop belonging to the tribe *Vicieae* in the family of Fabaceae (BISWAS and BISWAS, 1997) is under grown for food and feed purposes (VAZ PATTO *et al.*, 2011). The seeds of *L. sativus* contain 31% protein, 41% carbohydrate, 17% total dietary fiber, 2% fat and 2% ash on a dry matter basis (AKALU, *et al.*, 1998). *Lathyrus genus is a sum of 187 species and subspecies (MATHUR* et al.*, 2005), including species grown for grain (e.g. Lathyrus sativus L.), forage and grain (e.g. L. cicera, L. clymenum L. and L. ochrus L.), and solely for green forage (e.g. L. tingitanus, L. latifolius and L. sylvestris L.).* The world demand for legume proteins is increasing for animal feeding. Grass pea would be a nice alternative for cropping systems in the marginal lands and environments (VAZ PATTO *et al.*, 2006; 2011). Owing to the tolerance of grass pea to the adverse environmental conditions; this crop has the potential of being a staple food during famines, crop failures and in cases of extreme poverty as well as in times of food crisis (GIRMA and KORBU, 2012). It is a low-input crop mostly planted on marginal lands on residual moisture (DADI *et al.*, 2003). Overall, this crop is relatively tolerant to several abiotic stresses; makes it a reliable candidate for expansion in the semiarid areas of the world which are predicted to become more drought-prone due to climate change (GIRMA and KORBU, 2012). More than 100 million people in drought-prone areas of Asia and Africa consider grass pea as a traditional popular crop, because of its easy cultivation, its relative resistance to drought, flood, moderate salinity and insect attack, and its good yield of tasty seeds, which has an edible portion content of about 30% (*ABDELMONEIM et al., 2015)*.

Soil salinity is one of the most severe abiotic stresses affecting *the* production of the crops worldwide (*WANG et al., 2004*). This problem is more severe in arid and semiarid regions, and legume plants already face a notable impact of salt stress in these regions (*GRAHAM* and *VANCE, 2003*). *Lathyrus sativus is a relatively salt-tolerant leguminous forage plant. This plant gro*ws naturally in the high alkaline soils with a pH>9 (ZHENG and LI, 1999).

Salinity imposes unfavorable physiological and growth restrictions on plants and inhibit the crop production (KHADRI *et al.*, 2006). In general, soil salinity is believed to be mainly responsible for low land use as well as for the reduced cropping area (RAHMAN and AHSAN, 2001). A major constraint on grass pea production in coastal areas is soil salinity, predominately due to chloride and sulphate accumulation in the saline areas (ZHENG and LI, 1999). Even, some soils are naturally saline, the secondary salinization occurs by the use of irrigation systems, that is the main threat to legumes sustainable production in salinity exposed areas; where, water supplies are limited, and the irrigation is essential for common crop production (SHARMA *et al.*, 1982). Grass pea is a relatively salt-tolerant crop but, the yields are seriously reduced particularly by the chloride toxicity (MANCHANDA and SHARMA, 1990). The effects of salinity on grass pea are wide ranging. Seed germination is delayed and reduced as well as vegetative growth is suppressed under saline conditions (SHARMA *et al.*, 1982). In pea, phenolics content increased under the influence of salinity in both tolerant and sensitive cultivars (NOREEN and ASHRAF, 2009). Plants of the genus *Lathyrus* are less sensitive to drought and salinity than other members of the family *Fabaceae* (VAZ PATTO *et al.,* 2006), but there are few studies on this topic. The influence of salinity stress on the content of selected chemical constituents in *Lathyrus* tissues has been the subject of limited research (TYAGI *et al.,* 1995; XIONG *et al.,* 2006; VAZ PATTO *et al.,* 2011).

