

Genetic Divergence Of Introduced Upland Rice Genotypes At Fogera In North Western Ethiopia

Research Article

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Abstract

Genetic divergence is basic in order to provide information for plant breeding programs. Forty nine upland rice genotypes were tested in 7*7 simple lattice design at Fogera in Wereta station of Adet Agricultural Research Center in 2012/13. The objectives of the study were to estimate the genetic divergence among the genotypes and cluster them in divergent clusters based on agro-morphological traits. Cluster analysis grouped 49 genotypes in to 9 distinct clusters. Clusters I and II were the largest clusters (34.7 %) containing 17 genotypes. Cluster III, IV and V had 21 genotypes (42.9%), 7 genotypes each. Principal component analysis showed that the first four principal components had explained about 85 % of the total variation. This study had indicated that there was significant genetic variability or divergence among the genotypes. Thus, the improvement program of the upland rice genotypes through direct selection rather than a lengthy crossing program is recommended.

Keywords: Principal Component; Agro-Morphological Traits.

Introduction

Rice belongs to the genus *Oryzae*, is one of the leading food crops in the world. As such, it is a staple food of over a half of the world's population, mostly in Asia (IRRI, 2013). In Ethiopia, the cultivation of the crop has begun at Asefa, Amhara region and Gambella plains in the early 1970's (Asefa Ayele, 2011). Divergence analysis is a technique used to categorize genotypes that are similar into one group and others into different groups (Sharma, 1998). Knowledge on the extent and pattern of genetic variability present and distance in a population is absolutely essential for further improvement of the crop. Besides, knowledge of the naturally occurring diversity in a population helps to identify diverse groups of genotypes that can be useful for the breeding program (Muhammad and Akbar, 2007). Such information is scarce in upland rice production system of Ethiopia.

Objective

To estimate the genetic divergence of introduced upland rice genotypes.

Material and Methods

The experiment was conducted at Woreta station (in Fogera) of Adet Agricultural Research Center which is a national testing site for rice research. Fogera is located 617 km away from Addis Ababa in the north western Ethiopia and it is only 50 km away to the north from Bahir Dar city, the capital of Amhara region. Nearly all of the land in the district is in the lowlands it has vertisol soil type and has an average elevation of 1812 m.a.s.l located at 11°54'N latitude and 37°41'E longitude with an average temperature of 14.2 °C minimum and 29.9 °C maximum temperatures. The area gets a unimodal annual average rain fall amount of 1556.8mm which extends from early June to September. Forty-nine upland genotypes/lines which are comprised from different preliminary variety trials and variety adaptation trial accessions were evaluated with two check varieties. The experiment was conducted in a simple lattice design with two replications. Clean seeds of each genotype were selected and planted on well prepared plots. The plot size was 2.5 m long and 0.4 m wide, consisting of two rows per plot with 20 cm spacing between them and 0.3m spacing between

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plots as well as 1m spacing between blocks. Sowing was done by hand drilling at a seed rate of 60 kg/ha. The experimental plots were prepared by tractor ploughing and harrowing. Nitrogen was

applied in the form of urea at the rate of 100 kg/ha, in three splits i.e., one third at planting, tillering and panicle initiation. Phosphorus was applied in the form of Di-Amonium phpsphate (DAP) at

Table 1. Forty nine upland genotypes/accessions used in the study.

