Genetic variability and correlation analysis of rice (*Oryza sativa* L.) inbred lines based on agro-morphological traits

Abdourasmane K. Konate¹*, Adama Zongo², Honore Kam¹, Ambaliou Sanni³ and Alain Audebert⁴

¹Institut de l’Environnement et de Recherches Agricoles (INERA) BP 910 Bobo-Dioulasso, Burkina Faso.
²Université Ouaga 1 Pr Joseph Ki-Zerbo BP 7021 Ouagadougou, Burkina Faso.
³Université d’Abomey-Calavi, BP 526 Cotonou, Bénin.
⁴Centre de Coopération International en Recherche Agronomique pour le Développement (CIRAD), CA UPR, Riziculture Montpellier, France.

Received 10 July, 2016; Accepted 12 August, 2016

In order to evaluate genetic variability of agro-morphological traits and also determine the correlation between grain yield with its components in rice lines, 17 recombinants inbred lines, their parents and a check variety were grown in research station of Africa rice center in Benin republic during two consecutive years 2013 and 2014. The experiments were laid out in a randomized complete block design with four replications. Phenotypic coefficients of variance were higher than genotypic coefficients of variance in all the characters across the two years. High heritability in broad sense (H²) estimates were obtained for biomass (68.77%), date of 50% flowering (98.11%), plant height (81.94%), leaf area (82.90%), number of panicles (64.40%), leaf dry weight (72.91%), root weight (67.43%) and yield/plant (62.23%) suggesting that the traits were primarily under genetic control. A joint consideration of broad sense heritability (H²) and genetic advance as per cent mean expected (GAM) revealed that leaves dries weight and roots weight combined high heritability and high GAM. Furthermore, high (H²) and high GAM recorded in these characters could be explained by additive gene action. However, high estimates (H²) combined with moderate GAM recorded for biomass, day to 50% flowering, leaf area, number of panicle and yield/plant could be due to non-additive gene effect. Grain yield/plant recorded positive and significant correlation with stem weight (r=0.5262) and biomass (r=0.9291). This result indicates that selection based on these two characters will be highly effective for yield improvement in rice.

Key words: Agro-morphological traits, correlation, genetic variability, heritability, rice.

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important food crops in the world. It is a staple food crop for more than half of the world’s human population. Rice grain contains 75 to 80% starch, 12% water and 7% protein (Oko et al., 2012; Hossain et al., 2015). Minerals like calcium, magnesium and phosphorus are present along with some traces of iron, copper, zinc and manganese. In addition, rice is a good source of niacin, thiamine and riboflavin (Yousaf, 1992; Oko et al., 2012).

Rice is grown in 117 countries across all habitable
continents covering a total area of about 163 mha with a
global production of about 740 mt and an average yield of
about 4,539 kg / ha (FAOSTAT, 2014). The Asian
continent ranks first with over 90.1% of world production,
followed by the American continent (5.1%), African
continent (4.2%), Europe (0.5%) and Oceania (0.1%).
The major producing countries are China (206.5 million
tons), India (157.2 million tons), Indonesia (70.8 million
tons), Bangladesh (52.2 million tons) and Viet Nam with
44.9 million tons (FAOSTAT, 2014). In Africa, rice is
grown and consumed in more than 40 countries. Its
production has increased significantly from year 2000 to
2013. More than 20 million farmers in Africa are engaged
on rice production in these countries and about 100
million people are dependent on it directly for their
livelihood (Nwanze et al., 2006). For example in Burkina
Faso, rice production has grown from 103,087 tons on
year 2000 to 305,382 tons on 2013. It is no longer a
luxury food but has become the cereal that constitutes a
major source of calories for almost urban and rural
people of Africa (Seck et al., 2013).

In a report published by United Nations the world
population is going to cross the 8 billion mark by 2030
and 9.6 billion by the year 2050 and rice production must
be increased by 50% in order to meet the growing
demand. This demand in Sub-Saharan Africa is expected
to grow substantially as the population is currently
growing at the rate of 3 to 4% per annum (Ogunbayo et
al., 2014). To meet the future demand resulting from
population growth, development of new high yielding
rice genotypes is therefore a necessity. Thus, to meet
this demand and attend rice self-sufficiency, plant
breeders have to develop high yielding cultivars with
desirable agronomic traits for diverse ecosystems.

