

# Genetic variability and Aroma studies in landraces and cultivars of *Oryza sativa*

Akhtar Sabina

College of Education, American University in the Emirates, Dubai, UAE

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## ABSTRACT

Nature and magnitude of genetic variability was estimated in 116 genotypes (42 landraces and 74 cultivars) of rice. These rice cultivars/landraces were grown in replicated trials during the *kharif* season. Morphological traits were characterized using standard procedure of IRRI on the basis of scales (scores 0 to 9). Leaf blade colour and collar colour was predominantly green in more than 80.0 percent genotypes, while auricle colour, ligule colour and seed coat colour was desirable in most of the genotypes (54 to 90%). Flag leaf angle was erect/intermediate in nearly 60 per cent genotypes. Panicle type was compact/intermediate in nearly 85 per cent population with its threshability as intermediate to easy in about 77 per cent. Estimates of coefficient of variation (phenotypic and genotypic) was high (>30%) for leaf width, tillers plant<sup>-1</sup> and grain yield (q ha<sup>-1</sup>). Heritability estimates (broad sense) were high (>60%) for all the 10 quantitative traits studied. Expected genetic gain (% of the mean) was high (>30%) for all the traits except plant height and leaf length (data pooled over years). Preliminary screening of these cultivars/landraces for their kernel aroma on cooking revealed that the majority (71.6%) had no aroma, 25.0 per cent were having slight aroma while 4 landraces viz. *Tilazaq*, *Mushka budji*, *Larbeol* and *Kamad* had a presence of good kernel aroma on cooking.

**Key words :** Genetic variability, Variability, Kernel aroma

## Introduction

Rice (*Oryza sativa* L.) is one of the world's most important cereal crops that provides more calories per 100 g (447) than wheat (436) together with the highest digestible energy (>96%), biological values and protein efficiency ratio. It is the staple food of over half the world's population, with much higher dependence as a source of food energy in Asia. Rice is the staple diet of the majority of people in Jammu and Kashmir State as well and its demand is increasing day by day with the increase in its human population. At present rice in the State is cultivated on an area of 263.25 thousand ha, whereas in temperate zone (Kashmir valley) alone the crop occupies an area of 140849 thousand ha with a produc-

tion of 3468 and productivity of 24.79 q ha<sup>-1</sup> (Anonymous, 2017). The production in the state is not sufficient to feed its population and its demand is likely to increase in times to come. Rice improvement programmes through development of high yielding varieties suitable for valley conditions have been underway for a number of years. However, cultivation of rice growing areas with a few high yielding varieties has brought in its wake the danger of genetic vulnerability, as the genetic uniformity of improved HYVs has replaced the cultivation of large number of location specific rice cultivars/landraces. The genetic uniformity has set the stage for higher risks from biotic stresses. Therefore, scientists have been concerned to increase the genetic diversity of improved rice varieties, which calls for

strong and continuous breeding programmes using genetically diverse gene pools. The strategy holds true for Kashmir valley situations as well.

Genetic variability is the basic essential component of crop improvement. Amelioration of this genetic variability together with exploitation of other related genetic parameters vis-à-vis, gene action, correlated response and G x E interaction determines the success of any crop improvement programme. Knowledge on the extent of genetic variation and diversity for morphological, grain yield, maturity and yield component traits in cultivars/landraces has become important in modern crop improvement programmes (Rezaia and Frey, 1990). Characterization and evaluation of genetic variability provides plant breeders information necessary in the identification of basic germplasm materials for hybridisation so as to produce a variety that gives higher productivity under location specific eco-system (Buu *et al.*, 2002). In order to have a result oriented successful breeding programme and to overcome unforeseen challenges in the changing environment, it is essential to have a wider genetic base in the hybrid F<sub>1</sub> generations that would increase the spectrum of elite segregants. Chauhan *et al.* (1995) have emphasized the importance of such gene pools in the development of rice cultivars. Rice landraces especially from the diversity centres are important reservoirs of useful genes for widening of genetic base and enriching of the existing varieties with important agronomic traits.

