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Development of End-User Preferred Sweetpotato Varieties

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Abstract

Sweetpotato (*Ipomoea batatas* (L.) Lam) is the fourth most important root and tuber crop in Ghana, in terms of production. Attainment of increased sweetpotato utilization has become an important breeding objective in Ghana recently. The major emphasis in breeding is on the development of farmer/consumer preferred varieties. This study aimed at developing farmer/consumer preferred sweetpotato cultivars for increased utilization in Ghana and beyond. One hundred and fifteen sweetpotato accessions were collected and evaluated at two ecozones in the major and minor cropping seasons in 2011 to identify low sugar parents for hybridization. Two released varieties (Histarch and Ogyefo) and eight breeding lines (AAT-03-025, CIP 442264, CRIWAC 25-10, CRIWAC 30-10, DOS 03-006, CRIWAC 11-10, CIP 440095 and CRIWAC 19-10) were selected and used as parents. Genetic variability was significant for all the traits studied. Sufficient useful genetic variation was present in the materials studied and was exploited to provide for substantial amount of improvement through selection of superior genotypes. Negative heterosis was observed for sugar content and this is very important for breeding because Ghanaians prefer non-sweet varieties. Fifteen percent of the F_1 hybrids of Histarch and Ogyefo were non-sweet. These will meet the staple food needs of Ghanaians. Eight hybrids were identified as potential non-sweet varieties for further testing multilocation on-farm for release. These were Ogyefo × Histarch-11, Histarch × Ogyefo-13, Histarch × Ogyefo-52, Histarch × Ogyefo-37, Histarch × Ogyefo-65, Histarch × Ogyefo-88, Histarch × Ogyefo-39 and Histarch × Ogyefo-16.

Keywords: diallel design, end-user, heterosis, non-sweet, sweetpotato

1. Introduction

Sweetpotato (*Ipomoea batatas* (L.) Lam) is one of the most important root crops in the world with more than 133 million tonnes produced worldwide annually (Warammboi et al., 2011). It is the fourth most important root and tuber crop in Ghana in terms of production, after cassava, yam and cocoyam. Its annual production is estimated at 135, 000 tonnes, representing just under 0.6% of all root and tuber crops produced in Ghana (FAOSTAT, 2013). The attainment of improved crop yield is an important objective in most breeding programmes (Rausul et al., 2002), as is the development of end-user preferred improved varieties. Consumers in Ghana prefer non-sweet sweetpotatoes with high dry matter content (Baafi, 2014; Baafi et al., 2015; Sam & Dapaah, 2009). However, locally available clones have very sweet taste, which limits their consumption as a staple food (Missah & Kissiedu, 1994). Increased sweetpotato utilization has become an important objective in Ghana recently. The major emphasis in breeding is on the development of farmer/consumer preferred varieties. Dry matter content, starch content, sugar content and storage root yield are quantitatively inherited in sweetpotato (Jones, 1986). Heterosis for these traits is present in sweetpotato hybrids between certain varieties (Baafi, 2014; Grüneberg et al., 2009), and the identification and use of heterosis is important for breeding sweetpotato. The objective of this study was to develop farmer and consumer preferred sweetpotato varieties using a diallel mating scheme and to estimate the level of heterosis and heterobeltiosis among F_1 hybrids obtained from a diallel between low sugar sweetpotato genotypes.

2. Materials and Methods

2.1 Germplasm Collection and Evaluation

Germplasm were collected from farmers' field in the major sweetpotato growing areas in Ghana in 2010. These were the Northern, Upper East, Upper West, Volta, Eastern, Central and the Brong Ahafo Regions. Collections from the CSIR-Crops Research Institute, Kumasi and the CSIR-Plant Genetic Resources Research Institute (PGRRI), Bunsu, were also included. In addition, accessions were collected from the Crop Science Department, University of Ghana and the International Potato Centre (CIP) gene bank in Accra and Kumasi, respectively. A total of 115 sweetpotato accessions (Table 1) were collected. These represent four groups, namely local accessions (32), local improved accessions (13), exotic and local accessions in National Agricultural Research Systems (NARS) or Programmes (43), and exotic accessions from CIP, Kumasi germplasm (27). Evaluation of the sweetpotato germplasm was carried out under rain-fed conditions in two replications at Fumesua (Forest ecozone) and Pokuase (Coastal Savanna ecozone) in the major and minor cropping seasons from May to December, 2011 to identify low sugar parents for hybridization. Planting distance was 1 m between ridges and 0.3 m within row of ridge length 3.6 m and a total of 12 plants per ridge.

2.1.1 Data Collection

Harvesting was done at three and half months after planting. The 10 central plants were harvested and one large, one medium, and one small storage roots were randomly selected for determination of sugar content. Storage roots used for observations were those approximately over 3 cm in diameter and without cracks, insect damage or rotten parts (Ekanayake et al., 1990). The Workflow for Sample Preparation and near-infrared reflectance spectroscopy (NIRS) analysis of sweetpotato developed by the Quality and Nutrition Laboratory of the International Potato Centre (CIP), Lima, Peru was used. Fifty grams (50 g) fresh sample was used.

2.1.2 Data Analysis

Only data for 102 out of the 115 accessions were analyzed due to missing information. The analysis also excluded minor cropping season data for Pokuase because the experiment failed due to erratic rainfall. The data were subjected to Analysis of Variance (ANOVA) using Genstat statistical package (Genstat, 2007). The relative efficiency (RE) of an alpha lattice design over randomized complete block design (RCBD) was not significant. The RE was determined as shown below;

$$RE = \frac{MSe_{RCBD}}{MSe_{\alpha-lattice}} \quad (1)$$

Where, *MSe* = Error means square; *RE* is significant if the ratio is > 1 and vice versa. Hence, *RCBD* in two replications was used to analyze the data.

2.2 Hybridization and Genetic Material Used

The hybridization block was established at the research field of the CSIR-Crops Research Institute (CSIR-CRI), Fumesua in 2012. The list of parents used is shown in Table 2. The parents were selected from the germplasm collected and evaluated based on their low sugar content (Bottom 10% of accessions). They were ten genotypes, and were made up of two released varieties (Histarch and Ogyefo) and eight breeding lines (AAT-03-025, CIP 442264, CRIWAC 25-10, CRIWAC 30-10, DOS 03-006, CRIWAC 11-10, CIP 440095 and CRIWAC 19-10). The hybridization block was established during the minor cropping season in 2012 at planting distance of 0.3 × 1 m. The full diallel mating design was used. Flowers ready for pollination the next morning, were tied the previous afternoon using a piece of drinking straw to prevent out-crossing by insects. At the time of pollination, the corolla was carefully opened, pollinated and carefully tied again afterwards to avoid insect contamination after pollination. Although self-fertilization occurs only rarely in sweetpotato (Poole, 1955), emasculation was done on the female parents to eliminate such a possibility.

