Full Length Research Paper

Phenotypic and genotypic correlation for some characters in Lentil (\textit{Lens culinaris} Medik.)

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Responses of environmental change clearly depend upon the interaction between phenotypic and genetic variation. In this study, phenotypic and genotypic variation were examined in 2 cultivars (Fırat-87 and Kışlık Kırmızı-51) and 10 genotypes of lentil collected from farmers, who usually use own seeds year after year in Yozgat province, in Turkey. These cultivars and genotypes were evaluated at the field of farmers during 2009-2011 seasons. Treatment was made a randomized complete block design with four replications. Results indicated general similarities between the species in their trait correlation structure and level of integration among traits, but characteristic differences were observed in the patterns of change. The interactions were significant between year and characters in all characters except number of branches/plant. The similar pattern of genetic variation and phenotypic integration observed in these genotypes. This may be due to their close phylogenetic relation and to their ecological distributions. We further examined phenotypic and genotypic correlation for lens genotypes. Many of the traits measured had significant genotype effects.

Key words: Lens, \textit{Lens culinaris} medic., phenotypic and genotypic correlation

INTRODUCTION

Lentil (\textit{Lens culinaris} L. Medik.) is one of the most important sources of protein in Turkey. Therefore, it has a very wide planting area. Lens is grown at the 318 000 ha planting area. It has 131 000 ton production and 411 kg/ha yield (Anonymous, 2010). Yield of lens seem small, but generally lentil is produced on marginal lands that are relatively dry and without fertilizer inputs or irrigation. The yield performance of lens varieties is very low compared with the average global lens yield. But local varieties contain higher variation. This situation is very important for breeders. Plant breeders have always interested in world and local variety.

The genotype of an organism is the description of the genetic code. The phenotype of an organism is the description of the physical and behavioral characteristics of the organism, for example its size and shape, its metabolic activities, susceptibility to pathogens, or response to stress (Rose and Mileusnic, 1999). They have also paid variety of different species maximizing genetic variability for plant breeding programs. In the field of breeding, researcher may be interested in the extent to which phenotypic differences are influenced by differences in environmental conditions (Muehlbauer \textit{et al.}, 2006; Frederick \textit{et al.}, 2006). Estimating the genetic components of phenotypic variation and heritability may help the researcher. They evaluated and characterized the germplasm accessions for breeding programs (Polignano and Ugetti, 1984; Bakheit and Mahdy, 1988; Havey and Muehlbauer, 1989; Muehlbauer \textit{et al.}, 1989; Sarker \textit{et al.}, 1999; Kahraman \textit{et al.}, 2004; Muehlbauer, \textit{et al.}, 2006; Weller \textit{et al.}, 2009; Kökten \textit{et al.}, 2010; Udensi \textit{et al.}, 2011).

Genotypic and phenotypic conditions are dominant factors for yield formation. Environmental conditions are partially controllable, but genotype of the plant can only be changed by breeding programs. Information about phenotypic stability is useful for the selection of crop varieties as well as for breeding programs (Akçura \textit{et al.}, 2005). Sharma (1999) has been observed that higher genotypic correlation caused phenotypic correlation.

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Rakesh et al. (1999) reported high genotypic and phenotypic coefficients of variability for seed yield per plant. The phenotypic performance of a genotype is not necessarily the same under diverse agro-ecological conditions (Ali et al., 2003; Kole et al., 2008).

The coefficient of variation, heritability and repeatability of traits are important guides to selecting polygenic yield determining traits (Ortiz and Ng, 2000). Grain yield improvement through breeding for yield components would be most effective if their variability, heritability and genetic advances are understood (Adewale et al., 2010). Positive and significant correlations of seed yield with 100-seed weight, harvest index and plant height have also been reported in lentil (Kumar et al. 2004). Some researchers reported on the association between some characters of plants and path analyses have very useful as selection criteria for genetic improvement of yield (Abdalla, 1976; Salem, 1982; Sindhu et al., 1985; Ghafoor et al., 1990; Ciftci et al. 1998; Yadav et al., 2003; Kakde et al, 2005; Karadavut, 2009).

In this study, we aimed to determinate (i) genetic variability in yield and some characters, (ii) phenotypic and genotypic correlation between pairs of characters, (iii) path analysis seed yield and some yield components.

