EFFECT OF THE ENVIRONMENT ON THE ADAPTABILITY OF BIOFORTIFIED BEAN GENOTYPES IN THE EASTERN DEMOCRATIC REPUBLIC OF CONGO: CASE OF SOUTH KIVU

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ABSTRACT: *Faced with climatic, soil deterioration and technical constraints, bean production is low and very variable in space and time. The selection of the best performing genotypes is faced with the presence of significant interaction between genotype x environment which significantly reduces effectiveness. An experiment following a randomized complete block design was conducted during two cultural seasons B2012 and B2013 in 3 edapho-climatic characteristic sites in eastern Democratic Republic of Congo: Luvungi, Kashusha and Bitese and aimed to analyze the interaction genotype x environment yield of six biofortify bean genotypes, in order to identify the best in these ecosystems. Germination rate, day number to the flowering stage, days number to the physiological maturity stage, harvested plants number, pods per plant number, number of seeds per pod, weight of 100 seeds were observed. The interaction was analyzed using AMMI model and typological with by the Chord similarity indices. On one hand, genotypes with specific adaptability, namely Maharagi Kalanga in Luvungi; CodMLB001 in Kashusha and BRB194 and RWK10 in Bitese. On other hand, those broad adaptations as HM21-7 for Kashusha and Luvungi and RWR2245 for Kashusha and Bitese were also highlighted. Popularization and positive exploitation the interaction on high production potential sites and the general adaptation on relatively lower potential sites improves yield by valorizing each environment and the adoption of these genotypes by farmers.*

KEYWORDS: Biofortified bean, Kashusha, Luvungi, Bitese, selection, genotype.

