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RESEARCH ARTICLE

Investigating the Genetic and Agronomic Factors Influencing Yield in Clustered Spikelets Rice (*Oryza sativa* L.)

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Abstract

In the present study, 32 rice genotypes with clustered spikelets, along with 4 checks, were evaluated for a total of 14 yield and yield attributing traits were evaluated at the Research cum Instructional farm IGKV, Raipur (C.G.) in *Kharif* 2023 under RCBD design. The aim was to estimate genetic variability and associations for yield traits across 36 lines. A total of 14 yield and yield-attributing traits were evaluated. Among the traits like filled grains per panicle, total grains per plant, biological yield, harvest index, 100-grain weight, primary and secondary branches per panicle, grains per cluster, and grain yield per plant had high PCV, GCV, h^2, and GAM. Traits like effective tiller, spikelet fertility, biological yield, 100-grain weight, and harvest index positively correlated with grain yield. Selecting these traits and parents from clusters I and III, which had the highest inter-cluster distance, will enhance yield. PCA identified genotypes like *Hathi panjara, Naykain jhaba, Amajhopa, Ganga dhara, Tuphi bora-1, Haruna luchai, Amaruthi, Nariyal phool-1, Chhind guchchhi, Kalinga, Khajur jhopa, Gadakhuta*, and *Nariyal phool-2* as donor parents for specific traits.

Keywords: Cluster, Clustered spikelets rice, Correlation, Heritability, PCA, Variability parameters.

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Introduction

Rice (*Oryza sativa* L.) is a staple crop for more than one-third of the world's population and plays a key role in ensuring food security. Chhattisgarh state of India, popularly known as the "Rice Bowl of India," harbors a rich biodiversity of Rice germplasm. Indira Gandhi Krishi Vishwavidyalaya (IGKV) Raipur, Chhattisgarh, is currently conserving a collection of more than 23250 rice germplasm accessions, thereby playing a pivotal role in preserving the heritage of the State (Sarawgi *et al*., 2017). These rice germplasm accessions have a wide range of unique characteristics, which include clustered spikelets, distinct colors, exceptional taste, and potential medicinal properties (Dwivedi *et al*., 2016).

There are several agronomic traits that directly and indirectly affect rice yield. Among them, seed size, number of grains per panicle and panicle structure play a crucial role. While most of the rice cultivars have panicles with single spikelets (Non-clustered), however, there are some rare rice genotypes that have panicles with clustered spikelets where 2 to 10 spikelets are present in a tight group (Sahu *et al*., 2014; Sarawgi *et al*., 2017). This character of rice can be utilized in rice breeding programmes to improve the yield by increasing the number of grains per panicle. Till now, most of the research for improving grain yield in rice has been focused majorly on positively correlated traits such as tiller numbers, panicle length, flag leaf length, etc and limited studies have been conducted to evaluate the clustered spikelets rice genotypes towards their impact on grain yield. A clustered spikelet may provide a new epitome for improving yield in rice.

Variability is the most important for selection to be effective in any breeding program. Genetic parameters, such as the genetic coefficient of variation and the phenotypic coefficient of variation, can be used to quantify the degree of diversity present in the population for specific traits. Estimates of heritability help breeders to select parents for crop improvement programs by providing more information about the concerned trait (Kumar *et al*., 2014). The selection procedure will be further aided by knowledge of character associations and the direct and indirect effects of each character on yield. The degree of correlation between grain yield and its contributing traits can be determined using correlation and path analysis. This type of analysis could ultimately assist the breeder in creating his selection techniques to achieve an improvement in grain yield (Singh *et al*., 2018). In contrast, multivariate techniques such as Principal Component Analysis (PCA) and Agglomerative Hierarchical Cluster Analysis help to classify genotypes in various groups and thereby help to identify superior lines for hybridization programs (Dhakal *et al.,* 2020).

Taking the above points into consideration, the present study was undertaken to study grain yield and contributing traits in 36 rice genotypes, which includes clustered spikelet genotypes along with non-clustered check varieties to access the genetic variability correlation patterns between the yield contributing traits.

Materials and Methods

The present experiment was conducted at the Research cum Instructional Farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur -492012 (C.G.).

Experimental Materials

A total of 36 rice genotypes were used, including 32 genotypes with clustered spikelets and 4 non-clustered (single spikelets) check varieties (TCDM-1, Vikram-TCR, CG Devbhog and Rajeshwari). The details of the genotypes, along with the number of spikelets per cluster, are presented in Table 1. All of the genotypes used in the study were obtained from the Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur -492012 (C.G.).

Experimental Details

For the experiment, all of the experimental materials were planted following a randomized complete block design (RCBD) with two replications at the Research cum Instructional Farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya (IGKV), Raipur during *Kharif* season 2023. Throughout the experiment, all standard agronomic practices were adopted.

