



Variability Studies in Upland Rice (*Oryza sativa* L.) Genotypes of Nagaland

B. Lalhruaitluangi^{a*}, M. B. Sharma^a and Pankaj Shah^a

^a Department of Genetics and Plant Breeding, School of Agricultural Sciences and Rural Development, Nagaland University, Medziphema-797106, India.

Authors' contributions

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

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ABSTRACT

A study was conducted in the Experimental Farm of Genetics and Plant Breeding, Nagaland University, Medziphema in Kharif 2021. The study consists of 28 genotypes laid in Randomized Block Design (RBD). To choose efficient genotypes in breeding programmes for boosting rice production in poor rice soils, it will be helpful for resource-poor farmers who have restricted access to the usage of N fertilizer. From the results, ANOVA revealed that all the traits studied are significant except for root dry weight. Similarly, traits like stem dry weight (g), harvest index and grain yield per plant (g) have high GCV (%) and PCV (%) and high heritability (%) is also observed among these traits. High heritability (%) along with high genetic advance as percent of mean was found for grain yield per plant, panicle weight, stem dry weight and harvest index which indicates the function of additive gene in regulating these traits.

Keywords: Rice; genetic variability; genetic advance.

*Corresponding author: E-mail: bhruaii21@gmail.com;

1. INTRODUCTION

With chromosome number $2n=24$, rice (*Oryza sativa* L.) is a self-pollinated plant belonging to the gramineae family. There are 25 genera in the *Oryza* species, of which two, *Oryza sativa* and *Oryza glaberrima*, are domesticated. The other 23 genera are wild species. Additionally, rice can be grown as a ratoon crop for up to 30 years and as a perennial crop. Both temperate and tropical nations cultivate it as an annual crop. In most Asian countries, rice is the main food crop. In Asia, rice is an important part of both culture and society, and it also gives people jobs. More yields must be produced for farmers who can sell high-quality rice grains at competitive prices. In India, rice is another common food crop that is grown in both lowland and highland regions.

In order for selection to be successful, there needs to be heterogeneity in breeding materials for crops [1]. Yield is an extremely complex attribute that is controlled by many different circumstances. To boost rice productivity and break through the yield plateau to a higher level, it is crucial to improve variability in currently available genotypes and eventually selection effectiveness through breeding initiatives. Heritability information reveals how easily selected breeding characteristics will be passed on to succeeding generations. Therefore, heritability assessment is crucial for selection-based crop varietal improvement [2]. Improving yield and understanding the type and extent of genetic variation are the main breeding goals in rice breeding in order to carry out the inheritance of quantitative traits like yield and yield components. Breeders in crop development projects must analyze genetic variability measures including Genetic Coefficient of Variability (GCV %) and Phenotypic Coefficient of Variability (PCV%), heritability (%), and genetic advance for distinct traits. The goal of the current study was to provide explanations for specifics of Genetic Advance (GA), heritability, and variability in upland rice genotypes.

2. MATERIALS AND METHODS

The experiment was carried out during Kharif 2021 at Experimental Farm of Genetics and Plant Breeding, School of Agricultural Sciences and Rural Development, Nagaland University, Medziphema. The genotypes consist of 28 upland rice genotypes grown in Randomized Block Design with three replications with spacing of 20 x 15cm. Sowing was done on 21st May,

2021 and dose of fertilizer was given as N: P: K @ 60: 30: 30 kg/ha. Urea was applied in granular form and one half of the total requirements of urea was applied at the time of final land preparation as a basal dose. Data were recorded on five randomly selected plants for each replications for the traits (Table 1). The data analysis was done by using WINDOSTAT software to study genetic coefficient of variation (%), phenotypic coefficient of variation (%), Heritability (%) (Broad sense) and Genetic Advance. The variability estimation was given by Burton and Devane [3] and heritability percentage (broad sense) by Allard [4] and genetic advance by Miller et al. [5].

The upland rice genotypes used in this study were gathered from SASRS, Mokochung Nagaland, and the ICAR NEH Region, Nagaland. The experimental site is situated on Medziphema, 310 metres above mean sea level, in the foothills of Nagaland, at 25°45'43"N latitude and 95°53'04"E longitude, respectively.