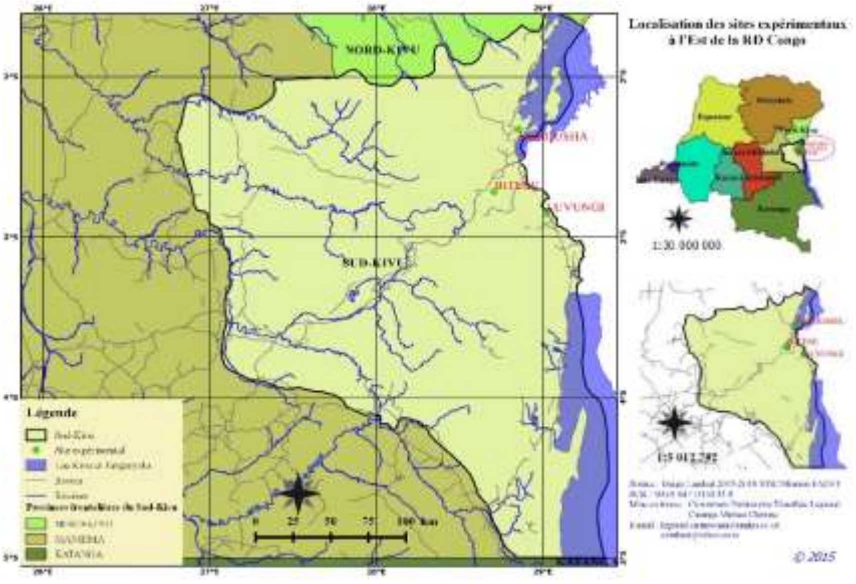
INTRODUCTION

Through agriculture, humans have exploited the environment and its natural resources for thousands of years to ensure their autonomy and meet food needs (Kammoun, 2014). Indeed, studying the behavior of genotypes in different environments has long been a major concern for the agronomist to seek to adapt cultivation techniques to crops varieties (Sassi, 2008). In fact, the breeder aims to develop cultivars with specific or wide adaptations (Crossa, 1990). This variation is the result of interaction between genotype and environment (Brancourt-Hulmel *et al.*, 1997). The variety-environment interactions and crop behavior can be a handicap for the dissemination and adoption of varieties due to wide variations in their performance (Casadebaig, 2008). Because of the large environmental variations, increasingly numerous and unpredictable varieties must have a great ability to adapt to various stresses. But the standardization of genotype does not allow it to achieve this objective (Rey *et al.*, 2014) and yield stability is an important criterion for the development and popularization of a variety (Westerman et Lawrence, 1970; Becker et Leon, 1988). However, phenotypic stability characterizing the importance of performance fluctuations observed for the same genotype grown in different environments highlights the effects of environments and interactions between genotypes and environment (Thoday, 1953; Brancourt-Hulmel *et al.*, 1994). This situation gets more and more complex since through the great diversity of cropping systems, correlated with the diverse edaphic and in a climate of increasingly unstable in the Democratic Republic of Congo (Sanginga, N. et Woomer, P.L., 2009; FAO, 2014), pure lines of biofortified beans lose their core capabilities to dab their abiotic and biotic stress affecting their adaptabilities in various ecological niches of South Kivu (Sally *et al.*, 2014). Moreover, apart from its dietary advantages, beans is a staple for all people and a source of revenue for the humans' to improve their well-being (Mastaki, 2006). The aim objective of this study is to evaluate the interaction between genotype x and the environment and analyze the stability of yield performance of biofortified bean genotypes adaptable to various soil and climatic conditions of the South Kivu in order to popularize among farmers and households to eradicate malnutrition in this area and improve their daily experiences.

MATERIALS AND METHODS

Location

The experiment was carried out in three sites representing the agro-ecological and edapho-climatic richness of the South Kivu in particular and in general those of the eastern part of the Democratic Republic of Congo.



Luvungi, in Uvira territory, in Ruzizi plain with a low altitude (S 02°51.166'; E 029°01.114' and Alt. :907 m); Kashusha in Kabare territory with middle altitude (S 028˚4772; E 02˚19005 and Alt. :1640 m) and Bitese in Walungu in the high altitudes (S 02°43.034'; E 028°42.391' and Alt. :2045 m).

Figure 1. Location of the three experimental sites in Eastern DRC

These sites get a rainfall varying between 800 and 1000mm in Luvungi and 1600 and 1750 in Kashusha and Bitese, respectively.

Materials

The basic material of this experiment consists of six biofortified bean genotypes whose main characteristic is high in Iron and Zinc: CODMLB001, HM21-7, RWR2245, BRB194, Kalanga and RWK10 Maharagi.

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Elaboration of the trials

After clearing with machete, the experimental plot of land of 162.5m^2 was plowed twice with a hoe at a depth of 30 cm within an interval of 10 days and then harrowed manually with rakes. The land was then divided into blocks and plots. Blocks, three of them, were aligned parallel to the slope. Their dimensions were 3m x 12.5m each containing six plots. The blocks were separated from each other by a distance of 2 m. Within the different blocks, each plot measured 3m x 1.2m and were separated from one another with 0.5m. The layout of the above described plots of land allowed to carry out the experiment according to a design in randomized complete blocks. The six varieties of biofortified beans were randomized and sown in lines at a depth of 4 cm with two seeds per hole and spacing of 20x20cm. The experiment was conducted over the period from February to June 2012 and from February to June 2013 corresponding to the suitable time for bean cultivation in South Kivu.

Observed parameters

The vegetative and reproductive parameters typical for the different phenological stages of the crop were determined. This is the rise rate, the number of days to fruit set (nouaison), the number of days to the flowering, number of days to physiological maturity, the number of harvested plants, the number of pods per plant, number of seeds per pod, weight of 100 seeds and yield. These were determined according to the norms of standard evaluation of CIAT's bean germoplasm (Schoonoven *et al.*, 1998). The hierarchical classification of biofortified bean genotypes per site was made on the basis of the index of Chord dissimilarity index (Hammer *et al.*, 2001) generating a dendrogram. Its reading is reversed compared to the rate expressed in similarity. A high dissimilarity rate means that both genotypes or both sites are different and the lower rates, the more similar are genotypes or sites.

