



Identification of suitable genotypes of lentil (*Lens culinaris*) for improved adaptation to rice fallow areas of Gangetic Alluvial Zone

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Received: 01 July 2022; Accepted: 13 July 2023

ABSTRACT

Rice fallows (RF) are the low lying *kharif* sown rice (*Oryza sativa* L.) areas that remain uncropped due to dearth of suitable cultivars of winter (*rabi*) pulses. A panel of 30 promising high yielding lentil (*Lens culinaris* Medik.) genotypes of diverse origin were assessed at both no till RF and with till condition at the Regional Research Sub-station (RRSS), Chakdah under the aegis of Bidhan Chandra Krishi Vishwavidyalaya, Nadia, West Bengal for two years (2019–20 and 2020–21). Multi-trait performance (earliness, biomass and grain yield) of each genotype was considered during recommendation of suitable genotype for specific ecology deploying GGE biplot. The present study recommended IC 560183 for no till RF ecology and Moitree, IC 559996, ILL 7978 and L 1112-19 for with till ecology having specific adaptation. Additionally, 2011S-56212-2 and ILL 8006 were identified as ideal and desirable genotypes for both the ecologies and therefore, recommended for commercial cultivation across the areas of Gangetic alluvial zone for augmenting lentil production and productivity.

Keywords: Desirability index, GE interaction, Lentil, Rice fallow, Stability

Globally, lentil (*Lens culinaris* Medik.) is farmed as a significant cool-season staple legume in 5.51 million hectares' area with production of 6.54 million tonnes (FAOSTAT 2018). Being a coffer of prebiotic carbohydrates, vitamins and essential minerals, lentil hold immense place in the food platter of many developing countries including India. A major share of rice fallow (RF) areas of around 11.65 million ha in Indo Gangetic plains and central zone of India remains fallow during winter season after harvesting of monsoon rice due to technological and socio-economic constrains (Maji *et al.* 2019). Therefore, targeting rice fallow areas through introduction of winter legumes like lentil will augment production and productivity with better sustenance (Pramanik *et al.* 2020).

Choosing early-maturing lentil genotypes with the highest potential yield and stable performance in RF niches is of paramount importance to the breeders for improving self-sufficiency in lentil production. However, there is no report till date regarding recommendation of suitable

genotypes of lentil for RF ecology considering genotypic stability on multiple traits. The foremost way of comparing several genotypes in target environments provides crucial information for selecting and endorsing crop cultivars for the release (Yan and Tinker 2006). Several univariate and multivariate statistical methodologies are available to analyse the genotype \times environment (GE) interaction and subsequently to recommend a suitable genotype for a specific environment. Recently, genotype main effect plus genotype by environment interaction (GGE) biplot is commonly extended for understanding the cause of GE interaction to ensure better identification of ideal genotypes and test environment in many pulses (Das *et al.* 2019, Das *et al.* 2020). The present investigation aimed to develop a selection index to resolve the ambiguities emerged due to multiple traits association followed by deployment of selection index in GGE biplot analysis as a variable for appraisal of superior lentil genotypes for their suitability in RF niches considering the important yield traits.

MATERIALS AND METHODS

The present study was carried out with 30 lentil genotypes of diverse origin consisting of germplasm accessions, advanced breeding lines and released varieties. These materials were grown in no till RF and with till conditions for two years 2019–20 and 2020–21 at Regional Research Sub-station (RRSS), Chakdah (23° 05' N; 88°

