Plant Archives Vol. 26, No. 2, 2026 pp. 987-997 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org

DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2026.v26.no.2.134

HARNESSING GENETIC VARIABILITY AND DIVERSE SEASONAL PERFORMANCE BASED SELECTION FOR STABLE FINGER MILLET GENOTYPES WITH HIGHER GRAIN YIELD

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(Date of Receiving-20-06-2026; Date of Revision-28-08-2026; Date of Acceptance-04-09-2026)

ABSTRACT

Diet imbalance among humans arises due to excessive consumption of cereals that are deficient in certain amino acids, minerals, micronutrients, and fiber. Finger millet, as one of the millets with a nutrient-rich and climate-resilient nature, was targeted to improve grain yield and its associated traits. The finger millet genotypes comprised 72 and 79 recombinant inbred lines (RILs) in Summer 2020 (E1) and *Kharif* 2020 (E2), respectively, along with 10 advanced breeding lines (ABLs) and eight check varieties. These lines were grown at GKVK, Bengaluru, across three seasons, E1, E2 and Summer 2021 (E3). Mean sum of squares of ANOVA for traits *viz*., plant height (cm), days to 50 percent flowering, number of productive tillers, finger length (cm), grain yield plant^{-1} (g), and 1000-grain weight (g) revealed significant differences ($p<0.01$) among genotypes (RILs/ABLs and checks) in E1 and E2.To assess the stability of grain yield, 15 genotypes (11 RILs/ABLs and four checks) were selected for the third season, E3, based on the *per se* performance of the mean grain yield reported from E1 and E2. Across three seasons, the stability and genotype-environment interaction (GEI) of 15 genotypes for grain yield were assessed using additive main effects and multiplicative interaction (AMMI), genotype, and genotype-by-environment (GGE) interaction models. RILs/ABLs 9-2, 65-4, 103-2, 36-3-1, and 93-1 expressed superior and stable grain yield across the three seasons and the same will be forwarded for ascertaining adaptability across diverse locations. The selected finger millet genotypes will be utilized for breeding varieties with higher-grain yield and enriched nutrients.

Key words : Finger millet, RILs/ABLs, Stability, AMMI model, G×E interaction, GGE biplot.

Introduction

There is a paradigm shift from cereals to millets due to drastic yield losses in cereals because of climate change factors, like terminal heat stress due to heat waves, etc. With the importance of nutrition, advancements in food processing technologies for consumption, and millets as a less resource-intensive crop, they have come into the spotlight. Millet production in Asia occupies 50.10 percent of the share, followed by Africa (47.30%), Europe (1.30%), and Oceania (0.10%). India ranks first in millet production with 11.57 million metric tonnes, accounting for 39.70% of global production, followed by Niger with 3.84 million metric tonnes (USDA, 2024-25). Finger millet is one of the minor millets that offers a source of food, fodder, forage, energy and nutritional security. It can be consumed as cakes, cookies, and biscuits, etc. Finger millet, as an ecologically sustainable crop, draws attention nowadays. Finger millet (*Eleusine coracana* L. Gaertn), known as 'ragi', belongs to the family Poaceae and is a highly self-pollinated crop. Its chromosome number is 2n=4x=36 (AABB, tetraploid) (Choudhary *et al*., 2025). *Eleusine coracana* originated from *Eleusine africana* as a gene introgression mutant (Hilu and Wet, 1976). India leads in Asia, covering an area of 1.23 million hectares and producing 1.83 million metric tonnes, with a productivity of 1,492 kg ha^{-1} (DA and FW, New Delhi,

2024-25). It is grown under various agro-climatic and agroecological zones (Ashoka and Halikatti, 1997). Genetic variability and stability analysis of genotypes based on grain yield and its related traits helps in evolving high-yielding varieties. Selecting high-yielding genotypes (G) should not depend just upon grain yield *per se*; their contributing traits also play a key role. When genotypes are grown in different seasons/environments, they show wide fluctuations in their yield ability. Hence, studies on genotype × season/environment interaction (GEI), which inform about the stability of grain yield and its related traits, are imperative. Lack of stable and bumper-yielding varieties is one of the major setbacks for increasing the production of finger millet. The first step in plant breeding is assessment and selection of superior and stable-yielding genotypes across seasons before releasing them as a variety. Hence, the research study was carried out with the objectives (i) genetic variability in RILs/ABLs, (ii) identification of promising RILs/ABLs for seed yield and its component traits, and (iii) differential performance of RILs/ABLs across three seasons, along with highly adapted promising varieties as check varieties. This study collectively provides a comprehensive understanding of the genetic variability and stability of the evaluated finger millet genotypes for diverse seasons.

Materials and Methods

Genetic materials

The material consists of 72 and 79 recombinant inbred lines (RILs), F_{11}-generation advanced lines derived from the cross between IE 2885 and IE 2912, in Summer 2020 (E1) and *Kharif* 2020 (E2) 'respectively' and 10 advanced breeding lines (ABLs) along with eight check varieties *viz.*, KMR-630, KMR-204, KMR-301, MR-6, GPU-66, GPU-67, GPU-48 and ML-365 procured from "AICRP on Seed (Crops), National Seed Project, GKVK, Bengaluru" were common in both season/environments *i.e.*, in E1 and E2. For the next season, Summer 2021 (E3), promising 11 RILs/ABLs, along with four check varieties (viz., KMR-204, KMR-301, KMR-630, and MR-6), were selected and evaluated for their stability performance in terms of grain yield and its attributing traits across three seasons, E1, E2 and E3.

