

## ABSTRACT

The yam bean (*Pachyrhizus* spp) is a high yielding storage root legume, rich in protein and micronutrients. The crop is constituted by three species, *P. ahipa*, *P. erosus* and *P. tuberosus* that are in cultivation but remain orphaned in research. The yam beans were recently introduced into Rwanda to determine its adaptability, adoption and breeding potential for integration into the diverse farming agro-ecologies and improvement of diets of root crop dependent communities. This study presents first comprehensive findings based on three objectives namely; i) to identify and evaluate the genetic control of adaptability and stability of diverse yam bean accessions based on agronomic performance across agro ecologies, ii) to determine the mode of gene action, combining ability for earliness and associated traits in yam beans, iii) to determine genetic parameters, variability, heritability and advance for yield and associated traits in F<sub>2</sub> yam bean populations.

Field evaluation of 22 yam bean accessions was done across three experimental sites (Karama, Musanze and Rubona) representing the major root crop growing regions of Rwanda. The study involved crossing three yam bean accessions of early maturing *P. ahipa* and late maturing *P. tuberosus* were crossed using North Carolina II mating design followed by field evaluation of F<sub>1</sub> and their parents to determine genetic control for earliness. Seven F<sub>2</sub> progenies were further evaluated at Rubona research station located in southern province of Rwanda and assessed for genetic variability, heritability and genetic advance of yield traits to determine potential for yam bean improvement. A randomized completed block design (RCBD) with 3 replications was used and data collected on yield and yield components of the progenies.

The GGE bi-plot revealed that EC209018 was high yielding but unstable. However, genotypes, AC209034, AC209035 and EC209046, were outstanding in terms of adaptation and relative stability across the 3 locations, suggesting consistent root yields irrespective of location and environmental conditions. The GGE scatter plot showed that all environments formed one mega-environment for storage root yield and two mega-environments for biomass suggesting that yam bean is adapted in the Rwandan environment and can easily be integrated into the farming systems of Rwanda to supplement diets of communities with a root crop rich in protein, zinc and iron. The crosses were significantly ( $P < 0.01$ ) different for key earliness traits, days to emergence, days to start flowering, days to 50% flowering and days to maturity in addition to storage root yield, plant height, number of cluster, and seed yield. High and significant GCA and SCA were observed for several traits, with a predictability ratio ( $\sigma^2_{gca} / \sigma^2_{sca}$ ) being higher than unity for all earliness traits, indicating predominance of additive gene actions.

These findings suggested that earliness traits could be improved through selection during early generation phase which would effectively lead to selection of lines with short time to 50% flowering, and days to maturity. Cultivars with high GCA can be used to transfer suitable genes of earliness into yam bean genotypes as our effective breeding strategy for earliness in new lines. The results demonstrated highly significant ( $p < 0.01$ ) genetic variability for yield and yield traits; plant vigor (PV), weight of pods (WOP), plant height (PHT), 100 seed weight (100SW), total biomass yield (TBY), storage root yield (SRY), dry matter content (DMC), and starch content (STA). High genetic and phenotypic variances and genotypic coefficients of variation ( $GCV > 25\%$ ) were observed for WOP, PHT, 100SW, TBY, DMC, and STA. Estimates of heritability were greater than 0.5 for all traits except seed yield, number of roots and number of pods. The genetic advance as percentage of the mean (GAM%) was high for PV (91.39%), WOP (133.88%), PHT (73.56%), 100SW (17.78), TBY (25.15%) and DMC (33.95%). Correlational analysis revealed positive and

significant ( $p < 0.05$ ) associations between PV and PHT, protein content (PRO), 100SW, TBY, SRY, and DMC while DMC had positive and significant ( $p < 0.01$ ) correlations with STA. These results indicated presence of high genetic variability, heritability and expected genetic gain and confirmed potential for genetic improvement of plant vigor, weight of pods, plant height, 100 seed weight, total biomass yield, storage root fresh yield, dry matter content and starch content of yam beans in Rwanda.

In conclusion, the three studies demonstrated that yam beans are adapted and high yielding in the major agro-ecological zones of Rwanda, with Karama, the low altitude zone, the most suitable environment for evaluation and selection for yield components. Accessions AC209034, AC209035 and EC209046 were well adapted and stable across the three agro-ecological zones. The findings revealed that storage root yields and associated traits could be improved through selection given the high genetic variability and significant ( $p < 0.01$ ) genotypic variance ( $\sigma^2_G$ ) components for SRFY, BIOM, DMC and HI. Combining ability analysis revealed that earliness and associated traits were conditioned majorly by additive gene effects with high predictability ratios ( $\sigma^2_{gca} / \sigma^2_{sca}$ ). The Phenotypic correlation coefficients revealed the possibility for simultaneous selection of earliness traits; SRY, BF and NR, and BF and DtF as well as DE, BF, DtF, and DM and SYP. These findings showed that it should be possible to recombine the earliness attribute from *P. ahipa* with SRY and SYP attributes of *P. tuberosus* to develop high yielding and early maturity yam bean varieties. These findings also proved that heterosis exists in yam bean for yield increases for both seed and root tubers production which will be of benefit to yam bean growers. The high genetic variability coupled with high heritability and genetic advance for yield (SRFY) and associated traits [number of roots (NR), storage root yield (SRY), plant height (PH), number of clusters (NC), seed yield (SYP), days to emergence (DE), days to start flowering (BF), days to flowering 50% (DtF), and days to maturity (DM)] in yam bean populations which clearly showed potential for genetic improvement if a breeding program is established.

In a short term, the high yielding and well adapted accessions that were identified in this study *viz.*, AC 209033, AC 209035 and EC209018 should be assessed through participatory farmer's selection for quick adoption. In the medium term, a yam bean breeding program should be established to further evaluate the yam bean populations in advanced generations. Many crosses should be initiated using either few parental germplasms available in Rwanda to form base populations for recurrent selection of yam bean for earliness and high yield. The number of parents should depend on the genetic diversity among them and the balance desired between high initial yielding selected genotypes such as AC 209033, AC 209035 and EC209018 (to increase short-term gains) and high genetic variance (to increase the potential for long-term genetic advancement by predicting gain for some new hybrids). In the long term, a breeding program should be initiated targeting the development of high yielding and early maturing yam bean varieties by utilizing the high genetic variability and predominance of additive genetic effects that were found to control these traits.