



ISSN: 2218-1768

Comparing the efficiency of base and multiplicative selection indices for yield and quality traits in Cassava

Severin Ntivuguruzwa^{1,2*}, R. Edema¹, P. Gibson¹, M.E.B. Alladassi¹,
A. Nduwumuremyi², W.Abincha^{1,4}, R. Kawuki³

¹Department of Agricultural production, College of Agricultural and Environmental Sciences, Makerere University, P.O Box 7062, ²Rwanda Agricultural and Animal Resources Board, P. O Box 5016, Rubona, Huye, Rwanda, ³National Crop Resources Research Institute, P.O Box 7084, Kampala, Uganda, ⁴Mount Kenya University, P.O Box 4441, Kisii, Kenya, Kampala, Uganda

ABSTRACT

The efficiency of two selection indices; base index and multiplicative index was compared to determine the effectiveness of each in identifying superior genotypes in cassava (*Manihot esculenta* Crantz) population. Genotypic data on various yield and quality traits among 570 cassava genotypes were used to construct these selection indices. The efficiency of these indices was compared by determining the performance means of each genotype for studied traits and computing selection differentials of each index. Best linear unbiased predictions (BLUPs) for dry matter content and harvest index were also used for comparison of the two selection indices. Base index produced high performance means of all five studied traits and proved to be more efficient compared to multiplicative index in improvement of cassava genotypes. In addition, base index produced high selection differentials for three out of five studied traits. It was concluded that base index is useful in cassava germplasm selection.

KEYWORDS: Selection index, efficiency, cassava, base index, multiplicative index

Received: May 23, 2020
Accepted: September 20, 2020
Published: October 07, 2020

*Corresponding Author:
Severin Ntivuguruzwa
Email: ntiseverin@yahoo.fr

INTRODUCTION

Cassava (*Manihot esculenta* Crantz) is a key staple food crop in Uganda, ranking second to bananas in terms of area occupied, total production and per capita consumption [1, 2, and 3]. Since its introduction in the early 1860's, cassava continues to play a significant role in the diet of Ugandans. The crop contributes a considerable proportion of the calorie intake with its per capita consumption estimated at 132 kg per person per year [4]. About 75% of farmers grow cassava for home consumption and about 25% grow it for cash and other uses.

Cassava is responsible for increased food security in most parts of Uganda. The crop is used on its own or as an additive to either millet or sorghum flour to make local bread. This is typical in the millet-cotton farming areas covering west Nile, north, east and north-eastern parts of Uganda. In the banana-coffee farming areas covering south and south-western parts of Uganda, cassava is mainly cultivated for fresh storage root consumption [5]. The crop is usually intercropped with legumes and cereals on small plots of land. The average yield of cassava in Uganda is estimated at 14.6 tons per hectare while the annual production

is estimated at 11.3 million tons, which accounts for about 3.4% of Africa's total cassava production and 1.9% of total cassava production worldwide [5]. Due to the increasing demand for cassava as a basic food and source of income for smallholder farmers, as well as its future potential as an industrial crop, research interventions involving farmers are urgently needed to improve cassava production and productivity.

The effectiveness of a plant breeding programmes depends on the ability of a breeder to select superior individuals or families as defined by the breeding objective. Breeders are generally interested in improving more than one trait at a time, or improving one trait without affecting the performance of others. In a multistage selection scheme, breeders begin with creation of genetic diversity by crossing elite clones which are selected based on their performance; this process is carried on through different stages and often ends with a few clones in the regional trials (RT) that have survived the selection process. In the RT, greater emphasis is put on yield and/or other critical farmer-preferred traits. This process takes about six to seven years or more starting from the initial crosses which is too long especially when the demand for new varieties is urgent.

Copyright: © The authors. This article is open access and licensed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0/>) which permits unrestricted, use, distribution and reproduction in any medium, or format for any purpose, even commercially provided the work is properly cited. Attribution — You must give appropriate credit, provide a link to the license, and indicate if changes were made.