Table 1. List of the 115 accessions collected and their source

Local accessions	Local improved accessions	NARS accessions		CIP accessions
CRIWAC 01-10	SANTOMPONA	TAG 03-019	B-REGARD	CIP 442903
CRIWAC 02-10	FARAA	NS 001	FIASO RED	CIP 442291
CRIWAC 03-10	TEKSANTOM	OK 03-015	TAG 03-030	CIP 440069
CRIWAC 04-10	OGYEFO	DOS 03-021	GWERI	CIP 440390
CRIWAC 05-10	OKUMKOM	CARROT C	BD 96-029	CIP 442462
CRIWAC 06-10	OTOO	HUMBERCHERO	FREMA	CIP 442776
CRIWAC 07-10	HISTARCH	B/FASO 002	DOS O3-006	CIP 440062
CRIWAC 08-10	SAUTI	FA 10-026	NS 003	CIP 442589
CRIWAC 09-10	APOMUDEN	RESISTO	AAT 03-004	CIP 442145
CRIWAC 10-10	LIGRI	NASPOT 1	OK 03-021	CIP 442147
CRIWAC 11-10	BOHYE	AAT 03-017	BOT 03-030	CIP 440095
CRIWAC 12-10	PATRON	OK 03-014	OK 03-017	CIP 441771
CRIWAC 13-10	DADANUIE	JONATHAN	KAYIA WHITE	CIP 442901
CRIWAC 14-10		H-ASIATOR	UKEREWE	CIP 443016
CRIWAC 15-10		TANZANIA	OK 03-018	CIP 440071
CRIWAC 16-10		NINGSHU 1		CIP 442896
CRIWAC 17-10		BOT 03-021		CIP 442162
CRIWAC 18-10		KEMB 37		CIP 442775
CRIWAC 19-10		BOT 03-028		CIP 443027
CRIWAC 20-10		BOT 03-020		CIP 443129
CRIWAC 21-10		J-ORANGE		CIP 442264
CRIWAC 22-10		BOT 03-027		CIP 442654
CRIWAC 23-10		ADA 001		CIP 443035
CRIWAC 24-10		DOS O3-017		CIP 442913
CRIWAC 25-10		NAV 001		CIP 442237
CRIWAC 26-10		AAT 03-025		CIP 443019
CRIWAC 27-10		B/FASO 001		CIP 442850
CRIWAC 28-10		ZAMBEZI		
CRIWAC 29-10				
CRIWAC 30-10				
CRIWAC 31-10				
CRIWAC 32-10				

Table 2. List of sweetpotato parents used for the establishment of the crossing block and their attributes

Parents	Sugar content (%)
CRIWAC 25-10	12.54
CRIWAC 30-10	12.45
DOS 03-006	12.26
AAT 03-025	12.26
CRIWAC 11-10	12.26
CIP 440095	12.06
Ogyefo	11.67
CIP 442264	11.06
Histarch	10.43
CRIWAC 19-10	9.83

2.3 Evaluation of F_1 Hybrids and Parents

2.3.1 Field Layout

The F_1 progenies produced and their parents were evaluated at three locations across three ecozones of Ghana in the minor cropping season in 2013. The locations were the CSIR-CRI research station at Fumesua (Forest ecozone), and the National Agricultural Research Stations at Wenchi (Transition ecozone) and Pokuase (Coastal Savanna ecozone). Since sweetpotato is highly heterozygous, each cross between two different parent plants is genetically distinct and the variation in the F_1 families produced is equivalent to an F_2 generation in a crop like maize. Therefore, there was a need to evaluate variation between different F_1 families as well as the variation within crosses. For this reason, twelve full-sib families obtained from crosses among four parents (Histarch, Ogyefo, CIP 442264 and AAT 03-025) out of the ten parents selected for hybridization were evaluated. The families consisted of one hundred and eleven F_1 progenies but, due to poor vigour of some progenies, 92 were evaluated alongside their parents at the three locations in two replications. All entries were planted in a single row on ridges at five plants per progeny at planting distance of 0.3 m within row and 1m between rows. Four node vines from the middle portion to the tip were used for planting. Genotypes within family were randomised into adjacent plots.

2.3.2 Data Collection

Harvesting was done at three and half months after planting. The three middle plants for each progeny row were harvested, and one large, one medium, and one small, storage root were randomly selected for physico-chemical analysis after yield data were taken. Storage roots taken for the yield data were those approximately 3 cm or more in diameter and without cracks, insect damage or rotten parts (Ekanayake et al., 1990). The physico-chemical traits determined were dry matter, starch, and sugar contents. This was done at the Quality and Nutrition Laboratory of the International Potato Centre (CIP) at Fumesua, Ghana. The physico-chemical traits were determined using the Workflow for Sample Preparation and near-infrared reflectance spectroscopy analysis of sweetpotato developed by the Quality and Nutrition Laboratory of CIP Lima, Peru. Fifty grams fresh sample was used. The fresh sample was freeze-dried for 72 hours. The dry matter content was calculated as the ratio of the weight of the dry sample to that of the wet sample expressed as a percentage.

2.3.3 Data Analysis

Data were analysed using the approach of Buerstmayr et al. (2007). Analysis of Variance (ANOVA) was performed on data for all parents and their F_1s to ascertain the performance among and between the F_1s and the parents in 8 × 12 alpha lattice design. After this, data for the different F_1 families were analysed separately with their parents to estimate heterosis. All the analyses of the different F_1 families were carried out in a randomized complete block design (RCBD) except for the crosses between Histarch and Ogyefo which was done using an 8 × 11 alpha lattice design. This was because the relative efficiency (RE) of alpha lattice design over randomized complete block design (RCBD) was significant for the data involving crosses between Histarch and Ogyefo. The analyses were done using Genstat version 9.2.0.152 (Genstat, 2007). The percent increase or decrease of F_1 hybrids over mid-parent as well as better parent performance was calculated to estimate heterosis for the traits studied (Fonseca & Patterson, 1968), as shown below,

$$Ht(\%) = \frac{F_1 - MP}{MP} \times 100 \quad (2)$$

$$Hbt(\%) = \frac{F_1 - BP}{BP} \times 100 \quad (3)$$

Where, *Ht* = Heterosis; *Hbt* = Heterobeltiosis; *MP* = Mid-parent value; *BP* = Better parent value; F_1 = F_1 hybrid value.