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54' E; altitude of 14 m amsl) under the aegis of Bidhan Chandra Krishi Viswavidyalaya, Nadia, West Bengal. In no till condition of fallow ecology, lentil was sown after harvesting of rainy (*kharif*) season rice in a narrow furrow between the rows of the preceding rice maintaining the left-over rice stubbles of 20 cm length in the field whereas standard cultivation protocol was followed for the normal till condition. Among the 4 different environments, no till RF ecology for the two years 2019–20 and 2020–21 were henceforth designated as E1 and E3, respectively, whereas E2 and E4 were with till ecology for the same pre-mentioned years. The genotypes were grown in a randomized complete block design (RCBD) with 3 replications maintaining proper plant geometry of 6 rows each of 3 m length with 25 cm spacing between rows and having a plot size of 4.5 m². To grow a productive crop, standard agronomic procedures were used. Data were recorded for days to 50% flowering, biological yield (kg/ha) and seed yield (kg/ha). Yield data were recorded at physiological maturity from the whole plot and expressed in kg/ha using the plot size as factor.

Analysis of variance (ANOVA) was performed to elucidate the effects of environments, genotype and their interactions over the years across the locations using R software (R Development Core Team 2018). Mean significant difference within genotypes and environments was computed by LSD test at P=0.05 probability level. Hierarchical cluster was generated using Ward method to exhibit the relatedness of the genotypes and environments. Considering the days to 50% flowering, plant biomass and seed yield of the lentil genotypes, Base Linear Phenotypic Selection Index was generated (BLPSI) following genetic correlation matrix of these traits. The combined data were formed both using the genotypes and the environments. This index value was utilized as a variable in GGE biplot based on the first two principal components (PC) resulting from singular value decomposition (SVD) of the mean selection index for the second principal component (PC2).

$$Y_{ij} = \mu + e_j + \sum_{n=1}^N \lambda_n \gamma_{in} \delta_{jn} + \varepsilon_{ij}$$

where Y_{ij} , yield of the i^{th} genotype ($i=1, \dots, I$) in the j^{th} environment ($j=1, \dots, J$); μ , grand mean; e_j , environment deviations from the grand mean; λ_n , The eigen value of PC analysis axis; γ_{in} & δ_{jn} , genotype and environment principal components scores for axis n ; N , number of principal components retained in the model; ε_{ij} , error term $\sim N(0, \sigma^2)$.

For genotype evaluation Average Environment Coordination (AEC) view of the GGE biplot was constructed which facilitated genotype comparisons based on mean of BLPSI and stability across environments within a mega-environment (Yan 2002). Correspondingly, for test environments appraisal, the discriminating power vs. representativeness view of the GGE biplot was prepared where the ideal test environment should be able in both discriminations of the genotypes and representative of the average environment (Yan *et al.* 2007). In addition, to ascertain superiority of the genotypes in different test environments, which-won-where view of the GGE biplot was prepared (Yan and Tinker 2006).

RESULTS AND DISCUSSION

Mean per se performance of the genotypes: Analysis of variance and relative contribution of each source of variation to the total variations is depicted in Table 1. The ANOVA revealed that for all the traits the effects of genotype (G), environment (E) and genotype \times environment (GE) interaction were significant. Regarding relative contribution of each source of variation it was observed that in case of all the 3 characters under study, environment was the major contributor to the total variation. In case of days to 50% flowering and biological yield, environment contributed 75.68 and 43.90% of the total variation, respectively. However, for seed yield, the contribution of environment was 47.25% of the total variation. The effect of genotypic

Table 1 Analysis of variance of 30 lentil genotypes evaluated in 4 environments

Trait	Source of variation	Degrees of freedom	MSS	P value	Per cent contribution of TSS
50% flowering	Geno	29	133.7401	<0.001	11.56
	Env	3	197.5115	<0.001	75.68
	Geno \times Env	87	6.0188	<0.001	10.22
	Residuals	120	1.08173	<0.001	2.53
Biological yield (kg/ha)	Geno	29	1565178	<0.001	31.33
	Env	3	10795328	<0.001	43.90
	Geno \times Env	87	42049.61	<0.001	3.54
	Residuals	120	182868.3	<0.001	21.23
Seed yield (kg/ha)	Geno	29	245845.8	<0.001	35.61
	Env	3	1790909	<0.001	47.25
	Geno \times Env	87	9737.266	<0.001	5.61
	Residuals	120	14482.41	<0.001	11.52

