
**GENOTYPE X ENVIRONMENT INTERACTION EFFECTS ON GRAIN YIELD,
BLAST DISEASE REACTION AND ADAPTABILITY OF FINGER MILLET
GENOTYPES IN UGANDA**

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ABSTRACT

Finger millet is grown in a wide range of agro-climatic conditions in Uganda and thus affected by an inevitable genotype x environment interaction (GEI) that affects performance of genotypes and therefore, effective selection. The objectives of the study were to: i) identify the best performing genotypes in terms of grain yield and blast disease resistance across environments, and in specific environments, and ii) evaluate the influence of genotype, environment, and genotype-environment interaction on grain yield. To achieve these objectives, 100 genotypes were evaluated in four environments with three replications in each environment. Analysis of variance and AMMI analyses were used to identify superior and stable genotypes, sources of stable resistance to blast disease, and least segregating environments. The grain yield results indicated highly significant ($p \leq 0.01$) differences between environments, genotypes and genotype x environment interaction. On partitioning the GEI, genotype x location, genotype x season and genotype x location x season were all highly significant ($p \leq 0.01$). From the AMMI analysis, genotype had the greatest effect accounting for 57.69%, GEI 32.27%, with environment main effects accounting for only 10%. This showed a higher variability among the genotypes and lower variability in the test environments. The highly significant ($p \leq 0.01$) effect of environment from AMMI II analysis showed high differential genotypic responses across environments. Twelve genotypes were high yielding and stable, whereas thirteen were high yielding but unstable. Eleven genotypes exhibited stable performance with regard to blast resistance. Overall the study revealed that six genotypes, that is, G84, G4, G60, G95, G23, and G29 combined both stable high grain yield and stable resistance to blast disease.

Keywords: adaptability, AMMI analysis, finger millet, G x E interaction, stability

Introduction

Finger millet is the second most important cereal in Uganda (FAOSTAT, 2012), grown in a wide range of environments by small-scale resource poor farmers both as a food security and cash

crop. Data from FAOSTAT (2012) indicates increasing acreage over the years which is however, not matched by corresponding increase in yield and in certain cases declining yield trends have been reported (Kidoido et al., 2002; Wanyera, 2007). There are many factors for this trend which include: the ever increasing unpredictability of agro-climatic conditions, lack of appropriate adapted varieties and finger millet blast disease. The decline in yield per unit area may also explain the increase in acreage to compensate for the yield gap. The lack of appropriate adapted varieties, declining yield trend and expansion to new crop areas will require basic understanding of performance of varieties in relation to the environment, and to determine whether genotype by environment interaction (GEI) is important. Such information is currently limited on finger millet which is mainly associated with subsistence small-scale farming. Reports from elsewhere on finger millet, however, indicate that finger millet is affected by GEI (Joshi et al, 2005; Misra et al., 2009; Solanki et al., 2000). The occurrence of large GEI poses a major problem for predicting performance which makes it difficult to decide which genotypes to be selected. It is therefore important to understand the nature of GEI to make testing and ultimately selection of genotypes more efficient.

According to Crossa et al. (2002), a significant GEI means that a selection from one environment may perform poorly in another. This would necessitate breeding for specific adaptation, which is not possible under limited resource conditions like the case is for Uganda on finger millet. In addition, the targeting of genotypes to specific locations is difficult when GEI is present, since yield is less predictable and cannot be interpreted based only on Genotype and Environment means (Samonte et al., 2005; Solanki et al., 2000). This would inevitably complicate the process of selecting genotypes with superior performance. Coupled with resource constraints, this slows progress from selection, since different genotypes would have to be chosen in different environments. As a result, multi-environment trials (METs) have been severally used and recommended to identify superior varieties with wide adaptation for farmers especially in low resource areas. The stable genotypes which perform well under stress and low-input conditions are desirable under farmers' conditions for sustainable finger millet and indeed crop production.

Multi-environment trials also assist in the identification of production environments that best suit certain genotypes (Crossa et al., 2002; Yan et al., 2000). It is therefore important to identify the causes of GEI in order to set up appropriate finger millet breeding objectives since Solanki et al. (2000) inferred that grain yield in finger millet is highly influenced by agro-climatic conditions, Andrew (1993) also suggested growing the materials in sufficient test environments to evaluate for superior stable entries of finger millet so as to increase production. Evaluation of interaction of genotypes with environments and other agro-management conditions would thus help in obtaining information on adaptability and stability of performance of genotypes and consequently improve productivity.

This study is on the premise of lack of information on finger millet genotypes adapted to diverse agro-ecological conditions in Uganda. Obtaining such information would lead to identification of cultivars that perform well across environments. To explore the impact of GEI, standard statistical methods have been applied and these include analysis of variance, principal component analysis, linear regression and Additive Main effects and Multiplicative Interaction (AMMI). Each of these methods employs statistical parameters to measure genotypic stability or response to environments according to different concepts of stability. The advantages and disadvantages of each of these methods have severally been dealt with (Balestre et al., 2010; Gauch, 1988; Yan and Hunt, 1988; Yan and Kang, 2003; Zobel et al., 1988). However, for this study, analysis of variance and AMMI were used since these have successfully and more often been used, and are considered better models in finger millet (Misra et al., 2009; Solanki et al., 2000).

Additive Main effects and Multiplicative Interaction analysis according to Purchase (1997) gives estimate of total GEI effects of each genotype and also further partitions it into interaction effects due to individual environments. Low GEI of a genotype indicates stability of the genotype over the range of environments. A genotype showing high positive interaction in an environment obviously has the ability to exploit the agro-ecological or agro-management conditions of that specific environment. The AMMI analysis permits estimation of interaction effect of a genotype in each environment and it helps to identify genotypes best suited for specific conditions. Though analysis of GEI interaction of multi-location data has been reported severally in other crops, for finger millet little is available and particularly for Uganda it is not available. All these workers however, stressed the usefulness of AMMI analysis for selection of promising genotypes for specific locations or environmental conditions. In general therefore, by examining AMMI biplot, the following questions can be answered for a MET according to Crossa et al. (2002):

1. What are the genotypes that give the highest average yields across environments?
2. What are the environments that gave the highest average yields across the genotypes?
3. Is there a significant GE interaction in this MET?
4. What are the positive and negative GE combinations?
5. Which genotype(s) are most (least) responsive to the environments?
6. Which are the environment(s) that best (least) differentiate the genotypes?.

1.1 Objectives

The objectives of this study were to: i) identify the best performing genotypes in terms of grain yield and blast disease resistance across and in specific environments, and ii) evaluate the influence of genotype, environment, and genotype-environment interaction on grain yield.

