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Genotype x environment interaction and stability analysis for yield and its contributing traits in rice

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Abstract

Twenty-eight cross combinations obtained through crossing of seven female lines with four testers in line x tester mating fashion were evaluated to study stability and genotype x environment interactions for yield and yield contributing characters in rice over three different locations in Gujarat state of India during *Khariif*, 2021. The coincidence of genotypic performance with environmental values was observed for five characters studied (Grains per panicle, Straw yield per plant, Kernel length, Kernel breadth and Amylose content), evident from significant G x E (linear) mean square when tested against pooled deviation. This suggested that the performance of genotypes over environments could be predicted reasonably for these traits.

Keywords: Rice, stability analysis, genotype, environment interaction

Introduction

Rice (*Oryza sativa* L.) is the world's single most important crop and a primary food source for half of the human kind on the planet. The living and livelihood of majority of the Indian farming population also depends on growing rice. It is the grain that has created and shaped the religions, communities, cultures, diets and economies of millions of people in society as well as occupies a significant position in the culture and heritage of many Asian countries.

In breeding programme, it is necessary to screen and develop stable genotypes, which perform more or less uniform under varying environmental conditions. Thus, knowledge of genotype x environment interaction helps the breeder to select high yielding and most adaptable varieties and hybrids. In any crop, plant breeders are mostly interested and continuously engaged in improvement of yield character. Yield is complex character which depends on many component characters, type of genotype, environmental conditions and genotype x environment interactions. When interaction between genotype and environment exists, ranking of genotypes will be different under different environments. Crop production is dependent on the release of such stable hybrids that gives consistently desirable performance under wide range of agro-climatic conditions. The stability of productivity is therefore very important factor to achieve high and continuous returns over wide geographical area through agriculture. Hence, it is always desirable to isolate genotypes manifesting stability in respect of economically important characters.

The present investigation therefore, was undertaken to study the stability performance and understand the differential G x E interaction of eleven parents and their 28 hybrids for yield and yield attributing characters.

Material and Methods

The experimental materials for the present investigation consisted of 11 genotypes (7 lines - NVSR- 494, NWGR- 15018, NVSR- 496, NVSR- 453, NVSR- 6172, NVSR- 6206 and NVSR- 494 and 4 testers- GR-17, GNR-3, NVSR-418 and NVSR-6287) as parents and their 28 resultant hybrids along with "Gurjari" as standard check.

The crossing programme was carried out at Main Rice Research Centre, NAU, Navsari during summer-2020. Twenty-eight crosses were made in Line x Tester mating design using 7 parents as lines and 4 as testers, by hand emasculation and pollination.

Three complete sets of 40 entries comprising of 28 F₁'s, 11 parents and one check were evaluated during *khariif*-2021 in Randomized Block Design (RBD), replicated thrice at three research stations of the university viz., Main Rice Research Centre, Navsari (Loc.-I), Regional Rice Research Station, Vyara (Loc.-II) and Hill Millets Research Station, Waghai (Loc.-III).

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The parents and F₁'s were represented by a single row plot of 10 plants, placed at 20 x 15 cm. All the agronomical practices and plant protection measures were followed as per recommendations.

Five random competitive plants excluding border ones were selected from each row in each replication to record observations. The thirteen characters viz., days to 50 % flowering, productive tillers per plant, plant height, panicle length, grains per panicle, grain yield per plant, straw yield per plant, kernel length, kernel breadth, L:B ratio, 100 grain weight, protein content and amylose content were recorded in field as well as in laboratory and mean values were subjected for statistical analysis. The mean values for all the characters across the environments were subjected to stability analysis as suggested by Eberhart and Russel (1966) [3].