The development of new genotypes requires some
knowledge about the genetic variability presents in the
germplasm of the crop to build efficient breeding
programme. The knowledge about genetic variability can
help to know if these variations are heritable or non-
heritable. The magnitude of variation due to heritable
component is very important because, it would be a guide
for selection of parents for crop improvement (Dutta et
al., 2013). Therefore, selection for high yield requires
knowledge about genetic variability and good
understanding of correlation between yield and yield
components regarding to the genetic material that is on
hand. Genetic variability for agronomic traits is the key
component of breeding programme for broadening the
gene pool of rice (Dutta et al., 2013).

Heritability estimates provide authentic information
about a particular genetic attribute which will be
transmitted to the successive generations and constitute
an efficient guide for breeders in the choice of parents for
crop improvement programmes (Rafi and Nath, 2004).
However, heritability in broad sense alone may not be
helpful for selection based on phenotype, because it's
influenced by environment. Thus, estimate heritability
along with genetic advance conjointly are reliable helpful
in predicting the gain under selection than heritability
alone (Ogunbayo et al., 2014). Moosavi et al. (2015)
reported that grain yield is a complex trait, quantitative
in nature and a combined function of a number of
constituent traits. Consequently, selection for yield may
not be satisfying without taking into consideration yield
component traits. Thus, positives correlated between
yield and yield components are requires for effective yield
component breeding increasing grain yield in rice
(Ogunbayo et al., 2014). So, it is important for plant
breeders to understand the degree of correlation between
yield and its components.

Therefore, the objective of the present study was to
assess and evaluate genetic variability of rice
recombinant inbred lines based on agro-morphological
traits and analyse the relationships between these traits.

MATERIALS AND METHODS

The experiment was conducted in the greenhouse of Africa rice
center research station in Cotonou (Benin republic) from March to
July 2013 and from February to June 2014. The site is located
between 6°25.415N and 2°19.684E at an altitude of 21 m above
sea level. Experiments were conducted in greenhouse using a
randomized complete block design with four replications. Individual
plant of each genotype was grown in 2 L pots containing natural
field soil. Management practices such as irrigation and fertilization
were performed by following the standard procedures (IRRI, 2002).

A total of 20 genotypes consisting of 17 F₁ inbred lines from the
indica’s cross included their two parents and the indica variety APO
were used in this study. The inbred lines were obtained from the
indica’s cross IR64 X B6144F-MR-6-0-0. The parent, B6144F-MR-6-
0-0, a drought resistant landrace was crossed with the variety IR64,
a variety which possesses many agronomical superior traits. The
variety APO, a popular variety known for its long term adaptation in
drought prone ecosystem was used as a control.

Observations were recorded on one plant of each pot. Thus,
morphological and agronomical data were collected for 11
quantitative characters at appropriate growth stage of rice plant
following the standard evaluation system indicated by IRRI (IRRI,
2002). The characters that were evaluated included days to 50%
flowering (50%DF, day), plant height (PH, cm), leaf area (LA, cm²),
number of tillers (NT), number of panicles (NP), number of fertile
spikelets (NFS), leaf dry weight (LDW, g), roots weight (RW, g),
panicles weight (PW, g), stem weight (SW, g), 1000 grains weight
(1000GW, g), biomass (biom, g) and grain yield per plant
(yield/plant, g/plant).

The data recorded on 12 morphological and agronomical traits
from the genotypes used, were subjected to statistical analysis.
Analysis of variance (ANOVA) was carried out to access the
genotype effect and their interaction using R program package. The
correlation analysis was performed using the same software to

*Corresponding author. Email: kadougoudiou@gmail.com.

