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Genotype environment interaction analysis for fruit yield in okra (*Abelmoschus esculentus* L.) under alkaline environments

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Abstract

Twenty four Okra genotypes were evaluated for marketable fruit yield and its related traits for genotype environment interaction during 2015-16 and 2016-17. The genotypes were exposed to alkaline environment with a pH range of 8.0±0.2, 8.5±0.2, 9.0±0.2 and 9.5±0.2. A significant level of deviation in expression of different traits was observed in all the genotypes with increasing pH. Based on Additive Main Effects and Multiplicative Interaction (AMMI), Genotype and Genotype Environment Interaction (GGE) biplot, Wrick's ecovalence (Wi^2), AMMI Stability Value (ASV) and Yield Stability Index (YSi) stable genotypes with high fruit yield were identified over the eight environments. The combined AMMI analysis of variance indicated that genotype main effect, environment and genotype-by-environment interaction effects showed variation of 19.83%, 63.07% and 17.10%, respectively for fruit yield. On the basis of different stability measures, VRO-112, VRO-110, Kashi Kranti, VROB-178, AE-70 and VRO-108 were differentiated as high yielding and stable genotypes over the tested environments. This study will be helpful for selecting alkali tolerant okra parents for further breeding programme and recommending the suitable genotypes for alkalinity prone area.

Key words: Yield stability, AMMI, GGE, okra, yield traits

Introduction

Okra is one of the economically important vegetable grown across the world including tropical and subtropical regions. Most popular terms for okra are lady's finger (England), gumbo (United States of America), guino-gombo (Spanish), guibeiro (Portuguese) and bhindi (India). Earlier known as *Hibiscus esculentus,* presently okra is accepted as *Abelmoschus esculentus,* due to presence of distinguished characteristics of the calyx, corolla and staminal column which are fused at the base and fall together after the anthesis (Dhankhar and Mishra 2004). The term *Abelmoschus* is probably derived from Arabian word "*abul-l-mosk"* which means "source of musk," indicating musky smell of seeds (Charrler 1984). Maximum cultivation (99%) of okra is being done in the Asian and African countries but productivity is very poor in African countries (2.25 MT ha^{-1}) in comparison to other okra growing regions. Global average yield of okra is 5.26 MT ha^{-1} from an area of 1.83 M ha with annual productivity of 9.62 MT. 72% of total world production occurs in India, ranking first with 6.3 million MT productivity in 0.5 million ha area (FAOSTAT 2018).

Globally, about 1128 m ha area is affected by salinity and sodicity stresses (Wicke et al. 2011). In India, 6.73 million hectares fall under salt affected area and projected to increase to 20 million ha by 2050 (Sharma 2014). Such salt affected areas have either land or crops with very low yields. Crop productivity including vegetables is limited due to accumulation of salts in arid and semi-arid areas across the world (Rui and Ricardo 2017). Salt tolerant genotypes can be the suitable strategy for saline or alkaline areas since it will lower down the cost of soil reclamation. Among all vegetables, okra is considered a semi tolerant or moderately tolerant crop, yet salinity stress has been reported to adversely affect the growth and productivity (Unlukara et al. 2008; Sanwal et al. 2019). Fifty per cent reduction in fresh fruit yield of okra has been reported at salinity of 6.7 dS m^{-1} (Minhas and Gupta 1993). Another study showed the reduction in okra yield by 30-40% (ECe 6 dS m^{-1}), 10-40% at pH 9.45 and 80% at pH 9.7 (Annual Report CSSRI 1997).

Yield is a complex polygenic trait with significant

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variations under different environments and hence performance of genotypes in single environment cannot be considered as a criterion for selection and identification of variety (Shrestha et al. 2012). Hence, the best strategy is to evaluate the genotypes in multiple environments for stable yield and average performance (Islam et al. 2015). One major effect for evaluating different performances of vegetable/field crops under different environments has been identified as the genotype environment interaction (GE). The study of GE is must, before release of any new variety/ cultivar for high mean performance and stability in multi-environment trials (MET).

Various conventional analytical methods are being adapted for evaluating genotype × environment interactions of traits along with stability. Rank sum method was modified by Kang (1993) by giving a single selection criterion with merging yield and stability as yield stability static (YSi). Still, the most reliable and explored analytical methods in use include AMMI, GGE and genotypes main effects. Through this method the genotype environment interaction can be quantified in terms of PCA and graphical representation and hence adopted widely specifically for multi-environment cultivar trials (Kempton 1984; Gauch and Zobel 1997).

