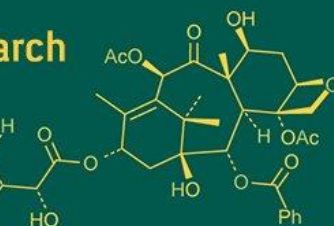
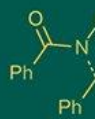


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Agro-morphological characterization and genetic variability analysis in rice (*Oryza sativa* L.)

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Abstract

The present study was undertaken to assess the agro-morphological characterisation and genetic variation in 55 rice accessions, including 5 check varieties (IR 64, Swarna, Jaya, Dagad Desi, and MTU 1010). The field experiment was conducted in a Randomized Complete Block Design (RCBD) with two replications during the *Kharif* season of 2025 at the Instructional Cum Research Farm, IGKV, Raipur, Chhattisgarh. Agro-morphological characterisation revealed considerable variation for most qualitative traits, while ligule shape and aroma showed no variation among the genotypes. Analysis of variance indicated highly significant differences among the accessions for all evaluated quantitative traits, validating the presence of substantial genetic variability within the experimental material. For all traits, the phenotypic coefficient of variation (PCV) was marginally higher than its corresponding genotypic coefficient of variation (GCV), denoting a minimal environmental influence on trait expression. High heritability coupled with high genetic advance as a percentage of mean were observed for grain yield per plant, harvest index, plant height, days to 50% flowering, and number of filled grains per panicle. This pattern reveals the predominance of additive gene action, indicating that direct phenotypic selection for these attributes would be highly effective for yield improvement.

Keywords: Rice, agro-morphological, genetic parameter, heritability and genetic advance

Introduction

Rice (*Oryza sativa* L.) $2n = 2x = 24$ is a monocotyledonous, semi-aquatic, self-pollinated annual grass belonging to the family Poaceae and subfamily Bambusoideae. It stands as a global staple, frequently feeding more than one-third of humanity and providing nearly 27% of global dietary energy and 20% of protein intake. Cultivated across a vast spectrum of geographic environments, its nutritional profile includes essential carbohydrates, vitamins (thiamine, riboflavin, niacin), and minerals (Verma *et al.*, 2006) [4]. As a result, global rice cultivation spans approximately 173.20 million hectares, yielding an output of 545.73 million tonnes (Anonymous, 2026a) [2]. India acts as a major global hub for production, within which the state of Chhattisgarh traditionally celebrated as the “Rice Bowl of India” ranks fifth nationally, producing 10.36 million tonnes across 3.8 million hectares (Anonymous, 2026b) [3].

With steady population expansion and diminishing arable land resources, global rice production must expand by an estimated 40% by 2030 to secure future food security (Khush, 2005) [18]. Surpassing current yield plateaus requires the continuous development of high-yielding, elite cultivars. Evaluation and characterization of existing landraces of rice are very important in order to achieve the varietal improvement. Because grain yield is a complex, polygenic trait determined by the interaction of multiple independent components, raw phenotypic selection based on yield alone is often inefficient. Systematic crop improvement relies heavily on assessing the nature and magnitude of genetic variability present in available germplasm lines (Adhikari *et al.*, 2018) [1]. Quantifying genetic parameters like the Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) helps distinguish heritable variation from environmental noise. Furthermore, estimating broad-sense heritability alongside genetic advance offers a more accurate prediction of genetic gain under selection, confirming whether target characteristics are governed by predictable additive gene action.

Materials and Methods

The experimental material includes 55 rice accessions including 5 check varieties (IR 64, Swarna, Jaya, Dagad Desi and MTU 1010) were used. These fifty rice germplasm accessions were taken from DBT Network Project. The accessions of rice were transplanted in the field of Research Cum Instructional Farm, Department of Genetics and Plant Breeding, IGKV, Raipur during *kharif* 2025. Seeds were

sown directly on July 7th, 2025, and the seedlings were transplanted to the field with a complete randomized block design with two replications. All necessary agronomical practices were followed to raise the crop. Days to 50% flowering, plant height (cm), panicle length (cm) number of effective tillers per plant, number of filled grains per panicle, spikelet fertility (%), 100 grain weight (g), harvest index (%) and grain yield per plant (g) were recorded.