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determine the degree of correlation between yield and its components. In order to assess and quantify the genetic variability among the genotypes for the characters under study the variance components and values of heritability and genetic advance were estimated following the formula given by Burton and De Vane (1953); and Johnson et al. (1955) and applied by Tuhina-Khatun et al. (2015).

Phenotypic and genotypic variances were estimated using the following formula:

\[ Vg = (MS_g - MS_{gxy}) / r \]

\[ Vgxy = (MS_{gxy} - MS_e) / r \]

\[ Ve = MS_e \]

\[ Vp = Vg + Vgxy + Ve / ry \]

Where, \( Vg \) = genotypic variance; \( Vgxy \) = genotype x year variance; \( Ve \) = environment variance; \( Vp \) = phenotypic variance; \( MS_g \) = mean square of genotypes; \( MS_{gxy} \) = mean square of genotype x year; \( MS_e \) = mean square of error; \( r \) = number of replications and \( y \) = number of year.

Both genotypic and phenotypic coefficients of variability were estimated using the formula below:

\[ GCV = \sqrt{Vg} \cdot 100 \]

\[ PCV = \sqrt{Vp} \cdot 100 \]

Where \( GCV \) = genotypic coefficient of variability; \( PCV \) = Phenotypic coefficient of variability; \( \sqrt{Vg} \) = genotypic standard deviation; \( \sqrt{Vp} \) = phenotypic standard deviation and \( X \) = general mean of the character.

Heritability in broad sense \( (H^2) \) was computed as the ratio of genetic \( (Vg) \) variance to the total phenotypic variance \( (Vp) \).

\[ H^2 = \frac{Vg}{Vp} \cdot 100 \]

The genetic advance (GA) and genetic advance as percentage of mean (GAM) were estimate using the formula given below:

\[ GA = H^2 \cdot k \cdot \sqrt{Vp} \]

\[ GAM = \frac{GA}{X} \cdot 100 \]

Where \( H^2 \) = heritability in broad sense; \( k \) = Selection differential which is equal to 2.06 at 5% intensity of selection; \( X \) = general mean of the character.

**RESULTS**

**Analysis of variance**

The results of combined analysis of variance for the all characters are shown in Table 1. Significant effects of genotype were observed for all the characters under study. High significant effect of year for all the characters except the leaf area (LA) and stem weight (SW) were shown from this analysis. The genotype x year was highly significant only for the characters leaf area (LA) and 1000 grain weight (1000 GW). Environmental conditions were not similar in two years, meaning that climate changes were observed during the study suggesting that the differences among genotypes were not stable across years.

**Estimate of genetic parameters**

Estimates of genotypic \( (Vg) \) and phenotypic variances \( (Vp) \), genotypic coefficient of variation \( (GCV) \) and phenotypic coefficient of variation \( (PCV) \), broad sense heritability \( (H^2) \), genetic advance (GA) and genetic advance as percentage of the mean (GAM) are shown in Table 2.

High genotypic and phenotypic variances were recorded with leaf area, 332.34 and 400.89, respectively. High genotypic and phenotypic variances were equally observed for 50% flowering day (41.88 and 42.68) and the number of fertile spikelets 22.71 and 53.97, respectively. The low values of genotypic and phenotypic variances were observed with the characters panicle weight (0.10 and 0.26), stem weight (0.81 and 2.01) leaf dries weight (0.53 and 0.73), number

Table 1. Mean square of combined analysis of variance for all the characters studies of 20 rice genotypes.

