Correlation analysis for morpho-physiological traits of maize (Zea mays L.)

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Abstract: The present study was conducted in the glasshouse of Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan during crop growing season 2011. It was concluded that higher heritability was recorded for all traits while higher genetic advance was recorded for fresh root-to-shoot weight ratio (49.07%), dry root weight (62.86%), dry shoot weight (47.75%), total dry weight (51.19%), dry root-to-shoot weight ratio (58.66%), chlorophyll contents (193.59%), photosynthetic rate (138.40%), sub-stomata CO2 concentration (145.28%), water use efficiency (181.28%), transpiration rate (96.29%) and stomata conductance (75.98%). It was found that significant genotypic and phenotypic correlations were shown by fresh root length, fresh shoot length, total fresh weight, dry root weight, dry shoot weight, total dry weight, photosynthetic rate, chlorophyll contents, leaf temperature and water use efficiency. Higher heritability, genetic advance and significant correlation indicated that selection on basis of these morpho-physiological traits may be helpful to improve maize grain yield.


Key words: Zea mays, heritability, genetic advance, genotypic, phenotypic, correlation

1. Introduction

Zea mays L. is the most important cereal food crop of world with supplementary importance for countries akin to Pakistan where swiftly increasing population has already outstripped the existing food provisions. Maize is the third vital cereal in Pakistan after wheat and rice. Maize contributes 5.67 % of the worth of agriculture outputs. It was grown on 1083 thousands hectares with annual production of 4271 thousands tons (Anonymous, 2011-12). Maize is used as food for human while feed for livestock and also used as industrial raw material to produce diverse types of by-products. It has highest 9.9% crude protein at early and at full bloom stages that decreases to 7% at milk stage (grain formation starting stage) and to 6% at maturity. Maize contains 72% starch, 10% protein, 4.80% oil, 9.50% fiber, 3.0% sugar, 1.70% ash, 82% endosperm, 12% embryo, 5% bran testa and 1% tip cap (Chaudhary, (1983) and Bureau of Chemistry, U.S., (2010)). The production of Pakistan is low as compared to other maize growing countries due to non-availability of resources and potential germplasm. Grain yield is related with various morphological, physiological and agronomic traits of maize. By improving these traits production of maize genotypes may be increased. Genotypic correlation provides an opportunity to a plant breeder to select genotypes on the basis of strong correlation among grain yielding contributing traits as reported by Mehdi and Ahsan (2000a); Grzesiak et al. (2007); Ali et al. (2011a, b); Ali et al. (2012); Ali et al. (2013); Jehangir et al. (2013); Anwar et al. (2013); Ali et al. (2014); Muhammad et al. (2014) and Qamar et al. (2014a,b). The present study was conducted to evaluate maize accessions for morpho-physiological seedling traits.

2. Material and methods

The current study was conceded out in the glasshouse of the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad to assess the maize genotypes for seedling traits for the period of the crop season in February 2011. The experimental material was comprising of 80 accessions including ten check varieties namely: F-121, F-130, F-140, F-143, F-113, F-111, F-105, F-148, F-146, B-303, F-128, B-306, B-303, B-313, F-117, B-316, EV-324, EV-335, EV-310, F-114, F-136, F-122, F-134, F-147, F-135, VB-06, EV-334, EV-330, EV-329, EV-338, B-314, B-305, B-321, B-326, B-308, F-118, B-304, EV-343, F-150, F-142, F-151, POP/209, BF-337, BF-248, BF-212, BF-236, EV-342, EV-323, BF-238, B-15, EV-347, F-96, B-312, EV-344, E-352, E-341, E-351, E-322, E-346, F-98, B-96, EV-340, E-349, B-121, E-336, B-11, Sh-213, Sh-139, SWL-2002, Pak-Afgoee, Islamabad W, EV-7004Q, EV-1097, Raka-Poshi, VB-51, Gold Islamabad, Sawan-3, BS-2 and POP/2007). The seeds of all accessions were sown in iron trays filled with sand following a randomized complete...
block design (RCBD) with three replications at the depth of 2.5 cm and twenty seedlings of each accession were established in each replication. The data of 5 plants was recorded for physiological traits including chlorophyll contents measured with the help of Chlorophyll Meter and leaf temperature, stomata conductance, transpiration rate, photosynthetic rate, sub-stomata CO₂ concentration, water use efficiency help of IRGA (Infrared Gas Analyzer), fresh root length, fresh shoot length, root-to-shoot length ratio, fresh root weight, fresh shoot weight, total fresh weight, fresh root-to-shoot weight ratio, dry root weight, dry shoot weight, total dry weight and dry root-to-shoot weight ratio by using meter rod (length) and electronic balance (weight). The data was statistically analyzed by using analysis of variance technique (Steel et al. 1997). The genotypic and phenotypic correlations were calculated by Kwon and Torrie (1964) technique. The genetic advance was calculated by using Falconer (1989) formula. Heritability was recorded by using Burton, (1951) technique.

