

## Limited trait based analysis to diversify upland rice genotypes

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### Abstract

The present experiment was conducted to identify suitable parental population for upland rainfed rice improvement programme among local bred material and introduced national varieties. Variable levels of water deficit in upland rice cultivation cause negative alteration in crop architecture resulting lowered down of root and shoot biomass and eventually grain yield. Mahalanobis Euclidian distance separated the genotypes into six clusters among which maximum intracluster diversity was recorded for cluster III (3.13) followed by cluster II (2.85) and Cluster I (2.05). For cluster IV, V and VI intra cluster distance was not observed since each harbored single genotype only. Cluster IV, V and VI excluded genotypes Sahbhagidhan, R-1572-1171-1-124-1 and Ananda from rest of the population indicating the most diverge genotypes. In present experiment, days to 50 percent flowering contributed 60 percent towards total divergence followed by grain yield (18 percent), plant height (13 percent) panicles per square meter (9 percent). Based on morphological assessment Sahbhagidhan, R-1572-1171-1-124-1 and Ananda have been found to be most diverse genotypes and can be used in recombination breeding programmes particularly for Bastar Plateau region.

**Keywords:** Upland Rice, rainfed, water stress, genetic diversity

### Introduction

Rice (*Oryza sativa* L.) is the world's most important cereal crop, providing the caloric needs of millions of population daily comprising all economic classes of society. Being the staple food for two third of the population, rice forming staging a central role in Indian economy. China occupies the first place with 144.0 million tons in the world's production table of 479.3 million tons followed by India with 108.0 million tons annual production [1]. It is of great concern to researchers and policy makers that the rate of rice production enhancement has reached plateau level since last decade and situation is being more complicated with reports that the population growth in most of the Asian countries, except China, continues to rise around 2 percent per year [2]. Hence it is very important to critically consider whether the rice production can be further increased while keeping pace with population growth particularly for below poverty line residents who are not able to manage food shortage linked price hike. Estimated revealed that by 2020 at least 115-120 million tons of milled rice is to be produced in India to maintain the present level of self-sufficiency. Since horizontal expansion of irrigated rice area is not possible, the upland rice is emerging as viable option which is still unexplored wing of scientific research. Nearly, hundred million people depend on the upland rice for their livelyhood globally [3], of which India contributes about 6 mha (13 per cent of total area). Uniqueness and clause of upland rice is entirely dependency upon the monsoon and production under rainfed conditions. Variable levels of water deficit in upland rice cultivation cause negative alteration in crop architecture resulting lowered down of root and shoot biomass and eventually grain yield. Moreover, poor productivity of existing cultivars, making rice production in upland regions risky and unattractive to poor and marginal farmers due to low yield of 1200 kg ha<sup>-1</sup> as compare to 3600 kg ha<sup>-1</sup> for irrigated rice. Consequently, the quest for further understanding of

water deficit tolerance for increased productivity has continued to attract intensive research in upland paddies which still remain scientifically untouched. Further limited reference is available in upland rice research and diversity is prerequisite to initiate any breeding work, genetic diversity analysis is carried out to explore suitable parents for breeding programme.

The experiment was undertaken with 27 genotypes under rainfed conditions during *Kharif* 2013 at Upland Rice Breeding Block of S. G. College of Agriculture and Research Station, Jagdalpur, IGKV, Raipur, Chhattisgarh. An upland ecology simulation model was created by choosing experimental plot where no water accumulates and cent percent rainfed treatment was given during entire life cycle of crop. Sowing was completed June last week by direct seeding in agronomically standardized geometry in 10sq M plot with two replications. Trench was made in periphery of experimental plot to avoid no water accumulation. The data was recorded for four quantitative characters namely days to flowering, plant height, panicles per sq M and grain yield. The mean over replication of each character were subjected to statistical analysis. For statistical analysis software Window State Version 9.1 was used.

Twenty seven genotypes were grouped in six diverse clusters which comprised 11 genotypes (Cluster II), seven genotypes (cluster III), six genotypes (cluster II) one genotype each in cluster IV, V and VI (Fig 01). The maximum number of genotypes were felled in cluster II, namely R-1595-2152-1-258-1, R-1262-1567-1-1, R-1577-642-1-208-1, R-1695-2152-2-269-1, Samleshwari (local check), R-1700-2240-1-2292-1, NS 1030, R-1583-830-1-268-1, R-1672-126-1-64-1, R-1695-2193-6-2171-1, R-1519-1134-1-115-1, which indicates most of test entries are having somewhat similar or close parentage. Cluster IV, V and VI excluded genotypes Sahbhagidhan, R-1572-1171-1-124-1 and Ananda from rest of the population

indicating the most diverge genotypes. Previous workers have reported geographical diversity as source of genetic diversity in sunflower, rice and many other crops, similarly in present experiment, Sahbhagidhan (origin of Hazaribagh, Jharkhand), R-1572-1171-1-124-1 (Raipur, Chhattisgarh) and Ananda (Bihar/Jharkhand) showed considerable heritable diversity. It is suggested that genotypes as parents in combination breeding programmes should be selected from diverse cluster to obtain maximum heterosis.