To shorten this process, it is recommended to evaluate genotypes based on multiple trait selection. One of the common methods used in multiple traits selection is tandem selection, which selects for one trait at a time until that is improved prior to focusing on other traits. A second one is independent culling level, where a certain level of merit is established for each trait, and all individuals that fall below that threshold are discarded, regardless of their superiority or inferiority for other traits. And lastly, selection index which is a procedure that provides a single criterion for selection among genotypes by including combinations of several traits [6].

Selection indices have been an effective selection criterion to increase grain yield in corn [7]. More recent studies [8] on the efficiency of selection indices in sweet corn reported that base index proved to be more efficient as compared to Smith-Hazel index in the improvement of aggregate genotype for eight yield and four quality traits simultaneously. Also, it has been reported [9] that multiplicative index was found to be useful in potato breeding programs compared to base index based on the sum of ranks proposed [10]. In addition, base and multiplicative indices provided superior genetic progress in the selection of common bean lines [11]. The objective of this study was to compare base and multiplicative selection indices and determines if they can be useful in cassava selections as they have shown high efficiency in other breeding program.

MATERIALS AND METHODS

Initial Testing Materials and Data Collection

A total of 570 genotypes were selected from a seedling trial at Buginyanya for having resistant clones to diseases. Together with other 5 checks, these clones were planted at Zombo in September 2014 using an augmented design with 6 blocks. Planting was done at 1x1m plant spacing, with 10 plants per plot of single row. Data were collected on disease severity and incidence of Cassava Mosaic Virus Disease (CMD) at three, six, and nine months after planting (MAP), Harvest Index (HI) and Dry Matter content (DMC).

In addition, at harvest, all plants were uprooted and number of roots per plot, root weight per plot and biomass weight per plot was recorded to compute the harvesting index (HI) of each genotype. Both the harvested roots weight and the biomass weight were measured in kg using weighing scale. Harvesting index (HI) was computed as the proportion of fresh weight of roots to total biomass as shown in the formula below:

$$HI = \frac{\text{weight of roots / plot}}{\text{weight of roots / plot} + \text{weight of the above ground biomass / plot}}$$

Dry matter content was also estimated based on the principle of a linear relationship between specific gravity with root DMC in cassava [12]. Here, root samples that were free of soil and also weighing 3-5 kg were weighed in air using a suitable scale,

and then weighed again, while emerged in water. Based on the weight of the samples in air and in water, the percentage DMC was obtained using the formula below:

$$DMC = [(Specific\ gravity \times 158.3) - 142]$$

Whereby: Specific gravity = weight of cassava roots sample in air divided by the difference between weight of cassava roots sample in air and cassava roots sample in water [12].

Using the collected data, base and multiplicative selection indices were used separately to select the top 120 clones each. The selection procedure for each index is described below.

Clonal Selection using Base Index

Base index was constructed for different selection strategies to improve plant traits as described in earlier reports [13]. The base index does not require the use of genotypic and phenotypic variance and covariance matrices [14]. It uses the economic weight as index weight as described in the equation below

$$I = a_1x_1 + a_2x_2 + a_3x_3 + \dots \dots \dots a_nx_n = \sum a_ix_i \tag{1}$$

Where; I is the index value, a_i is economic weight attributed to the trait n and x_i is the actual recorded value for each variate of the i^{th} genotype or average of the trait included in the index. In this study, five traits were considered and used in the index as outlined in step 2. This selection index is similar to the one used at the International Center for Tropical Agriculture (CIAT) [14].

$$I = (RWT \times 10) + (RTN \times 8) + (DMC \times 8) + (HI \times 5) - (CMDs \times 5) \tag{2}$$

Where RWT= root weight per plot; RTN= root number per plot; DMC= dry matter content; HI= harvest index; and CMD= cassava mosaic disease.

Once the selection index value for each genotype is obtained, the entire data set was ranked using the selection index, and the top 120 genotypes were selected and replanted to constitute the set of materials to evaluate the base index.

