International Journal of Bioresource Science
Citation: IJBS: **11**(01): 27-33, June 2024
DOI: 10.30954/2347-9655.01.2024.4

ASSOCIATION FOR AGRICULTURE ENVIRONMENT AND BIOTECHNOLOGY

RESEARCH PAPER

Synchronized Selection of White Seeded Finger Millet (*Eleusine coracana* L.) Genotypes for Yield and Stability

N. Anuradha[1*], TSSK Patro[1], Nagappa Govankoppa[2], C. Nandini[3], Y. Sandhya Rani[1], U. Triveni[1] and P. Kranthi Priya[1]

[1]Agricultural Research Station, Vizianagaram, Acharya NG Range Agricultural University, Andhra Pradesh, India
[2]University of Agricultural Sciences, Dharwad, India
[3]College of Agriculture, Gandhi Krishi Vigyana Kendra, Bengaluru, India

*Corresponding author: anuradha.pragnya@gmail.com (**ORCID ID:** 0000-0001-6244-9143)

Received: 20-02-2024 **Revised:** 09-05-2024 **Accepted:** 22-05-2024

ABSTRACT

A multi-location field experiment was conducted with 39 white seeded finger millet genotypes including one check which were laid out in Randomized Block Design (RBD) with two replications at research station farms of Vizianagaram, Bangaluru, Hanumanmatti, Mandya, Ranchi and Coimbatore. The study aimed to identify stable white seeded finger millet genotypes across the locations. AMMI analysis and thirteen stability indices based on AMMI were estimated and further non-parametric method of simultaneous selection index was calculated. Large portion of variation was captured by locations (66.7%) followed by GEI and genotypes. Four principal components significantly contributed 94.6% GEI. The AMMI1 biplot identified VR 1000 27.9 q/ha) and GE 4803 (25.7 q/ha) as stable high yielding genotypes. AMMI2 biplot identified GE 4943, GE 4916, GE 2329, GE 5155 and PRM 901 as highly stable genotypes irrespective of yield. Thirteen AMMI based stability indices revealed that PRM 901, GE 2329, PRM 902 and GE 4916 were most stable genotypes. However, synchronized selection for yield and stability revealed VR 1000 as the best white seeded finger millet with both high yield and stable expression over six locations.

HIGHLIGHTS

- Large amount of Environmental variation dominated more compared to interaction and genotypic variation.
- GEI was significantly explained by four interaction principal components.
- Genotypes; VR 1000 and GE 4803 recorded more than 25 q/ha as well as highly stable as per AMM1 Biplot.
- AMM1 based stability parameters identified GE 4943, GE 4916, GE 2329, GE 5155 and PRM 901 as stable among high yielders.
- Non parametric indices for synchronized selection revealed, R 1000 as the best white seeded finger millet over multi environments.

Keywords: Stability, Finger millet, AMMI, Simultaneous selection

Millets are crops of antiquity and are source of food assurance in semi-arid regions of Asia and Africa. They are small-grained cereals and belong to grasses family. Millets are mainly classified as major millets which include Sorghum and Pearl millet and minor millets which include finger millet, foxtail millet, kodo millet, browntop millet, barnyard millet, proso millet, little millet and foeno. After Sorghum and pearl millet, finger millet (*Eleusine coracana* L. Garetn) is the third most important millet crop grown in many states of India. It is an allotetraploid crop with basic chromosome number $2n = 4x = 36$. It is rich in micronutrients and especially for

How to cite this article: Anuradha, N., Patro, T.S.S.K., Govankoppa, N., Nandini, C., Sandhya Rani, Y., Triveni, U. and Kranthi Priya, P. (2024). Synchronized Selection of White Seeded Finger Millet (*Eleusine coracana* L.) Genotypes for Yield and Stability. *Int. J. Bioresource Sci.*, **11**(01): 27-33.

Source of Support: IUCEA; **Conflict of Interest:** None

calcium it has three times than that in milk and 10 times more compared to other major cereals. It is also rich in antioxidants and fibre content which helps in reducing diabetes and heart disease. Moreover, the crop can be grown under diverse climatic conditions. It thrives even under harsh environments such as sandy rocky soils with less or minimal irrigation facilities (Maitra *et al.* 2022; Shailja *et al.* 2023; Ambati Mounika *et al.* 2023).