The 't' test was used to determine whether F_1 hybrid means were significantly different from mid-parent and better parent means (Wynne et al., 1970), as follows;

$$t_{ij} = \frac{F_{1ij} - MP_{ij}}{\sqrt{3/8EMS}} \quad (4)$$

$$t_{ij} = \frac{F_{1ij} - BP_{ij}}{\sqrt{1/2EMS}} \quad (5)$$

Where, F_{1ij} = Mean of the ijth F_1 cross; MP_{ij} = Mid-parent value for the ijth cross; BP_{ij} = Better parent value for ijth cross; *EMS* = Error mean square.

3. Results

Numerous ANOVA tables were obtained because numerous ANOVA were carried out for the different separate analysis involving genotypes within family (to estimate mid-parent and better parent heterosis). Only ANOVA table from the combined analysis (i.e. involving all the hybrids irrespective of family and the parents) is reported (Table 5).

3.1 Performance of the 102 Sweetpotato Accessions Based on Sugar Content

The phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) (Table 3). The broad-sense heritability was 0.70. The expected gain from selection and genetic advance (as percent of grand mean) were 5.10 and 30.95%. There were significant differences in the sugar content of the sweetpotato accessions (Table 4). Sugar content ranged from 9.83% to 30.34%. These values were given by CRIWAC 19-10 and CIP 442850.

3.2 Performance of the Parents and F_1 Hybrids

There were challenges with most of the crosses due to cross incompatibilities which was either due to poor or lack of flowering and/or genetic incompatibilities. This occurs frequently with sweetpotato hybridization. The mean squares from the combined ANOVA showed highly significant ($p < 0.01$) differences among the genotypes for all the traits except sugar content which was significant at $p < 0.05$ (Table 5). Range of values for the traits were 36–48% for dry matter content, 9.01–17.53% for sugar content, and 68.27–76.25% for starch content (Table 6). Some genotypes did not produce storage roots but the highest root yield was 36.31 t/ha. The mean values for the traits were 43% (dry matter content), 13.45% (sugar content), 72.64% (starch content), and 16.04 t/ha (storage root yield). Their coefficients of variation were 6.3% (dry matter content), 20.7% (sugar content), 2.9% (starch content), and 46.9% (root yield).

Table 3. Genotypic and phenotypic coefficient of variation, heritability and expected genetic advance for sugar content of the 102 sweetpotato accessions

Genetic parameters	Value
Genotypic coefficient of variation (GVC)	18.01
Phenotypic coefficient of variation (PVC)	21.59
Heritability (H^2_b)	0.70
Expected Selection Gain (R)	5.10
Expected Selection Gain (R % of mean)	30.95

Table 4. Storage root sugar content for the 102 accessions evaluated across three locations

Accession	Total sugar (%)	Accession	Total sugar (%)	Accession	Total sugar (%)
CIP 442850	30.34	NAV 001	17.23	LIGRI	14.87
APOMUDEN	28.97	CRIWAC 27-10	17.22	CRIWAC 14-10	14.63
B/FASO 002	24.04	CRIWAC 16-10	17.16	CIP 443129	14.62
CIP 440062	23.30	BD 96-029	17.10	CIP 442162	14.58
B-REGARD	22.90	KAYIA WHITE	17.06	OK 03-017	14.49
CRIWAC 12-10	22.84	CIP 442147	17.04	CRIWAC 23-10	14.24
B/FASO 001	22.69	CIP 440069	16.94	CRIWAC 29-10	14.05
TAG 03-030	21.92	ZAMBEZI	16.88	CRIWAC 20-10	13.86
CIP 440071	21.84	CIP 442237	16.87	CRIWAC 22-10	13.85
UKEREWE	21.10	J-ORANGE	16.80	CIP 442589	13.84
AAT 03-017	20.86	TANZANIA	16.43	CRIWAC 10-10	13.77
AAT 03-004	20.85	CIP 442145	16.36	CIP 440390	13.74
CRIWAC 15-10	20.83	CIP 441771	16.15	CRIWAC 26-10	13.63
FA 10-026	20.64	CIP 442896	16.10	NS 003	13.52
BOT 03-028	20.03	JONATHAN	16.08	CRIWAC 24-10	13.49
CIP 442775	19.46	CRIWAC 17-10	15.99	CRIWAC 06-10	13.18
SANTOMPONA	19.10	OK 03-018	15.92	CIP 442291	13.14
OK 03-014	19.07	CRIWAC 07-10	15.91	CIP 442903	12.77
CRIWAC 21-10	18.76	NASPOT 1	15.76	BOT 03-027	12.75
OK 03-015	18.70	BOHYE	15.75	CIP 443027	12.73
BOT 03-020	18.60	DOS 03-021	15.74	FIASO RED	12.69
RESISTO	18.53	CIP 442462	15.73	SAUTI	12.61
CRIWAC 18-10	18.39	CRIWAC 02-10	15.71	NS 001	12.60
ADA 001	18.15	CRIWAC 31-10	15.71	FARAA	12.56
CRIWAC 05-10	18.06	0KYEREKO	15.65	CRIWAC 25-10	12.54
CRIWAC 28-10	18.04	CIP 442776	15.58	CRIWAC 30-10	12.45
CIP 442654	17.88	NINGSHU 1	15.50	DOS O3-006	12.35
CRIWAC 08-10	17.83	CRIWAC 04-10	15.45	AAT 03-025	12.26
CRIWAC 03-10	17.77	CRIWAC 01-10	15.42	CRIWAC 11-10	12.26
OKUMKOM	17.72	OTOO	15.38	CIP 440095	12.06
CIP 443016	17.62	TAG 03-019	15.34	OGYEFO	11.67
OK 03-021	17.59	CIP 443035	14.98	CIP 442264	11.06
DADANUIE	17.43	CIP 442913	14.90	HISTARCH	10.43
CIP 442901	17.30	H-ASIATOR	14.90	CRIWAC 19-10	9.83
SED (5%)	2.63	SED (5%)	2.63	SED (5%)	2.63

Table 5. Mean squares from combined ANOVA for the parents and their F_1 hybrids

Source of variation	Df	Total sugar	Dry matter	Starch	Total root yield
Rep stratum	2	15.41	0.0002	198.04	2040.33
Rep.Blk. Stratum					
Genotype	7	8.54^{ns}	0.0023^{ns}	11.03^{ns}	301.61**
Residual	14	8.06	0.0010	6.40	65.13
Rep.Blk.Plot Stratum					
Genotype	74	10.13*	0.0018**	7.55**	142.90**
Residual	190	7.77	0.0007	4.42	55.17