PARIHAR *et al.*, (2013) applied principal component analysis, correlation, biplot drawing and cluster analysis for the various agronomic traits studies in grass pea (*Lathyrus* spp) germplasms. BADO *et al.*, (2016) tried principal component analysis and canonical discriminant analysis for the prediction of salt tolerance. Principal component analysis (PCA), principal coordinate analysis (PCoA) and cluster analysis were performed by AL-ASHKAR *et al.*, (2019) to detecting the salt tolerance in wheat lines. SHAHBA *et al.*, (2012) performed regression analysis to determine the relationship between the measured parameters and the salinity levels in Seashore Paspalum cultivars. LOVATO *et al.,* (1999) employed regression analysis to investigate equations of growth responses of *Stylosanthes humilis* (Fabaceae) populations to salinity stress. BAYUELO-JIMENEZ *et al.,* (2002) used Ward’s minimum variance clustering method to classify the accessions into discrete clusters and the optimum number of clusters determined by the sum of squares index (E) (ROMERSBURG, 1988).

Investigating the relationships between yield and its components, improves the efficiency of breeding programs. One of the most useful methods for identifying these relationships is to analyze phenotypic correlations and to find direct and indirect effects using path coefficients analysis (BOARD *et al.,* 1997). Salt tolerant and sensitive genotype(s) have to be identified to cope with the salinity problem (VAZ PATTO *et al.,* 2006). On the other hand, in tolerant and sensitive genotypes, shoot dry weight is very important trait, since, it is used to feed and is the determinant of final yield (PARIHAR *et al.,* 2013). Increased economic yield; including grain and forage yield, is an important goal in the breeding programs of grass pea. To achieve this, it is necessary to identify traits playing important role in improving the yield and the use them in the breeding programs. Therefore, the objective of this experiment was to identify traits that affect yield and yield components. Path analysis investigates the causal relationships between traits and their direct effects on yield. The other idea with this study was to estimate the correlations and to determine some selection criteria for improving the forage yield of grass pea genotypes.

MATERIALS AND METHODS

This research was carried out in the Research Field and Laboratory of Plant Production and Breeding Department, Faculty of Agriculture, University of Maragheh, Maragheh, East Azerbaijan Province, Iran. 25 grass pea genotypes were provided by the Dryland Agricultural Research Institute, Maragheh, Iran (Table 1). Those were exposed to four salinity levels (0, 40, 80, 120 mM). The salinity was imposed with NaCl during the season and until harvesting time. Based on the primary screening (results were not published) in the fourth level of salinity, eight tolerant genotypes (8, 9, 10, 12, 13, 14, 23 and 24) and 17 sensitive genotypes (1, 2, 3, 4, 5, 6, 7, 11, 15, 16, 17, 18, 19, 20, 21, 22 and 25) were selected.

Data were averaged on a plant basis, and the individual means were used for the analysis. Principal components analysis was used to distinguish important traits in the tolerant and sensitive genotypes. NTSYS software applied For PCA analysis and PCA three-dimensional scatterplot of grass pea genotypes. Correlation coefficients were computed and path analysis performed for shoot weight to reveal cause and effect relationships by SPSS. Cluster analysis was performed to ensure that genotypes were correctly screened based on the measured traits.

Table 1. The grass pea (Lathyrus sativus L.) genotypes used in salinity tolerance experiment

Genotype Number	Tolerant (T) or Sensitive (S)	Origin
1	S	ICARDA
2	S	ICARDA
3	S	ICARDA
4	S	ICARDA
5	S	ICARDA
6	S	ICARDA
7	S	ICARDA
8	**T**	ICARDA
9	**T**	ICARDA
10	**T**	ICARDA
11	S	ICARDA
12	**T**	ICARDA
13	**T**	ICARDA
14	**T**	ICARDA
15	S	ICARDA
16	S	ICARDA
17	S	ICARDA
18	S	ICARDA
19	S	ICARDA
20	S	ICARDA
21	S	ICARDA
22	S	ICARDA
23	**T**	ICARDA
24	**T**	ICARDA
25	S	Local Check

Measurements

Plant height (cm), plantlet length (cm), plantlet weight (g), leaf length (mm), leaf width (mm), leaf number, leaf angle (angle of leaf to the shoot), root length (mm), plumule length (mm), radicle length (mm), plumule length/radicle length, shoot number, shoot fresh weight (g), shoot dry weight (g), root fresh weight (g), fruit fresh weight (g), fruit dry weight (g), seed dry weight (g), seed fresh weight (g), radicle dry weight (g), plumule dry weight (g), plumule dry weight/radicle dry weight, pH, pudding date, flowering date, germination percent, Rhizobium number, EC, first shoot location, Rhizobium depth, germination speed, pod number and grain number were measured.