MATERIAL AND METHODS

2 cultivars (Fırat-87 and Kışlık Kırmızı-51) and 10 genotypes of lentil collected from farmers, who usually use own seeds year after year in Yozgat province. Yozgat located in Central area of Turkey. These cultivars and genotypes were evaluated at the field of farmers during 2009-2010 and 2010-2011 growing seasons. Treatment was made a randomized complete block design with four replications. Seeds were sown a plot size 5x1.8=9.0 m² and 4x1.2=4.8 m² of each plot was harvested. Sowing (200 seeds/m²) was made by hand as 10x30 cm on 24, 21 October in the first and the second year, respectively. 3 kg N/da (21% Ammonium Sulfate) and 5 kg P₂O₅ (43% Triple Super Phosphate) fertilizer were given at sowing time. The soil was clay textured and it contains calcareous 18.32%, pH 7.76%, EC 0.021% and organic matter 1.66%. The amount of precipitation during the vegetation period was 398 and 412mm in the first and the second year, respectively. Measurements and observation of examined characters were done on five plants randomly chosen in each plot.

In each plot, plant height, number of primary branches, number of pods/plants, seed yield, number of seeds/pod and 1000 seed weight were measured and the analysis of variance and combined analysis of variance were done. Heritability is the ratio of the genetic variance over the phenotypic variance. Genotypic and phenotypic variances, genotypic and phenotypic coefficients of variability were calculated and heritability was estimated by Burton (1951). Simple correlation was also done by Kwon and Torri (1964) and Keller et al. (2001).

\[ V_g = \frac{GMS - EMS}{r} \]
\[ V_e = EMS \]
\[ V_p = V_g + \frac{V_e}{r} \]
\[ H^2 = \frac{V_p}{V_p} \]

Where; \( V_g \) : Genetic variance
\( V_e \) : Environmental variance
\( GMS \): Genotypes mean squares
\( EMS \): Error mean squares
\( H^2 \): Heritability
\( r \): Number of replication

Expected response to selection (ERS) for each traits was calculated as following equation (Khan et al. 2009);

\[ ERS = k \sqrt{vpH^2} \]

Where; \( k \) : 1.40 at 20% selection intensity for a traits
\( vp \) : Phenotypic variance for a trait
\( H^2 \) : Broad sense heritability for a trait

The data were analyzed by the MINITAB V13 statistical programs. All of the relationships between plant characters were investigated and the direct and indirect effects of plant characters on yield were determined (Steel and Torrie, 1985). Phenotypic and genotypic coefficients of variation (PCV and GCV), phenotypic, genotypic and environmental variations, genetic advance and broad sense heritability were estimated according to the methods of Dewey and Lu (1959) and Singh and Chaudhary (1985). The following measurements and observations were made; seed yield/plant (g/plant), plant height (cm), the first pod height (cm), the number branches/per plant (numbers), number of pod/per plant (numbers), 1000 seed weight (g) and number of seed/per pod (numbers).

RESULTS AND DISCUSSION

The results of variance analysis are shown in Table 1. Combined analysis of variance showed significant differences. The interactions were significant between year and characters in all characters except number of branches/plant. This indicated that environmental factors (year and location) can be significantly and years did not
Table 1. Combined analysis of variance for different traits for cultivar and lines.

<table>
<thead>
<tr>
<th>Source of Variance</th>
<th>DF</th>
<th>Plant height (cm) Mean Squares</th>
<th>Number branches/per plant</th>
<th>Number of pod/per plant</th>
<th>First pod height (cm)</th>
<th>Number of seed/pod</th>
<th>1000 Seed weight (g)</th>
<th>Seed yield/plant</th>
</tr>
</thead>
<tbody>
<tr>
<td>Years</td>
<td>1</td>
<td>16569.32**</td>
<td>1.25</td>
<td>463.12**</td>
<td>7612.41**</td>
<td>0.92**</td>
<td>2426.77**</td>
<td>1654.62**</td>
</tr>
<tr>
<td>Replication/Year</td>
<td>4</td>
<td>86.17</td>
<td>1.72*</td>
<td>28.56</td>
<td>52.15</td>
<td>0.34</td>
<td>34.56</td>
<td>173.15</td>
</tr>
<tr>
<td>Genotypes</td>
<td>11</td>
<td>155.23**</td>
<td>0.84**</td>
<td>15.32**</td>
<td>97.60**</td>
<td>0.41**</td>
<td>1152.63**</td>
<td>88.69**</td>
</tr>
<tr>
<td>Genotypes*Year</td>
<td>11</td>
<td>125.34**</td>
<td>0.54</td>
<td>10.43**</td>
<td>63.79**</td>
<td>0.37**</td>
<td>518.91**</td>
<td>41.62**</td>
</tr>
<tr>
<td>Error</td>
<td>44</td>
<td>30.14</td>
<td>0.23</td>
<td>5.03</td>
<td>16.44</td>
<td>0.11</td>
<td>26.88</td>
<td>16.39</td>
</tr>
</tbody>
</table>

Table 2. Genotypic and phenotypic variance (GV and PV), heritability estimate (HE), their coefficient of variations (GCV and PCV) and expected response to selection (ERS) from combined data.

