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GENETIC VARIABILITY AND GAIN FOR STORAGE ROOT YIELD AND YIELD COMPONENTS IN YAM BEANS

J. NDIRIGWE^{1,2}, P. RUBAIHAYO¹, P. TUKAMUHABWA¹, R. AGABA¹, S. TUMWEGAMIRE³, R.O.M. MWANGA⁴, B. HEIDER⁵ and W. GRÜNEBERG⁵

¹ Department of Agricultural Production, Makerere University, P. O. Box 7062, Kampala, Uganda

² Rwanda Agriculture and Animal Resources Board, Roots and Tubers Programme, P. O. Box 7231, Kigali, Rwanda

³ International Institute of Tropical Agriculture (IITA), P. O. Box 34441, Dar-es-Salaam, Tanzania

⁴ International Potato Center (CIP), P. O. Box 22274, Kampala, Uganda

⁵ International Potato Center (CIP), La Molina 1895, Apartado 1558, Lima 12, Peru

Corresponding author: ndrick3@gmail.com

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ABSTRACT

There is limited information on the genetic parameters and genetic gain of yam bean (*Pachyrhizus* species) accessions introduced to Rwanda. No comprehensive literature exists on the inheritance of yield and yield components, on segregating populations. This study investigated variability, heritability and genetic advance in F₂ yam bean genotypes. Seven F₂ yam bean hybrids were evaluated at the Rubona Research Station located in Southern Province of Rwanda, during growing season 2014B. Results revealed significant ($P < 0.01$) genetic variability in plant vigour (PV), pod weight (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 (σ_g^2) and phenotypic (σ_p^2) variances, and genotypic coefficients of variation ($GCV > 25\%$) were observed for WOP, PHT, 100SW, TBY, DMC and STA. Estimates of heritability (H^2) were high (greater than 50%) for all traits, except for seed yield, number of roots and number of pods. The GA and genetic advance, as percentage of the mean (GAM%), were high for PV, WOP, PHT, 100SW, TBY and DMC. There were positive and significant ($P < 0.05$) associations between PV and PHT, protein content (PRO), 100SW, TBY, SRY, and DMC. Dry matter content also had positive and significant ($P < 0.01$) correlations with STA. These results indicate presence of high genetic variability, heritability and expected genetic gain suggesting potential for genetic improvement of plant vigour, 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.

Key Words: Heritability, *Pachyrhizus*, protein, starch

RÉSUMÉ

Il existe peu d'informations sur les paramètres génétiques et le gain génétique des accessions de haricot-igname (espèce *Pachyrhizus*) introduites au Rwanda. Il n'existe pas de littérature complète sur l'hérédité du rendement et des composantes du rendement, sur la ségrégation des populations. Cette étude a étudié la variabilité, l'héritabilité et l'avancée génétique des génotypes de haricot-igname F2. Sept hybrides de haricot-igname F2 ont été évalués à la Station de Recherche de Rubona située dans la Province Méridionale du Rwanda, pendant la saison agricole 2014B. Les résultats ont révélé une variabilité génétique significative ($P < 0,01$) de la vigueur de la plante (PV), du poids de la gousse (WOP), de la hauteur de la plante (PHT), du poids de 100 graines (100SW), du rendement total en biomasse (TBY), du rendement des racines de stockage (SRY), teneur en matière sèche (DMC) et teneur en amidon (STA). Des variances génétiques (σ^2_g) et phénotypiques (σ^2_p) élevées et des coefficients de variation génotypiques ($GCV > 25\%$) ont été observés pour WOP, PHT, 100SW, TBY, DMC et STA. Les estimations de l'héritabilité (H^2) étaient élevées (supérieures à 50%) pour tous les caractères, à l'exception du rendement en graines, du nombre de racines et du nombre de gousses. Le GA et l'avance génétique, en pourcentage de la moyenne (GAM%), étaient élevés pour PV, WOP, PHT, 100SW, TBY et DMC. Il y avait des associations positives et significatives ($P < 0,05$) entre PV et PHT, la teneur en protéines (PRO), 100SW, TBY, SRY et DMC. La teneur en matière sèche avait également des corrélations positives et significatives ($P < 0,01$) avec le STA. Ces résultats indiquent la présence d'une variabilité génétique, d'une héritabilité et d'un gain génétique attendus élevés suggérant un potentiel d'amélioration génétique de la vigueur des plantes, du poids des gousses, de la hauteur des plantes, du poids de 100 graines, du rendement total en biomasse, du rendement en racines fraîches de stockage, de la teneur en matière sèche et en amidon de haricot-ignames au Rwanda.

