Assessment of major determinants of phenotypic variation for a transplanting seedling

Muhammad Abid Khan¹, Fida Muhammad Abbasi*, Habib Ahmad², Inayat Ur Rahman¹, Hamid Ali³

¹Department of Botany, Hazara University, Mansehra, KP, Pakistan
²Department of Genetics, Hazara University, Mansehra, KP, Pakistan

Key words: Rice, Basmati, Seedling, Genotype, Determinant.

http://dx.doi.org/10.12692/ijb/5.9.197-205 Article published on November 10, 2014

Abstract

Selections of desirable traits and exploration and utilization of genetic diversity have always been used as an essential tool in plant breeding. The present study was an attempt to investigate general and specific determinants of phenotypic variation among a data set of seedling characters and genotypes efficiency for a transplanting seedling. For this purpose 48 advance genotypes with three control cultivars Basmati-385, JP5 and Kangnai29 were grown in a replicated field trial and evaluated for 16 traits that were reported earlier as contributing traits of seedling vigor. ANOVA showed high CV% for SRFW, SRDW, WC, SSFW, SSDW, SFW, SDW, while lowest was found for SH followed by SLL. PCA extracted two components with 66.75% of variability. The PC1 comprised of SFW, SDW, SSFW, SSDW, SRFW, SRDW, WC as positive meaningful loading while one DG as negative one with overall 38.69% of variability. The PC2 carried 5 significant loadings i.e. SVI, SH, SLL, SLW and SLA with 28.068% of variation. The meaningful traits of PC1 and PC2 were the sub-derived variables of SH and SFW respectively. These findings pave a criterion for selection which will enable one to choose a best genotype at seedling that withstands lodging and having the ability to carry large and heavy panicle at adult stage. Apart from these, the less variability for SH and high variation in SFW indicated the capability of elite lines. The elite lines 97-m, 111-m, 161-s, Abbasi2, 105-m, 86-L, 29-s, 136-L, 158-2-L, 130-s, 14-L, 10-s, 127-m, 26-L, 179-s, 19-L, 79-L, 184-s, 07-m, 17-L, 109-L, 186-m, 12-L, 52-L, M2, 69-m and 07-m were more vigorous and withstand disease attack due to its high seedling biomass and short stature that one could effectively use in further improvement of rice.

*Corresponding Author: Fida Muhammad Abbasi ☐ drfidaabbasi6@gmail.com
Introduction

In Pakistan, rice is grown on about 10% of total cropland area of all the four provinces; with Punjab and Sindh as major producers. Rice is a staple food and a good source of income for the country. Pakistan is one of the major rice exporter countries. Besides key importance of rice in the national economy, the regular paddy yield is 3000 kg/ha which is much lesser than the other rice producing countries of the world.

Seedling vigor plays an important role in the successful crop performance. Under direct seeding varieties with high seedling vigor are required to better compete against weed (Mackill and Redona, 1997). Varieties possessing high seed and seedling vigor are, therefore, attaining the maximum production through this technique because the seedling that emerge earlier would have an advantage over the later emerging one, in that they will be stronger, will be able to compete well with weeds and withstand the pest attack. Seed and seedling vigor is genetically controlled and modified by the environment (Perry, 1972) and it is possible to incorporate this trait in high yielding varieties (Seshu & Krishnasamy, 1987).

Isley, 1957 defined vigor as “the sum total of all seed attributes which favor stand establishment under favorable field condition”. Delouche and Caldwell 1960 modified Isley's definition stating “sum total of all seed attributes which favor rapid and uniform stand establishment in the field”. Woodstock 1969 stated that “vigor is the condition of active good health and natural robustness in the seeds, which upon plant permits germination to process rapidly under a wider range of experimental conditions”. McDenial 1973 describes seedling vigor as the superior performance of seeds after plant compared to the seed of same genotype or other genotype under different environmental conditions. During the 18th international seed testing congress, a comprehensive definition of seedling vigor was approved which state that “vigor is the sum of those properties of seed that determine the potential level of activities and performance of seed during germination and seedling emergence” Perry, 1978. According to McDonald 1975 vigor is comprised of those properties which determine the potential for rapid and uniform emergence and development of normal seedlings under a wider range of field conditions. Matthews 1995 describe that “seedling vigor is not an absolute term but a relative measure”.

