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Review Article

A Research Review on Assessment of Genetic Variability in Bambara Ground Nut Accessions Using Agro-Morphological Traits

Melak Agajie*
Ethiopian Biodiversity Institute, Assosa Biodiversity Center, researcher in crop and Horticulture case team

***Corresponding Author**
Melak Agajie

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Abstract: Bambara groundnut (Vigna subterranea L. Verdc.) is an edible legume that represents one of the main income sources for women activities. For the improvement of desirable characters such as yield and ability to resist to abiotic and biotic stress, knowledge of the magnitudes of variation in the available accessions, the relation of characters with yield, extend of environmental influences on these is essential. The aim of this review was to identify the major agro-morphological characters that allow differentiating bambara groundnut accessions, that could be use to set up selection strategies for varieties improvement. Characters like canopy spread, number of pods per plant, number of seeds per pod, seed length, seed width and weight of 100 seeds are positively correlated to yield per plant. A negative correlation was revealed between days to 50% flowering and yield per plant indicating that plants which take more time on vegetative stage have fewer yields in semi-arid conditions of production. The phenotypic characters therefore provide a useful measure of genetic variability among bambara genotypes and will enable the identification of potential parental materials for future breeding programs.

Keywords: Genetic Variability Bambara Ground Agro-Morphological Traits.

1. INTRODUCTION

Agricultural policy in developing countries focuses mainly on cash crops. This choice has not significantly improved the population’s food situation. However, it has encouraged growers to abandon many local crops, which have declined as a result. Because of their nutritional quality, these crops could have played a major role in providing a balanced diet for an ever-increasing human population, but have been under-exploited. Their yields have therefore remained low and unstable.

In West Africa, Bambara groundnut is mainly cultivated by women, together with maize, millet or groundnut [1, 7]. The proteins found in its seeds have high lysine content and combining them with cereals as part of the diet represents a beneficial nutritional supplement for many local populations [14]. The flour obtained from its seeds could provide a viable substitute for “conventional” flours in the composition of various manufactured products [2]. The popularization of Bambara groundnut cultivation and increasing its production could provide farmers with a substantial income and contribute to food safety in Africa [15].

Over the last few decades, the scientific community has shown renewed interest in this neglected and under-used crop. From 1992 - 2006, three major research projects funded by the European Union were implemented by the Universities of Nottingham and Wageningen, in cooperation with various countries, including Botswana, Namibia, Malawi, Tanzania and Sierra Leone.

Bambara groundnut (Vignea subterranea) is an under -utilized African legume widely cultivated in Sub - Saharan Africa. It is an important grain legume, which is mainly grown by subsistence farmers in sub - Saharan Africa in a wide range of agro ecological zones (Ntundu et al., 2006)

Bambara groundnut is the third most important legume crop after cowpea and groundnut (Howell, 1994; Somta et al., 2011) and it is widely consumed in Southern Africa. The crop has unrealized potential to contribute to income generation, improved food security and nutrition.

Bambara groundnut is grown for its edible seeds for protein content and shows complementary advantage when consumed with cereals crops (Doku 1996; Ntundu et al., 2006; Olukolu et al., 2012). The crop tolerates drought, have high nutritional variability, have the ability to adapt to adverse environmental conditions and is resistant to pests and diseases prevailing during the growth period of the crop (Heller et al., 1997; Sesay et al.,1999). The Bambara groundnut seeds can also be used as livestock feed (Brought et al.,1993; Ntundu et al., 2006).

Research has paid little emphasis to this neglected and underutilized crop species. Understanding the level of genetic variability in Bambara groundnut would help in the selection of potential parent lines for the Bambara groundnut improvement programme in South Africa. Agro -morphological characterization is the first step for the assessment of genetic variability and identification of desirable traits of interest. Therefore, the objective of the review is to determine the extent of genetic variability and the relationship among Bambara groundnut accessions.

2. DISCUSSION

Evaluation of agro-morphological variability and its characterization are the first step in the assessment of genetic diversity. Previous studies have shown that the choice of 15 to 20 agronomic characteristics is very useful to assess bambara groundnut genetic diversity (Goli et al., 1997; Sesay et al., 2003; Ouedraogo et al., 2008). The statement in multivariate analysis is based on the use of accessions with maximum genetic divergence (Amurrio et al., 1995).

The Bambara groundnut accessions studied by shegro et al. (2013) showed a considerable level of morphological variability which can be exploited for use in future breeding programme. High coefficient of variation was particularly observed for number of pod among the accessions studied and this could be due to the heterogeneity existing among Bambara groundnut germplasm accessions as reported by Madamba (1997). Ntundu et al. (2006) also found considerable quantitative morphological variation among 100 Bambara groundnut landrace accessions in Tanzania. Similarly, Masindeni (2006) found large genetic variability among eight Bambara groundnut germplasm accessions using quantitative traits. Among twenty, three early flowering accessions identified in this study could be selected for early maturity. Similar results for early maturing accessions in Bambara groundnut was also reported by Brink et al. (2006). Ouedraogo et al. (2008) reported that flowering ranged from 32 to 42 days after sowing among Bambara groundnut germplasm accessions. These values were lower than the values reported in the present investigation. The variation of the days to flowering among accessions might be due to genotypic factor as well as the environmental conditions that prevailed during the crop growth period. Swanevelder (1997) also reported several variations in flowering among Bambara groundnut germplasm accessions. Number of pods per plant reported in the present study varied from 44.70 to 110.51 which are considerably lower than the values reported by Masindeni (2006). Yield per plant varied from 10.20 g to 57g indicating that the yield of Bambara groundnut also widely varied depending on the accessions and environmental conditions.