RESULTS AND DISCUSSION

Principal components analysis for the sensitive and tolerant genotypes showed that the first four components explained approximately 71-80% of variance (Table 2). For high explanation, theses amount indicates analysis efficiency. DANESHGILVAEI *et al.,* (2011) based on a study with 27 traits in the grass pea genotypes reported six principal components in PCA that explanted about 90% of variation among the data.

Table 2. Total variance explained for the tolerant and sensitive genotypes of grass pea exposed to salinity stress

Component	Initial Eigenvalues for tolerant genotypes			Initial Eigenvalues for sensitive genotypes		
	Total	% of Variance	Cumulative %	Total	% of Variance	Cumulative %
1	11.776	34.636	34.636	11.494	33.807	33.807
2	6.073	17.862	52.499	5.211	15.325	49.132
3	5.435	15.986	68.484	4.563	13.420	62.552
4	**3.924**	**11.541**	**80.025**	**2.953**	**8.686**	**71.238**
5	2.605	7.663	87.688	1.974	5.807	77.045
6	2.230	6.560	94.248	1.705	5.014	82.059
7	1.956	5.752	100.000	1.540	4.528	86.588

Table 3 shows the components matrix for the tolerant and sensitive genotypes. In the leaf related traits, coefficients of components in tolerant genotypes for leaf number (0.814) and leaf width (-0.498) were higher than sensitive genotypes. Leaf length (0.664) and leaf angle (0.118) had lower data. The coefficients associated with leaf show that in tolerant genotypes, leaf length and leaf number increased but, leaf width decreased (Table 3). In other words, salinity stress makes the leaves grow larger and longer, but the width of the leaves decreases and angle of the leaf becomes tighter. So, these traits may be used as an index of salinity tolerance in grass pea selection programs.

Table 3. Components matrix for the tolerant and sensitive genotypes of grass pea exposed to salinity stress (PCA)

Trait	PC1-Tolerant	PC1-Sensitive	PC2-Tolerant	PC2-Sensitive
Shoot Fresh Weight	0.919	0.824	0.558	0.228
Pod Number	0.914	0.916		
Plant Height	0.868	0.827		
Grain Number	0.865	0.908		
Shoot Dry Weight	0.856	0.707		
Plumule Length	-0.815	-0.723	-0.313	-0.148
Leaf Number	0.814	0.651		
Fruit Fresh Weight	0.804	0.917		
Plantlet Length	-0.785	-0.787	0.149	-0.287
pH	-0.784	-0.604		
Radicle Length	-0.749	-0.686	0.344	-0.361
Fruit Dry Weight	0.716	0.749	0.417	0.132
Leaf Length	0.664	0.925		
Plumule Dry Weight/Radicle Dry Weight	0.628	-0.353	-0.511	-0.140
Shoot Fresh Weight	-0.599	-	0.558	0.228
Pudding Date	-0.105	0.622	0.409	0.856
Seed Dry Weight	0.480	0.454	0.504	0.801
Flowering Date	0.139	0.616	0.406	0.723
Seed Fresh Weight	0.592	0.225	0.445	0.731
Germination Percent	0.317	0.191		
Leaf Angle	0.118	0.645	0.363	-0.594
Shoot Number	0.448	-0.385	-0.216	-0.308
Plumule Dry Weight	-0.177	-0.560	0.255	0.435
Plantlet Weight	-0.413	-0.514	0.565	0.494
Rhizobium Number	0.295	0.722	-0.312	-0.572
Radicle Dry Weight	-0.511	-0.297	0.804	0.456
Leaf Width	-0.498	0.198	0.617	0.422
Plumule Length/ Radicle Length	-0.358	0.353	-0.633	0.585
Root Fresh Weight	-	-	0.656	0.369
EC	0.258	-	-0.208	-0.124
First Shoot Location	-0.305	0.173	0.585	-
Root Length	-0.258	0.262	-0.186	-0.387
Germination Speed	0.348	-	-0.332	-0.408