Field evaluation

The study was carried out at "AICRP on Seed (Crops), National Seed Project, GKVK, Bengaluru" during Summer 2020 (E1), *Kharif* 2020 (E2) and Summer 2021 (E3). The augmented design comprised 10 blocks and eight check varieties, which were replicated twice in each block, along with randomized RILs/ABLs in two seasons/environments, *i.e.*, E1 and E2. Observations were recorded on five randomly selected plants in each row for plant height (cm), days to 50 percent flowering, number of productive tillers, finger length (cm), grain yield plant^{-1} (g) and 1000-grain weight (g). The criteria to choose check varieties were their better agronomic performance in all seasons.11 promising RILs/ABLs that outperformed or were on par with all the 8 check varieties were selected for the third season based on the *per se* performance of grain yield from among the RILs/ABLs which were grown in the previous two seasons, i.e., E1 and E2. In the third season/environment, i.e., Summer 2021 (E3), the trial was laid out in a randomized complete block design (RCBD) (Panse and Sukhatme 1985) with two replications.

Statistical analysis

Genetic variability parameters

Genetic variability parameters and analysis of variance (ANOVA) for augmented design (Federer and Raghavarao, 1975) were performed for genotypes in E1 and E2 separately with the statistical package 'Augmented RCBD' (Mendiburu, 2019) using a programming language, R-studio V. 3.6.2. Bar diagram with error bars for grain yield among 15 genotypes was prepared with the package 'ggplot2 V. 3.5.1' (Wickham, 2016) using a R programming language, RStudio 2024.12.1. Pearson's correlation coefficient (r) for grain yield and its contributing traits was ascertained using the package 'correlation V. 0.8.7' and the correlation graph was illustrated in package 'corrplot version 0.95' (Friendly, 2002) with RStudio 2024.12.1.

AMMI ANOVA

The selected stable and superior lines that were grown across three seasons/ environments were subjected to the additive main effects and multiplicative interaction (AMMI) model (Gauch and Zobel, 1988). Analysis was implemented using AMMI analysis in "Analysis of variance by ANOVA, REML or regression" with the help of the software 'Genstat V. 18.1'.

$$Y_{ij} = \mu + G_i + E_j + \sum_{k=1}^{n} \lambda_k \alpha_{ik} \gamma_{jk} + \in_{ijk}$$

Where, Y_{ij}, μ, G_i, E_j, λ_k, α_{ik} γ_{jk} and $\in_{ijk}$ are trait mean of ith genotype in the jth season /environment, seasonal/ environmental trait means, ith genotype mean deviation from seasonal /environmental trait mean, jth season/ environment mean deviation from seasonal/environment trait mean, square root of the eigen value of the kth interaction principal component (IPC) axis, the IPC scores for kth IPC of ith genotype, the IPC scores for kth IPC of

j^{th} season/environment and Residual, respectively.

Genotype and genotype-by-environment (GGE) interaction biplot analysis

Genotype and genotype-by-environment (GGE) interaction biplot analysis (Yan *et al*., 2000) was illustrated by genotype × environment analysis with R (GEA-R v.4.1). Four views of the GGE biplot were harnessed here to decipher genotype and G×E interaction for 15 genotypes across the three seasons (Asghar *et al*., 2010). (i) Discriminativeness and representativeness of test seasons/environments view of GGE biplot. In the present study, discriminating ability and representativeness of the test season/environment relative to grain yield plant^{-1} (g) across three seasons/environments were deciphered in the GGE biplot graph. (ii) Average environment coordination axis (AEC) view of the GGE biplot based on genotype-focused scaling for ranking of the test genotypes relative to the ideal genotype; the ideal genotype is the one whose point is located in the center of concentric circles in the GGE biplot.In the present study, ranking RILs/ABLs and checks was based on the ideal RIL/ABL or check (which is superior in mean performance) for grain yield plant^{-1} (g) across three seasons/environments, represented in the GGE biplot graph (iii) AEC view of bi-plot based on season/ environment-focused scaling for interpreting mean performance of the genotypes *vs* their stability patterns. In the present study, the stability of the RIL/ABL or check for grain yield plant^{-1} (g) across three seasons/ environments can be known based on the position of the RIL/ABL or check away from the origin and this can be known by the length of the projection from the average environment axis **(**AEA) shown in the GGE biplot graph. (4) Polygon view of GGE bi-plot based on symmetrical scaling for determining 'which-won-where/what' pattern of genotypes with test season/environment. One of the features of the 'GGE biplot graph' is its ability to display the 'which–won–where/what' pattern of genotypes. The vertices of the polygon are occupied by either a winning genotype or an inferior genotype in a particular season/ environment. The "which won where/what" graph shows which genotype gives the highest yield plant^{-1} in which season/environment and that particular genotype is called the winning genotype; these winning genotypes are present at the vertices of the polygon (Yan andTinker, 2006). Thus, a polygon view of a GGE bi-plot indicates the presence or absence of cross-over GEI (Yan and Rajcan, 2002).

Results and Discussion

The present investigation disclosed significant genetic variability among the tested genotypes. ANOVA (Augmented design) for characters *viz*., plant height (cm), days to 50 percent flowering, number of productive tillers, finger length (cm), grain yield plant^{-1} (g) and 1000-grain weight (g) revealed significant differences among RILs/ ABLs chosen in Summer 2020 and *Kharif* 2020 (Table 1). For breeding stable and high-yielding varieties of finger millet, finger millet RILs/ABLs were grown across the seasons (Fentie *et al*., 2013).