2. Materials and Methods

The experimental material consisted of 100 diverse genotypes of finger millet planted at the National Semi Arid Resources Research Institute (NaSARRI) (Latitude 1° 29' 39N Longitude 33° 27' 19E 1085 m.a.s.l.) and Ikulwe satellite station (0° 27' 3N; 33° 28' 16E; 1157 m.a.s.l.) for two seasons (making four environments, Table 1). The 100 genotypes consisted of different cultivars and landraces collected from different regions of the country from which data were collected for this study. The crops were grown under rain-fed conditions in a 10 x 10 lattice design replicated three times in all the locations and seasons. Cultivars E 11 and Seremi 2 were checks for susceptibility and resistance respectively.

Table 1: Environments used for evaluation of the 100 genotypes during the 2011 seasons

Environment	Location	Year/season	Code	Rainfall (mm) [‡]
1	NaSARRI	2011 (LR)	NaS 11LR	616.9
2	NaSARRI	2011 (SR)	NaS 11SR	915.2
3	Ikulwe	2011 (LR)	IKU 11LR	485.9
4	Ikulwe	2011 (SR)	IKU 11SR	677.9

[‡] = amount of rain fall during the growing periods, LR and SR are long and short rainy seasons respectively.

Each genotype was directly sown in six rows of three metres long and 1.5 m wide with row spacing of 30 cm and plant to plant spacing of 10 cm. Measurements were recorded from ten randomly selected plants in each season for leaf blast, head blast and grain yield. The grain yield was obtained on a per plot basis and then converted to yield ha⁻¹. Leaf blast (LB) incidence and severity were assessed at booting stage approximately 45 to 50 days after emergence as recommended by Babu et al. (2013). Head blast (HB) ratings were recorded at the time of grain maturity. The disease incidence was calculated as the number of diseased plants divided by the total number of plants sampled per plot, whereas for severity, different approaches were used for leaf and ear blast respectively. Percent disease index (PDI) on LB was calculated using the formula given by Wheeler (1969) to determine leaf blast severity with the resultant percentages expressed as proportions of 1.00 and categorized as follows: immune – 0.0%, highly resistant 0.1 – 5%, resistant 5.1 – 10%, moderately susceptible 10.1 – 25% and susceptible >25%. For head blast severity, 40 heads from two mid row plants in a plot were randomly selected to determine head blast severity at maturity. For each head a proportion of the spikelets affected by the disease

were estimated using the Standard Evaluation System (SES, IRRI, 1996). Based on the number of heads, then head blast severity was computed as follows:

$$HBS = \frac{(10 \times N1) + (20 \times N3) + (40 \times N5) + (70 \times N7) + (100 \times N9)}{\text{Total number of panicles observed}}$$

N1 – N9 are number of panicles infected with disease, multiplied with the corresponding portion infected. The plants were then categorised as: 0 = no disease or immune, less than 5% = highly resistant, 5-10% = resistant, 11 -25% = moderately resistant, 26 – 50% = susceptible and more than 50% = highly susceptible.

3. Data analysis

The components of variance, the GEI and residual were estimated by the method of general analysis of variance using GenStat (edition 12.1, Payne et al., 2009) software package. Genotype x environment interaction was further analysed using AMMI model as described by Zobel et al. (1988) and Gauch (1992) to identify finger millet accessions adapted to the different environments.

The approach based on analysis of variance and use of phenotypic means considered the effects of genotype, environment and interaction as fixed in the model. Then a combined analysis of variance was performed considering genotypes as fixed effects in GenStat version 12.1 (Payne et al., 2009). Significance of all effects was tested against mean square of error and also genotype-environment interactions. Genotype means were ranked and compared using t-test ($p \leq 0.05$) for both yield and blast reaction scores.

Meteorological data during the experimentation period are presented in Table 2 showing higher rainfall and lower temperatures at NaSARRI compared to Ikulwe. The relative humidity was more or less the same but slightly higher at NaSARRI compared to Ikulwe during the experimentation periods.

Table 2: Meteorological data for year 2011

Site	Month	Rain fall (mm)	Maximum temperature (°C)	Minimum temperature (°C)	Relative humidity (%)
Ikulwe	Jan	31.7	32.5	19.0	62
	Feb	2.3	33.9	19.6	67

	March	121.2	32.2	19.9	71
	April	89.5	31.8	19.4	79
	May	142.4	29.4	19.3	85
	June	82.6	28.7	19.2	83
	July	50.3	29.1	18.5	82
	August	184.7	28.0	18.3	84
	September	116.5	28.3	18.5	83
	October	177.4	28.9	18.8	79
	November	162.2	28.4	18.7	83
	December	37.1	30.3	18.9	70
NaSARRI	Jan	60.0	30.0	15.1	78
	Feb	27.2	29.9	15.4	80
	March	201.2	28.7	16.3	78
	April	132.8	28.3	16.7	80
	May	130.6	27.3	16.4	84
	June	92.5	27.7	15.5	87
	July	59.8	27.9	15.0	86
	August	159.6	26.8	15.3	89
	September	191.6	27.2	16.2	88
	October	331.4	27.6	17.8	80
	November	177.3	27.4	17.7	88
	December	55.3	27.6	17.6	82

The following model was used for the combined data:

$Y_{ij} = \mu + G_i + E_j + GE_{ij} + e_{ij}$ where; μ , is the general mean, G_i , E_j , and GE_{ij} represent the effects of genotype, environment and GEI respectively, and e_{ij} is the average of random errors associated with i^{th} plot that receives the i^{th} genotype in the j^{th} environment (Crossa, 1990).

Additive main effects and multiplicative interactions analysis method which integrates analysis of variance and principle components into a unified approach (Gauch, 1988) was also performed. The AMMI model for t genotypes and S environments may be written as:

$$Y_{ij} = \mu + g_i + e_j + \sum e_n \hat{a}_{in} \tilde{a}_{jn} + \hat{a}_{ij}$$

$$I = 1, 2, 3, \dots, t; j = 1, 2, 3, \dots, S$$

Where Y_{ij} is the yield of the i^{th} cultivar in j^{th} location, μ is the overall mean, g_i is the i^{th} cultivar effect, e_j is the j^{th} environment effect, $\sqrt{e_n} \hat{a}_{in}$ and $\sqrt{e_n} \tilde{a}_{jn}$ are the principal component scores for i^{th} genotype and j^{th} environment respectively. Error $\hat{a}_{ij} \sim N(0, \sigma^2)$; with $\sum_i \hat{a}_{in}^2 = \sum_j \tilde{a}_{jn}^2 = 1$ and the multiplicative interaction term satisfy the constraints, $\hat{e}_1 \hat{e}_2 \dots \hat{e}_n > 0$. Biplots derived by plotting the genotypes and environments markers (scores) of the first two multiplicative terms summarizing interaction patterns. The biplot analyses permits visualisation of differences in interaction effects (Misra et al., 2009) since the two axes use the same physical scale.

Cultivar superiority index for yield and blast disease resistance across the four environments was determined by calculating the superiority index (Lin and Binns, 1994) using the model:

$P_i = \sum (X_{ij} - M_j) / 2n$. Where; P_i = superiority of the i^{th} genotype in the j^{th} environment, M_j = maximum yield for all the genotypes in the j^{th} environment, n = number of environments ($n = 1, 2, 3, 4$). Genotypes with the lowest P_i values are regarded as the most superior and stable across the test environments. For blast disease however, the highest P_i values were regarded as the most superior and stable across test environments since in disease, lower score values are desired unlike yield.