Table 1: List of rice accessions used in the experiment

S. No.	IC No.	S. No.	IC No.
1	IC211155	26	IC464242
2	IC467048	27	IC214441
3	IC459831	28	IC390288
4	IC583022	29	IC464524
5	IC460191	30	IC199588
6	IC459811	31	IC206977
7	IC323905	32	IC459308
8	IC256788	33	IC458773X
9	IC618927	34	RL 12432
10	IC455308	35	IC124860
11	IC594032	36	IC205994
12	IC555058	37	IC459987
13	IC99243	38	IC459258X
14	IC135168	39	IC114244
15	IC618941	40	IC379591
16	IC300216	41	IC459710
17	IC134812	42	IC463770
18	IC596795	43	IC114448
19	IC85796	44	IC114349
20	IC462798	45	IC253461
21	IC466426	46	IC125764
22	IC459371	47	IC134863
23	IC389225	48	IC513436
24	IC124428	49	IC596814
25	IC462049	50	IC519103

Results and Discussions

Agro-morphological characterisation

Each variety can be distinguished on the basis of its unique, and reliable, morphological characters. Such characters may be controlled by one gene (monogenic) or many genes (polygenic). In an attempt to differentiate among varieties, it would be preferable to use stable morphological characters as recognizers. Each variety needs to be composed from characteristic diagnostic characters in order to differ from the other varieties. These characters need to be heritable and reliably detected over several generations in order to be considered as valid morphological markers. Distinct rice accessions were identified based on agro-morphological traits, basal leaf sheath colour (IC466426), purple stigma

colour (IC214441), horizontal flag leaf angle (IC390288), long fully awning (IC124860), purple hull colour (IC379591), black hull colour (IC459308), red kernal colour (IC459308), black kernal colour (IC618941), purple apiculus colour (IC459258X), threshability difficult (Swarna and Jaya). The most variable traits among the germplasm were leaf blade colour, basal leaf sheath colour, panicle type, flag leaf angle, leaf senescence, awning hull colour, kernel colour and threshability. In contrast, traits like ligule shape and aroma did not show any variation among the 55 germplasm samples. Similar findings have been reported by Lavanya *et al.* (2021)^[15], Sao *et al.* (2025)^[19] and Kumar *et al.* (2026)^[14].