Landraces have been found to be important repositories of gene pools, which could be useful in cultivar development programmes involving exotic and local adapted germplasm. The resultant variability is useful in identifying superior genetic materials for stabilizing the higher yield potential on a sustainable basis. Collection, evaluation and screening of genetic variation and diversity for yield and yield components, identification of photosynthetically efficient plant types together with, maturity and quality traits in traditional cultivars/landraces as a potential of gene repository is now becoming more important in the rice breeding programmes.

The local germplasm resources have now been pushed into smaller areas and if not conserved properly, this important rice gene pool is likely to face genetic erosion and extinction. These local rice materials are known for several important attributes like good quality characteristics, resilience to withstand low temperatures and presence of aroma in

some cases (typical for commercial exploitation and higher economic returns). Their use in crop improvement programmes would lead to genetic enhancement, broadening of the genetic base, promoting sustainable agriculture and value addition through incorporation of elite genes (e.g. aroma) in the high yielding commercial varieties. The present study was, therefore, carried out to know the nature and extent of genetic variability, heritability, genetic advance and some important traits of rice.

## Materials and Methods

One hundred and sixteen local and cultivated rice cultivars (42 landraces and 74 cultivars) were evaluated at one location for two years in a randomized block design with three replications. The cultivars selected comprised commercial high yielding varieties, promising lines in advance, multi-location testing programme and new breeding lines received from wide agro-geographical regions of the rice growing countries. The experimental plot consisted of 2 rows each of 4 m length with rows spaced 20 cm apart. At each hill 2-3 seedlings were planted maintaining hill to hill spacing of 15 cm. The experimental field was well prepared, and a standard recommended package of practices followed to raise a good crop. Observations were recorded on the various morphological, agronomical, yield and quality traits in order to study the magnitude of variability in the materials. Ten competitive plants were selected at random from each experimental plot in a replication and tagged for recording the observations. Mean values for all the characters and median values for days to flowering and maturity were worked out. The rice cultivars/landraces were also scored for grain aroma as per the descriptors for rice formulated by IBPGR-IRRI Advisory Committee (IRRI, 1980). A simple laboratory test to evaluate aroma, developed at IRRI, Philippines was used by placing 20 to 30 freshly harvested milled grains in a test tube containing 20ml of distilled water. The test tube opening was closed with a stopper and placed in boiling water for 10 minutes (rice requires approximately 20 minutes of cooking). Test tube was withdrawn, and contents were cooled. The aroma was rated as strong, intermediate, light or absent. Variety in each test tube gave a basis for comparison. The data collected for the entire experiment was subjected to appropriate statistical and biometrical analyses.

## Results and Discussion

Morphological characterisation, as per the Standard Evaluation System of IRRI, revealed that colour of leaf blade was predominantly green in about 87.00 per cent genotypes. The remaining genotypes (12.94%) were with different shades of purple colour. Collar colour was also green in about 79.00 per cent genotypes. Similarly, ligule colour was white in nearly 90.00 per cent and auricle colour was light green in about 54.00 per cent genotypes. The colour of leaf blade, collar, auricle and ligule was desirable in majority of the landraces/cultivars and such landraces would be of no hindrance for their introgression programme involving exotic x landrace hybridization. Flag leaf angle was erect/intermediate in about 60.00 per cent genotypes. Panicle type was erect/intermediate in nearly 95.0 per cent, while its threshability was intermediate to easy in 77.0 per cent genotypes. The majority of landraces/cultivars (59.48%) had desirable (erect/intermediate) flag leaf angle. Significant genetic variance was observed for all the 10 quantitative traits viz., plant height, tiller plant<sup>-1</sup>, days taken to 50.0 percent flowering, panicle length, leaf length and its width, grain length and its width, 100-grain weight and grain yield (q ha<sup>-1</sup>). Grain length and its width also exhibited significant variation in the genotypes. This revealed the presence of significant genetic variation among the genotypes for all the traits. Significant variance for environments (years) revealed significant influence on the mean performance of genotypes. Genotype x environment (years) interaction was also significant revealing that the genotypes did not behave similarly over two years (Table 1).