| Entry no | Genotypes | Seed source |
|----------|----------------------------|-------------|
| 1 | IR 28635-B-B-23-1 | AARC |
| 2 | IR 83399-B-B-52-1 | “ |
| 3 | IR 82310-B-B-67-2 | “ |
| 4 | IR 82639-B-B-115-1 | “ |
| 5 | IR 79915-B-83-4-3 | “ |
| 6 | IR 78937-B-4-B-B-B | “ |
| 7 | IR 82319-B-B-103-2 | “ |
| 8 | IR 78913-B-10-B-B-B | “ |
| 9 | IR 78877-048-B-B-3 | “ |
| 10 | IR 78948-B-1-B-B-B | “ |
| 11 | UPLR1-7 | “ |
| 12 | IR 78937-B-3-B-B-2 | “ |
| 13 | IR 82039-B-B-103-4 | “ |
| 14 | IR 82635-B-B-32-4 | “ |
| 15 | IR 82638-B-B-147-1 | “ |
| 16 | IR 82639-B-B-118-3 | “ |
| 17 | IR 82589-B-B-114-3 | “ |
| 18 | IR 82635-B-B-58-1 | “ |
| 19 | IR 82635-B-B-88-2 | “ |
| 20 | IR 82639-B-B-140-1 | “ |
| 21 | IR 82635-B-B-4 7-1 | “ |
| 22 | IR 82635-B-B-72-2 | “ |
| 23 | IR 82589-B-B-7-2 | “ |
| 24 | IR 78937-B-3-B-B-1 | “ |
| 25 | IR 78940-B-22-B-B-B-5B1 | “ |
| 26 | IR 77298-14-1-2-10 | “ |
| 27 | KMP34 | “ |
| 28 | IR 60080-46A | “ |
| 29 | ACCU16 bar 9-16-17-3-B-1 | “ |
| 30 | ACCU 16 bar 5-6-22-2B-1 | “ |
| 31 | ACCU 16 bar 12-13-14-B-1 | “ |
| 32 | ACCU 16 bar 12-12-33-2B-1 | “ |
| 33 | ACCU 16 bar 15-3-22-2-B-B | “ |
| 34 | ACCU 16 bar 12-14-19-3-B-B | “ |
| 35 | ACCU 16 bar 9-4-16-3-B-1 | “ |
| 36 | ACCU 16 bar 13-13-2-2-B-B | “ |
| 37 | ACCU 16 bar 9-7-20-4-B-B | “ |
| 38 | ACCU 16 bar 4-8-17-2-8-8 | “ |
| 39 | NERICA 11 | “ |
| 40 | FOFIFA 3730 | “ |
| 41 | FOFIFA 3737 | “ |
| 42 | NERICA 14 | ” |
| 43 | NERICA 15 | “ |
| 44 | NERICA 8 | “ |
| 45 | NERICA 9 | “ |
| 46 | NERICA 15 | “ |
| 47 | FOFIFA 4129 | “ |
| 48 | NERICA 4 (Check) | “ |
| 49 | HIDASIE (Check) | “ |

the rate of 100 kg/ha at planting. All other management practices were uniformly applied to all plots using recommended practices. Data on plot and plant basis was collected. Data on plant basis were recorded by randomly taking six plants from each experimental plot.

Methods Of Data Collection

The data collection was based on quantitative descriptors. The data for the following characters were recorded from six randomly taken plants from each experimental plot and the average was considered per plant basis.

Culm length (cm): measured from the base of the plant to the base of the panicle.

Flag leaf length (cm): measure length of the flag leaf, from the ligule to the tip of the blade.

Flag leaf width (cm): measure width at the widest portion of the flag leaf.

Number of tiller per plant: recorded as the total number of grain-bearing and non bearing tillers.

Number of panicles per plant: number of primary panicle branches attached to the basal whorl of the panicle.

Panicle length (cm): Length of main axis of panicle measured from the panicle base to the tip.

Number of spikelet per panicle: total counted spikelets with inn a single panicle.

Flowering cycle: Number of days until 50% flowering starting from germination.

Maturation Cycle: Number of days until 50% of the panicles was mature.

1000-grain weight (gm): Random sample of 1000 well-developed, whole grains and dried to 13% moisture content weigh on a precision balance.

Grain yield (kg): estimated from the harvestable rows of the plot.

Data Analysis

Genetic divergence analysis was computed based on multivariate analysis using Mahalanobis's D2 statistic (Mahalanobis, 1936) by SAS Software program.

Estimation of distances

Distances (D) for each pair of genotype combinations were computed using the following formula:

$$D_{ij} = (X_i - X_j) S^{-1} (X_i - X_j)$$

Where, D_{ij} = the distance between any two genotypes i and j,

X_i and X_j = the vectors for the values for genotype i^{th} and j^{th} genotypes, and

S^{-1} = the inverse of pooled variance covariance matrix.

Clustering of genotypes

Based on the distances (D) values, clustering of genotypes was done using Tocher's method as described by Singh and Chaudhary (1999).

Principal component analysis

Principal component analysis (PCA) was used to find out the characters, which accounted more to the total variation. The data were standardized to mean zero and variance of one before computing principal component analysis. Principal component analysis (PCA) is one of the multivariate statistical techniques which is a powerful tool for investigating and summarizing underlying trends in complex data structures (Legendre and Legendre, 1998). Principal component analysis reflects the importance of the largest contributor to the total variation at each axis for differentiation (Sharma, 1998). Principal components based on correlation matrix were calculated using SAS 9.1 computer software.

Results and Discussion

Genetic Divergence Analysis

In the present study, the variation among the tested genotypes for all the characters studied justified the need to estimate distance values among the genotypes.

