International Journal of Agriculture, Forestry and Fisheries
2015; 3(5): 202-205
Published online October 22, 2015 (http://www.openscienceonline.com/journal/ijaff)

Dissecting Genotype by Environment Interactions in Sesame (*Sesamum indicum* L.) Genotypes Form Niger

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To cite this article

Abdou Razakou Ibrahim, Moutari Adamou, Djibo Moussa, Bachari Moussa. Dissecting Genotype by Environment Interactions in Sesame (*Sesamum indicum* L.) Genotypes form Niger. *International Journal of Agriculture, Forestry and Fisheries.* Vol. 3, No. 5, 2015, pp. 202-205.

Abstract

The adaptability of a variety over diverse environments is usually tested by its degree of interaction with different growing environments. JRA was used in this study to dissect G x E interaction in sesame genotypes. The results showed significant differences for genotypes, environments and genotypes x environment interactions indicating that genotypes behaved differentially across environments. Genotypes SN203 and SN403 recorded the highest seed yields mean of 187 kg/ha and 206 kg/ha respectively and had a regression coefficient closer to unity (0.98 and 0.89 respectively) across the six (6) environments. These genotypes performed consistently well in these environments. Therefore, SN203 and SN403 sesame genotypes could be recommended in LUCOP-Ti project intervention area located in the western part of Niger.

Keywords

Genotypes, Environments, Genotypes x Environment, Join Regression Analysis, Stability

1. Introduction

Sesame (*Sesamum indicum* L.), is an oleaginous crop that seems to be originated from Africa (Ethiopia) (Weiss, 1971; Yahya, 1998). But, countries like India, China and Japan where wild types of sesame exist are secondary centers of diffusion (Yahya, 1998). In Niger, sesame constitutes the second oleaginous crop after groundnuts, which both provide the most important source of local oil. However, the mean productions during the last five years (2009-2013) were 79,490 tons in an area of 163,954 ha with a mean yield of 482 kg /ha, which is very low compared to world average of 692 kg/ha (FAOSTAT, 2014). The reason of this low productivity obtained at farmers field level resulted in large genotypes by environment (G x E) effects.

The studies on genotype × environment interaction are very common in sesame (Yebio et al., 1993; John et al., 2001; Boshim et al., 2003; Mekonnen and Mohammed, 2009; Suvarna et al., 2011; Muhammad Yasin Mirza et al., 2013). Recently in 2013, Narendra Kumar et al., stated that the pooled analysis of variance due to genotypes, environments as well as genotype × environment interactions were highly significant for seed yield/plant while assessing the genotype × environment interaction and their stability across four environments for seed yield and physiological traits.

Since a genotype is considered to be more adaptive or stable if it has a high mean yield but low degree of fluctuation in yielding ability when grown over diverse environments. The present study was designed to dissect G x E interaction in sesame genotypes in order to identify the most adapted and stable one in LUCOP-Ti intervention area at Western agro ecological region of Niger.

2. Materials and Method

A set of 8 sesame genotypes (SN-103, SN-203, SN-303, SN-403, L1, L5, BS and S42) were sown in a randomized complete block design with three replications in six environments (Gotheye, Djambala, Dabaraye, Maïkogo, Doumba, Bangario) of Tillaberi region located in western part of Niger in 2010. The elementary plot was 50 m^2 and spacing was 50 cm intra and inter rows. NPK fertilizer was applied after sowing in a rate of 150 kg/ha.

The climate of this area is typical tropical type characterized by arid condition. The mean annual rainfall was 417.12 ± 96.10 mm, with a mean temperature of 37.62 ± 0.83°C and relative humidity of 59.6 ± 2.07%. All recommended agronomical practices and plant protection measures were adopted for raising a good crop establishment. Data were recorded from two central rows of each genotype in each replication for seed yield/plant. Join Regression Analysis (JRA) was used to dissect G x E interactions by characterizing each environment in terms of its quality. With this model, G x E is explained in terms of differential sensitivities to environmental improvement (slope = sensitivity). SAS software and R studio package (version 3.1.1) were used for analyzing data.

3. Results and Discussion

The analysis of variance revealed significant effects for environment, genotypes and their interactions indicating that variations exit among genotypes and environment (table 1).

These findings are in agreement with the results obtained of Kangbo *et al*. (2003) and Narendra Kumar *et al.,* (2013). They reported that environment had large effects on sesame yield followed by genotypes and genotypes x environment interactions, which explained that genotypes behaved differently to different environments.