Clonal Selection using Multiplicative Index

Unlike base index, the multiplicative index does not require economic weights [15]. This weight free index instead requires that lower acceptable limits of performance be specified for each trait [14]. The lower acceptable limits are analogous to independent culling levels. The multiplicative index is obtained as:

$$I = (x_1 - l_1) (x_2 - l_2) \dots \dots (x_n - l_n) \tag{3}$$

Where; l_i is the lower acceptable limit for the i^{th} trait. As with independent culling levels, the l_i values among traits need to represent the same selection intensity. Just like for the base index, five traits were considered for the multiplicative index, and assigned the lower acceptable limits (Table 1).

Evaluation of Selected Clones

After applying the selection indices, as specified in equations (2) and (3), the top 120 with the highest index values for each of the two indices were selected and planted in clonal evaluation trials that were established at Namulonge, Zombo, and Bundibugyo (Table 2) during the second rainy season of 2015. At each site, clones assigned to the respective selection index were established in separate experiments. Thus, at each site up to 240 clones were evaluated using augmented designs that comprised 3 blocks each with 40 plots per block, and 4 checks per block. The experimental unit consisted of a single row plot of 1 m length with 10 plants spaced 1 m and 1 m between rows. Similar data collection described above for the initial clonal evaluation was done at each site on plant vigor, CMD, HI and DMC.

Data Analysis

Separate analyses were conducted. First, summary statistics were computed for each location for all the evaluated traits. Secondly, selection differentials were calculated for each trait at a specific location. In this case, means of the unselected clones were separated from the means of the top 15 clone ($\approx 15\%$ selection). In addition, Linear mixed model effects with *lme4* package was used to generate the Best Linear Unbiased Predictions (BLUPs) of 15 top and 15 bottom clones (Bernardo, 2010). This enabled comparison of the BLUPs to the respective selection index.

RESULTS

Datasets generated for CMD, root, DMC, HI were used to compare the two selection indices. There was a slight difference between base index and multiplicative index in the measurement of CMD severity across locations. From the result, CMD severity means ranged between 1.02 to 1.10 in base index, while means of CMD severity in multiplicative index ranged between 1.17 to 1.24 (Figure 1). For CMD incidence,

Table 1: Lowest acceptable limit given to the traits under the multiplicative index

Traits	Lowest acceptable limit
Flesh Root weight per plot (FRW)	3 kg
Root number per plant (RN)	10
Dry matter content (DMC)	35%
Harvest Index (HI)	0.5
Cassava mosaic disease severity	1

Table 2: Geographical and physical characteristics of the testing sites

Location	Longitude	Latitude	Altitude (masl)	Temperature (°C)	Annual average Rainfall (mm)
NaCRRRI (Namulonge)	32°53'E	0°32'N	1150	21-27	1200
Zombo	30°54'E	02°30'N	1522	23.4	1340
Bundibugyo	30°04'E	0°43'N	1700	22.9	1270

9% of the tested materials from multiplicative index presented foliar symptoms at Namulonge whereas, 8% of the tested materials from base index were diseased. The same situation occurred at Bundibugyo where 2.5% of the tested materials from multiplicative index had CMD foliar symptoms against 1.5% from base index which were diseased. At Zombo, CMD incidence was 3% for both selection indices.

Harvest index showed low differences between the two selection indices in all locations. Results from Figure 1 revealed that base index had a HI 0.45 at Zombo, while multiplicative had mean a HI of 0.40. The same difference was observed in Namulonge, where base index was having a HI of 0.26 versus 0.25 from multiplicative index. Similarly, Bundibugyo site as well showed small differences between the two selection indices with 0.38 for base index and 0.33 for multiplicative index.

Results further revealed low differences in DMC between the two selection indices at Namulonge and Bundibugyo. There was a DMC of 32.4% and 31.6% at Namulonge for base and multiplicative selection indices respectively. At Bundibugyo, the difference was also very low where base had a DMC of 30% versus 29.3% of multiplicative index. At Zombo, base index showed a higher DMC, than multiplicative index with respective values of 33.18% and 30.5% (Figure 1).