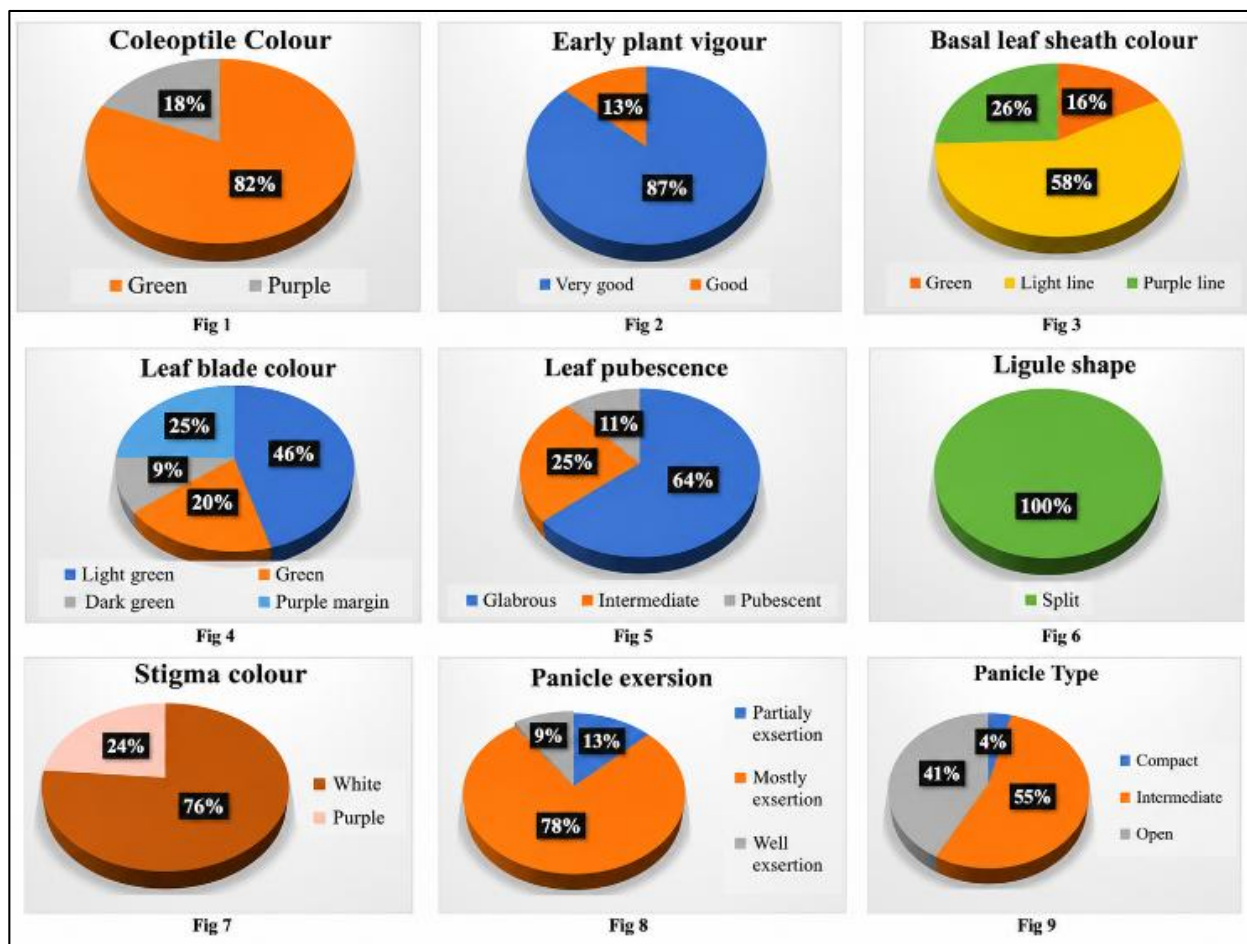


Fig 1: Frequency distribution of agro-morphological traits coleoptile colour (1), early plant vigour (2), basal leaf sheath colour (3), leaf blade colour (4), leaf pubescence (5), ligule shape (6), stigma colour (7), panicle exsertion (8), panicle type (9).