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>Biom</th>
<th>D50F</th>
<th>PH</th>
<th>LA</th>
<th>NT</th>
<th>NP</th>
<th>NFS</th>
<th>LDW</th>
<th>RW</th>
<th>PW</th>
<th>SW</th>
<th>1000GW</th>
<th>Yield/plant</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rep</td>
<td>3</td>
<td>31.6</td>
<td>4.126</td>
<td>49.06</td>
<td>95.51</td>
<td>1.22</td>
<td>48.35</td>
<td>75.88</td>
<td>8.32</td>
<td>15.47</td>
<td>3.26</td>
<td>20.73</td>
<td>9.68</td>
<td>24.95</td>
</tr>
<tr>
<td>Geno</td>
<td>19</td>
<td>89.1**</td>
<td>337.24**</td>
<td>66.37**</td>
<td>2992.44**</td>
<td>6.20**</td>
<td>11.66**</td>
<td>234.93**</td>
<td>4.72**</td>
<td>31.20**</td>
<td>1.03**</td>
<td>8.89**</td>
<td>11.35**</td>
<td>80.94**</td>
</tr>
<tr>
<td>Year</td>
<td>1</td>
<td>278.44**</td>
<td>120.16**</td>
<td>1836.36**</td>
<td>14.5ns</td>
<td>46.71**</td>
<td>30.11**</td>
<td>1956.69**</td>
<td>27.23**</td>
<td>38.43**</td>
<td>3.48**</td>
<td>1.52ns</td>
<td>47.91**</td>
<td>222.34**</td>
</tr>
<tr>
<td>G x Y</td>
<td>19</td>
<td>6ns</td>
<td>2.23ns</td>
<td>4.80ns</td>
<td>333.7**</td>
<td>0.22ns</td>
<td>0.20ns</td>
<td>53.25ns</td>
<td>0.49ns</td>
<td>2.59ns</td>
<td>0.21ns</td>
<td>2.40ns</td>
<td>6.21**</td>
<td>14.44ns</td>
</tr>
<tr>
<td>Error</td>
<td>117</td>
<td>10.58</td>
<td>1.4</td>
<td>2.923</td>
<td>71.56</td>
<td>1.26</td>
<td>2.04</td>
<td>65.6</td>
<td>0.36</td>
<td>3.74</td>
<td>0.33</td>
<td>2.38</td>
<td>2.57</td>
<td>8.64</td>
</tr>
</tbody>
</table>

1000 GW: 1000 grains weight; D50F: day to 50% flowering; LA: leaf area; LDW: leaf dry weight; NP: number of panicle; NFS: number of fertile spikelets; NT: number of tiller; PH: plant height; PW: panicle weight; RW: root weight; SW: stem weight; Yield/pl: yield per plant; biom: biomass; ns: no significant; *: significant at 5% level probability; **: significant at 1% level probability.
number of tiller (0.75 and 1.25) and 1000 grains weight (0.64 and 2.39), respectively. In general, the phenotypic variances were higher than genotypic variances for all the characters.

Genotypic coefficients of variance (GCV) were ranged from 3.18% for plant height to 20.03% for root weight, whereas phenotypic coefficients of variance (PCV) were ranged from 3.51% for plant height to 24.39% for root weight. According to Sivasubramanian and Menon (1973) PCV and GCV values more than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10 and 20% to be moderate. Based on this delineation, GCV and PCV values were low for biomass, day to 50% flowering, plant height and 1000 grains weight; medium for number of panicle, leaf dry weight and stem weight; high for root weight. The panicle weight and plant height were recorded with low GCV and moderate PCV. In addition, PCV values were higher than theirs corresponding GCV values for all the characters considered. However, this difference was low for all the characters except the panicle weight and stem weight.

Heritability analyses estimate the relative contributions of differences in genetic and non-genetic factors to the total phenotypic variance in a population. It is an important concept in quantitative genetics, particularly in selective breeding. The heritability in broad sense ($H^2$) estimate varied from 26.95% to 98.11%, respectively for 1000 grains weight and day to 50% flowering. All the characters studies had high heritability (>60%) except the numbers of fertile spikelets, panicle weight, stem weight and 1000 grains weight. This result indicates that these characters could be easily improved by selection.

Genetic advance (GA) under selection refers to the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at a given selection intensity (Wolie et al., 2013). The high value of GA was recorded with leaves area (34.19) and the low (0.42) with panicle weight. Estimates of GA for yield/plant was 4.69 g/plant indicating that whenever we select the best, 5% high yielding genotypes as parents, average grain yield/plant of progenies could be improved by 4.69 g/plant.