The prediction performance of top 15 and least 15 genotypes in both selection indices showed a significant difference (Table 3). For example, for DMC, the highest BLUP value for base index was 3.69 with a mean of 47.37 (UGH 150129), whereas the highest BLUP in multiplicative index was 1.58 with an average of 39.34 (UGH 150211).

The same difference was also observed for HI, where the best genotype (UGH 150066) in base index had BLUP of 0.05 with mean of 0.59, while the best genotype for multiplicative index had BLUP and mean values of 0.03 and 0.49 respectively (Table 3).

Data on selection differentials associated with the evaluated traits and selection indices are presented in Table 4. Selection differentials results showed significant differences between the two selection indices for all selected traits except CMD severity and HI which had the same selection differentials for both indices (Table 4). For example, under the base index, selection differentials for root number per plot were 20, while for multiplicative were 2; this showed a 10 fold differences between the two indices. Similar observations were evident for roots weight were base index had a 28 fold difference. Overall, the base index was better than multiplicative index since it had the highest selection differentials for most of the traits.

DISCUSSION

Visual selection can provide reliable response for traits that are highly phenotypically expressed like vigor, day to flowering, or plant height. However, visual evaluation is of questionable

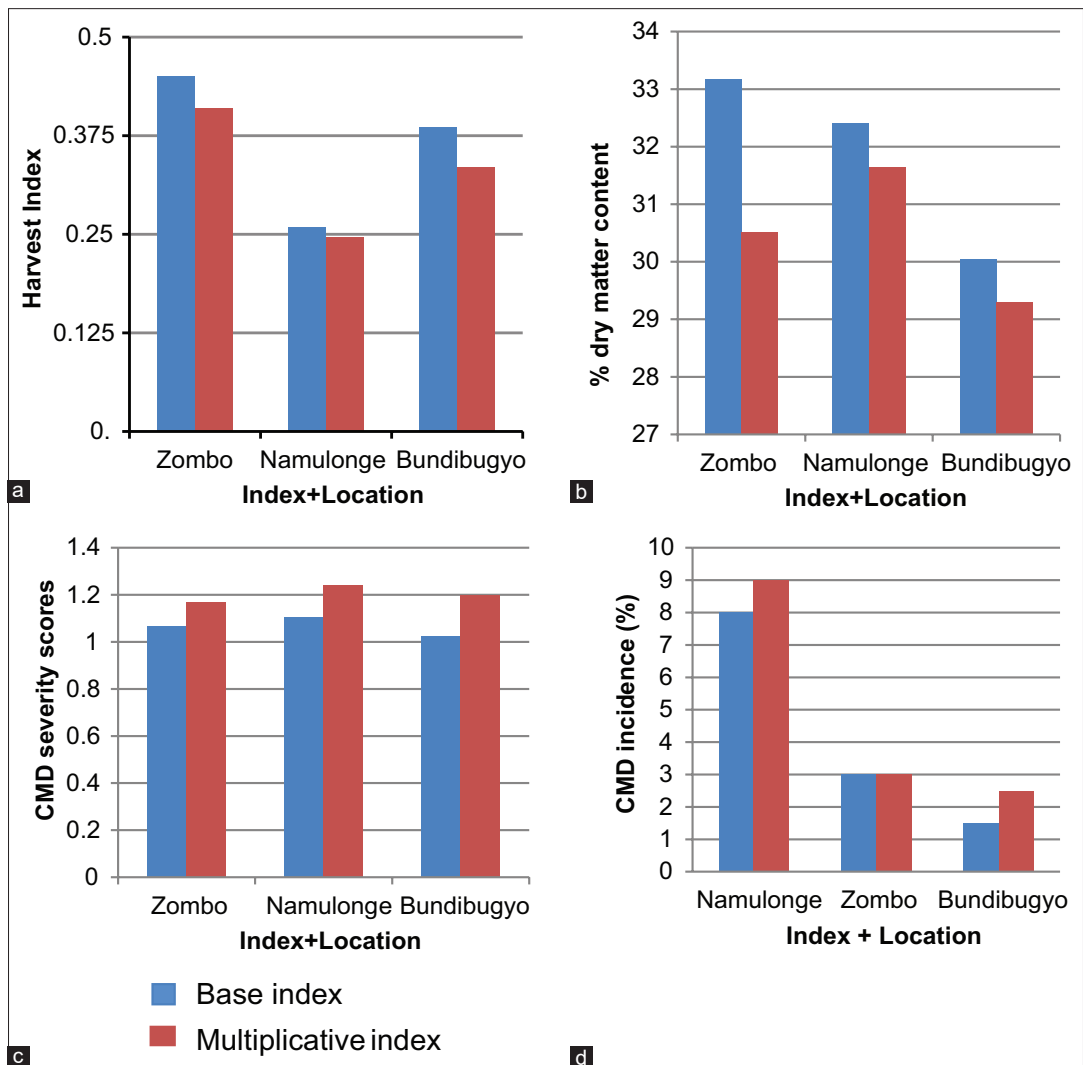