Numerous investigations on the determination of rice architectural designing at adult stage and also much previous research studies on rice seedling characterization are filed. Many researchers used various traits for describing seedling vigor in rice as well as in other crops. Among these traits seedling height was used as primary criterion for evaluation, Seedling dry weight was calculated by Ching et al 1974 in barley, speed of germination by Copeland 2001, germination rate by Krishnsamy and Ramaswamy 1987 in sorghum, leaf length by Rangel et al 2006, seedling height, seedling fresh and dry weight and water content by Abdel-khaliq et al 2010 determining genotype x environment interaction, rate of germination index, seedling shoot weight and seedling dry weight by Akram et al 2001. Herdt 1991 identified “seedling vigor problem as key research priority”. Glewen and vogal 1984 stated that seedling vigor is the combination of all component of seedling growth”.

Association among various traits is an important and useful feature which helps to identify different traits that can potentially be focused for further consideration and crop improvement. However, the previous studies poorly understood no instance of measures among correlated traits and their dependence on some major hidden components which are best explained by more less variables that could efficiently be utilize in robust genotype (ideotype) selection at seedling. Therefore, the present study was an attempt to investigate general and specific determinants of seedling phenotypic variation among a data set of seedling characters and genotypes efficiency at early stages.
Materials and methods

The experiment was conducted at Hazara University, Mansehra, Pakistan. In this experiment rice forty eight advance lines of different crossing background along with three control varieties Bas-385, JP5 and Kangnai29 were used. The seeds of each genotype were treated at 50C before testing for four days to remove remaining dormancy (Datta et al 1997). Later the seeds were subjected to seedling vigor characterization.

Germination %age

Three set of 25 seeds were dipped in broth of bacterial isolates for ten minutes and then placed on filter paper in petri dishes. To keep the filter papers moist we added 3ml of distils water to each petri dish. The petri dishes were then placed in growth germinator at 50C. After seven days germinated seeds were counted, the radical that showed 2 mm of length was counted as germinated. Germination percentage was calculated using following formula.

\[
\text{Germination percentage} = \frac{\text{No of seeds germinated}}{\text{No of seeds sown}} \times 100
\]

Kim et al. (1999) found more vigorous stem elongation and higher tillering production of 10-day old seedlings compared to 15- and 40-day old seedlings. Similarly, (Khatun 1995) observed that the tiller ability was higher among 30-day old seedlings transplanted in aman season than others. However, in Pakistan, almost all the rice crop is established by transplanting 25-30 days old seedlings from nursery in the puddled field manually. Therefore, in Pakistan it is not more critical for seedling to germinate early, like ones need to compete against weeds in direct seeding. That’s why we mainly focused on the traits after germination that will strive better after transplanting and will determine the blueprints of rice improvement at early stages.

To characterize 25 days old seedling for morphological and physiological replies, seedling of various elite lines were grown along with conventional check varieties in randomized complete block design was followed with three replications (Fig: 1). Sixteen important traits linked to seedling vigor and relative ideotype breeding, were evaluated. These traits comprised rate of germination index (RGI), days to five leaves (DFL), days to initiation of tillering (DIT), seedling vigor index (SVI), seedling height (SH), seedling leaf length (SLL), seedling leaf width (SLW), seedling leaf area (SLA), seedling fresh weight (SFW), seedling dry weight (SDW), seedling shoot fresh weight (SSFW), seedling root fresh weight (SRFW), seedling shoot dry weight (SSDW), seedling root dry weight (SRDW) and water content (WC). The seedling vigor index was calculated adopting the method suggested by Abdul-Baki and Anderson (1973) and expressed in whole number.

\[
\text{Vigor Index} = \text{Germination percentage} \times \text{Seedling length}
\]

Statistical analysis

The data were subjected to analysis of variance, which was subsequently followed by LSD test. Correlation was carried out using Pearson correlation method. We also performed principal component analysis in order to understand the combination of variables which can best explain the group of associated trait using STATISTICA 7 and SPSS.V16.

Results

Selection of desirable traits and active physiological functions enhance the potentiality and high yield performance of a genotype. Determinations of these characteristics are important for ideotype breeding. All the elite lines along with the conventional check varieties were characterized for seedling vigor.

