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RESEARCH ARTICLE

Principle Component and Cluster Analyses for Yield and Yield Components in Some Indigenous Rice (*Oryza sativa* L.) Genotypes

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ABSTRACT

The present study was conducted with 25 rice genotypes at research field of Institute of Agriculture Sciences, Banaras Hindu University, Varanasi during the kharif, 2012 to assess the extent and pattern of genetic divergence. Cluster analysis exhibited that genotypes fall into four clusters, in which cluster I is mono genotypic cluster, indicated the uniqueness of the genotype from rest ones. Principle component analysis (PCA) showed that the first three PCs had eigen value >2.00 and accounted 60% of total variation. IC 337588 was found most suitable genotypes may be chosen and involved in hybridization programme as a one of the parent for rice improvement. IC 337588 and IC 145605 were found most divergent with each other indicated the possibility of improvement of rice by manipulation of various traits viz., PL, DFF, DM, NETPI, GW, GWPa, GYP and HI. Besides, the representative genotypes from each cluster may also be utilized in hybridization programme to get good heterotic response.

Keywords: Cluster analysis, Genetic diversity, Indigenous collections, Principle component analysis (PCA), Rice.

INTRODUCTION

The increase in global population has gradually led to food shortage and hence, increases in poverty. This issue is a major challenge to breeders due to increasing population day by day and limited cultivable land [3 & 14]. Crop improvement technique, therefore remains a major concern to plant breeders [1, 2 & 16]. Thus, there is a need to develop the high yielding varieties to increase the production and productivity. Genotypes have wide and diverse origin and genetic background known as genetic diversity.

Knowledge of genetic variability is a pre requisite of any crop improvement programme [18]. Germplasm constitutes the foundation for genetic improvement of crops. The pace and magnitude of genetic improvement are generally dependent on the amount of genetic diversity present in a population [19]. To boost the yield potential of rice, it is necessary to identify cultivars with improved yield and other desirable agronomic characters, to overcome the global problem of hunger and starvation [6]. Genetic variation is the basis of plant breeding and provides a great array of genotypes that can be selected to develop new varieties or breeding materials [12]. Therefore, grouping of genotypes based on major yield attributing traits may be useful [16]. Genetic diversity study is a major breakthrough in understanding the crop performance leading to crop improvement [3]. Knowledge of

performance in genetic diverse population reveals the differences in the nature of genetic materials used. Genetic diversity studies therefore, is a step wise process through which existing variations in the nature of individual or group of individual crop genotypes are identified using specific statistical method. Measuring genetic diversity and grouping of genotypes is useful for developing germplasm conservation strategies, trait specific groups and its utilization. Keeping the above facts under consideration the present investigation was undertaken to study of genetic diversity to isolate the suitable parents for rice improvement.

MATERIALS AND METHODS

The present investigation was conducted with 25 genotypes of rice. The genotypes were received from Department of Genetics and Plant Breeding, IAS, BHU, Varanasi, India and numbered serially 1 to 25. The germplasm used in present investigation were IC 145605 (G1), IC 145704 (G2), IC 145706 (G3), IC 351712 (G4), IC 520304 (G5), IC 447325 (G6), EC 491422 (G7), Annada (G8), Tetep (G9), IC 280466 (G10), IC 282418 (G11), IC 282443 (G12), IC 282471 (G13), IC 282514 (G14), IC 282822 (G15), IC 282824 (G16), IC 337051 (G17), IC 337558 (G18), IC 337588 (G19), IC 341351 (G20), IC 346002 (G21), IC 356117 (G22), IC 356448 (G23), IC 382604 (G24) and IC 383396 (G25). The experiment was conducted at Crop Research Farm of IAS, BHU, Varanasi. Field experiment was performed in randomized complete block design (RCBD) with three replications during kharif, 2014-15 at two different locations. Each genotype was sown in six rows in 4 m length plot with 20 x 15 cm spacing. Recommended dose of fertilizer was applied at the time of sowing. The observations were recorded on 13 yield and yield components viz., plant height (PH), panicle length (PL), net effective tillers (NET), first leaf area (PLA), second leaf area (SLA), 50% flowering (DFF), days to maturity (DM), spiklets per panicle (SP), 1000 grain weight (GW), grain weight per panicle (GWP), grain weight per plant (GWPP) and harvest index (HI). Five random plants were tagged from each plot to record the data (quantitative traits) for all the yield and yield components except DFF and DM. These traits were computed on plot basis. The data on yield and its other related traits were subjected to pooled genetic divergence analysis by using statistical package SAS.