ANOVA and genetic variability for grain yield and its contributing attributes under study

The traits *viz*., plant height, number of productive tillers plant^{-1}, days to 50 percent flowering, finger length, 1000 grain weight and grain yield plant^{-1} differed significantly among finger millet RILs/ABLs (Table 1). This was inferred by the significant mean sum of squares for all traits in E1 and E2 (Suryanarayana *et al*., 2019). This indicated that the genotypes for the traits under study were genetically diverse in E1 and E2, as studied in Gebreyohannes *et al*. (2025). Genetic variability revealed that the PCV for all the traits studied was higher than the GCV values (Table 2). For days to 50 percent flowering, low genotypic (GCV percent: 6.52 in E1 and 6.12 in E2) and phenotypic coefficients of variation (PCV percent: 8.82 in E1 and 8.41 in E2) were observed, coupled with moderate heritability (54.70 percent in E1 and 52.90 percent in E2). The narrow difference between the estimates of PCV and GCV indicated little influence of season on the expression of (Table 2). Plant height exhibited low GCV percent (8.61-9.89) and moderate PCV percent (9.13-11.17 percent) across seasons, with high heritability (78.42 percent in E1 and 89 percent in E2), suggesting the influence of additive gene action and effectiveness of selection for this trait. The high PCV (29.62 percent) and high GCV (21 percent) were recorded for the productive tillers plant^{-1} in Summer 2020 (SR and Patil, 2013), along with moderate to high heritability (50.26 percent in E1 and 71.92 percent in E2). High heritability was observed for finger length (>94 percent) with moderate GCV and PCV in both seasons (Lule *et al*., 2012). This indicated the role of the additive component of genetic variance, where selection would be effective for the trait. The 1000-grain weight displayed moderate GCV and PCV with very high heritability (>95 percent). A narrow difference between the estimates of PCV and GCV indicated a marginal influence of season on the expression of 1000 grain weight and finger length in both E1 and E2 (Table 2). Higher PCV (20.46 percent) and GCV (19.38 percent) were recorded for grain yield plant^{-1} in E1, with a high heritability of 89.69 percent (Malambane and Jaisil, 2015). Grain yield plant^{-1} exhibited

Table 1 : Analysis of variance for finger millet genotypes (RILs/ABLs and checks) evaluated during Summer 2020 and *Kharif* 2020.

Source of variation	Degrees of freedom		DFF		PH		NPT		FL		TW		GYP	
Season (E)	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2
Blocks	9	9	72.30**	6.97	290.58**	16.36	0.66	0.01	0.09	0.06	0.02	0.05	2.78	6.45
Genotype (G)	89	96	56.43**	7.42 ns	176.56**	170.19**	2.59**	1.07 **	1.66 **	0.01 **	0.27**	0.26 **	42.46**	36.95**
RILs/ABLs	81	88	37.55**	5.37ns	144.85**	102.94**	2.35**	0.41 **	1.33 **	0.01 **	0.13**	0.13 **	18.60**	33.60**
Checks	7	7	275.30**	34.22**	50 7.89**	961.05**	5.06**	6.17 **	5.00**	0.03 **	1.88**	1.88 **	276.64**	72.84**
RILs/ABLs *vs* checks	1	1	53.33ns	0.03*	425.79**	552.51**	5.06*	23.48**	4.55 **	0.03 **	0.84**	1.22 **	336.34**	80.72**
Error	63	63	17.01	5.23	31.26	11.32	1.17	0.11	0.07	0.01	0.02	0.05	1.92	6.78

E1: Summer 2020; E2: *Kharif* 2020; RILs/ABLs: Recombinant inbred lines/Advanced breeding lines; ns: nonsignificant; * and ** indicate significance at P<0.05 and 0.01, respectively; DFF: Days to 50 percent flowering; PH: Plant height(cm); NPT: Number of productive tillers; FL: Finger length (cm);TW:1000-grain weight (g);GYP: Grain yield plant^{-1} (g).

Table 2 : Genetic variability for grain yield and its attributing traits among finger millet genotypes evaluated during Summer 2020 and *Kharif* 2020.

Trait	Mean		Genetic variability parameters							
			GCV		PCV		h^2		GAM	
	E1	E2	E1	E2	E1	E2	E1	E2	E1	E2
Days to 50 percent flowering	69.32±0.66	55.3±0.22	6.52	6.12	8.82	8.41	54.70	52.90	9.95	9.15
Plant height (cm)	108.14±1.24	111.16±1.05	9.89	8.61	11.17	9.13	78.42	89.00	18.07	16.76
Number of productive tillers	5.21±0.16	3.25±0.07	21.00	16.62	29.62	19.60	50 .26	71.92	30.71	29.08
Finger length (cm)	7.51±0.17	6.79±0.09	19.68	12.48	19.93	12.82	97.53	94.81	41.18	25.07
1000-grain weight (g)	3.28±0.04	3.30±0.05	10.37	10.63	10.54	10.69	96.76	95.14	22.25	22.07
Grain yield plant^{-1} (g)	21.07±0.48	18.58±0.58	19.38	27.88	20.46	31.20	89.69	79.84	37.86	51.38

E1: Summer 2020; E2: *Kharif* 2020; GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; h^2: Broad sense heritability; GAM: Genetic advance as percent mean.

high GCV (27.88 percent in E2) and PCV (31.20 percent), along with high heritability (79.84 percent in E2) (Table 2).

Estimates of broad-sense heritability were medium for the number of productive tillers plant^{-1}, days to 50 percent flowering, and high heritability for plant height, 1000 grain weight, finger length and grain yield plant^{-1} in E1. High heritability for the number of productive tillers plant^{-1}, finger length, 1000 grain weight, and grain yield plant^{-1} was recorded in E2, indicating ample scope for improvement of grain yield by selecting these contributing traits. The trait 'grain yield plant^{-1} (E2)' contributed more to variability, and it was followed by the trait 'number of productive tillers' (E1). The difference between PCV and GCV was lower for most of the traits, suggesting a negligible role of environment in the expression of traits; therefore, improvement by phenotypic selection was possible. High estimates of PCV and GCV, accompanied by high heritability for finger length (cm), 1000-grain weight (g), and grain yield plant^{-1} (g) and plant height (cm) for both seasons, indicate a greater opportunity for improvement of grain yield through selection of these traits.

