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RESEARCH ARTICLE

Genotypes stability and genotype by environment interaction for selection index in rice (*Oryza Sativa* L.)

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Abstract

Selection index is effective selection criterion that has often been used in many breeding programs for diverse crops including rice. Ten (10) rice promising lines and a local check were assessed for yield, selection index and selection index stability over 3 locations in southern west of Niger republic. The experimental design was a randomised complete bloc design with three replications. Genotypes showed good performances in terms of yield, yield components and index selection. 3 different mega environments were observed with the two being close and slightly overlapped. The ideal environment to screen for high index selection was the environment 1. The genotypes TXD 88, WAB 2101-WAC4-1-TGR1-WAT B6 and Gambiaka performed well in environment 3 and 1, while the winners in environment 2 were genotypes WAB 2056-1-FKR-4, WAB 2056-2-FKR2-5-TGR1-B and JARIBU 220. The most stable genotypes across environments were WAB 2076-WAC2-TGR1-B, TXD 88, WAB 2101-WAC4-1-TGR1-WAT B6, L-22-26-WAC B-TGR4-B and WAB 2125-WAC B-1-TGR3-WAT B8, while the ideal was the genotype WAB 2101-WAC4-1-TGR1-WAT B6. These varieties are promising candidates for farmer's adoption and release.

Keywords: Rice, selection, stability, genotypes, interaction

Introduction

The rapid growing of human population and the sharp decreasing of agricultural resources are threatening food security in the world. Consequently, the average current global yield increase of the four major crops (rice, maize, wheat, and soybean) ranging from 0.9-1.3% per year are insufficient to meet food demand for the estimated nine billion people in 2050 (Kim *et al.*, 2016; Ray *et al.*, 2013). Rice is one of the most important crops in the world. It supplies food for half the word population. In Africa, Seck et al., reported in (2012), that rice is the most rapidly growing food crop and about 30 million tons more of rice will be needed by 2035. Thus, within existing agricultural lands, the genetic improvement of yield potential in rice could be the ideal way to increase yield. Hence, it is urgent to increase rice production, which can be achieved by increasing grain yield with favorable related traits preferred by farmers (Rosegrant and Cline, 2003). Rice yield and related traits have improved with breeding programs (*et al.*, 2018). Grain yield of rice is a complex trait and is associated with many components traits such as tiller number, panicle number, grain weight (Ikeda *et al.*, 2013). Usually, breeder needs to select for more than one trait in rice development process. Several methods have been used to improve desirable traits at the same time.

These include tandem selection, independent cooling and index selection. According to Smith (1936) selection indices are an aid to the breeder for simultaneous selection of multiple traits. This tool can help the breeder in spotting the desirable genotype of a crop species in a population improvement program (Asghar and Mehdi, 2010). Index selection has often been used in many breeding programs for diverse crops (Sezegen and Carena, 2009; Sharma and Duveiller, 2003; Vivas *et al.*, 2012) as an effective selection criterion (Vikram and Roy, 2003; Xie *et al.*, 1998). It is of foremost importance to identify and develop genotypes that could produce high yield and index selection in a range environmental conditions that really happen in farmers' rice fields. Hence, in above respect the study was carried out to evaluate the long-term performance of rice genotypes with the objective of identifying and selecting those with high and stable selection index in farmer's field conditions.

Materials and methods

Plant materials were composed of 10 breeding lines with 1 local check, resulting in total of 11 varieties (Table 1). The study was carried out in three environments (sites) namely Sebery (environment 1), Kollo (environment2) and Sekoukou (environment 3). The geographic positions of the sites are 13°20'31"N, 2°19'01"E for Kollo, 13°17'42"N, 2°20'43"E for Sebery and 13°15'59"N, 2°22'00"E for Sekoukou. The experimental design was a randomized complete-block design with 3 replicates. Each plot consisted of 5 rows of 5 m long. The distance between and within the rows was 20 x 20 cm. The transplanting was used as seeding method with 2 seedlings per hill. Transplanting was performed 25 days after nursery seeding. Fertilizer application was done as followed: A pre-drilling base application of 200 kg.ha-1 of complex fertilizer (NPK: 15-15-15) was made at transplanting stage. A total of 200 kg.ha-1 of urea was also made in two applications; at two weeks after seeding (130 kg ha-1) and at panicle initiation or booting stage (70 kg ha-1). Weeding was done before fertilizer application. The harvest was done by eliminating one row from each side of the plot. Thus, the harvested area was 2.76 m2 (4.6 m x 0.60 m). The winnowing and weighing were performed at 14% moisture content.