A total of 19 quantitative traits were measured in five randomly selected plants, including days to 50% flowering, days to maturity, plant height (cm), flag leaf length (cm), flag leaf breadth (cm), flag leaf area (cm²), number of ear-bearing tillers, panicles per plant, panicle length (cm), panicle weight (g), spikelet fertility, root dry weight (g), stem dry weight (g), harvest index, total nitrogen (%), crude protein, 100 grain weight and grain yield per plant (g). Days to 50% flowering and days to maturity are two traits that were measured when 50% of the plants in a row flowered and, respectively, when 80% of the plants reached maturity. The flag leaf area was calculated using following the formula given by [6].

$$\text{Flag leaf area} = \text{Flag leaf length} \times \text{breadth} \times 0.75$$

No. of ear bearing tillers, panicles per plant, panicle length (cm), panicle weight (g) and spikelet fertility were recorded after tillering stage. The spikelet fertility was worked out using the following formula:

$$\text{Spikelet fertility (\%)} = \frac{\text{Number of filled spikelets/panicle}}{\text{Total number of spikelets (filled + unfilled)/panicle}} \times 100$$

Root length, root dry weight (g) and stem dry weight (g) were recorded after harvesting and harvest index was calculated using the formula given by Donald, [7].

Table 1. List of all the varieties used for study

S.No	List of varieties	Source of collection
1	Sungmangtsuk (SARS-1)	SARS, Mokokchung, Nagaland
2	Apuapa (SARS-61)	SARS, Mokokchung, Nagaland
3	Kezie (SASRS-94)	SARS, Mokokchung, Nagaland
4	Korea Tsuk	SARS, Mokokchung, Nagaland
5	Longkhum Tsuk (SASRS-2)	SARS, Mokokchung, Nagaland
6	Yarba (SARS-3)	SARS, Mokokchung, Nagaland
7	Tsushvuri	SARS, Mokokchung, Nagaland
8	Chali	SARS, Mokokchung, Nagaland
9	Chishoghi	SARS, Mokokchung, Nagaland
10	Thangmo Red	SARS, Mokokchung, Nagaland
11	Thangma White	SARS, Mokokchung, Nagaland
12	Chahashye	SARS, Mokokchung, Nagaland
13	Taposen Youli	SARS, Mokokchung, Nagaland
14	Kedayishye	SARS, Mokokchung, Nagaland
15	Shyekenyii	SARS, Mokokchung, Nagaland
16	Amusu	SARS, Mokokchung, Nagaland
17	Ongpangsuk	SARS, Mokokchung, Nagaland
18	Moyatsuk	SARS, Mokokchung, Nagaland
19	Sulijak	SARS, Mokokchung, Nagaland
20	Moya Chali	SARS, Mokokchung, Nagaland
21	Tsungmiki	SARS, Mokokchung, Nagaland
22	Manen Red (SARS-5)	SARS, Mokokchung, Nagaland
23	Pfukhi Lha	ICAR NEH Region, Nagaland
24	Rosho Lha	ICAR NEH Region, Nagaland
25	Tungo	ICAR NEH Region, Nagaland
26	Ngoni	ICAR NEH Region, Nagaland
27	Thupfu Lha	ICAR NEH Region, Nagaland
28	RCM-9	ICAR NEH Region, Nagaland

Harvest index= (Economic yield)/(Biological yield)

Total nitrogen and crude protein was estimated using Micro-Kjeldahl method given by by AOAC [8].

Crude protein content (%) = micro-kjeldahl nitrogen content (%) x 6.25 (based on the assumptions that nitrogen constitutes 16% of protein).

3. RESULTS AND DISCUSSION

From the present study, analysis of variance revealed significant among all the genotypes studied [9] except for root dry weight (Table 2). The estimates of genetic variability like genetic coefficient of variability (GCV %), phenotypic coefficient of variability (PCV%), heritability (%) and genetic advance are presented in Table 3. Mean performance of genotypes were presented in Table 4. Overall mean was highest for days to maturity (124.33), followed by days to 50% flowering (112.88) and plant height (112.19) and lowest on total nitrogen (0.94) followed by root dry weight (1.06) and flag leaf breadth (1.94). Mean for days to 50 percent flowering was highest in variety 27 followed by variety 28 indicating that this genotype can be used as a donor in hybridization program to develop early maturing varieties [10] whereas it was lowest in