Variability parameters and correlation studies for grain yield and its associated traits

The mean, standard error, minimum value, maximum value, absolute range, and standardized range for grain yield and its associated traits of RILs/ABLs and check varieties of both seasons were given (Table S1). In E1, the standard error was high for all traits except for 1000-grain weight (g) and grain yield plant^{-1} (g) when compared

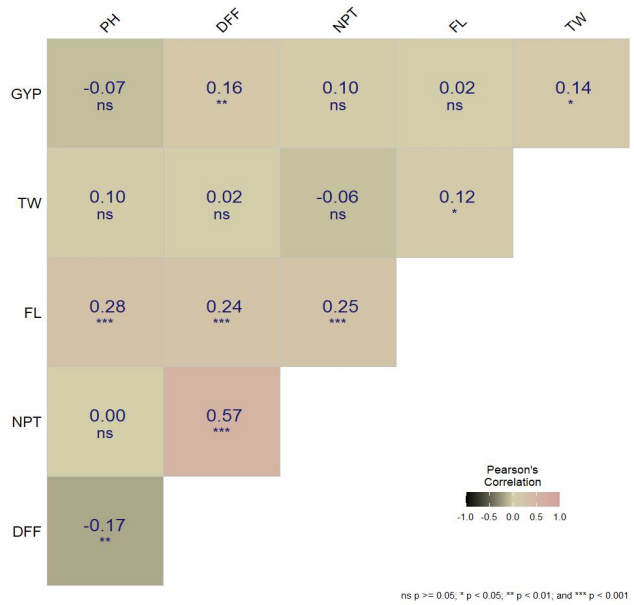


Fig. 1 : Corrgram for grain yield plant^{-1} (g) and its associated traits. PH: plant height (cm), DFF: days to 50 percent flowering, NPT: number of productive tillers, FL: finger length (cm), GYP: grain yield plant^{-1} (g),TW:1000-grain weight (g);***: Significant at 0.001 level; **:Significant at 0.01 level; *:Significant at 0.05 level; ns: Non significant at 0.05 level.

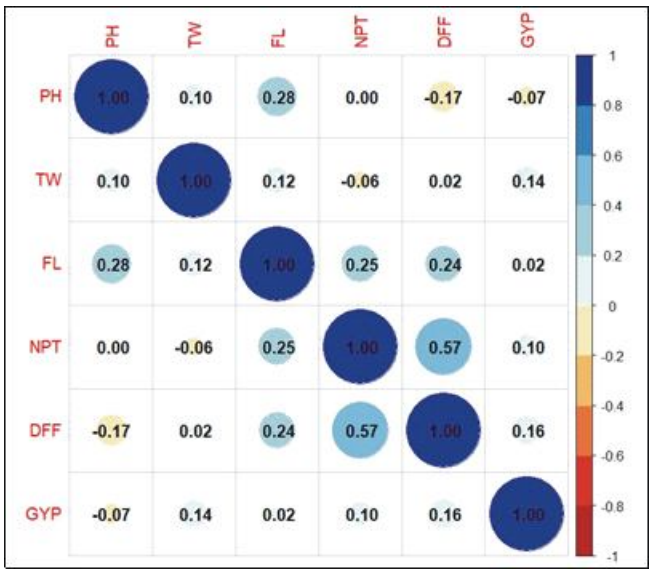


Fig. S1 : Detailed Correlation plot for grain yield plant^{-1} (g) and its associated traits. PH: plant height (cm); DFF: days to 50 percent flowering; NPT: number of productive tillers, FL: finger length (cm); GYP: grain yield plant^{-1} (g); TW:1000-grain weight (g);***: Significant at 0.001 level; **: Significant at 0.01 level; *: Significant at 0.05 level; ns: Non significant at 0.05 level.

Table S1 : Descriptive statistics for grain yield and its attributing traits among finger millet genotypes evaluated during Summer 2020 and *Kharif* 2020.