India has large area under salt stress, thus there is a need to develop stable genotypes with high yield which can be recommended for sodic environments. Therefore, the present experiment is need of the hour and was planned and executed for identification of suitable okra genotypes across different alkaline environments.

Table 1. List of okra genotypes used in the study

S.No.	Genotypes	Code	Type	Origin
1	VRO-5	G1	Variety	ICAR-IIVR, India
2	VRO-105	G2	Advance line	ICAR-IIVR, India
3	Arka Abhay	G3	Variety	ICAR-IIHR, India
4	No. 315	G4	Advance line	ICAR-IIVR, India
5	VROB-181	G5	Advance line	ICAR-IIVR, India
6	VRO-102	G6	Advance line	ICAR-IIVR, India
7	VRO-107	G7	Advance line	ICAR-IIVR, India
8	VRO-109	G8	Advance line	ICAR-IIVR, India
9	Parbhani Kranti	G9	Variety	MAU, India
10	Pusa Sawani	G10	Variety	ICAR-IARI, India
11	VRO-103	G11	Advance line	ICAR-IIVR, India
12	VRO-111	G12	Advance line	ICAR-IIVR, India
13	VRO-112	G13	Advance line	ICAR-IIVR, India
14	VRO-104	G14	Advance line	ICAR-IIVR, India
15	VRO-110	G15	Advance line	ICAR-IIVR, India
16	Kashi Kranti	G16	Variety	ICAR-IIVR, India
17	VROB-178	G17	Advance line	ICAR-IIVR, India
18	Arka Anamika	G18	Variety	ICAR-IIHR, India
19	Varsha Uphar	G19	Variety	CCS HAU, India
20	VRO-108	G20	Advance line	ICAR-IIVR, India
21	VRO-106	G21	Advance line	ICAR-IIVR, India
22	AE-70	G22	Advance line	TNAU, India
23	VRO-101	G23	Advance line	ICAR-IIVR, India
24	VRO-6	G24	Variety	ICAR-IIVR, India

Table 2. Description of the environments

S.No.	Code	Environments	Year
1	E1	pH 8.0±0.2	2015-16
2	E2	pH 8.5±0.2	
3	E3	pH 9.0±0.2	
4	E4	pH 9.5±0.2	
5	E5	pH 8.0±0.2	2016-17
6	E6	pH 8.5±0.2	
7	E7	pH 9.0±0.2	
8	E8	pH 9.5±0.2	

Materials and methods

The genetically pure seed of 24 diverse okra genotypes tolerant to yellow vein mosaic virus (YVMV) and okra enation leaf curl virus (OELCV) were used for this experiment (Table 1). Seeds were surface sterilized in a solution of 2% (0.02 g per ml) hypochlorite for 5 min and rinsed thoroughly with distilled water. Seeds were sown in micro-plots (2m × 2 m) having 10 plants/ replication of each genotype in normal (pH 8.0±0.2), sodic (pH 8.5±0.2), medium sodic (pH 9.0±0.2) and highly sodic (pH 9.5±0.2) environments during 2015-16 and 2016-17 (Table 2). Plant to plant distance was kept as 40 cm with 50 cm row spacing. Sodic soil was prepared by adding sodium bi-carbonate, the quantity being calculated on the basis of pH and exchangeable sodium percentage (ESP). Thus, for making the sodic soils as per treatments, 3.68 kg, 6.44 kg and 7.83 kg sodium bi-carbonate was added to increase the pHs from 8.0 (normal soil) to 8.5, 9.0 and 9.5 respectively. The experiment was randomized in triplicate with complete block design. The data was recorded on plant

height (cm), days to 50% flowering, number of fruits/ plant, fruit length (cm), fruit weight (g), fruit yield/plant (g), total chlorophyll (mg/g fw), proline (mg/g fw), sodium and potassium content of root and shoot.

Statistical analysis

The genotype × environment interaction for fruit yield was analyzed through additive main effect and multiplicative interaction (AMMI) and GGE-biplot analysis using software package PB Tools version 1.4 (http://bbi.irri.org/products). AMMI utilize the ANOVA for calculation of additive part (main effects) and principal component analysis for non-additive part (Gauch and Zobel 1989). In addition to AMMI and GGE biplot, the following stability statistics was also measured.