Table 1: List of experimental material

Entry	*Genotype*	*No. of grain per cluster*	*Entry*	*Genotype*	*No. of grain per cluster*
1	KHANDSAR	2	19	HATHI PANJARA	2
2	NARIYAL PHOOL	3	20	KALINGA	3
3	SAARIPHOOL	2	21	GANGA DHARA	3
4	KUSUMBHOG	2	22	TUPAI BORA	3
5	OONI	2	23	TUPAI BORA 1	3
6	GADAKHUTA	2	24	GURMATIYA	2
7	CHANDANI DHAN	3	25	JHILLI MUT DHAN 13-2	2
8	BARKI BARI	2	26	AMAJHOPA	3
9	JHUMMA CHUDI	2	27	KOUDI DHULL	3
10	SABRI KENDUWA	2	28	CHHIND GUCHHI	3
11	RADHE DHAN	2	29	NARIYAL PHOOL SEL-1	2
12	NARIYAL PHOOL -1	3	30	AMARUTHI	2
13	CL-1	3	31	KHAJUR JHOPA	7
14	BHAJNA	2	32	NAYKEIN JHOPA	2
15	LAL DHAN	2	33	TCDM-1 (Check-1)	1
16	HARUNA LUCHAI	2	34	VIKRAM-TCR (Check-2)	1
17	MANKI	2	35	CG-DEVBHOG (Check-3)	1
18	SHANKARJATA	2	36	RAJESHWARI (Check-4)	1

Observations

Observations for a total of 14 traits, which include Days to 50% Flowering (DFF), Plant Height (cm), number of effective tillers per plant, Panicle length (cm), Number of filled grains per panicle, Total number of grains per panicle, Spikelet fertility (%), Biological yield (g/plant), Grain yield per plant (g), Harvest index (%), Hundred seed weight (g), Number of primary branches per panicle, Number of secondary branches per panicle, number of grains per cluster, were recorded on 5 randomly selected plants per replication for each genotype under test.

Statistical analysis

The observations recorded for 14 yield and attributing traits on 36 genotypes under test were subjected to statistical analysis specifically for the analysis of variance (ANOVA), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, correlation coefficient analysis, path coefficient analysis, cluster analysis (ward algorithm and Euclidean distance) and principal component analysis (PCA) using R program using a suitable statistical package.

Result and Discussion

Analysis of variance

The replicated data for all 14 traits were subjected to analysis of variance based on randomized complete block design (RCBD) and the results are presented in Table 2. Analysis of variance (ANOVA) indicated that the treatment mean sum of squares for all 14 yield and yield attributing traits were highly significant ($p = 0.01$), indicating the presence of substantial genetic variability among the genotypes under test for all yield and yield attributing traits. Among the yield-contributing traits, the highest variation is exhibited by the number of total grains per panicle and the lowest variation is exhibited by hundred seed weight (g).

Furthermore, while comparing the genotypes based on the CN and GY it was found that the clustered rice genotypes *Khandsar* produced significantly higher grain yield compared to all four of non-clustered check rice varieties used in the study, while rice genotypes *Koudi dhull*, and *Chhindguchhi* produced significantly higher grain yields than the three checks except for the check rice variety *Rajeshwari* (Table 3). The pattern of clustering and panicle of each of the 36 rice genotypes under test is presented in Fig. 1 and Fig. 2(a-b), respectively.

Genetic variability parameters

Parameters of genetic variability such as general mean, range, genotypic and phenotypic coefficient of variance (%), heritability in a broad sense (%) and genetic advance as % of mean were used to decipher the nature and magnitude of variation existing for each of the 14 yield and attributing traits. The results are presented in Table 4.

The phenotypic coefficient of variance (PCV) was, in general, higher than the genotypic coefficient of variance (GCV) for all the yield and attributing traits, showing some influence of environmental factors on these traits. The estimates of GCV and PCV were categorized as low (0–10%), moderate

Table 2: Analysis of variance for 14 yield and attributing traits

SN	*Source of variation*	*Mean sum of square*		
		Replication	*Treatment*	*Error*
1	DFF	6.13	99.709 **	1.21
2	PH	0.18	1890.68 **	2.71
3	ET	7.67	9.41 **	1.75
4	PL	0.12	10.792 **	0.42
5	FGP	0.32	4421.965 **	2.31
6	TGP	0.14	5329.938 **	2.92
7	SF	0.08	195.831 **	0.23
8	BY	1.23	999.896 **	2.60
9	H.I.	14.56	105.756 **	2.28
10	HSW	0.01	0.949 **	0.01
11	PB	0.41	21.836 **	0.80
12	SB	17.01	265.225 **	2.72
13	CN	1.53	2.51 **	0.13
14	GYP	2.15	110.497 **	2.65

* and ** significant at 5% and 1% probability level
DFF = Days to 50% flowering; PH = Plant height (cm); ET = Effective tillers; PL = Panicle length (cm); NFG = Number of filled grains per panicle; TNG = Total number of grains; SF = Spikelet fertility; BY = Biological yield (g); EY= Economic yield (g); HI = harvest index; HSW = Hundred seed weight (g); PN= Panicle number per plant; PB = Primary branch; SB = Secondary branch; CN= Number of grain per cluster; GYP = Grain yield per plant (g)