Statistical Analyses

The complexity of the research results on the interaction Genotype x Environment (GxE) led us to the use of Genstat 13th édition.1, Excel 2013, and 2.4.0 R XLSTAT. These results were evaluated by analysis of variance (ANOVA), correlation and regression between yield and its components and the site averages were separated by the test LSDα = 0.05 and distribution of interaction GXX principal component (PCA) was performed using the AMMI model as written by Zobel *et al*. (1988).

RESULTS

In parallel with the performance, breeders should opt for other less volatile character in a multi character approach to combine yield potential and adaptation to the environment (Annchiarico and Iannucci, 2008). Seasonality did not induce significant differences in all parameters examined in the different study sites.

Phenotypic characterization of the vegetative stages of genotypes in sites

The results of the separate analysis of variance during the vegetative stage of the six genotypes

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Table 1. Mean square of ANOVA vegetative parameters per site

Sites	Varieties	Rise rate (%)	Number of day to the Nouaison (N°)	Number of days to the Flowering (N°)	Number of days to the Physiological Maturity(N°)
LUVUNGI	BRB194	83 ± 2,93	40 ± 0,81***	37 ± 0,81***	95 ± 0,81***
	CODMLB 001	83 ± 3,16	41 ± 0,81***	38 ± 0,81***	96 ± 0,81***
	HM 21-7	87 ± 5,72	42 ± 1,24***	39 ± 1,24***	97 ± 1,24***
	Maharagi kalanga	51 ± 32,21	39*	31***	99***
	RWR 2245	78 ± 6,35	39**	31**	99**
	RWR10	83 ± 5,65	47*	44***	102*
KASHUSHA	BRB194	71 ± 4,1	39*	43 ± 1,41**	99
	C0DMLB 001	78 ± 3,85*	39**	42**	99
	HM 21-7	74 ± 11,14*	39	45*	99
	Maharagi kalanga	83 ± 6,12**	39	44 ± 1,41**	99
	RWR 2245	76 ± 2,16*	39*	42**	96
	RWR10	57 ± 10,87	32 ± 1,88*	45*	99
BITESE	BRB194	98 ± 1,13	49 ± 1,69***	48 ± 1,24***	99 ± 0,47***
	CODMLB 001	97 ± 3,17	52 ± 0,81***	48***	100***
	HM 21-7	95 ± 1,58	50 ± 0,47***	46 ± 1,24***	98 ± 0,81***
	Maharagi kalanga	96 ± 2,49	47***	31***	100***
	RWR 2245	96 ± 2,53	47***	31***	100***
	RWR10	98 ± 1,04	55 ± 0,47*	51 ± 1,24*	96 ± 0,47*

***, **,* : Significance level corresponding respectively to P≤ 0.001, P≤0.01 et P≤0.05; N° : Number ; % : Percentage demonstrates the lack of significant differences in the rate of rise in the Luvungi sites and Bitese, as well as the number of days in Physiological Maturity in Kashusha. However, the results of the analysis of variance combined including all genotypes and the environment have shown the existence of highly significant differences (P<0,001) for genotypes within different sites for the remaining phenological stages.

Interaction genotype x environment based on biofortified bean production parameters in the 3 sites

The general additive model of Analysis of Variance AMMI (Table 2) on yield components and the yield of six biofortified bean genotypes Biofortified evaluated within the three sites shows that these parameters were significantly (P <0.001) affected by genotypes (G), environment (E) and the genotype x environment interaction (GxE). These results indicate that the behavior of genotypes varies by sites. This inter-site variation is very high because the wide variation in the interaction (GxE) is explained by the diversity of environmental conditions from one site to another, characterizing Eastern Congo and specifically South Kivu.

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Table 2. Analysis of Variance AMMI on yield components as well as yield (kg.ha^{-1}) of six biofortified bean genotypes evaluated in three typical environments of the Eastern D.R. Congo.