(1) AMMI stability value

The method given by Purchase et al. (2000) was used for AMMI stability value (ASV) using following formula: ASV= $[\{(SSIPCA1/SSIPCA2)\ (IPCA1\ score)\}^2 + (IPCA2\ score)^2]^{1/2}$ Where, SSIPCA1/SSIPCA2 - the weight derived by dividing the sum of squares of IPCA1 by the sum of squares of IPCA2. The specific adaptability of a genotype to certain environment is directly proportional to ASV value in both positive and negative directions. Lower ASV value means a more stable genotype across the environments.

(2) Yield stability index

The yield stability index (YSI) was calculated using the formula: YSI = RASV + RY where, RASV - rank of the AMMI stability value and RY - rank of the mean grain yield of genotypes.

A low value of yield stability index indicates desirable genotypes with high mean yield and stability.

(3) Wricke's ecovalence (W_i)

$$W_i = [Y_{ij} - Y_{i.} - Y_{.j} - Y_{..}]^2$$

where

Y_{ij} - is the mean performance of i^{th} genotype in j^{th} environment

$Y_{i.}$and $Y_{.j}$ represents genotype and environment mean deviations,

$Y_{..}$- overall mean.

Genotypes with a smaller value have minimum deviations from the mean across environments and are thus more stable (Wricke 1962).

The correlation analysis was done by R Core Team (2019).

Results and discussion

Mean performance

Wide range of variation in mean performance of genotypes throughout the environments was observed in yield and yield contributing traits (Table 3). The genotypic average for days to 50% flowering which is a sign of earliness ranged from 38.38 to 47.38 with mean 42.32. The average number of fruits per plant ranged from 6.38 to 8.87 with a mean value of 7.57, while average fruit length varied from 7.38 to 8.50 cm. Fruit weight ranged from 6.25 to 8.69 g with mean 7.41 g and fruit yield per plant varied from 42.42 to 79.99 g with mean of 57.14. Total chlorophyll content which helps in photosynthesis varied from 4.41 to 8.52 mg/g with mean 6.76 mg/g, while proline an amino acid, plays a highly beneficial role in plants exposed to various stress conditions ranged from 2.30 to 3.90 mg/g with mean 3.28 mg/g. Similarly, K/Na ratio ranged from 0.82 to 1.31 with mean 1.00 mg/g in roots while it varied from 2.54 to 4.49 with mean 3.32 mg/g in shoot. Among different genotypes G13 performed better for fruit yield per plant, number of fruits per plant and total chlorophyll content. G10 took minimum days for 50% flowering followed by G8 and G16. G21 had highest fruit length and G8 had maximum value for root K/Na. G18 scored highest value for proline content and G20 for shoot K/Na. All the genotypes showed a significant reduction in the expression of different traits at pH 9.5 in comparison to pH 8.0. High amount of salt in leaf and deficiency of water results in closing of stomata which lead to the reduction in rate of transpiration and concentration of CO_2 and ultimately affects the total chlorophyll content, plant height and yield (Redondo-Gómez et al. 2007; Saleem et al. 2011; Wani et al. 2013). Under salt stress conditions, plant height, fresh weight, dry weight and root length, chlorophyll and proline content were significantly reduced in Okra crop as reported by Sanwal et al. (2019), leaf area index and shoot length by Abbas et al. (2013) and germination percentage and root length by Shahid et al. (2011).

Stability analysis based on ASV, YSI and Wi^2 ecovalence

Initially analysis of variance was carried out for individual environment and then data was used to identify generally adapted specifically adapted genotypes using PB Tool. Homogeneity of variance was tested using Bartlett's test. Stable genotypes with

Table 3. Mean performance of Okra genotypes under the study across the environments