Table 3: Top-performing rice genotypes based on the number of grains per cluster

S. No.	*Name of Genotypes*	*Number of grains per cluster*	*Grain yield per plant (g)*
1	KHANDSAR	2	43.445
2	KOUDI DHULL	3	32.015
3	CHHIND GUCHHI	3	31.705
4	HATHI PANJARA	2	28.680
5	SHANKARJATA	2	27.940
6	CL-1	3	27.815
	RAJESHWARI (Check-4)	1	38.750
	CG-DEVBHOG (Check-3)	1	27.655
	VIKRAM-TCR (Check-2)	1	23.595
	TCDM-1 (Check-1)	1	18.520
CD at 5%=3.3			

(10–20%) and high (>20%), as proposed by Johnson *et al.,* (1955). The traits that exhibited low GCV and PCV are days to 50% flowering. The traits that showed moderate GCV and PCV are plant height (cm), effective tillers per plant, panicle length (cm) and spikelet fertility (%). Traits that exhibited a high range of GCV and PCV are the number of filled grains per panicle, number of grains per panicle, biological yield (g), harvest index, 100-grain weight (g), primary branches per panicle, secondary branches per panicle, number of grains per cluster and grain yield per plant (g). Similar high GCV and PCV were also reported by Prakash *et al*. (2018) for traits grain yield per plant and biological yield (g) and by Saha *et al*. (2019) for traits number of filled grains per panicle and number of grains per panicle. The higher estimates of GCV and PCV indicate towards preponderance of genetic variability among the genotypes for these traits. Therefore, direct selection would be rewarding for achieving improvement in these traits.

Among the 14 yield and attributing traits high heritability coupled with high genetic advance as % of mean was observed for plant height (cm), number of effective tillers, panicle length (cm), number of filled grains per panicle, number of total grains per panicle, spikelet fertility (%), biological yield (g), harvest index, 100-grain weight (g), primary branches per panicle, secondary branches per panicle, number of grains per cluster, grain yield per plant (g). High heritability coupled with high genetic advance as a percentage of the mean indicates the preponderance of additive gene action in these traits. Therefore, selection (mass selection and progeny selection) methods would be effective in the accumulation of additive genes, resulting in the improvement of mean performance for these traits in the populations. Eswaran *et al*., (2016) and Kumar *et al*., (2018) have also reported high heritability coupled with high genetic advance as % of the mean for most of the agro-morphological traits in their experiments, which supports the outcome of the present study.

Fig 1: Clustering pattern observed in the clustered spikelets rice genotypes

The trait days to 50% flowering showed high heritability with moderate genetic advance as % of the mean. Heterosis breeding will be successful in enhancing these traits since the combination of high heritability and modest genetic advancement indicates that the character is governed by both additives as well as non-additive gene activity. The results are in line with the findings of Hasan *et al*., (2013) who have also reported high heritability coupled with moderate genetic advance as % of the mean for days to 50 % flowering.

Table 4: Genetic Variability parameters

Traits	*GM*	*Range*		*Variance*		*Heritability (%)*	*GA % mean*
		Min	*Max*	*GCV (%)*	*PCV (%)*		
DFF	111.90	95.00	124.50	6.27	6.35	97.60	12.76
PH	155.05	94.80	197.20	19.82	19.84	99.71	40.76
ET	11.01	6.40	16.10	17.78	21.45	68.66	30.34
PL	22.36	15.10	27.16	10.19	10.59	92.59	20.19
NFG	153.36	87.40	321.20	30.65	30.67	99.90	63.11
TNG	189.27	117.60	345.20	27.27	27.28	99.89	56.14
SF	81.22	46.53	93.04	12.18	12.19	99.76	25.05
BY	77.41	41.00	138.40	28.85	28.92	99.48	59.27
HI	35.53	23.33	56.86	20.25	20.69	95.79	40.82
HSW	2.05	1.22	3.99	33.37	33.76	97.74	67.97
PB	12.91	9.70	28.20	25.11	26.05	92.94	49.87
SB	52.73	28.60	74.60	21.73	21.95	97.97	44.30
CN	2.40	1.00	7.00	45.52	47.96	90.06	88.99
GYP	21.57	8.36	43.45	34.04	34.87	95.31	68.46

DFF = Days to 50% flowering; PH = Plant height (cm); ET = Effective tillers; PL = Panicle length (cm); NFG = Number of filled grains per panicle; TNG = Total number of grains; SF = Spikelet fertility; BY = Biological yield (g); EY= Economic yield (g); HI = harvest index; HSW = Hundred seed weight (g); PN= Panicle number per plant; PB = Primary branch; SB = Secondary branch; CN= Number of grain per cluster; GYP = Grain yield per plant (g)

Fig 2(a): Panicle of all 36 rice genotypes

Fig 2(b): Panicle of all 36 rice genotypes

Correlation analysis

Correlation analysis was carried out to compute the correlation coefficient both at the genotypic and phenotypic levels (Table 5) to understand the relationship between the characters. The results showed a significant and positive correlation of grain yield per plant (g) with the number of effective tillers, spikelet fertility (%), biological yield (g), 100-grain weight (g) and harvest index. Further grain yield showed a significant negative correlation with secondary branches per panicle. Interestingly, the number of spikelets per cluster showed a non-significant but positive correlation with the grain yield per plant (g).