The following data were collected: date of 50% flowering, date of maturity (85% of grains on panicle were mature). Plant height at harvest (cm) was collected from 3 randomly selected plants by measuring from soil surface to the tip of the tallest panicle (awn excluded). The grain yield data was collected by excluding the border rows. The panicle and tiller number was calculated from the 3 plants used for measurement of plant height. The traits contributed to the index were determined according to farmer preferred rice traits reported by Souleymane *et al.,* (2015) including the height, tiller and panicle number, the duration and the yield. The selection index was calculated by using the following formula:

Selection index=height *1.1 +panicle number *1.5+tillernumber*1.5+Yield*1.8.

This was because we wanted to improve the height by about 10%, the tiller number, panicle number by 50% and the yield by 80%. Data were analyzed using Genstat software version 18th GGE biplot method was performed for genotypes by environment interaction study and index stability analysis.

Table 1: List of the genotypes used in the present study

Entry Number	Designation
1	FAROX 508-3-10-F43-1-1
2	JARIBU 220
3	TXD 88
4	WAB 1436-20N-3-B-FKR2-WAC1
5	L-22-26-WAC B-TGR4-B
6	WAB 2056-1-FKR-4
7	WAB 2056-2-FKR2-5-TGR1-B
8	WAB 2076-WAC2-TGR1-B
9	WAB 2101-WAC4-1-TGR1-WAT B6
10	WAB 2125-WAC B-1-TGR3-WAT B8
11	Gambiaka

Results and discussions

Genotypes average height across environments (fig.1) ranged from 96 cm for genotype 6 to 150 cm for genotypes 4 in environment 3. All the tested genotypes but one (genotype 4) were equal or above the local check. Six out of eleven including the check had the height reduced in environment 2. Genotypes tiller number (fig.2) and panicle number (fig. 3) differed with environments. In environment2 all the tested genotypes bore more tillers and panicles than the local check (Var11). The later performed better than all but one (genotype 4) in environment1. In environment 3 only genotype4 (Var4) and 6 (Var 6) had more panicles and tillers than the check. In term of yield genotypes performances ranged from 1.2 to 4Tha-1 in environment 2. In environment 1the average yield varied from 1.2 to 5 tha-1 en in environment 3 it ranged from 1.4 to 4.8 Tha-1 (fig.4). Eight genotypes out of eleven performed better in environments 1 and 3 than environment 2 in term of both selection indices (fig.5) and yield. The best selection indices in environment1 were observed for genotype 9 followed by genotypes 2, 3, 11 and 5. In the environment 3 the local check had the greatest selection index followed by genotypes 3, 5, 9 and 10. The duration (time to 85% maturity) of genotypes across environments ranged from 105 to 130 days (fig.6). However, slight differences existed within a given variety across environments. 2.2. Index stability. The scatter plot (fig. 7) explaining 97.4% of the variability shows 3 different mega-environments. However, environments 3 and 1 were very close meaning that they are similar. These environments were totally different from environment 2. Genotypes 10, 9, 8, 3 had similar selection index and had performances near to the average across environments, while genotypes 2, 6 and 7 were also similar. Genotypes that did well in environment 3 and 1 were genotype 3, 9 and 11 (local check) that is highly responsive to the environment. Genotype 4 did poorly in all the environments and was highly responsive to the environment. In the environment 2 the winner genotypes were 6, 7 and 2. The genotypes ranking plots (fig.8) shows that the best genotype was 9 followed by 3 and 5 while the worst were the 4 and 1. However the most stable genotypes across environment were 8, 3, 9, 5 and 10. The genotypes 6, 7 and 11 were responsive to the environments. The Environments comparison plot (fig. 9) shows that the best environment to discriminate the genotypes was the environment 1 that was close to the ideal. The second best environment was the environment 3 than lastly the 2. The best genotype to discriminate environments was the 9 that is close to the ideal (fig. 10). It was followed by 3, 5 and 10.