Genotypes	PH	DF	NFPP	FL	FW	FY	TC	P	RKN	SKN
G1	61.33	42.88	8.13	8.36	7.37	61.19	7.37	3.28	0.83	3.06
G2	94.38	40.63	6.90	7.38	6.56	45.51	7.41	3.31	0.85	3.64
G3	80.93	43.00	7.02	8.10	6.47	46.52	6.74	3.46	0.91	3.59
G4	59.96	43.63	6.63	7.65	8.13	54.26	6.60	3.05	0.92	3.27
G5	47.68	47.38	8.05	7.86	8.50	69.72	6.98	3.17	1.24	2.78
G6	88.18	41.13	7.53	8.06	7.25	55.23	6.34	3.03	0.99	3.24
G7	78.51	41.25	6.56	7.55	6.55	42.42	7.50	3.12	0.96	2.99
G8	88.01	38.38	8.16	7.97	6.91	57.13	7.67	3.71	1.31	2.98
G9	98.93	43.88	8.06	7.89	6.49	53.67	6.06	3.63	0.82	2.86
G10	84.50	38.38	7.99	8.25	7.33	60.60	6.27	3.72	1.23	3.46
G11	86.41	42.25	8.16	7.55	7.17	58.61	6.16	2.93	0.95	3.98
G12	66.01	46.75	7.25	7.77	6.25	45.02	7.66	2.30	1.15	3.45
G13	86.63	41.63	8.87	8.32	8.20	79.99	8.52	3.83	1.08	4.15
G14	75.16	42.25	6.73	7.58	7.72	52.18	5.60	3.29	0.87	3.31
G15	88.29	40.75	7.42	7.68	8.20	61.45	5.83	3.36	1.00	2.54
G16	87.46	39.38	8.45	8.33	8.32	70.93	7.78	3.45	1.03	2.94
G17	66.13	43.13	7.30	8.00	8.69	64.13	7.07	2.86	0.83	3.79
G18	80.25	41.38	7.10	7.48	6.44	46.65	6.72	3.90	1.00	2.97
G19	94.19	40.13	7.68	8.26	6.94	53.72	6.32	2.53	1.02	3.03
G20	94.33	42.75	7.66	7.55	7.39	57.08	7.16	2.81	1.00	4.49
G21	88.88	43.13	8.06	8.50	7.40	60.74	7.19	3.68	0.87	3.44
G22	104.00	45.00	7.62	8.13	8.12	62.91	4.41	3.26	1.04	2.73
G23	81.95	43.50	6.38	7.67	8.09	52.61	6.35	3.33	1.05	3.72
G24	82.50	43.13	7.95	8.34	7.33	59.20	6.59	3.43	1.15	3.32
Mean	81.86	42.32	7.57	7.93	7.41	57.14	6.76	3.27	1.00	3.32
Min	47.68	38.38	6.38	7.38	6.25	42.42	4.41	2.30	0.82	2.54
Max	104.00	47.38	8.87	8.50	8.69	79.99	8.52	3.90	1.31	4.49
Variance	179.32	4.99	0.42	0.11	0.54	79.19	0.74	0.16	0.02	0.23
SD	13.39	2.23	0.65	0.33	0.74	8.90	0.86	0.40	0.14	0.48
CV	16.36	5.28	8.58	4.23	9.96	15.57	12.71	12.13	13.59	14.33

PH=Plant height (cm), DF=days to 50% flowering, NFPP=number of fruits/plant, FL=fruit length (cm), FW=fruit weight (g), FY=fruit yield/plant (g), TC=total chlorophyll (mg/g fw), P=proline (mg/g fw), RKN=root potassium sodium ratio, SKN=shoot potassium sodium ratio

high mean yield across different environments were identified using AMMI stability value (ASV), yield stability index (YSI) and Wricke's ecovalence (1962) (Table 4). According to ASV method a genotype with low ASV value is considered as stable genotype while a high ASV value either in positive or negative direction indicates specific adaptability of a genotype to particular environment (Purchase et al. 2000). For fruit yield, G20 with mean fruit yield (57.08 g), G19 with mean fruit yield (53.72 g), G9 with mean fruit yield (53.67 g) and G17 with mean fruit yield (64.13 g) have low ASV value. Yield stability index incorporates both mean yield and stability in a single criterion. Low values of both parameters show desirable genotypes with high mean yield and stability (Bose et al. 2014). Genotypes with low ASV value are given rank one while in case of mean yield the high yielding genotypes is given rank one. For fruit yield genotypes, G13, G17, G16 and G20 were observed as stable genotypes with mean fruit yield 79.99 g, 64.13 g, 70.93 g, and 57.08 g,

Table 4. IPCA Score and yield-stability statistics of 24 okra genotypes for fruit yield