Genotype X environment interaction and stability analysis

The statistical analysis for genotype-environment interactions and stability parameters were worked out according to Eberhart and Russel (1966) [3] for different characters under study. Consistent high performance together with (i) the regression of each genotype in an experiment on environment index and (ii) a function of squared deviations from this regression would provide estimates of the desired stability parameters. These parameters are defined with Eberhart and Russel (1966) [3] model as follow:

$$Y_{ij} = \mu_i + b_i I_j + \delta_{ij}$$

The estimates of stability factor b_i is obtained for i^{th}

$$\text{genotype as } - b_i = \frac{\sum_{j=1}^n Y_{ij} I_j}{\sum_{j=1}^n I_j^2}$$

Squared deviation from the regression is obtained as –

$$S_{di}^2 = \left[\sum_j \frac{\delta_{ij}^2}{(e-2)} \right] - \frac{S^2 e}{r}$$

Test of significance

Individual deviation from the linear regression was tested as follows.

$$F = \frac{\left\{ \frac{\sum_j \delta_{ij}^2}{(n-2)} \right\}}{\text{pooled error}}$$

Result and Discussion

Analysis of variance

The analysis of variance for genotype x environment interaction and stability parameters were estimated and are presented in Table 1 for all 13 characters. The variance due to genotype were significant for all traits when tested against pooled deviation and pooled error, which indicated presence of substantial variation in the material studied. The analysis also indicated significant variation among the imposed environments for all the characters (except productive tillers per plant and plant height) when tested against pooled error.

The genotypes x environment interactions were significant for all the traits when tested against pooled error. This indicated that genotype interacted significantly in different environments. The significance of G x E interactions in rice for plant growth characters, yield and quality parameters has also been reported by Sreedhar *et al.* (2011), Shinde and Patel (2014), Haradari *et al.* (2017) [14, 13, 4] and contrast with Dushyantha Kumar *et al.* (2010), Swapna *et al.* (2014) [2, 15].

The genotype x environment interactions were also significant for grains per panicle, straw yield per plant, kernel length, kernel breadth and amylose content when tested against pooled deviations. The lack of significant G x E interaction for rest of the traits under study indicated that genotypes responded consistently over the environments for these traits. Similar results were reported by reported by, Pande *et al.* (2006), Nayak (2008) and Shinde and Patel (2014) [13, 8, 7]. The results of these traits are not therefore included in the study.

The environment (linear) component was also found non-significant for all the traits except kernel breadth and 100 grain weight when tested against pooled error, indicating the influence of environment on the expression of these characters. Similar results were earlier reported by Narayanswami and Dushyanthkumar (2003), Pande *et al.* (2006), Reddy *et al.* (2015), Haradari *et al.* (2017), Manjunatha *et al.* (2018), Venkatesan and Karthikeyan (2019) [4, 8].

The mean sum of squares due to G x E (pooled deviation) were found to be significant for grains per panicle, straw yield per plant, kernel length and kernel breadth which suggested that the prediction of the performance of genotypes over environment based on regression analysis for these traits might not be very reliable. Similar results were earlier reported by Pande *et al.* (2006), Reddy *et al.* (2015), Haradari *et al.* (2017), Manjunatha *et al.* (2018), Venkatesan and Karthikeyan (2019) [4, 8].

Stability parameters

The stability performance is one of the most desirable properties of a genotype for its wide adaptation. Hence, three stability parameters *i.e.*, mean performance, regression coefficient (b_i) and deviation from regression (S^2_{di}) for parents and their hybrids were estimated and computed as per Eberhart and Russel (1966) [3] to appraise relative stability over different environments.

A genotype is believed to be stable for the trait and adaptable to varied environmental conditions in its performance if it exhibits high mean performance, regression co-efficient is around unity ($b_i=1$) and non-significant deviation from linear regression ($S^2_{di}=0$). However, genotypes with a higher mean value and value of regression coefficient more than unity with non-significant deviation from linear regression were considered to be responsive and suitable for favourable environmental conditions. Further, the genotypes with higher mean values and regression coefficient less than unity or negative and non-significant deviations from linear regression were considered to be responsive and suitable for poor environmental conditions. Accordingly, the genotypes were classified as suitable for varied environmental conditions.

