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Introduction

Rice (*Oryza sativa L.*) is a major and vital cereal grain, next only to wheat in terms of global cultivated area. It is the staple food of more than half of the population of world. In addition to calories, rice is a good source of magnesium, phosphorus, manganese, selenium, iron, folic acid, thiamine and niacin; but it is low in fibre and fat (Fukagawa and Ziska, 2019). In India rice is cultivated over an area of about 45.07 million hectares in India with production and productivity of 122.27 million tons and 2.71 tons per hectare respectively (Anonymous, 2022), while in Union Territory of Jammu and Kashmir it was cultivated over an area of 267.58 thousand hectares with production and productivity of 5186 thousand quintals and 21.74 quintals per hectare respectively (Anonymous, 2022). Rice is one among few cereal crops with large amount of genetic variation and is being cultivated from sea level to higher elevations. The availability of significant genetic diversity for key characteristics in the parents being hybridized is the most important pre-requisite for starting a successful breeding operation which in turn helps in realizing the true production potential for developing improved rice varieties adapted to various agro-climatic zones [3-5].

A quantitative assessment of genetic diversity directs breeders towards speedy progress in breeding programs to get preferred recombinants in segregating generations. Hybrids with high heterosis are typically derived from parental genotypes differing in common ancestry, ecotype, and geographic origin and so on. Morphological, biochemical and DNA markers can be used to assess genetic diversity

kernel breadth (-0.20) and grain yield per plot (-0.38) were reported to negatively contribute to the genetic variation accounted by this component. Among six principal components or vectors first five components all together were reported to account for 81.30 % total genetic variation. Sathish and Senapati (2017) also reported similar trends while investigating advanced breeding lines of rice grown in low land conditions of West Bengal. Mahendran et al. (2013) suggested that potential morphological and quality traits which remain side by side in various principal components and contributing maximum towards total available genetic variation within breeding population have likelihood to remain together and provide ample scope and opportunity to be utilized in hybridization programmes [20].

From the foregoing discussion, it is apparent that there is a possibility for transferring the genes available within these advanced breeding lines of rice to create transgressive segregants with desired traits through selection and hybridization. Parents for hybridization should be chosen from separate clusters with a large inter and intra-cluster distance and the chosen parents should perform exceptionally well for the characters that contribute the most to genetic divergence. Mono-genotypic clusters with a single genotype could be used in hybridization programmes to exploit heterosis predominantly as testers. However, it is clear from the present study that crosses between genotypes from cluster II and those from cluster III, IV, V and VI are likely to express or demonstrate a high percentage of heterosis and generate potential recombinants with desirable traits. Further results of principal component or canonical vectors analysis classified the total genetic variation within advanced breeding lines by considering potential traits such as number of effective tillers per plant, grain yield per plot, plant height, panicle length and days to 50 per cent flowering, because these agro-morphological traits account for maximum contribution towards genetic diversity among advanced breeding lines. Selection for these traits will ensure efficient and goal oriented improvement of rice cultivars.

References