Code	FY	IPCA1	IPCA2	Wi^2	ASV	YSi
G1	61.19	-3.97	0.23	1456.94	15.17	29
G2	45.51	1.44	0.62	251.45	5.54	36
G3	46.52	3.67	0.25	1236.02	14.02	42
G4	54.26	-1.47	-1.42	535.25	5.79	30
G5	69.72	-2.19	-0.85	689.22	8.41	20
G6	55.23	1.88	0.28	398.38	7.19	30
G7	42.42	-1.67	3.31	790.01	7.19	40
G8	57.13	-0.95	1.01	154.38	3.77	21
G9	53.67	0.35	-0.74	197.65	1.53	20
G10	60.60	-4.17	-0.37	1587.58	15.93	32
G11	58.61	-1.07	-0.09	215.03	4.09	23
G12	45.02	-0.67	0.60	178.80	2.63	30
G13	79.99	-0.04	-2.51	380.27	2.51	7
G14	52.18	-0.94	0.67	154.73	3.65	27
G15	61.45	0.95	1.68	278.32	4.00	17
G16	70.93	0.03	-3.96	853.85	3.96	12
G17	64.13	0.42	0.90	367.61	1.84	8
G18	46.65	2.45	0.87	681.25	9.40	38
G19	53.72	-0.06	1.10	111.47	1.12	18
G20	57.08	-0.20	-0.16	91.40	0.78	14
G21	60.74	2.61	-0.46	636.90	9.98	27
G22	62.91	1.42	-0.94	271.28	5.51	18
G23	52.61	2.72	-0.23	799.89	10.39	38
G24	59.20	-0.53	0.19	246.47	2.03	15

respectively. Genotypes with low Wi^2 value indicates less deviation from mean value across the environments and hence are most stable (Wricke 1962). G20, G19, G8 and G14 with mean value 57.08 g, 53.72 g, 57.13 g, 52.18 g, respectively were reported as stable genotypes for fruit yield.

AMMI 1 biplot analysis

The pooled analysis of variance revealed that mean squares due to environments, genotypes, and genotype environment interaction were significant for fruit yield indicating significant variability among different environments and genotypes (Table 5). Genotypes, environment and genotype environment interaction (GEI) depicts 19.83%, 63.07% and 17.10% of the total variation for fruit yield. Twenty five genotypes of okra were evaluated for five planting seasons from 2006 to 2009 using AMMI model by Alake and Ariyo (2012) and reported that 77.2%, 4.6% and 18.1% of total variation by genotype, environment and GE respectively. Nwangburuka et al. (2011) studied GE interaction for 29 accessions of okra in four environments and observed that 70.8% of the total variation was mainly due to environment, 10.2% due to genotype and 19% due to GE interaction. Choudhary et al. (2019) also reported 72.4-87.0% of the total variation due to environment, 2.5-7.3% due to genotype and 10.5-24.1% due to GE interaction in baby corn over eight locations. Srivastava et al. (2011), Hamed and Hafiz (2012) and Javia (2014) used Eberhart and Rusell (1966) model to analyse GE interaction and identified stable and high yielding okra genotypes. The first two principal component accounts for 78.78% of the total genotype × environment interaction for fruit yield. For grain yield of basmati rice, AMMI analysis revealed that the first two significant IPCA scores together explained 77.18% of the total interaction variance (Dwivedi et al. 2020). Genotypes, G22, G15 and G17 for fruit yield (Fig. 1) were found as generally adaptable and high yielding genotypes as these genotypes showed IPCA 1 value close to zero. These genotypes are less influenced by the environments. Among the environments, E1, E2, E5 and E6 were found high yielding environment for fruit yield. However, these environments have large IPCA 1 score so they are suitable for the identification of specifically adapted genotypes.

Table 5. Analysis of variance for fruit yield of 24 okra genotypes across the environments

		Fruit yield	
Source	df	MS	% explain
Trial	95	384.71*	
Genotypes (G)	23	633.48*	19.83
Environments (E)	3	6620.55*	63.07
G × E	69	78.05*	17.10
PCA 1	25	274.17*	62.27
PCA 2	23	76.86*	16.51
PCA 3	21	41.07*	8.17

*significance at the 0.01 % levels

GGE biplot analysis

Discriminating ability and representation of test environments

The most representative and most discriminating

environment is considering as the most ideal environment (Yan 2001). The length of the vector from the origin of biplot and angle between vector and average environment axis (AEC) measures the discriminating ability and representativeness of the test environment (Yan and Kang 2003). The longer vector length means high discriminating ability and smaller angle means more representativeness of the environments (Yan et al. 2007). The AEC is the line which goes through the origin of biplot and average environment. Environment E1 and E5 for fruit yield (Fig. 2) were identified as most discriminating and found suitable for the identification of specifically adaptable genotypes. The test environments should have high IPCA 1 value to discriminate among the environments and small IPCA 2 value for more

