



Plant Archives

Journal homepage: <http://www.plantarchives.org>
DOI Url : <https://doi.org/10.51470/PLANTARCHIVES.2023.v23.no1.024>

MULTIVARIATE ANALYSIS OF SEEDLING VIGOUR TRAITS IN INDIGENOUS RICE (*ORYZA SATIVA*.L) GENOTYPES OF MANIPUR INDIA

Sushilkumar S.*, E.V. Divakara Sastry, Sakthivel G,Th., Renuka Devi, G, Bireswar Sinha and N. Gopimohan Singh

College of Agriculture, Central Agricultural University, Manipur- 795004, India

*Corresponding author Email: plantdoc@rediffmail.com

(Date of Receiving : 09-10-2022; Date of Acceptance : 17-01-2023)

ABSTRACT

Access to a diverse range of genetic material is quite important for the success of any plant breeding effort. An evaluation was commenced to determine genetic diversification of 30 genotypes of rice based on 14 seedling traits by employing multivariate analyses i.e., hierarchical cluster and Principal Component Analyses (PCA). Cluster analysis segregated the genotypes into five classes which are in contrast for germination, seedling length, root length, seedling vigour Index-I and seedling vigour index-II. The first three PCs explained 89.07% of the total variability were the major traits in discriminating the genotypes. In grouping of genotypes, the hierarchical cluster and PC analyses was used. Parental combinations from the five clusters with higher value of Euclidean distance could be used for genetic improvement. Generally, is the most diverged genotype from others. Thus, crossing of this genotype with Ashangbrokakara, Moliro, Stejari, and Kawnglang might result in heterotic expression in the F_1 and substantial variability in the successive segregating population.

Keywords : Cluster analysis, Genetic diversity, Germination, Principal component analysis, vigour.

Introduction

Rice (*Oryza sativa* L.) is one of the most important staple crops in the global agriculture. It belongs to poaceace family and is native of South East Asia (Indo-burma). The chromosome number of rice is $2n=24$. It is self-pollinated crop. Rice is mainly used for food, fodder, feed and fuel purpose. Due to increasing of population the demand for rice is increasing among the cereals. More than 2 billion of people in Asia obtain their 60-70% of caloric intake from rice.

For higher seed yield, good crop stand is equally important along with high yield potential. Crop stand is dependent on the seedling vigour. Like seed yield, seedling vigour is also a complicated trait. Some characters like root length, shoot length and seedling dry weight has been identified as standard indicator of seed vigour (Regan *et al.*, 1992). Seed vigour involves those properties that regulate the potential for uniform and rapid emergence and development of normal seedling under broad range of field circumstances. Cultivars, ageing, position of seeds on the panicle, weather during maturity, time of harvest, specific gravity, nutrition, mechanical integrity, storage conditions and pathogen are the main causes of variation in seedling vigour (Seshu *et al.*, 1988). Seed lot exhibiting the higher Seed Vigour Index (SVI) is esteemed to be more vigorous. Rice is considered to be the most important crop in India as well as in the world. So, the genotypes with potent seed vigour are profitable for the farmers to obtain ideal stand establishment in the direct sowing culture system.

In India more than 50% of the area is under rain fed condition. In this condition direct seeded rice are suitable. So

high seed vigour is crucial for direct seedling because it doesn't enhances only crop development (Wang *et al.*, 2010), but also increases the plant ingenuity to compete against weeds (Rao *et al.*, 2007).

Materials and Method

In the present study, 30 indigenous rice genotypes of Manipur were used for the evaluation. Of these, 26 rice genotypes were selected randomly from the collection maintained at Regional Rice Research station (RRRS), Thoubal, Manipur and 4 genotypes selected randomly form a collection maintained at College of Agriculture, Central Agriculture University (COA, CAU) Imphal, Manipur (Table 1). The seeds of 2018 *kharif* season harvest was used for evaluation. 100 seeds was placed for germination using between the paper method using roll towels and was incubated inside Plant Growth Chamber maintained at 25°C. the germination towels was placed in tray containing Hoagland's solution as per the composition given by Salisbury and Ross (1991) such that the solution moved up through capillary force. The whole set was replicated thrice in a RBD design. The whole experiment was maintained up to 14 days, following that the germination percentage was reported. Observations on other traits namely shoot length, root length, seedling length, seedling vigour index-I and seedling vigour index-II were noted on all the healthy seedlings and averaged. Anova was conducted to know the variance among the genotypes and Multivariate analysis *viz.*, principal component analysis (PCA), cluster analysis was accomplished using the software STAR (Ver 2.0.1.0) of IRRI, Philippines.