The yield of a genotype is determined by the potential of a genotype and also the environment in which it is grown. In other words, Genotype × environment interaction (GEl) is a major factor in the final output of the yield which is quiet challenging to a breeder to bred a genotype which yields high at all environments. Further, it is impossible to assess the yield of a genotype at broader level when the selection and evaluation was done at one environment only. Stable expression of yield is an important aspect of yield trials. Multi location evaluation helps to estimate the GEI. Additionally, partitioning of the variation into main effects and interaction effects will help to resolve the issue to some extent and helps in identifying better stable genotypes. However, identifying stable genotypes is of limited use until and unless the genotype has high yield. Considering both high yield and its stability is utmost important for successful breeding of a cultivar (Anuradha *et al.* 2022; Rao and Prabhakaran, 2005).

MATERIALS AND METHODS

A set of 39 white seeded finger millet genotypes (Table 1) obtained from All India Coordinated Research Project (AICRP) on Small millets, ICAR-Indian Institute of Millet Research (IIMR), Hyderabad were evaluated in a Randomized Block Design with two replications during *Kharif* 2010 at six locations which include research Station farms of Vizianagaram, Bangaluru, Hanumanmatti, Mandya, Ranchi and Coimbatore. Each genotype was sown in four rows of 3 meters length with a spacing of 22.5 × 10 cm. At the time of seeding, a fertiliser dose of 60:40:30 kg NPK/ha (full P and K plus 50% N) was applied, and seeds were sown by hand dibbling. Three weeks after sowing, the remaining 50% N was added. During the crop-growing season, standard pest management procedures were followed.

The data was subjected to statistical analysis and estimates of GEI and interaction principal components were obtained using AMMI analysis as suggested by Gauch *et al.* (1996). Unlike regression models, the AMMI analysis captures non-linear GEI and uses singular value decomposition (SVD) to break down residual matrices once main effects are fitted. Further estimates of stability indices like ASV (Purchase,1997), AMMI-based stability parameters (ASTAB, Rao and Prabhakaran, 2005), sum across environments of the absolute value of GEI mode (AVAMGE; Zali *et al.* 2012), Zhang's D parameter (DZ; Zhang *et al.* 1998), averages of the squared eigen vector values (EV; Zobel, 1994), stability measure based on fitted AMMI model (FA; Zali *et al.* 2012), MASI (Ajay *et al.* 2018b), MASV (Ajay *et al.* 2019), sums of absolute value of the interaction principal component (IPC) scores (SIPC; Sneller *et al.* 1997) and absolute value of the relative contribution of IPCs to the interaction (Za; Zali *et al.* 2012), were estimated and their synchronized selection indices were also estimated for concurrent selection The Spearman's rank correlations among all the 13 stability values were computed.

RESULTS AND DISCUSSION

The statistical analysis for the yield of 39 white seeded finger millet genotypes at six locations recorded significant variation for locations, genotypes and GEI (Table 1).

Locations contributed a large portion of total variation (66.7%), whereas the GEI and genotypes contributed about 21.9 and 5.6%, respectively. Furthermore, the analysis revealed that GEI was significantly explained by the first four PC and the cumulative percent of four PCs was 94.6%. This is in accordance with Molla *et al.* (2013), Seyoum *et al.* (2019) in finger millet and Patro *et al.* (2022) in groundnut where they observed higher variance for environments than genotypes, however Anuradha *et al.* (2022) recorded minimal variance for grain yield in finger millet. Four principal components were significant and the first two contributing to 70% of GEI. Few earlier workers (Sood *et al.* 2017; Mamo *et al.* 2018) in finger millet noticed nearly 90% of GEI by the first two Principal components.

