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# Stability analysis of quantitative and qualitative traits in heritage rice landrace Zag (red rice) of Kashmir Himalayas

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#### Abstract

Eighteen red rice collections from different sites of the Kashmir Himalayas valley were evaluated during kharif-2017, 2018 and 2019 for stability performance for yield along with its related traits and cooking quality traits. The genotype effect had a significant mean square for all traits except panicle length based on analysis of variance. The genotype×environment interaction showed a significant difference for some of the studied traits, which included kernel elongation ratio, grain yield, number of panicles, 1000 seed weight, kernel length before cooking and kernel length after cooking. When the environment + (G  $\times$  E) interaction is divided into environment (linear), G x E (linear) and congruent deviation, the mean square by environment (linear) shows that all attributes are taken into consideration. These results showed a significant difference between the environments that can have a great impact on the expression of the studied traits. Similarly, G x E (linear) was observed to be significant for all traits except 50% flowering days, plant height and maturity days, which means that the genotype behaviour of these traits is environmentally predictable and indicates that this is the function of the components of the linear environment. Mean squares due to pooled deviation (nonlinearity) were significant for all traits except 1000 grain weight and kernel breadth before cooking, suggesting that nonlinear composition is important for characteristics that contribute to the total G×E interaction. Thus, the genotypes differ significantly in terms of stability to the environment for such traits. C-5 has a low average for flowering days up to 50% and ripening days relative to the population mean, the row also has a uniform regression coefficient and the least deviation from the regression of yield showing consistent behaviour of the stream over the years. Likewise, C14 has a uniform regression coefficient and the least deviation from the regression for yield as well as a low mean for days up to 50% flowering and days until ripening, showed suitability of the line for consistent yield and early maturity.

Key words: Stability; Eberhart and Russel model; Zag; Red Rice; Adaptability

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# 1. Introduction

Rice (Oryza sativa L.) is the staple food for most people and the most important cereal crop and is widely cultivated in many parts of the world and is associated with economic, social and cultural heritage of the region (Amir et al 2019). Rice is grown under various agro climatic conditions thus having greater variability in local germplasm which needs to evaluated (Divya et al., 2020). Rice cultivars with red pericarp are prevalent in the Southern, Eastern, and the hilly tracts of the North-East and North-Western parts of India. The bran layer is rich in polyphenols and anthocyanins which confer antioxidant properties besides characteristic red hue to rice kernel (Chaudhary, 2003). Kashmir valley inhabits number of rice landraces such as Zag, Nunbeoul, Noor Miri, Qadir Beigh, Kawkadur, Kamad, Mushk Budji and several others. Of these a red rice, Zag is an important landrace of Kashmir known for its red colour and for its high iron and zinc content compared to the white rice varieties (Khan et al., 2020). The Karnah Tehsil of district Kupwara of Kashmir valley is recognized as geographical niche where 'Zag', a rare red rice landrace, was used to be grown in more than 5000 ha area at an altitude of 1900 m msl (34°02 N latitude and 74°32 E longitude) few decades back. Apart from this, the Zag rice landrace is cultivated sporadically elsewhere also in the valley.

Since yield is a quantitative trait, and is highly dependent on the environment, it is rewarding to select a superior genotype based on yield itself when conducted in different environments or over several years (Shrestha et al., 2012) and a stable genotype has potential to perform equally under different environments and years (Suresh et al 2020). Stability assessments in determining genotype performance in different environments can help recommend varieties for general or specific cultivation. Consistency of harvest potential and performance of varieties in different environments are highly desirable (Manjunatha et al, 2018). A number of ecotypes of red rice collected from different identified niches of Kashmir Himalayas were collected, evaluated and conserved at Khudwani centre of Shere Kashmir University. The ear to row method was adopted for their purification followed by multiplication. The varietal trial was constituted and conducted in 2017 and repeated in 2018 and 2019 to identify promising lines with respect to consistency in

yield and other associated parameters. In this connection, red rice samples from different corners of the valley were collected and tested for their stability. The objective was to test the collections for their consistency in yield, early maturity *vis. a vis.* for general and specific adaptability.

# 2. Material and Methods

The experimental materials comprised 18 red rice collections from different ecological niches of the valley (designated as C1 to C18). Access sessions were grown in random block designs replicated 3 times on the experimental farm of MRCFC Khudwani at SKUASTK in spring season 2017, 2018 and 2019. The Khudwani centre is located between elevation 33° 70°N latitude and 75°10°E longitude with average of 1590 meters (amsl) above sea level. Five rows were used for planting each cultivar, the length of each row was 3 meters and the distance between the rows was 20 cm. A standard practice package has been employed to grow healthy crops.