Sources of variation		Number of pods per plant (N°)		Number of seeds per pod (N°)		Weight of 100 seeds (g)		Yield (kg.ha^{-1})	
	ddl	SM	F	SM	F	SM	F	SM	F
Genotype (G)	5	2,6	0,0463*	3,7	0,0000***	463,8	0,0000***	144637	0,0397*
Environment (E)	2	49,5	0,0002***	2,0	0,0026**	659,8	0,0000***	1368282	0,0314*
Blocks	6	4,3	-	0,3	-	36,6	-	351638	-
Interaction (GxE)	10	4,7	0,0004***	0,5	0,4531	35,9	0,0220*	433315	0,0065**
PCA 1	6	7,8	0,0000***	0,7	0.2006	54,0	0,0056**	528267	0,0065**
PCA 2	4	0,1	0,9724	0,1	0.9150	8,9	0,6406	290887	0,0053**
Résiduelles E x G	30	7,762	-	0,456	-	14	-	135486	-

ddl : freedom degree ; SM : Square Mean; F : FISHER SNEDECOR's F Value; PCA : Principal Component Analysis; N°: Number; g : gramme; kg: kilogramme; ha: hectar; ***, **,* : Significance level corresponding respectively to P≤ 0.001, P≤0.01; AMMI : Additive main effects and multiplicative interaction

Besides, these results highlight the complexity of edapho-climate and altimetric of the environment in the East, indicating that the variation between sites is very high.

Yield performance of biofortified bean genotypes per and inter-site

Stability is one of the breeding objectives in demanding environments (Bouzerzour et Dekhili, 1995; Bouzerzour *et al*., 1998). The Analysis of Variance of the genotypes' performance per site indicates a differential behavioral effects of genotypes, very significant 1% for all sites (Table 1). This is an indication of sufficient and exploitable genetic variability in breeding and extension for each site.

Table 3. Square Means of Analysis of Variance differences of the genotypes' yield obtained per site and performant genotypes per site

Source of variation	ddl	SITES		
		LUVUNGI	KASHUSHA	BITESE
Génotypes	5	0,012**	0,002**	0,002**
Erreurs	11	0,046	0,082	0,324
Mean yields (kg.ha^{-1})		571,9	1024,96	1031,76
Best genotypes per site		[1]Maharagi Kalanga	[1]HM 21-7	[1]BRB194
		[2]RWR 2245	[2]CodMLB001	[2]RWK10
		[3]HM 21-7	[3]RWR 2245	[3]RWR 2245

ddl: degree of freedom; ** significant effect with a threshold of 1%; [1, 2, 3]: Classification of specific genotypes according to the adaptive performance

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From table 3 above and figure 2 below transpires a specific identification of genotypes according to their performances in descending order testifying to the existence of very significant interaction between genotypes and sites.

The genotype and hierarchic typology on basis of similarity indices of dendrogram following the group of genotypes in three main blocks which are equivalent to the 3 sites of the the d'experiment. The genotypes HM21-7 and CodMLB001 are 24 % distant from each other (a similarity of 76 %), these two are the best adapted at Kashusha. The Maharagi Kalanga and RWR2245 genotypes have similarity degree of 61 % and adapt better at Luvungi. At Bitese, the best adapted genotypes are RWK10 and RBR194 and have a similarity degree of 55 %. Two big blocks come out from this dendrogram. The site of Kashusha and that of Luvungi are 55 % distant from each other (low similarity rate 45 constitutes the first big block grouping the genotypes HM21- 7, CodMLB001, Maharagi Kalanga and RWR2245. The second big block is that of the site of Bitese 64 % (36 % similarity) distant from the first big block.