Table 6. Performance of sweetpotato parents and F_1 hybrids

Genotype code	Genotype name	Dry matter (%)	Total sugars (%)	Starch (%)	Total root yield (t/ha)
61 × 87-11	Ogyefo × Histarch-11	45	9.01	75.14	16.03
87 × 61-26	Histarch × Ogyefo-26	38	9.13	70.22	-
87 × 61-13	Histarch × Ogyefo-13	45	9.50	76.25	16.53
87 × 61-21	Histarch × Ogyefo-21	44	9.94	72.92	12.08
87 × 61-52	Histarch × Ogyefo-52	42	10.33	70.45	-
87 × 61-37	Histarch × Ogyefo-37	43	10.79	72.56	28.26
CIP 442264 (64)	CIP 442264	42	10.80	68.27	5.07
87 × 61-65	Histarch × Ogyefo-65	45	11.18	74.13	14.94
87 × 61-87	Histarch × Ogyefo-87	42	11.72	72.05	7.57
87 × 61-88	Histarch × Ogyefo-88	44	11.76	74.27	14.54
87 × 61-39	Histarch × Ogyefo-39	43	11.77	72.89	31.61
87 × 61-16	Histarch × Ogyefo-16	46	11.80	75.11	15.97
61 × 87-13	Ogyefo × Histarch-13	43	11.82	72.79	20.16
87 × 61-15	Histarch × Ogyefo-15	43	11.98	70.99	2.80
87 × 61-86	Histarch × Ogyefo-86	42	12.07	71.35	5.33
61 × 87-2	Ogyefo × Histarch-2	40	12.07	72.54	12.14
87 × 61-92	Histarch × Ogyefo-92	45	12.09	73.32	18.75
87 × 61-68	Histarch × Ogyefo-68	48	12.13	74.39	14.00
87 × 61-32	Histarch × Ogyefo-32	36	12.19	71.91	22.54
87 × 61-93	Histarch × Ogyefo-93	45	12.25	72.49	11.03
64 × 87-3	CIP 442264 × Histarch-3	46	12.25	72.94	-
87 × 61-76	Histarch × Ogyefo-76	43	12.38	73.74	11.93
87 × 61-94	Histarch × Ogyefo-94	42	12.40	71.08	9.65
87 × 61-75	Histarch × Ogyefo-75	42	12.46	72.61	18.67
87 × 61-69	Histarch × Ogyefo-69	44	12.47	74.69	17.11
AAT-03-025 (72)	AAT-03-025	43	12.47	72.32	19.87
87 × 61-63	Histarch × Ogyefo-63	47	12.51	73.84	14.83

Table 6. Continued

Genotype code	Genotype name	Dry matter (%)	Total sugars (%)	Starch (%)	Total root yield (t/ha)
87 × 61-56	Histarch × Ogyefo-56	44	12.53	74.43	15.72
64 × 87-2	CIP 442264 × Histarch-2	48	12.59	72.96	12.04
87 × 61-19	Histarch × Ogyefo-19	45	12.62	73.99	7.76
61 × 87-18	Ogyefo × Histarch-18	43	12.64	73.64	11.21
87 × 61-24	Histarch × Ogyefo-24	42	12.66	73.13	19.17
87 × 61-36	Histarch × Ogyefo-36	41	12.69	73.48	13.13
87 × 61-40	Histarch × Ogyefo-40	41	12.69	72.08	25.49
61 × 87-10	Ogyefo × Histarch-10	42	12.74	73.72	22.97
61 × 87-20	Ogyefo × Histarch-20	44	12.77	73.65	14.33
61 × 87-19	Ogyefo × Histarch-19	44	12.77	74.41	15.99
87 × 61-78	Histarch × Ogyefo-78	41	12.87	72.85	18.67
87 × 61-80	Histarch × Ogyefo-80	45	12.91	74.88	26.33
87 × 61-3	Histarch × Ogyefo-3	43	12.94	73.91	26.01
87 × 61-31	Histarch × Ogyefo-31	41	12.96	70.97	14.02
87 × 61-50	Histarch × Ogyefo-50	41	13.01	74.10	16.64
61 × 87-14	Ogyefo × Histarch-14	44	13.03	74.36	14.79
61 × 87-9	Ogyefo × Histarch-9	43	13.04	72.90	12.86
87 × 61-8	Histarch × Ogyefo-8	45	13.16	74.18	8.92
87 × 61-64	Histarch × Ogyefo-64	44	13.20	73.93	23.53
87 × 61-28	Histarch × Ogyefo-28	42	13.28	73.91	12.53
87 × 61-71	Histarch × Ogyefo-71	43	13.44	72.93	13.03
61 × 87-7	Ogyefo × Histarch-7	42	13.49	73.32	13.53
87 × 61-41	Histarch × Ogyefo-41	44	13.50	74.19	18.72
61 × 87-3	Ogyefo × Histarch-3	41	13.58	73.50	26.33
Ogyefo (61)	Ogyefo	41	13.62	72.92	13.61
87 × 61-38	Histarch × Ogyefo-38	43	13.62	72.29	27.17
87 × 61-58	Histarch × Ogyefo-58	42	13.70	72.91	36.31
87 × 61-49	Histarch × Ogyefo-49	42	13.73	70.04	6.96
87 × 61-1	Histarch × Ogyefo-1	44	13.85	74.79	11.46
87 × 61-29	Histarch × Ogyefo-29	43	13.95	74.74	22.58
87 × 61-45	Histarch × Ogyefo-45	45	14.03	74.63	11.41
87 × 61-67	Histarch × Ogyefo-67	40	14.09	72.58	13.68
87 × 61-66	Histarch × Ogyefo-66	42	14.09	72.12	16.80
87 × 61-6	Histarch × Ogyefo-6	43	14.10	72.49	24.25
87 × 64-2	Histarch × CIP 442264-2	48	14.14	72.59	15.93

