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## Assessment of genetic variability and heritability in dry direct seeded rice (*Oryza sativa* L.)

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### Abstract

Nearly 202 genotypes from Bengal and Assam Aus panel were tested for variability of yield and yield attributing characters under dry direct seeded rice conditions at ICAR-National Rice Research Institute, Cuttack. The yield per plant showed a significant amount of variety; the largest yield was 31.4 g, the lowest was 0.45 g, and the grand mean was 9.40 g. According to the study's average performance of the 202 genotypes, no single genotype of rice fared better than any other for any of the attributes assessed. The examined genotypes showed a large level of variability between them in all of the observations. Characters like Days to 50% flowering, Plant height, number of tillers per plant, SPAD, Flag leaf length and Panicle length shown higher phenotypic variance (PV), Genotypic variance (GV). Higher PCV, GCV estimates obtained for Yield per plant and Productive tillers per plant. High Heritability estimates obtained for all the traits except Panicle length. High heritability coupled with high Genetic advance obtained for Plant height, Days to 50% flowering, Productive tillers per plant, Flag leaf length and SPAD. Thus, it may be suggested that these characters are predominantly controlled by additive genes.

**Keywords:** PCV, GCV, heritability, variability

### 1. Introduction

More than half of the world's population depends on rice (*Oryza sativa* L.) as a primary food crop <sup>[1]</sup>. A significant obstacle to food security is the rice industry's efficient and sustainable development <sup>[2]</sup>. Statistics show that seedling transplantation accounts for 77% of the world's rice output, with a peak of 95% in China <sup>[3]</sup>. The seedling transplantation culture technology wastes water resources since it uses a lot of water for irrigation <sup>[4]</sup>. Emissions of greenhouse gases during the production of rice are another issue. Due to the majority of the growth stage of rice being spent submerged in water due to transplanting cultivation technology, a significant amount of greenhouse gas emissions is produced as a result of the oxygen-deficient environment <sup>[5]</sup>. Statistics show that rice paddy fields generate more than 30% of the world's methane gas <sup>[6]</sup>. The technology for direct seeding rice cultivation has steadily gained popularity in light of the aforementioned issues. Rice seeds are spread directly in the field using the cultivation technique known as direct seeding, skipping the seedling stage. According to Mahender *et al.* <sup>[7]</sup>. Direct seeding can currently be divided into three categories: dry, moist, and water direct seeding. Wet direct seeding refers to planting newly sprouted rice seeds in moist soil, whereas water directed seeding refers to planting rice seeds that have already borne fruit in flooded fields.

According to studies, direct seeding can greatly boost production efficiency compared to seedling transplantation and can reduce overall labor requirements from 11 to 66% depending on the season, region, and type of direct seeded rice <sup>[8]</sup>. Nitrogen fertilizer consumption in direct-seeded rice can increase to 80% with better water management practices <sup>[9]</sup>. Delaying the initial flooding of direct-seeded rice can lower greenhouse gas emissions, which in turn lowers global warming <sup>[10, 11, 12]</sup>. Direct-seeded rice yields can be increased by promoting tillering, improving weed control, and seedling emergence and establishment rates using optimal water management practices during the seedling stage <sup>[13, 14]</sup>. Direct seeding has thus taken over as the primary method of rice production around the world as labor costs rise and the amount of agricultural equipment rises <sup>[15]</sup>.

Although the direct seeding of rice technology has many benefits, there are still substantial issues and difficulties with its use and promotion. Low seedling rates, significant weed infestations, and rice that lodges easily in the middle and late phases of growth are major issues with direct seeding of rice [16]. A low seedling rate, which immediately impacts the initial number of seedlings and subsequently affects the quality and final yield of the rice [17] is the main cause of the poor and inconsistent yield of direct-seeded rice.