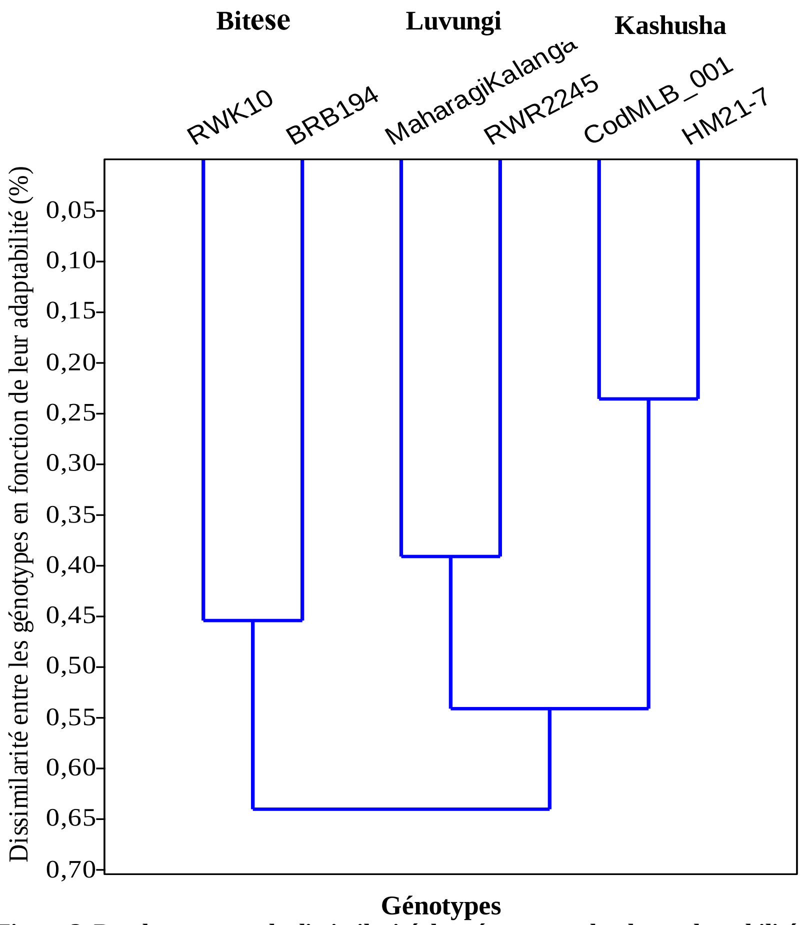

Figure 2. Dendrogramme de dissimilarité des génotypes selon leur adaptabilité illustrant les trois sites d'expérimentation et leurs meilleurs génotypes en fonction des indices de similarité de Chord (Hammer *et al.*, 2001)

The biplot AMMI suggests three possible alternatives for the breeder (Abdelkader *et al.*, 2011). In the light of Figure 3 below, the first alternative is to adopt the choice of a performant genotype and general adaptation such as RWR2245 genotype. The second alternative is to use interaction positively, through the choice of genotype specifically suited to high production potential sites, associated with the choice of genotype broad adaptation for low production potential sites. Hence HM21-7 will be used in Luvungi and Kashusha sites while RWR2245 will be used for both Kashusha, Luvungi and Bitese. The third alternative is to assign each site its stable and specific genotype and so BRB194 will be for Bitese, HM21-7 for Kashusha and Maharagi Kalanga for Luvungi.

The selection of genotypes adapted to the high yield potential sites associated with the selection of wide adaptation genotypes for low yield potential environments leads to the same conclusions as those of the results-based analysis of the model of linear regression.

