Studies of genetic variability and correlation among morphological traits of maize (Zea mays L.) at seedling stage.

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Abstract:
The present investigations aimed to evaluate the genetic diversity and character association in twenty maize accessions at seedling stage. The experiment was laid out in completely randomized design and correlation analysis both at genotypic and phenotypic levels were practiced. Heritability estimates were used to determine the selection criteria under drought stress conditions. The higher magnitude of heritability and genetic advance were recorded for fresh shoot weight, fresh and dry biomass of seedlings. The significant genotypic and phenotypic correlations were found between root and shoot length, fresh and dry biomass of the seedlings. However, fresh shoot weight had positive association with fresh biomass of seedlings and dry root weight with dry biomass of seedlings. It was suggested that traits like fresh and dry biomass of seedling, root and shoot length may be used as selection criteria to obtain high yielding maize genotypes under normal and drought stress conditions.

Key words: genotype, drought, heritability, genetic advance, inbred lines.

1. Introduction

Maize is one of the most important cereal crop in the world after wheat and rice. It is grown in Pakistan as a major cash crop under the area of 1083 thousand hectares with production of 3990 thousand tones [3]. Maize is dual purpose crop it is used as a food for human and feed for livestock. It is also used as a raw material in medicine, food and textile industries. Maize has high nutritive value as it contains 72 % starch, 10 % protein, 4.80 % oil, 8.50 % fiber, 3.0 % sugar, and 1.70 % ash [4].

The intelligent exploitation of maize inbred lines for genetic analyses requires a detailed knowledge of genetic and historical relationships between these lines and an understanding of the partitioning of genetic diversity among them. For example, developmental mutants of maize can exhibit strikingly different phenotypes when assayed in the genetic backgrounds of different maize inbred lines [8]. Knowledge of the relationships among lines would help to identify a set of inbred lines that have maximal diversity for the analysis of the effects of genetic background. Single-nucleotide polymorphism discovery in maize can be optimized by selecting a set of lines that capture the maximum number of alleles or haplotypes [13]. The present study was conducted to evaluate various maize genotypes for seedling traits.
seedling, dry root weight, dry shoot weight and dry biomass of seedlings.

**Table 1:** The detail of experimental material

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Status</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>B-316</td>
<td>Inbred line</td>
<td>PBG, UAF</td>
</tr>
<tr>
<td>F-96</td>
<td>Inbred line</td>
<td>PBG, UAF</td>
</tr>
<tr>
<td>F-113</td>
<td>Inbred line</td>
<td>PBG, UAF</td>
</tr>
<tr>
<td>F-111</td>
<td>Inbred line</td>
<td>PBG, UAF</td>
</tr>
<tr>
<td>F-114</td>
<td>Inbred line</td>
<td>PBG, UAF</td>
</tr>
<tr>
<td>EV-340</td>
<td>Inbred line</td>
<td>PBG, UAF</td>
</tr>
<tr>
<td>EV-347</td>
<td>Inbred line</td>
<td>PBG, UAF</td>
</tr>
<tr>
<td>B-322</td>
<td>Inbred line</td>
<td>PBG, UAF</td>
</tr>
<tr>
<td>F-146</td>
<td>Inbred line</td>
<td>PBG, UAF</td>
</tr>
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<td>EV-323</td>
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<td>PBG, UAF</td>
</tr>
<tr>
<td>F-140</td>
<td>Inbred line</td>
<td>PBG, UAF</td>
</tr>
<tr>
<td>F-143</td>
<td>Inbred line</td>
<td>PBG, UAF</td>
</tr>
<tr>
<td>F-130</td>
<td>Inbred line</td>
<td>PBG, UAF</td>
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<tr>
<td>F-117</td>
<td>Inbred line</td>
<td>PBG, UAF</td>
</tr>
<tr>
<td>B-327</td>
<td>Inbred line</td>
<td>PBG, UAF</td>
</tr>
<tr>
<td>Sh-139</td>
<td>Inbred line</td>
<td>PBG, UAF</td>
</tr>
<tr>
<td>EV-1097Q</td>
<td>Variety</td>
<td>NARC</td>
</tr>
<tr>
<td>Pop/209</td>
<td>Variety</td>
<td>NARC</td>
</tr>
<tr>
<td>Raka-poshi</td>
<td>Variety</td>
<td>NARC</td>
</tr>
</tbody>
</table>

2.1. Statistical Analysis

The data were subjected to analysis of variance [12]. The genotypic and phenotypic correlations were calculated by Kwon and Torrie technique [7]. The genetic advance was calculated by using Falconer formula [5].