P<0.01; *P<0.001.

variance followed the contribution of environment in all the traits. Residual variance contributed more than GE effect in all the traits except for days to 50% flowering. In earlier literature, Gauch and Zobel (1997) confirmed that in multi-environment trial (MET) data, environment is the main sources of variation and should contribute more than 80% of the total variation. In soybean (Bhartiya *et al.* 2017), fieldpea (Das *et al.* 2019), mungbean (Das *et al.* 2020), chickpea (Tamang *et al.* 2021) and lentil (Bhattacharya *et al.* 2022), published reports corroborated with the present findings where environment variation was highest among the sources of variation. In the present study, variation due to GE interaction was also significant which depicted the importance of reckoning stable genotypes based on their least interaction with environment (Rakshit *et al.* 2012).

The mean per se performance of individual genotype over varied locations along with BLPSI is presented in Table 2. Across the locations, among the genotypes 2011S-56212-2 was the highest yielder (1589.86 kg/ha) followed by IC 560183 and ILL 8006 whereas L 1112-19 was the earliest flowering genotype followed by L 1112-17 and IC 560183. Similar trend of seed yield was also detected in biological yield where 2011S-56212-2 showed the best vegetative growth with exceptionally good plant biomass followed by IC 560183 and ILL 8006. Wide variability was observed for the studied traits: 50% flowering ranged from 55 to 72 days, biological yield ranged from 2757.03 to 4727.92 kg/ha and seed yield varied from 838.81 to 1589.86 kg/ha. The genotypic performance in individual location depicted that the highest seed yield was obtained at E4 followed by E2 i.e. at with till condition. However, at no till condition (E1 and E3), genotypes matured early. The highest plant biomass was observed in E4 whereas lowest plant biomass was detected at E3. The BLPSI value indicates the ideal genotype to be selected considering multiple key traits for a specific environment. In our study, combined mean BLPSI value considering days to 50% flowering, biological yield and seed yield of 30 lentil genotypes detected that 2011S-56212-2 was the ideal one with the highest index value followed by IC 560183 and ILL 8006. Contemplating mean BPLSI, it was observed that RKL 22-10 was the poor performer across both the ecologies. Among the environments the combined performance of the genotypes was observed the best in E4 (with till) and poorest in E3 (no till). In the present study, we had visualized the GE effect based on the combined yield trait performance of lentil genotypes where beside yield performance, earliness and plant biomass were also taken into consideration which are the key traits for judging the performance of lentil at rice fallow niche (Maji *et al.* 2019).

Evaluation of genotypes across the environments based on mean vs. stability: Mean performance and stability of the genotype across the locations were graphically portrayed through AEC view of the yield-trait combination biplot (Fig 1). The AEC coordination view of the biplot is basically genotype-metric-preserving (SVP=1) biplot considering combined performance of the genotypes to

visualize genotype discrimination. The first two principal components (PCs) explained 99.38% variation for yield-trait combination which affirmed the previous reports (Yan *et al.* 2007) regarding the adequate elucidation of the biplot analysis. The genotypes having greater vector length from the AEC abscissa are less stable and *vice versa*. It can be clearly depicted that G10 followed by G2 and G15 were the good performer considering their multi-trait performance whereas, G11, G29, G4 were the poor performers as they placed in the extreme left side of the AEC ordinate. The most stable genotype was G27 (IC 281600) followed by G6 (Moitree) G10 (2011S-56212-2) and G15 (ILL 8006) having short projection from AEC abscissa, though, the performance of G27 and G6 was moderate. The present study demonstrated that G10 was the most ideal genotype as it performed well in terms of combined yield-trait profile coupled with high stability. Genotypes placed in proximity to ideal genotype were considered as desirable genotypes and the distance between them should be considered as the Euclidian distance (Yan and Tinker 2006). Though G2 was positioned in proximity of ideal genotype (G10) however, owing to its incongruous performance G15 was the most suitable candidate to be considered as desirable genotype. This strategy has been utilized in previous studies for selecting ideal genotype (Gore *et al.* 2021) considering single trait performance. Genetic homeostasis or buffering capacity of genotypes determines their sensitivity with environments. So, genotypes with low homeostasis exhibit high responsiveness towards environments.