Table 1 : List of rice (*Oryza sativa*. L) genotypes and their source of origin used in this study

S. No	Genotype	Source / Place
1	Asangbrokakra	RRS, Thoubal
2	Atiya tungla	RRS, Thoubal
3	Ayangleima	RRS, Thoubal
4	CAU R2	COA,CAU,Imphal
5	CAU R3	COA,CAU,Imphal
6	Kankchengphou	RRS, Thoubal
7	Kawngalwng	RRS, Thoubal
8	Khokmaha km	RRS, Thoubal
9	Kio phou	RRS, Thoubal
10	Kobra	RRS, Thoubal
11	Kumbi	RRS, Thoubal
12	Leimaphou	RRS, Thoubal
13	Malmal sang	RRS, Thoubal
14	Mangalphou	COA,CAU,Imphal
15	Mazinlu	RRS, Thoubal
16	Moilro	RRS, Thoubal
17	Napnang	RRS, Thoubal
18	Phoungang	RRS, Thoubal
19	Phouoibi	RRS, Thoubal
20	PhourenKhoganbi	RRS, Thoubal
21	Picharo	RRS, Thoubal
22	RCM 5	RRS, Thoubal
23	RCM 6	RRS, Thoubal
24	RCM-10	RRS, Thoubal
25	Sangsangba	RRS, Thoubal
26	Stejari	RRS, Thoubal
27	Tamphaphou	COA,CAU,Imphal
28	Tathai	RRS, Thoubal
29	Thangjing	RRS, Thoubal
30	Tora	RRS, Thoubal

Results and Discussion

The Analysis of variance (ANOVA) exhibited that there is significant difference between the genotypes for all the features studied, depicting that the differences are genetical. (Table 2). It also indicates that direct or indirect selection will be effective for various traits.

Table 2 : Analysis of Variance for 14 quantitative characters of 30 rice genotypes

Character	Replication	Genotypes	Error
Degrees of freedom	2	29	58
Germination	8.533	1484.781**	81.728
Root Length	2.7313	20.8974**	2.3221
Shoot Length	0.1439	10.254**	0.6902
Seedling length	3.062	47.043**	3.973
Root fresh Wt	4140.97	7219.67**	5378.242
Shoot Fresh Wt	665.544	9283.114*	1236.234
Seedling fresh Wt	7441.3444	24079.938**	7590.5169
Seedling Dry Wt	26.433	1005.025**	94.134
Root dry Wt	8.633	365.218**	36.369
Shoot Dry Wt	28.433	307.727**	57.536
RSR	0.012	0.2109**	0.0551
SVI-I	22468.4402	1173460.824**	40889.953
SVI-II	0.2263	18.9711**	0.5359
DMA	2.4477	6.8457**	1.6702

* indicate significance at p=0.05 and ** at p=0.01 respectively.
 Wt – Weight, RSR-Root shoot Ratio, SVI-I - Seed Vigour Index-I, SVI-II - Seed Vigour Index-II,
 DMA – Dry matter accumulation.

Multivariate statistical designs have found profound use in encapsulating and delineating the inherent dissimilarity in a group of genotypes. Few techniques include Principal component analysis (PCA), cluster analysis (CA) and Discriminant canonical analysis (DCA). PCA is one of the popular flexible techniques available for compiling and expressing the innate genetic differences in the genotypes of crop. The procedures are often stretched to genotypes' grouping in to cluster and thus lead in the preference of parents for hybridization. Hence, principal component analysis (PCA) and Cluster analysis (CA) were conducted to know the genetic divergence among the genotypes studied for seed vigour traits.

Principal Component Analysis

Principal component analysis indicated that that the first three main PCAs explained a cumulative variance of above 80%. Of these, the first two accounted for nearly 70% of the variance. In other words most of the variance is explained by the first two components. More than total of the area extracted from the complicated components. The first four components have an eigen value >1 (Brejda *et al.*, 2000). PC1 for maximum variability in the data with respect to succeeding components is similar to the finding of Basnet *et al.* (2014), Md Rahim *et al.* (2008) in mungbean. Adebisi *et al.* (2013) and Adekoya (2008) observed that first three principal components were pivotal in reflection the variation. he biological meaning of the principal component can be determined from the contribution of the unlike variables to each principal component according to the eigen vectors Adebisi *et al.* (2013). Results of principal component analysis showed that various characters contributed uniquely to the total variation as depicted by the eigen vectors (Table 3) and presented in Fig 1.