Correlation among seedling different traits

In the present investigation significant correlation was calculated for each trait because morphological associated traits provide a proficent selection criterion for a crop improvement. DG revealed high significant correlation at p<0.01 level with DFL and DIT while highly non-significant to SFW, SSFW, SRFW, SDW, SSDW, SRDW and WC which showed that these traits are badly affected by interruption to
germination. The DG is also non-significant to SLW at p<0.05 which means that it is dependent to some extent on germination. Similarly, DFL were high significant to DIT while non-significant to SFW, SSFW, SRFW and WC. DIT showed negative association with SRFW while highly correlated with DFL. RGI revealed no significant correlation while SVI indicated high correlation with SH, SLL, SLW, SLA, SFW, SSFW, SRFW, SSDW, SRDW and WC.

Table 1. Correlation among seedling different traits.

<table>
<thead>
<tr>
<th>Traits</th>
<th>DG</th>
<th>DFL</th>
<th>DIT</th>
<th>RGI</th>
<th>SVI</th>
<th>SH</th>
<th>SLL</th>
<th>SLW</th>
<th>SFW</th>
<th>SDW</th>
<th>SSFW</th>
<th>SRFW</th>
<th>SSDW</th>
<th>SRDW</th>
</tr>
</thead>
<tbody>
<tr>
<td>DFL</td>
<td>.545**</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DIT</td>
<td>- .53**</td>
<td>.979**</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>RGI</td>
<td>-.125</td>
<td>-.134</td>
<td>.122</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SVI</td>
<td>-.186</td>
<td>-.205</td>
<td>-.102</td>
<td>.041</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SH</td>
<td>-.131</td>
<td>-.156</td>
<td>-.143</td>
<td>-.183</td>
<td>.945**</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SLL</td>
<td>-.106</td>
<td>-.208</td>
<td>-.201</td>
<td>-.129</td>
<td>-.934**</td>
<td>.951**</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SLW</td>
<td>-.341**</td>
<td>-.256</td>
<td>-.280</td>
<td>.027</td>
<td>.629**</td>
<td>.660**</td>
<td>.544**</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SFW</td>
<td>-.522**</td>
<td>-.278**</td>
<td>-.253</td>
<td>-.017</td>
<td>.556**</td>
<td>.59**</td>
<td>.470**</td>
<td>-.444**</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SDW</td>
<td>-.476**</td>
<td>-.249</td>
<td>-.222</td>
<td>-.056</td>
<td>.579**</td>
<td>.541**</td>
<td>.496**</td>
<td>-.574**</td>
<td>.967**</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SSFW</td>
<td>-.502**</td>
<td>-.280**</td>
<td>-.253</td>
<td>-.031</td>
<td>.570**</td>
<td>.542**</td>
<td>.494**</td>
<td>-.573**</td>
<td>.994**</td>
<td>-.961**</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SRFW</td>
<td>-.541**</td>
<td>-.266**</td>
<td>-.272</td>
<td>.071</td>
<td>.518**</td>
<td>.475**</td>
<td>.458**</td>
<td>-.543**</td>
<td>.843**</td>
<td>.796**</td>
<td>.795**</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SSDW</td>
<td>-.477**</td>
<td>-.234</td>
<td>-.215</td>
<td>-.076</td>
<td>.589**</td>
<td>.603**</td>
<td>.584**</td>
<td>.592**</td>
<td>.927**</td>
<td>-.979**</td>
<td>.926**</td>
<td>-.755**</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SRDW</td>
<td>-.469**</td>
<td>-.23</td>
<td>-.187</td>
<td>.021</td>
<td>.388**</td>
<td>.374**</td>
<td>.320**</td>
<td>.344**</td>
<td>.357**</td>
<td>.824**</td>
<td>.790**</td>
<td>.806**</td>
<td>.703**</td>
<td>.850**</td>
</tr>
<tr>
<td>WC</td>
<td>-.533**</td>
<td>-.283**</td>
<td>-.259</td>
<td>-.003</td>
<td>.547**</td>
<td>.533**</td>
<td>.504**</td>
<td>.454**</td>
<td>.527**</td>
<td>.996**</td>
<td>-.941**</td>
<td>.990**</td>
<td>.847**</td>
<td>.896**</td>
</tr>
</tbody>
</table>