2.1. Statistical Analysis Formulae:

Phenotypic and genotypic coefficients of variation were calculated according to the formula given below:

\[ GCV = \text{Genotypic coefficient of variation (%),} \]

\[ PCV = \text{Phenotypic coefficient of variation (%),} \]

\[ \bar{X} = \text{Grand mean of the trait,} \]

\[ \sigma^2 = \text{phenotypic variance,} \]

\[ \sigma^2_g = \text{genotypic variance} \]

\[ GCV = \frac{\sqrt{\sigma^2_g}}{\bar{X}} \times 100 \]

\[ PCV = \frac{\sqrt{\sigma^2_p}}{\bar{X}} \times 100 \]

Broad sense heritability for each recorded trait was calculated as a ratio of the genotypic variances to phenotypic variances. Phenotypic \( r_p \) and genotypic \( r_g \) correlation coefficient was calculated as outlined by Kwon and Torrie (1964).

\[ r_p = \frac{M_{ij}}{\sqrt{(M_{..})(M_{ij})}} \quad r_g = \frac{\text{Cov}_{gij}}{\sqrt{\text{Var}_g} \sqrt{\text{Var}_i}} \]

Where, \( r_p \) is the estimate of phenotypic correlation coefficient, \( M_{ij} \) is the mean product of genotypes for the ith and jth traits, Mii and Mjj = Variety mean squares for ith and jth traits, respectively.

\[ r_g = \text{Genotypic correlation coefficient} \]

\[ \text{Cov}_{gij} = \text{Genotypic covariance of ith and jth traits} \]

\[ \text{Var}_g = \text{Genotypic variance of ith traits} \]

\[ \text{Var}_j = \text{Genotypic variance of jth traits} \]

Standard error of genotypic correlation coefficients (SE of rg) were calculated according to Reeve (1955). Genotypic correlation coefficient was considered significant if their absolute value exceeded twice their standard error.

\[ S.E. \text{ of } r_g = \frac{1 - r_g^2}{\sqrt{2}} \frac{\sqrt{\text{Var}_g \text{Var}_i}}{h_i^2 h_j^2} \]

Where,

\[ r_g^2 = \text{The genotypic correlation coefficient between the traits I and j,} \]

\[ h_i^2 = \text{The heritability of ith trait,} \]

\[ h_j^2 = \text{The heritability of jth trait.} \]

The estimates of heritability and genotypic correlation coefficient were considered significant if their absolute value exceeded twice of their standard error. Phenotypic correlation coefficients were tested using t-test (Steel and Torrie, 1997) as given below.

\[ t = \frac{r_p}{\sqrt{(1 - r_p^2) / n - 2}} \]

Where, \( r \) is the phenotypic correlation coefficient, n-2 = correlation error degree of freedom

Genetic advance (GA) was calculated by the following formula.

\[ \text{GA} = \sigma_p x h_i^2 x i \]

Where, \( \sigma_p \) = the phenotypic standard deviation, \( h_i^2 \) = Estimate of broad sense heritability, i = constant value (1.755) that reflects selection intensity (10%)}

3. Results and discussions

It was persuaded from table 1 that heritability was found between the ranges of 82.35% to 100%.

\[ \text{Table 1: heritability and genetic advance for various morpho-physiological traits of maize} \]