In the roots related traits; root length (-0.258) and radicle length (-0.749) in tolerant genotypes were lower than sensitive genotypes (0.262 and -0.686, respectively). Also, plumule length/radicle length ratio was very low in tolerant genotypes (-0.358 vs 0.353 in sensitive genotypes). The idea is that salinity selects more dwarf plants. Plant growth decreases with any increase in the salinity of root zone. The decrease in plant growth is related to increase in osmotic tension of soil solution which reduced absorption of water by roots due to the accumulation of various ions in toxic amount (SAQIB *et al.,* 2005, 2008).

Coefficients of pudding and flowering dates in tolerant genotypes (-0.105 and 0.139) were lower than the sensitive genotypes (0.662 and 0.616, respectively). In other words, tolerant genotypes tend to earliness and to complete the growing season earlier (DANESHGILVAEI *et al.,* 2011).

Plumule dry weight/radicle dry weight ratio and shoot dry weight increased in tolerant genotypes (Table 3). Since, the cultivars with less root development are sensitive to salinity (BAYUELO-JIMENEZ, 2002). Negative effects of salinity on agriculture are a concern because, they affect growth, development and yield of crop plants. Typically, decline in plant growth occurs linearly after attending the threshold values of salinity. Salinity decreases root growth as well as shoot growth but, this reduction is lower in roots compared to above ground growth (FAGERIA, 1992).

Coefficients of seeds fresh and dry weight in tolerant genotypes (0.592, 0.480) were higher than sensitive genotypes (0.225, 0.454). However, the fruits fresh and dry weights in tolerant genotypes (0.804, 0.716) were lower than sensitive ones (0.749, 0.917). The tops dry weight can also be used as a criterion to classify cultivars tolerant to salinity. In this case, at least, two levels of salinity should be imposed. One is control and another stressful level which can affect the plant growth significantly (FAGERIA, 1992). There are two main stresses imposed by salinity on plant growth. One is water stress imposed by the increase in osmotic potential of the rhizosphere as a result of high salt concentration. Another stress is the toxic effect of high concentration of ions (SHARMA *et al.,* 1982). The high amount of Na^+ and Cl^- reduce the uptake of cations and anions and creates nutritional disequilibrium in the plants, leading to the reduced yield (KUMAR *et al.,* 2008; FAGERIA *et al.,* 2011). Meanwhile, the plants tolerant to salinity, exclude Na^+ absorption process and maintain high concentration of K^+ in tops (DAVENPORT *et al.,* 2005; SAQIB *et al.,* 2005).

Cluster Analysis

Cluster analysis based on Ward's algorithm and Euclidean distance measure effectively separated the tolerant and sensitive genotypes (Figure 1). Cut off dendrogram located tolerant genotypes (8, 9, 10, 12, 13, 14 and 23, except 24) in the same subgroup. This fact shows that cluster analysis efficiently divided and/or separated semi-tolerant tolerant genotypes. DANESHGILVAEI *et al.,* (2011) performed cluster analysis on grass pea genotypes and reached three distinct groups. The first group consisted of 16 genotypes, the second group had 3 genotypes and the third one contained just one genotype.

PCA three-dimensional scatter plot of grass pea genotypes subjected to salinity stress confirmed the results of cluster analysis (Figure 2) and the tolerant genotypes (except 24) were located close to each other.