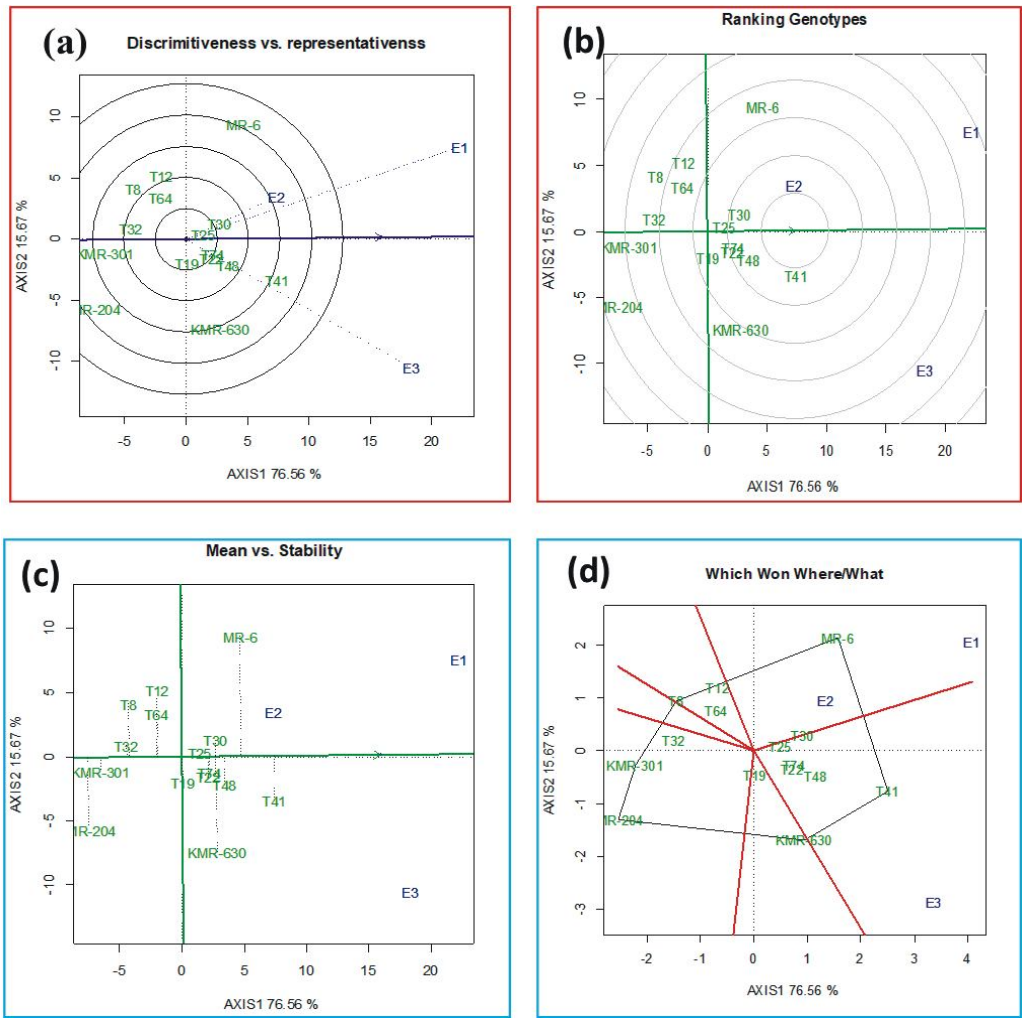
Trait	Minimum value		Maximum value		Absolute range		Standardized range	
	E1	E2	E1	E2	E1	E2	E1	E2
DFF	52.04	50.28	83.04	62.03	31.00	11.75	0.45	0.21
PH	71.17	80.72	132.17	133.71	61.00	52.99	0.56	0.48
NPT	2.96	2.01	8.96	5.00	6.00	2.99	1.15	0.92
FL	4.03	4.09	13.42	8.66	9.39	4.57	1.25	0.67
TW	2.57	2.33	4.07	4.17	1.50	1.84	0.46	0.56
GYP	12.40	8.26	33.62	32.52	21.22	24.26	1.01	1.31

E1: Summer 2020; E2:*Kharif* 2020; DFF: Days to 50 percent flowering; PH: Plant height(cm); NPT: Number of productive tillers; FL: Finger length (cm); TW:1000-grain weight (g); GYP:Grain yield plant^{-1} (g).

Table S2 : AMMI ANOVA for 15 finger millet genotypes evaluated across three seasons.

Source of variation		Grain yield plant^{-1}(g)	
	Degrees of freedom	Mean sum of squares	Percent variance
RILs/ABLs+ checks (G)	14	40.27***	99.08
Seasons/environment (E)	2	229.89***	0.08
Blocks	3	0.03	0.00
GEI	28	26.66***	0.67
IPCA1	15	36.81***	93.40
IPCA2	13	14.95***	7.55
Error	42	0.03	0.17

RILs/ABLs: Recombinant inbred lines/Advanced breeding lines; GEI: Genotype × Season/Environment interaction; IPCA: Interaction principal component analysis; *** indicates significance at P<0.001



Seasons	
E1	Summer 2020
E2	*Kharif* 2020
E3	Summer 2021
RILs/ABLs	
T8	43-2
T12	103-2
T19	17-2-1
T22	6-5
T25	66-1
T30	5-3
T32	93-1
T41	9-2
T48	65-4
T64	36-3-1
T74	KMR-316

Fig. 2 : (a) Discriminating ability *vs* representativeness of test seasons **(b)** AEC view of GGE bi-plot based on finger millet genotype-focused scaling for comparison of genotypes with the ideal RIL/ABL/check **(c)** AEC view of GGE bi-plot based on season-focused scaling for comparison of finger millet genotypes with the ideal 'RIL/ABL/check' (g) **(d)** Polygon view of GGE biplot based on symmetrical scaling for 'which won where/what' pattern of finger millet genotypes and seasons in the expression of grain yield plant^{-1}(g).

to E2. In the case of E2, it recorded low 'minimum values' when compared to E1, except for plant height (cm) during E1. In the case of E1, higher 'maximum values' were recorded for all traits except for plant height (cm) when compared to E2. The absolute range was high for plant height (cm), number of productive tillers, days to 50 percent flowering, and finger length (cm), whereas in E2, grain yield plant^{-1} (g) and 1000-grain weight (g) recorded higher values. In general, the standardized range is low in E2 for all the traits except for grain yield plant^{-1} (g). Furthermore, the standardized range was relatively high for the number of productive tillers, finger length (cm), and grain yield plant^{-1} (g). It was apparent that for all the traits under study, RILs/ABLs and checks exhibited a wide range of values, indicating the presence of significant variability in the RILs/ABLs and check varieties. The level and significance of correlation plots for grain yield plant^{-1} (g) and its associated traits for all genotypes were shown (Fig. 1 and Fig. S1). The symmetry of the frequency distribution was positively skewed, and the tailedness of the frequency distribution was platykurtic for grain yield plant^{-1} (g) in both Summer 2020 (Fig. S2) and *Kharif* 2020 (Fig. S3).

