

# GENETIC DIVERSITY ANALYSIS FOR SUBMERGENCE TOLERANCE IN RICE (*Oryza sativa* L.)

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## INTRODUCTION

Rice improvement programme depends on selected germ plasm, which virtually determine the success and nature of the end product which we are concern. The development of superior rice population involved the effective use of available genetic resource both indigenous as well as exotic in order to suit the various farming situations of rice (Paikhomba *et al.*, 2014). In rice the grain yield is primary trait targeted for improvement interns of productivity in case of favorable and unfavorable environmental condition. Apart from grain yield, now a day's breeders are showing interest towards nutritional aspects. Being a staple food crop, it provides approximately 20 percent of per capita energy and 13 percent of protein for human beings. But in case of developing countries, the dietary contribution of rice is highest at 29.3 and 29.1 percent for energy and protein respectively. The per capita consumption of rice varies from 62 to 190 kg year (Bouis , 2003). However, rice is a poor source of micronutrients (Fe and Zn ) content (Bouis and Welch, 2010). Micronutrients deficiency is a global problem, contributing to world's widespread malnutrition and high rate of children and women's mortality (WHO, 1996). It is estimated that more than 2 billion people in the world are deficient in Vitamin A, Iodine and Iron and more than 2.5 billion people in the developing world are Zinc deficient (Panopio, 2010).

The success of any plant breeding programme depends on knowledge of the genetic architecture of the population and selection and adoption of appropriate breeding methodology for the improvement of traits of interest (Sathya and Jebaraj, 2013). Hence it is essential to find out the relative magnitude of additive and non-additive genetic varianness, heritability and genetic advance with regard to the characters of concern to the breeders (Pratap *et al.*, 2013). Keeping in mind the genetic studies on rice both under flooded and aerobic conditions were undertaken to estimate the genetic component of variance for drought tolerance, yield and yield components and micronutrient content (Fe and Zn) and to compute the heritability and genetic advance for 14 characters.

## MATERIALS AND METHODS

The present investigation was conducted with 38 local land races of rice obtained from IRRI, Phillipinesto access the genetic variability and diversity for five quantitative traits related to submergence tolerance. The experiment was conducted at Crop Research Farm, Rajendra Agricultural University (RAU), Pusa, Bihar, India. Field experiment was performed in randomized block design (RBD) during two years *i.e.* *Kharif*2014 and 15. Each genotype was sown in four rows in plot of 5 m length with 20 × 15 cm plant geometry in water tank. The submergence stress was created at 30 days after transplanting for 14 days with 1.3m water level. Fertilizer was applied as per recommendation. Five random plants were tagged in each plot to record the data for allthe submergence related traits. Stress indices were calculated as follows:

## ABSTRACT

Genetic parameters for yield and its correspondent characters in rice were estimated in 98 doubled-haploid lines (Azucena/IR 64) for 14 characters under contrasting moisture regimes. Among the character studied, biological yield traits like number of tillers per plant (37.74 and 35.39), number of productive tillers per plant (41.67 and 40.60), grain yield per plant (78.86 and 75.73), straw yield per plant (45.02 and 49.63) and roots traits like root dry weight (63.50 and 62.18), root length (27.18, 29.30, 16.34, 22.09 and 36.86, 32.76, 29.83, 30.76), root volume (59.43 and 57.51), root number (42.48 and 47.57) and root number at 15 cm from the base (48.24 and 41.16) were recorded high percentage of PCV and GCV. Moderate values (10-20 %) of PCV and GCV were recorded for plant height, test weight, grain Fe and Zn content. The heritability for shoot and root morphological traits under flooded condition was higher than the heritability under aerobic condition this indicates the effectiveness of Azucena alleles on root related traits was more than the IR64 alleles in aerobic condition where the genotypes express themselves to their fullest potential and effectively combat environmental factors and also environment variability would be more due to induce stress. This augments the scope for estimation of genetic parameters for genetic improvement with respect to drought tolerance

## KEY WORDS

Rice, PCV, GCV, heritability, genetic advance, flooded and aerobic condition

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$$\text{Percent plant survival (RSE)} = \frac{\text{Total number of survived seedlings}}{\text{Total number of seedling before submergence}} \times 100$$

Toojinda *et al.*, 2003)

Total shoot elongation (TSE) = Height of shoot after de-submergence – Height of shoot before de-submergence.