Environment appraisal based on discriminativeness vs. representativeness: In the GGE biplot approach, discrimination power (ability to discriminate genotypes), representativeness (representation ability corresponding to

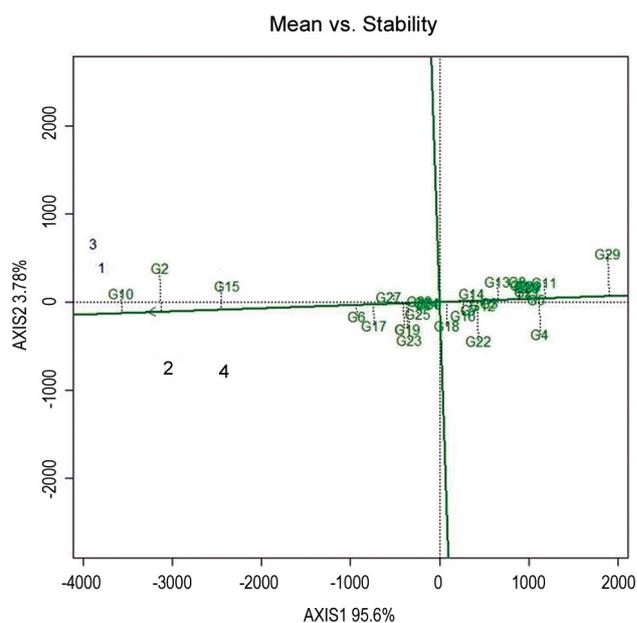


Fig 1 GGE biplot of mean vs. stability analysis of 30 lentil genotypes studied in 4 environments considering combined yield trait profile.

Table 2 Mean performance as well as selection index considering yield trait combination of the 30 lentil genotypes evaluated in 4 environments

Code	Genotype/Environments	Days to 50% flowering	Biological yield (kg/ha)	Seed yield (kg/ha)	BPLSI
<i>Based on genotype</i>					
G1	IC 560335	66.26	3729.78	1058.67	4854.71
G2	IC 560183	57.13	4581.44	1505.73	6145.05
G3	RKL 16-304	57.88	3356.69	938.81	4352.63
G4	BCL-10209	61.81	3142.69	899.90	4104.40
G5	LL 1522	62.60	3048.61	980.95	4092.16
G6	Moitree	62.75	3822.40	1218.52	5103.67
G7	ILL 10802	71.98	3341.80	1058.07	4471.86
G8	4605/4380/2SPS	66.66	3109.00	1003.49	4179.16
G9	KLS 1451	60.10	3210.51	902.76	4173.37
G10	2011S 56212-2	59.02	4727.92	1589.86	6376.81
G11	IC 560212-S1	57.48	3077.12	898.53	4033.13
G12	ILL 5883	58.46	3274.60	1064.31	4397.38
G13	LIRL-22-46	62.02	3202.51	1028.28	4292.82
G14	ILL 10951	68.11	3305.26	1072.57	4445.94
G15	ILL-8006	61.25	4315.49	1441.34	5818.08
G16	BM 8	68.4	3420.36	1026.87	4515.62
G17	IC 559996	62.08	3756.45	1193.8	5012.33
G18	IC 560111	66.94	3472.70	1072.67	4612.31
G19	ILL 7978	57.83	3637.06	1143.03	4837.92
G20	ILL 10961	63.06	3087.92	986.69	4137.67
G21	Masoor	60.70	3091.28	984.66	4136.63
G22	L 1112-17	54.98	3310.89	1085.88	4451.75
G23	L 1112-19	54.69	3696.63	1082.38	4833.70
G24	ILL 8006-S3	64.26	3512.24	1129.78	4706.28
G25	IPL 539	62.60	3652.32	1044.51	4759.44
G26	WBL 58	60.50	3219.46	847.03	4126.99
G27	IC-281600	59.01	3660.00	1160.75	4879.76
G28	ILL 10971	59.81	3656.07	1024.37	4740.25
G29	RKL 22-10	58.22	2757.03	838.81	3654.16
G30	2011S-56234-1	62.48	3529.95	1103.64	4696.08
<i>Based on environment</i>					
E1	No till (2019–20)	59.70	3240.00	989.77	4289.45
E2	With till (2019–20)	63.27	3716.01	1139.90	4919.18
E3	No till (2020–21)	60.50	3040.95	897.54	3999.00
E4	With till (2020–21)	63.10	3963.86	1291.01	5317.98
Mean		61.63	3490.20	1079.55	
Range (Min -Max)		54.69-71.98	2757.03-4727.92	838.81-1589.86	
LSD		2.38	335.41	108.20	

