Study on morphometric characterization for yield and yield contributing attributes in traditional rice (Oryza sativa L.) varieties

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Abstract

The present study was carried out at Agricultural College and Research Institute, Killikulam, Tuticorin district during Rabi 2021-22 to characterize the inherent genetic variability among 105 traditional rice varieties against nine morphometric yield contributing traits in a randomized block design with three replications. Univariate analysis among rice genotypes elucidated significant differences for all the traits studied. Phenotypic coefficient of variation (PCV) was relatively higher than genotypic coefficient of variation (GCV) for all the traits. The traits such as number of productive tillers per plant, number of filled grains per panicle, and thousand-seed weight (g) exhibited the higher estimates for both PCV and GCV. Heritability and genetic advance were also recorded high for all the yield attributes, indicating the role of additive gene for heritability, suggesting the direct selection for yield contributing trait always will be rewarding.

Keywords: Rice, genetic variability, heritability, genetic advance and yield

Introduction

Rice (Oryza sativa L. 2n=2x=24), is an important cereal food crop of the Poaceae family with a haploid chromosome number (n=12), widely portrayed as a “global grain” or “Life of people”. It can be either diploid (or) tetraploid, with the autogenously mode of reproduction Baroudy et al., (2020) [3]. It is a substantial food crop cultivated around the globe, which accounts for 35-80 per cent of total calorific intake Vijay et al., (2019) [30]. Around, 40 per cent of the global and 65 per cent of the Indian population depends on rice as their staple diet, to satisfy their regular dietary intake Singh et al., (2021) [21]. Rice has been domesticated for ages, making it suitable for cultivation in diverse locations around the globe with an extreme environment. Vigueira et al., (2019) [29]. China and India are the two most populous nations and are the largest consumers and producers of rice. FAO (2019) [5]. On a global scale, paddy occupies 75 per cent of cereal grain production followed by wheat, with a cultivable area of 164.0 million hectares and yielding about 516.3 million tonnes with average productivity of 3.15tonnes/ha. FAO/OCED (2022) [16]. India ranked second only to China in terms of total rice production (118.4 million tonnes) and productivity (2.79 t/ha), with a global lead of 43.86 million hectares India stat (2020-21) [10]. Population forecast indicated a rise in the national population may shoot up the production to 130 million tonnes from standard projections, to meet an average of 42 per cent increase in the demand for grain across the nation by 2035 Gaballah et al., (2022) [6].

To meet the reckoning demand for rice shortly, agronomically superior rice varieties with multiple stress resistance must be bred with progressive breeding approaches and biotechnological tools. Several rice varieties have been successfully developed after the green revolution through repeated selection and hybridization programs, eventually, leading to a trivial loss of variations among landraces Nandhini et al., (2017) [15]. Since Traditional rice varieties hold up a high level of heterogenity, it is crucial to utilize them in present-day breeding programs. To do so it requires an elaborate survey of genetic variability, and a thorough understanding of the genetic makeup of the Traditional rice varieties is essential Govintha Raj et al., (2016) [17]. Mostly, any variation in the given population is due to interaction between the genetic and environmental components of the variation, where the genetic one must be heritable Roy and Shil (2020) [18]. Regarding the aforementioned considerations, the current study has been carried out to estimate variability, heritability, genetic advance for yield and yield contributing traits in rice genotypes.
The current investigation was conducted during Rabi 2021 – 2022 at the B block farm of Agricultural College and Research Institute, Killikulam. The experimental material consists of 105 rice genotypes obtained from AC&RI, Killikulam, and sown in a uniform raised bed nursery with the recommended doses of fertilizer of 1.0kg N, 1.0kg P₂O₅, and 0.5kg K₂O per 50 m² area. Twenty-five days old robust rice seedlings of each genotype were transplanted into the main field with one seedling per hill, by adopting a spacing of 30cm between rows and 20cm between plants within a row in a Randomised Block Design replicated thrice. Required agronomic practices and essential prophylactic remedies were adopted during the entire crop period to raise a good crop. Observations were taken randomly from ten competitive plants of each genotype in every replication for nine yield contributing biometrical traits viz. plant height (cm), number of productive tillers, panicle length(cm), number of grains per panicle, single plant yield (g), grain length(mm), and grain breadth(mm) and data for days to 50% flowering was recorded on a plot basis, thousand seed weight(g) was observed for randomly drawn grain samples from each genotype for every replication. The collected data were subjected to standard statistical analysis using WINDOWSTAT software. Univariate analysis of each character (ANOVA) was carried out as suggested by Panse and Sukhatme (1957) [17]. Genetic variability parameters such as GCV and PCV, heritability, and genetic advance as percent of mean were enumerated according to Burton et al., (1953) [4], Lush (1940) [12], and Johnson et al., (1955) [11] respectively.