Additionally, traits such as plant height (cm), panicle length (cm), number of filled grains per panicle and number of primary branches per panicle exhibited non-significant correlation in positive direction. In contrast, traits such as days to 50% flowering and the total number of grains per panicle showed a non-significant negative correlation with the grain yield per plant (g). A similar high correlation of effective tiller, biological yield and 100-grain weight with grain yield was also reported by Surek and Beser (2003).

A positive correlation between characters is advantageous as it facilitates the concurrent development of both attributes through indirect selection. Conversely, a negative correlation will hinder the simultaneous improvement of two traits, necessitating some form of economic trade-off in such an instance.

Path analysis

Path coefficient analysis was performed to get a clearer and more accurate picture of a complex event at the correlation level. The grain yield per plant (g) was used as a dependent

Table 4: Genotypic and Phenotypic coefficient of correlation

Traits	**r**	DFF	PH	ET	PL	NFG	TNG	SF	BY	HI	HSW	PB	SB	CN	GYP
DFF	r_p	1	0.677**	-0.132^{NS}	0.137^{NS}	0.079^{NS}	-0.031^{NS}	0.226^{NS}	0.329**	-0.822**	-0.040^{NS}	0.015^{NS}	-0.296*	0.491**	-0.015^{NS}
	$\mathbf{r_g}$	1	0.685**	-0.173^{NS}	0.161^{NS}	0.079^{NS}	-0.032^{NS}	0.229^{NS}	0.334**	-0.849**	-0.037^{NS}	0.025^{NS}	-0.304**	0.520**	-0.018^{NS}
PH	r_p		1	-0.186^{NS}	0.480**	0.043^{NS}	-0.008^{NS}	0.120^{NS}	0.581**	-0.644**	0.445**	0.251*	-0.211^{NS}	0.452**	0.118^{NS}
	$\mathbf{r_g}$		1	-0.232*	0.496**	0.043^{NS}	-0.009^{NS}	0.121^{NS}	0.583**	-0.654**	0.452**	0.261*	-0.215^{NS}	0.476**	0.121^{NS}
ET	r_p			1	0.065^{NS}	-0.129^{NS}	-0.195^{NS}	0.048^{NS}	0.296*	0.315**	-0.001^{NS}	-0.154^{NS}	-0.302**	-0.101^{NS}	0.493**
	$\mathbf{r_g}$			1	0.074^{NS}	-0.162^{NS}	-0.241*	0.056^{NS}	0.341**	0.398**	-0.014^{NS}	-0.216^{NS}	-0.393**	-0.151^{NS}	0.617**
PL	r_p				1	-0.039^{NS}	-0.046^{NS}	-0.001^{NS}	0.327**	-0.125^{NS}	0.421**	0.273*	-0.104^{NS}	0.129^{NS}	0.183^{NS}
	$\mathbf{r_g}$				1	-0.039^{NS}	-0.047^{NS}	0.001^{NS}	0.336**	-0.115^{NS}	0.434**	0.276*	-0.110^{NS}	0.152^{NS}	0.185^{NS}
NFG	r_p					1	0.877**	0.397**	0.220^{NS}	-0.008^{NS}	-0.313**	0.026^{NS}	0.389**	-0.219^{NS}	0.156^{NS}
	$\mathbf{r_g}$					1	0.877**	0.398**	0.221^{NS}	-0.009^{NS}	-0.316**	0.027^{NS}	0.394**	-0.235*	0.159^{NS}
TNG	r_p						1	-0.075^{NS}	0.036^{NS}	0.054^{NS}	-0.448**	0.085^{NS}	0.552**	-0.264*	-0.025^{NS}
	$\mathbf{r_g}$						1	-0.075^{NS}	0.037^{NS}	0.054^{NS}	-0.451**	0.089^{NS}	0.557**	-0.281*	-0.026^{NS}
SF	r_p							1	0.366**	-0.122^{NS}	0.191^{NS}	-0.077^{NS}	-0.246*	0.016^{NS}	0.336**
	$\mathbf{r_g}$							1	0.368**	-0.124^{NS}	0.191^{NS}	-0.081^{NS}	-0.247*	0.013^{NS}	0.345**
BY	r_p								1	-0.257*	0.499**	0.231^{NS}	-0.291*	0.218^{NS}	0.516**
	$\mathbf{r_g}$								1	-0.258*	0.502**	0.238*	-0.298*	0.230^{NS}	0.530**
HI	r_p									1	-0.027^{NS}	-0.034^{NS}	0.189^{NS}	-0.467**	0.269*
	$\mathbf{r_g}$									1	-0.021^{NS}	-0.037^{NS}	0.193^{NS}	-0.507**	0.281*
HSW	r_p										1	0.318**	-0.207^{NS}	0.185^{NS}	0.338**
	$\mathbf{r_g}$										1	0.328**	-0.208^{NS}	0.193^{NS}	0.349**
PB	r_p											1	0.073^{NS}	0.154^{NS}	0.036^{NS}
	$\mathbf{r_g}$											1	0.071^{NS}	0.154^{NS}	0.046^{NS}
SB	r_p												1	-0.346**	-0.262*
	$\mathbf{r_g}$												1	-0.365**	-0.267*
CN	r_p													1	0.050^{NS}
	$\mathbf{r_g}$													1	0.060^{NS}
GYP	r_p														1
	$\mathbf{r_g}$														1