Stability analysis of the selected 15 genotypes across three seasons

To get stable, high-yielding varieties of finger millet, there is a need to grow finger millet RILs/ABLs across the multi-season/environments. Promising and high-yielding finger millet RILs/ABLs were selected for E3 based on their mean grain yield from both E1 and E2 data. AMMI ANOVA and GGE biplot patterns of interaction of 'RILs/ABLs and checks' with season/ environments were used for selecting the best stable lines

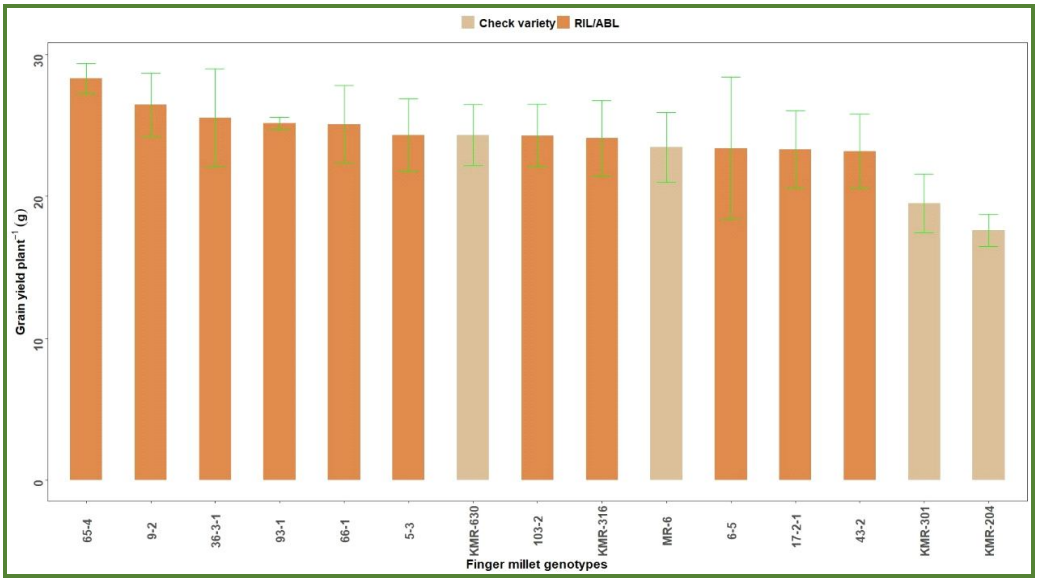


Fig. 3 : Barplot showing stable finger millet genotypes for grain yield plant^{-1} evaluated across three seasons. RILs/ABLs: Recombinant inbred line/Advanced breeding line; the standard error was represented by the green error bars.

Table S3 : Mean grain yield plant^{-1} (g) and parameters to assess stability of finger millet genotypes evaluated across Summer 2020, *Kharif* 2020, and Summer 2021.

RILs/ABLs	Grain yield plant^{-1} (g)							
	Mean	Rank	IPCA1	IPCA2	ASV	Rank	SI	Rank
43-2	23.17	13	-1.21	-0.44	4.06	11	24	**12**
103-2	24.28	8	0.21	0.63	0.94	3	11	**5**
17-2-1	23.31	12	0.51	0.98	1.98	6	18	**8**
6-5	23.37	11	-2.60	-0.05	8.69	15	26	**15**
66-1	25.06	5	-1.33	-0.53	4.47	13	18	**9**
5-3	24.31	6	1.38	-0.35	4.64	14	20	**10**
93-1	25.13	4	0.29	-1.48	1.77	5	9	**4**
9-2	26.44	2	-0.19	0.56	0.84	2	4	**1**
65-4	28.31	1	-0.34	-0.83	1.42	4	5	**2**
36-3-1	25.51	3	-0.76	1.27	2.83	8	11	**6**
KMR-316	24.09	9	0.78	0.85	2.75	7	16	**7**
KMR-204*	17.60	15	0.89	-1.30	3.25	9	24	**13**
KMR-301*	19.51	14	1.10	0.00	3.67	10	24	**14**
KMR-630*	24.29	7	-0.03	0.53	0.54	1	8	**3**
MR-6*	23.44	10	1.29	0.17	4.32	12	22	**11**
SE(M)±	0.07							
CD@p=0.01	0.27							

IPCA: Interaction principal component analysis; ASV: AMMI stability value; SI: Stability index; SE(M): standard error of mean; CD: Critical difference; *: Finger millet varieties used as check.

across three seasons. These results were studied in accordance with the stability analysis models used in the estimation of grain yield in finger millet (Ishwarya *et al*., 2025 and Kumar *et al*., 2023).

AMMI ANOVA

AMMI ANOVA based on mean sum of squares (MSS) attributable to RILs/ABLs and checks × seasons showed significant differences for grain yield plant^{-1} (g) and its component traits (Table S2). The percent variance attributable to genotype×season-interaction (GEI) towards total variability of RILs/ ABLs and checks was less than that attributable to main effects of RILs/ABLs and checks and seasons/environments for the trait grain yield plant^{-1} (g). The main effects of RILs/ABLs and