4. Results

4.1 Analysis of Variance

The pooled analysis of variance for grain yield and reaction to blast disease across the four environments showed the main effects of environment, genotypes and their interactions to be highly significant ($p \leq 0.01$, Table 3). Yield performance therefore revealed wide variation in

cultivars between environments. Some cultivars produced significantly greater grain yield in one environment. Likewise genotype reaction to disease was also variable according to environment. On partitioning the GEI component, genotype x location, genotype x season and genotype x season x location effects were highly significant ($p \leq 0.05$) for both blast reaction traits and grain yield. Single environment analysis showed genotypes to be significantly different in all the environments and single location analysis revealed no seasonal effect on head blast severity at NaSARRI and head blast incidence at Ikuwe.

Table 2: Pooled analysis of variance for finger millet blast disease and grain yield ha⁻¹ of 100 finger millet accessions grown in two locations and two seasons during 2011

S.O.V	DF	Mean squares				
		LBI	LBS	HBI	HBS	Grain yield
Environment	3	4.286**	1.64**	4.081**	0.268**	14.131**
Rep (Environment)	8	0.018	0.006**	0.052**	0.0016	0.674**
Genotype	99	0.072**	0.013**	0.228**	0.092**	2.462**
G x E	297	0.029**	0.007**	0.041**	0.0155**	0.459**
• G x Location	99	0.032**	0.005**	0.038**	0.013**	0.602**
• G x Season	99	0.033**	0.01**	0.061**	0.021**	0.535**
• G x Location x season	99	0.022**	0.005**	0.024**	0.012**	0.24**
Residual	792	0.01	0.002	0.009	0.003	0.09
C.V.		23.0%	28.1%	16.5	26.4%	10.3%

*, ** significant ($p \leq 0.05$ and 0.01 respectively), S.O.V, Df, LBI, LBS, HBI, HBS and G.yield are source of variation, degrees of freedom, leaf blast incidence, leaf blast severity, head blast incidence, head blast severity and grain yield ha⁻¹ respectively.

4.2 Top ranked genotypes

Table 4, shows 20 top ranked genotypes by environment. The highest mean grain yield was obtained in NaS 11SR whereas the lowest was in IKU 11SR. The maximum yield ranged from 4.01 to 4.92 t ha⁻¹ in IKU 11LR and NaS 11SR respectively. The minimum yield on the other hand, ranged from 1.07 to 1.47 t ha⁻¹ in NaS 11SR and IKU 11LR respectively. Among the top yielding 20 genotypes, three were open head shaped, six top-curved, five incurved and six fist head shaped in NaS 11LR. At NaS 11SR; two were open head shaped, four top-curved, nine incurved and seven fist head shaped. Environment IKU 11LR had three genotypes with open head shape, eight top-curved, five incurved and three fist head shaped; whilst one was open head shaped, eight top-curved, seven incurved and four fist head shaped in IKU 11SR. The pooled genotypic means across all the four environments had three open shaped genotypes, six top-curved, six incurved and five fist head shaped genotypes.

4.3 Ranking top 20 genotypes on resistance to head blast severity

The means, minimum and maximum head blast severity scores for the top 20 most resistant genotypes in each environment, and pooled for all environments is presented in Table. 5. The means ranged from 0.159 to 0.221 in IKU 11SR and NaS 11LR respectively. The maximum head blast scores ranged from 0.669 to 0.97 in NaS 11SR and IKU 11SR respectively; while the minimum scores were between 0.00 in NaS 11LR and IKU 11SR to 0.064 in NaS 11SR.

Table 3: Ranking top 20 genotypes in terms of grain yield (tons ha⁻¹) based on ANOVA across environments and pooled for all four environments

Rank	Environments								Pooled	
	NaS 11LR		NaS 11SR		IKU 11LR		IKU 11SR		‡Genoty pe	GM
	‡genotyp e	Mea n	‡genotyp e	Mean	‡genotyp e	Mea n	‡genotyp e	Mea n		
1	⁴ G84	3.80	³ G86	4.36	⁴ G84	3.66	⁴ G22	3.82	⁴ G84	3.80
2	³ G86	3.57	² G77	4.35	⁴ G22	3.56	² G61	3.67	³ G86	3.56
3	⁴ G4	3.53	⁴ G84	4.34	² G51	3.54	² G64	3.66	² G51	3.54
4	² G77	3.52	⁴ G29	4.31	² G64	3.45	² G51	3.60	⁴ G4	3.53
5	¹ G89	3.49	⁴ G4	4.35	² G61	3.41	⁴ G84	3.51	² G77	3.52

6	² G51	3.48	¹ G89	4.21	¹ G38	3.39	³ G67	3.49	⁴ G95	3.51
7	⁴ G95	3.47	⁴ G91	4.20	⁴ G95	3.38	² G37	3.40	³ G60	3.50
8	³ G60	3.47	³ G60	4.18	² G37	3.38	¹ G38	3.39	¹ G89	3.49
9	¹ G38	3.39	² G6	4.15	² G100	3.33	² G100	3.32	¹ G38	3.44
10	² G37	3.35	³ G66	4.10	³ G86	3.32	⁴ G95	3.29	² G37	3.43
11	³ G19	3.35	¹ G21	4.02	⁴ G4	3.31	² G90	3.24	⁴ G22	3.39
12	² G100	3.34	⁴ G41	3.95	¹ G67	3.20	³ G94	3.21	² G100	3.39
13	³ G49	3.31	³ G26	3.90	¹ G89	3.27	³ G49	3.20	³ G19	3.38
14	⁴ G22	3.30	⁴ G95	3.90	³ G60	3.26	² G68	3.17	³ G49	3.34
15	³ G23	3.28	³ G19	3.79	³ G19	3.26	³ G19	3.18	³ G23	3.34
16	⁴ G29	3.28	³ G65	3.76	³ G49	3.26	³ G3	3.16	² G64	3.32
17	¹ G21	3.28	³ G23	3.74	² G77	3.25	⁴ G4	3.09	¹ G21	3.31
18	² G64	3.25	³ G80	3.68	³ G23	3.18	² G31	3.07	² G61	3.27
19	⁴ G91	3.20	² G55	3.66	² G68	3.15	³ G23	3.07	⁴ G29	3.25
20	² G61	3.15	³ G49	3.66	² G90	3.14	³ G86	3.06	³ G87	3.21
Mean		2.76		3.12		2.70		2.64		2.81
Min		1.09		1.07		1.47		1.11		1.07
Max		4.24		4.92		4.01		4.57		4.92
C.V.		11.7		10.7		7.8		10.0		0.23
Lsd (0.05)		0.52		0.54		0.34		0.42		10.3
P value		< 0.00		< 0.001		< 0.00		< 0.00		< 0.00

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NaS 11LR, = NaSARRI long rains of 2011, NaS 11 SR, = NaSARRI short rains of 2011, IKU 11LR Ikulwe long rains of 2011, IKU 11SR, Ikulwe short rains of 2011, ‡ Type of head shape: ¹ = open, ² = top-curved, ³ =incurved and ⁴ = fist types of head shapes. GM = Genotypic pooled means.