Estimation of coefficient of variation (phenotypic and genotypic) for each quantitative trait revealed the presence of moderate values (10.0-30.0%) for plant height; panicle length, 100-grain weight, days taken to 50.0 per cent flowering, grain length and its width, and leaf length. It was high (>30%) for grain yield, leaf width and tillers plant<sup>-1</sup>.

Heritability (b.s) estimates were high (>60.0%) for all the quantitative traits. This heritability and genotypic variance was used to calculate expected genetic gain (% of mean). The performance of the traits was not affected much by environmental variations and sampling error. Expected genetic gain was high (>30.0%) for all these traits except plant height and leaf length (for data pooled over

years) where it was moderate. Normally in self-pollinating crops like rice estimation of expected genetic gain is not having that much significance. However, identification of a few high yielding varieties in yield traits and their selection *per se* from a large number of cultivars under cultivation can provide a logistic approach to increase production/productivity of that crop species. The expected genetic gain for these 10 quantitative traits was high (>30.0%) on the basis of both single year's and pooled over years data except for plant height and leaf length (pooled data over years).

Screening of the landraces/cultivars for kernel aroma on cooking revealed that majority of the genotypes (69.82%) had no kernel aroma on cooking, while 30 genotypes (including 13.79% landraces) gave slight kernel aroma on cooking. However, 5 genotypes viz., *Tilazag*, *Mushkabuji*, *Larbeoul*, *Kamad* and SK/PBG/49 presence of good kernel aroma on cooking. This revealed that the majority of landraces had good cooking quality parameters (Table 2). *Mushka budji* and *Kamad* are highly priced rice cultivars and the sale price is almost equal to some best Basmati rice varieties. Because of low yielding potential of these landraces their cultivation has been pushed to some minor pockets and much areas are characterised by low input management.

Incorporation of allelic resources for grain quality into some high yielding commercial varieties would make available some transgressive segregants possessing good yielding, potential and very good grain quality. Even if there would be some decline in yielding potential, yet the pricing structure of these resultant segregants would be almost double as compared to their high yielding parent.

Several workers have reported significant genetic variability in the materials of rice together with moderate to high coefficient of variation (genotypic and phenotypic), heritability (broad sense) and expected genetic gain. High genetic variability and its coefficient of variation has been observed for plant height (Chauhan, 2017; Sawant and Patil, 2018), while as Ganesan and Subramanian (1994) reported moderate genetic coefficient of variation for this trait. Similarly, for tillers plant<sup>-1</sup> high genotypic coefficient of variation was recorded in this crop (Parmasivan, 1988; Ganesan and Subramanian, 1994), while Selvarian and Rangasamy (1997) reported moderate genotypic coefficient of variation.

**Table 1.** Analysis of variance for morphological, maturity, yield and yield component traits of the landraces and cultivated rice varieties of Kashmir Valley

Source of variation	d.f.	Mean squares								
		Plant height			Tillers plant <sup>1</sup>			Panicle length		
		<i>Kharif</i> 2008	<i>Kharif</i> 2009	Pooled over years	<i>Kharif</i> 2008	<i>Kharif</i> 2009	Pooled over years	<i>Kharif</i> 2008	<i>Kharif</i> 2009	Pooled over years
Environments (years)	1	-	-	498.33**	-	-	9.568**	-	-	31.534**
Replications	2	102.63*	25.48**	33.60**	3.35*	11.68**	6.42**	6.154**	6.54**	0.714
Genotypes	115	946.80**	1037.36**	324.98**	39.69**	50.33**	40.69**	60.78**	60.12**	14.082**
Environments x genotypes	115	-	-	3.158*	-	-	8.627**	-	-	0.755
Error	230	2.73	0.83	-	0.99	0.92	-	1.85	0.63	-
	<b>462</b>	-	-	<b>0.98</b>	-	-	<b>1.26</b>	-	-	<b>0.58</b>

Contd.