According to earlier studies, seeds with higher vigor always emerge more uniformly than seeds with lower vigor [18]. Second, weeds are a significant issue limiting the output of direct-seeded rice and affect more than 30% of its yield [19]. The majority of the existing high-yielding types statistically endure a 20-50% yield reduction when planted via direct seeding [20]. Therefore, the key to removing the obstacle preventing the promotion and use of direct-seeded rice is to find the suitable varieties for direct seeded condition and functional genes for the qualities needed for direct seeding and introduce them into current high-yielding varieties via molecular marker-assisted selection. On the genetic basis of plant morphological features and root system architecture related to nutrient uptake, yield, and yield-contributing traits under DDSR, no thorough investigation has been done so far. Determining an optimal plant and root system design is therefore crucial for enhancing nutrient uptake, grain output, and adaptability under DDSR.

In the present study, we performed ANOVA and Genetic variability studies for 9 traits including plant morphological traits, yield and yield attributing traits in a Bengal and Assam

Aus Panel (BAAP) developed by Norton *et al.* [21] with the aim to assess the range of variability, heritability and genetic advance of the traits then to be used directly to breed high yielding and nutrient-efficient rice varieties for DDSR condition.

## 2. Materials and Methods

In the current study studies, over 202 genotypes from the Bengal and Assam Aus Panel (BAAP) presented in the Table 1 were used. The experiment was carried out using a Randomized Block Design with two Replications during the Rabi season of 2020-2021 at the ICAR-National Rice Research Institute in Cuttack, Odisha. At a distance of 20 cm between rows and 15 cm between plants, each genotype was directly seeded in soil. The field was immediately irrigated following fertilization in order to encourage proper germination. Following that, irrigation was given once every 5-7 days. To keep aerobic conditions, the plots were kept dry throughout the crop season. Recommendations for cultural practices and plant protection measures were put into action in order to maintain a steady and healthy crop stand. For three randomly selected plants, nine morphological traits were noted, including SPAD, Days to 50% flowering, Plant height, Flag leaf length, Flag leaf breadth, Panicle length, Number of tillers per plant, Productive tillers per plant, and single Plant yield per plant. The genetic parameters were estimated based on the method suggested by Al Jibouri *et al.* [22]; Johnson *et al.* [23] and Burton *et al.* [24]. The statistical analysis was done using the R-software.