**. Correlation is significant at the 0.01 level.
*. Correlation is significant at the 0.05 level.

Table 2. Mean, coefficient of variability and critical values for seedling growth parameters.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>SH</th>
<th>SL</th>
<th>SLW</th>
<th>SLL</th>
<th>SFW</th>
<th>SDW</th>
<th>SSFW</th>
<th>SRFW</th>
<th>SSDW</th>
<th>SRDW</th>
<th>RWC</th>
</tr>
</thead>
<tbody>
<tr>
<td>Min</td>
<td>12.167</td>
<td>8.067</td>
<td>0.333</td>
<td>2.373</td>
<td>0.177</td>
<td>0.041</td>
<td>0.157</td>
<td>0.02</td>
<td>0.029</td>
<td>0.009</td>
<td>0.118</td>
</tr>
<tr>
<td>Max</td>
<td>28.6</td>
<td>18.733</td>
<td>0.833</td>
<td>11.392</td>
<td>0.957</td>
<td>0.264</td>
<td>0.752</td>
<td>0.204</td>
<td>0.227</td>
<td>0.057</td>
<td>0.692</td>
</tr>
<tr>
<td>Grand mean</td>
<td>17.808</td>
<td>12.411</td>
<td>0.500</td>
<td>5.088</td>
<td>0.4381</td>
<td>0.1137</td>
<td>0.3597</td>
<td>0.0761</td>
<td>0.0904</td>
<td>0.0233</td>
<td>0.3244</td>
</tr>
<tr>
<td>LSD</td>
<td>0.05</td>
<td>3.0202</td>
<td>2.2911</td>
<td>0.113</td>
<td>1.982</td>
<td>1.764</td>
<td>0.0452</td>
<td>0.1498</td>
<td>0.0495</td>
<td>0.0374</td>
<td>0.0135</td>
</tr>
<tr>
<td>Groups</td>
<td>24</td>
<td>21</td>
<td>11</td>
<td>19</td>
<td>24</td>
<td>21</td>
<td>20</td>
<td>22</td>
<td>16</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Mean with same letters aren't significantly different at 5% probability.

Seedling growth parameters

Furthermore, ANOVA was performed which was subsequently followed by LSD test (Table 3). Seedling height (SH) displayed high correlation with SLL, SLW, SLA, SFW, SSFW, SRFW, SSDW, SRDW and WC. For SH 17.808 cm grand mean was recorded while it ranged from 12.167 - 28.6 with coefficient of variability of 10.48%. The elite line 149-s revealed lowest SH while Abbasi2 showed the maximum. LSD value at (0.05) exhibited the 24 clusters with critical value 3.0202 in which the mean were not significantly different from one another. SLL was highly correlated with SLW, SLA, SFW, SSFW, SSDW, SRFW, SRDW and WC. The elite lines showed significant difference (p> 0.05) for SLL and recorded 21 groups with critical value 2.2911 in which the mean were not significantly different from one another. The minimum value 8.067 was measured for 117-s and maximum value 18.733 was noted for 97-m. The grand mean 12.411 was recorded with coefficient of variability 11.41%. The SLW was highly correlated with SLL, SLA, SFW, SSFW, SSDW, SRFW, SRDW and WC. The mean of SLW ranges from 0.333 - 0.833 with grand mean 0.500 and CV of 14.03%. The 161-s was detected for highest seedling broad leaves genotype while 66-R were the narrowest one after 21 days. There were 11 groups at 5% probability in which the mean were not significantly different from one another with critical
value 0.1135. High coefficient of variability of 21.48% was observed for SLA in the genotypes. Their mean values ranged from 2.373 to 11.392 with genotypic mean of 5.088. The genotype 29-s showed the highest SLA while 117-s revealed the lowest one. There were total 19 groups in which the means are not significantly different from one another with critical value 1.982 at level p>0.05. High correlation was observed with SLL, SLW, SFW, SSFW, SSDW, SRFW, SRDW and WC. SFW high significant correlation was found with SSFW, SRFW, SDW, SSDW, SRDW and WC. Average mean for SFW was 0.4381 with 24.89% coefficient of variability. High mean was detected for 97-m while lowest mean was observed for 133-m. There were 24 sets in which the mean were not significantly different from one another at critical value 0.1764 at 5% probability. SDW revealed high correlation to SFW, SSFW, SRFW, SSDW, SRDW, and WC at (p>0.01). The grand mean was 0.1137 with % variation of 24.58 which revealed high diversity of the trait among the genotype. Probability level at 5% showed LSD value of 0.0452 for the trait with 21 groups in which the means were not significantly different from one another. The SSFW seedling shoot fresh weight was highly correlated at 1% probability with SFW, SDW, SRFW, SSDW, SRDW, and WC. Grand mean of 0.3597 was calculated with 25.75 % of variability among the means of SSFW. The LSD value was 0.1498 at 5% probability and revealed 21 groups in which the means were not significantly different from one another. Highest mean was recorded for 97-m while lowest one was recorded for 133-m. Significant genotypic correlation was calculated for SRFW with SFW, SDW, SSFW, SSDW, SRDW and WC. The critical value of 0.0495 at 5% probability showed 20 groups with least significant difference. The grand mean of 0.0761 was measured with 40.22% highest coefficient of variability. The maximum SRFW was exhibited by 97-m while lowest was recorded for 02-s. SSDW showed high correlation with SVI, SH, SLL, SLW, SLA, SFW, SDW, SSFW, SRDW and WC while highly negatively correlated with DG. Highest mean was recorded for while lowest for. SSDW also has enough variation of 25.57%. It categorized 22 groups where means were not significantly different from one another. LSD value of 0.0374 for SSDW at p>0.05 was recorded. SRDW expressed highest coefficient of variability on the basis of dry matter among all variables which helps one to choose a genotype against drought. The SRDW ranged from 0.009 and 0.057 with lowest for and highest for. Grand mean and LSD of 0.0233 and 0.0135 was recoded, respectively. LSD also discriminated 16 groups where means were not significantly different from one another. Similarly, it was correlated with SLL while highly correlated with SVI, SH, SLL, SLW, SLA, SFW, SDW, SSFW, SRFW, SSDW and WC and highly negatively associated with DG. The WC showed high correlation with SVI, SH, SLL, SLW, SLA, SFW, SDW, SSFW, SRFW, SSDW while negatively correlated to DFL and highly negatively correlated to DG. The WC also shows high coefficient of variation of 26.24, which demonstrate the different water absorption pattern of genotypes. Grand mean of 0.3244 were recorded. The water absorption ranged from 0.118-0.622. Maximum mean was recorded for while minimum was noted for Principal axes method was performed to identify trends in seedling morphological and physiological traits for the selection of diverse genotype. The scree plot (Fig. 2) extracted four meaningful components in the transformed data with Eigenvalue more than 1, in which the 1st components, 2nd component, 3rd component and fourth component contributing 55.492%, 14.498%, 12.193% and 6.41% of variance to seedling vigor, respectively. All the four components were accountable for 88.596% cumulative variability in seedling.