Figure 1: Comparison of base and multiplicative index for selected traits at three locations in Uganda. (a) comparison of harvest index; (b) comparison of root dry matter content; (c) comparison of CMD severity; (d) comparison of CMD incidence

Table 3: Comparison of best linear unbiased predictions (BLUPS) for dry matter content and harvest index of selected clones in base and multiplicative indices

Clones	Base Index					Multiplicative Index					
	DMC		HI			DMC		HI			
	Blups	Mean	Clones	Blups	Mean	Blups	Mean	Clones	Blups	Mean	
Top 15											
UGH150129	3.69	47.37	UGH150066	0.05	0.59	UGH150211	1.58	39.34	UGH150453	0.03	0.49
UGH150253	1.51	38.21	UGH150035	0.05	0.59	UGH150595	1.07	36.48	UGH150045	0.03	0.49
UGH150669	1.30	37.31	UGH150067	0.05	0.53	UGH150096	0.94	35.76	UGH150066	0.02	0.47
UGH150090	1.21	36.97	UGH150577	0.04	0.51	UGH150227	0.76	34.89	UGH150348	0.02	0.46
UGH150210	1.10	36.48	UGH150054	0.04	0.49	UGH150319	0.67	34.24	UGH150239	0.02	0.44
UGH150383	1.09	36.32	UGH150569	0.04	0.48	UGH150035	0.67	34.22	UGH150262	0.02	0.44
UGH150525	1.07	36.12	UGH150570	0.03	0.47	UGH150214	0.67	34.22	UGH150232	0.01	0.43
UGH150447	1.01	34.91	UGH150491	0.03	0.46	UGH150217	0.64	34.04	UGH150107	0.01	0.43
UGH150489	0.90	34.54	UGH150253	0.03	0.46	UGH150453	0.63	32.99	UGH150078	0.01	0.41
UGH150058	0.84	34.22	UGH150399	0.03	0.46	UGH150166	0.59	33.76	UGH150229	0.01	0.41
UGH150319	0.80	33.92	UGH150551	0.03	0.46	UGH150445	0.59	33.75	UGH150151	0.01	0.41
UGH150209	0.80	33.88	UGH150207	0.03	0.45	UGH150075	0.57	33.62	UGH150490	0.01	0.41
UGH150410	0.78	32.82	UGH150122	0.02	0.44	UGH150163	0.55	33.57	UGH150560	0.01	0.4
UGH150419	0.78	32.16	UGH150402	0.02	0.44	UGH150196	0.55	33.12	UGH150096	0.01	0.4
UGH150374	0.78	32.09	UGH150415	0.02	0.44	UGH150150	0.54	33.03	UGH150677	0.01	0.38

(Contd...)