Table 1. *ANOVA for seed yield of 8 sesame genotypes harvested from six environments.*

	Df	SS	MS	F cal
Environment	5	3277950	655590**	61.81
Genotypes	7	551670.07	78801.01*	7.43
Environment x block	12	1253267	10272 ns	0.97
Environment x genotypes	35	21492436	614069.6**	57.89
Residuals	82	869768	10607	

**= significant at 1%, *=significant at 5%, ns= not significant, Df= degree of freedom, SS = Sums of squares and MS = Means of squares,

3.1. Seed Yield (kg/ha)

The mean seed yield over different environments ranged from 518 kg/ha to 81 kg/ha. The highest environmental mean was obtained at Bangario followed by Doumba, while le lowest was obtained at Djambala (table 2). Expected Bangario where seed yield means performance seemed to be normal with maximum, minimum and mean of 687 kg/ha, 400 kg/ha and 518 kg/ha respectively, the other environments showed relatively low performance.

Table 2. *Mean performances.*

Variable	Environment					
	Gotheye	Djambala	Dabaraye	Maïkogo	Doumba	Bangario
Minimum	36	22	140	73	125	400
Maximum	196	108	233	260	250	687
Mean	81	70	181	134	158	518
SE	27,32	21,60	51,42	51,40	43,83	11,62
CV (%)	53	53	49	66	48	37

SE=standard error, CV=coefficient of variation

Table 3. *Individual means performance of 8 sesame genotypes tested under 6 environments.*

Genotype	Environment						
	Gotheye	Djambala	Dabaraye	Maïkogo	Doumba	Bangario	Mean
SN103	39 b	108 a	193 a	103 a	125 a	513 a	180
SN203	95 ab	93 a	193 a	83 a	150 a	507 a	187
SN303	134 ab	103 a	160 a	260 a	150 a	473 a	213
SN403	44 b	90 a	233 a	213 a	150 a	507 a	206
L1	55 b	72 a	140 a	73 a	250 a	400 a	165
L5	49 b	47 a	193 a	147 a	150 a	567 a	192
BS	36 b	22 a	167 a	78 a	125 a	493 a	154
S42	196 a	27 a	167 a	113 a	167 a	687 a	226
Env. Mean	81	70	181	134	158	518	
CV (%)	53	52	49	66	48	37	

Env. mean= environmental mean, CV(%) = coefficient of variation

Table 4. *Genotypes scoring and ranking.*

Genotype	Gotheye	Djambala	Dabaraye	Maïkogo	Doumba	Bangario	Sum	Mean	SDV
SN103	7	1	2	5	7	3	25	4.2	2.6
SN203	3	3	3	6	3	4	22	3.7	1.2
SN303	2	2	7	1	4	7	23	3.8	2.6
SN403	6	4	1	2	5	5	23	3.8	1.9
L1	4	5	8	8	1	8	34	5.7	2.9
L5	5	6	4	3	6	2	26	4.3	1.6
BS	8	8	5	7	8	6	42	7.0	1.3
S42	1	7	6	4	2	1	21	3.5	2.6

SDV = standard deviation

Table 3 showed mean seed yield (kg/ha) of individual environment. Overall mean seed yield ranged from 22 kg/ha for genotype BS at Djambala to 687 kg/ha for S42 at Bangario. The highest mean seed yields across environments were show by genotypes S42 (226 kg/ha), SN303 (213 kg/ha), SN403 (206 kg/ha) and L5 (192 kg/ha), which were higher than grand mean of 190 kg/ha, whereas the lowest mean seed yields were recorded by BS (154 kg/ha) followed by L1 (165 kg/ha). The other counterpart SN103 and SN203 with respectively 180 kg/ha and 187 kg/ha performed relatively better because their means seed yields were closer to grand mean. The results of mean seed yields obtained in this study were much lower than that of Misganaw et al., (2015), who reported that the highest overall mean seed yield of 1035 kg/ha was recorded by G6 at Shewarobit in 2011. They also reported that across environment, the highest mean seed yields were shown by Acc.00047, NN-0143 and Acc.202-344 with 712.8 kg/ha, 679.2 kg/ha and 639.9 kg ha, respectively. Similar results were obtained by Ahmed et al., (2007), and Kumaresan D and N. Nadarajan (2010) and Hagos Tadesse and Fetien Abay (2011). Sesame genotypes performed differently to the different environments for their seed yield, indicating that mean performances should be an indicator for selection of adapted genotypes.