Table 1: Analysis of variance (mean square) for phenotypic stability for different characters in rice

Source of variation	d.f.	Days to 50% flowering	Productive tillers/plant	Plant height (cm)	Panicle length (cm)	Grains per panicle	Grain yield per plant (g)	Straw yield per plant (g)
Genotypes (G)	39	73.73**++	5.52**++	563.34**++	26.74**++	1817.81**++	24.03**++	53.40**++
Environments (E)	2	6.41*	0.861	56.63	7.51*	1696.92*	13.67*	45.02*+
Genotype x Environment (G x E)	78	4.20**	0.243**	71.89**	2.22**	109.02**++	1.03**	3.17**++
E+ (G x E)	80	4.25**	0.25**	71.51**	2.35**	148.71**++	1.34**	4.22**++
Environments (Linear)	1	12.83	1.721	113.26	15.03	3393.84	27.34	90.05
G x E (Linear)	39	4.98**	0.213**	84.58**	1.87**	159.18**++	0.54	4.78**++
Pooled deviation	40	3.33**	0.266**	57.72**	2.51**	57.38**	1.48**	1.59**
Pooled error	234	0.10	0.079	18.43	0.35	27.84	0.42	0.50
Source of variation	D.F.	Kernel length (mm)	Kernel breadth	L:B ratio	100 grain weight (g)	Protein content (%)	Amylose content (%)	
Genotypes (G)	39	0.63**++	0.091**++	0.22**++	0.15**++	1.18**++	5.41**++	
Environments (E)	2	1.53*+	1.16**+	0.67*	0.71**	1.56*	3.53*+	
Genotype x Environment (G x E)	78	0.11**++	0.02**++	0.05**	0.04**	0.30**	0.18**++	
E+ (G x E)	80	0.14**++	0.04**++	0.07**	0.05**	0.33**	0.26**++	
Environments (Linear)	1	3.06	2.33*	1.35	1.42*	3.13	7.07	
G x E (Linear)	39	0.15**++	0.02**++	0.06**	0.042**	0.24**	0.264**++	
Pooled deviation	40	0.068**	0.013**	0.053**	0.041**	0.364**	0.104	
Pooled error	234	0.031	0.003	0.009	0.005	0.038	0.112	

*, ** - indicates 5 % and 1 % probability levels of significance, respectively tested against pooled error

+, ++ - indicates 5 % and 1 % probability levels of significance, respectively tested against pooled deviation.

1. Grains per panicle [Table 2]

The parental mean and cross mean were 189.12 and 225.10, respectively. Out of 40 genotypes, 33 genotypes had non-significant deviation from linear regression, and 20 genotypes had higher grains per panicle than population mean; out of these genotypes, three genotypes were as ($b_i > 1$ and non-significant: one, $b_i = 1$ and non-significant: two and $b_i < 1$ and non-significant: zero) well adapted to various environments.

Among the parental genotypes NVSR-453 (Mean = 191.3; b_i

= 1.00; $S^2_{di} = -11.19$ NS) and hybrid, NVSR-496 x NVSR-418 (Mean = 235.7; $b_i = 1.02$ non-significant; $S^2_{di} = 2.55$ NS) had average stability, whereas hybrid NVSR-6206 x NVSR-418 (Mean = 259.5; $b_i = 1.13$; $S^2_{di} = -6.36$ NS) showing below average stability for grains per panicle.

These results are similar to the findings of Sreedhar *et al.* (2011), Shinde and Patel (2014), Swapna *et al.* (2014), Reddy *et al.* (2015), Pande *et al.* (2006), Manjunatha *et al.* (2018), Al-kordy *et al.* (2019) and Patel *et al.* (2019) [14, 13, 15, 8].