The AMMI1 biplot which shows the relationship between the genotypes and locations was presented as "grain yield vs. PC1 scores" (Fig. 1). The

Table 1: ANOVA and AMMI ANOVA of 39 white seeded finger millet over six locations

Source of variation	Degrees of freedom	Mean sum of squares	Pr(>F)	% contribution toward total variation	Cumulative
REP (ENV)	6	7.0	0.62		
ENV	5	5085	2.93E-08	66.68	
GEN	38	56.2	< 2.2e-16	5.60	
ENV: GEN	190	44.0	< 2.2e-16	21.93	
Residuals	228	9.5			
PC1	42	87.1	0.00	43.7 ofGEI	43.7
PC2	40	54.9	0.00	26.3 ofGEI	70.0
PC3	38	31.4	0.00	14.3 ofGEI	84.3
PC4	36	23.9	0.00	10.3 ofGEI	94.6
PC5	34	13.3	0.08	5.4 ofGEI	100

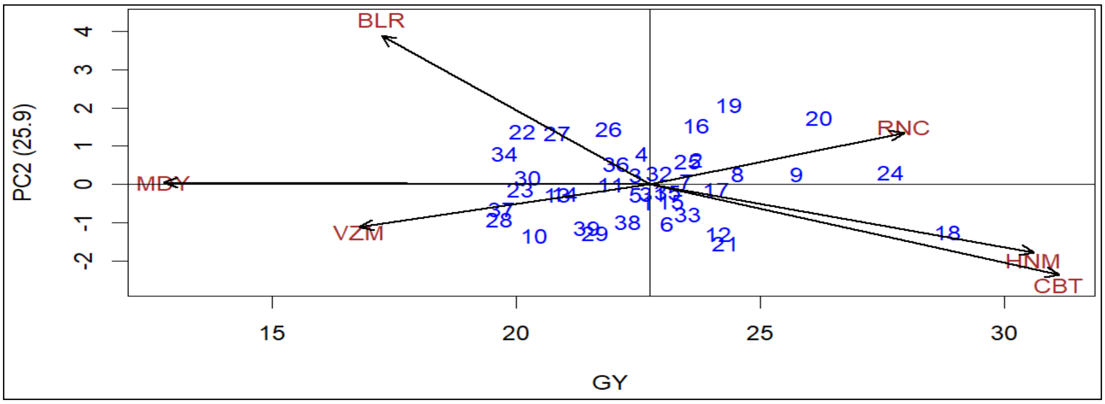

Fig. 1: AMMI1 biplot for 39 white seeded finger millet

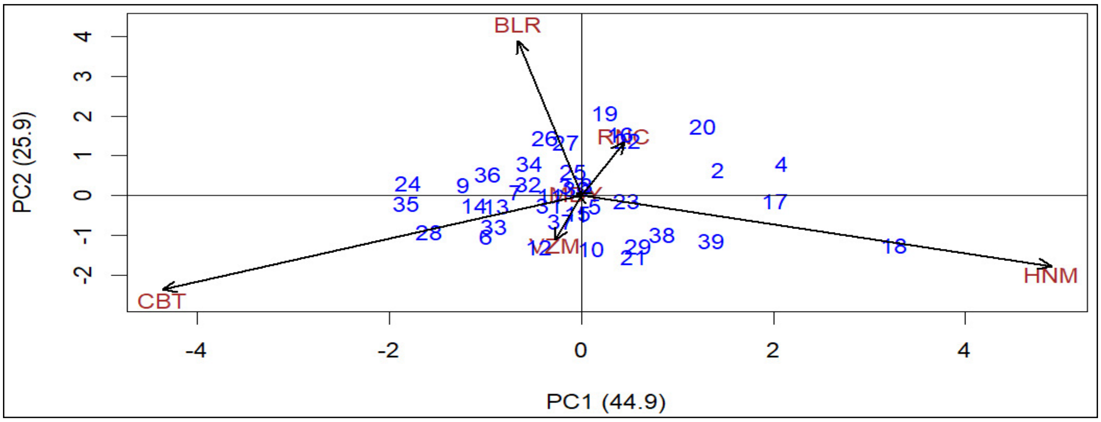

Fig. 2: AMMI2 biplot for 39 white seeded finger millet

genotypes 24 (VR 1000) and 9 ((GE 4803) were having more than the average yield score (27.9 q/ha and 25.7 q/ha respectively) and are very nearer to the X-axis indicating that both of them are highly stable with higher grain yield while the genotype, 18 (GE 4921, 28.9 q/ha) was far away from X-axis and was nearer to Hanumanmatti and Coimbatore locations indicating its specific adaptation to those two locations. On the other side, 30 (PRM 9-1, 20.1 kg/ha) and 23 (GE 5387, 20.1 kg/ha) were poor yielders with high stability. The location Mandya was the farthest from biplot origin, with long vector denoting strong interaction forces while Vizianagaram was having shorter vector and was nearer to the origin implying weak interaction forces. The AMMI2 biplot with PC1 and PC2 on X and Y axes (Fig. 2) which is an indicative of stability showed genotypes, 1 (GE 4943), 3 (GE 4916), 8