Table 6. Continued

Genotype code	Genotype name	Dry matter (%)	Total sugars (%)	Starch (%)	Total root yield (t/ha)
87 × 61-4	Histarch × Ogyefo-4	41	14.16	72.22	22.68
87 × 61-74	Histarch × Ogyefo-74	44	14.18	72.78	13.42
87 × 61-82	Histarch × Ogyefo-82	41	14.23	73.11	8.81
87 × 61-62	Histarch × Ogyefo-62	45	14.26	74.12	15.61
64 × 87-1	CIP 442264 × Histarch-1	48	14.29	72.06	13.31
87 × 61-73	Histarch × Ogyefo-73	39	14.34	72.20	20.44
87 × 61-27	Histarch × Ogyefo-27	40	14.38	72.05	30.88
87 × 61-53	Histarch × Ogyefo-53	40	14.39	72.94	10.83
87 × 61-44	Histarch × Ogyefo-44	41	14.42	71.75	13.69
61 × 87-17	Ogyefo × Histarch-17	42	14.44	71.14	10.14
87 × 61-70	Histarch × Ogyefo-70	42	14.46	72.26	9.54
87 × 61-30	Histarch × Ogyefo-30	41	14.51	72.51	22.36
61 × 87-8	Ogyefo × Histarch-8	42	14.56	72.31	13.64
87 × 61-72	Histarch × Ogyefo-72	40	14.70	70.38	11.13
61 × 87-16	Ogyefo × Histarch-16	41	14.86	71.84	11.68
61 × 87-1	Ogyefo × Histarch-1	42	14.90	72.56	28.96
87 × 61-51	Histarch × Ogyefo-51	43	14.91	73.83	20.47
87 × 61-54	Histarch × Ogyefo-54	40	14.93	72.71	16.95
87 × 61-83	Histarch × Ogyefo-83	41	14.98	69.97	20.88
87 × 61-89	Histarch × Ogyefo-89	43	15.02	72.04	15.09
87 × 61-23	Histarch × Ogyefo-23	43	15.19	72.50	15.50
87 × 61-20	Histarch × Ogyefo-20	42	15.32	72.38	15.22
61 × 87-15	Ogyefo × Histarch-15	42	15.33	71.75	8.21
87 × 64-1	Histarch × CIP 442264-1	46	15.44	69.74	13.57
61 × 87-6	Ogyefo × Histarch-6	39	15.63	68.34	9.64
87 × 61-77	Histarch × Ogyefo-77	38	15.64	72.20	21.97
87× 61-42	Histarch × Ogyefo-42	41	15.95	70.54	11.53
87 × 72-2	Histarch × AAT-03-025-2	40	16.16	70.36	6.89
61 × 87-4	Ogyefo × Histarch-4	40	16.26	72.23	22.47
87 × 61-47	Histarch × Ogyefo-47	40	16.29	71.37	19.17
Histarch (87)	Histarch	46	16.33	72.82	20.71
87 × 72-1	Histarch × AAT-03-025-1	43	16.90	71.25	17.36
87 × 61-46	Histarch × Ogyefo-46	40	17.18	70.30	3.56
87 × 61-57	Histarch × Ogyefo-57	39	17.53	69.78	20.19
SED (5%)		2	2.28	1.75	6.13
Range		36-48	9.01-17.53	68.27-76.25	nil-36.31
CV (%)		6.3	20.7	2.9	46.90

Note. *SED =Standard error of difference.

3.3 Estimation of Heterosis and Family Performance for the Sweetpotato Genotypes

Significant variation ($P < 0.05$) was seen between the parents, the F_1 hybrids and between the parents and the F_1 hybrids for all the traits in the crosses between Histarch and Ogyefo (Table 7). Fifty-five per cent of the F_1 hybrids had sugar content lower than Ogyefo (13.58%). Crosses Histarch × CIP 442264 and Histarch × AAT-03-025 had significant differences ($P < 0.05$) for only dry matter content and root yield (Table 9 and 11). There were no significant estimates for heterosis between crosses Histarch × CIP 442264 (Table 10), but some F_1 progeny had significant heterosis for dry matter content, sugar content and storage root yield in crosses between Histarch and Ogyefo (Table 8). Heterosis was significant for dry matter content and storage root yield for crosses between Histarch and AAT-03-025 (Table 12). Both positive and negative heterosis was seen. For example, Histarch × Ogyefo-26 (Table 8) had significant negative mid-parent and better parent heterosis for dry matter content (-14% and -18%), and sugar content (-39.1% and -33.0%) while Histarch × Ogyefo-13 had positive heterosis for starch content (4.6% and 4.6%).

Table 7. Performance of Histarch (87) and Ogyefo (61), and their F_1 hybrids

Genotype code	Dry matter (%)	Total sugars (%)	Starch (%)	Total root yield (t/ha)
61 × 87-11	45	9.01	75.14	16.03
87 × 61-26	38	9.13	70.22	-
87 × 61-13	45	9.50	76.25	16.53
87 × 61-21	44	9.94	72.92	12.08
87 × 61-52	42	10.33	70.45	-
87 × 61-37	43	10.79	72.56	28.26
87 × 61-65	45	11.18	74.13	14.94
87 × 61-87	42	11.72	72.05	7.57
87 × 61-88	44	11.76	74.27	14.54
87 × 61-39	43	11.77	72.89	31.61
87 × 61-16	46	11.80	75.11	15.97
61 × 87-13	43	11.82	72.79	20.16
87 × 61-15	43	11.98	70.99	2.80
87 × 61-86	42	12.07	71.35	5.33
61 × 87-2	40	12.07	72.54	12.14
87 × 61-92	45	12.09	73.32	18.75
87 × 61-68	48	12.13	74.39	14.00
87 × 61-32	36	12.19	71.91	22.54
87 × 61-93	45	12.25	72.49	11.03
87 × 61-76	43	12.38	73.74	11.93
87 × 61-94	42	12.40	71.08	9.65
87 × 61-75	42	12.46	72.61	18.67
87 × 61-69	44	12.47	74.69	17.11
87 × 61-63	47	12.51	73.84	14.83
87 × 61-56	44	12.53	74.43	15.72
87 × 61-19	45	12.62	73.99	7.76

Table 7. Continued

Genotype code	Dry matter (%)	Total sugars (%)	Starch (%)	Total root yield (t/ha)
61 × 87-18	43	12.64	73.64	11.21
87 × 61-24	42	12.66	73.13	19.17
87 × 61-36	41	12.69	73.48	13.13
87 × 61-40	41	12.69	72.08	25.49
61 × 87-10	42	12.74	73.72	22.97
61× 87-20	44	12.77	73.65	14.33
61 × 87-19	44	12.77	74.41	15.99
87 × 61-78	41	12.87	72.85	18.67
87× 61-80	45	12.91	74.88	26.33
87 × 61-3	43	12.94	73.91	26.01
87 × 61-31	41	12.96	70.97	14.02
87 × 61-50	41	13.01	74.10	16.64
61 × 87-14	44	13.03	74.36	14.79
61 × 87-9	43	13.04	72.90	12.86
87 × 61-8	45	13.16	74.18	8.92
87× 61-64	44	13.20	73.93	23.53
87 × 61-28	42	13.28	73.91	12.53
87 × 61-71	43	13.44	72.93	13.03
61 × 87-7	42	13.49	73.32	13.53
87 × 61-41	44	13.50	74.19	18.72
61 × 87-3	41	13.58	73.50	26.33
Ogyefo (61)	41	13.62	72.92	13.61
87 × 61-38	43	13.62	72.29	27.17
87 × 61-58	42	13.70	72.91	36.31
87 × 61-49	42	13.73	70.04	6.96
87 × 61-1	44	13.85	74.79	11.46
87 × 61-29	43	13.95	74.74	22.58
87 × 61-45	45	14.03	74.63	11.41
87 × 61-67	40	14.09	72.58	13.68
87 × 61-66	42	14.09	72.12	16.80