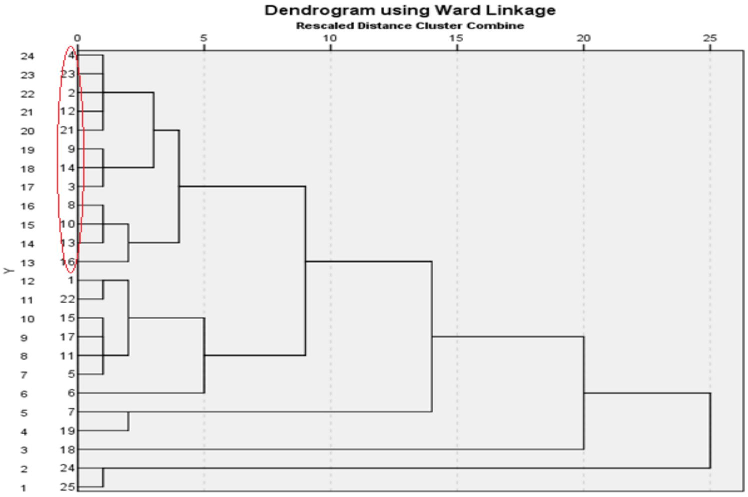

Figure 1. Dendrogram of cluster analysis based on Ward's algorithm and Euclidean distance measure for the several genotypes of grass pea exposed to diverse salinity levels

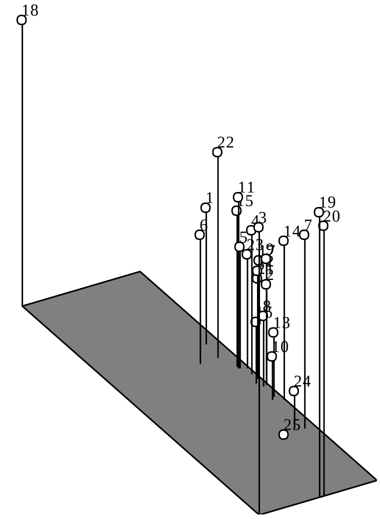

Figure 2. Three-dimensional scatterplot of grass pea genotypes (PCA) subjected to salinity stress

Correlation coefficients

Improvements in grain and forage yields are important breeding goals of the crop plants (PARIHAR *et al.*, 2015). Therefore, it is necessary to identify the related attributes playing dominant role in improving the crop yield and to have consideration in the selection programs (BHATT, 1973). Path coefficient analysis is a method that determines the causal relationships between traits and their direct effects on a dependent trait such as yield, and that genetic correlation coefficients are more effective than phenotypic correlations for selecting traits that contribute to the yield improvement (BOARD *et al.*, 1997).

Table 4. Significant correlation coefficients between several traits in genotypes of grass pea subjected to salinity stress

	Shoot Dry Weight	*PH*	Plumule Length	Plantlet Length	Seed Dry Weight	Rhizobium Number	Leaf Angle	Leaf Length	Shoot Fresh Weight	Fruit Fresh Weight	Leaf Number	Grain Number	Pod Number	Plant Height
Shoot Dry Weight	1	-.639**	-.474*	-.464*	.593**	.458*	.418*	**.823****	**.944****	**.833****	**.900****	**.816****	**.808****	**.885****
pH	-.639**	1	.433*	.559**	-.207	-.324	-.136	-.598**	-.654**	-.641**	-.638**	-.694**	-.599**	-.606**
Plumule Length	-.474*		1	**.819****	-.510**	-.415*	-.644**	-.716**	-.546**	-.590**	-.405*	-.571**	-.561**	-.568**
Plantlet Length	-.464*			1	-.365	-.565**	-.438*	-.636**	-.511**	-.543**	-.423*	-.611**	-.577**	-.503*
Seed Dry Weight	.593**				1	.044	.379	.575**	.557**	.546**	.382	.499*	.492*	.527**
Rhizobium Number	.458*					1	.368	.551**	.455*	.482*	.459*	.541**	.559**	.591**
Leaf Angle	.418*						1	.656**	.461*	.537**	.320	.514**	.552**	.520**
Leaf Length	.823**							1	**.831****	.764**	.724**	.782**	.794**	**.845****
Shoot Fresh Weight	.944**								1	**.908****	**.913****	**.857****	**.845****	**.904****
Fruit Fresh Weight	.833**									1	.738**	**.933****	**.902****	**.802****
Leaf Number	.900**										1	.708**	.694**	**.867****
Grain Number	.816**											1	**.961****	**.801****
Pod Number	.808**												1	.792**
Plant Height	.885**													1