Mots Clés: Héritabilité, *Pachyrhizus*, protéine, amidon

INTRODUCTION

Yam bean (*Pachyrhizus* spp.) is an annual leguminous root crop native of Mexico, Central America and South America, with wide adaptation in various tropical and subtropical regions of Asia, West and Central Africa (Zanklan *et al.*, 2007; Ndirigwe *et al.*, 2017). It is grown under rainfed conditions and is placed taxonomically in the subtribe *Diocleinae*, tribe *Phaseoleae*, within the legume family (*Fabaceae*), and having chromosomes, $2x = 2n = 22$ (Pati *et al.*, 2019). The genus *Pachyrhizus* comprises five species (Silva and Ticona-Benavente, 2016). Three of these are cultivated for their edible tubers, and the remaining two are wild.

The name 'yam bean' is mainly used to designate the three cultivated species, which develop storage roots (Grüneberg *et al.*, 2003). The natural distribution of yam bean is in tropical lowlands with rain forests. It is

restricted to areas with annual precipitation rates between 640 and 4100 mm, an annual temperature ranges of 21 to 27°C, and soil pH value of 4.3 to 6.8 (Sørensen *et al.*, 1997).

In spite of the economic and agronomic importance of the introduced yam bean as resource base for food, feed and forage rich in protein, they are still underutilised and neglected; and deserve consistent evaluation of their genetic resources toward enhancing their narrow gene pool and diversity (Heider *et al.*, 2011; Grüneberg, 2016). Yet, there has never been a concerted steady effort to explore and advance yam bean research in term of genetic variability for yield and yield components traits in offspring. Agaba *et al.* (2017) reported genetic variability for dry matter content in yam beans population that is controlled by additive and non-additive gene effects. But no comprehensive studies on variability, heritability and genetic advance in

yam bean segregating populations have been conducted on yield and yield traits.

Genetic variability is vital for continued genetic improvement of any crop species (Sandhu *et al.*, 2015). Biometrical methods to assess the genetic variability and the extent of heritability of the economic characters serve as useful tools in evaluating the segregating population. These techniques provide an insight into their magnitude of variability available in a crop and are effective in reducing the environmental effects substantially to project the real genetic effects with discrimination of better genotype from the rest (Kalaiyarasi *et al.*, 2019). The development of an intensive breeding and improvement programme needs detailed inherent information and an understanding of genetic variation for yield and its components in the segregating population (Saxena and Bisen, 2016). To determine and formulate an effective selection technique for increasing yield, the association or correlation analysis among yield and yield contributing characters are also paramount. In addition, relationships between yield and yield attributing traits are of prime important for direct and indirect selection of traits which contributes to yield (Aditya and Bhartiya, 2013).

It is known that the effectiveness of plant breeding programmes, particularly, in selection depends on the relative importance of genetic and non-genetic factors in the expression of phenotypic differences among genotypes in a population, referred to heritability (Gangadhara, 2012). Heritability gives a measure of the relationship between phenotypic and breeding values, as the basis for predicting the performance of the offspring based on the performance of their parents in a particular combination of breeding materials (Shumbusha *et al.*, 2014). Thus, it becomes necessary to partition the observed variability into heritable and non-heritable components measured as genotypic and phenotypic coefficients of variations (PCV and GCV), heritability and genetic advance to account for created variability to be used in breeding programmes

(Sandhu *et al.*, 2015). The objective of this study was to investigate the genetic variability, heritability, combining abilities and gene action controlling inheritance of yield and related traits in introduced yam bean to develop suitable genotype in Rwanda.

MATERIALS AND METHODS

The study was carried out at Rubona Research Station, located in the Southern Province of Rwanda, during growing season 2014B. Rubona is sited at 2.29°South and 29.46°East, 1650 meters above sea level representing the mid-elevation agricultural zone of Rwanda, and experiences mean annual rainfall of 413 mm and temperature average of 19.15 °C. The soils of the mid-elevation zone (the most important agricultural production zone of roots and tubers in Rwanda), are granitic, light gravel loams (Ndirigwe, 2006).

Seven yam bean F₂ hybrids generated from parental materials obtained from the International Potato Center Lima-Peru (Table 1), were used for this study. The experiment was carried out by sowing F₂ seed and parental lines (Table 1) in a randomised completed block design (RCBD), with 3 replications. Each plot consisted of two rows, each containing eight plants spaced at 0.3 m within row and 1 m between rows. Two seeds were sown by hand per hole, at approximately two cm depth.