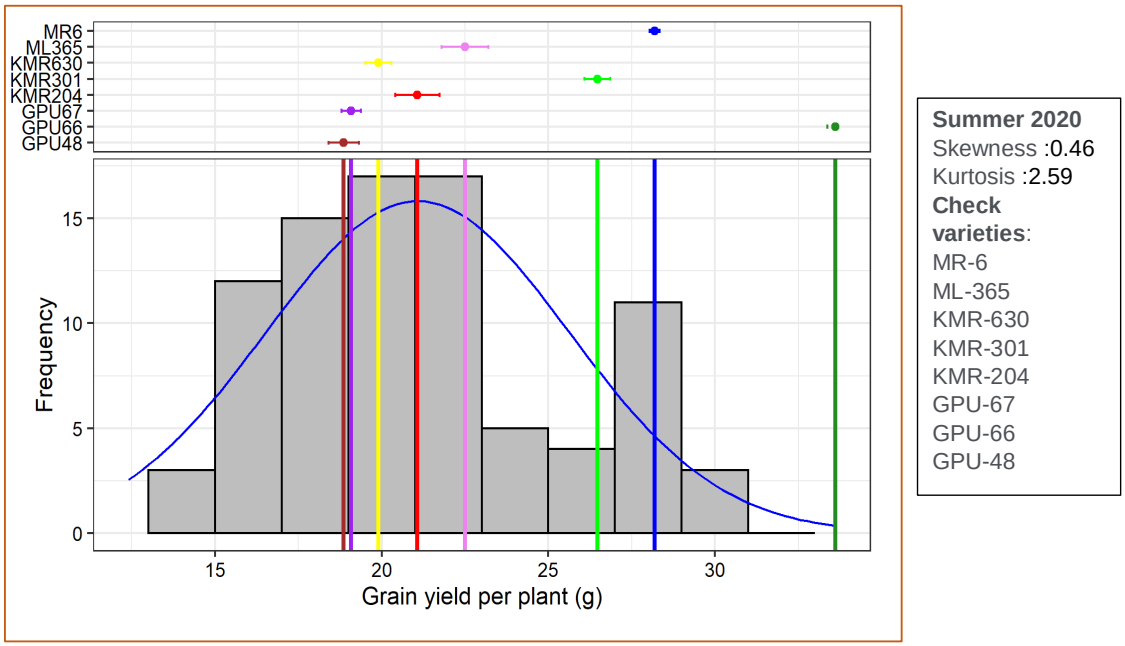


Fig. S2 : Frequency distribution of RILs/ABLs for grain yield plant^{-1}(g) in Summer 2020

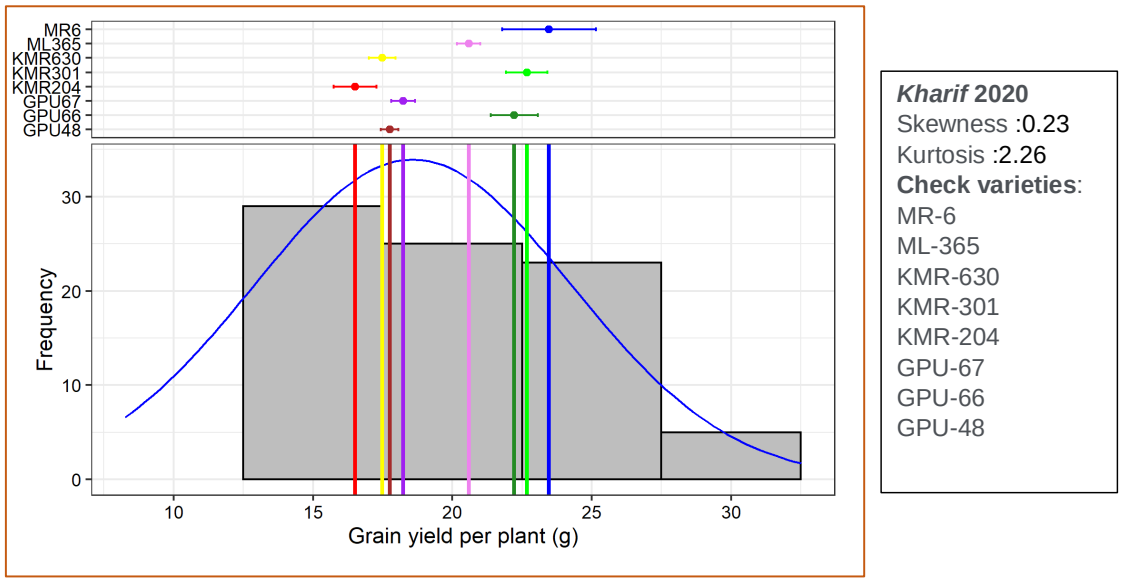


Fig. S3 : Frequency distribution of RILs/ABLs for grain yield plant^{-1}(g) in *Kharif* 2020.

checks contributed more towards the total variability of the RILs/ABLs and checks than those of GEI for grain yield plant^{-1}. Estimates of the mean of grain yield plant^{-1} (g) and parameters like 'AMMI stability value (ASV)' to assess the stability of 11 finger millet RILs/ABLs and four checks evaluated across three seasons, i.e., Summer 2020, *Kharif* 2020, and Summer 2021 (Table S3).

GGE Biplot patterns of interaction of 'RILs/ABLs and checks' with seasons/environments

Discriminating ability and representativeness

The longest vector of E2 has more length, so it has more discriminating ability among RILs/ABLs and checks with respect to grain yield plant^{-1} variation, and was followed by E1 (Fig. 2a). E1, with the shortest season/environment vector, showed the least discriminating ability over RILs/ABLs and checks, i.e., low variation in grain yield plant^{-1} (g) of RILs/ABLs. The average of the test season/environment was denoted by the average environment axis (AEA) with a small circle with an arrow. The angle between the AEA and E2 was less, so it denoted the more representativeness of all three test seasons/environments, whereas E1 had a greater angle with AEA, thus denoting the less representativeness of all the test seasons/environments. Hence, E2, with high representativeness and high discriminating ability, was the best season/environment when compared to the other

two test seasons/environments. Concentric circles denote the season/environment standard deviation to assess the length of the season/environment vectors, *i.e.*, discriminating ability of the test season/environment. E2 and E3 exhibited little correlation as the angle between them was an acute angle, and E2 and E1 exhibited 'no correlation' as they have a right angle between vectors. If the correlation between both seasons/ environments was higher, we could draw the same information from the RILs/ABLs and checks in both corresponding seasons/ environments.