In order, to rank genotypes across the six environments studied, we scored genotypes in such a way that genotype with the highest mean yield received a rank of one. After, ranks were added together, and the genotype with the lowest score is considered to be the best. According to table 4, the most performant sesame genotypes across different environments were S42 followed by SN203, SN303 and SN403, while the least genotype was BS.

3.2. Stability

Genotypes respond differently across a range of environments i.e., the relative performance of varieties depends on the environment. In order to structure and understand Genotype by Environment Interaction (GEI), Joint Regression Analysis (JRA) has been widely used in crop sciences, (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Gusmão, 1985; Pereira and Mexia, 2008; Zheng et al., 2009), and in genetics, to analyse quantitative trait loci (QTL) by environment interaction (Korol et al., 1998; Emebiri and Moody, 2006).

According to Eberhart and Russell, (1966), genotypes with the regression coefficient (bi) greater than one have below average stability, above average mean yield and highly sensitivity to environmental change, so these genotypes were best fit for specific adaptation in favorable or high potential environments, the genotypes with the regression coefficient less than one, have greater resistance to environmental change (above average stability), and thus increases the specificity of adaptability to low potential environments. As a result, genotypes: S42, L5 and BS with regression coefficients greater than one, indicating their responsiveness to favorable environments, whereas, SN403, SN303 and L1 had regression coefficient significantly lower than unity, indicating their adaptation to low yielding environments (figure 1).

The other counterpart SN103 and SN203 closer to unity; therefore, these genotypes had average responsiveness, and this result was in agreement with the findings of Misganaw et al., (2015) in sesame and Firew (2003) in common bean.

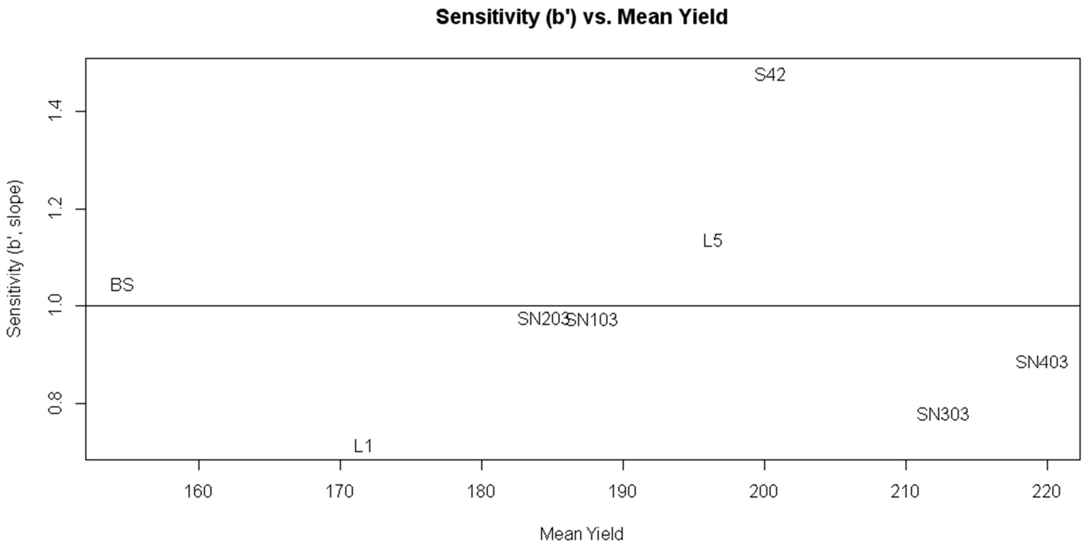

Figure 1. *Seed mean yield vs. Environmental sensitivity.*

4. Conclusion

Join Regression Analysis (JRA) has proven to be an important model for analyzing and interpreting the GEI as a complement of traditional statistical analysis in genetics, plant breeding, and agronomy, for determining yield stability of different genotypes or agronomic treatments across environments. The results revealed that genotypes SN203 and SN403 with a relatively high seed yield mean of 187 kg/ha and 206 kg/ha respectively across the six (6) environments and a regression coefficient closer to unity (0.98 and 0.89 respectively) shown a broad adaptation. These genotypes performed consistently well in these environments. Therefore, SN203 and SN403 sesame genotypes could be recommended in LUCOP-Ti project intervention area located in the western part of Niger.

Acknowledgments

The authors were thankful to National Agricultural Research Institute of Niger (INRAN) and Projet Lutte Contre la Pauvrete dans la zone de Tillaberi Nord (LUCOP-Ti) for financial support; to CERRA Kollo for providing genotypes and to extension services for providing technical support.

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