Figure 1: Genotypes height across environments

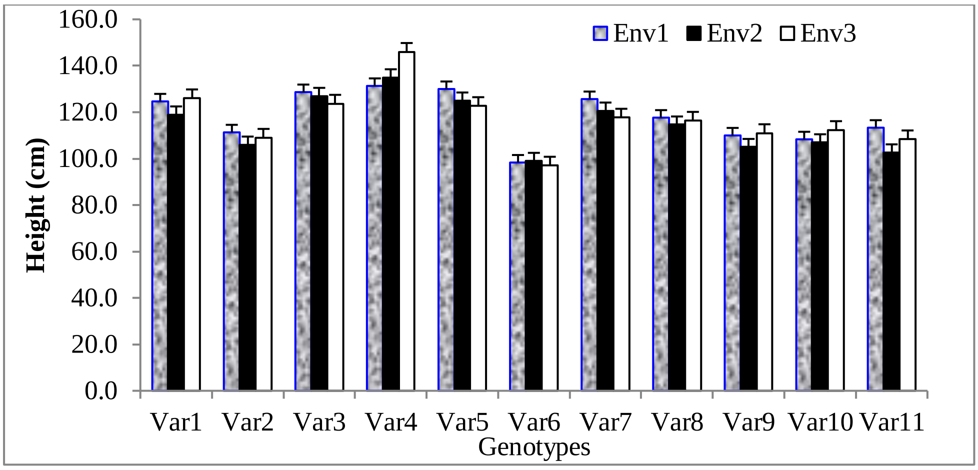


Figure 2: Average tiller number across environments

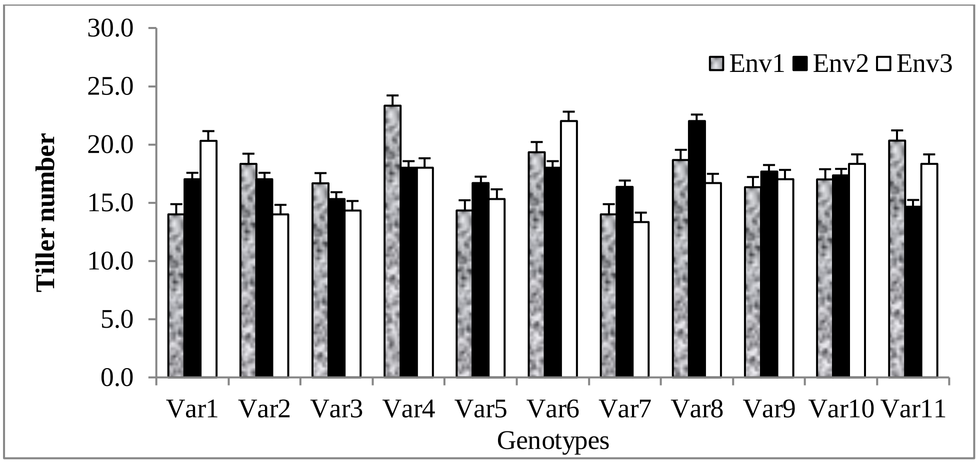


Figure 3: Panicle number of 11 genotypes in 3 environments