Table 7. Continued

Genotype code	Dry matter (%)	Total sugars (%)	Starch (%)	Total root yield (t/ha)
87 × 61-6	43	14.10	72.49	24.25
87 × 61-4	41	14.16	72.22	22.68
87 × 61-74	44	14.18	72.78	13.42
87 × 61-82	41	14.23	73.11	8.81
87 × 61-62	45	14.26	74.12	15.61
87 × 61-73	39	14.34	72.20	20.44
87 × 61-27	40	14.38	72.05	30.88
87 × 61-53	40	14.39	72.94	10.83
87 × 61-44	41	14.42	71.75	13.69
61 × 87-17	42	14.44	71.14	10.14
87 × 61-70	42	14.46	72.26	9.54
87 × 61-30	41	14.51	72.51	22.36
61 × 87-8	42	14.56	72.31	13.64
87 × 61-72	40	14.70	70.38	11.13
61 × 87-16	41	14.86	71.84	11.68
61 × 87-1	42	14.90	72.56	28.96
87 × 61-51	43	14.91	73.83	20.47
87 × 61-54	40	14.93	72.71	16.95
87 × 61-83	41	14.98	69.97	20.88
87 × 61-89	43	15.02	72.04	15.09
87 × 61-23	43	15.19	72.50	15.50
87 × 61-20	42	15.32	72.38	15.22
61 × 87-15	42	15.33	71.75	8.21
61 × 87-6	39	15.63	68.34	9.64
87 × 61-77	38	15.64	72.20	21.97
87 × 61-42	41	15.95	70.54	11.53
61 × 87-4	40	16.26	72.23	22.47
87 × 61-47	40	16.29	71.37	19.17
Histarch (87)	46	16.33	72.82	20.71
87 × 61-46	40	17.18	70.30	3.56
87 × 61-57	39	17.53	69.78	20.19
SED (5%)	2	2.28	1.75	6.13
Grand Mean	43	13.45	72.64	16.04
Range	36-48	9.01-17.53	68.27-76.25	nil-36.31
CV (%)	6.3	20.7	2.9	46.90

Note. *SEM = Standard error of mean.

Table 8. Estimates of mid-parent heterosis (Hb) and heterobeltiosis (Hbt) for the F_1 hybrids of Histarch (87) and Ogyefo (61)

Genotype code	Dry matter		Total sugars		Starch		Root yield	
	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)
61 × 87-11	3^{ns}	-3^{ns}	-39.9*	-33.9*	3.1^{ns}	3.0^{ns}	-6.6^{ns}	-22.6^{ns}
87 × 61-26	-14*	-18*	-39.1*	-33.0*	-3.6^{ns}	-3.7^{ns}	-	-
87 × 61-13	3^{ns}	-2^{ns}	-36.6*	-30.3*	4.6*	4.6*	-4.0^{ns}	-20.2^{ns}
87 × 61-21	1^{ns}	-4^{ns}	-33.6*	-27.0*	0.1^{ns}	0.0^{ns}	-29.6^{ns}	-41.7^{ns}
87 × 61-37	-1^{ns}	-6^{ns}	-28.0*	-20.8*	-0.4^{ns}	-0.5^{ns}	64.7^{ns}	36.5^{ns}
87 × 61-65	2^{ns}	-3^{ns}	-25.4^{ns}	-17.9*	1.7^{ns}	1.7^{ns}	-12.9^{ns}	-27.9^{ns}
87 × 61-87	-4^{ns}	-9^{ns}	-21.8^{ns}	-14.0^{ns}	-1.1^{ns}	-1.2^{ns}	-55.9^{ns}	-63.5*
87 × 61-88	1^{ns}	-4^{ns}	-21.5^{ns}	-13.7^{ns}	1.9^{ns}	1.9^{ns}	-15.3^{ns}	-29.8^{ns}
↓								
87 × 61-20	-3^{ns}	-8^{ns}	2.3^{ns}	12.5^{ns}	-0.7^{ns}	-0.7^{ns}	-11.3^{ns}	-26.5^{ns}
61 × 87-15	-3^{ns}	-9^{ns}	2.3^{ns}	12.6^{ns}	-1.5^{ns}	-1.6^{ns}	-52.2^{ns}	-60.4^{ns}
61 × 87-6	-11*	-16^{ns}	4.3^{ns}	14.8^{ns}	-6.2*	-6.3*	-43.8^{ns}	-53.5^{ns}
87 × 61-77	-12*	-16^{ns}	4.4^{ns}	14.8^{ns}	-0.9^{ns}	-1.0^{ns}	28.0^{ns}	6.1^{ns}
87 × 61-42	-6^{ns}	-11^{ns}	6.5^{ns}	17.1^{ns}	-3.2^{ns}	-3.3^{ns}	-32.8^{ns}	-44.3^{ns}
61 × 87-4	-7^{ns}	-12^{ns}	8.5^{ns}	19.4^{ns}	-0.9^{ns}	-1.0^{ns}	30.9^{ns}	8.5^{ns}
87 × 61-47	-9^{ns}	-14^{ns}	8.7^{ns}	19.6^{ns}	-2.1^{ns}	-2.1^{ns}	11.7^{ns}	-7.4^{ns}
87 × 61-46	-8^{ns}	-13^{ns}	14.7^{ns}	26.1^{ns}	-3.5^{ns}	-3.6^{ns}	-79.3*	-82.8*
87 × 61-57	-9^{ns}	-14^{ns}	17.0^{ns}	28.7^{ns}	-4.2*	-4.3^{ns}	17.7^{ns}	-2.5^{ns}

Note. *Significant at $P < 0.05$; **Significant at $P < 0.01$; ^{ns}Not significant.