Genetic advance as per cent mean expected (GAM) had a general range between 3.65% for 1000 grains weight and 33.87% for roots weight. Among the characters high values of GAM (>20%) were recorded only for roots weight and leaf dry weight (25.16%). It was moderate (10 to 20%) for biomass, day to 50% flowering, leaf area, number of tillers, number of panicle, panicle weight, stem weight and yield/plant; low (<10%) for plant height, number of fertile spikelets and 1000 grains weight. Leaf dry weight and roots weight had high heritability and high GAM, whereas biomass, day to 50% flowering, leaf area, number of panicle and yield/plant had high heritability but moderate GAM. Panicle weight and stem weight had both moderates heritability and GAM.

**Correlation**

The degree of correlation between the traits is important in plant breeding. It can be used as tool for indirect selection. Correlation studies help the plant breeder during selection and provide the understanding of yield components. The results of correlation analysis showed in Table 3 reveals that there was positive and highly significant correlation between day to 50% flowering (50%DF) with leaf dry weight ($r=0.6223$), number of panicle ($r=0.7091$) and stem weight ($r=0.5566$). The characters which had positive relationship with grain yield/plant were day to 50% flowering ($r=0.3997$), leaf area ($r=0.0382$), leaf dry weight ($r=0.101$), number of

<table>
<thead>
<tr>
<th>Characters</th>
<th>Min</th>
<th>Means</th>
<th>Max</th>
<th>Vg</th>
<th>Vp</th>
<th>GCV</th>
<th>PCV</th>
<th>H2 (%)</th>
<th>GA</th>
<th>GAM</th>
</tr>
</thead>
<tbody>
<tr>
<td>Biomass (g)</td>
<td>39.79</td>
<td>50.34</td>
<td>62.85</td>
<td>10.39</td>
<td>15.11</td>
<td>6.40</td>
<td>7.72</td>
<td>68.77</td>
<td>5.51</td>
<td>10.94</td>
</tr>
<tr>
<td>Day to 50% flowering</td>
<td>81.60</td>
<td>92.67</td>
<td>118.30</td>
<td>41.88</td>
<td>42.68</td>
<td>6.98</td>
<td>7.05</td>
<td>98.11</td>
<td>13.20</td>
<td>14.25</td>
</tr>
<tr>
<td>Plant height (cm)</td>
<td>79.00</td>
<td>87.24</td>
<td>100.30</td>
<td>7.70</td>
<td>9.39</td>
<td>3.18</td>
<td>3.51</td>
<td>81.94</td>
<td>5.17</td>
<td>5.93</td>
</tr>
<tr>
<td>Leaf area (cm²)</td>
<td>175.20</td>
<td>213.60</td>
<td>264.70</td>
<td>332.34</td>
<td>400.89</td>
<td>8.53</td>
<td>9.37</td>
<td>82.90</td>
<td>34.19</td>
<td>16.01</td>
</tr>
<tr>
<td>Number of tillers</td>
<td>10.00</td>
<td>13.43</td>
<td>16.89</td>
<td>0.75</td>
<td>1.25</td>
<td>6.44</td>
<td>8.33</td>
<td>59.79</td>
<td>1.38</td>
<td>10.26</td>
</tr>
<tr>
<td>Number of panicles</td>
<td>6.50</td>
<td>10.29</td>
<td>15.07</td>
<td>1.43</td>
<td>2.23</td>
<td>11.63</td>
<td>14.50</td>
<td>64.40</td>
<td>1.98</td>
<td>19.23</td>
</tr>
<tr>
<td>Number of fertile spikelets</td>
<td>8.81</td>
<td>86.39</td>
<td>101.30</td>
<td>22.71</td>
<td>53.97</td>
<td>5.52</td>
<td>8.50</td>
<td>42.08</td>
<td>6.37</td>
<td>7.37</td>
</tr>
<tr>
<td>Leaf dry weight (g)</td>
<td>3.02</td>
<td>5.09</td>
<td>9.35</td>
<td>0.53</td>
<td>0.73</td>
<td>14.31</td>
<td>16.75</td>
<td>72.91</td>
<td>1.28</td>
<td>25.16</td>
</tr>
<tr>
<td>Roots weight (g)</td>
<td>3.05</td>
<td>9.44</td>
<td>16.86</td>
<td>3.58</td>
<td>5.30</td>
<td>20.03</td>
<td>24.39</td>
<td>67.43</td>
<td>3.20</td>
<td>33.87</td>
</tr>
<tr>
<td>Panicle weight (g)</td>
<td>1.17</td>
<td>2.17</td>
<td>8.73</td>
<td>0.10</td>
<td>0.26</td>
<td>14.78</td>
<td>23.30</td>
<td>40.25</td>
<td>0.42</td>
<td>19.32</td>
</tr>
<tr>
<td>Stem weight (g)</td>
<td>3.48</td>
<td>8.00</td>
<td>13.78</td>
<td>0.81</td>
<td>2.01</td>
<td>11.27</td>
<td>17.71</td>
<td>40.49</td>
<td>1.18</td>
<td>14.77</td>
</tr>
<tr>
<td>1000 grains weight (g)</td>
<td>12.85</td>
<td>23.49</td>
<td>29.28</td>
<td>0.64</td>
<td>2.39</td>
<td>3.41</td>
<td>6.58</td>
<td>26.95</td>
<td>0.86</td>
<td>3.65</td>
</tr>
<tr>
<td>Yield/plant (g/plant)</td>
<td>22.79</td>
<td>36.04</td>
<td>45.79</td>
<td>8.31</td>
<td>13.36</td>
<td>8.00</td>
<td>10.14</td>
<td>62.23</td>
<td>4.69</td>
<td>13.00</td>
</tr>
</tbody>
</table>
panicle (0.1286), plant height (r=0.2794), panicle weight (r=0.112), stem weight (r=0.5262) and biomass (r=0.9291). Among these characters only stem weight and biomass showed significant positive correlation with grain yield per plant. On the contrary 1000 grains weight (r=0.024), number of fertile spikelets (r=0.3007), number of tiller (r=0.1425) and root weight (r=0.1489) were inversely but no significant correlated with grain yield per plant. Plant height had positive correlation with all the characters except leaves area, number of fertile spikelets and root weight. In the same time, number of fertile spikelets had negative correlation with almost the characters except 1000 grains weight and leaf dry weight. Positive and significant correlation were shown for biomass with root weight (r=0.5556) and for number of panicle with number of tillers and panicle weight (r=0.5345 and r=0.5134, respectively). However, plant height and number of panicle showed significant negative correlation with number of fertile spikelets (r=-0.4627) and leaf (r=0.5265), respectively.