(GE 2329), 11 (GE 5155) and 30 (PRM 901) were at the centre of origin demonstrating highly stable genotypes. Biplots are helpful for visualization of the stability and performance of genotypes but the actual scores of stability indices will let us know the exact ranking of genotypes based on stability or yield. Moreover, the significance of more than two PCs indicates the necessity of the stability estimates which can cover the all the significant PCs (Anuradha *et al.* 2022; Ajay *et al.* 2019). Thirteen stability estimates which were based on AMMI analysis were given in Table 2 and the correlations among stability estimates were given in Fig. 3. AMGE and EV were almost nearer to zero score and hence not listed in the table. All the stability estimates had higher and positive correlation which can be viewed by the dark-red colour of boxes. Anuradha *et al.* (2022) in finger millet and Ajay *et al.* (2020) in peanut had observed quiet analogous results. PRM 901, GE 2329, PRM 902 and GE 4916 were found to be most stable genotypes as demonstrated in almost all the stability estimates. However, except GE 2329, rest three genotypes recoded below average yield while GE 2329 recorded just nominal above average yield.

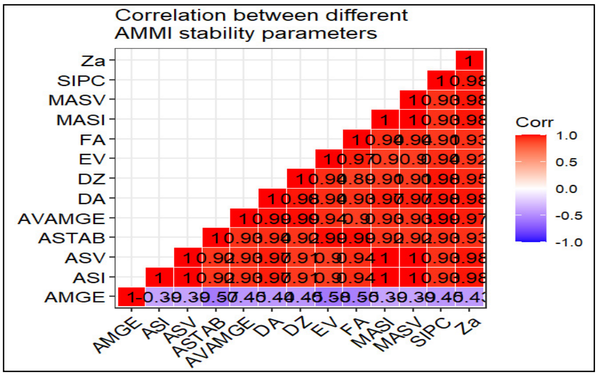

Fig. 3: Correlation among various stability indices

Table 2: Eleven stability index scores for 39 white seeded finger millet

Genotype	Entry	Yield (q/ha)	ASI	ASV	ASTAB	AVAMGE	DA	DZ	FA	MASI	MASV	SIPC	Za
1	GE 4943	22.5	0.1	0.4	1.6	11.0	6.3	0.3	39.3	0.2	1.7	2.1	0.1
2	GE 5103	23.5	0.6	2.5	3.8	20.5	11.4	0.4	129.4	0.7	2.9	3.3	0.2
3	GE 4916	22.5	0.1	0.4	0.9	8.4	4.7	0.2	21.9	0.2	1.3	1.5	0.1
4	GE 5087	22.5	0.9	3.6	5.7	24.4	14.9	0.4	223.0	0.9	3.9	3.9	0.2
5	GE 4969	22.3	0.1	0.3	1.4	11.1	5.8	0.2	34.2	0.2	1.6	1.6	0.1
6	GE 6834-1	23.1	0.5	2.0	2.7	18.3	9.7	0.3	94.1	0.5	2.7	3.0	0.1
7	VR 984	23.4	0.3	1.2	1.9	15.8	7.3	0.3	53.5	0.4	1.9	2.5	0.1
8	GE 2329	24.6	0.1	0.3	0.3	4.5	2.6	0.1	6.8	0.1	0.7	0.9	0.0