Morphological agronomic traits studied in this study included 13 traits which are: length: breadth ratio (LBR), plant height (PH), number of effective tillers (NT), panicle length (PL), spikelets per panicle (SP), grain yield per plant (GY), spikelet fertility (SF), kernel length before cooking (KLBC), kernel elongation ratio (KER), kernel breadth before cooking (KBBC), kernel length after cooking (KLAC), kernel breadth after cooking (KBAC) and aroma. Twenty grains were randomly sampled from each replication and were dehusked by mini-huller and polished by mini-rice polisher (Kett, Japan). Brown rice was used for kernel length before cooking (KLBC) and kernel breadth before cooking (KBBC) and these traits were measured on them. Also, by dividing the average length by the average width of rice kernel, the L/B ratio was calculated. The method of Juliano et al. (1966) was also used to measure the KLAC trait. The method of Murthy (1965) was used to measure the Kernel elongation ratio (ER) trait and this ratio was obtained by dividing the average length of cooked kernel by the average length of the raw rice.

The stability parameters were calculated based on the proposed linear model of Eberhart and Russell (1966) and observations on the phenotypic performance of the 18 genotypes studied in the years 2017, 2018 and 2019



were used for this analysis and was performed using WINDOSAT 9.1.

#### 3. Results and Discussion

In this study, the results of analysis of variance showed that the studied traits (days to 50% flowering, plant height (cm), number of panicles, days to maturity, grain yield, 1000 seed weight, KLBC, KLAC, KBBC, KBAC, KER except panicle length) have very significant mean squares for genotypes. It was found that the mean square of the environment is very important for all characteristics that reveal the various performance of the whole environment. For some traits such as number of panicles, grain yield and 1000 seed weight, KLBC, KLAC and KER, the genotype  $\times$  environment interaction was significant. When the environment +  $(G \times E)$  interaction is divided into environment (linear), G x E (linear) and congruent deviation, the mean square by environment (linear) shows that all attributes are taken into consideration. This confirmed that there was a significant difference between the environments and had a great influence on the expression of studied traits. Similarly, G x E (linear) was observed to be significant for all traits except 50% flowering days, plant height and maturity days, which means that the genotype behaviour of these traits is environmentally predictable and indicates that this is the function of the components of the linear environment. For all studied traits, the mean squares due to the pooled deviation (nonlinearity) was significant except 1000 grain weight and KLBC, suggesting that nonlinear composition is important for characteristics that contribute to the total G×E interaction. Thus, the genotypes differ significantly in terms of stability to the environment for such traits.

A pool of ANOVAs showed very significant mean-squared sums of genotypes and environments of all characters investigated. This shows that there is a substantial variation between genotypes in the global environment, as reported by Rashmi *et al* (2017). Substantial (linear) environmental variability indicates a linear contribution of environmental effects and additive environmental variances in these characteristics and is striking with the others researchers' findings such as Saidaiah *et al.* (2010) and Manjunatha *et al.* (2018). In addition, the linear component of the GE interaction was found to be significant for six characters by Babu *et al.* (2005) and Ramya and Senthil Kumar (2008). The stability of 18 sets of red rice based on 10 traits was evaluated by three stability parameters, namely regression coefficient (bi), mean (x), and deviation from the regression (S<sup>2</sup>di) using the proposed model of Eberhart and Russell (1966). Based on the model, a reliable genotype for the entire environment is to have high mean yield (xi), unit regression (bi) and minimum deviation ( $\delta^2$ di) around the slope of the regression. Since the variance of  $\delta^2 di$  is a function of environmental water, we argue that multiple environments with at least a replica for each environment are needed to get a reliable estimate of  $\delta^2$ di. Therefore, we tested the cultivar response using linear regression taking into account the stability of the mean and deviation in the regression of each genotype. A genotype of bi = 1 with a high mean and not significant  $\delta^2$ di is suitable for general adaptation.