Thinning of the plants to one per hole was done four weeks after sowing. Staking using *callandria sp* was done at 6 to 8 weeks after planting to ensure upright growth and to avoid ground spreading for ease of data collection, and enhanced growth and yield characteristics (Zanklan, 2003). No fertilisers or chemicals were applied during the experiment.

Data were recorded for yield and yield components, namely, (i) plant vigour (PV) as width of first leaf time of development of third leaf within plot, (ii) number of pods per cluster (NOP) counted at harvest, (iii) plant height (PHT) at time of full flowering, (iv) seed yield (SYD) at physiological maturity, (v) 100 seed

TABLE 1. Characteristics of the crosses and parental genotypes used in the yam bean study

Hybrids	Pedigree		Source of seed
	Female	Male	
Hybrid 1	PA-209004	PT-209013	CIP gene bank
Hybrid 2	PA-209004	PT-209014	CIP gene bank
Hybrid 3	PA-209004	PT-209015	CIP gene bank
Hybrid 4	PA-209022	PT-209013	CIP gene bank
Hybrid 5	PA-209022	PT-209014	CIP gene bank
Hybrid 7	PA-209031	PT-209013	CIP gene bank
Hybrid 8	PA-209031	PT-209014	CIP gene bank

Accessions obtained from International Potato Center, Lima - Peru

weight (100SW) at physiological maturity, (vi) number of roots (NOR) counted at harvest, (vii) total biomass yield (TBY) as fresh storage root yield plus vine yields (FBY = RFY + VNY) expressed at physiological maturity, and (viii) storage root yield (SRY) as weight of storage roots harvested from the experimental plots and expressed at physiological maturity. Others included (ix) dry matter content (DMC) as the percentage ratio of dry weight to fresh weight (RDM = 100 * Dry weight / Fresh weight according to Wilken *et al.* (2008), (x) starch content (STA) was obtained through precipitation in excess ethanol while stirring; and (xi) protein content (PRO) as crude protein by Kjeldahl method which is the total protein equivalent including nitrogen from both protein and non-protein sources as recommended by Tumwegamire *et al.* (2011). All data were recorded on individual plants basis and expressed as means per plot.

The data were subjected to Analysis of Variance using GenStat 14th edition (VSN International Ltd, Hemel Hempstead, UK) (Payne *et al.*, 2011). The mean data were analysed to work out the variance components and coefficient of variance following Burton (1952). The estimations of variance components (phenotypic, environmental and genotypic variances), were done following the formulae:

Genotypic variance (σ_g^2) =

$$\frac{\text{Genotypic mean square (GMS)} - \text{Error means squares (EMS)}}{\text{Number of replications (r)}}$$

Environmental variances (σ_e^2) = Error means squares

Phenotypic variance (σ_p^2) = $\sigma_g^2 + \sigma_e^2 / r$

Genotypic coefficient of Variation (GCV), environmental coefficients of variation (ECV) and phenotypic coefficient of variation (PCV) were estimated following the methods suggested by Chaudhary and Singh (1985).

$$\text{GCV \%} = \frac{\sqrt{\sigma_g^2}}{\bar{x}} * 100; \text{ ECV \%} = \frac{\sqrt{\sigma_e^2}}{\bar{x}} * 100,$$

$$\text{and PCV \%} = \frac{\sqrt{\sigma_p^2}}{\bar{x}} * 100$$

Where:

GCV% = genotypic coefficient of variation, σ_g^2 = genotypic, PCV% = phenotypic coefficient of variation, σ_p^2 = genotypic variance, ECV% = environmental coefficient of variation, and σ_e^2 = environmental variance and \bar{x} = grand mean of the trait.

The broad sense heritability (H^2_b) was determined following Kearsy and Pooni (1996) as:

$$h^2_b = \frac{\sigma_g^2}{\sigma_g^2 + \sigma_e^2/r} * 100$$

The expected Genetic Advance (GA) of the genotypes at 5% selection pressure was calculated according to Chaudhary and Singh (1985) as follows:

Genetic advance (GA): $H^2_b * k * \sigma^2_p$,

Genetic advance as percentage of mean (GAM%):

$$\frac{GA}{\bar{x}} * 100$$

RESULTS

The results of the combined analysis of variance revealed highly significant ($P < 0.01$) genetic variability for all yield and yield traits assessed, except for the number of pods per cluster (NOP), seed yield (SYD), 100 seed weight (100SW) and Protein content (PRO) of the yam bean storage roots (Table 2).