Table 3. Rotation sum of squared loadings.

<table>
<thead>
<tr>
<th>PCs</th>
<th>Total</th>
<th>% of Variance</th>
<th>Cumulative %</th>
</tr>
</thead>
<tbody>
<tr>
<td>PC1</td>
<td>6.19</td>
<td>38.69</td>
<td>38.69</td>
</tr>
<tr>
<td>PC2</td>
<td>4.491</td>
<td>28.068</td>
<td>66.758</td>
</tr>
<tr>
<td>PC3</td>
<td>2.402</td>
<td>15.011</td>
<td>81.769</td>
</tr>
<tr>
<td>PC4</td>
<td>1.092</td>
<td>6.827</td>
<td>88.596</td>
</tr>
</tbody>
</table>
The extraction was followed by rotated factor pattern for first four retained components which was linearly transformed using varimax (uncorrelated orthogonal rotation which maximize the explained variance and interpret the dimension of loadings). The rotation altered the extraction that 1st components, 2nd component, 3rd component and fourth component contributed 38.69%, 28.068%, 15.011% and 6.827% of variability to seedling vigor, respectively (Table 3).

We found some general patterns created by principal component analysis. The seven traits water content, seedling fresh weight, shoot fresh weight, seedling dry weight, shoot dry weight and root fresh weight donating 96.9%, 96.9%, 93.3%, 92.7%, 92.6%, 84.3% and 81.8% loading on the 1st component, respectively (Fig. 3). The loadings of 1st PC revealed that increase in one loading confer an increase to other loadings while the negative value suggests the adverse effect of DG on the rest of significant loadings. The 2nd pattern was formed by leaf area (94.2%), seedling vigor index (93.9%), leaf length (92.9%), seedling height (92%) and leaf width (71.4%). The third component has three meaningful loadings; days to initiation of tillering (98.9%), days to five leaves stage (97.7%) and days to germination (54.6%). The loading, days to germination was explained as factorial complex trait (meaningful loading for more than one component) by rotated component matrix and therefore ignore the whole component due to fewer loadings than rock-bottom lower bound. The only one loading rate of germination index (99.7%) lies on the 4th component and was also washed out due fewer loadings than lower. Accordingly, the only two clean components were retained after rotation.