2.2. Statistical Analysis Formulae:

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

\[
GCV = \frac{\sigma_g}{\bar{X}} \times 100
\]

\[
PCV = \frac{\sigma_P}{\bar{X}} \times 100
\]

Where,

GCV = Genotypic coefficient of variation (%)

PCV = Phenotypic coefficient of variation (%)

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

\[
\sigma^2_P = \text{phenotypic variance}, \quad \sigma^2_g = \text{genotypic variance}
\]

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 [7].

\[
r_p = \frac{M_{ij}}{\sqrt{(M_{ii})(M_{jj})}}
\]

Where,

\[r_p = \text{the estimate of phenotypic correlation coefficient}
\]

\[M_{ij} = \text{the mean product of genotypes for the } i^{th} \text{ and } j^{th} \text{ traits}
\]

\[M_{ii} \text{ and } M_{jj} = \text{ Variety mean squares for } i^{th} \text{ and } j^{th} \text{ traits, respectively.}
\]

\[
r_g = \frac{\text{Cov}_{ij}}{\sqrt{(\text{Var}_i)(\text{Var}_j)}}
\]

Where,

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

\[\text{Cov}_{ij} = \text{Genotypic covariance of } i^{th} \text{ and } j^{th} \text{ traits}
\]

\[\text{Var}_i = \text{Genotypic variance of } i^{th} \text{ traits}
\]

\[\text{Var}_j = \text{Genotypic variance of } j^{th} \text{ traits}
\]

Standard error of genotypic correlation coefficients (SE of rug) was calculated according to Reeve [9]. The Genotypic correlation coefficient was considered significant if their absolute value exceeded twice their standard error.

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

Where,

\[r^2_g = \text{The genotypic correlation coefficient between the traits } i \text{ and } j.
\]

\[h_i^2 = \text{The heritability of } i^{th} \text{ trait.}
\]

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

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 according to Steel and Torrie [12] as given below.

\[
t = \frac{r}{\sqrt{(1 - r^2) / n - 2}}
\]
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Where,
\[ r = \text{the phenotypic correlation coefficient, } n-2 = \text{correlation error degree of freedom} \]

Genetic advance (GA) was calculated by the following formula [5].
\[ \text{GA} = \sigma_p \times h^2 \times i \]

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

3. Results and discussion:

It is clear from Table 2 that higher genotypic and phenotypic variances were recorded for fresh biomass of seedling (80.793, 81.471) followed by fresh shoot weight (43.450, 44.241) respectively. The higher genotypic and phenotypic coefficient of variation was recorded for dry root weight (42.419, 43.911) followed by dry shoot weight (47.271, 40.442) respectively. The higher environmental variance and coefficient of variance were recorded for fresh root weight (8.140, 7.176) respectively. Similar results were found by [10, 11& 2]. The highest estimates of heritability and genetic advance were recorded for fresh and dry shoot weight, fresh and dry biomass of seedlings. Selection of higher yielding maize genotypes may be helpful on the basis of higher genetic advance and heritability.

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Figure 3: Fresh shoot weight (FSW) and Dry shoot weight (DSW) of maize seedlings

It is clear from Figure-3 that higher fresh shoot weight was recorded for B-322, B-327 and B-316 while lower for F-111 and F-130 but dry shoot weight was for F-140, EV-323, B-316 and F-114 while lower for F-111 and F-130. The higher values of fresh and dry shoot weights indicated that lines B-316 may be used to develop drought tolerant genotype [1&2].