(Toojinda *et al.*, 2003)

$$\text{Relative shoot elongation} = \frac{\text{elongation growth under}}{\text{elongation growth under non}} \times 100$$

(Toojinda *et al.*, 2003)

Tolerance score (TS) = Scored on the basis of percent plant survival

(Toojinda *et al.*, 2003)

Leaf senescence (LS) = Chlorophyll content non-stress condition - Chlorophyll content after 10 days of de-submergence

(Toojinda *et al.*, 2003)

The data were subjected to pooled analysis of variance, genetic parameters, association analysis and genetic diversity by using statistical package WINDOSTAT version 9.2 (INDOSTAT Service, Hyderabad).

## RESULTS AND DISCUSSION

### Analysis of variance and genetic parameters

The analysis of variance showed significant differences ( $P < 0.01$ ) among treatments for the different submergence attributing traits, indicated the presence of sufficient variability in population (Table 1). The coefficient of variation studies indicated that the magnitude of phenotypic coefficient of variation (PCV) were slightly higher than the corresponding genotypic coefficient of variation (GCV) for all the characters

studied, indicated the little influence of environmental factor on expression of these traits. All the traits exhibited high magnitude of GCV, PCV,  $h^2$  coupled with high GAM, indicated the involvement of additive gene action in expression of these traits. Similar findings have earlier been reported by Toojinda *et al.* (2003) Devi *et al.* (2013), Kumar *et al.* (2015), Roy *et al.* (2013) and Kumar *et al.* (2015) for percent plant survival, tolerance score, total shoot elongation, leaf senescence and other traits. Several workers *viz.*, Yimram *et al.* (2009), Singh *et al.* (2014) suggested the consideration of variance components, heritability estimates and genetic advance together gives better chance of selection of appropriate traits. Keeping this view, all the traits *viz.* PPS, TSE, RSE, and TS may be directly selected and added in rice improvement with reference to submergence tolerance.

### Tochers Clustering

All the 38 genotypes were grouped into 7 clusters (Fig 1). Cluster I consisted of 17 genotypes, cluster II consists of three genotypes, cluster III has 10 genotypes, cluster IV and V consists of three genotypes each whereas cluster VI and VII consists of single genotypes. The intra-cluster and inter-cluster distances are presented in Table 3. Maximum inter-cluster distance was observed for cluster II & VII followed by cluster V & VI, VI & VII, III & III, V & V indicated that the genotypes included in these different cluster may throw high heterotic response and there by better segregants. Per cent contribution of five characters towards the genetic divergence presented in Table 3. Percent plant survival (%) contributed maximum manifestation of genetic divergence followed by leaf senescence, TSE and RSE. The character i.e. tolerance score has no contribution towards manifestation of genetic divergence indicated that there is no genetic variability was present for this trait. The diversity in the present material was also supported by the appreciable amount of variation among cluster means for different characters. Cluster V & VII (PPS), VII & IV (TSE), VI, III & VII (RSE), IV & VI (TS) and V & II (LS) were identified as diverse cluster for respective traits given in parenthesis (Table 5). Therefore,

**Table 1: Analysis of variance for various submergence related traits in rice (Pooled of two years)**

GP/ Trait	Percent plant survival	Total shoot elongation (cm)	Relative shoot elongation (cm)	Tolerance score	Leaf Senescence
Range	3.84 - 50.43	1.45 - 37.05	18.52 - 613.41	1.00 - 9.00	2.39 - 36.93
Mean	20.87	14.41	161.45	5.49	16.12
GCV (%)	63.85	64.23	83.76	44.91	50.21
PCV (%)	64.49	65.56	85.83	45.67	51.85
$h^2_{bs}$ (%)	98.00	96.00	95.00	97.00	96.00
GAM (0.05)(%)	130.24	129.61	168.40	90.98	102.98

GP = Genetic parameters, GCV = Genetic coefficient of variation, PCV = Phenotypic coefficient of variation,  $h^2_{bs}$  = Heritability in broad sense, GAM = Genetic advance as % of mean

**Table 2 : Rice genotypes present in seven clusters formed by Tochers clustering method (Pooled of two years)**

Clusters	Genotypes Present
I	Sugapankh, Lalka Dhan, Singhara, Swarna Sub 1, Rom Runtik, Kalonchi, Kariyawa, Changpaljom Phai, Zobgui, Nang Quot, Moroberekan, Jalkanathi, Dudha Ladu, Kola Joha, Dihawan, Ai Chih Ai K Who 2, Paiam
II	Maintimolotsy, Swarna, Sarjoo 52
III	Suraha, Jadhan, Anh Hsung Seln (Ci 1), Karnal Local, Fr-13b, Sathi, S-150, Bpt 5204, Sub 1, Fr-13a, Karkati 87
IV	Chakia 59, Karahani, Cr 1009
V	Lunishree, Rajbhog, Kala Bunde
VI	Ir-36
VII	Hsung Tieng