<table>
<thead>
<tr>
<th>Traits</th>
<th>Heritability (h²_b, %)</th>
<th>Genetic advance %</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fresh root length</td>
<td>99.88</td>
<td>41.01</td>
</tr>
<tr>
<td>Fresh shoot length</td>
<td>99.19</td>
<td>28.95</td>
</tr>
<tr>
<td>Fresh Root-to-shoot length ratio</td>
<td>99.49</td>
<td>41.67</td>
</tr>
<tr>
<td>Fresh root weight</td>
<td>96.67</td>
<td>36.10</td>
</tr>
<tr>
<td>Fresh shoot weight</td>
<td>96.67</td>
<td>36.10</td>
</tr>
<tr>
<td>Total fresh weight</td>
<td>98.63</td>
<td>30.59</td>
</tr>
<tr>
<td>Fresh root-to-shoot weight ratio</td>
<td>98.51</td>
<td>49.07</td>
</tr>
<tr>
<td>Dry root weight</td>
<td>97.07</td>
<td>62.86</td>
</tr>
<tr>
<td>Dry shoot weight</td>
<td>92.31</td>
<td>47.75</td>
</tr>
<tr>
<td>Total dry weight</td>
<td>97.47</td>
<td>51.19</td>
</tr>
<tr>
<td>Dry root-to-shoot weight ratio</td>
<td>98.73</td>
<td>58.66</td>
</tr>
<tr>
<td>Chlorophyll contents</td>
<td>99.99</td>
<td>193.59</td>
</tr>
<tr>
<td>Photosynthetic rate</td>
<td>100.00</td>
<td>138.40</td>
</tr>
<tr>
<td>Stomata conductance</td>
<td>82.35</td>
<td>57.98</td>
</tr>
<tr>
<td>Transpiration rate</td>
<td>99.30</td>
<td>96.29</td>
</tr>
<tr>
<td>Sub-stomata CO₂ concentration</td>
<td>99.99</td>
<td>145.28</td>
</tr>
<tr>
<td>Water use efficiency</td>
<td>98.70</td>
<td>181.28</td>
</tr>
<tr>
<td>Leaf temperature</td>
<td>99.63</td>
<td>9.88</td>
</tr>
</tbody>
</table>

Higher heritability was reported for photosynthetic rate (100%) followed by chlorophyll contents (99.99%) while lower for dry root/shoot weight ratio (88.73%) followed by stomata conductance (82.35%). Higher genetic advance was found for chlorophyll contents (193.59%) followed by water use efficiency (181.28%) and sub-stomata CO₂ concentration (145.28%) while lower for fresh shoot length (28.95%) followed by total fresh weight.
was positively and significantly correlated with fresh and dry shoot weight, dry root weight, total dry weight showed positive and significant genotypic and phenotypic selection of higher yielding maize genotypes may be helpful to improve maize grain yield (Afarinesh et al. (2005); Ali et al. (2011a); Ali et al. (2011b); Fang et al. (2011) and Ali et al. (2012) and Ahsan et al. (2013)).

It was suggested from tables 2 and 2a that positive and significant genotypic and phenotypic correlation of fresh root length was found with fresh shoot length, fresh root/shoot length ratio, fresh and dry root and shoot weight, total fresh and dry weight and photosynthetic rate. Significant correlations with fresh and dry root and shoot weight indicated that selection on the basis of fresh root length for drought condition may be helpful to improve maize grain yield (Afarinesh et al. (2005); Ali et al. (2011a); Ali et al. (2011b); Fang et al. (2011) and Ali et al. (2012)). Fresh shoot length showed positive and significant genotypic and phenotypic correlation with fresh shoot length, fresh and dry shoot weight, dry root weight, total dry weight and leaf temperature while fresh root/shoot length ratio was positively and significantly correlated with fresh root length, sub-stomata CO2 concentration and water use efficiency at genotypic and phenotypic levels. Similar results were obtained by Ali et al. (2011a); Ali et al. (2011b); Fang et al. (2011) and Ali et al. (2012). Fresh root weight was positively and significantly correlated with fresh root length, total fresh and dry weight, photosynthetic rate, fresh root/shoot weight ratio, chlorophyll contents, sub-stomata CO2 concentration and water use efficiency at genotypic and phenotypic levels while dry root weight was correlated with fresh root and shoot length, fresh root and shoot weight, dry shoot weight, total fresh and dry weight, photosynthetic rate, dry root/shoot weight ratio and chlorophyll contents (Afarinesh et al. (2005); Fang et al. (2011) and Ali et al. (2012)).

### Table 2: Genotypic correlations of various morphological and physiological traits of maize seedlings

<table>
<thead>
<tr>
<th>Traits</th>
<th>FRL</th>
<th>FSL</th>
<th>RSLR</th>
<th>FRW</th>
<th>TFW</th>
<th>FRSWR</th>
<th>DRSWR</th>
<th>TDW</th>
<th>DSW</th>
<th>TFW/DRW</th>
<th>FRL/FSW</th>
<th>FRL/FRW</th>
<th>LT</th>
<th>Chl. C</th>
<th>gs</th>
<th>E</th>
<th>Ci</th>
<th>WUE</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1.0000</td>
<td>0.3948**</td>
<td>0.2868**</td>
<td>0.3994**</td>
<td>0.4249**</td>
<td>-0.0722</td>
<td>0.3080**</td>
<td>0.3027**</td>
<td>0.0781</td>
<td>0.0733</td>
<td>0.0414*</td>
<td>0.3766*</td>
<td>0.2561**</td>
<td>0.0200*</td>
<td>0.4846**</td>
<td>0.3212**</td>
<td>0.0912</td>
<td></td>
</tr>
</tbody>
</table>