Understanding the association of morphological quantitative traits is incredibly important in crop improvement programme. The positive correlation of estimated leaf area with terminal leaf length and leaf width might be due to the functional relationship between leaf length and width. Ouedraogo et al. (2008) also reported similar relationships to the present findings. The positive associations among the various traits observed in this study clearly indicated that selecting for any of these traits will have a positive effect on selecting the associated traits for Bambara groundnut improvement programme. A negative significant correlation was also observed among some traits. Negative correlation was observed between number of pods and hundred seed weight and could be due to the variation in seed size.

The PCA biplots provide an overview of the similarities and differences between the quantitative traits of the different accessions and of the interrela-tionships between the measured variables. The biplot demarcated the accessions with characteristics explained by the first two dimensions.

The PCA grouped the accessions over the four quadrants based on the quantitative traits. The accessions are scattered in all four quadrants, showing large genetic variability for the traits studied. Accessions close to each other in the principal component axes had similar relationships for some traits. The actual genetic relationship among these closely associated accessions could be further revealed through detail quantitative, biochemical and molecular chracterization. However, other 3 accessions were completely distinct compared to the rest of the accessions. This whole data set confirmed that sufficient genetic variability was present for the measured quantitative traits which can be exploited for use in Bambara groundnut improvement programme. Genetic distances from 0.86 to 1.79 that were observed in the pair-wise combinations indicate that the Bambara groundnut accessions were diverse for the morphological quantitative traits measured and this could play a great role in the Bambara groundnut improvement programme in the country.

All the results by Ndiang et al. (2014) showed existence of an important diversity in the species. Evaluation of accessions presenting the same seed colours (NOR1 and NO1Y, NOR2 and NOR2Y) confirm this diversity. This important phenotypic variability should derive to the expression of high genotypic heterogeneity and/or to the environmental factors. The clustering pattern of the Bambara groundnut accessions did not indicate any relationship between morphological divergence and agro-ecological distribution. This finding supports the work of Aremu et al. (2007), Ariyo (1991) on cowpea and okro, respectively. However, reduced plant forms would allow enough sunshine penetration to every crop parts. Plant height and internode length have been identified as variables that permit to define the variability among the groups of Bambara groundnut (Bonny and Dje, 2011; Ndiang et al., 2012).

By the Principal Component Analysis (PCA) procedure, plant height and internode length, petiole length, terminal leaflet length, terminal leaflet width, number of leaves, number of nodes per stem, number of pods per par plant and number of seeds per plant were important in genotype grouping. These characters were the most discriminant factors, suggesting their consideration when selecting is for agronomic superior traits. PCA was confirmed this important agro-morphological variability between the different accessions indicating existing of higher genotypic and phenotypic organization of used biological material. In some studies, PCA is a descriptive technique which reveals the pattern of character variation among genotype (Aremu et al., 2007). It further reduces a multivariate data into units or component thereby accounting for a meaningful amount of variation in a population.

Considering PCA, it is noteworthy that it is one of the techniques in multivariate analysis in that it sufficiently provides a clearer and more informative display of the relative positions of the accessions. Similar results have been reported earlier for yam, okra and cowpea (Onyilagha, 1980; Ariyo, 1990; Aremu et al., 2007). The generally very low Coefficient of Variation observed for the nine traits indicated a high level of uniformity in the group from which data were obtained. The positive and significant relationship observed for number of pods with terminal leaflet width ($r = 0.92^{**}$) and terminal leaflet length ($r = 0.68^{*}$) means that increase in number of pods increase the terminal leaflet width and terminal leaflet length. Plants with large leaves and less growth habit show that these plants have stems open or spreading type. When collar diameter of plant is important, the aerial part of plant is more vigorous with branches, leaves and abundant petioles. A negative correlation revealed between date to 50 % flowering and yield per plant indicates that plants with longer vegetative stage yield less in our experimental area. Similar results have been reported in Burkina Faso by Ouedraogo et al. (2008).

According to the study done by Amara et al. (2016) Eighteen quantitative traits were recorded to estimate the level of genetic variability among accessions. The analysis of variance revealed significant differences among the phenotypic traits evaluated. The UPGMA cluster analysis based on the quantitative traits produced four distinct groups of genotypes and a singleton. Genotypes SB11-1A, SB19-1A, SB12-3B and Bambara-12 were found to possess good vegetative characters and are recommended for use as suitable parents when breeding cultivars for fodder production. Desirable yield and yield-related traits were identified in B7-1, SB4-4C, SB19-1A, Bambara-12 and SB16-5A and were recommended as suitable parental lines for bambara groundnut grain production improvement. The phenotypic characters therefore provide a useful measure of genetic variability among bambara genotypes and will enable the identification of potential parental materials for future breeding programs in South Africa.

3. CONCLUSION

Characterization and evaluation of bambara groundnut germplasm and identification of the best parents is important for improvement of the crop. Accessions of Bambara groundnut mainly collected from Northern Burkina Faso showed that there is a phenotypic diversity in seed coat and eye colour and pattern. It is well known that phenotypic variability is a non exhaustive representation of genetic diversity. Agronomic and morphological evaluations have provided more accurate estimation of genetic diversity, the raw material of plant breeding. According to several studies done sofar in Africa, Bambara groundnut germplasm revealed a wide range of variability for the studied phenotypic traits. This has provided estimation of the extent of genetic variability, which is the raw material of plant improvement. This information would help in facilitating the management and utilization of the accessions in Bambara groundnut improvement programs in Africa. Some studies revealed that some accessions were associated with desirable grain yield characteristics and may be suitable parental lines for improvement of grain production. Similarly, others some accessions were identified as possessing favorable vegetative traits and these accessions could be used as parents when breeding bambara groundnut for use as fodder production.

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