9	GE 4803	25.7	0.6	2.2	5.0	26.1	12.4	0.4	153.3	0.6	3.3	3.5	0.2
10	VR 996	20.3	0.3	1.3	4.6	17.7	11.0	0.4	121.7	0.4	3.2	3.7	0.1
11	GE 5155	21.9	0.1	0.6	1.3	9.9	5.4	0.2	29.2	0.2	1.3	1.8	0.1
12	GE 6834	24.2	0.4	1.5	2.5	14.6	8.9	0.3	79.9	0.4	2.7	2.9	0.1
13	GE 4853	20.9	0.4	1.5	2.3	18.4	8.5	0.3	72.0	0.4	2.3	2.4	0.1
14	GE 4885	21.1	0.5	1.9	2.6	18.9	9.3	0.3	87.3	0.5	2.4	2.9	0.1
15	GE 5141	23.2	0.1	0.5	3.7	20.6	9.3	0.4	86.2	0.3	2.5	3.1	0.1
16	VR 997	23.8	0.4	1.7	4.3	22.4	11.0	0.4	121.7	0.5	3.2	3.4	0.1
17	GE 4945	24.2	0.9	3.4	6.6	32.9	15.2	0.5	232.0	0.9	3.9	4.4	0.2
18	GE 4921	28.9	1.5	5.6	13.3	40.3	23.1	0.6	532.0	1.5	6.1	6.0	0.3
19	GE 728	24.3	0.6	2.1	4.5	22.9	12.2	0.4	149.4	0.6	3.9	2.8	0.1
20	VR 998	26.1	0.7	2.8	5.3	22.8	13.6	0.4	184.2	0.7	3.9	3.9	0.2
21	GE 5042	24.3	0.5	1.8	5.1	25.0	11.9	0.4	141.0	0.5	3.4	3.7	0.1
22	VR 999	20.1	0.4	1.6	2.3	17.1	8.9	0.3	78.3	0.4	2.7	2.4	0.1
23	GE 5387	20.1	0.2	0.8	0.8	10.0	4.7	0.2	22.4	0.2	1.2	1.6	0.1
24	VR 1000	27.9	0.5	1.9	2.2	16.1	8.7	0.3	74.8	0.5	2.1	2.2	0.1

25	VR 936	23.8	0.2	0.6	3.0	16.1	8.7	0.3	75.9	0.3	2.5	2.5	0.1
26	SURVA	22.0	0.4	1.6	2.4	18.5	8.9	0.3	79.2	0.4	2.8	2.2	0.1
27	JWM-1	20.9	0.4	1.4	2.2	18.3	8.4	0.3	70.1	0.4	2.6	2.3	0.1
28	PRM 801	19.6	0.8	2.9	3.6	23.9	12.0	0.3	143.6	0.8	3.2	3.0	0.2
29	PRM 802	21.6	0.4	1.6	2.6	16.8	9.0	0.3	80.9	0.4	2.7	2.9	0.1
30	PRM 901	20.2	0.1	0.2	0.4	5.7	3.0	0.1	9.1	0.1	0.8	1.1	0.0
31	PRM 902	22.8	0.2	0.7	0.4	6.6	3.5	0.1	12.4	0.2	0.9	1.1	0.0
32	VL 356	22.9	0.3	1.0	3.0	16.9	8.6	0.4	73.7	0.3	2.1	3.1	0.1
33	VL 360	23.5	0.5	1.8	2.9	15.9	9.6	0.3	92.0	0.5	2.6	3.2	0.1
34	Indaf 11	19.8	0.3	1.2	2.7	15.7	8.7	0.3	76.0	0.4	2.5	3.2	0.1
35	VR 1034	23.1	0.8	3.1	3.5	19.9	12.2	0.3	149.2	0.8	3.1	2.1	0.1
36	GPU 71	22.1	0.5	1.7	1.4	13.9	7.4	0.2	55.1	0.5	2.0	2.0	0.1
37	GE 4922	19.6	0.2	0.7	1.9	13.3	6.8	0.3	46.9	0.2	1.8	2.4	0.1
38	GE 526	22.3	0.4	1.7	2.0	14.8	8.3	0.2	68.8	0.4	2.4	2.4	0.1
39	GE 4976	21.3	0.6	2.5	4.5	23.4	12.4	0.4	153.3	0.7	3.5	4.0	0.2

Table 3: Synchronized ranking of 39 white seeded genotypes for yield and stability