**DISCUSSION**

Genetic diversity in breeding is very important. It is the key of crop improvement. More variability is observed in the basic population more is the chance of improvement. In the present study, results from ANOVA showed highly significant difference among the genotypes for all the characters, indicating huge genetic variability existing among the genotypes. So, the parents used for crossing were genetically different. Significant year effects were observed for all the characters except leaf area and stem weight, meaning that climate change were observed during the study. Environmental conditions were not similar during the two years. The results are in accordance to those found by Ogunbayo et al. (2014). All the characters, except leaf area and 1000 grains weight, exhibited stability across the seasons since the significance of genotype × year interaction was not detected and the differences among genotypes were clear. This appears to show that further improvement through selection for these characters may be effective. On the other hand, the significant effect of genotype × year interaction for leaf area and 1000 grains weight, indicating that genotypic difference in these characters was greatly influenced by the environment.

The current study suggests that phenotypic variance (Vp) and phenotypic coefficient variance (PCV) were higher than theirs corresponding genotypic variance (Vg) and genotypic coefficient of variance (GCV) respectively for all the characters studies, indicating that the expression of these
characters was influenced by environment. Similar results were reported by Dutta et al., (2013); Singh et al., (2014) and Tuhina-Khatun et al., (2015) in rice. It is interesting to note that this difference was low for all the characters except panicle weight and stem weight, indicating that these characters were less influenced by environment. It also suggests that selection based on these characters would be effective for future crossing. Similar result was also found by Prajapati et al., (2011) and Singh et al., (2014) for these traits. However the other traits like panicle weight and stem weight which showed a higher difference between PCV and GCV indicated that environmental effect on the expression of those traits is higher.