Table 2: Stability parameters of different genotypes for Grains per panicle and Straw yield per plant (g)

Sr. No	Genotypes	Grains per panicle			Straw yield per plant		
		Mean	b_i	S^2_{di}	Mean	b_i	S^2_{di}
1.	NVSR-494	211.9	4.79	74.91	23.87	0.53	-0.08
2.	NWGR-15018	197.5	0.83	-26.90	25.12	0.17	-0.44
3.	NVSR-496	182.0	0.69	12.70	21.03	-0.51	2.10*
4.	NVSR-453	191.3	1.00	-11.19	23.97	0.09	-0.47
5.	NVSR-6172	189.6	0.46	-19.72	23.01	0.13	1.13
6.	NVSR-6206	180.1	0.30	-11.01	20.81	-0.41	0.96
7.	NVSR-2103	187.1	1.01	-29.16	21.38	0.27	3.22**
8.	GR-17	177.7	1.00	27.53	19.64	0.18*	-0.48
9.	GNR-3	184.6	-0.05	-5.70	21.27	0.53	3.65**
10.	NVSR-418	193.0	0.48	-28.95	24.43	0.92	-0.17
11.	NVSR-6287	185.3	0.37	-9.28	23.15	1.36	-0.34
	Parental mean	189.12			22.52		
12.	NVSR-494 x GR-17	228.4	1.20	-26.51	30.09	2.17	2.96**
13.	NVSR-494 x GNR-3	215.9	0.78	35.53	27.67	0.55	0.11
14.	NVSR-494 x NVSR-418	243.6	-0.16	202.86**	32.76	2.18	4.69**
15.	NVSR-494 x NVSR-6287	219.6	1.90	-27.55	28.23	1.51	-0.19
16.	NWGR-15018 x GR-17	238.2	-0.44	-24.47	32.22	1.25	1.35
17.	NWGR-15018 x GNR-3	209.4	0.18	32.58	24.20	-1.79*	-0.47
18.	NWGR-15018 x NVSR-418	259.6	0.63	25.41	35.22	3.90	2.30*
19.	NWGR-15018 x NVSR-6287	239.8	-1.63	-23.52	32.16	-0.16	0.07
20.	NVSR-496 x GR-17	189.7	0.88	46.54	23.40	1.53	-0.43
21.	NVSR-496 x GNR-3	197.8	0.23	185.77**	25.92	0.24	-0.12
22.	NVSR-496 x NVSR-418	235.7	1.02	2.55	31.24	1.10	2.70*
23.	NVSR-496 x NVSR-6287	218.8	1.90	-28.41	28.13	2.09	-0.24

24.	NVSR-453 x GR-17	230.9	-0.76	130.18*	29.20	-0.28	-0.36
25.	NVSR-453 x GNR-3	195.9	3.90	16.26	23.53	0.18	1.28
26.	NVSR-453 x NVSR-418	255.6	-0.23	25.30	34.38	3.38	0.53
27.	NVSR-453 x NVSR-6287	211.6	2.61	337.65**	25.58	-0.35	-0.45
28.	NVSR-6172 x GR-17	242.6	0.39	-19.77	31.60	0.93	0.29
29.	NVSR-6172 x GNR-3	238.6	-0.12	-22.61	28.11	1.66	12.16**
30.	NVSR-6172 x NVSR-418	244.1	1.29	179.12**	31.23	1.94	0.03
31.	NVSR-6172 x NVSR-6287	237.4	-0.06	12.10	30.57	0.48	0.62
32.	NVSR-6206 x GR-17	189.1	3.77*	-28.77	22.51	0.73	-0.38
33.	NVSR-6206 x GNR-3	214.7	-0.48	-25.91	26.52	-0.97	5.54**
34.	NVSR-6206 x NVSR-418	259.5	1.13	-6.36	31.72	6.86	0.22
35.	NVSR-6206 x NVSR-6287	231.1	1.90	167.68**	29.84	2.00	1.51*
36.	NVSR-2103 x GR-17	209.6	1.91	-27.22	27.15	1.25	-0.48
37.	NVSR-2103 x GNR-3	184.5	4.42	94.39*	21.37	0.60*	-0.49
38.	NVSR-2103 x NVSR-418	243.3	0.36	-24.09	31.87	1.68*	-0.49
39.	NVSR-2103 x NVSR-6287	218.1	0.89	-23.96	27.08	1.22	0.43
40.	Gurjari	202.0	1.62*	-29.14	25.50	0.76	-0.35
	Cross mean	225.10			28.70		
	General mean	214.95			26.95		
	S.E. \pm	5.4	0.8		0.87	0.82	

*, ** significant at 5 per cent and 1 per cent of probability levels, respectively.