Figure 4: Fresh biomass of (FB) and Dry biomass of (DB) of maize seedlings

It is clear from Figure-4 that higher fresh biomass of seedlings were recorded for B-327, Sh-139, B-316 and F-143 while lower for F-96 and F-130 but higher dry biomass of seedlings were recorded for F-140, B-327 and F-117 while lower for F-111, F-113 and F-114. The higher values of fresh and dry biomass of seedlings indicated that line B-327 may be used for developing drought tolerance genotypes [1&2].

3.1. Correlation:

It is clear from Table 3 that high and positive genotypic correlation of fresh root length was found with fresh shoot length, dry root and shoot weight. The high and significant phenotypic correlation was found for fresh shoot length, fresh biomass of seedling and dry root weight while negative and significant phenotypic correlation was found for dry shoot weight. Similar results were described by [2]. A positive and significant genotypic correlation was found between fresh shoot length and fresh root weight, fresh shoot weight and dry root weight but negative and significant genotypic correlation was found for dry biomass of seedlings. A positive phenotypic correlation was found between fresh shoot length and fresh shoot weight. Similar results were found by [6, 14 & 15]. Fresh root weight was positive and significantly correlated with fresh and dry biomass of seedling and dry shoot weight both at genotypic and phenotypic levels while positively with fresh shoot length at the genotypic level but negatively at the phenotypic level. Fresh shoot weight was positive and significantly correlated with fresh root and shoot length and fresh biomass of seedling at
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Genotypic and phenotypic levels. Fresh biomass of seedling was highly and significantly correlated with fresh and dry root weight, shoot weight and dry biomass of seedling both at genotypic and phenotypic levels. The strong genotypic correlation of fresh and dry biomass indicated that selection on the basis of fresh and dry weight may be useful to improve the yield of maize genotypes. Similar results were reported by [11, 2]. Dry root and shoot weight were significantly correlated with each other and with fresh and dry biomass of seedling at genotypic and phenotypic levels. Dry biomass of seedling was highly and significantly correlated with fresh root weight dry root and shoot weight at genotypic and phenotypic levels. The significant genotypic correlations indicated that selection can be made on the basis of these traits [11, 10&2].

Table 2: Estimates of various genetic components for maize genotypes

<table>
<thead>
<tr>
<th>Traits</th>
<th>GCV%</th>
<th>PCV%</th>
<th>GV</th>
<th>PV</th>
<th>ECV%</th>
<th>EV</th>
<th>GA</th>
<th>h²bs</th>
</tr>
</thead>
<tbody>
<tr>
<td>FRL</td>
<td>31.861</td>
<td>29.431</td>
<td>3.451</td>
<td>4.391</td>
<td>0.940</td>
<td>1.319</td>
<td>2.890</td>
<td>78.60</td>
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<tr>
<td>FSL</td>
<td>39.349</td>
<td>38.478</td>
<td>7.910</td>
<td>8.456</td>
<td>0.546</td>
<td>2.322</td>
<td>4.774</td>
<td>93.50</td>
</tr>
<tr>
<td>FSW</td>
<td>29.239</td>
<td>28.321</td>
<td>43.450</td>
<td>44.241</td>
<td>0.791</td>
<td>0.898</td>
<td>11.464</td>
<td>98.20</td>
</tr>
<tr>
<td>FB</td>
<td>37.424</td>
<td>38.988</td>
<td>80.793</td>
<td>81.471</td>
<td>0.678</td>
<td>1.769</td>
<td>15.709</td>
<td>99.20</td>
</tr>
<tr>
<td>DRW</td>
<td>42.419</td>
<td>43.911</td>
<td>6.518</td>
<td>7.213</td>
<td>0.695</td>
<td>2.176</td>
<td>4.259</td>
<td>90.40</td>
</tr>
<tr>
<td>DSW</td>
<td>47.271</td>
<td>40.442</td>
<td>26.729</td>
<td>28.471</td>
<td>1.742</td>
<td>3.769</td>
<td>8.791</td>
<td>93.90</td>
</tr>
<tr>
<td>DB</td>
<td>21.899</td>
<td>20.781</td>
<td>38.437</td>
<td>39.271</td>
<td>0.834</td>
<td>5.631</td>
<td>10.764</td>
<td>97.90</td>
</tr>
</tbody>
</table>

GV = Genotypic variance, PV = Phenotypic variance, EV = Environmental Variance, PCV = Phenotypic coefficient of variance, GCV = Genotypic coefficient of variance, ECV = Environmental coefficient of variance, GA = Genetic advance, h²bs = Broad sense heritability.