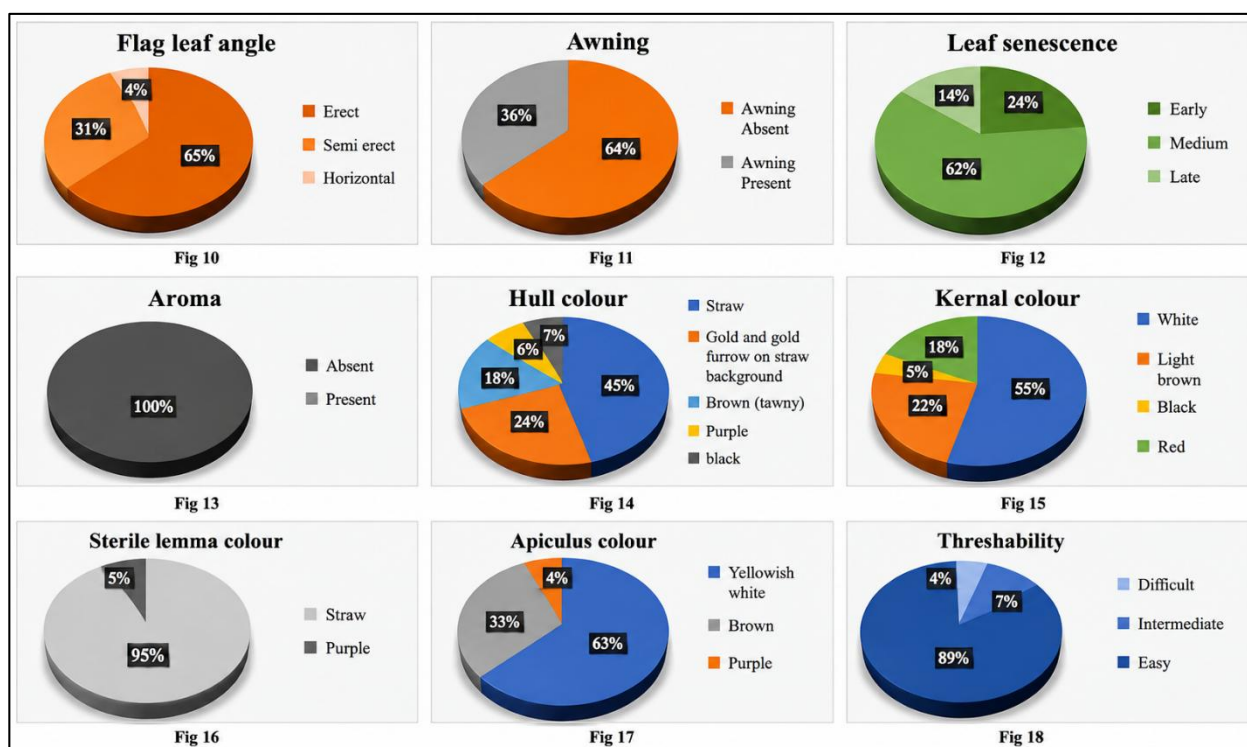


Fig 2: Frequency distribution of agro-morphological traits, flag leaf angle (10), awning (11) and leaf senescence (12), aroma (13), hull colour (14), kernal colour (15), sterile lemma colour (16), apiculus colour (17) and threshability (18).

Genetic variability analysis

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

Sl. No.	Source of variation	Mean sum of square		
		Replication	Treatments	Error
	Degree of freedom	1	54	54
1.	Days to 50% flowering	70.08	180.99**	3.63
2.	Plant height (cm)	64.37	737.19 **	140.70
3.	Panicle length (cm)	0.08	8.46**	0.06
4.	Number of effective tillers	0.79	3.76**	0.87
5.	Number of filled grains per panicle	7.99	581.11**	68.56
6.	Spikelet fertility percentage (%)	1.40	53.61**	8.76
7.	100 seed weight (g)	0.01	10.10**	2.07
8.	Harvest index (%)	2.58	226.56**	2.58
9.	Grain yield per plant (g)	0.01	250.25**	10.90

** Significant at 1% Probability level

The analysis of variance (ANOVA) (table 2.) performed indicated highly significant differences ($P \leq 0.01$) between the mean values of all the investigated traits among the rice genotypes. The significantly different mean sum of squares indicates the presence of a high variation among the studied characters, which signifies a greater variation among the experimental material. Genetic diversity is one of the major factors in the development of improved varieties through breeding activities. Therefore, the availability of enough genetic variation is the key factor for a successful crop improvement program. Similar results have been observed by Koli *et al.* (2026) ^[17], Kumar *et al.* (2026) ^[14], and Ali *et al.* (2026) ^[5] for the study of rice genotypes for yield and yield contributing characters, such as flowering time, plant height, effective tillers, panicle length, filled grains per panicle, and grain yield.

The estimated PCV and GCV values for yield and yield-related traits, giving an evaluation of the amount of variability available for crop improvement and selection presented in table 3. The PCV values for all the traits in the present study were higher than the corresponding GCV values, suggesting the effect of environmental factors. However, a strong correlation was observed between PCV and GCV revealing that the traits were mostly governed by the hereditary control. The GCV varied from 5.37 for the spikelet fertility to 25.32 for harvest index.

The highest genotypic coefficient of variation (GCV) was recorded for harvest index (25.32%). Traits that showed moderate GCV included the grain yield per plant (19.21%), the grain yield per plant (19.21), number of effective tillers per plant (18.81%), plant height (14.72), number of filled grains per plant (11.61), hundred seed weight (11.60) and days to 50% flowering (10.03). Traits with low GCV (less than 10%) are panicle length (7.57) and spikelet fertility percentage (5.37).

In the present study the phenotypic coefficient of variation (PCV) ranges from 6.33% in spikelet fertility percentage to 25.61% for harvest index. A high degree of PCV was

observed for harvest index (25.61%), followed by the grains yield per plant (19.21%) and number of effective tiller (18.81%).

Moderate percentage of PCV were recorded for plant height (14.72%), number of filled grains per panicle (11.61%), hundred seed weight (11.30) and days to 50% flowering (10.23%). A low degree of phenotypic variation was noted in days to 50% flowering (9.05), brown rice length (8.85%), paddy length (7.70%), and spikelet fertility (5.92%). Lower percentage of PCV were showed by panicle length (7.57%) and spikelet fertility percentage (5.37%).