2. Straw yield per plant [Table 2]

The parental mean and cross mean were 22.52 g and 28.70 g, respectively. Out of 40 genotypes, 30 genotypes had non-significant deviation from linear regression, and 19 genotypes had higher straw yield per plant than population mean; out of these genotypes, five genotypes were as ($b_i > 1$ and non-significant: two, $b_i = 1$ and non-significant: two and $b_i < 1$ and non-significant: one) well adapted to various environments.

Among the parental genotypes, NVSR-418 showing average stability (Mean = 24.43; $b_i = 0.92$; $S^2_{di} = -0.17$ NS) while, NVSR-494 (Mean = 23.87; $b_i = 0.53$; $S^2_{di} = -0.08$ NS)

showed above average stability and specifically adapted to unfavourable environment and NVSR-6287 (Mean = 23.15; $b_i = 1.36$; $S^2_{di} = -0.34$ NS) showing below average stability and specifically adopted to favourable environment.

Among the hybrids, NWGR-15018 x GR-17 ((Mean = 32.22; $b_i = 1.25$; $S^2_{di} = 1.35$ NS) showing below average stability whereas NVSR-6172 x GR-17 (Mean = 31.60; $b_i = 0.93$; $S^2_{di} = 0.29$ NS) had average stability for straw yield per plant.

The results were in correspondence to the findings of Vanave *et al.* (2014), Haradari *et al.* (2017), Patel (2017), Manjunatha *et al.* (2018), Patel (2019) and Patel *et al.* (2019)^[4].

Table 3: Stability parameters of different genotypes for Kernel length (mm) and Kernel breadth (mm)

Sr. No	Genotypes	Kernel length (mm)			Kernel breadth (mm)		
		Mean	b_i	S^2_{di}	Mean	b_i	S^2_{di}
1.	NVSR-494	6.39	1.71	-0.01	2.51	1.63	0.12**
2.	NWGR-15018	6.54	0.27	0.01	2.16	0.65	-0.00
3.	NVSR-496	5.36	2.75	-0.002	2.62	0.47	-0.002
4.	NVSR-453	6.14	1.12	0.04	2.39	0.18	-0.001
5.	NVSR-6172	6.12	0.70	-0.02	2.44	0.66	-0.001
6.	NVSR-6206	5.82	-0.20	0.09*	2.42	1.03	-0.002
7.	NVSR-2103	5.43	1.82	-0.028	2.41	1.13	0.0002
8.	GR-17	5.86	1.21	0.18**	2.44	0.52	-0.002
9.	GNR-3	5.58	1.31	0.13*	2.36	0.81	0.009*
10.	NVSR-418	6.34	1.10	-0.02	2.48	0.92	-0.002
11.	NVSR-6287	6.10	1.11	-0.02	2.48	0.56	-0.002
	Parental mean	5.97			2.43		
12.	NVSR-494 x GR-17	6.00	2.08	0.03	2.46	0.50	-0.002
13.	NVSR-494 x GNR-3	6.17	0.02	-0.02	2.52	-0.26*	-0.002
14.	NVSR-494 x NVSR-418	6.66	0.28	-0.02	2.38	1.31	-0.002
15.	NVSR-494 x NVSR-6287	6.46	0.51	-0.02	2.50	0.74	0.020**
16.	NWGR-15018 x GR-17	6.17	1.38	0.03	2.53	0.36	0.041**
17.	NWGR-15018 x GNR-3	6.01	0.53	-0.005	2.26	0.14	-0.001
18.	NWGR-15018 x NVSR-418	6.90	-1.22	-0.02	2.36	1.63	-0.001
19.	NWGR-15018 x NVSR-6287	6.58	-0.57	-0.01	2.57	0.19	-0.0001
20.	NVSR-496 x GR-17	5.50	2.53	-0.02	2.33	1.40	-0.001
21.	NVSR-496 x GNR-3	5.58	2.68	-0.02	2.10	0.10	0.042**
22.	NVSR-496 x NVSR-418	5.64	2.87	0.28**	2.10	1.29	-0.001
23.	NVSR-496 x NVSR-6287	5.76	1.74	-0.01	2.15	0.66	-0.002
24.	NVSR-453 x GR-17	6.29	0.80	0.01	2.23	1.29	0.002
25.	NVSR-453 x GNR-3	6.25	0.29	-0.02	2.11	0.91	-0.001
26.	NVSR-453 x NVSR-418	6.12	1.61	0.43**	2.25	1.15	0.005
27.	NVSR-453 x NVSR-6287	5.80	3.28	-0.02	2.26	1.13	0.007