Of the genotypes that exhibited the least head blast scores among the top 20, head shapes varied as follows: at NaS 11LR; three, three, ten and four genotypes had open, top-curved, incurved and fist type head shapes respectively, at NaS 11SR; two, two, eight and seven genotypes had open, top-curved, incurved and fist shaped head types respectively. At IKU 11LR, three genotypes were open head shaped, five top-curved, eight incurved and four fist head shaped whereas at IKU 11SR, one was open head shaped, three top-curved, eight incurved and fist head shaped.

Table 4: Ranking top 20 genotypes with least head blast scores based on ANOVA across environments and pooled for all four environments

Rank	Environments								Pooled	
	NaS 11LR		NaS 11SR		IKU 11LR		IKU 11SR		‡Genotype	GM
	‡genotype	Mean	‡genotype	Mean	‡genotype	Mean	‡genotype	Mean		
1	³ G45	0.008	³ G86	0.110	⁴ G84	0.042	⁴ G5	0.031	⁴ G84	0.068
2	⁴ G84	0.030	³ G35	0.110	⁴ G4	0.071	⁴ G84	0.048	³ G23	0.094
3	³ G23	0.031	³ G72	0.122	² G97	0.084	³ G62	0.053	⁴ G46	0.094
4	⁴ G4	0.049	⁴ G91	0.129	³ G63	0.085	³ G60	0.059	⁴ G4	0.095
5	³ G32	0.061	⁴ G41	0.126	³ G23	0.087	⁴ G46	0.062	¹ G36	0.099

6	¹ G36	0.06	³ G62	0.12	³ G32	0.09	¹ G36	0.074	³ G32	0.10
		5		7		5				5
7	¹ G83	0.08	⁴ G46	0.13	⁴ G46	0.10	² G2	0.075	² G30	0.11
		2		0		1				3
8	² G48	0.08	³ G60	0.13	³ G65	0.10	⁴ G95	0.075	³ G63	0.11
		2		4		6				6
9	⁴ G46	0.08	⁴ G95	0.13	¹ G36	0.10	² G30	0.076	³ G65	0.12
		3		5		8				5
10	¹ G85	0.09	⁴ G5	0.13	³ G60	0.11	³ G63	0.077	¹ G85	0.12
		3		7		0				5
11	³ G53	0.09	² G77	0.13	¹ G85	0.11	⁴ G29	0.078	⁴ G95	0.12
		5		8		4				7
12	⁴ G41	0.09	⁴ G29	0.13	² G30	0.11	⁴ G4	0.078	³ G56	0.12
		6		9		6				8
13	³ G82	0.10	¹ G36	0.14	¹ G50	0.11	⁴ G91	0.079	² G2	0.12
		3		0		8				9
14	² G76	0.10	¹ G21	0.14	³ G56	0.12	³ G99	0.081	³ G62	0.13
		7		2		1				1
15	³ G86	0.10	³ G99	0.14	² G10	0.12	³ G35	0.084	³ G99	0.13
		6		3		2				1
16	³ G87	0.10	² G13	0.14	³ G62	0.12	³ G65	0.084	⁴ G29	0.13
		9		4		3				4
17	³ G67	0.11	² G2	0.14	⁴ G28	0.12	³ G23	0.084	¹ G50	0.13
		0		5		5				6
18	² G30	0.11	³ G33	0.14	² G39	0.12	³ G32	0.088	³ G72	0.13
		3		5		5				7
19	³ G56	0.11	³ G16	0.14	³ G45	0.12	⁴ G34	0.088	² G10	0.14
		3		5		9				3

20	³ G63	0.11	⁴ G34	0.14	² G2	0.13	² G20	0.089	³ G81	0.14
		8		7		0				4
Mean		0.22		0.21		0.21		0.159		0.20
		1		5		9				4
Min		0.00		0.06		0.01		0.00		0.00
				4		1				
Max		0.82		0.66		0.84		0.97		0.96
				9						7
C.V.		25.8		19.6		25.6		36.7		26.4
Lsd		0.09		0.06		0.09		0.094		0.04
(0.05)		2		8						3
P value		<		<		<		<		<
		0.00		0.00		0.00		0.001		0.00
		1		1		1				1

NaS 11LR, = NaSARRI long rains of 2011, NaS 11 SR, = NaSARRI short rains of 2011, IKU 11LR Ikulwe long rains of 2011, IKU 11SR, Ikulwe short rains of 2011, ‡ Type of head shape: ¹ = open, ² = top-curved, ³ = incurved and ⁴ = fistid types of head shapes. GM = genotypic pooled means

4.4 Cultivar superiority index and mean rank

Cultivar superiority index P_i for grain yield ha^{-1} of the top 20 cultivars showed G84 had the lowest superiority index of 0.004 which implied the genotype is superior in terms of yield to all the other genotypes in this study (Table 6). The second most superior cultivar was G86. For blast disease, the cultivar with highest superiority index was still G84 and second most superior was G 46. This showed that G 84 was the most superior in terms of blast disease resistance.

Table 5: Superiority index (P_i) and mean rank for grain yield and blast disease resistance for 20 genotypes

Grain yield ha ⁻¹				Blast disease			
Genotype	P _i	Genotype	Mean rank	Genotype	P _i	Genotype	Mean rank
G84	0.004	G84	7	G84	0.87	G84	95
G86	0.006	G51	11.25	G4	0.81	G46	91
G95	0.007	G86	11.25	G23	0.80	G36	87.8
G4	0.007	G95	12	G46	0.80	G4	85.1
G77	0.009	G4	13	G36	0.79	G60	85.1
G51	0.009	G37	13.75	G45	0.78	G30	84.8
G38	0.010	G38	14.25	G32	0.78	G23	83.8
G60	0.011	G77	15.5	G63	0.76	G32	81.8
G37	0.011	G100	16.25	G30	0.75	G95	81.6
G89	0.011	G49	17.25	G60	0.75	G63	80.3
G49	0.012	G60	17.5	G65	0.74	G45	79.8
G100	0.012	G89	17.5	G62	0.73	G2	79.3
G23	0.012	G23	19.25	G85	0.72	G65	78.8
G21	0.013	G21	21.5	G95	0.72	G29	78.4
G29	0.016	G22	22.5	G2	0.72	G62	78.3
G19	0.017	G64	25.5	G56	0.72	G99	78.3
G87	0.017	G29	25.25	G99	0.71	G91	73.8
G8	0.018	G19	26.5	G29	0.71	G50	73.5

G68	0.018	G68	26.5	G50	0.71	G56	73
G64	0.019	G87	26.75	G10	0.70	G85	71.8

The cultivars among the top 20 that combined superiority for both grain yield and blast disease resistance were: G84, G4, G60, G95, G23 and G29. These showed both high and stable grain yield and stable resistance to blast disease.