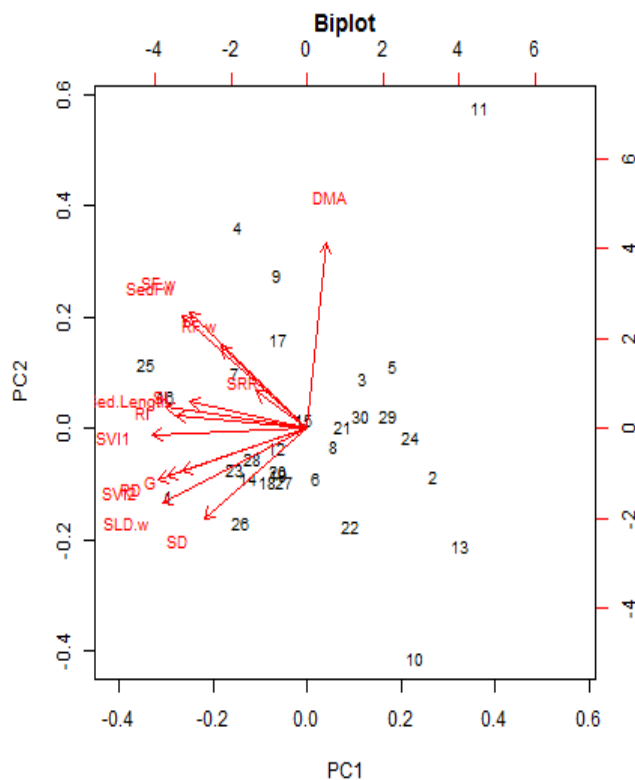


Fig. 1 : Biplot

Table 3 : Eigen Vector

Variables	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12	PC13	PC14
Germination	-0.278	-0.140	-0.286	0.295	-0.152	-0.480	-0.335	0.325	0.339	-0.440	-0.118	-0.111	0.073	-0.001
Root length	-0.290	0.044	0.032	-0.244	0.612	-0.224	0.364	-0.045	0.162	-0.012	0.003	0.034	0.000	0.517
Shoot length	-0.259	0.087	0.193	-0.521	-0.288	0.061	-0.621	-0.028	0.088	-0.064	-0.024	0.014	0.015	0.362
seedling length	-0.314	0.070	0.112	-0.406	0.274	-0.120	-0.048	-0.044	0.147	-0.379	-0.006	0.030	0.006	-0.776
Root fresh weight	-0.191	0.274	0.246	0.532	0.389	0.150	-0.416	-0.036	0.002	0.059	0.116	-0.008	0.424	0.000
Shoot fresh weight	-0.264	0.388	0.012	-0.136	-0.335	0.090	0.036	0.486	-0.131	0.109	0.166	-0.025	0.440	-0.004
Seedling fresh weight	-0.277	0.374	0.136	0.223	0.024	0.150	-0.012	0.314	-0.073	0.026	-0.127	0.083	-0.753	0.000
Seedling dry weight	0.320	-0.251	0.077	0.069	-0.079	0.353	0.152	-0.187	0.044	-0.332	0.506	-0.498	0.137	0.001
Root dry weight	-0.312	-0.158	-0.279	0.017	0.009	0.146	0.045	-0.084	0.087	0.324	-0.633	-0.304	0.109	-0.002
Shoot dry weight	-0.228	-0.299	0.430	0.129	-0.177	0.176	0.244	-0.139	-0.318	-0.310	-0.270	0.560	0.120	0.000
Root and shoot Ratio	0.113	0.123	-0.692	-0.070	0.128	0.331	-0.101	-0.080	-0.149	-0.295	0.166	0.455	0.023	0.001
Seedling vigour Index-I	-0.342	-0.023	-0.066	-0.058	-0.072	-0.411	-0.037	-0.284	-0.775	0.037	-0.066	-0.113	-0.007	0.001
Seedling vigour Index-II	-0.329	-0.170	-0.193	0.175	-0.238	-0.174	0.003	-0.196	0.315	0.596	0.360	0.311	-0.924	0.001
Dry matter accumulation	0.043	0.617	-0.030	0.077	-0.255	-0.096	0.191	-0.606	0.274	-0.174	-0.143	-0.082	0.006	-0.001