Table 1: Eigen values and variability explained by each principle components (PCs)

PCs	Eigenvalue	Proportion	Cumulative
1	2.89	0.22	0.22
2	2.57	0.20	0.42
3	2.35	0.18	0.60
4	1.19	0.09	0.69
5	1.02	0.08	0.77
6	0.91	0.07	0.84
7	0.58	0.04	0.89
8	0.49	0.04	0.92
9	0.34	0.03	0.95
10	0.28	0.02	0.97
11	0.19	0.01	0.99
12	0.16	0.01	1.00

RESULTS AND DISCUSSION

In order to maintain, evaluate and utilize germplasm effectively, it is important to investigate the available genetic diversity [10 & 15]. The use of germplasm can be determined from the extent of available variability in the material. The important objective of each genetic diversity study is to understand the possibility of classifying individual genotypes into different groups [8]. The success of plant breeding depends on the availability of genetic variation, knowledge about desired traits, and efficient selection strategies that make it possible to exploit existing genetic resource [11]. They also gave the emphasis to develop the segregating population, genetic distance estimates form the basis for selecting parental combinations with sufficient genetic diversity and for classifying germplasm into heterotic groups for hybrid crop breeding.

Several multivariate analyses of genetic diversity are available but in present investigation, PCA was used to identify the most significant variables in the traits studied. It was also used for establishing the genetic relationship among the genotypes. Association between traits emphasized by this method may correspond to genetic linkage between loci controlling the traits or a pleiotropic effect. The genetic variation present in breeding material was divided into 12 principle components explained 100% variation of gene pool (Table 2), whereas the first five principle components had eigen value >1.00 and accounted 77% of total variation. However, the first three PCs covered a high amount of genetic variation i.e. 60% and

Table 2: Correlation coefficient of each agro-morphological trait with respect to its principle components (PCs)

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12
PH	-0.010	0.199	-0.445	0.128	0.078	-0.154	0.795	-0.073	0.057	0.133	0.113	-0.206
PL	-0.284	0.321	-0.036	0.538	0.068	0.251	0.030	-0.098	-0.288	0.035	-0.255	0.544
NET	0.102	-0.209	0.320	-0.119	-0.600	0.287	0.406	0.215	-0.093	0.315	0.011	0.224
FLA	0.456	0.191	0.154	0.079	0.213	-0.105	0.005	0.395	-0.250	0.254	-0.554	-0.267
SLA	0.467	0.186	0.097	0.209	0.068	-0.195	0.072	0.354	-0.020	-0.412	0.450	0.322
DFP	-0.212	0.453	-0.104	-0.401	-0.157	0.046	-0.079	0.406	-0.017	-0.025	0.160	0.098
DM	-0.244	0.499	-0.006	-0.375	-0.028	-0.033	0.004	0.046	0.007	-0.056	-0.185	-0.034
SP	0.224	0.193	-0.233	0.238	-0.140	0.715	-0.145	0.087	0.345	-0.106	0.033	-0.326
GW	-0.363	-0.111	0.310	0.196	0.243	-0.078	0.146	0.409	0.667	0.030	-0.138	0.060
GWP	0.192	0.394	0.332	0.017	0.150	-0.027	-0.119	-0.349	0.233	0.598	0.350	0.056
GYP	0.117	0.201	0.501	-0.145	-0.004	0.114	0.317	-0.408	0.085	-0.519	-0.227	-0.075
HI	-0.381	0.046	0.379	0.264	0.047	0.081	0.029	0.149	-0.433	-0.041	0.375	-0.525
AUD-PC	0.032	-0.205	0.000	-0.377	0.671	0.490	0.184	0.081	-0.173	0.049	0.134	0.177

