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Identifying Rice Genotypes Suitable for Aerobic Direct-Seeded Conditions †

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Abstract: Direct-seeded rice (DSR) requires less labor and less water. The low input cost of DSR makes it a better alternative than the conventional transplanted system for rice. DSR helps to reduce production risk, facilitates crop production, and limits irrigation water use. In the present study, a total of 44 rice genotypes were evaluated in a randomized block design (RBD) with three replications over two seasons (2020 and 2021) under DSR conditions at the Central Soil Salinity Research Institute (CSSRI), Karnal. The average grain yield ranged from 1114 kg/ha (CSR 62) to 5198 kg/ha (CSR MAGIC-167), biomass ranged from 6670 kg/ha (CSR 52) to 14,744 kg/ha (CSR MAGIC-117), plant height ranged from 67 cm (CSR 52) to 113 cm (CSR 47), panicle length ranged from 19 cm (CSR 53) to 30 cm (CSR 66), and total tillers ranged from to 7 (CSR MAGIC-117) to 13 (CSR 2748-4441-193). Out of 44 genotypes, maximum grain yield was observed in genotype CSR MAGIC-167 (5198 kg/ha) followed by CSR 58 (5117 kg/ha), CSR 49 (5014 kg/ha), and CSR RIL-06-178 (4904 kg/ha). The best performing genotypes, namely CSR MAGIC-167, CSR 58, CSR 49, and CSR RIL-06-178, should be further evaluated in larger and multilocation trails under DSR situations, and stably performing lines could be released as commercial varieties of DSR.

Keywords: rice; DSR; aerobic; CSR

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1. Introduction

Rice (*Oryza sativa* L.) is a major food crop that plays a crucial role in national food security. It serves as a staple food for more than half of the world's population [1]. Hence, it is very important to increase rice production to meet the exorbitant growth in global population [2,3]. In India, rice is grown in an area of 43.79 million hectares with a production of 116.42 million tonnes [4]. Currently, the dominant method of rice planting is manual transplanting cultivation. Transplanted rice (TPR) is a traditional method that constitutes labor-intensive activities with low productivity [5] and the use of a vast quantity of irrigation water [6]. A shortage in labor and water lead to delayed transplanting which results in a reduction in rice yield and, due to this, a delay in wheat sowing occurs, which also further reduces wheat yield [7].

Recently, many farmers in the tropical region have shifted their cropping method from transplanting to direct-seeded rice (DSR). Direct-seeded rice is the most feasible alternative rice production technique because it not only saves labor requirements but also preserves natural resources, particularly underground water. It is a beneficial and profitable rice production system for current as well as future agricultural scenarios [8]. In Asia, DSR occupied a total of 21% of rice plantation areas at the beginning of the 21st century [9]. DSR refers to the process of establishing the crop from seeds sown directly in the field as compared to transplanting seedlings from the nursery [10]. Many studies have shown that 25% of labor inputs could be saved in DSR compared to the transplanting method [11]. DSR is endowed with multiple benefits, such as using water and labor more efficiently as well as reducing production costs [11]. It is faster and easier to plant, provides higher economic returns, and emits less methane than transplanting rice cultivation [12]. DSR also reduces production risk, facilitates crop production, and shortens crop growth duration, i.e., early maturity. Furthermore, weed infestations, which are a major constraint in DSR, can be overcome through the use of smart agricultural practices and strategies [13]. Although, DSR is very beneficial for cultivators, it still faces a lot of challenges, one of which is the limited accessibility of suitable cultivars [12,14]. In DSR cultivation, only those cultivars are used that have already been developed for transplanting rice. Consequently, this causes variations in grain yield, poor crop establishment, and high weed infestation [15]. So, the main objective of this study was to identify a suitable genotype for aerobic direct-seeded rice based on growth and yield parameters.

2. Materials and Methods

A field experiment was conducted to evaluate the performance of different rice genotypes in the DSR system in response to yield and yield-contributing parameters in an RBD design. A total of 44 rice genotypes were screened by direct-seeded rice at the Central Soil Salinity Research Institute (CSSRI), Karnal, during the two seasons of Kharif 2020 and Kharif 2021, in reclaimed sodic soils. The machinery used for the DSR was a Turbo Happy Seeder. Rice seeding depth ranged from 1 cm to 2 cm. Irrigation was given at intervals of 5 to 6 days depending on the rainfall during the crop growing period. Data were collected at the time of maturity. Yield and yield attributes such as plant height (cm), total tillers, panicle length (cm), yield (kg/ha), and biomass (Kg/ha) were recorded. The collected data were statistically analyzed using analysis of variance by STAR software (STAR 2.0.1) and correlation analysis was performed using the complot package in the R program.

3. Results and Discussion

Analysis of variance was performed for all characters concerning genotypes, year, and year–cultivar interaction for the direct-seeded rice, and the results are given in Table 1. Highly significant differences were observed among all parameters in the genotypes. The growth and yield parameters of the direct-seeded rice varied significantly between genotypes. Out of 44 genotypes, maximum grain yield was recorded in genotype CSR MAGIC-167 (5198 kg/ha) with optimal biomass (11,758 kg/ha), plant height (91 cm), panicle length (23 cm), and total tillers (9), while minimum grain yield was observed in CSR 62 (1114 kg/ha) with smaller plant height (85 cm), panicle length (21 cm), total tillers (9 No), and biomass (10,349 kg/ha).