4.5 Stability and adaptability analysis

The ANOVA table of the AMMI II model analysis of yield data presented in Table 7 showed that all the three components were highly significant ($p \leq 0.01$). The genotype, environment, and GE interaction explained 57.69, 10.04 and 32.27% of the total treatment variation, respectively. The G x E interaction was further partitioned into IPCA1 and IPCA2. The IPCA1 component explained 17.33% of the total variation, which was 53.71% of the GE interaction whereas ICPA2 component explained 14.94% of total variation, which was 46.29% of the GE, with residual effects explaining 0% of both total variation and GE interactions. Therefore, the genotypic and GE components explained 89.96 of the total treatment variation whereas environment only explained 10.04%

Table 6: AMMI ANOVA of 100 finger millet accessions for yield (tons ha⁻¹) in four environments

Source of variation	Df	SS	% G-E SS	MS	F	% of GXE Interaction SS
Treatment	399	422.4	100.00	1.059	12.78**	
Genotypes	99	243.7	57.69	2.462	29.71**	
Environments	3	42.4	10.04	14.131	20.97**	
Interactions	297	136.3	32.27	0.459	5.54**	
IPCA 1	101	73.2	(17.33)	0.724	8.74**	53.71

IPCA 2	99	63.1	(14.94)	0.638	7.70**	46.29
Residual	97	0.0	0.00	0.000	0.00	0.00
Error	792	65.6		0.083		

Df = degrees of freedom, SS = sums of squares, % G-E SS = percentage genotype/environment sum of squares, MS = mean square.

4.6 The four genotype selection from AMMI

AMMI generated best four selections from each environment as presented in Table 8. The genotypes which appeared among the top four yielders in at least two environments were G22, G51, G64, G84 and G86; G84 appearing three times. The least IPCA 1 score in terms of magnitude was obtained at NaSARRI during the long rainy season whereas the highest was at NaSARRI during the short rainy season.

Table 7: First four AMMI selections per environment

Environment	Mean grain yield (tons ha ⁻¹)	IPCA score	Rank			
			1	2	3	4
NaS 11LR	2.77	0.136	G84	G86	G4	G88
NaS 11SR	3.12	1.718	G86	G77	G84	G29
IKU 11LR	2.70	-0.573	G84	G22	G51	G64
IKU 11SR	2.64	-1.281	G22	G61	G64	G51

NaS 11LR, = NaSARRI long rains of 2011, NaS 11 SR, = NaSARRI short rains of 2011, IKU 11LR Ikulwe long rains of 2011, IKU 11SR, Ikulwe short rains of 2011.

4.7 AMMI – Biplots for classification of genotypes and environments

The most powerful interpretive tool in analysis of G x E interaction in AMMI model according to Crossa et al. (1991) is the biplot analyses since the biplots permit visualisation of differences in interaction effects (Misra et al., 2009). In the AMMI II biplot (Fig 1), the IPCA1 scores of genotypes and environments are plotted against their respective means. The results revealed that the main effects (Genotypes and environments) accounted for 67.73% and IPCA1 accounted for 17.33% of the total variation in the data and the rest accounted for by residual, therefore AMMI I biplot gave a model fit of 85.06%. The scatter of the genotype points in the AMMI I biplot showed three environmental clusters that is NaS 11SR with very high positive interaction, IKU 11SR with high negative interaction and NaS 11LR and IKU 11LR with low to moderate levels of interactions but in opposite directions. Genotypes close to IPCA1 value of zero indicate minimal interaction with the environment and among them with above mean yields were: G5, G9, G10, G19, G23, G49, G50, G59, G84, G86, G87, G96 and G100.

The results also showed that environments NaS 11SR and IKU 11SR were the highest and lowest yielding environments respectively as they produced the highest and least means, whereas NaS 11LR and IKU 11LR were close to each other and the origin with values above the mean. Since NaS 11LR and IKU 11LR were the long rainy season for NaSARRI and IkuIwe respectively, it is an indication that during the long rainy season the yields were stable, the differences observed being due to location. On the other hand, the great disparity observed in short rainy season, showed high variance in conditions during the season at the two locations. Environment NaS 11SR had the highest mean yield (3.12 t ha⁻¹) whilst IKU 11SR had the least mean yield (2.64 t ha⁻¹). Genotypes exhibiting high interactions were G52, G48, G67, G61, G64, G22 (negative) and G6 (positive) otherwise the other genotypes may be categorised as having moderate interaction. Environment NaS 11SR showed positive moderate interactions with G6, G66, G91, G29, G21, G41, G55, and G56 whilst IKU 11LR and IKU 11SR showed positive interactions with G52, G48, G42, G71, G44, G7, G15, G68, G13 and G85.