Table 9. Performance of Histarch and CIP 442264, and their F_1 hybrids

Genotype code	Dry matter (%)	Total Sugars (%)	Starch (%)	Root yield (t/ha)
Histarch (87)	46	16.33	72.82	20.71
CIP 442264 (64)	42	10.80	68.27	5.07
64 × 87-1	48	14.29	72.06	13.31
64 × 87-2	48	12.59	72.96	12.04
64 × 87-3	46	12.25	72.94	-
87 × 64-1	46	15.44	69.74	13.57
87 × 64-2	48	14.14	72.59	15.93
SED (5%)	2	3.38	4.33	6.13
Grand Mean	46	13.69	71.6	11.50
Range	42-48	10.80-16.33	68.27-72.96	nil-20.71
CV (%)	4.6	30.2	7.4	65.2

Table 10. Estimates of mid-parent heterosis (Hb) and heterobeltiosis (Hbt) for F_1 hybrids of Histarch (87) and CIP 442264 (64)

Genotype code	Dry matter		Total sugars		Starch		Root yield	
	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)
64 × 87-1	10^{ns}	5^{ns}	5.4^{ns}	32.3^{ns}	2.5^{ns}	-1.0^{ns}	3.3^{ns}	-35.7^{ns}
64 × 87-2	10^{ns}	5^{ns}	-7.2^{ns}	16.6^{ns}	3.8^{ns}	0.2^{ns}	-6.6^{ns}	-41.9^{ns}
64 × 87-3	4^{ns}	-1^{ns}	-9.7^{ns}	13.4^{ns}	3.8^{ns}	0.2^{ns}	-	-
87 × 64-1	4^{ns}	-1^{ns}	13.9^{ns}	43.0^{ns}	-0.8^{ns}	-4.2^{ns}	5.3^{ns}	-34.5^{ns}
87 × 64-2	10^{ns}	5^{ns}	4.3^{ns}	30.9^{ns}	3.3^{ns}	-0.3^{ns}	23.6^{ns}	-23.1^{ns}

Note. ^{ns}Not significant.

Table 11. Performance of Histarch and AAT-03-025, and their F_1 hybrids

Genotype code	Dry matter (%)	Total sugars (%)	Starch (%)	Root yield (t/ha)
Histarch (87)	46	16.33	72.82	20.71
AAT-03-025 (72)	43	12.47	72.32	19.87
87 × 72-1	43	16.90	71.25	17.36
87 × 72-2	40	16.16	70.36	6.89
LSD (5%)	4	5.7	2.90	13.74
Grand Mean	43	15.5	71.69	13.20
Range	40-46	12.47-16.90	70.36-72.82	6.89-20.71
CV (%)	4.2	22.6	2.5	63.5

Table 12. Estimates of mid-parent heterosis (Hb) and heterobeltiosis (Hbt) for F_1 hybrids of Histarch (87) and AAT-03-025 (72)

Genotype code	Dry matter		Total sugars		Starch		Root yield	
	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)	Hb (%)	Hbt (%)
87 × 72-1	-6^{ns}	-7*	17.4^{ns}	35.5^{ns}	-1.8^{ns}	-2.2^{ns}	-14.4^{ns}	-16.2^{ns}
87 × 72-2	-11**	-12**	12.2^{ns}	29.6^{ns}	-3.0^{ns}	-3.4^{ns}	-66.4*	-66.7^{ns}

Note. *Significant at $P < 0.05$; **Significant at $P < 0.01$; ^{ns}Not significant.

4. Discussion

Significant differences observed between the germplasm provided opportunity for identification and selection of superior genotypes as parents for hybridization. Significant differences demonstrate significant genetic diversity and indicates that meaningful selection and improvement of desired trait is possible (Mohammed et al., 2012; Nwangburuka & Denton, 2012). The observed difference between PVC and GVC could be attributed to environmental effects (Denton & Nwangburuka, 2011). GCV provides a measure to compare the genetic variability present in various quantitative traits. However, it is not possible to estimate heritable variation with GCV alone (Prasad et al., 1981). The use of GCV with heritability estimates give the best picture of the amount of advance to be expected from selection (Burton, 1952). Heritability indicates the effectiveness with which selection of genotypes can be based on phenotypic performance (Johnson et al., 1955). In this study, broad-sense heritability estimates for sugar content was high. Traits with medium to high heritability are influenced by additive gene effects (Denton & Nwangburuka, 2011). This suggests that selection based on phenotype will be effective. Two of the parents (CRIWAC 25-10 and CRIWAC 19-10) did not produce flowers, and for those that did, only Histarch, Ogyefo, CIP 442264 and AAT-03-025 gave successful crosses. Lack of seeds and fewer numbers of seedlings from some crosses may largely be attributed to poor flowering and genetic incompatibility. This is because, according to Martin (1967), Martin and Cabanillas (1968), the improvement of sweetpotato

through conventional breeding is impeded by poor flowering and incompatibility. According to Fekadu et al. (2013), flowering prolificacy in sweetpotato is variety dependent. While some varieties do not flower at all, others produce very few flowers. In addition, many sweetpotato clones rarely flower under normal conditions as a result of differential response to seasonal variation. Most sweetpotato genotypes are day length sensitive. Thus while some genotypes flower readily any season, flowering in others occurs only during short day length (Martin, 1988). Among the parents that gave successful crosses, AAT-03-025 and CIP 442264 were very low in flower prolificacy that is why fewer crosses involving them were made and subsequently fewer seeds were obtained.

The range of values obtained for this study were comparable to those reported by Grüneberg et al. (2009). Values for dry matter content were also comparable to those reported by Shumbusha et al. (2014). Significant negative heterosis observed for sugar content is important for sweetpotato improvement in Ghana because the main trait preferred for increased sweetpotato utilization in Ghana is non-sweetness (bland taste) (Baafi, 2014; Baafi et al., 2015; Missah & Kissiedu, 1994; Sam & Dapaah, 2009). Breeding for non-sweetness is the most important breeding objective of the crop currently in Ghana. The sugar contents of the hybrids evaluated agrees with Kays et al. (2005). The authors classified sweetpotatoes based on sugar content as very high ≥ 38; high 29-37; moderate 21-28; low 12-20; and non-sweet ≤ 12. Based upon this classification, 15% of the F_1 hybrids of Histarch and Ogyefo were non-sweet. These will meet the staple food needs of Ghanaians. Based upon sugar content (mainly), dry matter content and root yield, eight hybrids were identified as potential non-sweet varieties for release. They were Ogyefo × Histarch-11, Histarch × Ogyefo-13, Histarch × Ogyefo-52, Histarch × Ogyefo-37, Histarch × Ogyefo-65, Histarch × Ogyefo-88, Histarch × Ogyefo-39, and Histarch × Ogyefo-16. These genotypes had high dry matter content of 42-46%, sugar content of 9-12%, and root yield of 12-31 t/ha as compared to Histarch (46% dry matter, 16.33% sugar content and 20.7 1t/ha root yield) and Ogyefo (41% dry matter, 13.62% sugar content and 13.61 t/ha root yield). Yields of the selected hybrids were low compared to Histarch. The first documented non-sweet, staple-type sweetpotato breeding line GA90-16 yields less than the most widely grown traditional North American cultivars Beauregard and Jewel (Kays et al., 2001). According to the authors, GA90-16 in Athens, total yields are generally ≈ 70% to 80% of 'Jewel', varying with year and location. Relatively lower yields for non-sweet varieties may be because higher yields are sacrificed for non-sweetness. In terms of yield some of these hybrids may be low but their non-sweetness will contribute so much for their increased acceptance and utilization in Ghana. In addition, 26 other hybrids were identified for other purpose such as source of sugar flour for sweetening porridge and *aboolo*. One of the oldest uses of sweetpotato is sweetening porridges and maize products, such as *Aboolo* (steamed or baked sweetened fermented maize dough) (Osei-Opare & Adjei-Poku, 1977).