** = Significance at 5% level, * = Significance at 1% level

FRL = Fresh root length, FSL = Fresh shoot length, RSLR = Root-to-shoot length ratio, FRW = Fresh root weight, FSW = Fresh shoot weight, TFW = Total fresh weight (Fresh biomass per seedling), FRSWR = Fresh root-to-shoot weight ratio, DRSWR = Dry root-to-shoot weight ratio, A = Photosynthetic rate, LT = Leaf temperature, Chl. C = Chlorophyll contents, gs = Stomata conductance, E = Transpiration rate, Ci = Sub-stomata CO2 concentration, WUE = Water use efficiency.

Fresh shoot weight was positively and significantly correlated with fresh root and shoot length, total fresh and dry weight, dry root and shoot weight, photosynthetic rate and sub-stomata CO2 concentration, can be made to improve genetic potential of maize genotypes. Similar results were reported by Mehdi and Ahsan (2000); Afarinesh et al. (2005); Ali et al. (2011a); Ali et al. (2011b); Fang et al. (2011) and Ali et al. (2012) and Ahsan et al. (2013).
while dry shoot weight was correlated with fresh root length, fresh shoot length, root-to-shoot length ratio, fresh root weight, fresh shoot weight, total fresh weight, fresh root-to-shoot weight ratio, dry root weight, dry shoot weight, total dry weight and dry root-to-shoot weight ratio, stomata conductance, transpiration rate, photosynthetic rate and water use efficiency. Significant correlations suggested that photosynthetic rate was higher that leads towards the accumulation of organic compounds in the plant body and helped to improve grain and fodder yield of maize. Similar results were obtained by Afarinesh et al. (2005); Grzesiak et al. (2007); Ali et al. (2011a); Ali et al. (2011b); Fang et al. (2011); Ali et al. (2012) and Ali et al. (2014). Fresh root-to-shoot weight ratio was positively and significantly correlated with fresh root weight, dry root-to-shoot weight ratio, photosynthetic rate and water use efficiency while was positive and significant correlation of dry root-to-shoot weight ratio was found with fresh root-to-shoot weight ratio, dry root weight, total dry weight, leaf temperature, chlorophyll contents and water use efficiency at genotypic and phenotypic level. Significant positive genotypic and phenotypic correlation of total fresh weight was found with fresh root length, fresh and dry root and shoot weight, total dry weight, sub-stomata CO\(_2\) concentration and chlorophyll contents while total dry weight was positively and significantly correlated with fresh root length, leaf temperature, photosynthetic rate, dry root-to-shoot weight ratio, fresh and dry root and shoot weight, total dry weight, sub-stomata CO\(_2\) concentration and chlorophyll contents. Similar results were obtained by Mehdi and Ahsan (2000); Ali et al. (2011a); Ali et al. (2011b); Fang et al. (2011); Ali et al. (2012) and Ali et al. (2014). Photosynthetic rate was positively and significantly correlated with fresh root length, fresh root-to-shoot weight ratio, fresh and dry root and shoot weight, total dry weight, sub-stomata CO\(_2\) concentration and chlorophyll contents while fresh root weight, stomata conductance, transpiration rate, photosynthetic rate, leaf temperature and water use efficiency showed a significant positive genotypic and phenotypic correlation with fresh root-to-shoot length ratio, fresh root weight, stomata conductance, transpiration rate, sub-stomata CO\(_2\) concentration, total fresh and dry weight, fresh and dry root-to-shoot weight ratio and photosynthetic rate. Similar results were obtained by Mehdi and Ahsan (2000); Ali et al. (2011a); Ali et al. (2011b); Fang et al. (2011); Ali et al. (2012); Ali et al. (2013) and Ali et al. (2014).

**Conclusion:**
It was concluded from above study that significant genotypic and phenotypic correlations were shown by fresh root length, fresh shoot length, fresh root weight, fresh shoot weight, total fresh weight, dry root weight, dry shoot weight, total dry weight, photosynthetic rate, chlorophyll contents, leaf temperature and water use efficiency. Higher heritability, genetic advance and significant correlation indicated that selection on basis of these morpho-physiological traits may be helpful to improve maize grain yield.

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