28.	NVSR-6172 x GR-17	5.84	1.99	0.044	2.31	1.13	-0.002
29.	NVSR-6172 x GNR-3	6.39	-0.70	0.23**	2.37	1.00	0.01*
30.	NVSR-6172 x NVSR-418	6.49	1.33	-0.02	2.48	0.92	-0.002
31.	NVSR-6172 x NVSR-6287	6.58	0.74	0.05	2.40	1.08	0.003
32.	NVSR-6206 x GR-17	5.49	2.67	0.01	2.09	2.12	0.03**
33.	NVSR-6206 x GNR-3	5.29	3.58	0.007	1.89	2.75	0.004
34.	NVSR-6206 x NVSR-418	6.37	0.57	-0.004	2.42	1.43	-0.001
35.	NVSR-6206 x NVSR-6287	5.50	3.37	0.01	2.12	1.83	0.02**
36.	NVSR-2103 x GR-17	6.48	-0.28	0.05	2.13	2.05	0.02**
37.	NVSR-2103 x GNR-3	6.88	-2.87	0.18**	2.03	2.06	0.02**
38.	NVSR-2103 x NVSR-418	6.94	-1.25	0.02	2.16	2.29	0.06**
39.	NVSR-2103 x NVSR-6287	6.65	-0.90	-0.02	2.58	-0.25	0.002
40.	Gurjari	5.51	-0.05	-0.01	2.20	0.33	-0.001
	Cross mean	6.17			2.29		
	General mean	6.11			2.33		
	S.E. \pm	0.18	0.94		0.08	0.47	

*, ** significant at 5 per cent and 1 per cent of probability levels, respectively.

3. Kernel length [Table 3]

The parental mean and cross mean were 5.97 mm and 6.17 mm, respectively. Out of 40 genotypes, 33 genotypes had non-significant deviation from linear regression, and 22 genotypes had higher kernel length than population mean; out of these genotypes, 10 genotypes were ($b_i > 1$ and non-significant: five, $b_i = 1$ and non-significant: zero and $b_i < 1$ and non-significant: five) well adapted to various environments.

Among the parental genotypes, NVSR-453 (Mean = 6.14; $b_i = 1.12$; $S^2di = 0.04$ NS), NVSR-418 (Mean = 6.34; $b_i = 1.10$; $S^2di = -0.02$ NS) and NVSR-6287 (Mean = 6.10; $b_i = 1.11$; $S^2di = -0.02$ NS) showing below average stability and specifically adapted to favourable environment whereas, NVSR-6172 (Mean = 6.12; $b_i = 0.70$; $S^2di = -0.02$ NS) showing above average stability for kernel length.

Among the hybrids, NWGR-15018 x GR-17 and NVSR-6172 x NVSR-418 showing below average stability whereas, hybrids *viz.*, NVSR-494 x NVSR-6287, NVSR-453 x GR-17, NVSR-6172 x NVSR-6287 and NVSR-6206 x NVSR-418 showing above average stability for kernel length. These results are near about similar to the findings of Swapna *et al.* (2014), Patel (2019) [15].