DFF = Days to 50% flowering; PH = Plant height (cm); ET = Effective tillers; PL = Panicle length (cm); NFG = Number of filled grains per panicle; TNG = Total number of grains; SF = Spikelet fertility; BY = Biological yield (g); EY= Economic yield (g); HI = harvest index; HSW = Hundred seed weight (g); PN= Panicle number per plant; PB = Primary branch; SB = Secondary branch; CN= Number of grain per cluster; GYP = Grain yield per plant (g)

variable on thirteen independent variables mentioned beforehand. The direct and indirect effect of all traits on grain yield is presented in Table 6. The traits that showed the highest positive direct effect on gain yield per plant (g) were total number of grains per panicle (1.555) followed by number of effective tiller (1.115), 100 seed weight (g) (0.939), spikelet fertility % (0.708), number of grains per cluster (0.315), days to 50% flowering (0.281), harvest index (0.148), plant height (0.108), primary branches per panicle (0.039) and secondary branches per panicle (0.003). The trait number of grains per cluster exhibited a moderate positive direct effect on the grain yield per plant (g), suggesting a direct relationship of cause and effect, while its weak negative indirect effects through other traits is the possible reason why it has a non-significant correlation with the grain yield per plant (g) as discussed earlier. The traits that exhibited the highest negative direct effect on grain yield were the number of filled grains per panicle (-0.842) followed by biological yield (-0.581) and panicle length (-0.211). Similar to our findings, Maurya *et al*. (2018) have also reported a direct positive effect of plant height, effective tiller, total number of grains, spikelet fertility and test weight on grain yield.

Table 5: Path analysis

Character	*DTF*	*PH*	*ET*	*PL*	*NFG*	*TNG*	*SF*	*BY*	*HI*	*HSW*	*PB*	*SB*	*CN*	*r*
DTF	**0.281**	0.074	-0.193	-0.034	-0.067	-0.050	0.162	-0.194	-0.126	-0.034	0.001	-0.001	0.164	-0.018^{NS}
PH	0.192	**0.108**	-0.259	-0.105	-0.036	-0.013	0.086	-0.339	-0.097	0.425	0.010	-0.001	0.150	0.121^{NS}
ET	-0.049	-0.025	**1.115**	-0.016	0.136	-0.375	0.040	-0.198	0.059	-0.013	-0.008	-0.001	-0.048	0.617**
PL	0.045	0.053	0.082	**-0.211**	0.033	-0.073	0.001	-0.196	-0.017	0.408	0.011	0.000	0.048	0.185^{NS}
NFG	0.022	0.005	-0.180	0.008	**-0.842**	1.364	0.282	-0.129	-0.001	-0.297	0.001	0.001	-0.074	0.159^{NS}
TNG	-0.009	-0.001	-0.269	0.010	-0.738	**1.555**	-0.053	-0.021	0.008	-0.424	0.003	0.002	-0.089	-0.026^{NS}
SF	0.064	0.013	0.063	0.000	-0.335	-0.116	**0.708**	-0.214	-0.018	0.179	-0.003	-0.001	0.004	0.345**
BY	0.094	0.063	0.380	-0.071	-0.186	0.057	0.260	**-0.581**	-0.038	0.472	0.009	-0.001	0.072	0.530**
HI	-0.238	-0.070	0.444	0.024	0.008	0.083	-0.088	0.150	**0.148**	-0.019	-0.001	0.001	-0.160	0.281*
HSW	-0.010	0.049	-0.016	-0.092	0.266	-0.701	0.135	-0.292	-0.003	**0.939**	0.013	-0.001	0.061	0.349**
PB	0.007	0.028	-0.240	-0.058	-0.023	0.138	-0.057	-0.139	-0.006	0.308	**0.039**	0.000	0.049	0.046^{NS}
SB	-0.085	-0.023	-0.438	0.023	-0.332	0.866	-0.175	0.173	0.029	-0.196	0.003	**0.003**	-0.115	-0.267*
CN	0.146	0.051	-0.168	-0.032	0.198	-0.437	0.009	-0.134	-0.075	0.182	0.006	-0.001	**0.315**	0.060^{NS}

DFF = Days to 50% flowering; PH = Plant height (cm); ET = Effective tillers; PL = Panicle length (cm); NFG = number of filled grains per panicle; TNG = Total number of grains; SF = Spikelet fertility; BY = Biological yield (g); EY= Economic yield (g); HI = harvest index; HSW = Hundred seed weight (g); PN= Panicle number per plant; PB = Primary branch; SB = Secondary branch; CN= Number of grain per cluster.