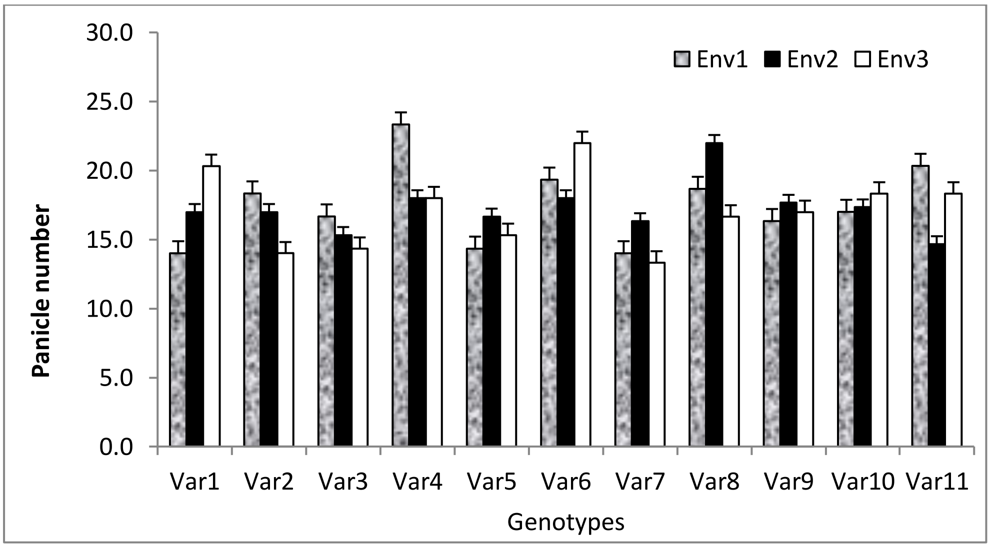


Figure 4: Yield performance of 11 genotypes

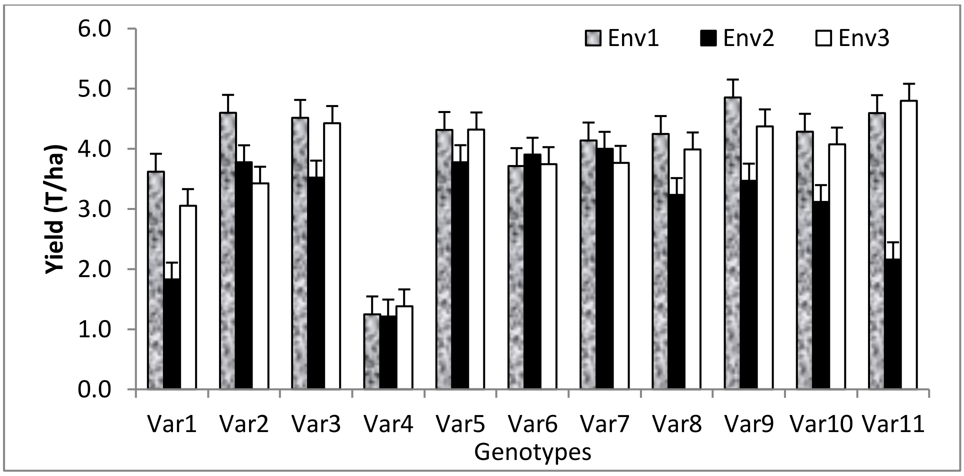


Figure 5: Selection index of genotypes across environments

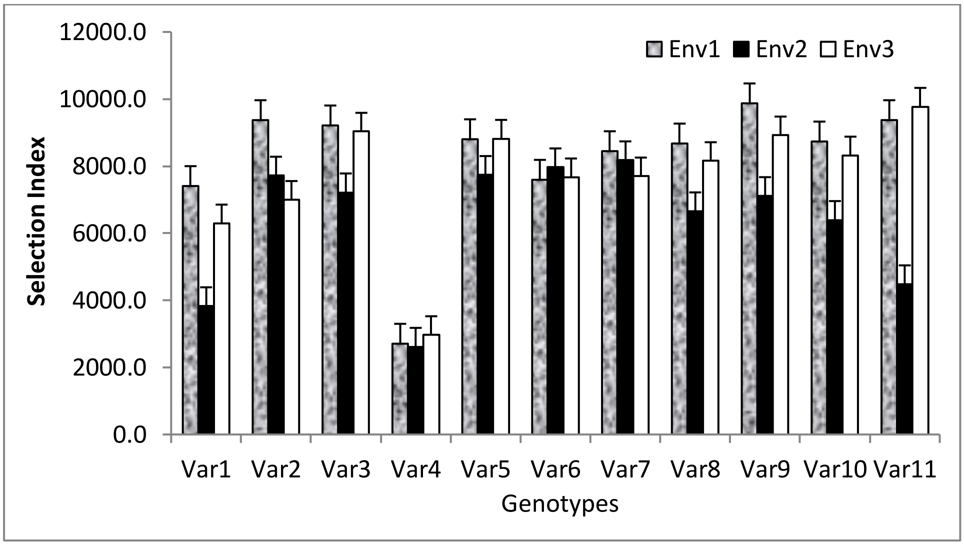


Figure 6: Plant duration (time to maturity)