4. Kernel breadth [Table 3]

The parental mean and cross mean were 2.43 mm and 2.29 mm, respectively. Out of 40 genotypes, 29 genotypes had non-significant deviation from linear regression, and 21 genotypes had higher kernel length than population mean; out of these, 11 genotypes were ($b_i > 1$ and non-significant: four, $b_i = 1$ and non-significant: three and $b_i < 1$ and non-significant: four) well adapted to various environments. Among the parental genotypes, NVSR-6172 (Mean = 2.44; $b_i = 0.66$; $S^2di = -0.001$ NS), GR-17 (Mean = 2.44; $b_i = 0.52$;

$S^2di = -0.002$ NS) and NVSR-6287 (Mean = 2.48; $b_i = 0.56$; $S^2di = -0.002$ NS), showing above average stability and specifically adapted to unfavourable environment whereas, NVSR-418 (Mean = 2.48; $b_i = 0.92$; $S^2di = -0.002$ NS) showing average stability for kernel breadth.

Among the hybrids, NVSR-6172 x NVSR-418 (Mean = 2.48; $b_i = 0.92$; $S^2di = -0.002$ NS) and NVSR-6172 x NVSR-6287 (Mean = 2.40; $b_i = 1.08$; $S^2di = 0.003$ NS) exhibited average stability for kernel breadth. Hybrid NVSR-494 x GR-17 (Mean = 2.46; $b_i = 0.50$; $S^2di = -0.002$ NS) showing above average stability whereas four hybrids *viz.*, NVSR-494 x NVSR-418, NVSR-496 x GR-17, NVSR-6172 x GR-17 and NVSR-6206 x NVSR-418 showing below average stability for kernel breadth. These results are near about similar to the findings of Swapna *et al.* (2014), Patel (2019) [15].

5. Amylose content [Table 4]

The parental mean and cross mean were 25.58 per cent and 24.50 per cent, respectively. Out of 40 genotypes, 37 genotypes had non-significant deviation from linear regression, and 18 genotypes had higher kernel length than population mean; out of these, six genotypes were ($b_i > 1$ and non-significant: three, $b_i = 1$ and non-significant: zero and $b_i < 1$ and non-significant: three) well adapted to various environments.

Among the hybrids, NVSR-494 X GNR-3 (Mean = 24.80; $b_i = 0.75$; $S^2di = -0.11$ NS), NVSR-496 X NVSR-418 (Mean = 26.06; $b_i = 0.79$; $S^2di = -0.10$ NS) and NVSR-6206 x NVSR-418 (Mean = 26.43; $b_i = 0.76$; $S^2di = -0.11$ NS) showing above average stability whereas, NVSR-494 x NVSR-6287, NWGR-15018 x NVSR-418 and NVSR-6172 x NVSR-418 showing below average stability for amylose content.

These findings similar with Shinde and Patel (2014) [13].

Table 4: Stability parameters of different genotypes for Amylose content (%)

Sr. No	Genotypes	Amylose content (%)		
		Mean	b_i	S^2di
1.	NVSR-494	26.33	0.34	-0.10
2.	NWGR-15018	27.23	0.34*	-0.11
3.	NVSR-496	27.07	-3.09	0.45*
4.	NVSR-453	26.12	0.46	0.18
5.	NVSR-6172	27.36	0.61*	-0.11
6.	NVSR-6206	24.22	0.33	-0.11
7.	NVSR-2103	24.86	0.57*	-0.11
8.	GR-17	23.20	0.62	-0.11