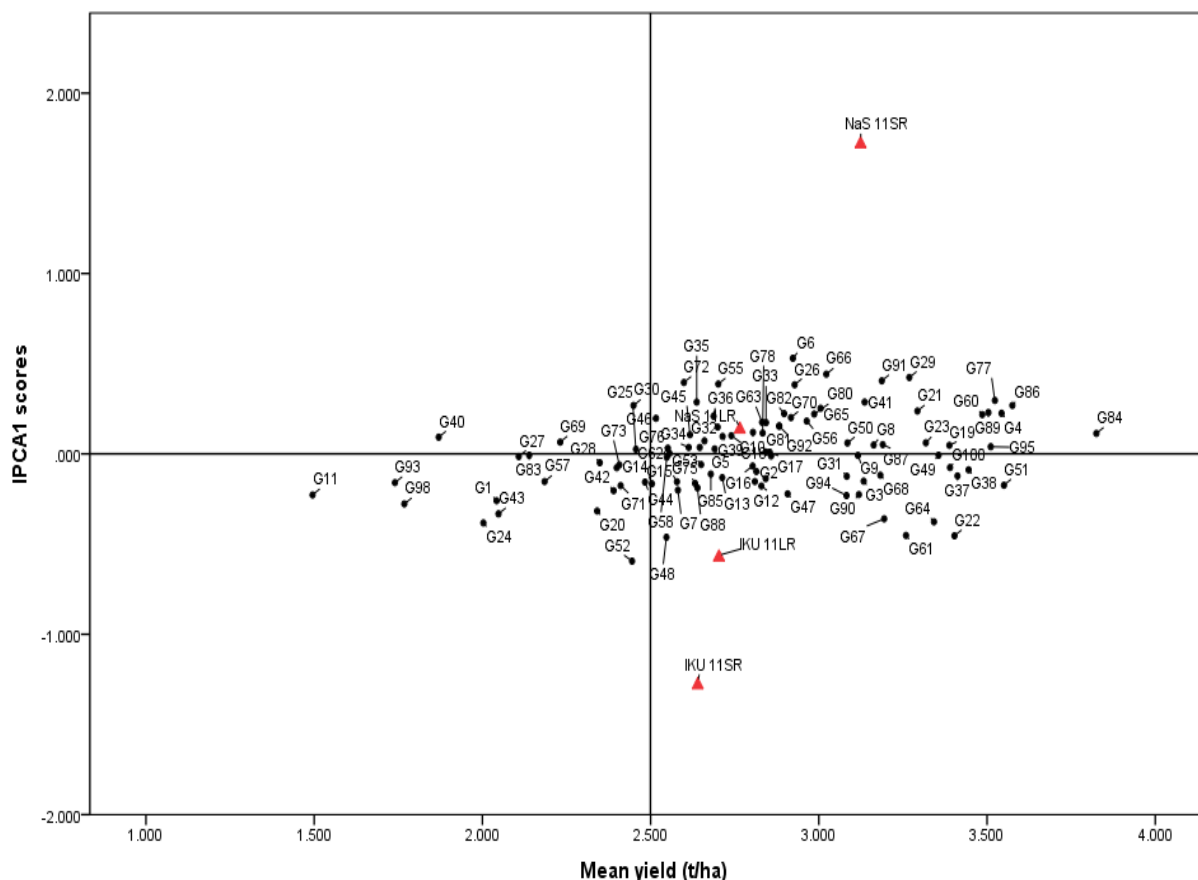


Figure 1: Plot of Genotype and environmental IPCA1 VS Means for the four environments. the environments; NaS 11LR, NaS 11SR, IKU 11LR and IKU 11 SR are NaSARRI long rainy season 2011, NaSARRI short rainy season 2011, Ikulwe long rainy season 2011 and Ikulwe short rainy season 2011 respectively.

▲ = Environments; ● = genotypes

5. Discussion

The significant environment, genotype main effects and GEI for grain yield indicated that the genotypes were different, environments diverse and the performance of a genotype was affected by environmental conditions. From the AMMI analysis, genotype had the greatest effect accounting for 57.69%, GEI 32.27%, with environment accounting for only 10%. This showed a higher variability among the genotypes and lower variability in the test environments. The first two IPCA scores explained 100% of the interaction sum of squares. The highly ($p \leq 0.01$)

significant effect of environment showed high differential genotypic responses across environments. Variations in rainfall amounts, temperatures, relative humidity and blast disease could have contributed to the observed differences. This is in line with a report by Verma (1989) who indicated that high mean daily temperature followed by frequent rainfall with low light intensity reduced grain filling in finger millet and thus limited yield.

5.1 Yield performance based on analysis of variance

Significant differences for yield across environments suggested genotypes performed differently under diverse environments and their performances were unpredictable across environments as was also reported by (Rasyad et al., 2012). Since GEI was also significant ($p \leq 0.01$) in the current study, it is an indication that selecting superior finger millet varieties in particular areas and seasons may not necessarily result in superior performance in other areas and/or seasons. It must therefore be decided whether to plant widely adapted varieties or locally adapted varieties. To choose a widely adapted variety, breeders and farmers need to choose varieties which are stable across locations and/or seasons since edaphic and climatic conditions tend to vary across locations and seasons which are highly likely to cause yield variation (Verma, 1989).

The significant genotype x location interaction observed in the current study indicated that genotypes performed differently in the different locations and therefore performance was less stable. From the results, there was expression of crossover (qualitative) interaction since there were genotypic changes in ranking from one environment to another. However, there were genotypes which were quite consistent in the top 20 best performers as they occurred in all environments indicating relative stability.

Genotype x season interaction was also significant, a reflection of inconsistency in performance of genotypes in different seasons. The genotype x location component of G x E, may be indicative of specific adaptation by subdividing target areas in homogeneous regions that minimise G x E within locations. Since the genotype x season and genotype x location x season were also significant, it makes spatial subdivision of the locations difficult for finger millet production. Therefore testing of genotypes in such a scenario would require a representative range of conditions as a reliable strategy since it would cover a representative sample of spatial and temporal variations, and according to Crossa et al. (1991), a selection environment in one year may have little relation to those experienced in the next. The observations made in the current study, therefore, would suggest testing finger millet genotypes for many cropping cycles. To save time however, several workers have suggested substituting temporal variation with spatial variation assuming that testing over wide locations can ensure a parallel degree of temporal buffering capacity in their germplasm (Romagosa and Fox, 1993). It has also been

statistically elucidated by Barah et al. (1981) that both spatial and temporal buffering rely on the same mechanism in experiments with sorghum, and in rice by Flinn and Garrity (1989).

5.2 Genotypic blast disease reaction across environments

The main effects of environment and genotype and genotype x environment interaction on blast disease were highly significant ($p \leq 0.01$), similar to findings of Takan et al. (2004) and Lenne et al. (2007) who demonstrated that there is a considerable variation in aggressiveness of *Magnaporthe grisea* isolates on different finger millet varieties. They also observed that aggressiveness varied according to source of isolates, a hint that isolates from different locations were different. They however, inferred that there was no gene-for-gene relationship between finger millet pathogen as in rice implying no major genes for resistance were involved in these interactions. *Pyricularia grisea*, the *Eleusine* pathotype is defined by its specific pathogenicity to *Eleusine* species such as *Eleusine coracana*, *Eleusine indica* and *Eleusine africana* (Tanaka et al., 2009). He further reported that though the pathogen seems to be uniform, its members are however not cultivar-specific. Dobinson et al. (1993) divided *Eleusine* isolates into at least two genetically distinct sub-groups, which were further divided by Tanaka et al. (2009) according to origin indicating variability of the *Pyricularia Eleusine* pathogen.

The significant effect of environment and genotype x season effect on blast disease was also reported by Takan et al. (2004) indicating differential reaction based on environments and seasons. The report indicated that during the short rainy season, the disease incidence and percentage severity were significantly low compared to the long rainy season. This could be attributed to low precipitation, low humidity and high temperature; factors which do not encourage blast pathogen development (Babu et al., 2013). So the seasonal differences in blast occurrence could explain the significant differences during the seasons. The higher levels of disease at NaSARRI compared to Ikulwe could also be due to the fact that the conditions were probably more favourable for disease development and multiplication at NaSARRI where there has been continuous cultivation of finger millet compared to Ikulwe. This could have led to accumulation of the pathogen making NaSARRI a hot spot area. The somewhat low yields obtained at Ikulwe compared to NaSARRI despite low pathogen levels may be explained by other unfavourable agro-climatic conditions that could have led to poor agronomic performance.