Table 7: Clustering pattern of genotypes

Cluster no.	*No. of Genotypes*	*Name of Genotypes*
C1	7	Khandsar, Shankarjata, Koudi dhull, CG-Devbhog, Rajeshwari, TCDM-1, Vikram-TCR
C2	21	Chandani dhan, Sabri kenduwa, Saariphool, Kusumbhog, Bhanjna, Haruna luchai, Barki bari, kalinga, Chhind guchchhi, Khajur jhopa, Ganga dhara, Tuphi bora, Tuphi bora-1, Nariyal phool-2, Nariyal phool, CL-1, Nariyal phool-1, Amaruthi, Amajhopa, Hathi panjara, Naykain Jhaba
C3	8	Jhilli mut dhan 13-2, Gadakhuta, Gurmatiya, Radhe dhan, Ooni, Jhumma chudi, Lal dhan, Manki

Cluster Analysis

The cluster analysis was performed using the package NbClust, which, after analyzing 30 indices, provides the best number of clusters following the majority rule, while the distance followed for clustering is Euclidean distance. The clustering method is the ward, which minimizes the within-cluster variance and merges the clusters that have minimum distance at each step. The clustering pattern of genotypes is presented in Table 7. Besides this, various inter and intra-cluster distances were also computed and presented in Table 8 and Fig 3.

In the case of yield characters, the genotypes were grouped into three clusters. The highest number of genotypes appeared in cluster II, which possessed 21 genotypes. The second highest number of genotypes was found in cluster III, which possessed 8 genotypes. The least number of genotypes appeared in cluster I having 7 genotypes.

Out of these three clusters identified, cluster I had the highest intra-cluster distance, followed by Cluster II and Cluster III. The highest inter-cluster distance was found between cluster I and cluster III, followed by cluster I and II.