The (Fig. 3) showed that these two components demonstrate simple structure, measuring different morphological and physiological trends and their corresponding loadings share same conceptual measure within respective components.

**Discussion**

The quantitative traits are polygenic traits, expressed in continuous phenotypic variations in natural population. These traits also provide insights for the genetic control of the trait variation. The genotype variability mostly depends on the genetic characteristic of these traits. Seed and seedling vigor in rice is associated with several quantitative characters (Petersen et al., 1978). These characters show some association among themselves which could be potentially utilized in rice improvement.
seed density of rice seed to seedling vigor, as these traits showed high relative expected genetic advance and heritability.

In the current study the 1st component (Fig. 3) could be a better pattern which has a prominent contribution to seedling internally which in some extent seem to be dependent upon the early emergence of seeding. Similar findings also reported by (Manzoor et al., 2007) that early germinated seedling gave maximum contribution to seedling traits. Seshu et al. (1988) used early germination as measuring tool for seedling vigor. Although DG is an important trait but in Pakistan as seedlings are transplanted to the puddled field where germination no more play significant role as in direct seeding therefore, we assumed DG as constant and denoted the content of preceding component as relative seedling biomass (SB). Similarly, the loading of 2nd component carry most of length traits with high positive coefficient value and (Table 2) submitted that SVI, SH, SLL, SLW and SLA were highly dependent on one another. Therefore, the PC2 was subsequently labeled as seedling elongation parameters (SEP). The small positive values for SEP in 1st component and minimum positive values for SB in 2nd component suggest that these two components support one another in very minor proportion. The interpretation showed that SB and SEP contribute more to seedling vigor and clarifies the phenotypic diversity among genotypes. These findings are helpful in the selection of more than two variables. However, in the current genotypes collection the SEP showed less coefficient of variability as compared to SB (Table 2).

As interested in studying the relationship among the meaningful traits of each component the correlation reveal that the plants with tall SH height tends to have long leaves and high SVI while plants with high SLL indirectly support SLA. Same conclusions were also derived by (Ray, 2013) from the 414 landraces from their adult morphology. Similarly, weight components seem to be dependent upon SFW which are adversely affected by delay in seed germination. Furthermore, the most of the elite lines were found to the opposite side of the control cultivars in 1st component with normal SH, SLL, SLW and SLA that bared the robustness in their biomass. The genotypes 97-m, 111-m, 161-s, Abbasi2, 105-m, 86-L, 29-s, 136-L, 158-2-L, 130-s, 14-L, 10-s, 127-m, 26-L, 179-s, 19-L, 79-L, 184-s, 07-m, 17-L, 109-L, 186-m, 12-L, 52-L, M2, 69-m and 96-m showed high performance (high SB) with respect to control i.e. Bas-385, JP5, Kangnaiz29 and Pulman sufaid (Fig. 4). The high positive value of JP5 for 2nd component and normal positive coefficient value for 1st component described its high elongation ratio with respect to biomass that’s why JP5 facing lodging at maturity which results in high yield loss.

**Conclusion**

In conclusion the study gave a better knowledge of understanding seedling vigor among a set of traits. The most contributed traits to phenotypic diversity i.e. DG, SVI, SH, SLL, SLW, SLA, SFW, SDW, SSFW,
SSDW, SRFW, SRDW and WC that are the sub-derived variables of two major ones SH and SFW which are adversely effected by DG. These findings pave a criterion for selection which will enable one to choose a best genotype at seedling that withstands lodging and having the ability to carry large and heavy panicle at adult stage. Apart from these, the less variability for SH and high variation in SFW indicate the capability of elite lines. The advance lines 97-m, 111-m, 161-s, Abbasi2, 105-m, 86-L, 29-s, 136-L, 158-2-L, 130-s, 14-L, 10-s, 127-m, 26-L, 179-s, 19-L, 79-L, 184-s, 07-m, 17-L, 109-L, 186-m, 12-L, 52-L, M2, 69-m and 96-m were vigorous and withstand disease attack due to its high seedling biomass and short stature that one could effectively use in further improvement of rice.

References


Mackill DJ, Redona ED. 1997. Breeding strategies