5.3 Top ranking of genotypes based on blast disease reaction and grain yield

From the results, genotypes that showed blast resistance irrespective of environment among the farmer varieties were: G23, G36 and G84; ICRISAT introductions G45 and G46 also showed resistance across environments, and an improved and released variety G99 was also resistant. These results showed that within the 100 accessions, there were genotypes with high levels of

blast resistance across the test environments; therefore sources of genes for stable and/or durable resistance against blast disease could be identified. There were also varieties that showed consistently higher yields across environments; among them were: G4, G21, G23, G37, G38, G77, G84 and G95 among the farmers' varieties, G49 an introduction from ICRISAT, G51 and G100, improved cultivars from NaSARRI. These identified varieties can be utilised further in the breeding programme to breed cultivars with both good agronomic traits and high levels of blast disease resistance. The stable resistance was a further indication of availability of genotypes that could be used as sources of genes for resistance against several races of the pathogen. The significance of GEI would also imply screening for both resistance to blast disease and yield must be conducted in target environments or a representative target environment where finger millet cultivars will be grown. Cultivar superiority index also identified high yielding genotypes across environments with stable resistance against blast disease. Six genotypes: G84, G4, G60, G23 and G29 combined both high grain yield potential and stable blast resistance.

5.4 AMMI Model analysis to classify genotypes and environments

From the AMMI biplot the environments fall into three groups: NaS 11SR with large positive IPCA 1 scores, which interact strongly with genotypes that have positive IPCA 1 scores and negatively with genotypes with negative scores; IKU 11SR with large negative IPCA 1 scores thus strongly interact with the genotypes but in the opposite direction to NaS 11SR; NaS 11LR and IKU 11LR with small IPCA 1 scores (between 0 and ± 0.5), suggesting that they had little interaction with the genotypes and therefore least differentiated genotypes unlike NaS 11SR and IKU 11SR. Environments can be sub grouped according to their average yield over the genotypes. Within the genotypes, G6, G19, G21, G22, G23, G26, G29, G41, G49, G64, G66, G84, G87, G91, G100 had higher average yields; of which G6, G26, G29, G41, G66, G91 were especially suitable to NaS 11SR, while G22, G61, G64 and G67 were specifically adapted to IKU 11SR.

The genotypes and environments of axis 1 showing values close to zero contributed little to the sum of squares of the genotype x environment interaction; they were therefore the most stable. Genotypes G9, G19, G23, G25, G49, G50, G59, G62, G87, and G99, were among those that contributed least to the genotype x environment interaction, in other words were less responsive to environmental changes. Genotypes G10, G19, G17, G37, G53, G96 and G100, had relatively high yields and showed intermediate IPCA1 values. These genotypes were moderately stable, showing wide adaptation to the test environments. The genotypes with high average yields making the highest contribution to this interaction were G6, G22, G52, G61, G64, and G67 clearly indicating specific adaptation and low stability (Yan and Kang, 2003), whereas genotypes; G1, G11, G24, G43, G93 and G98 were lowest yielding and least stable showing

non-adaptation to any of the test environments. The environments making the greatest contribution were NaS 11SR and IKU 11SR; the smallest contributions were made by NaS 11LR and IKU 11LR, that is, the long rainy season at both NaSARRI and Ikulwe. The most productive environment was NaS 11SR followed by NaS 11LR (NaSARRI short and long rainy seasons respectively) a further confirmation of NaSARRI being more favourable compared to Ikulwe probably due to the differences in agro-climatic conditions and better adaptation of the genotypes to NaSARRI.

Analysis of the genotype x environment interaction thus detected variability of environments for both grain yield and head blast disease reaction, with groups of some genotypes showing specific adaptability and others showing stability. Differential performances of genotypes due to the environmental variability was observed and explained by Broccoli and Burak (2004) who associated the variability with soil and water conditions as these are paramount to grain filling, and prevailing temperatures also affecting effective photosynthesis and photosynthates translocation. Pajic and Babic (1991) working with maize also reported that the size and weight of grain depended exclusively on environment although other workers like Broccoli and Burak (2004) found that genotype also had influence on these traits.

Displacement along the x-axis of the AMMI biplots reflected differences in main effects, whereas displacement along the y-axis exhibited differences in interaction effects. Genotypes with IPCA1 scores near zero had little interaction with environments. Genotypes or environments on the same parallel line relative to the y-axis had similar mean values for yield, and genotype or environment on the right hand side of the guidelines had yields above the mean. The impact of environment was highly significant on yield justifying MET to identify good performers in particular environments and/or across environments. Significant variation due to locations and seasons is a further pointer to the need of multi-locational performance trials for more than one season for reliability of performance to be made and therefore reliable decisions in finger millet breeding.

Partitioning the variance components revealed that Location and Genotype x Season were the main sources of G x E interaction for yield suggesting the possibility of identifying varieties with specific adaptation. Seasonal effect was the main source of GEI for both leaf blast severity and head blast severity. For yield the impact of environment is expected since yield is a polygenic trait (Lin and Binns, 1994), and therefore subject to influence from the environment. The environmental impact complicates potential genetic gain and advance in yield and resistance to blast disease and thus requires testing of genotypes in multi-environments to identify those with specific adaptation and/or stability.

Conclusion

The combination of ANOVA and AMMI analyses were sufficient to explain the effects of environments, genotypes and the GEI observed in the study and resulted in identification of genotypes with stable high yields and field resistance to blast disease across environments. Both ANOVA and AMMI analyses revealed the best genotypes, but AMMI further identified the best genotypes that had wide adaptation. The genotypes identified as stable and high yielding were: G9, G19, G23, G49, G50, G59, G62, G84, G87, G95, G99, and G100, whereas genotypes identified as high yielding but unstable and probably suitable for specific adaptation were: G4, G6, G22, G29, G51, G61, G64, G66, G77, G86, G88, G91 and G94.

Analysis of variance also revealed genotypes with the least blast scores, and those that exhibited both least blast scores and high yields. These included: G4, G23, G84 and G95. Additive Main effects and Multiplicative Interaction analysis also identified NaS 11SR as a high yielding environment but most segregating, whereas NaS 11LR and IKU 11LR were relatively high yielding and least differentiated genotypes. Cultivar stability index identified genotypes for both stable high grain yield and stable blast disease resistance. These were: G84, G4, G60, G23 and G29.

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References

- Andrew, D.J. 1993. P. 411 – 423. Riley, K.W., S.C. Gupta, A. Seetharam, and J.N. Mushonga. (Eds.). Advances in small millets. Oxford and IBH Publication Co. Pvt. Ltd. New Delhi.
- Babu, T.K., Thukar, R.P., Upadhyaya, H.D., Reddy, P.N., Sharma, R., Girish, A.G., and Sarma, N.D.R.K., 2013. Resistance to blast (*Magnaporthe grisea*) in a mini-core collection of finger millet germplasm. European Journal of Plant Pathology. Open Access Repository, International Crops Research Institute for Semi-Arid Tropics. Available online <http://dx.doi.org/10.1007/s10658-012-0086-2/> (date accessed: 10/04/2013).
- Balestre, M., dos Santos, V. B., Soares, A.A., and Reis, M.S., 2010. Stability and adaptability of upland rice genotypes. Crop Breeding and Applied Biotechnology, 10:357-363.