Variance components, heritability and genetic advance. The estimates of phenotypic and genetic variance, coefficients of variation (genotypic, phenotypic and environmental), heritability and genetic variance are presented in Table 3. Weight of pods, plant height, 100 Seed weight, total biomass yield, dry matter content, and starch content exhibited high genetic (σ^2_g of 2.56, 15.49, 2391.33, 7.99, 2.57, 6.44, 9.20 and 16.87) and phenotypic (σ^2_p of 17.19, 2442.30, 9.82, 2.95, 8.59, 10.41 and 20.89) variances, respectively. Similarly, the genotypic coefficients of variation were high (>25%) for plant height, 100 seed weight, storage root yield, dry matter content and starch content. Also, plant vigour, weight of pods, plant height and number of roots had

TABLE 2. Analysis of variances for different yield and associated quality traits in yam beans

Source of Variation	Df	Mean squares											
		PV	NOP	WOP	PHT	SYD	100SW	NOR	TBY	SRY	DMC	STA	PRO
Replication	2	0.24	1.40	107.49	541.1	0.026	1.046	0.739	3.848	9.80	25.015	33.91	7.66
Genotypic	6	7.84***	1.77	48.18***	7326.90***	0.099	29.46***	0.238	8.859***	25.77***	31.22***	62.67***	4.04
Error	154	0.47	1.54	5.09	152.90	0.12	5.48	0.132	1.16	6.44	3.63	12.06	0.44

PV = Plant vigour, NOP = Number of pods per cluster, WOP = Weight of pods, PHT = Plant height, SYD = Seed yield, 100SW = 100 seed weight, NOR = Number of roots, TBY = Total biomass yield, SRY = Storage root yield, DMC = Dry matter content, STA = Starch content, PRO = Protein content

TABLE 3. Genetic components of variance, coefficients of variation, heritability and genetic advance for twelve traits of F₂ yam bean population

Traits	σ_p^2	σ_g^2	σ_e^2	PCV (%)	GCV (%)	ECV (%)	H ²	GA	GAM (%)
Plant vigour	2.72	2.56	0.47	47.10	8.13	13.54	0.94	3.20	91.39
Number of pods	0.93	0.42	1.54	3.83	13.17	6.11	0.45	0.90	3.55
Weight of pods	17.19	15.49	5.09	72.10	10.03	88.49	0.90	7.70	133.88
Plant height (cm)	2442.30	2391.33	152.90	36.47	536.20	112.84	0.98	99.68	73.56
Seed yield (t ha ⁻¹)	0.06	0.02	0.12	7.95	1.22	3.99	0.32	0.16	5.22
100 Seed weight (g)	9.82	7.99	5.48	10.60	35.70	18.54	0.81	5.25	17.78
Number of roots	0.21	0.04	0.24	28.21	0.62	14.77	0.30	0.29	17.72
Total biomass yield (t ha ⁻¹)	2.95	2.57	1.16	14.04	18.25	9.44	0.87	3.08	25.15
Storage root yield (t ha ⁻¹)	8.59	6.44	6.44	16.26	29.04	35.73	0.75	4.53	25.12
Dry matter content (%)	10.41	9.20	3.63	18.65	27.52	20.98	0.88	5.87	33.95
Starch content (%)	20.89	16.87	12.06	11.50	46.99	30.33	0.81	7.60	19.12
Protein content (%)	1.33	1.20	0.38	11.69	17.53	3.85	0.90	2.15	21.79

PV = plant vigor, NOP = No of pods per cluster, WOP = weight of pods, PHT = plant height, SYD = seed yield, 100SW = 100 seed weight, NOR = Number of roots, TBY = Total biomass Yield, SRY = storage root yield, DMC = dry matter content, STA = starch content, PRO = protein content

high phenotypic coefficients of variation. However, the environmental coefficients of variation were unexpectedly high for weight of pods, plant height, storage root yield and dry matter content, and starch content.

Estimates of heritability ranged from 30% for seed yield to 98% for plant height, and were high (>50%) for storage root yield, 100 seed yield, starch content, total biomass yield, weight of pods, dry matter content, starch content, protein content, and plant vigour (Table 3).

The estimates for genetic advance at 5% selection intensity, and the corresponding genetic advance as percentage of mean values are presented in Table 3. The estimates for genetic advance (GA) and genetic advance as percentage of the mean (GAM%) were high for plant vigour, and weight of pods, plant height; and moderate for 100 seed weight, number of roots, total biomass yield, storage root yield, dry matter content, starch and protein content.