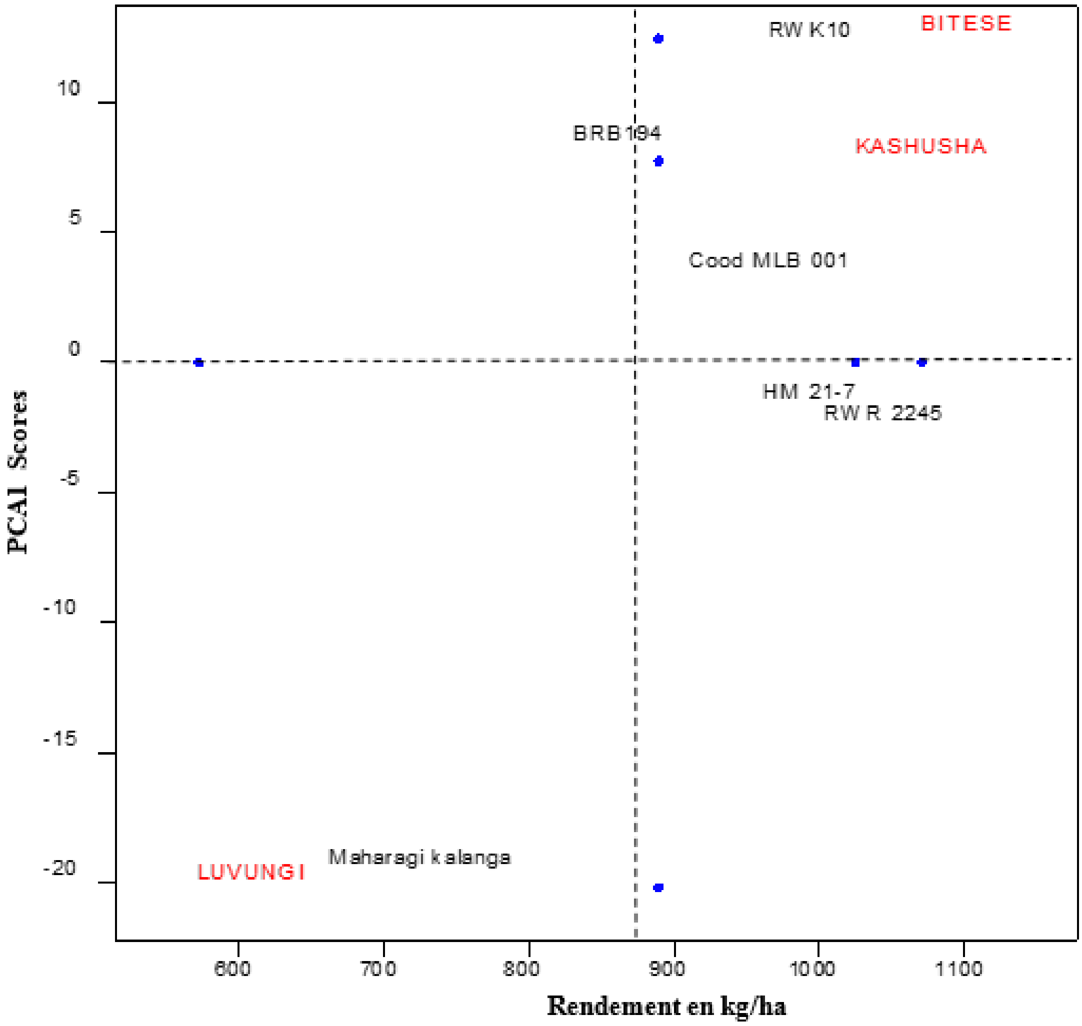

Figure 3. Biplot AMMI1 représentant la relation entre les scores de PCA1 et les effets moyens génotype et sites du rendement grain des 6 génotypes des haricots biofortifiés évalués

DISCUSSION

The results of this research attest the presence of significant statistical differences among genotypes, environments and interactions GxE, suggesting the need to share genotypes stability based, on typical environments confirming the work of Anley *et al.* (2013). Furthermore, they are similar to those of Lubobo (2012) as well as those of Eberhart et Russell (1966) for the analysis of phenotypic characterization parameters of genotypes vegetative stages has revealed significant differences in the different sites, highlighting the influence of edapho-climatic heterogeneity and altimetric on the performance of biofortified bean genotypes in the eastern Democratic Republic of Congo.