Table 3: (Continued)

Clones	Base Index						Multiplicative Index				
	DMC			HI			DMC		HI		
	Blups	Mean	Clones	Blups	Mean	Clones	Blups	Mean	Clones	Blups	Mean
	Top 15										
	Bottom 15										
UGH150460	-0.86	28.24	UGH150236	-0.02	0.29	UGH150393	-0.54	26.63	UGH150026	-0.01	0.26
UGH150122	-0.88	28.17	UGH150140	-0.02	0.29	UGH150171	-0.59	26.54	UGH150034	-0.01	0.26
UGH150461	-0.94	27.93	UGH150059	-0.02	0.28	UGH150307	-0.65	26.26	UGH150591	-0.01	0.26
UGH150051	-0.96	27.21	UGH150245	-0.02	0.28	UGH150134	-0.68	26.13	UGH150024	-0.01	0.25
UGH150023	-0.99	26.58	UGH150489	-0.02	0.28	UGH150079	-0.69	25.59	UGH150489	-0.01	0.23
UGH150078	-1.03	24.22	UGH150117	-0.03	0.27	UGH150026	-0.70	25.32	UGH150022	-0.01	0.23
UGH150393	-1.04	23.91	UGH150658	-0.03	0.27	UGH150677	-0.71	24.86	UGH150355	-0.01	0.23
UGH150145	-1.14	23.56	UGH150338	-0.03	0.27	UGH150335	-0.74	24.72	UGH150507	-0.01	0.23
UGH150293	-1.17	22.12	UGH150406	-0.03	0.26	UGH150164	-0.80	24.17	UGH150150	-0.01	0.22
UGH150121	-1.22	21.88	UGH150209	-0.04	0.26	UGH150043	-0.82	24.13	UGH150653	-0.01	0.21
UGH150451	-1.33	21.32	UGH150390	-0.04	0.25	UGH150317	-0.87	24.11	UGH150158	-0.01	0.2
UGH150382	-1.42	21.04	UGH150145	-0.04	0.25	UGH150078	-1.03	24.07	UGH150589	-0.02	0.2
UGH150100	-1.45	20.87	UGH150023	-0.04	0.21	UGH150051	-1.15	23.84	UGH150335	-0.02	0.2
UGH150112	-1.62	20.36	UGH150186	-0.05	0.19	UGH150551	-1.16	23.71	UGH150282	-0.02	0.19
UGH150236	-1.90	19.98	UGH150155	-0.05	0.18	UGH150158	-1.55	21.76	UGH150155	-0.02	0.18

Table 4: Selection differentials for yield and associated traits for two selection indices

Selection index	Selected traits				
	CMD severity	Root number per plot	Root weight per plot	Harvest index	Dry matter content
Base index					
Mean of unselected clones	1.55	39	8.47	0.43	34.59
Mean of selected clones	1	59	15.27	0.47	35.78
selection differential	-0.55	20	4.80	0.04	1.19
Multiplicative index					
Mean of unselected clones	1.55	39	8.47	0.43	34.59
Mean of selected clones	1	41	8.65	0.47	33.66
Selection differential	-0.55	2	0.17	0.04	-0.93

value for traits regarding yield and its components, which are targeted by breeders [16]. This study is one of the few cassava studies that present empirical data to compare selection indices. It's the first study that was done in the highlands of Uganda.

The frequency distribution of CMD, fresh root number, fresh root weight, HI and DMC at all locations showed that the genotype means for base selection index are higher than the means from multiplicative selection index. Similar results [17] were reported that base index proved to be more efficient compared to Smith-Hazel index and desired gain index in improving the yield of sweet corn genotypes.

Additionally, assessment of BLUP values revealed the significant difference between the two selection indices for DMC and HI index. Base index had higher BLUP values than multiplicative index for both traits. This confirmed that base index is better than multiplicative index in cassava selection. This is supported by previous reports that selection index is effective only when, in its development each trait is weighted accordingly to its relative importance in the final product [14].

In this study, the selection differentials of studied traits were assessed to measure the effectiveness of the indices in identifying superior genotypes for the traits of interest. The selection differentials showed that base index had superior

selection differentials for most of the traits evaluated. Conversely, multiplicative index had poor selection differentials for all traits compared to base index. Therefore, Base index was effective in selecting superior cassava genotypes for all traits studied. This is substantiated by earlier findings [18]. Thus, base index would be effective for use in cassava breeding programmes.