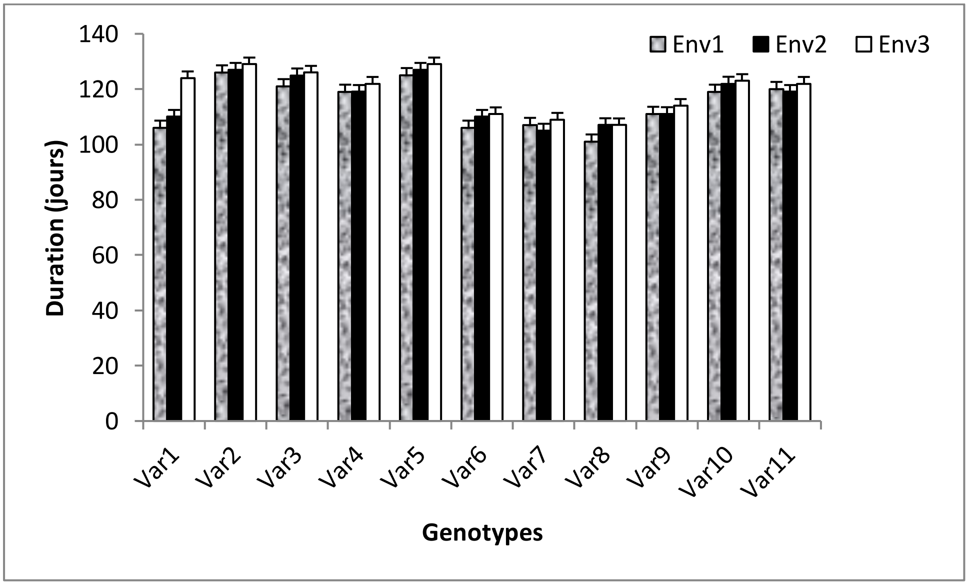


Figure 7: Scatter plot showing mega-environments and sectors

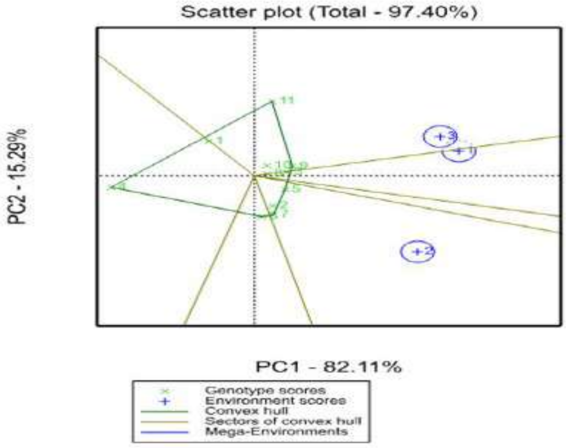


Figure 8: genotypes ranking plot

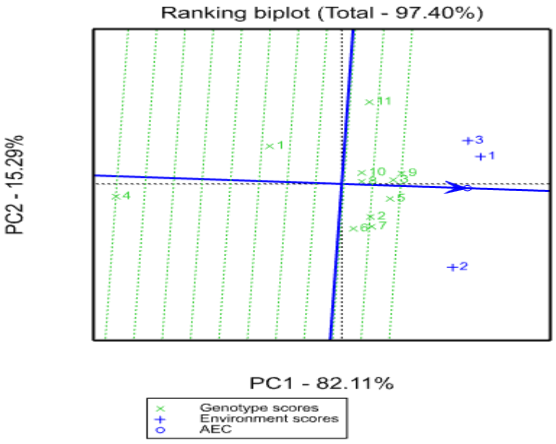


Figure 9: Environments comparison plot

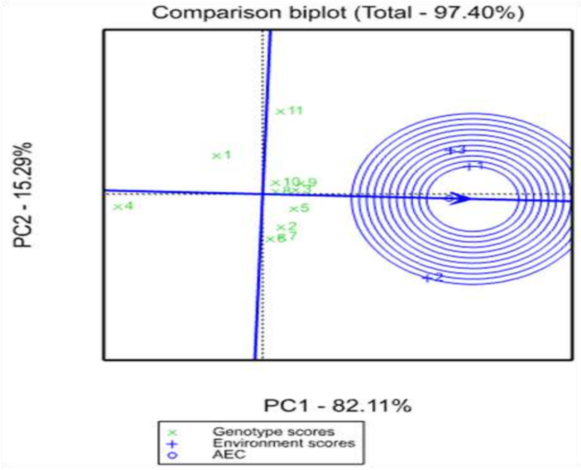
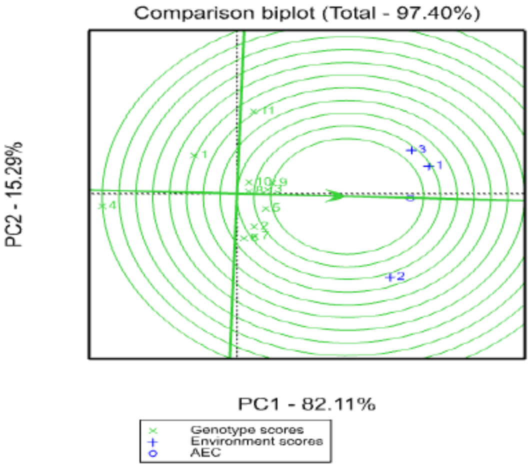


Figure 10: genotypes comparison plot



The study showed that majority of the genotypes had high performances in term of yield, and selection index as well. Direct selection for grain yield has recently been used in delivering improved rice varieties and it is proved to be an effective and feasible approach (Saikumar *et al.*, 2016). Nevertheless, selection based solely on grain yield may not be efficient in the development of widely adapted and adopted genotypes (Kumar *et al.*, 2007; Venuprasad *et al.*, 2007; Xangsayasane *et al.*, 2014), because crop development and production process is a strong interaction of environment effect with all the yield components. Additionally, farmers may be interested in many other traits apart from grain yield. This interest may be motivated and conditioned by economic or social factors (Souleymane *et al.*, 2015). Thus, genotypes with high selection index may easily be adopted by farmers because they combine almost all their preferred traits. Moreover, to be widely adopted genotypes should be stable across environments. Hence, stability is a major factor for increasing rice production and productivity in the Sahel. It is determined by genotype and environment interaction (Saikumar *et al.*, 2016). Genotypes 10, 9, 8, 3, 7 and 11 did well in environments 1 and 3 and could be recommended to farmers in these environments. Results indicated that genotypes 2, 6 and 7 performed better in environment 2 in term of selection index, hence, can be release to farmer of tha environment. Genotype 4 was the worst in term of selection index in all the environments. The environments were not conducive to this genotype to display its genetic potential.