variety 28. Similarly, mean for days to maturity was highest for variety 27 and variety 28. Mean for plant height, flag leaf length, flag leaf breadth, flag leaf area was highest in variety 16, variety 26, variety 4 and variety 26. Mean for no. of ear bearing tillers, panicles per plant, panicle length and panicle weight was highest in variety 19, variety 9, variety 4 and variety 16. Mean for Spikelet fertility and root length was highest in variety 13 and variety 3. Mean for root dry weight was same for almost all the variety (1.05) except for variety 1 (1.29) and 2 (1.20). Mean for stem dry weight and harvest index was highest in variety 11 and variety 10. Mean for total nitrogen (%) and crude protein was highest in variety 20. Mean for 100 grain weight (g) and grain yield per plant (g) was highest in variety 10.

100 grain weight (g) for variety 10 (Thangmo Red) was higher than the check variety 28 (RCM-9). Similarly, for grain yield per plant (g) variety 11 was higher than the check variety 28 (RCM-9) [11] (Figs. 1 and 2) indicating that variety 10 and 11 can be used for improving yield in future breeding programmes. Therefore, varieties 3, 4, 9, 10, 11, 13, 16, 17, 19, 20, 21, 26, 27, 28 have highest mean among all the traits studied so these varieties can be useful for further breeding improvement programmes.

Table 2. Anova table

	Df	Days to 50% flowering	Days to maturity	Plant height (cm)	Flag leaf length (cm)	Flag leaf breadth (cm)	Flag leaf area (cm ²)	No. of Ear Bearing Tillers (EBT)	Panicles/plant	Panicle length (cm)
Treatments	27	646.23***	549.18***	899.4***	140.91***	0.41***	830.37***	5.17***	0.85*	40.3***
Error	54	0.714	0.011	20.82	7.48	0.01	28.03	0.28	0.58	3.38

	Df	Panicle weight (g)	Spikelet fertility	Root length (cm)	Root dry weight (g)	Stem dry weight (g)	Harvest Index	Total nitrogen(%)	Crude protein	100 grain weight (g)	Grain yield/ plant (g)
Treatments	27	12.11***	402.32***	7.78***	0.008	11.51***	847.03***	0.01***	0.412***	2.15***	17.82***
Error	54	0.32	142.62	0.303	0.005	0.22	0.97	0.0001	0.004	0.005	0.017

Significance at 5%-*, Significance at 1%- **, Significance at 0.1%- ***

Table 3. Estimates of genetic variability for the traits studied

Character	GCV	PCV	Heritability	GA
Days to 50% flowering	12.995	13.016	0.997	34.25
Days to maturity	10.882	10.882	1	28.727
Plant height (cm)	15.253	15.786	0.934	38.909
Flag leaf length (cm)	19.548	21.129	0.856	47.747
Flag leaf breadth (cm)	18.73	19.491	0.924	47.52
Flag leaf area (cm ²)	31.647	33.264	0.905	79.485
No. of ear bearing tillers (EBT)	8.059	8.725	0.853	19.65
Panicles/plant	6.238	14.275	0.191	7.197
Panicle length (cm)	12.579	14.203	0.784	29.413
Panicle weight (g)	61.027	63.473	0.924	154.9
Spikelet fertility	11.2	18.225	0.378	18.172
Root length (cm)	19.509	20.66	0.892	48.636
Root dry weight (g)	2.995	7.44	0.162	3.183
Stem dry weight (g)	44.486	45.761	0.945	114.171
Harvest Index	43.956	44.032	0.997	115.844
Total nitrogen (%)	6.211	6.313	0.968	16.131
Crude protein	6.211	6.313	0.968	16.131
100 grain weight (g)	21.695	21.782	0.992	57.046
Grain yield/ plant (g)	47.33	47.398	0.997	124.773