Furthermore, our results confirm those of Laala *et al.* (2010) stipulating that indirect selection must be based on yield components in complex environments. So the breeder-popularization agent can, based on the number of pods per plant and number of seeds per pod and weight of

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100 seeds, choose the HM21-7 and RWK10 varieties for Kashusha and the BRB194 variety for Bitese. However, for Luvungi they can opt for the number of pods per plant for Maharagi Kalanga variety as best criterion for indirect adaptability selections. This genotypic specificity per site reflects the altimeter and weather variability correlated to the specific edaphic properties from one site to another.

In turn, the AMMI analysis of variance of the performance of these six genotypes at the three sites showed the existence of significant differences among genotypes, environments and genotype x environment interaction ($p < 0.01$) confirming the work of Ceyhan *et al.* (2012) and Karadavut *et al.* (2010) which found wide variations in yields depending on the site. The effect of genotype x environment interaction was three times higher than that of genotypes following the discriminatory binding and pressure of the environment as also found by Yan and Rajcan (2002) and Kaya *et al.* (2006), as well as Tolessa *et al.* (2013). Also, the inadaptability of several genotypes in specific sites is due to the fact that it is impossible for a genotype to contain all the genes responsible for best performance in any environment (Annicchiarico, 2002). Selective specific efficiency and direct adaptive genotype based on the performance of Maharagi Kalanga in Luvungi, HM21-7 in Kashusha and BRB194 in Bitese is due to the recurrence of environmental conditions that have allowed the realization of a given yield, repeated regularly as stipulated in Ceccarelli S. (2010) and Ceccarelli *et al*. (1998) as well as in Kadi *et al.* (2010) and Kadi (2012).

According Hakizimana et *al.* (2011), if the similarity between two genotypes or sites is greater than or equal to 50%, it means that the two are the same and when it is less than 50%, so compared genotypes or sites are different. Reading figure 2 shows that there is a degree of similarity greater than 50% between genotype 7 and CodMLB001 HM21-, Maharagi Kalanga and RWR2245 and finally between RWK10 and RBR194. This shows that the three genotypic couples are similar in pairs but the lowest similarity is between the genotypic couple RWK10 and RBR194 (55%). Comparison among sites shows that they are not similar because Kashusha and Luvungi have only 45% of similarity, therefore genotypes adapted to Kashusha are not suitable for Luvungi and even if we cultivated the genotypes for Kashusha in Luvungi, they would not behave better and vice versa due to their edapho-climatic and ecological characteristics. Bitese remains very different from the first large block formed by Kashusha and Luvungi (similarity 36%). The specific adaptation of these genotypes in Bitese causes their inadaptability in the other two areas, due to Bitese's location at high altitude. Between the Kashusha and Luvungi sites, there are two genotypes that have a wide adaptation (HM21-7 and RWR2245) which explains the fact that low as is the degree of similarity it nears the similarity threshold. This nearing threshold is due to the fact that the two sites are located, one in the middle transitional altitude zone (Kashusha) and the other in low altitude (Luvungi) with several common characteristics. The big difference that Bitese site shows in comparison to the other two is due to its location in the high altitude and the fact that it has only one genotype (RWR2245) common to the other two sites, confirming the work of Chennafi *et al. (*2006) and Richard *et al*. (2007) who found that the variation of the yield is caused by the sensitivity of new cultivars to various stresses which characterize the place of production.

CONCLUSION

The AMMI analysis models and the similarity indices used for the study of the interaction genotype x environment of seed yield were identified on the one hand, genotypes with a

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specific adaptability namely Maharagi Kalanga in Luvungi ; CodMLB001 in Kashusha and BRB194 and RWK10 in Bitese. On the other hand, those of large adaptation such as HM21-7 for Kashusha and Luvungi and RWR2245 for Kashusha and Bitese. Popularization and exploitation of the positive interaction on high production potential sites and the general adaptation on sites relatively lower potential yield and the adoption of these genotypes by farmers.

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