On the other hand, genotypes with insignificant  $\delta^2$ di, high mean and bi>1 are considered to be lower than the mean in terms of stability. These genotypes are suitable for a favourable environment because they respond positively in better environments but less efficiently in unfavourable environments. Also, a low mean, bi < 1 with intentioned  $\delta^2$  di does not respond favourably to improved environmental conditions and can therefore be considered adapted to particularly harsh environments. Finally, genotypes with any bi value with significant  $\delta^2$ di were unstable. Estimation of the stability parameters showed insignificant estimates of deviation from the regression ( $\delta^2$ di) for all traits. However, some genotypes showed significant mean square deviation from regression (S<sup>2</sup>di) for some traits that can be referred to days to 50% flowering for genotype C2,C10,C14,C15 and C18; plant height for genotypes C1,C 2, C4, C7,C9,C10,C11,C14 and C15; number of panicles for genotypes C1 and C10; panicle length for genotypes C1, C2, C3, C5, C9,C11, C12 and C16; days to maturity for genotypes C3, C6,C7,C10,C13,C14 and C18; grain yield for genotypes C3, C4,C7 C10,C12, C15, C16 and C18; KLBC for genotype C10, and KER for genotypes C4, C10 and C14. The regression showed that the genotype nonlinear component (the non-uniformity of the regression) exhibiting insignificant mean square deviation ( $\delta^2$ di) was equal to zero. Thus, it is possible to predict the performance of these genotypes in a specific environment. Therefore, genotypes that could predict performance (i.e.,  $\delta^2 di = 0$ ) were classified as stable.

Table 1:	Stability variance analysis for yield,	yield contributing	; traits in 'zag'	genotypes across random
	environments in the Kashmir valley			

Source of variation				Mean S	um of Suc	luares		
	d.f.	DF (50%)	РН	NP	PL	DM	GY (t/ha)	1000 SW(g)
Rep within Env.	6	2.9	4.4	0.6	1.0	0.6	0.2	2.2
Varieties	17	48.5**	439.3**	1.7**	3.2	58.9**	2.1**	13.8**
Env.+ (Var.* Env.)	36	36.90**	45.0	3.4**	5.5*	41.1**	3.2**	4.9**
Environments	2	619.5**	333.9**	31.9**	10.9*	562.8**	39.3**	21.4**
Var.* Env.	34	2.6	28.0	1.7**	5.2	10.4	1.1**	3.9**
Environments (Lin.)	1	1238.9**	667.8**	63.8**	21.9**	1125.6**	78.7**	42.7**
Var.* Env. (Lin.)	17	2.2	29.9	2.9**	7.8*	12.6	1.7**	6.8**
Pooled Deviation	18	2.8**	24.7**	0.4**	2.5**	7.7**	0.3**	0.9
Pooled Error	102	1.1	1.4	0.1	0.4	0.7	0.0	0.9
Total	53	40.6	171.5	2.8	4.8	46.8	2.8	7.7

#### Source of variation

#### Mean Sum of Suquares

	d.f.	KLBC	KBBC	KLAC	KBAC	KER
Rep within Env.	6	0. 4**	0.1**	0.02	0.03	0.02**
Varieties	17	0.1**	0.04**	0.3**	0.1*	0.01*
Env.+ (Var.* Env.)	36	0.2**	0.04**	0.3**	0.1**	0.02**
Environments	2	2.9**	0.5**	0.6**	0.8**	0.1**
Var.* Env.	34	0.1**	0.02	0.3**	0.04	0.01*
Environments (Lin.)	1	5.7**	1.01**	1.2**	1.5**	0.3**
Var.* Env.(Lin.)	17	0.1**	0.03*	0.5**	0.1*	0.02**
Pooled Deviation	18	0.02**	0.01	0.1**	0.03**	0.01**
Pooled Error	102	0.01	0.01	0.01	0.01	0.001
Total	53	0.2	0.05	0.3	0.1	0.02

 $\ast\ast$  Significant at 0.01,  $\ast$  significant at 0.05.

DF: days taken to 50% Flowering, NP: Number of Panicles, PH: Plant height (cm), PL: Panicle length (cm), GY: Grain yield t/ha, DM: Days to maturity, 1000 SW: 1000 Seed Weight (g).