Estimation Of Distance and Clustering Of Genotypes: The distance values, based on the pooled mean of genotypes, resulted in classifying the 49 genotypes in to nine distinct clusters (Table 3.3). This indicated that the presence of wide diversity among the genotypes. Clusters I and II were the largest clusters (34.7 %) containing 17 genotypes together. Cluster III, IV and V had 21 genotypes in total (42.9%), 7 genotypes each, Clusters VI and VII had 8 genotypes together 4 genotypes each (16.3%), Cluster VIII constituted 2 genotypes (4.1 %) and Cluster IX had 1 genotype (2.0 %). Cluster IX had the least performance than any other genotypes tested (Fig 3.1).

Muhammad and Akbar (2007) in his study of clustering of basmati rice mutants by metrograph analysis also found 11 clusters of rice genotypes with cluster-I and cluster-II possessed the highest scores i.e., 66 % and 56 % respectively on morphological basis which is nearly similar result to this study.

Cluster mean analysis: The mean value of the 11 quantitative characters in each cluster is presented in Table 3.2.

Cluster I consisted of 9 genotypes having the characteristic of high culm length (75 cm), higher panicle length (2 cm), relatively high number of spikelet per panicle (74.68) and relatively higher yield (4408.44 kg/ha) next to cluster V (5,200 kg/ha) and cluster VI (4,875 kg/ha). This cluster is relatively early maturing with values of lower flowering cycle (97.19 days) and maturation cycle (135.44 days).

Table 4. Eigenvectors and eigenvalues of the first four principal components (PCs) for 11 characters of 49 upland rice genotypes tested at Fogera (2011/12).

| Characters | Eigenvectors | | | |
|--|--------------|-------|-------|-------|
| | PC1 | PC2 | PC3 | PC4 |
| Flag leaf length | 0.11 | 0.49 | 0.73 | 0.22 |
| Flag leaf width | 0.35 | 0.17 | 0.01 | 0.05 |
| Culm length | -0.36 | -0.09 | 0.17 | -0.10 |
| Number of tiller per plant | -0.37 | 0.02 | -0.06 | -0.10 |
| Flowering cycle | 0.13 | -0.63 | 0.50 | -0.34 |
| Maturation cycle | 0.38 | 0.02 | 0.01 | 0.03 |
| Number of panicles per plant | 0.34 | -0.14 | 0.19 | 0.21 |
| Panicle length | -0.33 | -0.10 | 0.13 | 0.35 |
| Number of spikelet per spike | -0.28 | -0.11 | 0.06 | 0.66 |
| Thousand seed weight | 0.30 | 0.10 | -0.34 | 0.20 |
| Grain yield | -0.21 | 0.53 | 0.10 | -0.41 |
| Eigen value | 6.45 | 1.32 | 0.93 | 0.68 |
| Difference | 5.13 | 0.39 | 0.25 | 0.09 |
| Percent of total variance explained | 59 | 12 | 8 | 6 |
| Cumulative percent of total variance explained | 59 | 71 | 79 | 85 |

Figure 1. Dendrogram depicting cluster analysis among 49 upland rice genotypes.

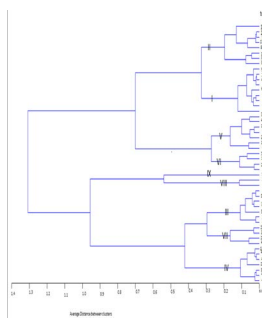
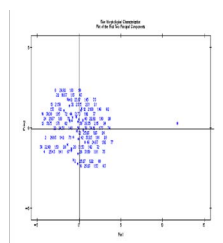


Figure 2. Scatter graph depicting the 49 upland rice genotypes tested at Fogera (2012/13).



Cluster II had consisted of 8 genotypes. This cluster is characterized by high number of panicles per plant (10.14), relatively high number of spikelet per plant (75.55), high panicle length (20 cm) and relatively moderate yield (4011.63 kg/ha) next to cluster V (5,200 kg/ha), cluster VII (4,875 kg/ha) and cluster I (4,408 kg/ha).

Cluster III had consisted of 7 genotypes, including the standard check Nerica-4, which are characterized by the following features, the highest culm length (75 cm) and relatively higher number of tillers per plant (9.80) next to cluster IX (10.9) and the earliest flowering types (93.63 days).

In cluster IV there are seven genotypes. The cluster is characterized by relatively higher flag leaf length (27 cm) next to cluster V

(28 cm), lower tiller number per plant (7.44) next to cluster VIII (6.95), relatively lower maturation cycle (133.86 days) next to cluster VIII (133.25 days) and relatively lower number of spikelet per panicle (69.14) next to cluster VIII (66.85).