The most important function of the heritability in the genetic study of quantitative characters is its predictive role to indicate the reliability of the phenotypic value as a guide to breeding value (Falconer and Mackay, 1996; Al-Tabbal et al., 2012). High heritability estimates for yield/plant, plant height, day to 50% flowering, biomass and number of tillers, indicated a high response to selection in these traits. Similar results were also reported by Al-Tabbal et al., 2012; Dutta et al., 2013; Rafii et al., 2014, which support the present findings. Heritability in broad sense and the genetic advance are also important selection parameters. It is more useful as a selection tool when considered jointly with heritability. The estimates of genetic advance can help to understand the type of gene action of various polygenic characters. Johnson et al. (1955) suggested that high heritability estimates along with the high genetic advance is more helpful in predicting gain under selection than heritability estimates alone. Thus, the heritability estimates will be reliable if accompanied by high genetic advance. The present study revealed high heritability accompanied with high genetic advance as percent of the mean for leaf dry weight and root weight; high heritability and moderate genetic advance as percent of the mean for biomass, day to 50% flowering, leaf area, number of panicle and yield/plant. These results could be explained by additive gene action and their selection may be done in early generations. Similar findings have been reported by Wolie et al. (2013), Ogumbayo et al. (2014) on rice and Reza et al. (2015) on wheat. However, panicle weight and stem weight had moderate heritability coupled with low to moderate genetic advance as percent of the mean indicates non-additive gene effects; suggesting that these characters could be improved by developing varieties through recurrent selection method (Ogumbayo et al., 2014).

Selection of traits contributing simultaneously to a character will improve it in subsequent segregation population (Nor et al., 2013). Hence, the correlation analysis is therefore necessary to determine the direction of selection and the numbers of characteristics need to be considered in improving any character such as grain yield. The present study showed that there was a highly significant correlation between grain yield per plant with biomass at the 1% level and stem weight at the 5% level indicating that simultaneous selection for these characters would result in improvement of yield. Similar findings were earlier reported by Gulzar and Subhasl (2012), Azarpour (2013) and Moosavi et al. (2015). Also, day to 50% flowering exhibits a significant positive correlation with leaf area, number of panicle and stem weight. The observed positive correlation of date to 50% flowering was supported by earlier researchers such as Zhou et al. (2010) and Khan et al. (2014) for number of panicle. Plant height has not significant correlated with yield per plant. This result is in accordance with those of Golam et al. (2011) and Nor et al. (2013). However, this is in contrast with the previous study of Khan et al. (2014) and Moosavi et al. (2015) that presented the negative correlation between plant height and yield per plant. Positive and significant correlation was shown between plant height and number of fertile spikelets. Similar results were early reported by Aris et al. (2010) and Kohnaki et al. (2013). Azarpour (2013) also reported that plant height in rice had significant and positive correlated with spikelet fertility per plant.

Conclusion

The present study highlighted the existence of diversity among the 17 rice recombinant inbred lines, their parents and the check variety. High heritability in broad sense recorded for biomass, day to 50% flowering, plant height, leaf area, number of panicles, leaf dry weight, roots weight and grain yield per plant demonstrates that these characters could be successfully transferred to offsprings if their selection is performed in hybridization programme. The correlation analysis revealed that 8 agronomical traits such as day to 50% flowering, leaf area, leaf dry weight, number of panicle, plant height, panicle weight, stem weight and biomass have the positive contribution to grain yield. Among these characters, biomass and stem weight showed significant correlation with grain yield. So, these two traits may be considered as the selection criteria for the improvement of grain yield in rice.

Conflict of Interests

The authors have not declared any conflict of interest.

ACKNOWLEDGMENTS

The authors are thankful to all the team of INERA in Burkina Faso, Africa Rice center in Benin, and CIRAD Montpellier in France. Financial support from General Challenge Program (GCP) is dully acknowledged.
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