 $KLBC: Kernel \ Length \ Before \ Cooking(mm), KBBC: Kernel \ Breadth \ Before \ Cooking(mm), KLAC: Kernel \ Length \ After \ Cooking(mm), KBAC: Kernel \ Breadth \ After \ Cooking(mm), KER: Kernel \ Elongation \ Ratio$ 



Genotype	Γ	05(50%)	(0)		Hd		Γ	M			NP			PL		Yie	I/T) bl	(AI	100	0 SW	~
	Mean	$\mathbf{b}_{i}$	$\mathbf{S}^2 \mathbf{d}_{\mathbf{i}}$	Mean	$\mathbf{b}_{i}$	$S^2d_i$	Mean	$\mathbf{b}_{i}$	$\mathbf{S}^2 \mathbf{d}_{\mathbf{i}}$	Mean	$\mathbf{b}_{i}$	$\mathbf{S}^2 \mathbf{d}_{\mathbf{i}}$	Mean	$\mathbf{b}_{i}$	$\mathbf{S}^2 \mathbf{d}_{\mathbf{i}}$	Mean	$\mathbf{b}_{i}$	$\mathbf{S}^2 \mathbf{d}_{i}$	Mean	$\mathbf{b}_{i}$	S
C1	81.0	1.0	0.2	118.2	0.3	22.9**	12.2a	1.0	$1.5^{**}$	20.3	0.0	$2.5^{**}$	116.2	0.8	-0.2	3.0	0.6	0.0	33.033b	2.1	2
C2	90.8	1.1	7.85**	127.1	2.0	$150.4^{**}$	9.2	2.8	-0.1	19.2	4.8	$6.1^{**}$	124.7	1.4	-0.2	4.0	2.2	0.0	29.9	3.4	2
C3	87.6	1.2	-0.2	132.5	1.8	-1.2	10.3	3.0	0.3	19.0	6.9	$9.2^{**}$	128.3	1.7	$46.1^{**}$	3.8	2.2	0.3**	29.6	4.2	0
C4	85.1	1.1	0.0	122.5	-1.4	7.8*	10.5	0.3	-0.1	21.6b	-0.4	0.7	123.2	1.4	-0.6	5.589a	0.7	$0.74^{**}$	36.0a	-1.0	0
C5	81.3	1.0	-1.0	113.7	0.5	0.1	10.4	0.8	-0.2	20.8	-0.8	2.3*	116.7	0.7	-0.4	3.8	1.2	0.1	31.3c	1.9	0
C6	81.1	1.0	0.7	101.1	-0.27*	-1.6	10.1	0.3	-0.1	20.0	0.3	-0.2	117.2	0.4	$6.1^{**}$	3.8	1.5	0.0	28.8	-0.85	*
C7	87.8	1.0	-1.1	118.4	1.4	$20.6^{**}$	11.383b	1.0	0.7*	20.933c	0.0	-0.4	127.5	0.6	52.7**	4.104c	0.2	$0.19^{*}$	30.2	0.5	Ŷ
C8	84.4	1.1	-0.4	123.3	0.8	0.2	10.1	0.9	0.9*	20.9	-0.4	0.6	122.5	1.2	-0.2	4.0	$0.31^{*}$	0.0	28.8	-1.4*	*
C9	82.8	0.9	-0.7	114.6	0.9	67.3**	10.3	0.6	-0.2	19.7	0.7	$2.1^{*}$	116.7	0.7	-0.2	3.7	1.3	0.0	28.3	-0.8	Ŷ
C10	77.8	0.7	4.23*	110.1	0.3	59.3**	10.8c	1.1	$1.6^{**}$	20.4	-1.0	-0.2	121.1	1.5	8.7**	2.2	0.2	$1.12^{**}$	28.7	1.4	Ŷ
C11	87.3	1.4	1.6	128.8	1.8	67.35**	8.8	2.9	0.1	18.7	7.1	8.9**	125.6	2.1	0.7	3.7	$2.07^{**}$	0.0	26.8	1.8*	~
C12	86.2	1.0	-1.1	132.3	1.5	1.9	9.7	0.8	0.1	21.08a	0.2	$5.20^{**}$	121.3	0.7	1.3	4.146b	0.6	$0.28^{**}$	30.6	0.9	0
C13	81.8	0.8	1.8	114.3	1.5	1.0	10.5	0.6	0.0	19.7	0.4	-0.1	115.9	0.7	7.3**	2.9	1.0	0.0	30.5	1.5	Ť
C14	80.8	0.7	$6.52^{*}$	120.0	1.7	$12.62^{**}$	9.8	0.5	-0.1	20.9	-0.1	0.0	116.2	0.6	2.9*	2.8	0.9	0.0	27.4	-2.1	Ŧ
C15	79.4	1.2	$5.50^{*}$	118.7	1.4	$5.79^{*}$	9.8	0.2	0.4	19.5	1.2	-0.4	116.1	0.8	-0.4	3.0	0.7	0.6**	32.9	2.8	0
C16	77.6	0.8	-0.3	88.0	1.8	0.3	10.7	0.5	0.0	17.4	0.5	$2.21^{*}$	122.4	1.0	0.2	3.1	1.0	$1.5^{**}$	32.7	1.7	0
C17	78.0	1.0	0.2	94.1	0.4	0.1	10.1	0.2	-0.1	19.1	-0.8	-0.3	114.8	0.7	-0.2	2.0	0.8	0.0	26.8	1.3	Ť
C18	78.0	1.0	$4.77^{*}$	113.7	1.6	0.5	10.7	0.8	-0.2	19.8	-0.5	-0.2	116.3	0.9	3.8*	2.9	0.7	$0.94^{**}$	31.6	0.7	1
Population	82.7			116.9			10.3			10.0			190.9			30			2 06		