**Table 1:** List of 202 Genotypes evaluated during Rabi 2020-21 under Dry direct seeded condition

S. No.	Genotype	S. No.	Genotype	S. No.	Genotype	S. No.	Genotype	S. No.	Genotype	S. No.	Genotype	S. No.	Genotype
1.	BAAP-2	30.	BAAP-47	59.	BAAP-82	88.	BAAP-116	117.	BAAP-154	146.	BAAP-187	175.	BAAP-230
2.	BAAP-3	31.	BAAP-48	60.	BAAP-83	89.	BAAP-117	118.	BAAP-155	147.	BAAP-189	176.	BAAP-231
3.	BAAP-4	32.	BAAP-49	61.	BAAP-84	90.	BAAP-118	119.	BAAP-156	148.	BAAP-190	177.	BAAP-232
4.	BAAP-5	33.	BAAP-50	62.	BAAP-85	91.	BAAP-119	120.	BAAP-157	149.	BAAP-191	178.	BAAP-233
5.	BAAP-6	34.	BAAP-51	63.	BAAP-86	92.	BAAP-120	121.	BAAP-158	150.	BAAP-197	179.	BAAP-234
6.	BAAP-12	35.	BAAP-55	64.	BAAP-87	93.	BAAP-121	122.	BAAP-159	151.	BAAP-198	180.	BAAP-235
7.	BAAP-13	36.	BAAP-56	65.	BAAP-88	94.	BAAP-122	123.	BAAP-160	152.	BAAP-199	181.	BAAP-236
8.	BAAP-20	37.	BAAP-57	66.	BAAP-89	95.	BAAP-123	124.	BAAP-161	153.	BAAP-200	182.	BAAP-237
9.	BAAP-21	38.	BAAP-58	67.	BAAP-90	96.	BAAP-125	125.	BAAP-162	154.	BAAP-204	183.	BAAP-238
10.	BAAP-22	39.	BAAP-59	68.	BAAP-91	97.	BAAP-127	126.	BAAP-163	155.	BAAP-205	184.	BAAP-240
11.	BAAP-23	40.	BAAP-60	69.	BAAP-92	98.	BAAP-129	127.	BAAP-164	156.	BAAP-206	185.	BAAP-241
12.	BAAP-25	41.	BAAP-62	70.	BAAP-93	99.	BAAP-130	128.	BAAP-165	157.	BAAP-209	186.	BAAP-242
13.	BAAP-26	42.	BAAP-63	71.	BAAP-96	100.	BAAP-131	129.	BAAP-166	158.	BAAP-210	187.	BAAP-243
14.	BAAP-27	43.	BAAP-64	72.	BAAP-99	101.	BAAP-132	130.	BAAP-167	159.	BAAP-211	188.	BAAP-247
15.	BAAP-28	44.	BAAP-65	73.	BAAP-101	102.	BAAP-133	131.	BAAP-168	160.	BAAP-212	189.	BAAP-248
16.	BAAP-31	45.	BAAP-67	75.	BAAP-102	103.	BAAP-134	132.	BAAP-169	161.	BAAP-213	190.	BAAP-250
17.	BAAP-32	46.	BAAP-69	75.	BAAP-103	104.	BAAP-135	133.	BAAP-170	162.	BAAP-214	191.	BAAP-254
18.	BAAP-33	47.	BAAP-70	76.	BAAP-104	105.	BAAP-138	134.	BAAP-171	163.	BAAP-215	192.	BAAP-255
19.	BAAP-34	48.	BAAP-71	77.	BAAP-105	106.	BAAP-139	135.	BAAP-172	164.	BAAP-216	193.	BAAP-257
20.	BAAP-35	49.	BAAP-72	78.	BAAP-106	107.	BAAP-141	136.	BAAP-174	165.	BAAP-218	194.	BAAP-259
21.	BAAP-36	50.	BAAP-73	79.	BAAP-107	108.	BAAP-144	137.	BAAP-175	166.	BAAP-219	195.	BAAP-262
22.	BAAP-37	51.	BAAP-74	80.	BAAP-108	109.	BAAP-145	138.	BAAP-177	167.	BAAP-220	196.	BAAP-264
23.	BAAP-38	52.	BAAP-75	81.	BAAP-109	110.	BAAP-146	139.	BAAP-178	168.	BAAP-222	197.	BAAP-269
24.	BAAP-40	53.	BAAP-76	82.	BAAP-110	111.	BAAP-147	140.	BAAP-179	169.	BAAP-224	198.	BAAP-270
25.	BAAP-41	54.	BAAP-77	83.	BAAP-111	112.	BAAP-148	141.	BAAP-180	170.	BAAP-225	199.	BAAP-287
26.	BAAP-42	55.	BAAP-78	84.	BAAP-112	113.	BAAP-148	142.	BAAP-181	171.	BAAP-226	200.	BAAP-290
27.	BAAP-43	56.	BAAP-79	85.	BAAP-113	114.	BAAP-151	143.	BAAP-182	172.	BAAP-227	201.	BAAP-296
28.	BAAP-45	57.	BAAP-80	86.	BAAP-114	115.	BAAP-152	144.	BAAP-185	173.	BAAP-228	202.	BAAP-298
29.	BAAP-46	58.	BAAP-81	87.	BAAP-115	116.	BAAP-153	145.	BAAP-186	174.	BAAP-229		

## 3. Results and Discussion

Analysis of variance (ANOVA) indicated statistically significant differences between each rice genotype and each of the investigated features (Table 2). Therefore, by careful

selection, these features may be enhanced. The table below (Table 3) provides an explanation of the mean, minimum and maximum values of the nine characters for the genotypes. Wide range of variability was found for SPAD reading among