Results and Discussion
Analysis of Variance (ANOVA)
Results of Univariate analysis (ANOVA) for all nine yield contributing traits were enumerated in Table 1. It revealed that the mean sum of squares due to treatment is significant for all the traits studied, indicating that genotypes included in the study have diverse genetic roots and hold up adequate variation among them. Therefore, this germplasm can be employed for an effective selection process of genetic advancement of yield attributes. Similar findings were reported by Girma et al., (2018) [8], Sujitha et al., (2020) [26], and Sowjanya et al., (2021) [22].

Per se performance
Mean values of all nine yield contributing traits of each genotype were given in brief (Table 2). Variation for the trait days to fifty per cent flowering ranged from 119 days to 42 days with a per se value of 90.5 days, implying that the genotype with a lower estimate for days to fifty percent flowering can be used as a donor parent to develop short duration variety. The variation for plant height ranged from 167.0cm to 71.7cm with an average value of 115.4cm. The number of productive tillers fluctuated between 29.0 to 10.70 with an average value of 18.9. The length of the panicle varied from 36.2cm to 15.0cm with a median value of 24.6cm. Trait number of grains per panicle differed between 340.7 to 86.7 per se value of 159.7. Thousand seed weight could be varied between 36.7g to 13.7g with a mean value of 25.4g. Grain length may differed between 10.5cm to 5.7cm with a mean of 7.7cm. The highest grain width was 4.9cm and the lowest was 2.0cm with an average of 2.9cm. The variation for single plant yield ranges from 77.9g to 34.9g with an average of about 55.5g. Hence, the per se performance of the given genotypes entails that no specific genotypes were significant for all the yield contributing traits, indicating that sufficient variation was present in the genotypes that can be exploited in the crop improvement schemes.

Range and variability parameters
The range and variability parameters of all the genotypes were depicted in detail (Table 2). In accordance with the results, the number of grains per panicle showed a high range of variability (86.7-340.7), whereas the least range of variability was observed for grain breadth (2.0-4.9) Madhububu et al., (2020) [13] and Sharma et al., (2021) [20]. Reports from journals quenched that the success of any selection process in a crop improvement scheme always rests on the presence of relative divergence among traits, calibrated using the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). The PCV estimates were kind of greater than the GCV estimates (Table 2 and Figure 1) for all traits evaluated, although the variation seemed extremely small, emphasizing that divergence may arise not only by genotype but also by an environmental effect on trait expression, which is invariably similar to the findings of Tiwari et al., (2019) [27], Sabri et al., (2020) [19], Sudeepthi et al., (2020) [23] and Sowjanya et al., (2021) [22]. PCV and GCV are higher for the trait number of grains per panicle (32.24 and 32.13) followed by thousand seed weight (23.56 and 23.42) and the number of productive tillers (21.77 and 21.61) respectively. Traits such as plant height (20.12 and 19.97), single plant yield (16.81 and 16.62), grain breadth (16.39 and 16.17), days to fifty per cent flowering (14.40 and 14.16), panicle length (13.49 and 13.22) and grain length (11.78 and 11.41) have moderate estimates for both PCV and GCV. These results were comparable with Srilakshmi et al., (2018) [24], Tiwari et al., (2019) [27] and Sabari et al., (2020) [19]. Traits that possessed moderate PCV and GCV are likely to be included in crop advancement plans. Similarly, yield attributes that have high PCV and GCV are predominantly influenced by genetic factors rather than the environment, suggesting that these traits are genetically divergent and hence there is an ample scope for selection.

Heritability and genetic advance as percent of mean
Measures of heritability and genetic advance as per cent of the mean are of great importance for selection. High heritability coupled with high genetic advance suggests a more precise prediction of genetic gain under selection Arora (1991) [2]. Estimates of heritability (Table 2 and Figure 2) ranged from 99.30 per cent for number of filled grains per panicle to 93.30 per cent for grain length. Values of heritability for all the yield contributing traits were high. Similar kinds of reports were given by Srilakshmi et al., (2018) [24], Sujitha et al., (2020) [26] and Sowjanya et al., (2021) [22]. (Table 2 and Figure 2) The results for genetic advance as a percentage of mean found high values for all the traits included in the study, which range between 65.97 per cent for the number of filled grains per panicle to 22.78 per cent for grain length. These results were in consonance with the earlier reports of Umarani et al., (2017) [28], Sreedhar and Reddy (2019) [23], and Sujitha et al., (2020) [26]. Yield attributes with high heritability coupled with high genetic advance per cent of mean are controlled by additive
gene action and substantial enhancement of these traits can be achieved through the direct selection which include mass selection, progeny selection, and pure line selection. Johnson et al., (1955) [4]. In the current study, high GCV and PCV coupled with high heritability and genetic advance were observed for traits that include the number of filled grains per panicle, thousand seed weight, and the number of productive tillers per plant, implying the predominance of additive gene action and hence the traits are potential for improvement by selection. Similar findings of the study were consistent with reports of Maurya et al., (2021) [14], Hake and Bhoite (2021) [9] and Akshay et al., (2022) [1].