Hence, this genotype cannot be recommended in all the tested environments but may be tested in other. Genotype 11 showed high potential of selection index only in environments 1 and 3 that were also similar but poor yielding potential in environment 2. Thus, it is a genotype with finite adaptability (Sedghi-Azar *et al.,* 2008). Results showed that out of 11 genotypes three (3) were the best performer and the most stable (genotype 9, 3 and 5). Theses genotypes could be recommended or released to farmers of the environments. However, the ideal was genotypes 9 for all the environments. Genotypes that were adapted throughout the three environments and showed spatial and temporal stability are the best suited for adoption (Mosavi *et al.*, 2013). The genotypes stability in term of index selection indicates their insensitivity and their adaptation to a range of environments. This implies that these genotypes deserve to be promoted on-farm and for subsequent release varieties for the rice growing irrigated ecologies in southern West of Niger. This is because according to Souleymane *et al.,* (2017) there is need to identify stable genotypes with relatively consistent performance. across a range of environments. Results showed that the ideal environment was the environment1. Hence, the environment 1 could be considered as the most stable site for high selection index and high yielding rice improvement compared to the two other locations. In this study, significant genotypes performances were observed in term of selection indices. Three genotypes have specific performances in environment 1 and 3, while 3 others performed well in environment 2. Four genotypes had high selection index and were stable across the three environments. The ideal genotype was the genotypes 9 while the ideal environment was environment1. The most performing and stable genotypes could be recommended for farmers adoption and release. This study was funding by Africa Rice Center for funding and provision of seeds.

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