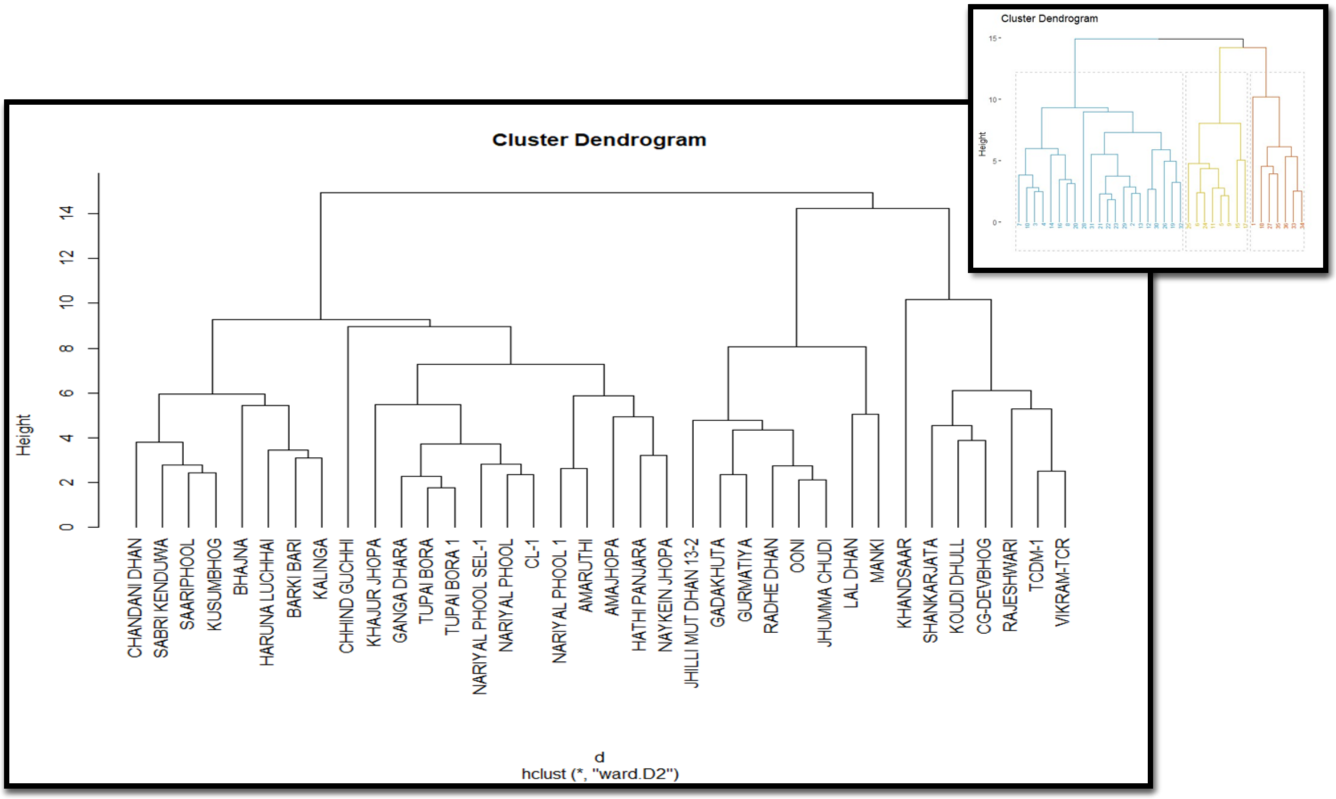

Fig 3: Cluster diagram for yield attributing traits

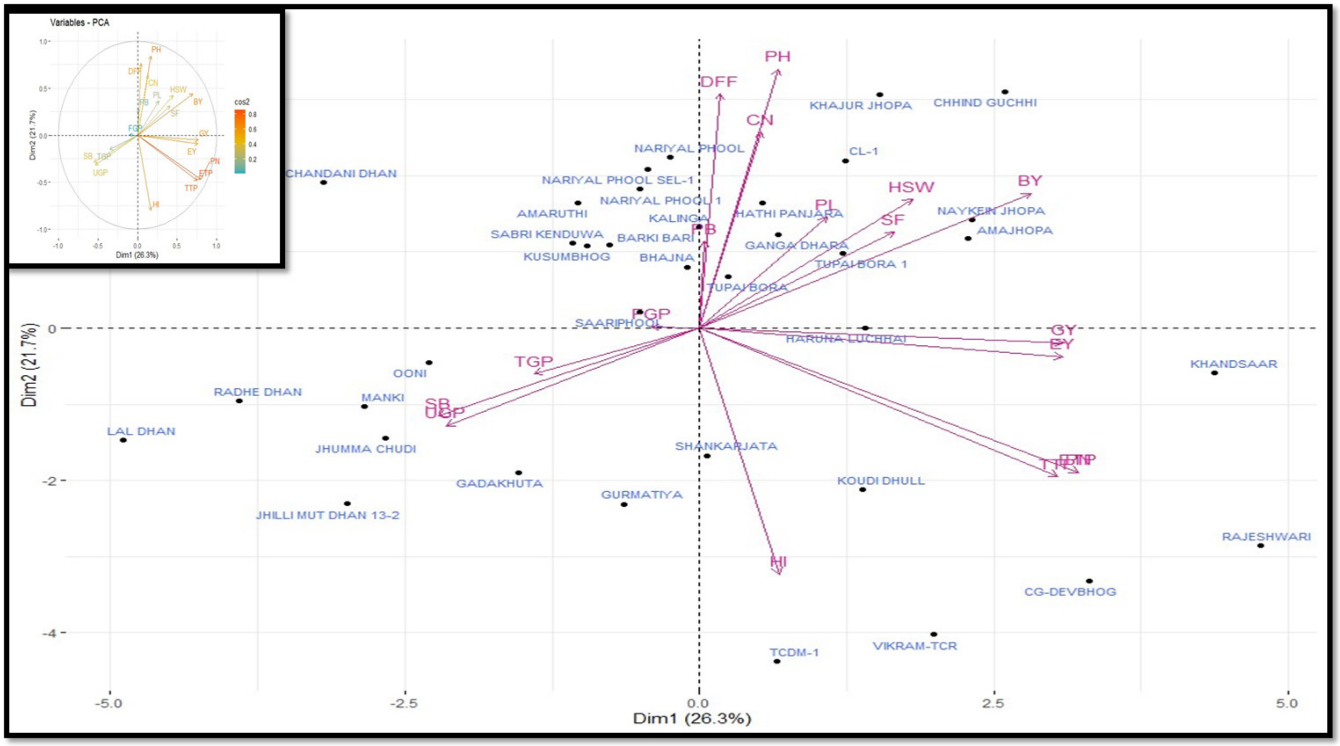

Fig 4: PCA biplot for yield traits

Table 8: Intra and Intercluster distance

Clustering component		*C1*	*C2*	*C3*
Intra cluster distance:				
Intra cluster: complete		9.04	8.63	7.10
Intra cluster: average		5.62	4.68	4.39
Intra cluster: centriod		3.66	3.20	2.88
Inter cluster distance:				
inter cluster: complete	C1	0.00	10.29	11.03
	C2		0.00	10.17
	C3			0.00
inter cluster: average	C1	0.00	6.79	6.89
	C2		0.00	5.98
	C3			0.00
inter cluster: centroid	C1	0.00	4.66	5.20
	C2		0.00	4.18
	C3			0.00

Minimum inter-cluster distance was found between cluster II and cluster III.

Cluster I had the highest cluster mean for harvest index, followed by grain yield per plant and effective tiller. Whereas, Cluster II had the largest mean value for plant height, followed by days to 50% flowering, biological yield (g), spikelet fertility, panicle length (cm), primary branches per panicle, number of grains per cluster and 100 grain weight (g). Cluster III had the largest mean value for the number of total grains per panicle, followed by the number of filled grains per panicle and secondary branches per panicle. The cluster mean is presented in Table 9.