Mean performance of yam beans. The mean values, ranges, standard error (SE) of means, and coefficients of variation for yield and related traits are shown in Table 4. A wide range of variations was observed with regard

to different yield and related traits. The differences among maximum and minimum values (range) of all characters were high for plant vigour (3.0), weight of pods (12.87 t ha⁻¹), 100 seed weight, total biomass yield (8.35 t ha⁻¹), storage root yield (19.7 t ha⁻¹), dry matter content (15%) and starch content (21%).

The genotypic mean performance of parents and F₂ progenies are presented in Table 5. For most of the traits evaluated, the mean performance of the progenies was higher than the lower parental lines. The results further identified progeny of hybrid1 (AC209004 x TC209013) to have transgressive segregants with mean plant vigour that was higher than values for the mean performance of both parental lines. For the number of pods per cluster, all the progenies had higher mean values than the low parental genotypes (*P. ahipa*). Plant height for progenies was higher than the values of the low parents, but lower than for the high parents. There was limited variability in seed yield between the parents and the progenies with the parents varied from 2.35 to 3.37 t ha⁻¹; while the seed yield of progenies varied from 2.97 to 3.16 t ha⁻¹.

The 100 seed weight of parental lines was higher (range: 31.25-32.94 g) than for all the

TABLE 4. Statistics information for yield and yield components in F₂ yam bean populations

Characters	Minimum	Maximum	Range	Mean	CV (%)	SE
Plant vigour	2.00	5.00	3.00	3.50	19.67	0.69
Number of pods	23.00	31.00	8.00	25.22	4.92	1.24
Weight of pods	3.13	16.00	12.87	5.75	39.24	2.26
Plant height (cm)	102.00	215.00	113.00	135.50	9.12	12.37
Seed yield (t ha ⁻¹)	1.98	3.98	2.00	3.09	11.35	0.35
100 Seed weight (g)	25.00	35.00	10.00	29.55	7.92	2.34
Number of roots	1.00	2.00	1.00	1.63	30.14	0.49
Total biomass yield (t ha ⁻¹)	8.50	16.85	8.35	12.24	8.78	1.08
Storage root yield (t ha ⁻¹)	13.00	32.70	19.70	18.03	8.74	3.47
Dry matter content (%)	14.00	29.00	15.00	17.30	11.02	1.91
Starch content (%)	28.00	49.00	21.00	39.76	8.74	3.47
Protein content (%)	8.25	11.86	3.61	9.85	6.25	0.62

CV = Coefficient of variation, SE = standard error of the mean

TABLE 5. Genotypic mean performance of yam bean genotypes (parents and F2 progenies) evaluated at Rubona Research Station, Rwanda

Accessions	PV	NOP	WOP	PHT (cm)	SYD (tha ⁻¹)	100 SW (g)	NOR	TBY (tha ⁻¹)	SRY (tha ⁻¹)	DMC (%)	STA (%)	PRO (%)
Hybrids												
Hybrid 1	4.57	25.28	4.72	169.30	2.97	31.62	1.63	13.42	19.91	19.50	36.76	9.79
Hybrid 2	3.37	25.00	5.85	135.50	3.11	29.19	1.67	12.03	18.27	16.65	39.81	9.70
Hybrid 3	3.51	25.22	5.92	131.20	3.12	28.30	1.66	12.07	17.57	17.02	40.38	9.85
Hybrid 4	3.42	25.38	5.11	127.80	3.16	28.63	1.62	11.97	17.27	16.36	40.96	9.99
Hybrid 5	3.32	25.50	4.03	125.10	3.08	29.56	1.59	11.95	18.12	16.87	41.20	9.77
Hybrid 7	3.17	25.42	6.62	124.40	3.13	29.19	1.71	11.97	17.29	16.85	40.39	9.79
Hybrid 8	2.87	24.71	8.38	124.30	3.12	29.45	1.54	11.88	17.11	17.09	40.15	9.99
Parents												
AC209004	4.04	21.54	4.81	54.50	2.35	31.17	1.67	10.15	13.22	15.44	50.61	8.79
AC209022	3.75	21.63	4.92	57.80	3.04	31.25	1.58	10.04	12.82	15.74	50.84	8.98
AC209031	4.25	21.25	5.82	62.10	3.37	32.94	1.71	10.98	14.31	16.14	50.13	8.94
TC209013	4.45	27.04	6.23	183.30	3.24	31.67	1.45	24.96	31.91	23.79	38.52	9.42
TC209014	4.25	26.25	5.83	190.00	3.37	32.94	1.67	15.39	23.92	24.25	35.37	9.76
TC209015	4.27	27.78	5.11	205.30	3.24	32.39	1.48	14.70	25.58	23.98	32.80	9.58
Mean	3.79	24.77	5.64	130.05	3.10	30.64	1.61	13.19	19.02	18.44	41.38	9.57
CV (%)	15.80	5.49	32.47	8.65	13.40	6.69	30.15	14.34	13.63	9.64	8.08	6.07
SE	0.60	1.35	1.83	11.00	0.41	2.05	0.49	1.88	2.55	1.76	3.37	0.58