Contribution of characters towards total divergence is critical criteria to screen genotypes based on specific characters i.e. trait oriented breeding. In present experiment, days to 50 percent flowering contributed 60 percent towards total divergence followed by grain yield (18 percent), plant height (13 percent) panicles per square meter (9 percent)

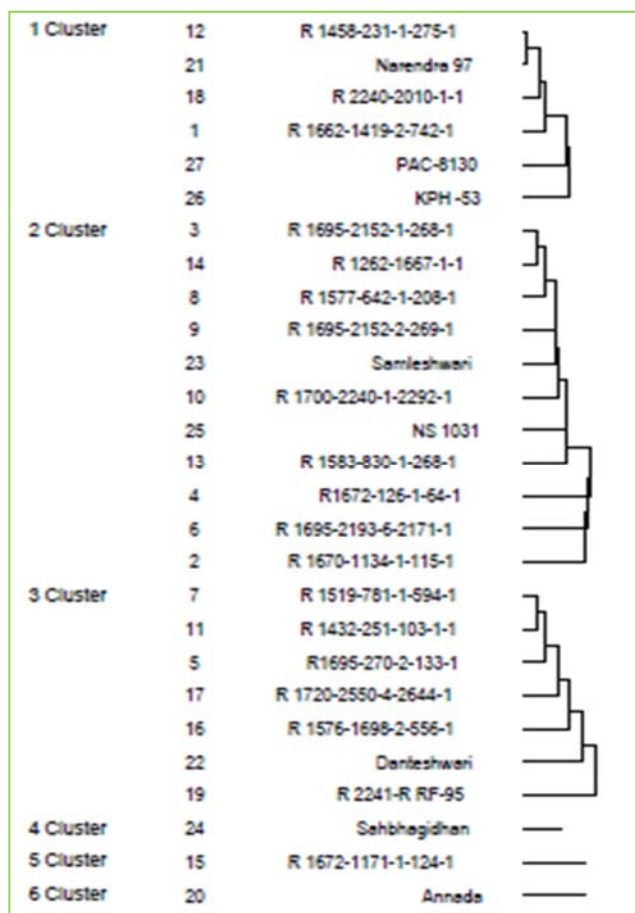


Fig 1: Clustering of Genotypes

(Fig 02). Heading span i.e. days to 50 percent flowering is most important parameter in rainfed rice survival because to produce sustainable crop yield, a genotypes must accomplish its growth and developmental cycle prior to offset of monsoon. To maintain life, when water stress is imposed, growth cycle is shortened by crop for which reproductive span is ultimately altered<sup>4</sup>. Those genotypes which are not able to reduce its growth period or having prolonged growth span faces reduced yield<sup>5</sup>. Hence days to flowering followed by crop duration are quite serious issue in upland rice breeding and owing to that only maximum divergence contribution was recorded. Mahalanobis Euclidian distance separated the genotypes into six clusters among which maximum intracluster diversity was

recorded for cluster III (3.13) followed by cluster II (2.85) and Cluster I (2.05). For cluster IV, V and VI intra cluster distance was not observed since each harbored single genotype only. Looking for intercluster distance, cluster V and II exhibited maximum variation (22.24) followed by cluster IV and II (16.3) and Cluster V and I (9.10)

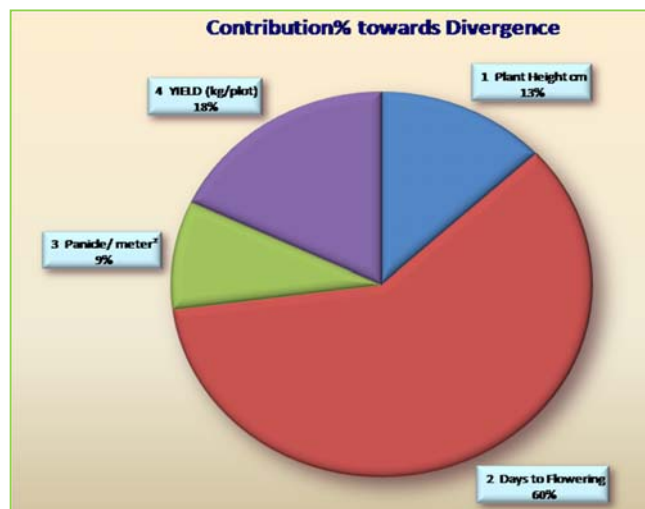


Fig 2: Contribution of Traits towards diversity

(Fig 03). The minimum cluster distance was seen between cluster VI and I which indicates hybridization should not be attempted between these cluster families. In contrast, clusters having greater inter and intra cluster distance should to deploy in crossing programmes as parents to achieve maximum heterosis and genetic advance.

Cluster mean analysis indicated the extent of genetic diversity among different clusters and that is of real value in plant breeding [6, 7]. The genotypes grouped into same cluster displayed the lowest degree of divergence from one another and in case crosses are made between genotypes belonging to the same cluster, no transgressive segregants are expected from such combinations [8]. Therefore, hybridization programmes should always be formulated in such a way that the parents belonging to different clusters with maximum divergence could be utilized to get desirable transgressive segregants [9].

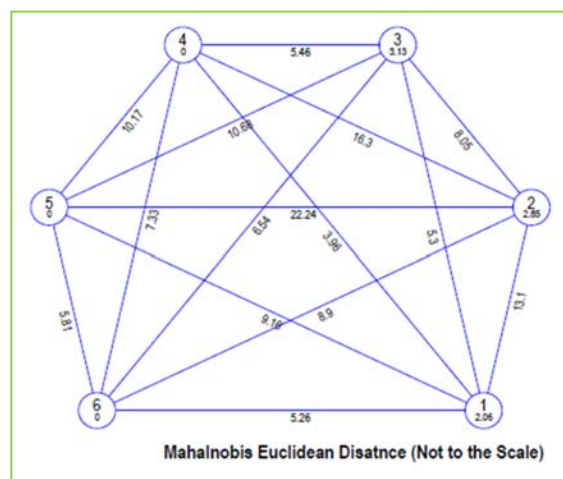


Fig 3: Inter and Intra Cluster Distance

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