Genotype	Entry	AMGE_ SSI	ASV_ SSI	ASTAB_ SSI	AVAMGE_ SSI	DA_ SSI	DZ_ SSI	MASI_ SSI	MASV_ SSI	SIPC_ SSI	Za_SSI
1	GE 4943	9	4	7	6	6	8	9	5	9	9
2	GE 5103	3	21	19	18	20	18	21	17	19	23
3	GE 4916	24	8	6	5	5	6	6	6	6	6
4	GE 5087	5	37	35	37	36	34	37	35	35	35
5	GE 4969	17	6	8	10	8	7	8	7	7	7
6	GE 6834-1	18	22	16	19	25	11	23	22	23	28
7	VR 984	11	7	4	8	4	4	7	4	11	8
8	GE 2329	6	1	1	1	1	1	1	1	1	1
9	GE 4803	16	15	17	21	21	20	15	15	15	15
10	VR 996	19	29	38	33	37	39	31	37	39	36
11	GE 5155	20	13	9	11	10	12	12	10	12	12
12	GE 6834	13	5	5	3	7	5	4	9	8	10
13	GE 4853	37	32	31	35	27	31	34	28	29	31
14	GE 4885	38	36	33	36	34	33	36	29	33	34
15	GE 5141	7	2	24	25	17	30	5	12	24	5
16	VR 997	25	14	22	22	22	24	16	24	26	17
17	GE 4945	4	23	29	28	28	29	27	26	30	29
18	GE 4921	1	20	20	20	23	21	20	20	21	19
19	GE 728	8	17	15	17	19	13	17	25	4	11
20	VR 998	2	18	18	12	18	17	18	23	17	18
21	GE 5042	10	12	23	24	16	25	13	19	20	16
22	VR 999	27	35	34	34	33	28	35	36	32	33
23	GE 5387	29	26	21	23	24	22	22	21	25	24
24	VR 1000	22	10	2	2	2	2	10	2	2	2
25	VR 936	23	3	14	9	9	19	3	11	10	4
26	SURVA	34	27	27	31	30	23	24	33	18	21
27	JWM-1	36	28	28	32	26	27	26	32	28	25

28	PRM 801	39	39	39	39	39	38	39	39	36	39
29	PRM 802	14	25	30	27	32	32	28	31	31	32
30	PRM 901	31	16	12	14	13	16	14	14	14	13
31	PRM 902	26	9	3	4	3	3	2	3	3	3
32	VL 356	32	11	25	16	11	26	11	8	27	14
33	VL 360	21	19	11	7	15	15	19	13	22	22
34	Indaf 11	30	33	36	30	35	37	32	34	37	37
35	VR 1034	33	34	26	26	31	14	33	27	5	27
36	GPU 71	35	31	10	13	12	9	30	16	13	20
37	GE 4922	28	30	32	29	29	35	29	30	34	30
38	GE 526	15	24	13	15	14	10	25	18	16	26
39	GE 4976	12	38	37	38	38	36	38	38	38	38

Simultaneous selection indices of giving rank were followed as per Ajay *et al.* (2020) where, 39th was given to lowest yielder and 1st rank given to highest yielder, but, in case of stability index, the highest score was given 39th rank and lowest score as 1st rank. Consequently, both the ranks were added for a genotype and then the final rank was given, the less score genotype was given the first rank and so on. In that pattern the ranks obtained for various simultaneous selection indices were given in table 3 which helps in synchronized selections of genotypes for yield and stability. The same ranking pattern was observed for ASI and ASV based simultaneous selection indices. Similarly for DA and FA; DZ and EV. From this table, it was observed that GE 2329 ranked first twelve times followed by VR 1000 which ranked first for nine times. Nevertheless, GE 2329 (24.6 q/ha) has nominal increase over mean value while VR 1000 (27.9 q/ha) was high yielding with greater stability. Henceforth, synchronized selection for yield and stability in white seeded finger millet, revealed that VR 1000 was both high yielding and stable in expression over six locations. Anuradha *et al.* (2022) in finger millet and Ajay *et al.* (2020) in peanut had earlier applied the simultaneous selection indices to identify better performing genotypes.

ACKNOWLEDGEMENTS

The authors are highly thankful to Acharya NG Ranga Agricultural University, Guntur and All India Coordinated Research Project on Small Millets, GKVK, Bengaluru for providing necessary facilities, plant material and financial support.

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