Principal Component Analysis

Five significant principal components were obtained as they had eigenvalue more than 1. The PC1 and PC2 had 48.04% of

Table 9: Cluster mean for yield attributing traits

Group/ Character	*DFF*	*PH*	*ET*	*PL*	*NFG*	*TNG*	*SF*	*BY*	*HI*	*HSW*	*GYP*	*PB*	*SB*	*CN*
C1	105.50	128.48	**14.33**	22.13	151.77	187.57	79.62	80.43	**44.89**	1.94	**30.27**	11.83	52.14	1.57
C2	**115.90**	**174.99**	10.52	**23.11**	151.76	177.90	**84.78**	**84.96**	31.27	**2.32**	21.28	**13.42**	50.00	**2.71**
C3	107.00	125.99	9.39	20.69	**158.95**	**220.60**	73.21	54.94	38.52	1.44	14.73	12.53	**60.41**	1.63

DFF = Days to 50% flowering; PH = Plant height (cm); ET = Effective tillers; PL = Panicle length (cm); NFG = Number of filled grains per panicle; TNG = Total number of grains; SF = Spikelet fertility; BY = Biological yield (g); EY= Economic yield (g); HI = harvest index; HSW = Hundred seed weight (g); PN= Panicle number per plant; PB = Primary branch; SB = Secondary branch; CN= Number of grain per cluster; GYP = Grain yield per plant (g)

Table 10: Percentage of variance contributed by each principal component towards total variance for yield attributing trait

Particulars	*Principal component 1*		*Principal component 2*		*Principal component 3*	
Trait	*Contribution*	*Correlation*	*Contribution*	*Correlation*	*Contribution*	*Correlation*
DFF	0.04%	0.044	14.88%	0.763	0.14%	-0.060
PH	0.58%	0.165	18.16%	0.843	0.91%	0.154
ET	13.43%	0.798	5.65%	-0.470	0.54%	-0.118
PL	1.53%	0.269	3.36%	0.362	1.01%	0.162
NFG	0.22%	-0.102	0.00%	0.005	30.86%	0.893
TNG	2.57%	-0.349	0.56%	-0.148	27.91%	0.849
SF	3.55%	0.410	2.50%	0.312	2.18%	0.237
BY	10.30%	0.698	4.92%	0.438	5.96%	0.392
EY	12.36%	0.765	0.22%	-0.094	9.38%	0.492
HI	0.59%	0.167	16.41%	-0.801	0.61%	0.126
HSW	4.24%	0.448	4.51%	0.420	0.04%	-0.034
GYP	12.42%	0.767	0.06%	-0.048	3.24%	0.289
PB	0.00%	0.011	2.04%	0.282	2.59%	0.259
SB	6.38%	-0.550	2.11%	-0.287	9.76%	0.502
CN	0.36%	0.130	10.43%	0.639	3.18%	-0.287
Eigenvalue	4.74		3.91		2.58	
% Variance	26.33		21.72		14.35	
Cumulative % variance	26.33		48.04		62.40	

DFF = Days to 50% flowering; PH = Plant height (cm); ET = Effective tillers; PL = Panicle length (cm); NFG = Number of filled grains per panicle; TNG = Total number of grains; SF = Spikelet fertility; BY = Biological yield (g); EY= Economic yield (g); HI = harvest index; HSW = Hundred seed weight (g); PN= Panicle number per plant; PB = Primary branch; SB = Secondary branch; CN= Number of grain per cluster; GYP = Grain yield per plant (g)

the variance present in the studied data set (Table 10). From 5 PCs total of 82.34% cumulative variance is explained in the studied data set. For PC1, the most important trait is the number of effective tillers, followed by grain yield per plant, economic yield, total tiller per plant, biological yield, and spikelet fertility. For PC2, plant height is the most significant trait contributing the maximum to PC2, followed by harvest index, days to 50% flowering, number of grains per cluster, 100 grain weight, and panicle length, as revealed by the eigenvalues. For PC3, the number of filled grains per panicle is the most important trait, followed by the total number of grains per panicle, secondary branches per panicle, and primary branches per panicle.

Based on the PCA Biplot analysis (Fig. 4), the rice genotype *Hathi panjara* moderately correlated with the trait plant height (cm) and number of grains per cluster. While the rice genotypes *Naykain Jhaba* and *Amajhopa* were highly correlated with trait biological yield (g). *Ganga dhara* as highly correlated with panicle length (g). *Tuphi bora-1* was highly correlated with spikelet fertility (%). *Haruna luchai* was moderately correlated with grain yield per plant (g).

Conclusion

The present study shows the presence of substantial genetic diversity among the 36 rice genotypes tested. All 14 yield and attributing traits studied had shown significant variation with high heritability coupled with high genetic advance as % of mean for traits such grain yield per plant (g), total number of grains per panicle, number of effective tillers, hundred seed weight (g), and spikelet fertility (%). These traits also exhibited a significant positive correlation along with a strong direct effect on grain yield per plant (g). Although the trait number of grains per cluster exhibited a non-significant correlation with grain yield per plant (g), the path analysis revealed a moderate positive direct effect. This indicates that the number of grains per cluster may contribute to a moderate enhancement in yield when combined with other key yield-attributing traits in the future breeding programs. Further, we found that clustered rice genotypes *Khandsar*, *Koudi dhull*, and *Chhindguchhi* produced significantly higher grain yields compared to non-clustered check rice varieties. The presence of multiple grains per spikelet (clustering) had a moderately positive influence on yield by increasing the number of fertile grains and overall plant productivity. However, the number of grains within each cluster did not directly correlate with yield due to lower grain density. Further research is needed to understand how the trait of clustered grains is inherited. Few mutants and genes have been identified by various researchers, which can be included in the future studies to get better understanding of its inheritance and contribution towards increased grain yield. Further they can be utilized to develop varieties that can break the current yield potentials.

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