Table 3: Genotypic and phenotypic correlation for various morphological traits of maize seedlings

<table>
<thead>
<tr>
<th>Traits</th>
<th>R</th>
<th>FSL</th>
<th>FRW</th>
<th>FSW</th>
<th>FB</th>
<th>DRW</th>
<th>DSW</th>
<th>DB</th>
</tr>
</thead>
<tbody>
<tr>
<td>FRL</td>
<td>G</td>
<td>0.7512**</td>
<td>0.0311</td>
<td>0.4579*</td>
<td>-0.0641</td>
<td>0.6398**</td>
<td>0.6647**</td>
<td>-0.0112</td>
</tr>
<tr>
<td>P</td>
<td>0.6213**</td>
<td>0.1213</td>
<td>0.0943*</td>
<td>0.2139**</td>
<td>0.6121**</td>
<td>-0.3411**</td>
<td>0.0449</td>
<td></td>
</tr>
<tr>
<td>FSL</td>
<td>G</td>
<td>0.4311*</td>
<td>-0.2179**</td>
<td>0.4421**</td>
<td>-0.0129</td>
<td>0.3528**</td>
<td>0.0292</td>
<td>-0.2176*</td>
</tr>
<tr>
<td>P</td>
<td>-0.2179**</td>
<td>0.3701*</td>
<td>-0.2101</td>
<td>0.1732</td>
<td>0.4471**</td>
<td>0.2911*</td>
<td></td>
<td></td>
</tr>
<tr>
<td>FRW</td>
<td>G</td>
<td>-0.0211</td>
<td>0.4319**</td>
<td>-0.1762</td>
<td>0.2123*</td>
<td>0.2921*</td>
<td></td>
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<tr>
<td>P</td>
<td>0.1101</td>
<td>0.4421**</td>
<td>-0.2711*</td>
<td>0.2679**</td>
<td>0.3129**</td>
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<tr>
<td>FSW</td>
<td>G</td>
<td>0.6671**</td>
<td>0.0217</td>
<td>0.0044</td>
<td>0.0121</td>
<td></td>
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</tr>
<tr>
<td>P</td>
<td>0.6319**</td>
<td>0.0217</td>
<td>-0.0023</td>
<td>0.0203</td>
<td>0.0373</td>
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</tr>
<tr>
<td>FB</td>
<td>G</td>
<td>0.3172*</td>
<td>0.4144**</td>
<td>0.4144**</td>
<td>0.9127**</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>P</td>
<td>0.3315**</td>
<td>0.4324**</td>
<td>0.9087**</td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>DRW</td>
<td>G</td>
<td>0.4811**</td>
<td>0.8921**</td>
<td></td>
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</tr>
<tr>
<td>P</td>
<td>0.4789**</td>
<td>0.8131**</td>
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<tr>
<td>DSW</td>
<td>G</td>
<td>0.1443*</td>
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<td></td>
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</tr>
<tr>
<td>P</td>
<td>0.2376*</td>
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</tr>
</tbody>
</table>

** = Highly significant, * = Significant, DRW = Dry root weight, DSW = Dry shoot weight, FRL = Fresh root length, FSL = Fresh shoot length, FB = Fresh biomass of seedling, DB = Dry biomass of seedling, FSW = Fresh biomass of seedling and dry root weight with dry biomass of seedlings. It was suggested that fresh and dry biomass of seedling, root and shoot length may be helpful to select higher yielding maize genotypes for normal and drought stress conditions.

4. Conclusion

It was concluded from the present study that the strong genotypic and phenotypic correlation was found between root and shoot length, fresh and dry biomass of seedling, fresh shoot weight and fresh biomass of seedling and dry root weight with dry biomass of seedlings. It was suggested that fresh and dry biomass of seedling, root and shoot length may be helpful to select higher yielding maize genotypes for normal and drought stress conditions.

5. References

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