Ranking genotypes relative to 'ideal genotype'

RIL 65-4 (T48) has high mean performance, and as we move towards the origin, away from the point where RIL 65-4 (T48) is present, the mean performance of finger millet RILs/ABLs decreased (Fig. 2b). RIL 5-3 (T30) got the last position in terms of RILs/ABLs, and check variety 'MR-6 (C4)' got the last position overall in the mean performance of grain yield plant^{-1} (g). The average environment coordinate axis (AEC) was used to know the position of the concerned 'RIL/ABL and check variety'.

'Mean *vs* Stability' GGE biplots

RIL 9-2 (T41) has high stability among all RILs/ABLs or checks, as it was on the AEA axis, and as distance increases from the AEA axis, the stability decreased (Fig. 2c). The length of the projection denotes the stability of the genotype. RIL 6-5 (T22) has instability among all RILs/ABLs, as it has a very lengthy projection from the AEA axis, and the position of this RIL or check can be known on the AEC axis.

"Which won where/what" patterns

In the present study, the "which won where/what" graph (Fig. 2d) revealed which RIL/ABL (winning genotype) produced more grain yield in which season/ environment. The winning finger millet RILs/ABLs were present at the vertices of the polygon. In a polygon, each side was separated perpendicular to a vertical line. This graph was divided into various sectors by lines that had acute angles between them. Therefore, RIL/ABL and check at the vertices exhibited a positive correlation with the season/environment between the lines. The polygon was formed by keeping either winning or inferior RIL/ ABL at the farthest position on the vertices in such a way that the polygon encompassed all finger millet RILs/ ABLs within it. GGE biplots revealed GEI for grain yield plant^{-1} (g) for 11 RILs/ABLs and four checks across the three seasons/environments. The results advised that high-yielding, stable RILs/ABLs E1, E2 and E3 were identified, some of which outyield, and others were on par with the checks that polygon encompasses all finger millet RILs/ABLs within it. As per the graph, RIL 6-5 (T22) gives the highest yield in E2. RIL 65-4 (T48) gives the highest yield plant^{-1} in E1 and E3 because both E1 and E3 fall in the same sector where RIL 65-4 (T48) was present. RIL 5-3 (T30), present at the vertex, has the lowest yield in E2.GGE biplots diagrammatically illustrated each finger millet RILs/ABL × season/ environment for the trait 'grain yield plant^{-1}' in each of three seasons. As the 11 RILs/ABLs were less influenced by seasonal variations indicated their utility in the breeding of high-yielding finger millet cultivars.

Table S4 : Mean grain yield plant^{-1} (g) of eleven finger millet RILs/ABLs and four checks evaluated across three seasons.

RILs/ABLs and check varieties	Grain yield plant^{-1} (g)			Mean (g)
	Summer 2020	*Kharif* 2020	Summer 2021	
65-4	27.89	30.29	26.75	28.31
9-2	29.25	28.07	22.00	26.44
36-3-1	28.74	29.18	18.60	25.51
93-1	24.51	24.87	26.00	25.13
66-1	23.45	30.42	21.30	25.06
5-3	28.93	23.88	20.11	24.31
KMR-630*	27.32	25.40	20.15	24.29
103-2	27.96	24.57	20.30	24.28
KMR-316	29.31	22.47	20.50	24.09
MR-6*	28.17	20.00	22.16	23.44
6-5	20.42	33.13	16.57	23.37
17-2-1	28.31	22.62	19.00	23.31
43-2	21.97	28.14	19.40	23.17
KMR-301*	23.52	16.70	18.30	19.51
KMR-204*	18.48	15.33	19.00	17.60
SE(M) ±	27.89	30.29	26.75	0.07
CD @ P=0.01	29.25	28.07	22.00	0.27

SE(M): standard error of mean; CD: Critical difference; *: Finger millet varieties used as check.

Identification of high-yielding and stable finger millet genotypes

The stable high-yielding RILs/ABLs such as 9-2 (26.44g), 65-4 (28.31g), 93-1 (25.13g), 103-2 (24.28g), 36-3-1 (25.51g), and KMR-316 (24.09g) evaluated across three seasons are shown in the barplot (Fig. 3 and Table

S4). High-grain-yielding, stable finger millet RILs/ABLs across E1, E2, and E3 were identified, which outyielded and were on par with the check varieties in yield and their related traits, based on the stability index (SI) combining both 'ammi stability value (ASV)' and the 'mean performance' of traits across three seasons/ environments. The findings unveiled the importance of stability parameters such as ASV and IPCC scores in selecting genotypes that combine high grain yield with stability, contributing to stable production in finger millet (Anuradha *et al*., 2022).

The presence of a high degree of genetic variability among the finger millet RILs/ABLs indicates substantial potential for selecting superior lines for varietal improvement. RILs/ABLs, including 9-2, 65-4, 103-2, 36-3-1, 93-1 and KMR-316, exhibited superior and stable yields on par with check varieties. These promising genotypes should be advanced to multilocation trials to evaluate their adaptability before varietal release. Upon demonstrating consistent performance across diverse locations, they can be considered for direct release as new varieties. Furthermore, with the aid of advanced molecular breeding techniques such as marker-assisted selection (MAS), these lines act as donor parents for transferring the trait 'high grain yield' into well-adapted finger millet varieties.

Competing interests : The authors declare that no conflict of interest exists.

Acknowledgements

The first author is thankful to the Indian Council of Agricultural Research (ICAR) for providing the ICAR-PG Scholarship for pursuing a Master's degree in Genetics and Plant Breeding. Highly Thankful to Mohan Rao, A. and Ramesh S. for their advisory role in research.

Author contribution : Botta Thandava Ganesh carried out the experiment, analysed data, and prepared the manuscript. Ramanappa T.M., conceptualized the experiment and reviewed the manuscript.

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