mega environment) and desirability index are the critical factors for identification of captivating testing locations and exclude out redundant one. In the discriminativeness vs. representativeness biplot the lines that connect the test environments are known as environment vectors. The biplot indicated that all the test environments exhibited acute angles with each other (Fig 2) which indicate their close relationship (Yan and Tinker 2006). E1 and E3 exhibited acute angles between their vectors and E2 and E4 revealed same response too. So, it can be deduced that these environments were positively correlated and having closer relationship with each other. Among the 4 environments, E1 and E3 were the most discriminative environments. The test environments' representativeness is displayed by projecting them onto the average environment axis (AEA). Environments with a good discrimination power and less representativeness such as E3 would be meaningful for winnowing genotypes with specific adaptation. Representativeness of the environment is generally denoted by angle between environment vectors and AEC. Environment with smallest angle with AEC is the most representative environment (Yan and Tinker 2006). It was observed that E1 (no till RF) reflected a smaller angle with AEC. The desirability index of the testing locations is the cumulative response of both the discriminating power and representativeness. The E1 with the highest desirability index (4.89), was identified as the ideal or Type-I testing environment for the appraisal of genotype with general adaptability (Table 3).

Identification of which-won-where: Another important feature of GGE biplot is identifying genotype for a specific test environment in the form of which-won-where graphical representation. In this graph a polygon was first drawn on genotypes that are positioned outermost from the biplot

Table 3 Standardized test location evaluation parameters

Environment	Discriminating power	Representativeness	Desirability index
E1	4.96	0.98	4.89
E2	4.53	0.98	4.44
E3	4.86	0.97	4.72
E4	4.55	0.96	4.38

origin so that all the other genotypes are placed within polygon (Yan 2002). Genotypes at the vertices of the polygon are either the best or poorest in one or more environments. Following that, perpendicular lines were formed from the biplot's origin to each side of the polygon, dividing the biplot into many sectors, each with a single genotype at the polygon's vertex. The perpendicular lines are termed as equality lines (Yan 2002). The equality lines partitioned the graph into six sectors of which all the 4 environments were present in a single sector (Fig 3). Among the 30 genotypes, G10 and G2, were in the vertices, thus, considered as the winning genotypes for no till RF ecology (E1 and E3). For with till ecology, G6, G17, G19 and G23 were the most promising genotypes under study. This strategy has been applied previously for mega environment identification in many crops (Singh *et al.* 2020, Gore *et al.* 2021).