Cluster V had consisted of seven genotypes. The cluster could be characterized by highest flag leaf length (28 cm), relatively higher flowering cycle (103.53 days) next to cluster IX (109.1 days), highest number of spikelet per panicle (76.7), highest panicle length (21 cm) and highest yield 5,200 kg/ha.

Cluster VI consisted 4 genotypes with a characteristic feature of higher flag leaf length (27 cm) next to cluster V (28 cm), shorter culm length (63 cm) next to cluster IX (61 cm), moderately higher flowering cycle (100.3 days) next to cluster IX (109.1 days) and

Table 3. Mean value of 11 quantitative characters of the nine clusters for 49 upland rice genotypes tested at Fogera (2012/13).

| Cluster | Parameters | | | | | | | | | | |
|---------|------------|------|------|------|-------|-------|------|------|------|----|--------|
| | FLL | FLW | CL | NTPP | FC | MC | NPP | NSPP | PL | TW | YLD |
| I | 0.26 | 0.02 | 0.75 | 8.67 | 97.2 | 135.4 | 8.7 | 74.7 | 0.2 | 2 | 4408.4 |
| II | 0.26 | 0.02 | 0.71 | 8.56 | 97.5 | 135.8 | 10.1 | 75.6 | 0.2 | 2 | 4011.6 |
| III | 0.27 | 0.02 | 0.75 | 9.8 | 93.6 | 134.6 | 8.9 | 73.2 | 0.19 | 2 | 3484.1 |
| IV | 0.27 | 0.02 | 0.73 | 7.44 | 98.5 | 133.9 | 8.1 | 69.1 | 0.19 | 2 | 3110.7 |
| V | 0.28 | 0.02 | 0.68 | 8.89 | 103.5 | 135.9 | 8.9 | 76.7 | 0.21 | 2 | 5200 |
| VI | 0.27 | 0.02 | 0.63 | 8.63 | 100.3 | 136.4 | 8.2 | 74.1 | 0.18 | 2 | 4875 |
| VII | 0.25 | 0.02 | 0.72 | 8.13 | 98.6 | 137 | 8 | 72.2 | 0.2 | 2 | 2750 |
| VIII | 0.24 | 0.02 | 0.75 | 6.95 | 95.6 | 133.3 | 8.5 | 66.9 | 0.18 | 3 | 2251 |
| IX | 0.22 | 0.01 | 0.61 | 10.9 | 109.1 | 138.5 | 7.9 | 70.5 | 0.16 | 2 | 1557 |

FLL: Flag leaf length (cm), FLW: Flag leaf width (cm), CL: Culm length (cm), NTPP: Number of tiller per plant, FC: Flowering cycle, MC: Maturation cycle, NPP: Number of panicle per plant, NSPP: Number of spikelet per panicle, PL: Panicle length (cm), TSW: Thousand seed weight (gm), YLD: Yield (kg/ha).

Table 2. Distribution of genotypes in to nine clusters based on distance analysis for 49 upland rice genotypes tested at Fogera (2012/13).

| Cluster | Total number Of genotypes | Genotypes |
|---------|---------------------------|---|
| I | 9 | IR 82635-B-B-58-1, IR 82639-B-B-140-1, FOFIFA 3730, FOFIFA 3737, NERICA 14, FOFIFA 4129, HIDASIE (Check), IR 79915-B-83-4-3, IR 78937-B-4-B-B-B |
| II | 8 | IR 28635-B-B-23-1, IR 82639-B-B-118-3, IR 82589-B-B-114-3, IR 83399-B-B-52-1, ACCU 16 bar 5-6-22-2B-1, ACCU 16 bar 15-3-22-2-B-B, ACCU 16 bar 12-14-19-3-B-B, IR 78913-B-10-B-B-B |
| III | 7 | IR 82039-B-B-103-4, IR 82635-B-B-72-2, NERICA 11, NERICA 8, NERICA 9, NERICA 15, NERICA 4 (Check) |
| IV | 7 | IR 78948-B-1-B-B-B, UPLR1-7, KMP34, ACCU 16 bar 12-13-14-B-1, ACCU 16 bar 12-12-33-2B-1, ACCU 16 bar 13-13-2-2-B-B, ACCU 16 bar 9-7-20-4-B-B |
| V | 7 | IR 78937-B-3-B-B-2, IR 82635-B-B-32-4, IR 82638-B-B-147-1, IR 78937-B-3-B-B-1, IR 78940-B-22-B-B-B-5B1, IR 82310-B-B-67-2, IR 82639-B-B-115-1 |
| VI | 4 | IR 82635-B-B-88-2, IR 77298-14-1-2-10, IR 60080-46A, IR 82319-B-B-103-2 |
| VII | 4 | IR 82589-B-B-7-2, ACCU16 bar 9-16-17-3-B-1, ACCU 16 bar 4-8-17-2-8-8, NERICA 15 |
| VIII | 2 | IR 82635-B-B-4 7-1, ACCU 16 bar 9-4-16-3-B-1 |
| IX | 1 | IR 78877-048-B-B-3 |