AC = Accession Code for *Pachyrhizus Ahipa* parents and TC = Accession Code for *Pachyrhizus Tuberosus* parents PV = plant vigor, NOP = No of pods per cluster, WOP = weight of pods, PHT = plant height, SYD = seed yield, 100SW = 100 seed weight, NOR = No. of roots, TBY = Total biomass yield, SRY = storage root yield, DMC = dry matter content, STA = starch content, PRO = protein content

crosses whose values varied from 28.30 - 29.56 g. Wide variations were observed for total biomass yield (TBY) among parental lines, ranging from 10.04 to 24.94 t ha⁻¹, as compared to the values for progenies (11.88-13.42 t ha⁻¹). The storage root yields were average for both parents and progenies, ranging from 12.82 t ha⁻¹ in parental lines AC209022 to 31.91 t ha⁻¹ in parental lines TC209013. For dry matter content, the progenies had values ranging from 16.65 to 19.50%; while the parental lines varied from 15.44 to 24.25%. There were high values for starch content (32.80 to 50.84%) and protein content (8.79 to 9.99%) for parents to progenies.

Principal component analysis of yield and associated traits. Principal component analysis of yield and associated traits are shown in Table 6. The total variation represents an equivalent of five variables and

indicated all traits (apart of 100SW) were important contributing variables. The first 5 components (PCA1, PCA2 and PCA3) with an eigenvalue >1 explained 84.08% of total variability among the genotypes. Principal components, PC1 to PC5 explained 43.93, 17.64, 9.28, 7.50, and 5.73% of the total variation, showing maximum eigenvalues of 5.271, 2.116, 1.113, 0.899 and 0.687, respectively. Apart of 100SW trait, all traits with high coefficients were the primary sources of variation in the PC1 score for the genotypes and contributed positively to PC1. Pearson's correlation coefficients

The phenotypic correlation coefficients among the twelve yield and yield traits are presented in Table 7. Plant vigour had a significant (P<0.05) positive correlations with plant height and protein content; and a highly significant relationship with 100 seed weight, total biomass yield, storage root yield and dry matter content. Number of pods showed

TABLE 6. Eigenvector values for principal components of yield and associated traits in yam bean (*Pachyrhizus* sp.)

Parameter	PCA1	PCA2	PCA3	PCA4	PCA5
PV	0.058	0.477	0.073	0.435	0.304
NOP	0.373	-0.133	-0.099	-0.090	0.034
WOP	0.065	-0.223	0.708	0.354	-0.322
PHT	0.407	0.033	-0.089	-0.056	0.118
SYD	0.133	-0.025	0.617	-0.618	0.247
100SW	-0.024	0.514	0.139	-0.099	0.411
NOR	0.063	-0.441	0.112	0.451	0.643
TBY	0.312	0.217	0.093	0.232	-0.308
SRY	0.377	0.164	0.041	0.121	-0.197
DM	0.370	0.258	0.035	-0.015	-0.023
STA	0.358	-0.293	-0.173	-0.068	0.075
PRO	0.401	-0.133	-0.146	-0.072	0.077
Eigen values	5.271	2.116	1.113	0.899	0.687
Total variance (%)	43.93	17.64	9.28	7.50	5.73
Cumulative (%)	43.93	61.57	70.85	78.35	84.08

PV = Plant vigor, NOP = Number of pods per cluster, WOP = weight of pods, PHT = Plant height, SYD = Seed yield, 100SW = 100 seed weight, NOR = Number of roots, TBY = Total biomass Yield, SRY = Storage root yield, DMC = Dry matter content, STA = Starch content and PRO = Protein content

TABLE 7. Phenotypic correlation coefficients for yield and associated traits among F2 yam bean progenies evaluated at Rubona Research Station, Rwanda