As a typical rule of thumb for determining the relevance of a trait, the arithmetic sign of coefficient is insignificant. When a coefficient is more than 0.3, it is assumed to have a large enough effect to be regarded significant (Raji, 2003). In this study traits with coefficient values less than 0.2 were considered to have no effect on the overall variation. The Eigen vector results showed that the character like seedling length, seedling dry weight, seedling vigour index I and seedling vigour index II were negatively influenced to the total variation in principal component 1. Likewise seedling fresh weight and shoot fresh weight exhibited positive influence to the variation of principal component 2. In principal component 3 shoot dry weight were contributed positively to the variation and shoot and root ratio influenced negatively to the variation. In principal component 4 root fresh weight was positively influenced to the variation shoot length and seedling length were negatively influenced to the variation. An additional perception was attained by plotting the PC scores for each observation with respect to the axes of PC 1 and PC 2 (Figure 1).

It can be inferred from Fig 1 that genotype 15 had nearly average values for most of the traits. Genotypes 11 is best as it had high Dry Matter Accumulation while it also has reasonably ideal values for most of the traits. Genotype 1 has lower values for traits like Seedling Dry Weight, Seedling Dry Weight, Seedling Vigour Index-I, Root Dry Weight. among the traits, it is seen that most of the traits pointed to one direction, which indicates that these traits influenced germination in one direction, which makes selection effective for better genotypes which will have high seedling establishment/ vigour.

Cluster analysis

Cluster analysis was conducted using the average linkage distance method of hierarchical clustering method on STAR software developed by IRRI. The 30 genotypes were grouped into 5 clusters as shown in the diagram. Clusters IV and V contained only one genotype each, all other 3 clusters exhibited multiple genotypes (Table 4).

Table 4: Distribution of 30 rice genotypes in different clusters

Cluster	Frequency	Membership
I	10	Ashangbrokakra, Kawnglang, Moliro, Napngang, Picharo, Phongang, RCM- 6, Sangsangba, Stejari, Tathai
II	5	Atiya tungla, CAU – R4, Kobra, Malmasang, RCM – 5
III	13	Ayanleima, Kakchengaba, Khokmacha, Kio phou, Leimaphou, Mangalphou, Mazinula, Phouoibi, PhourenKhongamba, RCM – 10, Tamphaphou, Thanjing, Tora
IV	1	CAU - R2
V	1	Kumbiphou

Table 5: Cluster means for 14 characters of 30 genotypes

Trait / Cluster	I	II	III	IV	V
Germination	83.33	40.47	74.36	73.33	25.33
Root Length	15.88	11.26	13.94	16.31	8.41
Shoot Length	9.29	5.86	6.16	6.42	6.29
Seedling length	25.18	17.12	20.1	22.73	14.7
Root fresh weight	77.1	43.4	63.44	290	11
Shoot Fresh weight	246.3	134.2	193.1	229	253
Seedling fresh weight	322.8	172	254.95	519	242
Seedling Dry weight	92.1	68.6	72.64	80.67	25
Root dry weight	43.17	24.33	38.74	30.67	12.33
Shoot Dry weight	48.93	45.53	34.41	50	12.67
Root and Shoot Ratio	0.9	0.53	1.14	0.61	1.06
Seedling Vigour Index -I	2061.84	699.76	1437.84	1948.01	484.2
Seedling Vigour Index-II	7.7	2.91	5.43	5.89	0.63
Dry Matter Accumulation	3.52	2.65	3.56	6.2	10.03

Characters based on cluster mean values

The cluster mean values for 14 characters are presented in the Table 5. The data indicated that mean values exhibited wide range for almost all the traits in the study. Cluster 1 obtained maximal mean value for germination, shoot length, root length, seedling length, seedling dry weight, root dry weight, seedling vigour index-I, seedling vigour index -II. For root fresh weight and seedling fresh weight cluster IV had supreme values. Cluster V obtained highest mean values for shoot fresh weight and dry matter accumulation. The genotypes from different clusters can be selected based on

the interest of the character to be enhanced. In the present investigation cluster I showed the highest mean value for seedling vigour index-I and seedling vigour index-II. So, selection of parents from this cluster will be useful for making superior seed vigour for directed seeded rice. These the results are in line with the findings of Tejasmini *et al.* (2016), Ovung *et al.* (2012).The above grouping shows the existent of broad genetic divergence amid rice genotypes. Thus, observations recommended that inter crossing of genotypes from non-identical cluster showing good mean performance may help in get quality genotypes