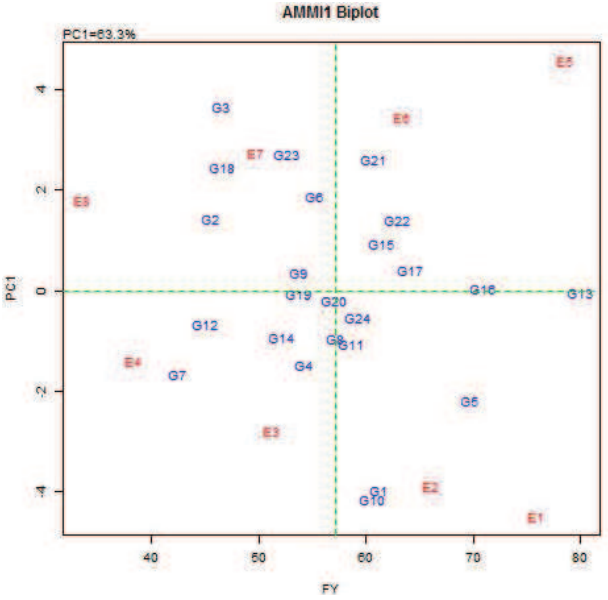


Fig. 1. AMMI-1 biplot for fruit yield of Okra genotypes across the environments

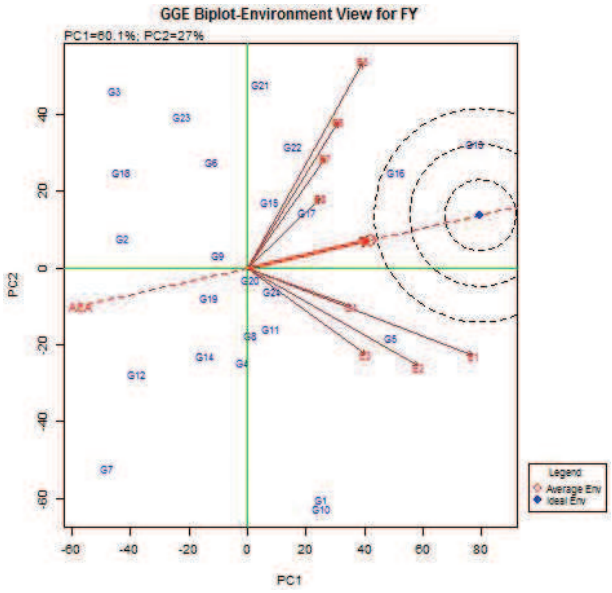


Fig. 2. Comparison of environments with ideal environment for fruit yield

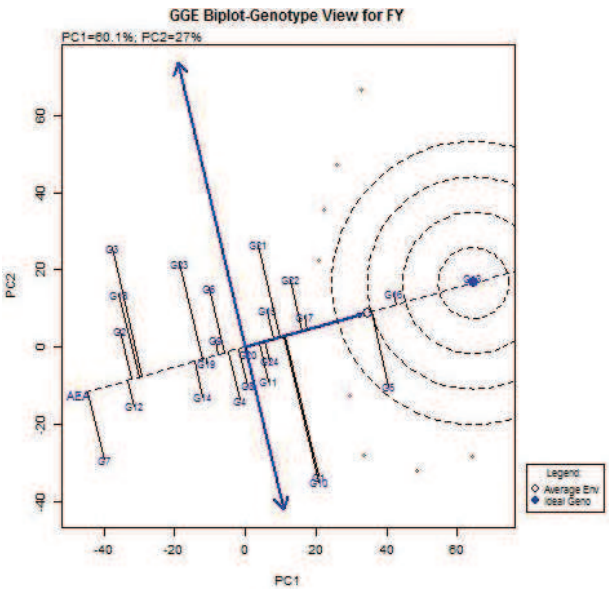


Fig. 3. Comparison of genotypes with respect to ideal genotype for fruit yield

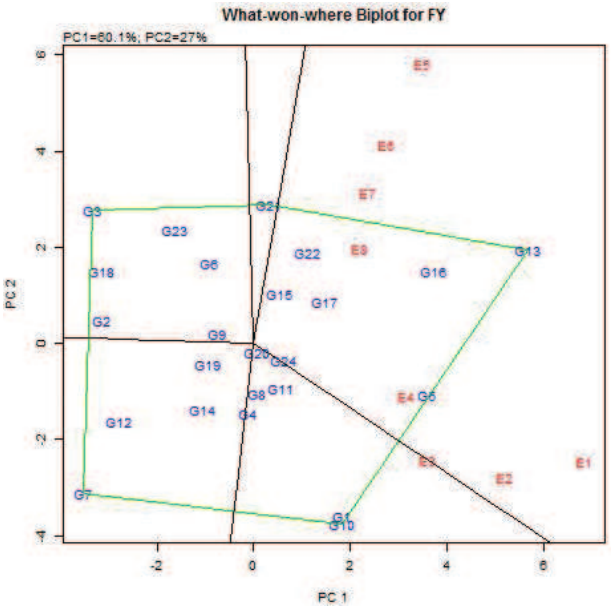
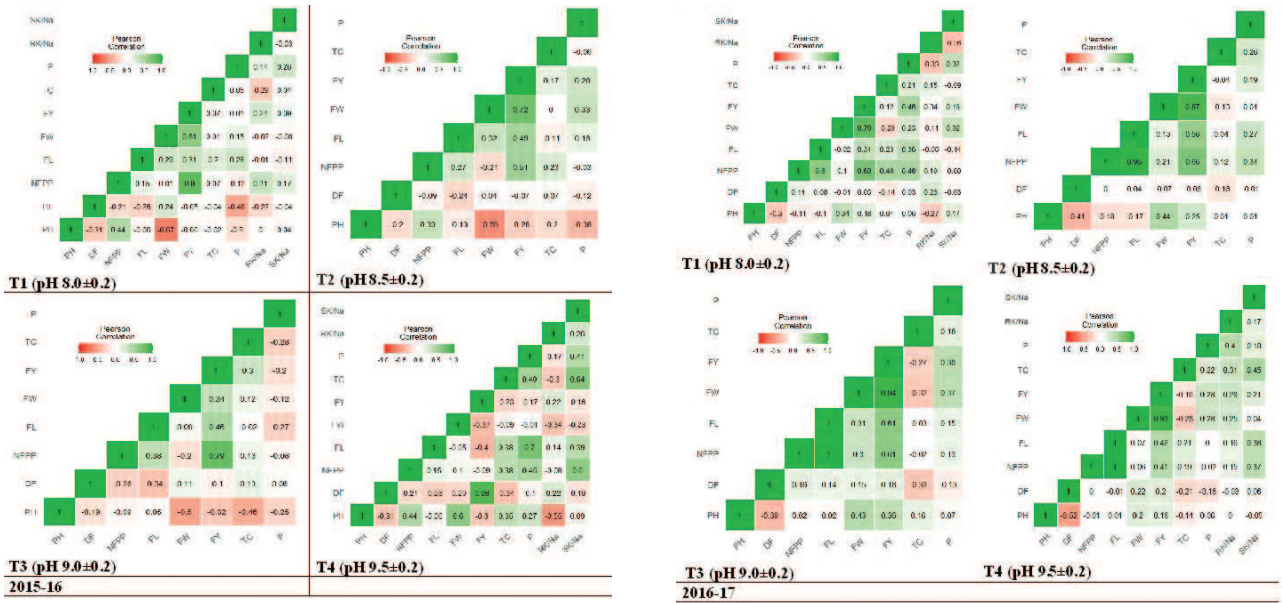


Fig. 4. Polygon view of genotype-environment interaction across the environments for fruit yield



(A) (B)

Fig. 5. Correlation heat map of yield traits in different environments

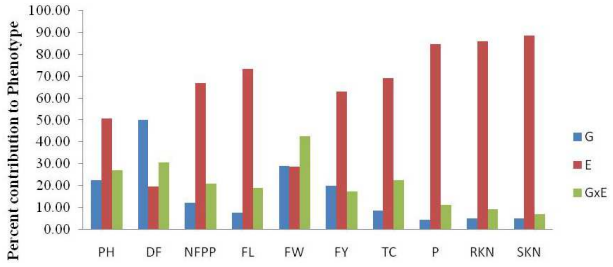


Fig. 6. Per cent contribution of genotype, environment and interaction effects in phenotypic expression of each trait across the environments

representativeness over the locations (Yan and Rajcan 2002). The environment E4 and E8 for fruit yield were found as most representative environment but are not discriminating. Non-discriminating environments do not significantly discriminate between genotypes and hence not recommended (Yan and Tinker 2006). Alake and Ariyo (2012) used Eberhart and Russell (1966), AMMI and GGE biplot techniques for the evaluation of twenty five West African okra genotypes in five different environments. Among the three techniques AMMI and GGE biplot was found more powerful than Eberhart and Russell (1966) in describing the GE interaction whereas GGE biplot is more suitable for environment and genotypic interactions as compared to AMMI model.