Stability and analysis of traits heritage rice landrace Zag (red rice)

166

Weight(g).

Mean     I     Seli	167	Genotype		KLBC			KBBC			KER	
C1     57     15     00     31     07     00     15     27*     00       C2     57     05     05     07     05     07     05     07     00       C3     59     12     00     27     15     01     15     01     15     01       C3     55     17     03     27     15     01     15     01     15     01       C4     54     17*     00     27     15     00     15     01     15     01       C4     55     11     00     23     15     01     15     01     01       C4     14*     00     24     14     0     15     01     15     01     01       C4     24     14*     0     24     15     01     15     01     01       C5     14     16     16     16     16     16     16     16     16			Mean	bi	S2di	Mean	bi	S2di	Mean	bi	S2di
C2     5.7     (6)     (2)		CI	5.7	1.5	0.0	3.1	0.7	0.0	1.5	2.7*	0.0
C3     59     12     00     28     09     01     15     00       C4     54     08     00     27     15     00     15     07     00       C5     56     17*     00     27     15     00     15     24     00       C5     56     17*     00     27     15     00     15     24     00       C6     57     01     02     00     27     15     00     15     01     01       C7     56     01     02     28     03     03     04     01     01       C9     03     04     03     04     04     04     04     04       C9     04     03     04     04     04     04     04     04     04       C4     04     04     04     04     04     04     04     04       C4     04     04     04     04		C2	5.7	0.6	0.0	2.8	0.9	0.0	1.5	0.9	0.0
C(1     5,4     0,8     0,0     2,7     1,5     0,0     1,5     0,7     0,1       C3     5,6     1,7*     0,0     3,0     0,00**     0,0     1,5     2,4     0,0       C4     5,7     0,7     0,7     0,00**     0,0     1,5     2,4     0,0       C4     5,5     1,1     0,0     2,9     0,1     1,5     2,4     0,0       C4     5,5     1,1     0,0     2,8     1,2     0,0     1,6     0,0     0,0       C4     5,6     0,0     0,0     2,9     0,0     1,6     0,0     0,0       C4     0,0     <		C3	5.9	1.2	0.0	2.8	0.9	0.0	1.4	1.5	0.0
C3     56     17*     00     30     00**     15     24     00       C6     57     07     07     00     15     07     07     00       C7     53     11     00     29     31     00     15     07     00       C7     55     11     00     29     31     00     16     13     00       C8     56     09     00     27     15     00     16     10     00       C10     56     17     00     29     11     00     16     23     00       C11     58     12     00     27     15     00     16     00     00       C12     54     13     01     02     14     00     00     16     00     00     00     00     00     00     00     00     10     00     10     00     10     00     10     10     10     10 </td <td></td> <td>C4</td> <td>5.4</td> <td>0.8</td> <td>0.0</td> <td>2.7</td> <td>1.5</td> <td>0.0</td> <td>1.5</td> <td>-0.7</td> <td><math>0.01^{*}</math></td>		C4	5.4	0.8	0.0	2.7	1.5	0.0	1.5	-0.7	$0.01^{*}$
C6     57     07     00     29     31     00     15     07     00       C7     55     11     00     28     12     00     16     18     00       C8     56     09     00     28     12     00     16     11     00       C9     56     14*     00     28     09     00*     16     10     10     00       C10     56     14*     00     28     09     00     16     10     00       C11     58     12     00     29     11     00     16     10     00       C12     56     17     00     27     15     00     16     00     00       C13     54     14     00     28     00     16     10     00     00       C13     54     14     00     29     00     16     10     00     00     00     00     00<		C5	5.6	$1.7^{*}$	0.0	3.0	0.00**	0.0	1.5	2.4	0.0