- Barah, B.C., Binswanger, H.P., Rana, B.S., and Rao, N.G.P., 1981. The use of risk aversion in plant breeding; concepts and application. *Euphytica*, 30:451-458.
- Broccoli, A.M., and Burak, R., 2004. Effect of genotype x environment interactions in popcorn maize yield and grain quality. *Spanish Journal of Agricultural Research*, 2:85-91.
- Crossa, J. 1990. Statistical analysis of multi-location trials. *Advances in Agronomy*, 44:55-85.
- Crossa, J., Cornelius, P.L., and Yan. W., 2002. Biplots of linear-bilinear models for studying crossover genotype x environment interaction. *Crop Science*, 42:619-633.
- Crossa, J., Fox, P.N., Pfeiffer, W.H., Rajaram, S., and Gauch, H.G., 1991. AMMI adjustment for statistical analysis of an international wheat yield trial. *Theoretical and Applied Genetics*, 81:27-37.
- Dobinson, K.F., Harris, R.E., and Hamer. J.E., 1993. Grasshopper, a long terminal repeat (LTR) retroelement in the phytopathogenic fungus *Magnaporthe grisea*. *Mol Plant Microbe Interaction*, 6:114-126.
- FAOSTAT. 2012. Production of finger millet in Uganda during 1999- 2010. Statistic database of Food and Agricultural Organisation Publications, Rome, Italy.
- Flinn, J.C. and Garrity. D.P., 1989. Yield stability and modern rice technology. P. 250 – 264. Anderson, J.R. and P.B.R. Hazell (Eds). In: *Variability in Grain Yields: Implications for Agricultural Research and Policy in Developing Countries*, John Hopkins University Press, Baltimore.
- Gauch, H.G. 1992. Statistical analysis of regional yield data: AMMI analysis of factorial designs. Amsterdam, Elsevier.
- Gauch, H.G. 1988. Model selection and validation of yield trials with interactions. *Biometrics*, 44:705-715.
- IRRI; Standard Evaluation System for rice 4th Edition; IRRI, INGER Genetic Resources Center, Manila, Philippines, 1996.
- Joshi, B.K., Tiwari, R.K., Amgain, R.B., Shrestha, P., Gyawali, S., Mudwari A., and Baniya, B.K., 2005. Stability and adaptation in finger millet (*Eleusine coracana* (L.) Gaertn.) landraces. *On-farm Conservation of Agricultural Biodiversity in Nepal*, 1:73-83.

- Kidoido, M.M., Kasenge, V., Mbowa, S., Tenywa, J.S., and Nyende. P., 2002. Socio-economic factors associated with finger millet production in eastern Uganda. *African Crop Science Journal*, 10:111-120
- Lenne, J.M., Takan, J.P., Mgonja, M.A., Manyasa, E.O., Kaloki, P., Wanyera, N., Okwadi, J., Muthumeenakshi, S., Brown, A.E., Tamale, M., and Sreenivasaprasad. S., 2007. Finger millet blast management: a key entry point for fighting malnutrition and poverty in East Africa. *Outlook on Agriculture*, 36:101-108.
- Lin, C.S. and Binns. M.R., 1994. Concepts and methods for analyzing of regional trial data for cultivar and location selection. *Plant Breeding Review*, 12:271-297.
- Misra, R.C., Das, S., and Patnaik. M.C., 2009. AMMI Model Analysis of Stability and Adaptability of late duration finger millet (*Eleusine coracana*) Genotypes. *World Applied Science Journal*, 6:1650-1654.
- Pajic, Z. and Babic. M., 1991. Interaction of popping volume and some agronomic characteristics in popcorn hybrids. *Genetika*, 2:137-144.
- Payne, R.W., Murray, D.A., Harding, S.A., Baird, D.B., and Soutar, D.M., 2009. An introduction to GenStat for Windows (12th edition). VSN International, 5 The Waterhouse, Waterhouse Street, Hemel Hemstead, UK.
- Purchase J.L. 1997. Parametric analysis to describe genotype x environment interaction and yield stability in winter wheat. *South African Journal of Plant and soil*, 17:101-107.
- Ramagosa, I. and Fox. P.N., 1993. Genotype x environment interaction and adaptation. In: Hayward, M.D., N.O. Bosemark, and I. Ramagosa (Eds.). *Plant Breeding: Principles and Prospects*. Chapman and Hall, London, 1993, Publication.
- Rasyad, A., Manurung, G. M. E., Van Sanford, D. A., 2012. Genotype x Environment interaction and stability of yield components among rice genotypes in Riau province, Indonesia. *SABRAO Journal of Breeding and Genetics*, 44:102-111.
- Samonte, S.O.P.B., Wilson, L.T., McClung A.M., and Medley, J.C., 2005. Targeting cultivars onto rice growing environments using AMMI and SREG GGE biplot analysis. *Crop Science*, 45:2414-2424.
- Solanki, J.S., Maloo, S.R., and Sharma. S.P., 2000. Stability analysis for seed yield in finger millet. *Indian Journal of Agricultural Research*, 34:268-270.
- Takan, J.P., Akello, B., Esele, P., Manyasa, E.O., Obilana, A., Audi, P.O., Kibuka, J., Odeno, M., Oduori, C.A., Ajanga, S., Bandyopadhyaya, R., Muthumeenakshi, S., Coll, R., Brown, A. E., Talbot, N.J., and Sreenivasaprasad, S., 2004. Finger millet blast pathogen

- diversity and management in East Africa: a summary of project activities and outputs. International Sorghum and Millets Newsletter, 45:66-69.
- Tanaka, M., Nakayashiki, H., and Tosa, Y., 2009. Population structure of *Eleusine* isolates of *Pyricularia oryzae* and its evolutionary implications. Journal of General Plant Pathology, 75:173-180.
- Verma, V.S., 1989. Variability pattern in quantitative traits of ragi (*Eleusine coracana* (L) Gaertn). Madras Agricultural Journal, 76:626-629.
- Yan, W., and Hunt, L.A., 1988. Genotype x Environment Interaction and Crop Yield. Plant Breeding Reviews, 16:135-228.
- Yan, W., Hunt, L.A., Sheng, Q., and Szlavnic, Z., 2000. Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Science, 40:597-605.
- Yan, W., and Kang, M.S., 2003. GGE biplot analysis: a graphical tool for breeders, geneticists, and agronomists. CRC Press LLC. 2000 N.W. Corporate Blvd., Boca Raton, Florida 33431, USA.
- Wanyera, N.M.W., 2007. Finger millet (*Eleusine coracana* (L) Gaertn) in Uganda. P. 1-9. In: Mgonja, M.A., J.M. Lenne, E. Manyasa, and S. Sreenivasaprasad (Eds). Proceedings of the first international finger millet stake-holders workshop, projects R8030 & 8445, UK Department for international development – crop protection programme held on 13th -14th September 2005 at Nairobi.
- Wheeler, B.E.J., 1969. An introduction to plant disease. John Wiley and Sons Ltd., London.
- Zobel, R.W., Madison, J.W., and Gauch, H.G., 1988. Statistical analysis of a yield trial. Agronomy Journal, 80:388-393