* and ** are significant at 0.01 and 0.05 levels, respectively

Table 4 shows only the traits that had significant relationship with shoot dry weight. Shoot dry weight had significant negative correlation with *pH*, plumule length and plantlet length. However, with the other traits shoot dry weight had significant positive correlation. Shoot fresh weight (0.944**), leaf number (0.900**), plant height (0.885**), fruit fresh weight

(0.833**) and leaf length (0.823**) had the highest correlations, respectively. The results of phenotypic correlations revealed that the traits including plumule length, plantlet length, rhizobium number, leaf angle, leaf length, fruit fresh weight, leaf number, grain number, pod number and plant height had significant correlations with shoot dry weight (Table 4).

In a research performed by JEBERSON *et al.,* (2018), seed yield per plant exhibited significant and positive correlation with biological yield per plant, plant height and number of pods per plant. Biological yield per plant had positively significant correlation with the number of pods per plant.

In another study on *Lathyrus sativus* L. (KUMARI and PRASAD, 2005); seed weight was negatively but, non-significantly correlated with seed yield and, plant height had a significant positive correlation with days to flower. Furthermore, days to flower and days to podding had strong positively correlations.

Path coefficient analysis of shoot dry weight

Path analysis of tolerant genotypes revealed the direct effects of leaf number and pod number on shoot dry weight. In stepwise regression, two traits including: leaf number and pod number were entered into the model. The results showed that leaf number and pod number had the most direct and positive effect on the shoot dry weight, plant height had the highest indirect effect through leaf number on the shoot dry weight. The strong positive correlations of plant height, pods per plant and seeds per pod have previously been reported in grass pea (KUMAR and DEBEY, 20001; SHARMA *et al.,* 2000).

About sensitive genotypes, two traits including leaf number and fruit fresh weight were entered into model. The results showed that leaf number and fruit fresh weight had the most direct and positive effect on the shoot dry weight and plant height had the highest indirect effect through leaf number on the shoot dry weight.

Path analysis showed that the selection of genotypes based on only the correlation coefficient may not be effective. Several characteristics were identified to explain shoot dry weight during path analysis. The selections based on the identified characters would be more effective in improving yield in breeding programs.

In *Lathyrus,* for the selection of yield contributing traits; path analysis showed that the importance should be given to the biological yield, plant height and number of pods/plants. Path coefficient was carried out based on the seed yield per plant as a dependent variable and all the other characters as independent variables. The biological yield per plant exhibited the highest positive and direct effect on grain yield followed by harvest index. Plant height and pods per plant showed significant positive indirect effect on seed yield. Therefore, these characters can be considered for selecting genotypes to improve the grain yield in the *Lathyrus sativus* breeding programs (JEBERSON *et al.,* 2018). The similar results were reported by PARIHAR *et al.* (2015) and KUMARI and PRASAD (2005).

Furthermore, path analysis revealed that plant height, days to podding, pods per plant and seeds per pod were the principal yield components. The trait days to flower also contributed to seed yield mainly via influencing pods per plant. Path coefficient analysis revealed that pods per plant, followed by plant height contributed the most toward seed yield and correlations also showed similar associations (KUMARI and PRASAD (2005). A strong positive correlation of plant height, pods per plant and seeds per pod have previously been reported in grass pea (KUMAR and DUBEY, 2001; SHARMA *et al.*, 2000).