C7     5.5     11     00     28     12     00     16     18     00       C8     5.6     0.9     0.0     27     1.5     0.0     1.4     0.0       C9     5.6     0.9     0.0     27     1.5     0.0     1.4     0.0       C9     5.6     0.9     0.0     2.9     0.0     1.5     0.0     1.6     1.0     0.0       C10     5.6     0.9     0.12*     0.0     2.9     1.1     0.0     1.6     0.0     0.0       C11     5.8     1.2     0.0     2.9     1.1     0.0     1.2     0.0     0.0       C13     5.5     1.5     0.0     2.9     0.0     0.0     0.0     0.0     0.0       C14     5.3     1.5     0.0     2.9     0.0     0.0     0.0     0.0     0.0     0.0       C13     5.4     0.0     0.0     0.0     0.0     0.0     0.0     0.0		C6	5.7	0.7	0.0	2.9	3.1	0.0	1.5	0.7	0.0
C8     5.6     0.9     0.0     2.7     1.5     0.0     1.4     1.1     0.0       C9     5.4     1.4*     0.0     2.8     0.9     0.0     1.6     1.1     0.0       C10     5.6     0.9     0.12*     3.0     0.00**     0.0     1.6     2.7     0.0       C11     5.8     1.2     0.0     2.9     0.0     1.6     2.5     0.0       C11     5.8     1.2     0.0     2.9     0.0     1.4     2.0     0.0       C12     5.4     1.5     0.0     2.1     0.0     1.4     2.0     0.0       C14     5.3     1.5     0.0     2.9     0.0     1.4     2.0     0.0       C14     5.3     1.5     0.0     2.9     0.0     1.5     0.0     1.5     0.0       C14     0.0     2.3     0.0     0.0     1.5     0.0     1.5     0.0       C14     0.0     1.5		C7	5.5	1.1	0.0	2.8	1.2	0.0	1.6	1.8	0.0
C9     54     14*     00     28     09     06     10     10     00       C10     56     09     012*     30     000**     0     16     25     001*       C11     58     12     00     29     11     00     14     20     00*       C11     58     12     00     29     11     00     14     20     00       C12     55     15     00     27     15     00     15     00     10     10     00       C13     53     15     00     29     00     15     00     15     00     00       C14     53     15     00     29     00     15     00     12     00     00       C15     54     14     00     29     00     15     00     15     00       C15     54     01     00     12     01     01     12     03		C8	5.6	0.9	0.0	2.7	1.5	0.0	1.4	-1.1	0.0
C10     5.6     0.9     0.12*     3.0     0.00**     0.0     1.6     2.5     0.01*       C11     5.8     1.2     0.0     2.9     1.1     0.0     1.4     2.0     0.0       C12     5.6     1.7     0.0     2.7     1.5     0.0     1.4     2.0     0.0       C13     5.5     1.5     0.0     2.1     0.0     1.5     0.0     1.5     0.0     0.0       C13     5.5     1.5     0.0     2.1     0.0     1.5     0.0     1.5     0.0     0.0     0.0     0.0       C14     5.3     1.5     0.0     2.9     0.0     0.1     0.0     1.5     0.0       C15     5.4     0.1     0.0     2.9     0.0     0.1     0.0     0.0     0.0       C15     5.4     0.0     2.9     0.0     0.1     0.0     0.1     0.0     0.0       C15     5.4     0.0     2.9     0.0		C9	5.4	$1.4^{*}$	0.0	2.8	0.9	0.0	1.6	1.0	0.0
CI1     5.8     1.2     0.0     2.9     1.1     0.0     1.4     2.0     0.0       CI2     5.6     1.7     0.0     2.7     1.5     0.0     1.5     0.9     0.0       CI3     5.5     1.5     0.0     2.7     1.5     0.0     1.5     0.9     0.0       CI3     5.5     1.5     0.0     2.8     0.9     0.0     1.5     0.9     0.0       CI4     5.3     1.5     0.0     2.9     0.0     1.5     0.0     1.5     0.0       CI5     5.4     0.4     0.0     2.9     0.0     1.5     0.0       CI4     5.4     1.4     0.0     2.9     0.0     1.5     0.0       CI5     5.4     0.1     0.0     1.2     0.0     1.5     0.0       CI7     5.4     0.1     0.0     1.5     0.0     1.5     0.0       CI8     5.4     0.0     2.9     0.0     1.5     0.0<		C10	5.6	0.9	$0.12^{*}$	3.0	0.00**	0.0	1.6	2.5	$0.01^{*}$
C12   5.6   1.7   0.0   2.7   1.5   0.0   1.5   0.9   0.0     C13   5.5   1.5   0.0   2.8   0.9   0.0   1.5   0.9   0.0     C14   5.3   1.5   0.0   3.1   0.7   0.0   1.5   0.9   0.0     C14   5.3   1.5   0.0   2.9   0.0   1.1   0.7   0.0   1.5   0.0     C15   5.4   0.4   0.0   2.9   0.4   0.0   1.5   0.3   0.0     C16   5.4   0.1   0.0   2.9   0.4   0.0   1.5   0.0   0.5   0.5   0.5   0		CII	5.8	1.2	0.0	2.9	1.1	0.0	1.4	2.0	0.0