the genotypes. It shown a range of 18.4 to 45.8 with a grand mean value of 32.74. Days to 50% flowering ranged from 71-105 and shown grand mean of 87.39 value. Plant height shown minimum of 67.87, maximum of 135.43 and exhibited a grand mean value of 106.34. Flag leaf length shown a range of 16.1 to 45.6 with a grand mean value of 27.24. Flag leaf width was shown minimum of 0.3 and maximum of 1.93 with a grand mean value of 1.18. Panicle length was shown a range of 13.93 to 94.2 and with a grand mean value of 21.6. Number of tillers per plant shown minimum of 1.33, maximum of 38 and grand value of 12.36. Productive tillers were shown 2.66 minimum, 27.33 maximum and 9.003 grand mean value. A considerable degree of variation was seen in yield per plant, maximum yield shown was 31.4, minimum was 0.45 with grand mean value of 9.40. No single genotype of rice performed better than any other for all of the qualities tested, according to the study's average performance of the 202 genotypes. All of the observations between the tested genotypes revealed a great deal of diversity between them. Genetic diversity and heritability have a significant impact on how a plant trait develops. Any breeding program can benefit from prior knowledge of population variability estimates and the trait's heritable components. Unless a sizable portion of the variance is heritable, trying to improve a character through selection would be more difficult. Knowing the character's heritability as well as its phenotypic and genotypic coefficient of variation would be helpful in breeding programme. Following Table 3 is a brief discussion of the variability parameters with respect to yield and traits associated with yield, including the grand mean, minimum, maximum, standard error, estimations of genotypic co-efficient of

variation (GCV), phenotypic co-efficient of variation (PCV), environmental co-efficient of variation (ECV), heritability (h<sup>2</sup>), genetic advance and genetic advance over mean. For all of the traits examined, the magnitude of PCV was greater than GCV, indicating environmental influences on these traits' expression [25]. Higher PCV, GCV estimates obtained for Yield per plant and productive tillers per plant. Highest PCV estimates obtained for Yield per plant and productive tillers per plant [26], number of tillers per plant [26] and panicle length [27]. Moderate PCV estimates obtained for SPAD, Plant height, Flag leaf length [28] and Flag leaf width [29]. There was therefore a lot of room for these qualities to be improved through careful selection and hybridization. Lowest PCV estimated obtained for Days to 50% flowering [27]. The examined characters had a moderate difference between PCV and GCV, indicating a moderate sensitivity to environment and, as a result, a stronger role for genetic factors in affecting the expression of these characters. This observation is similar to earlier findings of Ajmera *et al.* [30]; Khan *et al.* [31]; Nath and Kole [28]; Manivelan *et al.* [27]. The strategy for character selection is heavily influenced by heritability. Moderate heritability was noted in the current study for traits like Plant height, Days to 50% flowering, productive tillers per plant and Flag leaf width. These findings are accordance with Manivelan *et al.* [27]; Khan *et al.* [31]; Rajamadhan *et al.* [32] for plant height and days to 50% flowering. According to high heritability estimates, these qualities are highly transmittable to the next generation. Therefore, it is safe to rely on these characters, and practicing simple selection can help you get better.

**Table 2:** Analysis of variance (ANOVA) for 9 different characters

Source	D.F	SPAD	DFF	PH	FL	FW	PL	NT	PT	YIELD
Replication	1	31.88	55.79	3661.3	263.08	0.11	95.91	2.78	24.69	15.90
Genotypes	201	30.74**	81.47***	217.0***	31.90***	0.06***	33.37**	27.37**	18.70***	21.96***
Error	201	20.45	30.65	74.4	18.91	0.03	29.07	19.26	9.10	12.54

d.f = Degrees of freedom Values given in Parenthesis \*\*\*Significant at 5% level of significance \*\*Significant at 1% level of significance

SPAD = chlorophyll content, DFF = Days to 50% flowering, PH = Plant height (cm), FL = Flag leaf length (cm), FW = Flag leaf width (cm), PL = Panicle length (cm), NT = Number

of tillers per plant, PT = Productive tillers per plant, Yield per plant (g).