<table>
<thead>
<tr>
<th>Characters</th>
<th>P</th>
<th>G</th>
<th>PCV</th>
<th>GCV</th>
<th>H²</th>
<th>ERS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Seed yield/plant</td>
<td>14.87</td>
<td>3.98</td>
<td>6.17</td>
<td>2.49</td>
<td>18.41</td>
<td>112.45</td>
</tr>
<tr>
<td>Plant height</td>
<td>26.18</td>
<td>9.03</td>
<td>19.54</td>
<td>6.51</td>
<td>38.87</td>
<td>8.52</td>
</tr>
<tr>
<td>First pod height</td>
<td>1.54</td>
<td>0.07</td>
<td>12.41</td>
<td>7.43</td>
<td>47.65</td>
<td>6.57</td>
</tr>
<tr>
<td>Number branches/ plant</td>
<td>3.66</td>
<td>1.01</td>
<td>14.39</td>
<td>5.12</td>
<td>41.77</td>
<td>2.16</td>
</tr>
<tr>
<td>Number of pod/ plant</td>
<td>0.08</td>
<td>0.03</td>
<td>13.82</td>
<td>8.07</td>
<td>38.49</td>
<td>0.68</td>
</tr>
<tr>
<td>1000 seed weight</td>
<td>21.52</td>
<td>7.64</td>
<td>6.93</td>
<td>8.67</td>
<td>40.78</td>
<td>26.47</td>
</tr>
<tr>
<td>Number of seed/ pod</td>
<td>1.78</td>
<td>0.04</td>
<td>7.22</td>
<td>5.49</td>
<td>16.53</td>
<td>0.85</td>
</tr>
</tbody>
</table>

effect this number of branches/plant. Genotypes were significant in all characters (p>0.01), genotypes*year interactions and years were also significant in all characters except number branches/per plant. This character was not significant.

Genotypic and phenotypic variance, their coefficient of variation and broad sense heritability are showed Table 2. The influence of environment on seed yield/plant, plant height, the first pod height, the number branches/per plant, number of pod/per plant, 1000 seed weight and number of seed/per pod was estimated to be 86.13, 91.45, 56.75, 55.98, 63.27, 75.44 and 58.73% respectively. In generally phenotypic coefficient of variation was higher than genotypic variation of all characters.

According to Toker (2004), the heritability for plant height, number of stems and pods per plant, seed yield, biological yield, 100-seed weight, days to flowering and maturity were estimated as 83%, 63%, 43%, 62%, 52%, 99%, 97% and 97%, respectively. Researcher found that seed weight was the least affected trait across changing environmental conditions and followed by days to flowering and maturity.

Loss and Siddique (1997) explained that plant height, number of stems and pods per plant, biological yield, harvest index, 100-seed weight, days to flowering and maturity are the most important characters in faba bean improvement. Estimated values of the heritabilities in the study had the average yield values. Because, it didn’t show a significant deviation to the average climatic conditions for many years.

Genotypic coefficient of variation estimates for two growth seasons in all characters were higher than others. This could be due to the overestimated genetic variance in genotype*year interaction. Consequently, higher estimates of heritability in broad sense were obtained from the combined analysis. This data were supported by the result of Bakheit and Mahdy (1988). Heritability was lower for seed yield/plant and number of seed/per pod. These characters were widely affected by environmental conditions. On the other hand, first pod height, number of branch and 1000 seed weight was slightly affected by environment. Genotypes*year or genotypes*environment interactions reduced the association between phenotypic and genotypic values. Also, it may be the cause of poor performance of genotypes for selection from one environment to another, forcing plant breeders to examine genotypic adaptation (Toker, 2004).

Phenotypic and genotypic correlation coefficients among genotypes are shown Table 3. Seed yield was found to be negatively and significantly correlated with number branches/plant, number of pod/plant and 1000 seed weight at both genotypic and phenotypic levels indicating the importance of these characters for yield improvement. But, number of branch and seed yield/plant was negatively correlated with plant height. These results are supported by some researchers (Salem, 1982;
Table 3. Results of phenotypic and genotypic correlation for lens genotypes.