CONCLUSION AND RECOMMENDATION

Base selection index proved to be more efficient compared to multiplicative selection index since it had the highest mean for all evaluated traits, high breeding values and high selection differentials for all traits studied. With regards to this, base index would be more useful in cassava breeding programs. Further studies were recommended for multiplicative index and use the concept suggested that using the lower value of a specific trait in its construction instead of using the lower acceptable limit value for a certain trait [18]. In this present study, the lowest acceptable value was utilised

ACKNOWLEDGEMENT

We acknowledge Next Generation Cassava Breeding Project (NextGen) for the financial assistance in carrying out the study. We gratefully thank staffs of Root Crops programme, National

Crops Resource Research Institute (NaCRRI) Uganda, who have contributed a lot to this study.

REFERENCES

1. Ssemakula, G.N., W.S. Sserubombwe, A. Bua, J. Jagwe, R.S.B. Ferris, and J.B.A. Whyte. (2004). Constraints and potential for cassava commercialization in Uganda. In proceedings of regional workshop on improving the cassava subsector, Nairobi, Kenya. April 2002, 57-60.
2. Uganda Bureau of Statistics (UBOS) (2008). Agricultural production in Uganda, <http://www.ubos.org/> (Visited March 2017).
3. Food and Agriculture Organization (FAO), (2012). Food and Agriculture Organization, statistical database for agriculture. Crops and products domain. <http://faostat.fao.org/> (Accessed January, 2017).
4. Food and Agriculture Organisation (FAO). 2009. FAO food balance sheet. FAO, Rome. <http://www.faostat.fao.org/> (Visited February 2017).
5. Ministry of Agriculture, Animal Industry and Fisheries (MAAIF). The Republic of Uganda (2007). The national cassava policy p.1-18.
6. Smith, H.F., (1936). A discriminant function of a plant selection. *Annals of Eugenics*, 7: 240-250.
7. Modarresi, M., M.T. Assad and M. Kheradnam. 2004. Determining selection indices in corn hybrids (*Zea mays L.*) to increase grain yield. *J. Sci. & Tech. of Agric. and Natural Resources*, 7(4): 71-82.
8. Asghar & Mehdi, (2010). Selection indices for yield and quality traits in sweet corn. *Pakistan journal of Botany* V4 (2) p. 775-789.
9. Terres IR; Lenz E; Castro CM; Pereira AS. 2015. Estimativas de ganhos genéticos por diferentes índices de seleção em três populações híbridas de batata. *Horticultura Brasileira* 33: 305-310.
10. Mulamba & Mock (1978). Improvement of yield potential of the eto blanco maize (*Zea- Mays L.*) population breeding for plant traits. *Journal of Genetics and cytology*, V7, p 40-51.
11. Evandro J, Nerin, D.R, Sandra, M.M, Micheli T. D. F. P, Daniele P. R., and Lucas da Silva D. (2012). Comparison among direct, indirect and index selections on agronomic traits and nutritional quality traits in common bean. *Journal of Science and Food Agriculture* 2013; 93: 1097-1104
12. Ekanayake, I.J, (1994). Terminology for growth analysis of cassava. *Tropical Root and Tuber crops bulletin* 8(1);2: 4-5.
13. Williams, J.S. (1962). The evaluation of a selection index. *Biometrics*, 18:375-393
14. Bernardo, R., (2010). Breeding for quantitative traits in plants. Second edition, USA pp 323-336.
15. Eliston, R.C., (1963). A weight free index for the purpose of ranking or selection with respect to several traits at a time. *Biometrics*, 19: 85-97.
16. Hallauer, R.; Marcelo, c.; Miranda, F, J.B., (2010). Quantitative genetics in maize breeding book.
17. Muhammadi J., Syed S.M., (2010). Selection indices for yield and quality traits in sweet corn. *Journal of Botany*, 42(2): 775-789.
18. Mark S. Strefeler, Todd C. Wehner, (2007). Comparison of six methods of multiple traits selection for fruit yield and quality traits in three fresh market cucumber populations. *Horticulture Science* 5: 792-798.