9.	GNR-3	23.89	0.47*	-0.11
10.	NVSR-418	25.87	0.53**	-0.11
11.	NVSR-6287	25.24	0.50*	-0.11
	Parental mean	25.58		
12.	NVSR-494 x GR-17	25.25	3.35	0.12
13.	NVSR-494 x GNR-3	24.80	0.75	-0.11
14.	NVSR-494 x NVSR-418	26.45	-0.39	-0.02
15.	NVSR-494 x NVSR-6287	25.39	1.25	-0.07
16.	NWGR-15018 x GR-17	25.30	0.17	-0.09
17.	NWGR-15018 x GNR-3	24.02	3.57	0.31
18.	NWGR-15018 x NVSR-418	26.39	1.31	-0.09
19.	NWGR-15018 x NVSR-6287	23.28	3.04	0.24
20.	NVSR-496 x GR-17	25.58	-0.05	-0.10
21.	NVSR-496 x GNR-3	25.59	2.09	0.06
22.	NVSR-496 x NVSR-418	26.06	0.79	-0.10
23.	NVSR-496 x NVSR-6287	23.08	0.32	-0.10
24.	NVSR-453 x GR-17	22.27	0.94	-0.11
25.	NVSR-453 x GNR-3	24.12	0.62*	-0.11
26.	NVSR-453 x NVSR-418	23.71	4.12	0.55*
27.	NVSR-453 x NVSR-6287	24.37	2.49	0.04
28.	NVSR-6172 x GR-17	24.66	0.37	-0.08
29.	NVSR-6172 x GNR-3	24.13	0.65	-0.11
30.	NVSR-6172 x NVSR-418	26.52	1.12	-0.11
31.	NVSR-6172 x NVSR-6287	23.66	1.33	-0.11
32.	NVSR-6206 x GR-17	23.33	1.01	-0.11
33.	NVSR-6206 x GNR-3	23.89	2.32	0.03
34.	NVSR-6206 x NVSR-418	26.43	0.76	-0.11
35.	NVSR-6206 x NVSR-6287	23.44	1.28	-0.10
36.	NVSR-2103 x GR-17	22.43	1.59	-0.11
37.	NVSR-2103 x GNR-3	24.25	0.68	-0.11
38.	NVSR-2103 x NVSR-418	24.17	1.79	-0.09
39.	NVSR-2103 x NVSR-6287	23.42	0.80	-0.11
40.	Gurjari	24.42	0.10	0.61*
	Cross mean	24.50		
	General mean	24.80		
	S.E. ±	0.22	0.76	

*, ** significant at 5 per cent and 1 per cent of probability levels, respectively.

Table 5: Stable hybrids identified for five traits in rice

Sr. No.	Characters	Different environment (bi=1)	Unfavorable environment (bi<1)	Favorable environment (bi>1)
1.	Grains per panicle (g)	NVSR-496 x NVSR-418.	-	NVSR-6206 x NVSR-418.
2.	Straw yield (g)	NVSR-6172 x GR-17	-	NWGR-15018 x GR-17.
3.	Kernel length (mm)	-	NVSR-494 x NVSR-6287, NVSR-453 x GR-17, NVSR-6172 x NVSR-6287, NVSR-6206 x NVSR-418	NWGR-15018 x GR-17, NVSR-6172 x NVSR-418.
4.	Kernel breadth (mm)	NVSR-6172 x NVSR-418, NVSR-6172 x NVSR-6287.	NVSR-494 x GR-17,	NVSR-494 x NVSR-418, NVSR-496 x GR-17, NVSR-6172 x GR-17, NVSR-6206 x NVSR-418.
5.	Amylose content (%)	-	NVSR-494 x GNR-3, NVSR-496 x NVSR-418, NVSR-6206 x NVSR-418.	NVSR-494 x NVSR-6287, NWGR-15018 x NVSR-418, NVSR-6172 x NVSR-418.

Summary and Conclusion

Among 11 parents, NVSR-453 for grains per plant, NVSR-418 for straw yield per plant and NVSR-418 for kernel breadth exhibited average stability. Hybrids, NVSR-496 x NVSR-418 for grains per plant, NVSR-6172 x GR-17 for straw yield per plant while, NVSR-6172 x NVSR-418 and NVSR-6172 x NVSR-6287 for kernel breadth had shown average stability. A population with preponderance of additive genetic variance would lead to the improvement of a character through selection in segregating generations. The presence and magnitude of various components of non-

additive gene effect could be justified with heterosis breeding. Whereas, in case of equal magnitude of both additive and non-additive components of genetic variance, population improvement scheme such as reciprocal recurrent selection would be more effective.

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