	NOP	WOP	PHT (cm)	SYD (t ha ⁻¹)	100SW (g)	NOR	TBY (t ha ⁻¹)	SRY (t ha ⁻¹)	DMC (%)	STA (%)	PRO (%)
PV	-0.009	-0.100	0.164*	-0.035	0.355***	-0.042	0.263***	0.260***	0.310***	-0.031	-0.146*
NOP	-	0.097	0.756***	0.242***	-0.137*	-0.034	0.493***	0.625***	0.536***	-0.685**	0.323***
WOP		-	0.074	0.195***	-0.134*	-0.023	0.092	0.086	0.007	-0.114***	0.077
PHT (cm)			-	0.240***	0.066	-0.088	0.560***	0.752***	0.732***	-0.820***	0.3527***
SYD (tha ⁻¹)				-	0.034	-0.079	0.157*	0.228***	0.192***	-0.170**	0.146*
100SW (g)					-	-0.053	0.117*	0.065	0.245***	0.085	-0.204***
NOR							-0.108	-0.104	-0.061	-0.018	-0.024
TBY (t ha ⁻¹)							-	0.799***	0.606***	-0.361***	0.040
SRY (t ha ⁻¹)								-	0.737***	-0.548***	0.177**
DMC (%)									-	0.528***	0.081
STA (%)										-	-0.347***

*, **, *** = significant at P<0.05, 0.01, 0.001 respectively

PV = Plant vigour, NOP = Number of pods per cluster, WOP = Weight of pods, PHT = Plant height, SYD = Seed yield, 100SW = 100 seed weight, NOR = Number of roots, TBY = Total biomass yield, SRY = Storage root yield, DMC = Dry matter content, STA = Starch content, PRO = Protein content

significant ($P < 0.01$) positive correlations with plant height ($r = 0.756$), seed yield, total biomass yield, storage root yield dry matter content and protein content, but negative significant ($P < 0.05$) correlations with 100 seed weight and starch content. The dry matter content had positive and significant ($P < 0.01$) correlations with total biomass yield and storage root fresh yield, seed yield, 100 seed weight, plant height and starch content. The starch content had negative significant ($P < 0.01$) correlations with most traits; while number of roots had no significant correlations with any traits.

DISCUSSION

Seven F_2 yam bean crosses showed highly significant variability for yield and yield traits; namely plant vigour (PV), weight of pods (WOP), plant height (PH), 100 seed weight (100SW), total biomass yield (TBY), storage root fresh yield (SRY), dry matter content (DMC) and starch content (STA) (Table 2). Significant variability implies that genetic improvement of these traits is possible and could be exploited for improvement of yam bean germplasm in Rwanda. The observed genetic variability could be a result of the distinct yam bean species (*P. tuberosus*, *P. erosus* and *P. ahipa*) (Delêtre *et al.*, 2013; Santayana *et al.*, 2014;) that were intercrossed to obtain the base population (F_1) for this study. These results are similar to the findings reported in yam beans elsewhere (Zanklan *et al.*, 2007; Agaba *et al.*, 2016; Silva and Ticona-Benavente, 2016). Agaba *et al.* (2016) reported significant differences among yam bean accessions introduced in Uganda, and explained that such variability in yam beans was a precursor to effective selection and initiation of yam bean breeding programmes to improve yield and dry matter traits that were preferred by root crop farmers in the region. Previously, Zanklan *et al.* (2007) also reported significant genetic variances for root traits, seed yield, pod yield, seed number and pod

weight which suggested the possibility for yam bean breeding, adoption, establishment and utilisation in Africa.

The high estimates of genotypic coefficients of variation (GCV) for plant height, 100 seed weight, storage root yield, dry matter content and starch content indicated the presence of inherent variability in the evaluated germplasm (Table 2). According to Al-Tabbal and Al-Fraihat (2011), such GCV estimates indicate genetic variability that remains unaltered by environmental conditions, and forms the basis for exploitation in selection and hybridisation programmes. Heritability estimation was essential to determine the proportion of genetic variation in the parents that could be transmitted to the progenies, which is the foundation of all improvement programmes (Sandhu *et al.*, 2015). Heritability estimates were high for most traits (Table 3), which suggested potential to reliably predict breeding values based on the phenotypic mean values (Alemu *et al.*, 2017).