Table 1: ANOVA for nine yield attributes

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>Mean Sum squares</th>
<th>CV</th>
<th>S.E.D</th>
<th>CD (5%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Replication</td>
<td>Genotypes</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Days to fifty percent flowering</td>
<td>5.668</td>
<td>498.510**</td>
<td>2.59</td>
<td>1.92</td>
</tr>
<tr>
<td>Plant height (cm)</td>
<td>7.884</td>
<td>1600.345**</td>
<td>2.52</td>
<td>2.37</td>
</tr>
<tr>
<td>Number of productive tillers per plant</td>
<td>0.163</td>
<td>50.064**</td>
<td>2.57</td>
<td>0.40</td>
</tr>
<tr>
<td>Panicle length (cm)</td>
<td>0.079</td>
<td>32.071**</td>
<td>2.65</td>
<td>0.53</td>
</tr>
<tr>
<td>Number of filled grains per panicle</td>
<td>7.151</td>
<td>7919.646**</td>
<td>2.61</td>
<td>3.40</td>
</tr>
<tr>
<td>Thousand seed weight (g)</td>
<td>0.424</td>
<td>106.346**</td>
<td>2.59</td>
<td>0.54</td>
</tr>
<tr>
<td>Grain length (mm)</td>
<td>0.029</td>
<td>2.378**</td>
<td>2.91</td>
<td>0.18</td>
</tr>
<tr>
<td>Grain breadth (mm)</td>
<td>0.004</td>
<td>0.647**</td>
<td>2.67</td>
<td>0.06</td>
</tr>
<tr>
<td>Single plant yield (g)</td>
<td>0.029</td>
<td>257.144**</td>
<td>2.52</td>
<td>1.14</td>
</tr>
</tbody>
</table>

*Significant at 5% level **Significant at 1% level

Table 2: Summary statistics of genetic variability parameters for nine yield attributes

<table>
<thead>
<tr>
<th>Traits</th>
<th>Range</th>
<th>Mean</th>
<th>PCV (%)</th>
<th>GCV (%)</th>
<th>H (%)</th>
<th>GAM (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>DFF</td>
<td>42.00 – 119.00</td>
<td>90.54</td>
<td>14.40</td>
<td>14.16</td>
<td>96.8</td>
<td>28.69</td>
</tr>
<tr>
<td>PH</td>
<td>71.70 – 167.00</td>
<td>115.38</td>
<td>20.12</td>
<td>19.97</td>
<td>98.4</td>
<td>40.81</td>
</tr>
<tr>
<td>NoPT</td>
<td>10.70 – 28.97</td>
<td>18.86</td>
<td>21.77</td>
<td>21.61</td>
<td>98.6</td>
<td>44.21</td>
</tr>
<tr>
<td>PL</td>
<td>15.00 – 36.20</td>
<td>24.56</td>
<td>13.49</td>
<td>13.22</td>
<td>96.1</td>
<td>26.71</td>
</tr>
<tr>
<td>GPP</td>
<td>86.70 – 340.70</td>
<td>159.73</td>
<td>32.24</td>
<td>32.13</td>
<td>99.3</td>
<td>65.97</td>
</tr>
<tr>
<td>TSW</td>
<td>13.67 – 36.67</td>
<td>25.37</td>
<td>23.56</td>
<td>23.42</td>
<td>98.8</td>
<td>47.95</td>
</tr>
<tr>
<td>GL</td>
<td>5.70 – 10.50</td>
<td>7.72</td>
<td>11.78</td>
<td>11.41</td>
<td>93.9</td>
<td>22.78</td>
</tr>
<tr>
<td>GB</td>
<td>1.97 – 4.87</td>
<td>2.86</td>
<td>16.39</td>
<td>16.17</td>
<td>97.3</td>
<td>32.87</td>
</tr>
<tr>
<td>SPY</td>
<td>34.90 – 77.90</td>
<td>55.49</td>
<td>16.81</td>
<td>16.62</td>
<td>97.7</td>
<td>33.85</td>
</tr>
</tbody>
</table>

DFF - Days to fifty percent flowering, PH - Plant height, NoPT - Number of productive tillers per plant, PL - Panicle length, GPP - Number of grains per panicle, TSW - Thousand-seed weight, GL - Grain length, GB - Grain breadth, SPY - Single plant yield, PCV - Phenotypic coefficient of variation, GCV - Genotypic coefficient of variation, H - Heritability, GAM – Genetic Advance as per cent of mean.

Fig 1: Phenotypic and Genotypic coefficient of variation for nine yield attributing attributes
Heritability and Genetic advance as per cent

Fig 2: Heritability and Genetic advance as percentage of the mean for nine yield attributing attributes

Conclusion

The results of the analysis of variance suggest that the material under the present study have a significant level of variability. High magnitude of PCV and GCV were observed for the traits such as number of filled grains per panicle, thousand seed weight, and number of productive tillers per plant revealing that a substantial degree of variation present in the traits can be exploited in trait-based crop improvement schemes through efficient selection. Higher estimates of heritability in a broad sense and high genetic advance as per cent of mean were observed for all the traits under study, indicating that these traits were under the influence of additive gene action and hence direct selection of these traits is beneficial for improving yield in any future breeding programs.

References