Ranking of genotypes relative to ideal genotype

An ideal genotype is defined as having high mean yield over different environments with stable performance (Yan and Rajcan 2002; Yan and Kang 2003). The ideal genotype has high IPCA 1 (high yielding) value and low IPCA 2 value (more stable). The open blue circle with an arrow represents the point of average environment coordinates (AEC) for environments in Fig. 3, and the dark blue dot represents the ideal genotype. Those genotypes which are located near the ideal genotype are more desirable than others (Kaya et al. 2006; Mitrovic et al. 2012). Similarly, genotypes having small length of vector are more stable and with longer vector are less stable (Yan and Kang 2003). Hence, genotypes, G13, G16, G17, G22, G15 and G24 for fruit yield were found most desirable among the all tested genotypes (Fig. 3). G20, G9 and G19 for fruit yield were stable genotypes but are not desirable as they are present away from the ideal genotype. Olayiwola and Ariyo (2013) studied the GE interaction of twelve okra genotypes using GGE biplot and YSi technique of stability analysis and observed that YSi was less effective in the high yielding and stable genotypic selection. Both GGE biplot and AMMI model are equally efficient for the identification of stable and high yielding genotypes across the environments and stable and ideal environment for the genotypic evaluation (Nwangburuka et al. 2011).

Polygon view for specific adaptation

Which-won-where pattern represents the specific genotypic adaptation to a specific environment. Starting from the biplot origin perpendicular lines were drawn to each side of the polygon (Kaya et al. 2006). The four lines divide the graph into five sectors (Fig. 4). Genotypes G13, G1, G10, G7, G3 and G21 for fruit yield were present on the vertices. These genotypes are either better or poor performing for a particular or across the environments due to their scattering far away from the origin of biplot (Yan and Kang 2003). Genotypes, G13, G16, G22, G15, G17 and G5 fell into sector 1 with G13 as vertex genotypes for fruit yield were the high yielding genotypes for these eight environments. Similar findings in okra were also reported by Nwangburuka et al. (2011) and Olayiwola and Ariyo (2013). The genotypes present on vertices were the most sensitive, as they are present far from the origin (Yan and Tinker 2006). However genotypes present near the origin are less sensitive genotypes. Partitioning of genotype and environment interaction by GGE biplot showed that IPCA 1 and IPCA 2 accounted for 60.10 % and 27.00 % with sum of 87.00% for fruit yield of the total variance.

Correlation analysis

Correlation between yield and its related traits was analyzed for both years and each environment (Fig. 5). Fruit yield was positively and significantly associated with number of fruits per plant, average fruit weight and fruit length across the environments except the T4 environment of season 2015-16 indicating that fruit yield of okra can be increased by direct selection for these traits. Number of fruit per plant showed positive correlation with fruit yield and fruit length across the environments except in environment T4 of 2015-16. Root and shoot K/Na ratio had a positive correlation with fruit yield/plant in both the years. Positive correlation of fruit yield per plant with number of fruits per plant, fruit weight and fruit girth was also reported by Shivaramegowda et al. (2016), Koundinya and Dhankhar (2013) and Balakrishnan and Sreenivasan (2010) in Okra crop.

Phenotypic expression of each trait across the environments was studied by calculating the per cent contribution of genotype, environment and interaction effects and it was observed that fruit yield was contributed mainly by environment (63.07%), followed by genotype (19.83%) and their interaction (17.10%). The percentage of explanation of phenotype by environment was high for all the traits studied except DF and FW (Fig. 6). The genotypic contribution (50.04 %) in phenotypic expression was high only for days to 50% flowering (DF) while the contribution of interaction effect (42.47 %) was high for fruit weight (FW).

Results of the present study clearly showed the differences among the tested environments in determining the fruit yield per plant. Environments E1, E2, E5 and E6 are most suitable for the identification of specifically adaptable genotypes while E4 and E8 are most representative environment. On the basis of different stability and adaptability measures using AMMI, GGE biplot and Ysi statistics, we can say that VRO-112, VRO-110, Kashi Kranti, VROB-178, AE-70 and VRO-108 are high yielding and stable genotypes over the tested alkaline environments. This study will be helpful for selecting and recommending suitable genotypes for alkalinity prone area and for selecting the parents for alkalinity tolerance breeding.

Authors' contribution

Conceptualization of research (SKS, AM); Designing of the experiments (SKS, AKR); Contribution of experimental materials (SKS); Execution of field/lab experiments and data collection (GK, RK); Analysis of data and interpretation (SKS, HK); Preparation of manuscript (SKS, HK, AM).

Declaration

The authors declare no conflict of interest.

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