Source of variation	d.f.	Mean squares								
		100 grain weight			Days to 50% flowering			Grain yield/ha		
		<i>Kharif</i> 2008	<i>Kharif</i> 2009	Pooled over years	<i>Kharif</i> 2008	<i>Kharif</i> 2009	Pooled over years	<i>Kharif</i> 2008	<i>Kharif</i> 2009	Pooled over years
Environments (years)	1	-	-	0.210**	-	-	330.75**	-	-	34.53**
Replications	2	0.002	0.007	0.004**	1.71	47.65**	13.38**	0.22	0.99**	0.41
Genotypes	115	0.94**	1.01**	1.809**	810.72**	846.86**	827.51**	545.97**	549.37**	546.88**
Environments x genotypes	115	-	-	0.151**	-	-	2.55**	-	-	0.58**
Error	230	0.006	0.0057	-	1.59	0.64	-	0.49	0.06	-
	<b>462</b>	-	-	<b>0.0086</b>	-	-	<b>0.78</b>	-	-	<b>0.09</b>

Contd.

Source of variation	d.f.	Mean squares						
		Leaf length (cm)			Leaf width (cm)			
		<i>Kharif</i> 2008	<i>Kharif</i> 2009	Pooled over years	<i>Kharif</i> 2008	<i>Kharif</i> 2009	Pooled over years	Pooled over years
Environments (years)	1	-	-	37.978**	-	-	2.253**	
Replications	2	0.90	4.90**	16.729**	0.09*	0.018	0.041*	
Genotypes	115	232.98**	224.20**	68.150**	0.61**	0.55**	0.541**	
Environments x genotypes	115	-	-	5.309**	-	-	0.088**	
Error	230	3.25	0.34	-	0.016	0.022	-	
	<b>462</b>	-	-	<b>1.62</b>	-	-	<b>0.019</b>	

Contd.

Source of variation	d.f.	Mean squares						
		Grain length (mm)			Grain width (cm)			
		<i>Kharif</i> 2008	<i>Kharif</i> 2009	Pooled over years	<i>Kharif</i> 2008	<i>Kharif</i> 2009	Pooled over years	Pooled over years
Environments (years)	1	-	-	0.797**	-	-	1.327**	
Replications	2	0.006	0.074	0.018	0.01	0.004	0.005	
Genotypes	115	6.22**	7.03**	6.32**	1.36**	1.35**	1.27**	
Environments x genotypes	115	-	-	0.615**	-	-	0.178**	
Error	230	0.033	0.065	-	0.006	0.013	-	
	<b>462</b>	-	-	<b>0.015</b>	-	-	<b>0.014</b>	

**Table 2.** Screening of rice cultivars/landraces of Kashmir Valley for their aroma content

S. No	Genotype	Score
1.	<i>Tilzag</i>	2
2.	<i>Pren zagir</i>	0
3.	<i>Shala kew</i>	0
4.	<i>Safed braze</i>	0
5.	<i>Meer zag</i>	1
6.	<i>Qadir Beigh</i>	1
7.	<i>Babri safed</i>	1
8.	<i>Baber</i>	1
9.	<i>Zager (purple)</i>	1
10.	<i>Ramhall</i>	0
11.	<i>Rehman Batt-II</i>	0
12.	<i>Mushkandi</i>	1
13.	<i>Niverzag</i>	0
14.	<i>Khuch</i>	1
15.	<i>Begum</i>	0
16.	<i>Zaged</i>	1
17.	<i>Shala kew-III</i>	0
18.	<i>Mushke budgi</i>	2
19.	<i>Wazul kreer</i>	0
20.	<i>Potebrar</i>	0
21.	<i>Tumle hall</i>	0
22.	<i>Watezag</i>	0
23.	<i>Tral zagir</i>	0
24.	<i>Rehman Batt-I</i>	0
25.	<i>Loal Anzul</i>	1
26.	<i>Larbeoul</i>	2
27.	<i>Hapat china</i>	0
28.	<i>Chenebara</i>	0
29.	<i>Katwara</i>	1
30.	<i>Reshim</i>	0
31.	<i>Kamad</i>	2
32.	<i>Gurahh</i>	0
33.	<i>Gullabara</i>	1
34.	<i>Bale keoun</i>	0
35.	<i>Pren never</i>	0
36.	<i>Kalabrear</i>	1
37.	<i>Prun chwal</i>	0
38.	<i>Sige Safed</i>	1
39.	<i>Kanusa Rax</i>	1
40.	<i>Gurukeon</i>	1
41.	<i>Siga</i>	0
42.	SAW/GML14	0
43.	SAW/GML/252	0
44.	SAW/GML/270	0
45.	SAW/GML/317	0
46.	SAW/GML/292	1
47.	SAW/GML/310	1
48.	SAW/GML/804	0
49.	SAW/GML/234	1
50.	SAW/GML/224	0
51.	SAW/GML/294	0
52.	SAW/GML/806	0