Cluster Analysis

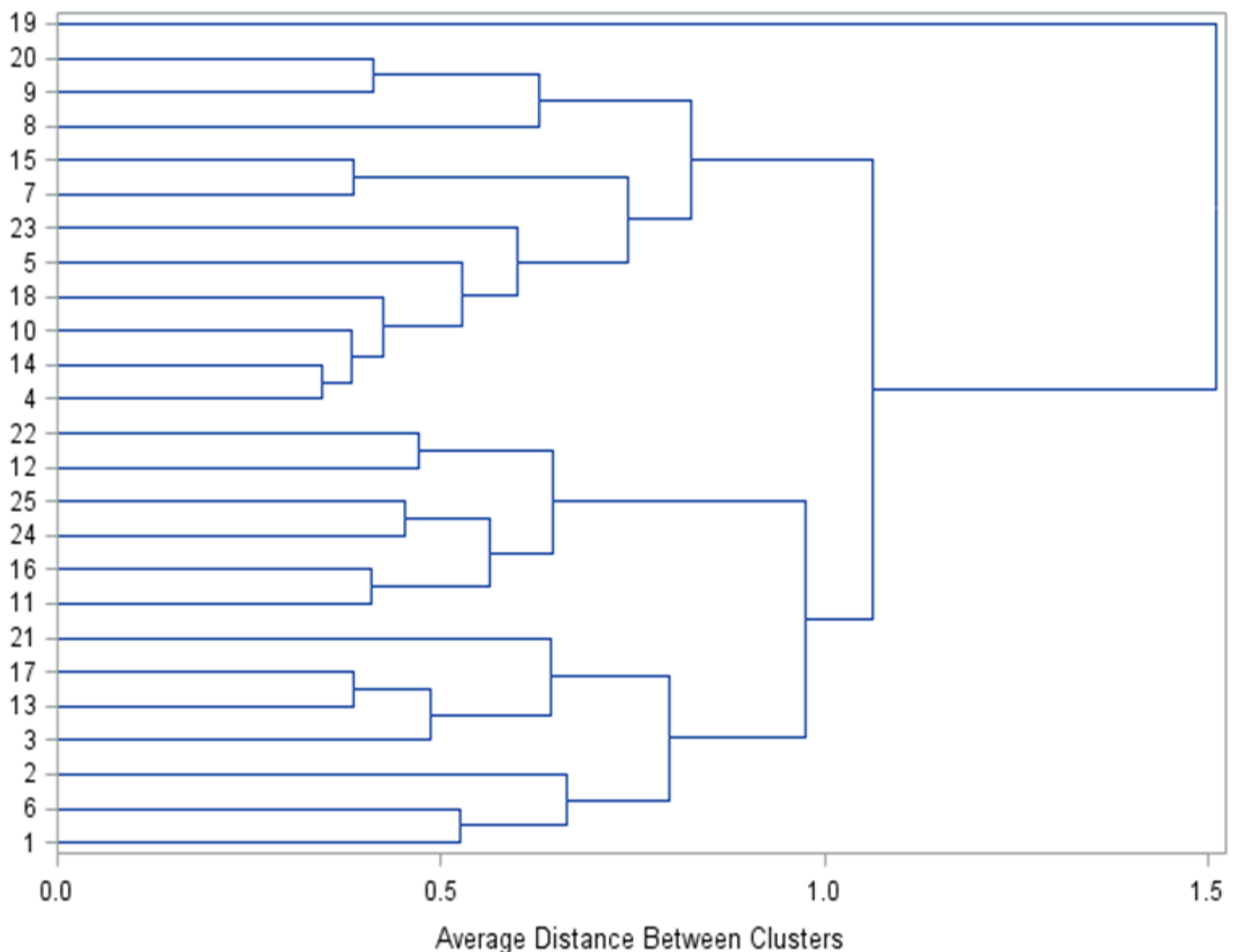


Fig-1: Grouping pattern (Euclidean) of rice genotypes into various clusters

had >2 eigen value. Similarly, Khatun *et al.* (2015) also observed about 72% variation explained by first four PCs. The first principle component (PC 1) explained 22% of the total variation and was mainly associated with FLA and number of spikelets per panicle [7]. The second PC (PC2) was responsible for 20% variation and was related PL, DF, DM and GWP. The third PC (PC3) contributed about 11.81% variation due to effect of NETPI, GW, GWP, GYP and HI. The association of characters in different principle component depends upon the nature of breeding material. Nachimuthu *et al.* (2014) also noted strong association of PCs with traits like DFF, DM, PL and GYP [11].

Cluster analysis help to select the suitable genotypes for hybridization to manipulate the important traits. Selection of proper parents plays a vital role for a successful plant breeding programme. Parents with more genetic distance can create higher variations, which can increase the genetic gain in selection. The distribution of 25 rice genotypes in four different clusters and their cluster means are presented in Fig 1 and table-2, respectively. The total genotypes of rice fall into four clusters. Cluster I comprised only one genotype (G19) forming a smallest and mono genotypic cluster, whereas cluster II comprised 11 genotypes forming a largest cluster. Cluster III and cluster IV consist of six and seven genotypes, respectively. Based on dendrogram, IC 337588 exhibited good to high diversity with remaining genotypes used in this study, whereas IC 337588 and IC 145605 was found most divergent (Fig 1). These IC 337588 and IC 145605 were used in crossing programme to generate higher recombinants. But several workers like Maji and Shaibu (2012) in rice, Gour *et al.*, (2017) in rice, Shukla and Singh (2006) in *Opium poppy*, Yadav *et al.* (2007) in *Opium poppy*; have also observed the non-correspondance between F₁ performance and their parents with high diversity (except some traits). Thus, the moderately diverse genotypes can also be included in breeding programme to isolate the good recombinants with high heterotic response [9,5, 13 &19].

Based on above discussion, IC 337588 and IC 145605 exhibited more diversity with other genotypes present in different clusters, indicated the possibility of improvement of rice by manipulation of various traits *viz.*, PL, DFF, DM, NETPI, GW, GWP, GYP and HI. Besides, the

representative genotypes from each cluster may also be utilized in hybridization programme to get good heterotic response.

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