The presence of highly significant genotypic coefficient of variation in specific phenotypes suggests the existence of large diversity at the population level. Since the PCV tends to be greater than GCV, this difference may be attributed to effects of environment. However, the difference between GCV and PCV was found to be relatively small, because of minimizing environmental effects on most of the measured traits. Corresponding results to this study have been documented by Pathak *et al.* (2024) ^[11], Sai Venkat *et al.* (2024) ^[12], Srividhya *et al.* (2025) ^[10], and Modarresi *et al.* (2026) ^[13].

Heritability (Broad Sense)

The percentage of phenotypic variation that may be ascribed to genetic factors or gene action is known as heritability. Higher heritability indicates more possibility for successful selection, making it a crucial indicator for choosing traits in a breeding program. Heritability is a statistical metric that measures the proportion of phenotypic variation (observed traits) in a population that is attributable to genetic variation among individuals as defined by Lush, 1936.

Three levels are typically used to classify heritability estimates: low (less than 30%), moderate (between 30% and 60%), and high (more than 60%).

As shown in table 4.3, heritability for yield and yield-related traits in the current study were computed broadly and expressed as a percentage.

Table 4.3: Genetic parameters of variation for yield and its contributing traits

Genetic parameters	Grand Mean	Range		GCV%	PCV%	h ² (bs)%	GA% Mean
		Max.	Min.				
Days to 50% flowering	93.87	116.10	71.00	10.03	10.23	96.07	20.25
Plant height (cm)	117.26	163.11	52.00	14.72	17.86	98.31	25.00
Panicle length (cm)	27.02	33.20	23.03	7.57	7.64	98.38	15.48
Number of effective tillers	6.39	10.00	2.66	18.81	23.81	62.46	30.64
Number of filled grains per panicle	137.83	191.33	94.33	11.61	13.07	78.89	21.25
Spikelet fertility percentage (%)	88.13	97.72	69.51	5.37	6.33	71.89	9.38
100 seed weight (g)	2.41	3.00	1.11	11.30	13.91	65.96	18.90
Harvest index (%)	41.78	61.93	24.77	25.32	25.61	97.75	21.58
Grain yield per plant (g)	7.74	12.03	5.04	19.21	20.06	91.65	37.88

It can be difficult to determine whether observed variability is inherited genetically. The degree to which a trait may be passed on from one generation to the next is known as its heritability. It expresses the reliability of phenotypic values and functions as a forecasting tool. Consequently, selection for a certain trait is more successful when heritability is large.

High heritability is shown by the following traits panicle length (98.38%), Plant height (98.31%), Harvest index (97.75%), Days to 50% flowering (96.07%), Grain yield per plant (91.65%), Number of filled grains per panicle (78.89%), Spikelet fertility percentage (71.89%), 100 seed weight (65.96%) and Number of effective tillers (62.46%). Corresponding results to this study have been documented by Sudeepthi *et al.* (2020) [8], Debsharma *et al.* (2022) [9] and Srividhya *et al.* (2025) [10].