The present study indicated that all the studied traits exhibited enormous variability with significant $G \times E$ interaction. GGE biplot and selection index judiciously appraised the lentil genotypes for specific environment based on their stability patterns. Finally, considering combined yield trait performance G10 (2011S-56212-2) could be recommended as ideal/best performing genotype whereas

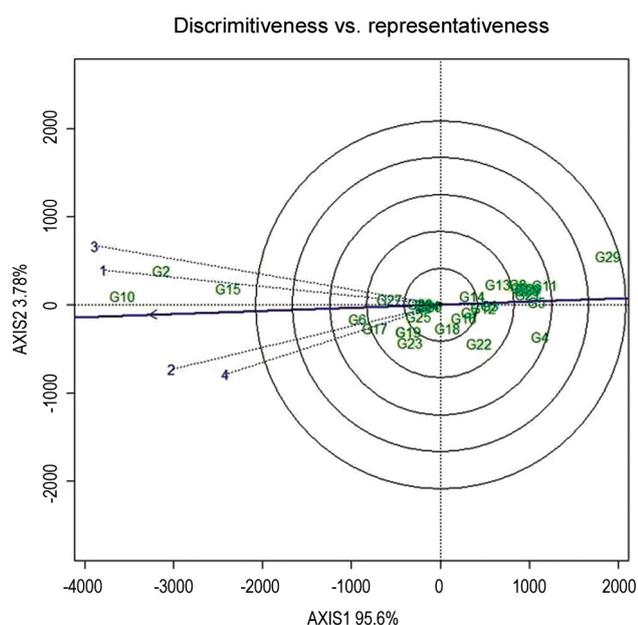


Fig 2 Discriminativness vs. representativeness of 30 lentil genotypes in 4 different environments based on combined yield trait profile.

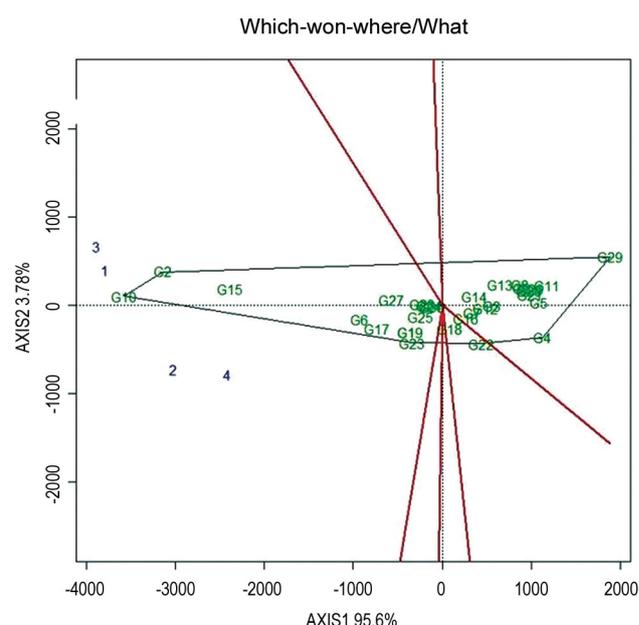


Fig 3 Which won where graph of 30 lentil genotypes studied in 4 different environments based on combined yield trait profile.

G15 (ILL 8006) as desirable genotype for both (with till and no till) the ecologies. All the testing environments were present in a single sector that further validated that, meagre differences were present between the no till and with till condition. Identification of ideal test environment E1 (no till of first year) can strengthen the substantial selection of testing environments for future trials. To the extent that we know, this is the first report of appraisal of lentil genotypes considering multiple traits at no till RF ecology. Irrespective of poor yield of lentil in rice-fallow condition, some genotypes performed equally well in both the ecologies and exhibited stable performance. The present study prudently advocated specific lentil genotypes, viz. G2 (IC 560183) for no till RF ecology and G6 (Moitree), G17 (IC 559996), G19 (ILL 7978) and G23 (L 1112-19) for with till ecology that will facilitate the lentil growers of this zone for best selection of their cultivars towards achieving sustenance and better nutritional security.

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