In addition to heritability, estimation of genetic advance is vital for effective selection and improvement of quantitative traits. This study demonstrated high estimates of genetic advance (GA) and genetic advance as a percentage of the mean (GAM %) for several traits (Table 3). Expected genetic advance as percentage of mean was generally high for most of the traits, except for number of pods and seed yield which depicted genetic advance values lower than 10%. Among the traits, the highest estimates of genetic advance as percentage of mean recorded were weight of pods (133.88%), plant vigour (91.39%) and plant height (73.56). Estimates of genetic advance, as percentage of mean values showed relatively high (>17%) genetic advance expectations for number of roots, 100 seed weight total biomass yield, storage root yield, dry matter, starch content and protein content. Such high genetic advance is indicative of additive gene action in the phenotypic expression of these traits in yam beans (Jha and Singh, 2014). The high heritability,

accompanied by high genetic advance. as percentages of the means for most traits, indicates that these traits are genetically controlled, inheritable and that selection may be effective in early generations of breeding (Jha and Singh, 2014). These results support the argument that the phenotypic expression of yield and yield traits in yam beans might be a good indicator of their genotypic potentiality, and, therefore, offer a wide scope for successful selection of elite genotypes from the breeding populations.

The mean performance of F₂ progenies was high for most traits, except for weight of pods (5.75 t ha⁻¹), seed yield (3.09 t ha⁻¹) and number of roots (1.63) (Table 4). Mean values recorded for storage root yields (18.03 t ha⁻¹), dry matter content (17.30%) and starch content (39.76%) were similar or slightly lower than yam bean performance reported elsewhere in Africa such as average yields of 24 t ha⁻¹ from on-farm trials involving two *P. erosus* accessions (CIP-209018 and CIP-209019) in Benin (Adegbola *et al.*, 2015; Grüneberg, 2016), 17 t ha⁻¹ from 10 *P. erosus* accessions in Senegal and 14 t ha⁻¹ from 15 *P. erosus* accessions in Sierra Leone (Belford *et al.*, 2001).

In Uganda, storage root yields of up to 22.1 t ha⁻¹, starch (52.3%), and dry matter content of 15.3 % have been reported (Agaba *et al.*, 2016). These results suggest that the evaluated yam beans were well adapted to the test environments in East and Central Africa. However, it is important to know the performance of any crop in early generations before the crop can be recommended for large scale adoption and utilisation (Joshi, 2001), especially for new crop introductions such as the yam beans.

The mean genotypic performance of parents and their F₂ progenies showed wide variation for all traits (Table 5). For plant vigour, apart from crosses 209076, all progenies had lower values than their corresponding parental lines. Whiles number of pods, plant height, 100 seed weight, total biomass yield, storage root fresh

yield, and dry matter content showed mean progeny values that were higher than the lower parents (AC-209004, AC-209022, and AC-209031). These findings suggest that heterosis can be exploited to improve these traits in yam beans (Burton and Brownie, 2006). In terms of storage root yield, dry matter content and protein; the best performing progenies were 209076, 209077 and 209080, but their mean values were less than those reported in Uganda (Agaba *et al.*, 2017).

The results of principal component analysis revealed that a total of 84.08% of the total variation could be explained by five principal components (Table 6). This variation represents an equivalent of five variables and indicated that all traits (apart of 100SW) were important contributor variables. These findings were similar to what was observed by Silva (2016), who characterised 64 yam bean accessions using PCA and cluster analysis and Tapia and Sørensen (2003) who studied the morphological variation in *P. tuberosus* germplasm collection. Similar reports were highlighted on recent performance investigations in yam beans using descriptive statistics and PCA in Rwanda and Uganda, respectively (Agaba *et al.*, 2016; Ndirigwe *et al.* 2017)

The correlation analysis revealed positive and significant correlations between several yield and yield traits such as plant vigour and plant height, protein content, 100 seed weight, total biomass yield, storage root yield and dry matter suggesting that these traits can be simultaneously improved through selection (Table 7). The results also revealed negative, but significant correlations between starch and number of pods, weight of pods, plant height, fresh biomass yield and storage root yield which demonstrated the inherent difficulty for simultaneous improvement of these traits in yam beans. Similar correlation estimates have been reported before by researchers working with yam beans (Agaba *et al.*, 2016).

The estimation of inter-trait correlations is vital in breeding programmes as an indicator

for successful selection of genotypes that would possess genetic capability for simultaneous improvement of several quantitative traits in a single selection cycle. Genetic association of characters is an important criterion for choice of the selection procedures (Acquaah, 2012). The storage root yields and dry matter contents are target traits for improvement of yam beans (Grüneberg *et al.*, 2003; Agaba *et al.*, 2016; Grüneberg, 2016) which suggests that the positive and significant correlation estimates obtained between them and several traits is a good basis for planning a breeding program that would target comprehensive improvement of yield and yield traits in yam beans.

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