C13     5.5     1.5     0.0     2.8     0.9     0.0     1.6     0.9     0.0       C14     5.3     1.5     0.0     3.1     0.7     0.0     1.5     0.3     0.0       C15     5.4     0.4     0.0     2.9     0.4     0.0     1.5     0.3     0.0       C15     5.4     1.4     0.0     2.9     0.4     0.0     1.5     0.3     0.0       C16     5.4     1.4     0.0     2.9     0.1     0.0     1.5     0.3     0.0       C17     5.4     0.1     0.0     2.8     1.2     0.0     1.5     0.3     0.0       C18     5.7     0.2     0.0     3.0     1.1     0.0     1.5     0.3     0.0       Population mean     5.6     1.2     0.0     1.5     0.0     1.5     0.0       Statistificant at <0.03 and <0.01, respectively.     5.0     0.0     1.5     0.0     1.5     0.0     0.0		C12	5.6	1.7	0.0	2.7	1.5	0.0	1.5	0.9	0.0
Cl4     5.3     1.5     0.0     3.1     0.7     0.0     1.5     0.8     0.0       Cl5     5.4     0.4     0.0     2.9     0.4     0.0     1.5     0.3     0.0*       Cl6     5.4     1.4     0.0     2.9     0.6     0.1     1.5     0.3     0.0*       Cl7     5.4     0.1     0.0     2.9     0.6     0.0     1.5     0.3     0.0       Cl7     5.4     0.1     0.0     2.9     1.1     0.0     1.5     0.3     0.0       Population mean     5.6     0.0     3.0     1.1     0.0     1.5     0.7     0.0       Population mean     5.6     2.9     3.0     1.1     0.0     1.5     0.7     0.0       RLBC: Kenel Length Before Cooking (mm), KBBC     5.6     0.0     1.2     1.5     1.5     1.5		C13	5.5	1.5	0.0	2.8	0.9	0.0	1.6	0.9	0.0
C15     5.4     0.4     0.0     2.9     0.4     0.0     1.6     1.7     0.02*       C16     5.4     1.4     0.0     2.9     0.6     0.0     1.5     0.3     0.0       C17     5.4     1.4     0.0     2.9     0.6     0.0     1.5     0.3     0.0       C17     5.4     0.1     0.0     2.8     1.2     0.0     1.5     0.3     0.0       C18     5.7     -0.2     0.0     3.0     1.1     0.0     1.6     0.7     0.0		C14	5.3	1.5	0.0	3.1	0.7	0.0	1.5	0.8	0.0
C16     5.4     1.4     0.0     2.9     0.6     0.0     1.5     0.3     0.0       C17     5.4     -0.1     0.0     2.8     1.2     0.0     1.5     0.8     0.0       C17     5.4     -0.1     0.0     2.8     1.2     0.0     1.5     0.8     0.0       C18     5.7     -0.2     0.0     3.0     1.1     0.0     1.6     0.7     0.0       Population mean     5.6     .     2.9     .     1.1     0.0     1.6     0.7     0.0       *, **, significant at <0.05 and <0.01, respectively.     .     2.9     .     1.5     .     1.5     .     1.5     .     1.5     .     I.0     I.0     I.5     .     I.5     .     I.5     .     I.5		C15	5.4	0.4	0.0	2.9	0.4	0.0	1.6	1.7	$0.02^{*}$
CI7     5.4     -0.1     0.0     2.8     1.2     0.0     1.5     -0.8     0.0       C18     5.7     -0.2     0.0     3.0     1.1     0.0     1.6     0.7     0.0       Population mean     5.6     -0.2     0.0     3.0     1.1     0.0     1.6     0.7     0.0       * **, significant at <0.05 and <0.01, respectively.     2.9     2.9     1.5		C16	5.4	1.4	0.0	2.9	0.6	0.0	1.5	0.3	0.0
Cl8     5.7     -0.2     0.0     3.0     1.1     0.0     1.6     0.7     0.0       Population mean     5.6     2.9     2.9     1.5     1.5     1.5     1.5       *, **, significant at <0.05 and <0.01, respectively.		C17	5.4	-0.1	0.0	2.8	1.2	0.0	1.5	-0.8	0.0
Population mean 5.6 2.9 1.5   *, **, significant at <0.05 and <0.01, respectively.		C18	5.7	-0.2	0.0	3.0	1.1	0.0	1.6	0.7	0.0
*, **, significant at <0.05 and <0.01, respectively. KLBC: Kernel Length Before Cooking(mm), KBBC : Kernel Breadth Before Cooking (mm), KER:Kernel Elongation Ratio		Population mean	5.6			2.9			1.5		
	∗ ⊻	, **, significant at <0.05 and LBC: Kernel Length Before	l <0.01, respectiv Cooking(mm), K	ely. CBBC : Kernel	Breadth Before C	ooking (mm), KEF	t:Kernel Elongat	ion Ratio			