cluster V (103.53 days) and relatively higher yield (4,875 kg/ha) next to cluster V (5,200 kg/ha).

Four genotypes made Cluster VII. This cluster had features of higher maturation cycle (137 days) next to cluster IX (138.5 days), lower number of panicle per plant (8.00) next to cluster IX (7.90), moderately lower number of spikelet per panicle (72.18) next to VIII (66.85) and IV (69.14) and relatively lower grain yield (2,750

kg/ha) next to cluster IX (1,557 kg/ha) and cluster VIII (2251 kg/ha).

Cluster VIII had only two genotypes. This cluster is also characterized by lower flag leaf length (24 cm) next to cluster VIII (22 cm), highest culm length (75 cm), lowest number of tiller per plant (6.95), relatively lower flowering cycle (95.60 days) next to cluster III (93.63 days), lowest maturation cycle (133.25 days),

lowest number of spikelet per panicle (66.85), lower panicle length (18 cm) next to cluster IX (16 cm), highest thousand seed weight (0.03 kg) and lower grain yield (2,251 kg/ha) next to cluster IX (1,557 kg/ha).

Cluster IX had one genotype which was the least type by its performance in most of the traits, the cluster is characterized by the following features, lowest flag leaf length (22 cm), lowest flag leaf width (1 cm), lowest culm length (61 cm), highest number of tiller per plant (10.90), highest flowering cycle (109.10 days), highest maturation cycle (138.5 days) or late maturing type, lowest number of panicle per plant (7.90), lowest panicle length (16 cm) and lowest yield (1557 kg/ha).

Principal component analysis

The principal component analysis revealed that four principal components i.e., PC1, PC2, PC3 and PC4 with eigenvalues of 6.45, 1.32, 0.93 and 0.68, respectively, have accounted for 85% of the total variation (Table 3.3). The first two principal components PC1 and PC2 with cumulative variance values of 71%, contributed more to the total variation. According to Chahal and Gosal (2002) characters with largest absolute values closer to unity with in the first principal component influence the clustering more than those with lower absolute values closer to zero. Therefore, in this study, differentiation of the genotypes into different cluster was because of a cumulative effect of a number of characters rather to the small contribution of each character.

Characters having relatively higher value in the first principal component (PC1) were flag leaf width, culm length, number of tiller per plant and maturation cycle. Characters like flag leaf length, flowering cycle and grain yield had contributed a lot for principal component (PC2); flag leaf length, flowering cycle and thousand seed weight had contributed in the third principal component (PC3); number of spikelet per panicle, grain yield, panicle length and flowering cycle in the fourth principal component (PC4) were the major contributors.

Ogunbayo et al. (2005) also found in his study of phylogenetic diversity and relationships among 40 rice accessions using mor-

phological and RAPDs techniques that the PCA re-ordered the accessions into four broad groups that had within cluster similarities which is very similar to the finding of this study.

Conclusion and Recommendation

The nine clusters indicated that the presence of wide diversity among the genotypes. Clusters I and II were the largest clusters (34.7 %) containing 17 genotypes together. Cluster III, IV and V had a total of 21 genotypes, 7 genotypes each (42.9 %), Clusters VI and VII had 8 genotypes together 4 genotypes each (16.3%), Cluster VIII constituted 2 genotypes (4.1 %) and Cluster IX had 1 genotype (2.0 %). Cluster IX had the least performance than any other genotypes tested. This study had indicated that there was significant genetic divergence among the genotypes. Thus, there is an enormous opportunity in the improvement program of the upland rice genotypes through direct selection rather than a lengthy crossing program and hybridization which involves technical expertise crossing of the genotypes from different clusters that would produce viable and a potential segregate population. Regarding this, due to its highly significance difference in yield and related traits I recommend specially Accessions IR 78937-B-3-B-B-1 for further breeding and selection procedures.

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