Table 1. Analysis of variance for yield, biomass, plant height, tillers, and panicle length of rice genotypes with the direct seeding method.

Source	DF	Yield	Biomass	Height	Tillers	Panicle Length
Genotype	43	8,124,772.54 **	14,051,913.10 **	670.98 **	9.06 **	29.85 **
Year	1	141,567.34	55,559,133.40 **	491.90 **	131.10 **	7.51 *
Genotype: Year	43	951,238.66 *	6,190,075.88 **	64.02 **	7.30 **	4.21 **
Pooled Error	132	597,957.95	2,153,000.63	18.29	3.87	1.45

*, ** = Significant at 5% and 1% level, respectively.

Grain yield ranged from 1114 kg/ha to 5198 kg/ha (Figure 1). The highest grain yield was observed in CSR MAGIC-167 (5198 kg/ha) followed by CSR 58 (5117 kg/ha) and CSR 49 (5014 kg/ha), while the lowest grain yield was recorded in CSR 62 (1114 kg/ha) followed by CSR27SM-132 (1174 kg/ha) and CSR 52 (1202 kg/ha). Maximum biomass was observed in genotype YET 72 (13,386 kg/ha) followed by CSR 53 (13,702 kg/ha) and CSR MAGIC-117 (14,744 kg/ha), while minimum biomass was observed in CSR 52 (6670 kg/ha) followed by CSR-2748-4441-193 (7620 kg/ha) and CSR-2748-140 (7834 kg/ha). Biomass was ranged from 6670 kg/ha to 13,386 kg/ha. These results conform with the findings of [16], who evaluated different Indian rice varieties for grain yield and quality attributes in direct-seeded and transplanted rice production systems.

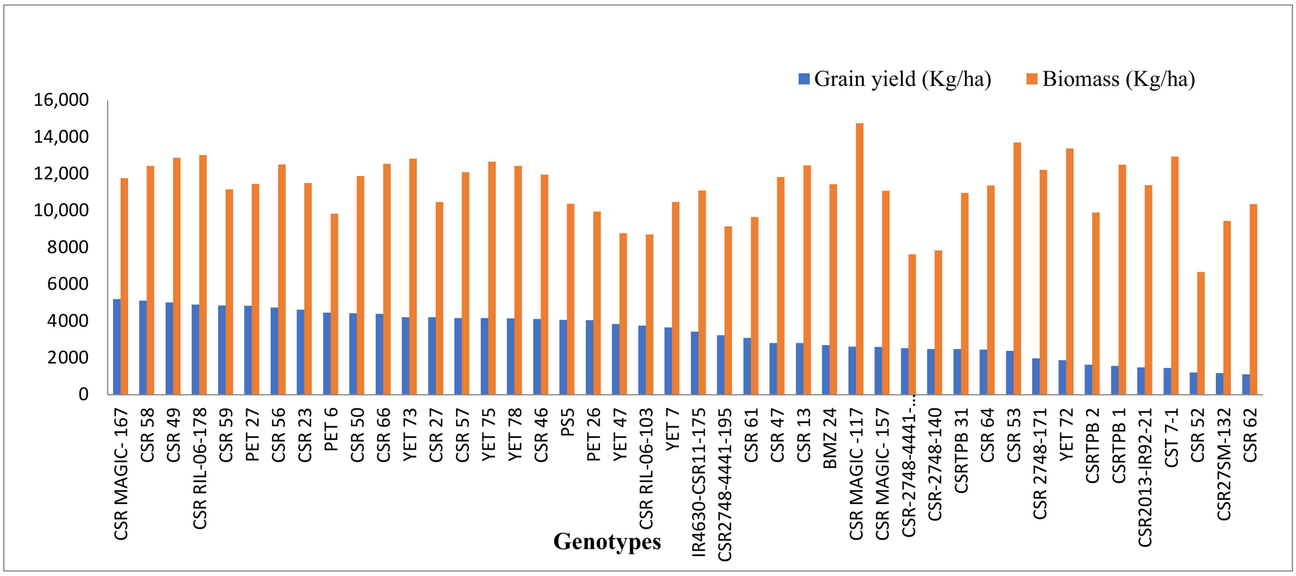

Figure 1. Grain yield and Biomass of rice genotypes in direct seeding method.

A positive association of grain yield was observed with its component traits. Grain yield showed a significant and positive correlation with tillers (0.51), biomass (0.22), plant height (0.41), and panicle length (0.52). A negative but non-significant correlation was observed between biomass and tillers (−0.06). Similar findings were reported by [17,18].

4. Conclusions

Based on the study findings, it is concluded that CSR MAGIC-167, CSR 58, CSR 49, and CSR RIL-06-178 were best performing genotypes. These lines should be evaluated in large trails in a farmer's field with multiplication trails of AICRP to identify the real potential of these genotypes. They could then be commercially released as optimal rice varieties for DSR situations. These genotypes could be utilized in subsequent breeding programs and could lay the foundation for genetic analysis.

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