Table 4. Mean table for all the traits under study

	Days to 50% flowering	Days to maturity	Plant height (cm)	Flag leaf length (cm)	Flag leaf breadth (cm)	Flag leaf area (cm ²)	No. of ear bearing tillers (EBT)	Panicles/plant	Panicle length (cm)	Panicle weight (g)	Spikelet fertility	100 grain weight (g)	Grain yield/plant (g)	Root length (cm)	Root dry weight (g)	Stem dry weight (g)	Harvest Index	Total nitrogen (%)	Crude protein
Variety 1	105.33	124	124.37	34.33	2.37	58.55	13.33	5.67	26.57	2.23	55.88	4.24	2.77	8.17	1.29	2.37	26.5	0.85	5.29
Variety 2	105	120	130.1	43.4	2.17	70.5	15	5.67	26.17	5.11	81.98	4.34	3.56	6.13	1.2	2.53	28.27	0.84	5.23
Variety 3	115	120	120.13	44.27	2.37	78.57	15.67	6	37.37	6	89.95	4.13	4.77	12.13	1.05	4.8	35.22	0.83	5.17
Variety 4	111	118	120.07	43.07	2.47	79.67	16	5.67	30	2.42	70.34	4.06	3.59	10.13	1.05	4.47	28.78	0.93	5.81
Variety 5	98.67	120	106.27	38.8	2.17	63.03	18	6	27.43	2.97	75.78	2.64	3.58	7.4	1.05	3.43	34.46	0.91	5.71
Variety 6	120	127	80.6	26.13	1.87	36.57	16.67	5	25.77	3.8	87.97	3.4	3.61	8.4	1.05	4.3	31.13	0.96	6
Variety 7	102.67	120	106.4	26.17	1.83	35.92	17.33	6.33	25.77	2.44	94.02	4.9	3.92	8.43	1.05	3.8	34.42	0.94	5.87
Variety 8	107	120	100.8	35.1	2.17	56.92	15.67	5.67	26.97	3.46	81.56	5	4.06	5.17	1.05	3.63	30.98	0.93	5.83
Variety 9	110.33	118	114.3	36.1	2.33	63.15	14.33	6.67	26.3	2.16	84.24	3.92	3.85	5.93	1.05	5.67	31.02	1.01	6.35
Variety 10	120	125.33	133.27	38.57	2.17	62.68	13.67	5	24.1	1.07	58.35	5.32	10.7	7.73	1.05	7.57	78.13	1.01	6.33
Variety 11	115	118	114.1	23.07	1.67	28.85	15.33	4.33	26.83	1.47	92.26	3.47	13.69	13.69	1.05	9.7	100.69	0.93	5.83
Variety 12	115	118	131.43	38.13	2.2	62.97	16.33	6	30.77	1.67	91.53	2.87	3.71	3.71	1.05	4	33.03	0.92	5.75
Variety 13	100	122	109.53	30.4	1.27	28.87	16.33	5.67	31.93	1.46	100	4.25	3.83	3.83	1.05	3.87	28.17	0.94	5.85
Variety 14	104.67	120	113.57	30.67	2.07	47.41	14.67	5	31.1	6.53	88.06	3.84	4.76	4.76	1.05	2.033	35.2	0.92	5.77
Variety 15	104	122	132.87	18.6	1.97	27.36	15.67	5.33	30.87	1.02	82.22	4.09	4.64	4.64	1.05	4.23	34.26	0.93	5.83
Variety 16	101.33	122	139.33	45.47	1.87	63.71	15.33	5	27.03	6.77	85.5	5.27	6.93	6.93	1.05	6.4	50.84	1.03	6.42
Variety 17	104.67	120	103.47	32.33	1.3	35.4	16.33	4.67	22.47	5.6	87.72	3.85	2.57	2.57	1.05	2.17	19	1.04	6.5
Variety 18	115	118	112.4	37.17	2.2	58.8	15	5.33	30.4	1.66	82.52	3.24	3.6	3.6	1.05	2.2	26.27	0.97	6.04
Variety 19	123	120	119.6	36.5	1.37	52.45	18.33	5.67	27.3	1.53	94.64	5.2	2.71	2.7	1.05	2.2	20.02	0.93	5.79
Variety 20	97.67	120	132.7	37.1	1.97	54.9	14	5.67	26.33	3.5	83.3	3.35	5.74	5.74	1.05	3.38	36.42	1.05	6.58
Variety 21	95.67	118	132.7	32	1.97	46.98	16	5.33	33.47	1.29	86.84	2.83	5.2	5.2	1.05	5.13	36.06	0.97	6.04
Variety 22	121	117	110.53	32	1.53	37.09	15.67	5.33	29.53	1.42	90.44	3.14	6.48	6.48	1.05	4.58	42.22	1.02	6.39
Variety 23	121	118	101.73	26.5	2.17	43.3	15.33	4.67	29	7.7	90.27	4.84	5.57	7.8	1.05	3.49	38.96	0.94	5.89
Variety 24	121	120	91.13	30.17	1.23	27.85	16.33	6	30.97	2.18	77.4	3.22	4.66	6.83	1.05	3.15	34.51	1.02	6.37
Variety 25	105.67	120	114.03	2.43	2.13	50.53	16.67	5.67	27.67	2.96	91.67	3.2	4.45	8.33	1.05	3.47	30.54	0.94	5.89
Variety 26	108	135	86.6	46.13	2.43	83.09	14.67	5.67	27.67	3.7	51.91	4.83	6.64	9.8	1.05	4.91	48.63	0.98	6.14
Variety 27	158	171	77.6	30.77	1.73	61.75	18	6	20.93	2.19	88.41	3.34	7.16	7.33	1.05	9.24	53.11	0.96	6
Variety 28	155	170	81.77	29.1	1.47	30.07	18	5	20.17	6.67	81.18	2.34	7.35	10.57	1.05	5.36	40.89	0.8733	5.46
Total Mean	112.881	124.33	112.19	34.11	1.94	51.68	15.84	5.5	27.89	3.25	83.07	3.9	5.15	8.09	1.06	4.36	38.2	0.95	5.93