**Table 3:** Variability and genetic parameters for different characters of rice genotypes under dry direct seeded condition

Character	SPAD	DFF	PH	FL	FW	PL	NT	PT	YIELD
Maximum	45.8	105	135.43	45.6	1.93	94.2	38	27.33	31.40
Minimum	18.4	71	67.87	16.1	0.3	13.93	1.33	2.66	0.45
Grand Mean	32.74	87.39	106.34	27.24	1.18	21.60	12.36	9.003	9.40
Standard Error of Mean (SEM)	3.12	3.82	5.98	3.01	0.12	3.72	3.03	2.08	2.44
Critical Difference (CD) 5%	8.70	10.65	16.69	8.38	0.34	10.38 NS	8.44	5.80	6.82
Critical Difference (CD) 1%	11.48	14.05	22.01	11.05	0.45	13.69 NS	11.13	7.66	8.99
Environmental Variance	19.50	29.21	71.73	18.08	0.03	27.71	18.35	8.70	11.95
Genotypic Variance	4.90	24.19	67.49	6.15	0.013	2.035	3.86	4.57	4.48
Phenotypic Variance	24.39	53.41	139.22	24.23	0.044	29.75	22.21	13.24	16.43
Environmental Coefficient of Variance	13.49	6.18	7.96	15.61	14.68	24.38	34.65	32.72	36.76
Genotypic Coefficient of Variance	6.76	5.63	7.73	9.10	9.92	6.61	15.90	23.74	22.51
Phenotypic Coefficient of Variance	15.09	8.36	11.09	18.06	17.71	25.26	38.12	40.42	43.10
Heritability (Broad Sense)	0.20	0.45	0.48	0.25	0.313	0.07	0.17	0.34	0.27
Genetic Advance	2.04	6.82	11.78	2.57	0.14	0.77	1.69	2.59	2.28
Genetic Advance as percentage of mean	6.24	7.81	11.08	9.45	11.44	3.56	13.66	28.72	24.22

SPAD = chlorophyll content, DFF = Days to 50% flowering, PH = Plant height (cm), FL = Flag leaf length (cm), FW = Flag leaf width (cm), PL = Panicle length (cm), NT = Number of tillers per plant, PT = Productive tillers per plant, Yield per plant (g)

High genetic advance estimates were obtained for characters like Plant height [31, 33], Days to 50% flowering [26], productive tillers per plant, Flag leaf length [26], yield [26] and SPAD [34].

Low genetic advance estimates obtained for panicle length and number of tillers per panicle. These findings in accordance with Anis *et al.* [33]; Khan *et al.* [31] for plant

height. Pavani *et al.* [26] for Days to 50% flowering, Flag leaf length and yield per plant. The difference in findings may be due to various reasons including the genetic material used and environmental conditions it might not be necessary to have traits with high heritability to produce high genetic advance. High heritability should be accompanied by high genetic progress, according to Johnson *et al.* [23]. Breeders need to exercise caution while analyzing heritability. High heritability and high genetic advance were demonstrated in the current investigation by plant height [33, 31], days to 50% flowering [26], productive tillers per plant [27], Flag leaf length [26], yield per plant [26] and SPAD. Present study in accordance with Anis *et al.* [33]; Khan *et al.* [31] for plant height, Manivelan *et al.* [27] for Productive tillers per plant, Pavani *et al.* [26] for Days to 50% flowering, Flag leaf length and yield per plant. High heritability accompanied with high genetic advance as percent of mean observed for the trait's productive tillers per plant [35], yield per plant [36], Flag leaf width and plant height [31]. It demonstrated that these features are mostly regulated by additive gene activity. In order to increase these qualities, selection based on phenotypic performance would be useful. These findings are in accordance with Khan *et al.* [31] for plant height, Pavani *et al.* [26]; Pragnya *et al.* [35] for Productive tillers per plant. High heritability and little to no genetic advance as percentage of the mean were seen for Days to 50% flowering Pragnya *et al.* [35] and SPAD Hussain *et al.* [34]. It demonstrated that these features could be controlled by both additive and non-additive gene action.

#### 4. Conclusion

The analyzed characters' high levels of variability show the range of practical selection. The majority of the traits described above showed strong heritability, which suggests that additive gene activity is largely at play. The current study demonstrated how the chosen genotypes performed differently. Breeders may be misled by traits that have a large difference between GCV and PCV, which indicates that they are strongly influenced by environment. Traits that have a relatively small gap between their GCV and PCV are least changed by their environment. Therefore, by using straightforward selection, these features can simply be improved.

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#### 6. Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

#### 7. Conflict of interest: None.

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