CONCLUSIONS

Path analysis via the correlation coefficients of the direct and indirect effects provides information on the actual contribution of a trait on the yield. Shoot dry weight was the trait most affected by the salinity. The decrease in shoot dry weight and its related traits occurs through osmotic effects reducing the ability of plants to gain water and by restricting the growth. A comparison of correlation coefficients and path analysis showed that; leaf number was the principal shoot dry weight component at both tolerant and sensitive genotypes. In grass pea, shoot dry weight decreased with any increase in salinity levels. Therefore, the identification of salinity tolerant genotypes could help overcome the effects of salinity on the crop productivity. The differential responses exhibited by the traits under the salinity conditions might be due to the complexity of the traits under stress. In both tolerant and sensitive genotypes, leaf number and plant height were the common components in determining of shoot dry weight. In PCA, the coefficients associated with leaf showed that in tolerant genotypes; leaf length and leaf number increased but, leaf width decreased. In other words, salinity stress makes the leaves grow larger and longer, but the width of the leaves decreases and angle of the leaf becomes tighter. In addition to the leaf number as a common trait; pod number in tolerant genotypes and fruit fresh weight in the sensitive genotypes were other important traits in determining the shoot dry weight. These results clearly indicated that the selection of genotype under the normal and saline conditions should be entirely different.

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KOMPONENTE PRINOSA KRME TOLERANTNIH I OSETLJIVIH KLIJANACA SASTRICE IZLOŽENIH STRESU SOLI

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Izvod

Sastrica (*Lathyrus sativus* L.) je relativno tolerantna na različite abiotičke stresove kao što je salinitet. Dvadeset i pet genotipova sastrice koje je obezbedio Poljoprivredni istraživački institut za zemljište, Marageh, Iran, bilo je izloženo raulličitim nivoima zaslanjenosti slanosti (0, 40, 80, 120 mM). Na osnovu primarne ocene, odabrano je 8 tolerantnih i 17 osetljivih genotipova. Analiza glavnih komponenata za osetljive i tolerantne genotipove pokazala je da su prve četiri komponente objasnile približno 71-80% varijanse. U PCA, koeficijenti povezani sa listom pokazali su da se kod tolerantnih genotipova dužina i broj listova povećala, ali se širina lista smanjila. Drugim rečima, stress zaslanjenosti utiče da lišće raste veće i duže, ali širina listova se smanjuje, a ugao lista postaje manji. Dakle, ove osobine se mogu koristiti kao indeks tolerancijena zaslanjenost u programima selekcije sastrice. Klaster analiza zasnovana na Ward-ovom algoritmu i euklidovoj meri rastojanja efikasno je razdvojila tolerantne i osetljive genotipove. U delu dendrograma tolerantni genotipovi (osim jednog genotipa) nalaze se u istoj podgrupi. Ova činjenica pokazuje da je klaster analiza efikasno podelila i / ili odvojila polutolerantne od tolerantnih genotipova. Suva masa izdanka imala je značajnu negativnu korelaciju sa pH, dužinom plumula i dužinom biljčica. *Path* analiza tolerantnih genotipova otkrila je direktne efekte broja lista i broja mahuna na suvu težinu izdanaka. Postupnom regresijom, u model su unete dve osobine, uključujući broj listova i broj Rezultati su pokazali da su broj listova i broj mahuna najdirektnije i pozitivno uticali na suvu masu izdanka, a visina biljke imala je najveći indirektni efekat kroz broj listova na suvu masu izdanka. Kod osetljivih genotipova, rezultati su pokazali da su broj listova i sveža težina ploda najdirektnije i pozitivno uticali na suvu masu izdanka, a visina biljke najveći indirektni efekat pokazala je kroz broj listova na suvu masu izdanka. Identifikovano je nekoliko karakteristika koje objašnjavaju suvu težinu izdanaka tokom *path* analize. Odabir na osnovu identifikovanih karakteristika bio bi efikasniji u poboljšanju prinosa u programima oplemenjivanja sastrice.

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