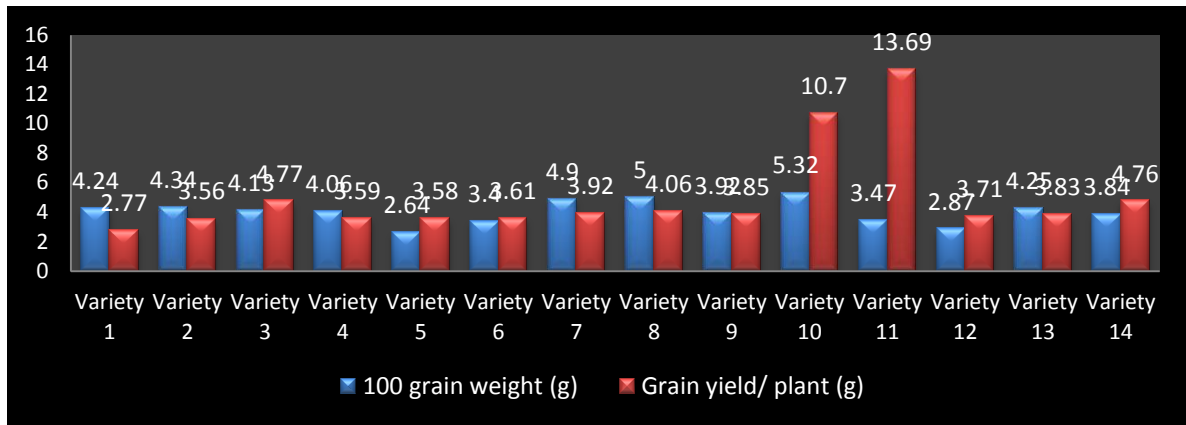


Fig. 1. Mean for 100 grain weight (g) and grain yield/plant for all the traits studied