**Table 2.** Continued ...

S. No	Genotype	Score
53.	SAW/GML/181	0
54.	SAW/GML/207	0
55.	SAW/GML/182	1
56.	SAW/GML/286	0
57.	SAW/TA/30	1
58.	SAWG/M/01	0
59.	SAWG/M/04/113	0
60.	SK/PBG/105	0
61.	SK/PBG/97	0
62.	SK/PBG/56	1
63.	SK/PBG/46	0
64.	SK/PBG/49	2
65.	SK/PBG/58	0
66.	SK/PBG/99	0
67.	SK/PBG/93	0
68.	SK/PBG/67	0
69.	SK/PBG/51	1
70.	SK/PBG/84	1
71.	SK/PBG/90	1
72.	SK/PBG/79	0
73.	SK/PBG/102	0
74.	SKAU-5	0
75.	SKAU-382	0
76.	SKAU-357	0
77.	SKAU-337	0
78.	SKAU-105	0
79.	SKAU-339	0
80.	SKAU-356	0
81.	SKAU-46	0
82.	SKAU-292	1
83.	<i>Jehlem</i>	0
84.	<i>Himdhan</i>	1
85.	<i>Chenab</i>	0
86.	<i>Kohsar</i>	0
87.	<i>Koshikikari</i>	0
88.	K-475	0
89.	K-332	1
90.	K-334	0
91.	K-116	0
92.	K-225	0
93.	K-110	0
94.	K-312	0
95.	China 1007	0
96.	China 988	0
97.	China 1039	0
98.	GRALDO	0
99.	IR-63347-AC 201-1	0
100.	Hexi-5	0
101.	SIJUNG 10	1
102.	OLBYE 2	0
103.	HAMNAM 15	0
104.	ECHCA	1

**Table 2.** *Continued ...*

S. No	Genotype	Score
105.	STEJAREE	0
106.	IR 61009-47-3-1-1	0
107.	MILYANG 80	0
108.	IR 61728-4B-2-1-1	0
109.	H257-2-1-1	0
110.	GIGANTE VERCELLI	1
111.	LIO 573	0
112.	RP 2421	0
113.	HPR 1178	0
114.	VL94-3027	0
115.	VL93-3635	0
116.	HPR-1149	0

  

Score	Description
0	Non scented
1	Lightly scented
2	Scented

For panicle length high GCV has been reported by Anees Salma (1992), but Vange (2008) observed low GCV for this trait. For days taken to 50.0 per cent flowering Sharma and Sharma (2007) recorded high GCV. For grain yield high GCV has been reported in rice crop (Babar, 2007; Mustafa and Elsheikh, 2018; Sharma and Sharma, 2007).

Presence of high genotypic and phenotypic coefficients of variation is expected to help in the identification of desirable genotypes. However, Burton (1952) has suggested that genotypic coefficient of variation would be meaningful only when the heritability estimates for a trait is also very high. Similarly, higher heritability estimate along with high expected genetic gain would be more useful when considered together to predict the resultant effect of selecting the best genotypes (Johnson *et al.*, 1955) and in self-pollinated crops especially while handling the advanced generations of segregating genotypes resulting from crosses of parents with diverse genetic base. In the present set of materials, the heritability and expected genetic gain estimates were high, while genotypic coefficient of variation was moderate for most of traits (except grain yield and taken plant<sup>-1</sup> that revealed high estimates).

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