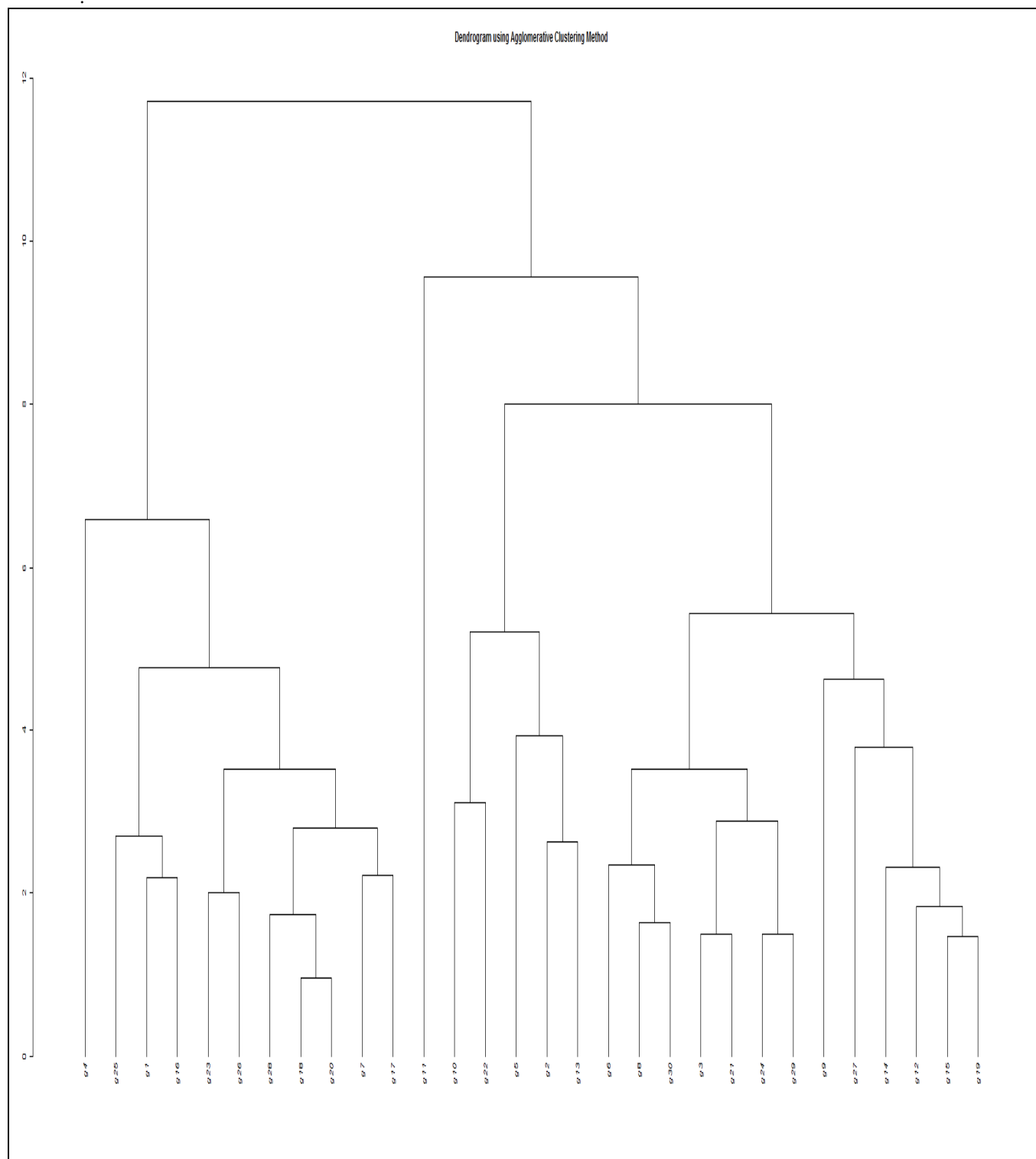


Fig. 2 : Dendrogram using agglomerative clustering method

Conclusion

This study, utilized multivariate technique to attain the degree of genetic variation in seed life of 30 rice genotypes, was a initial phase in acquiring an intuition into the germplasm divergence which is a significant stage towards an productive exploitation of genetic assets of rice genotypes. The principal component analysis distinguished dry matter accumulation, seedling fresh weight, shoot fresh weight, seedling length, root length, root and shoot ratio were impacting characters in fourth quarters. Move over seedling vigour index-I, seedling vigour index-II, seedling dry weight, shoot dry weight were the influencing characters of third quarter (-, -) so these are the characters were negatively influenced for the divergence and genotypes like Ashangbrokakra, Kawlang, Moliro, RCM-6, Sangsangbaand Stejari were found best genotypes because they have maximal seedling vigour index-I and also seedling vigour index-II. Cluster analysis showed that genotypes from cluster 1 gave good results when utilized in the hybridization programme.