**Table 3 : Inter and Intra cluster distance by Tochers clustering method (Pooled of two years)**

Cluster	I	II	III	IV	V	VI	VII
I	19.51	49.51	70.90	49.41	127.83	93.32	182.75
II		16.65	144.37	99.01	119.72	154.89	305.23
III			36.79	91.45	103.48	118.32	71.86
IV				6.63	197.86	101.41	148.07
V					35.02	267.74	170.14
VI						0.00	250.20
VII							0.00

**Table 4: Percent contribution of various characers towards the genetic diversity by Tochers clustering method (Pooled of two years)**

Source	Times Ranked 1	Contribution <sup>st</sup> (%)
1. Per cent plant survival	264	37.55
2. Total shoot elongation	125	17.78
3. Relative shoot elongation	92	13.09
4. Tolerance score	0	0.00
5. Leaf Senescence	222	31.58

**Table 5: Cluster mean of rice genotypes for seven clusters by Tochers' clustering method (Pooled of two years)**

Cluster	Traits	Percent Plant Survival	Total shoot elongation	Relative shoot elongation	Tolerance score	Leaf Senescence
I		14.22	8.80	103.02	6.72	13.45
II		10.07	9.12	82.53	7.42	29.44
III		31.78	18.34	253.99	3.22	12.62
IV		6.42	28.78	150.26	8.42	15.65
V		44.75	16.79	108.03	1.67	33.85
VI		5.97	13.41	613.40	8.25	9.67
VII		43.92	37.05	208.15	1.25	11.08

**Table 6 : Rice genotypes present in seven clusters formed by Euclidean clustering method (Pooled of two years)**

Clusters	Genotypes present
I	ANH HSUNG SELN (CI 1), KARNAL LOCAL, SURAHA, JADHAN, HSUNG TIENG, FR-13B, S-150, SATHI, FR-13A
II	LUNISHREE, RAJBHOG
III	SARJOO 52, KOLA JOHA, KARKATI 87, KALA BUNDE
IV	MAINTIMOLOTSY, SWARNA, MOROBEREKAN, JALKANTHI, NANG QUOT, KARIYWA, ZOBGUI, ROM RUNTIK, CHANGPALJOM PHAI, SINGHARA
V	PAIAM, BPT 5204 SUB 1, KALONCHI, SWARNA SUB 1, SUGAPANKH, LALKA, DHAN, DIHAWAN, DUDHA LADU, AI CHIH AI K WHO 2
VI	IR-36
VII	CHAKIA 59, KARAHANI, CR 1009

**Table 7: Inter and Intra cluster distance by Euclidean clustering method (Pooled of two years)**

Cluster No.	I	II	III	IV	V	VI	VII
I	137.64	429.75	434.62	551.97	239.14	551.05	392.79
II		47.62	289.92	697.13	552.79	1154.12	844.12
III			59.44	172.08	206.72	669.69	458.03
IV				66.17	154.09	444.94	252.76
V					59.20	306.21	176.62
VI						0.00	405.98
VII							26.52

hybridization between genotypes falling in different clusters may be useful for development of desirable recombinants.