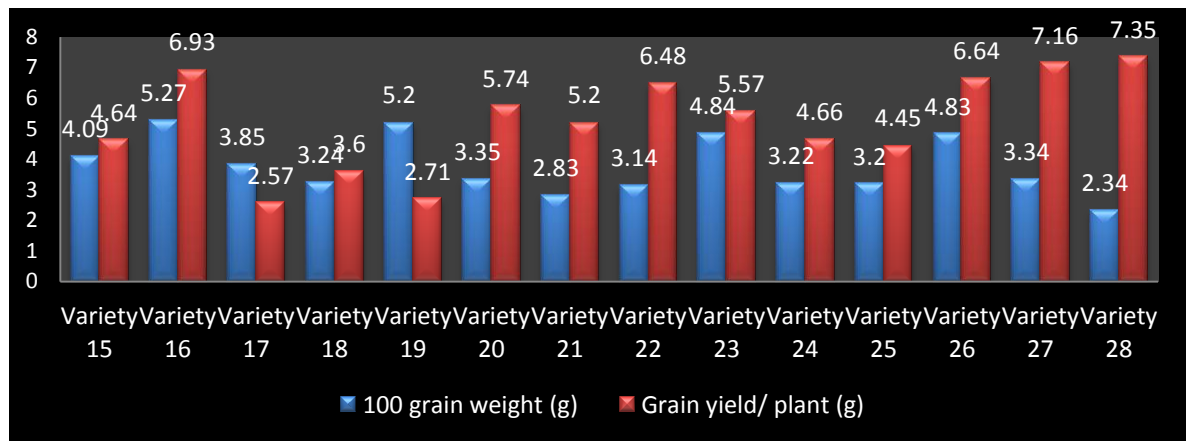


Fig. 2. Mean for 100 grain weight (g) and grain yield/plant for all the traits studied

Genetic coefficient of variability (%) was slightly lesser than phenotypic coefficient of variability (%). Similar results was reported by Sudeepthi et al. [12]. The GCV and PCV are classified as proposed by Sivasubramanian and Madhavamenon (1973). Traits like days to 50% flowering, days to maturity, plant height, flag leaf length, flag leaf breadth, panicle length, spikelet fertility [13] and root length have moderate GCV (%) and PCV (%) whereas no. of ear bearing tillers, panicles per plant, root weight, total nitrogen (%) and crude protein have low GCV (%) and PCV (%). The traits which have high GCV (%) and PCV (%) are flag leaf area [14], panicle weight, stem dry weight, harvest index, 100 grain weight and grain yield per plant. GCV (%) and PCV (%) were highest for grain yield per plant, stem dry weight, harvest index and flag leaf area. Similar findings were also found for high GCV (%) and PCV (%) in traits like yield and no. of grains/panicle [15].

Heritability (%) was observed to be high for almost all the traits studied viz., days to 50%

flowering (99.7%), days to maturity (100%), plant height (93.4%) [11], flag leaf breadth (92.4%), flag leaf length (85.6%), flag leaf area (90.5%), no. of ear bearing tillers (85.3%), panicle length (78.4%), panicle weight (92.4%), root length (89.2%), stem dry weight (94.5%), harvest index (99.7%) (Singh et al., 2011), total nitrogen (96.8%), crude protein (96.8%), 100 grain weight (99.2%) and grain yield per plant (99.7%) except for spikelet fertility (37.8%) which shows moderate heritability and panicles per plant (19.1%) [16,17] which shows possibility that these traits may be crucial for selecting superior genotypes in rice development programmes. Root dry weight (16.2%) also shows low heritability. The genetic advance as percentage of mean for 19 traits revealed that grain yield per plant is highest (124.77) which is followed by harvest index (115.84), stem dry weight (114.17) and flag leaf area (79.48) whereas moderate genetic advance as percentage of mean was moderate for no. of ear bearing tillers (19.65), total nitrogen and crude protein (16.13) and low for traits like panicles per plant (7.19) and root

dry weight (3.18) (Figs. 1,2). High heritability coupled with high genetic advance was found in grain yield per plant [18], harvest index, stem dry weight and flag leaf area indicating that these characters are governed by additive gene action. As a result, improved response to selection can be achieved to improve these qualities.

The presence of additive gene action was demonstrated by moderate heritability and high genetic progress, although moderate heritability was primarily caused by environmental factors. Low genetic progress and high heritability demonstrated non-additive gene activity, suggesting that selection may not be favourable [19-21]. Hybridization followed by progeny testing will be helpful for the development of such features.

4. CONCLUSION

The study concluded that yield contributing traits like days to 50% flowering (99.7%), days to maturity (100%), plant height (93.4%), flag leaf breadth (92.4%), flag leaf length (85.6%), flag leaf area (90.5%), no. of ear bearing tillers (85.3%), panicle length (78.4%), panicle weight (92.4%), root length (89.2%), stem dry weight (94.5%), harvest index (99.7%), total nitrogen (96.8%), crude protein (96.8%), 100 grain weight (99.2%) and grain yield per plant, spikelet fertility and panicles per plant showed moderate to high heritability indicating the predominant role of additive gene action. This study comes to the conclusion that simple selection can result in a significant improvement in the expression of these traits over the base population. Further, varieties 10,11 and 27 (Thangmo Red, Thangmo white and Thupfu La) may be valuable as donors in upcoming breeding programmes.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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