References

- Adebisi, M.A.; Okelola, F.S.; Ajala, M.O.; Kehinde, T.O.; Daniel, I.O. and Ajani, O.O. (2013). Evaluation of Variations in Seed Vigour Characters of West African Rice (*Oryza sativa* L.) Genotypes Using Multivariate Technique. *American Journal of Plant Sciences*. 4: 356-363.
- Adekoya, M.A. (2008). Evaluation of Variation, Inter-Character Correlation and Performance of Okra (*Abelmoschus esculentus*). MA Dissertation, University of Agriculture, Abeokuta, 111.
- Basnet, K.M.; Adhikari, N.R. and Pandey, M.P. (2014). Multivariate analysis among the Napalese and exotic mungbean (*Vigna radiata* (L.) Wilczek) genotypes based on the qualitative parameters. *Universal Journal of Agricultural Research*. 2(5):147-155.
- Brejda, J.J.; Moorman, T.B.; Karlen, D.L. and Dao, T.H. (2000). Identification of regional soil quality factors and indicators. Central and Southern High- Plains. *Soil Science Society of America Journal*. 64: 2115-2124.
- Khare, R.; Singh, A.K.; Eram, S. and Singh, P.K. (2014). Genetic variability, association and diversity analysis in upland rice (*Oryza sativa* L.). *SAARC Journal of Agriculture*. 12(2):40-51.
- Md. Rahim, A.; Mia, A.A.; Mahmud, F. & Afrin, K.S. (2008). Multivariate analysis in some mungbean (*Vigna radiata* L. wilczek) accession on the basis of agronomic traits. *American Eurasian journal of Scientific Research*, 3: 217-221.
- Ovung, C.Y.; Lal, G.M. and Rai, P.K. (2012). Studies on genetic diversity in Rice (*Oryza sativa* L.). *Journal of Agricultural Technology*, 8(3): 1059-1065.
- Raji, A. (2003). Assessment of Genetic Diversity and Heterotic Relationships in African Improved and Local Cassava (*Manihot esculenta* Crantz) Germplasm, Ph.D. Thesis, Obafemi Awolowo University, Ile Ife, 120.
- Rao, A.N.; Johnson, D.E.; Sivaprasad, B.; Ladha, J.K. & Mortimer, A.M. (2007). Weed management in direct-seeded rice. *Advances in Agronomy*. 93: 153-255.
- Regan, K.L.; Siddique, K.H.M.; Turner, N.C. and Whan, B.R. (1992). Potential for increasing early vigor and total biomass in spring wheat. II. Characteristics associated with early vigor. *Australian Journal of Agricultural Research*, 43: 541-553.
- Salisbury, F.B. and Ross, C.W. (1991). Plant physiology. Wood worth publishing company, Belmont, CA, USA.
- Seshu, D.V.; Krishnasamy, V. and Siddique, S.B. (1988). Seed vigor in rice. Rice seed health. *International Rice Research Institute, Los Banos*, p.315-329.
- Singh, A.; Singh, B.; Panda, K.; Rai, V.P.; Singh, A.K.; Singh, S.P.; Chouhan, S.K.; Rai, V.; Singh, P.K. and Singh, N.K. (2013). Wild rice of Eastern Indo-Gangetic plains of India constitutes two sub populations harbouring rich genetic diversity. *Plant Omics Journal*, 6(2):121-127.
- Tejaswini, K.L.Y.; Manukonda, S.; Rao, P.R.; Kumar, B.R.; Mohammad, L.A. and Raju, S.K. (2016). Cluster analysis studies in rice (*Oryza sativa* L.) using wards minimum variance method. *Journal of Agricultural and Crop Research*, 4(9): 129-139.
- Wang, Z.F.; Wang, J.F.; Bao, Y.M, Wang, F. and Zhang, H.S. (2010). Quantitative trait loci analysis for rice seed vigor during the germination stage. *Biomedical and Biotechnology research journal*, 11(12): 958-964.