<table>
<thead>
<tr>
<th></th>
<th>Seed yield/plant</th>
<th>Plant height</th>
<th>First pod height</th>
<th>Number branches/plant</th>
<th>Number of pod/plant</th>
<th>1000 seed weight</th>
<th>Number of seed/pod</th>
</tr>
</thead>
<tbody>
<tr>
<td>Seed yield/plant</td>
<td>1.00</td>
<td>-0.78</td>
<td>0.43</td>
<td>0.58</td>
<td>0.82</td>
<td>0.32</td>
<td>0.77</td>
</tr>
<tr>
<td>Plant height</td>
<td></td>
<td>1.00</td>
<td>0.37</td>
<td>-0.49</td>
<td>0.17</td>
<td>-0.67</td>
<td>-0.26</td>
</tr>
<tr>
<td>First pod height</td>
<td></td>
<td></td>
<td>0.32</td>
<td>0.41</td>
<td>-0.57</td>
<td>-0.33</td>
<td></td>
</tr>
<tr>
<td>Number branches/plant</td>
<td></td>
<td></td>
<td></td>
<td>1.00</td>
<td>0.64</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Number of pod/plant</td>
<td></td>
<td></td>
<td></td>
<td>1.00</td>
<td>-0.72</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1000 seed weight</td>
<td></td>
<td></td>
<td></td>
<td>1.00</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Number of seed/pod</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1.00</td>
</tr>
</tbody>
</table>

Sindhu et al., 1985; Bakheit and Mahdy, 1988; Sharma, 1999; Bicer and Sarker, 2008; Karadavit, 2009). Higher genotypic correlation than that of corresponding phenotypic correlation has been observed by Sharma (1999). The estimates of correlation coefficient between seed yield and yield components in general genotypic correlation were higher than their corresponding phenotypic correlations. Similar results were also obtained by Younis et al. (2008). The results of correlation coefficients implied that number of branch, plant height, number of pod/plant and number of seed/pod may be considered for selection for yield improvement.

Considering seed yield and other characters of causes, genotypic correlation coefficients were partitioned by using method of path analysis to find out the direct and indirect effects of yield contributing characters towards the grain yield. Shrivastava and Sharma (1976) suggested that only direct yield components should be used for path analysis. In this study, path analysis was done to determine direct and indirect effects. Plant height, first pod height, number branches/plant, number of pod/plant, 1000 seed weight and number of seed/pod on the seed yield/plant. The number of pod/plant showed the highest direct effect (0.781) and number of seed/pod (0.509). But, indirect effect of number of pods on seed yield via number of seed/pod was shown negative (-0.215). Other indirect minimum effect occurred via number of branches/plant (-0.004). This result was supported by Bakheit and Mahdy (1988).

Younis et al. (2008) found that days to flower, plant height, number of primary branches, biological yield, harvest index and hundred seed weight had positive direct effect on seed yield. Biological yield, hundred seed weight and harvest index also had positive and highly significant genotypic and phenotypic correlation with seed yield.

Om-Vir et al. (2001) explained that positive and significant correlations of seed yield with 100-seed weight, harvest index and plant height have also been reported in lentil. Path analysis is used to determine the amount of direct and indirect effects of the causal components on the complex component (Guler et al., 2001). The inheritance mechanism is from genomes in one generation to genomes in the next ideally without any influence on the genome of the events that occur in the development of the phenome during the life history of the organism (Rose and Mileusnic, 1999). A phenome is the set of all phenotypes expressed by a cell, tissue, organ, organism, or species. While the genome is an essential element in the path from the first stage in the life of the organism to the final individual, it is largely isolated from changes from the phenome of the developed organism (Hartl and Jones, 2004).

Conclusions

The results of this study illustrate some clear phenotypic and genetic variation. Although genotypes are found in different ecological positions and have been shown to differ response ecological conditions. They have similar patterns of genetic variation and phenotypic integration (Chazdon, 1992). Correlations among traits are similar for genotypes, as are the patterns of genotypic effects demonstrated by reaction norms and Anova (Nicotra et al., 1997). This suggests that genetic variation and phenotypic integration may be due to their close phylogenetic relation and ecological distributions. In addition, the results demonstrate that the relationship between genetic variation and phenotypic is likely to be influenced as much by the type of trait under consideration (Kumari et al., 1995). The differences between genotypic and phenotypic variability for all traits was small indicating that these traits were less influenced by environment (Kumar and Dubey, 1996). Coefficients of genotypic and phenotypic variation suggest that there is good scope for yield improvement through selection for pods/plant, seeds/plant and yield/plant (Kumar and Dubey, 2001).

REFERENCES

Abdalla, M.M.F. (1976). Natural variability and selection in some local and exotic population of field bean Vicia