Journal of Cereal Research 13(2): 162-170

167

Significant changes in linear regression uniformity for various traits have been reported in relation to genotypes such as C8 and C11 (grain yield); C8 and C11 (1000-seed weight); and C5 and C9 (KLBC); C5 and C10 (KBBC), C1 (KER). Significant and greater than 1 was found in C11 for grain yield and 1000 seed weight and for C8 for 1000- seed weight, C5 and C9 for KLBC, and C1 for KER. Rest of the genotypes showing non-significant regression coefficient (bi) value and deviation from the regression ( $\delta^2$ di) were average in stability and were either favourably or poorly adapted to the environments. Accordingly, the promising genotypes having maximum number of panicles/plants were C1, C7 and C-10; while those with longer panicle were C12, C4 and C7. For 1000 seed weight, C4, C1 and C5 showed higher mean than that of the population mean. For grain yield, genotypes C4, C12 and C7 were found to be the promising. The line C5 had less mean value for days to 50% flowering and days to maturity than the population mean with unity regression coefficient and least Stability and analysis of traits heritage rice landrace Zag (red rice)

deviation from regression for yield, indicating that this line could show consistent performance across the environments. Furthermore, C-14 had regression coefficient unity and least deviation from regression for yield (Fig. 1) and with low mean value for days to 50% flowering and days to maturity than the population mean, indicating that the consistent performance of the line across the environments (Fig. 2 and 3). The results are in consistency with Manjunathan *et al.* (2018).

The maximum temperature ranged between 21.7 (°C) to 32.7 (°C), 21.7 (°C) to 32.1 (°C) and 23.2 (°C) to 33.6, during 2017, 2018 and 2019 respectively. The corresponding figures for minimum temperature were 7.3 (°C) to 19.1 (°C), 8.0 (°C) to 18.6 (°C), 8.3 (°C) to 18.6 (°C), respectively. The total rainfall during the crop growing season was 360 mm, 500 mm and 398 mm during 2017, 2018 and 2019, respectively (Fig.3). Lowest yield was recorded in 2019 as compared to 2017 and 2018, This may be the higher average max temp during 2019 (Fig. 3) which would have concurrently resulted into the less





number of days to reach different phenological stages and finally to the reduction in the yield. Despite of the variation in weather parameters across the three years, C 14 and C5 performed in a consistent way throughout the three years.

## 4. Conclusion

Farmers are cultivating diverse population including local landraces not only to be penalised by various biotic and abiotic stresses but to get more farm income on the sale of local rice varieties. Growing local landraces in addition to high yielding varieties ensure the in-situ conservation of genetic resources for posterity. Since lot of admixtures is often been found in farmers varieties which discourage their cultivation by farmers and grain acceptance by consumers, therefore, pureline method is the option to derive out the better and uniform lines for general cultivation. From present study, it is suggested that the most stable lines identified from three years of continuous study need to be further tested over a greater number of locations to determine their utility for cultivation across broad range of ecologies in the temperate agro-ecosystems.



# Compliance with ethical standards

### NA

# **Conflict of Interest**

Authors declare that they have no conflict of interest

# Author contributions

GHK, conduct of trial, analysis of data, preparation of manuscript NRS exploration and collection of different zag lines, ABS, FAM, SHW, RSK, manuscript preparation data recording and data analysis, AH, analysis and interpretation of meteorological data MR, NAB Critical review and finalization

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Stability and analysis of traits heritage rice landrace Zag (red rice)

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