Genetic advance as a percent of mean

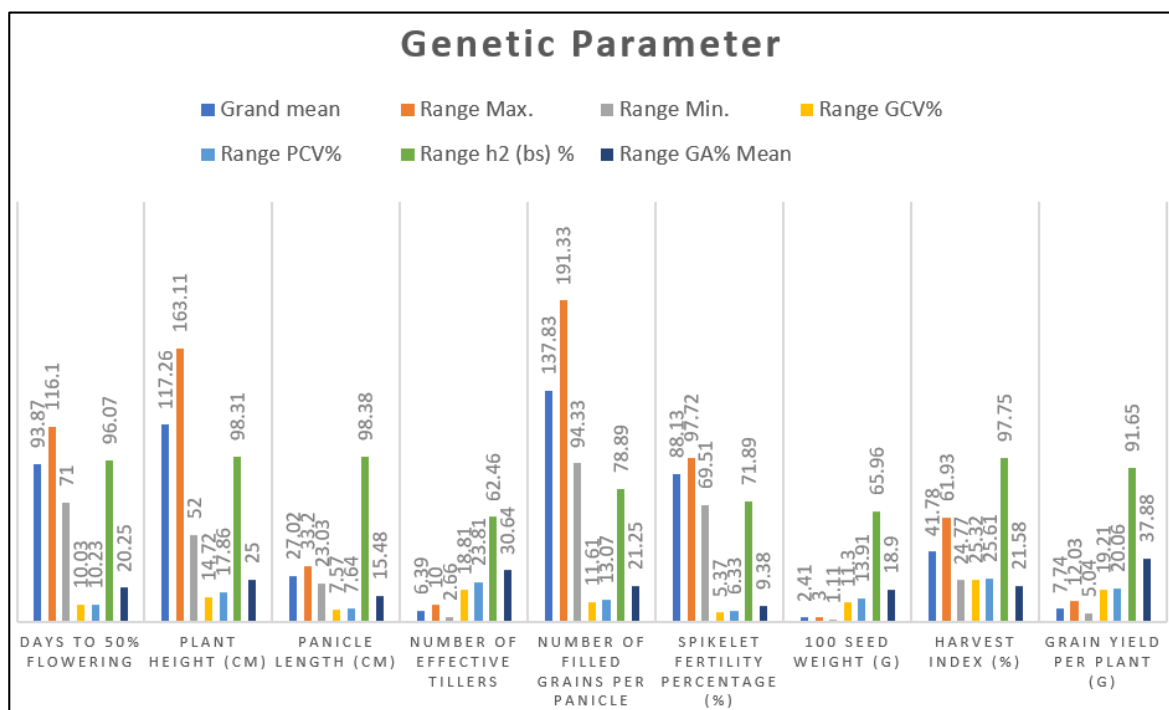
Genetic Advance as a Percent of Mean (GAM) is the predicted genetic gain or improvement in the mean genotypic value of a selected population over its base population expressed as a relative percentage of the grand mean of the selected population. It allows plant breeders to compare the efficiency of selection across many traits easily as it places the absolute genetic progress on a common scale regardless of the measurement units of a particular trait.

Genetic advance as a percent of mean is an important statistical parameter commonly used in plant breeding to predict the expected gain in a trait by selection. It is expressed as a percent of a population mean. The Johnson, Robinson and Comstock (1955) [7] classification system has divided Genetic Advance as a percent of Mean into low (<10%), moderate (10-20%) and high (>20%) categories.

High genetic advance as a percent of mean is shown by the following traits grain yield (37.88%), number of effective tillers per plant (30.64), plant height (25%), harvest index (21.58), number of filled grains per panicle (21.25%) and days to 50% flowering (20.25).

Moderate genetic advance as a percent of mean is shown by the following traits hundred seed weight (18.90%) and panicle length (15.48%).

A high genetic advance as a percent of mean together with high heritability indicates control of the target trait by additive gene action and thus indicates the high likelihood of success of phenotypic mass selection on future generations. Estimation of genetic advance as a percent of mean in combination with heritability provides a better estimate of the efficiency of selection than examination of heritability alone. Corresponding results to this study have been documented by Htwe *et al.* (2019) [6] and Ali *et al.* (2026) [5].

**Fig 3:** Estimation of variability parameters for yield and yield attributing traits in rice accessions

Conclusion

- Agromorphological traits display a substantial degree of hereditary control, making them reliable indicators for screening germplasm accessions during the early phases of crop selection.
- Distinct rice accessions were identified based on agromorphological traits, basal leaf sheath colour (IC466426), purple stigma colour (IC214441), horizontal flag leaf angle (IC390288), long fully awning (IC124860), purple hull colour (IC379591), black hull colour (IC459308), red kernal colour (IC459308), black kernal colour (IC618941), purple apiculus colour (IC459258X), threshability difficult (Swarna and Jaya).
- The presence of significant treatment mean squares in the ANOVA confirms that the current germplasm collection harbors vast genetic variability, opening immense avenues for future rice improvement initiatives.
- Traits such as harvest index, grain yield per plant, and number of effective tillers should be highly prioritized during selection because they combine high GCV values with high broad-sense heritability estimates.
- The simultaneous presentation of highly elevated heritability alongside maximum genetic advance as a percent of mean for grain yield per plant, number of effective tillers, and plant height implies that selection for these characters will be highly effective due to the control of additive gene action.

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