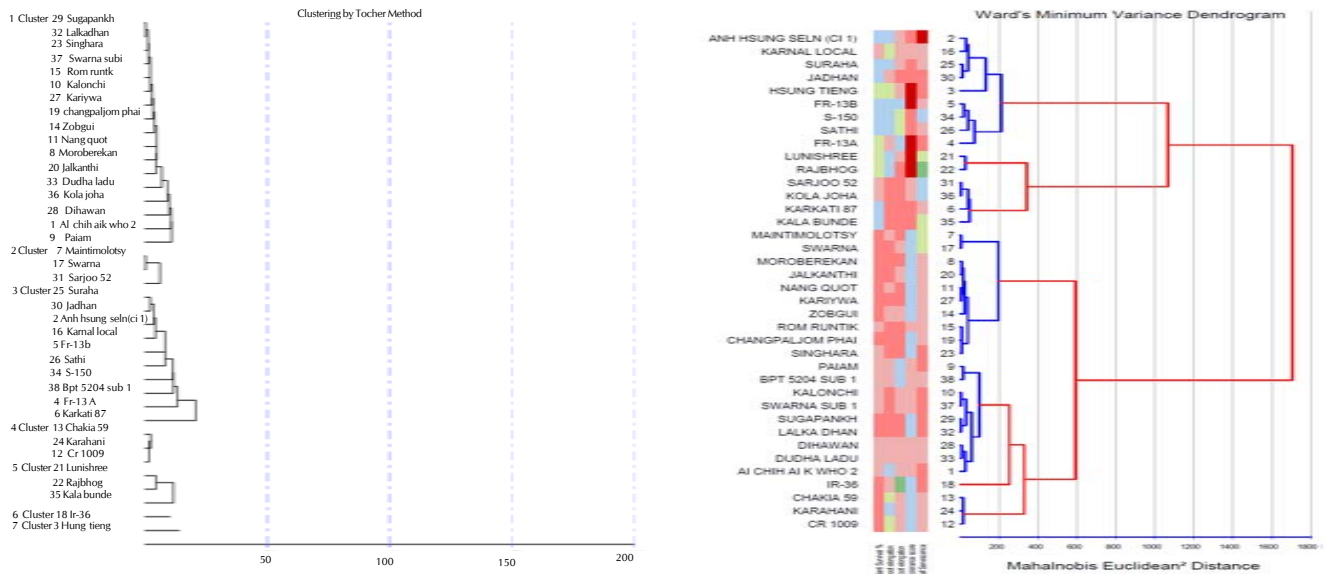
#### Euclidean clustering

Cluster IV comprised of 10 genotypes forming the largest cluster followed by cluster V & I comprised of 9 genotypes each, cluster III comprised of 4 genotypes, cluster VII comprised of 3 genotypes, cluster II comprised of 2 genotypes

and cluster VI comprised of single genotype, indicated the wide spectrum of diversity. (Table 6). Intra-cluster and inter-cluster distance among these clusters are presented in (Table 7). Maximum inter cluster distance was observed between cluster II & VI, followed by cluster II & VII, II & IV, III & VI, I & I, IV & IV and III & III indicated that the genotypes included in these different cluster may be gave high heterotic response

**Table 8: Cluster mean of rice genotypes for seven clusters by Euclidean clustering method (Pooled of two years)**

Cluster	Traits Percent Plant Survival	Total shoot elongation	Relative shoot elongation	Tolerance score	Leaf Senescence
I	34.32	22.96	261.85	2.75	11.98
II	50.15	22.64	144.03	1.00	35.84
III	26.31	6.35	53.48	4.38	24.35
IV	8.99	6.49	69.92	7.75	17.86
V	18.17	11.72	168.13	5.92	11.15
VI	5.97	13.49	613.41	8.25	9.67
VII	6.42	28.78	150.26	8.42	15.65



**Figure 1: Distribution of rice genotypes in to various clusters by Tochers (left) and Euclidean (right) methods**

and thereby better segregants. Maximum intra cluster distance was observed for cluster I & IV, Cluster II, I & III (PPS), VII, I & II (TSE), VI, I & V (RSE), VII, VI & IV (TS) and II, III & IV (LS) were identified as diverse cluster for respective traits given in parenthesis (Table 8). The genotypes from these clusters may be included in breeding programme to get promising segregants.

By considering both clustering methods, it was also noted that the rice genotypes of differences in origin were grouped in the same cluster, indicating absence of relationship between genetic diversity and geographic diversity. The genotypes collected from same geographical origin were spread over different clusters due to the fact that diverse parental materials from different sources were utilized in the hybridization programme to generate these advance breeding lines. The results were also confirmed with agreement of Singh *et al.* (2013) and Sarkar *et al.* (2014). To isolate the suitable genotypes in terms of submergence tolerance both clustering methods were taken care because each method has its own importance depending upon involvement of predominant traits. But Non-hierarchical Euclidean clustering method is more effective to group the genotypes and their effective utilization due to transformation of prominent traits on a single index. Stress parameters viz., PPS was found predominant and may be used as

selection criteria in breeding programme for screening of submergence tolerant genotypes. This study indicated that the germ plasm lines with high order of genetic divergence among cluster II & VI by Euclidean method will be expected to provide the best breeding material for achieving the maximum genetic gain.

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