5. Conclusion

Significant genetic diversity was found for sugar content. Sufficient useful genetic variation was present in the materials studied and was exploited to provide for substantial amount of improvement through selection of superior genotypes. Significant heterosis was found which is useful for the improvement of sweetpotato for increased utilization in Ghana and beyond. Negative heterosis observed for sugar content is very important because breeding for non-sweetness will raise sweetpotato to an increased staple food status in Ghana. The hybrids listed above will be further tested multi-locationally for potential release to farmers. These selected hybrids together with their parents used in this study will be used as the breeding population for sweetpotato improvement programme in Ghana. In addition to polyploidy and large chromosome number, this study suggested that flowering and self- or cross-incompatibility are major constraints to sweetpotato breeding in Ghana.

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References

Baafi, E. (2014). *Development of End-User Preferred Sweetpotato Varieties in Ghana* (Phd Thesis, West Africa Centre for Crop Improvemnt (WACCI), University of Ghana).

Baafi, E., Manu-Aduening, J., Carey, E. E., Ofori, K., Blay, E. T., & Gracen, V. E. (2015). Constraints and Breeding Priorities for Increased Sweetpotato Utilization in Ghana. *Sustainable Agriculture Research, 4*(4), 1-16. http://dx.doi.org/10.5539/sar.v4n4p1

Buerstmayr, H., Nicola, K., Uwe, S., Heinrich, G., & Elisabeth, Z. (2007). Agronomic Performance and Quality of Oat (*Avena sativa* L.) Genotypes of Worldwide Origin Produced under Central European Growing Conditions. *Field Crops Research, 101*, 92-97. http://dx.doi.org/10.1016/j.fcr.2006.12.011

Burton, G. W. (1952). Quantitative Inheritance in Grasses. *Proceedings of the sixth International Grassland Congress* (pp. 297-283). August. 17-23, Pennsylvania State College, USA.

Denton, O. A., & Nwangburuka, C. C. (2011). Heritability, Genetic Advance and Character Association in Six Yield Related Characters of Solanum Anguivi. *Asian Journal of Agricultural Research, 5*(3), 201-207. http://dx.doi.org/10.3923/ajar.2011.201-207

Ekanayake, I. J., Malagamba, P., & Midmore, D. J. (1990). Effect of Water Stress on Yield Indices of Sweetpotatoes. In R. H. Howeler (Ed.), *Proceedings of the eighth Symposium of the International Society for Tropical Root Crops* (p. 724). Bangkok, Thailand.

FAOSTAT. (2013). Food and Agriculture Organization of the United Nations. Rome, Italy.

Fekadu, G., Shimelis, H., & Mark, L. (2013). Self- and Cross-Incompatibilities in Sweetpotato and Their Implications on Breeding. *Australian Journal of Crop Science, 7*(13), 2074-2078.

Fonseca, S., & Patterson, F. L. (1968). Hybrid Vigour in Seven Parental Diallel Cross in Common Wheat (*Triticum aestivum* L.). *Crop Science, 8*, 85-88. http://dx.doi.org/10.2135/cropsci1968.0011183X000800010025x

Genstat. (2007). *For Windows Release 9.2.0.152*. Genstat-Ninth Edition at 2007, Lowes Agricultural Trust.

Grüneberg, W., Robert, M., Maria, A., & Harrison, D. (2009). Unleasing the Potential of Sweetpotato in Sub-Saharan Africa: Current Challenges and Way Forward. *Challenge Theme Paper 1: Sweetpotato Breeding* (pp. 1-42). CIP - Social Sciences Working Paper 2009-1.

Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1955). Estimates of Genetic and Environmental Variability in Soybean. *Agronomy Journal, 47*, 314-318. http://dx.doi.org/10.2134/agronj1955.00021962004700070009x

Jones, A. (1986). Sweetpotato Heritability Estimates and Their Use in Breeding. *Hortscience, 21*, 14-17.

Kays, S. J., Wang, Y., & McLaurin, W. J. (2005). Chemical and Geographical Assessment of the Sweetness of the Cultivated Sweetpotato Clones of the World. *Journal of the American Society for Horticultural Science, 130*(4), 591-597.

Kays, S. Y., McLaurin, W. J., Dukes, P. D., Thies, J., Bohac, R., & Jackso, D. M. (2001). GA90-16: A Nonsweet, Staple-Type Sweetpotato Breeding Line. *HortScience, 36*(1), 175-177.

Martin, F. W. (1967). The Sterility Incompatibility Complex of the Sweetpotato. *Proceedings of the first International Symposium on Tropical Root Crops* (pp. 3-15). St. Augustine, Trinidad 2-8 April 1967. University of West Indies.

Martin, F. W. (1988). Genetic and Physiological Basis for Breeding and Improving the Sweetpotato. In L. Degras (Ed.), *Proceedings of the seventh International Symposium on Tropical Root Crops* (pp. 749-761). Institute De La Reserche Agronomique (INRA), Paris France.

Martin, F. W., & Cabanillas, E. (1968). Classification of Sweetpotato Varieties for Incompatibility and Sterility. *Proceedings of American Society of Horticultural Science, 93*, 502-511.

Missah, A., & Kissiedu, A. F. K. (1994). Effect of Time of Harvesting on the Yield and Pest Incidence of Two Sweet Potato Varieties in the Forest Zone of Ghana. *Proceedings of the fifth International Symposium of Tropical Root Crops, AB* (pp. 276-280).

Mohammed, A., Geremew, B., & Amsalu, A. (2012). Variation and Association of Quality Parameters in Ethiopian Durum Wheat (*Triticum turgidum* L. Var. *Durum*) Genotypes. *International Journal of Plant Breeding and Genetics, 6*(1), 17-31. http://dx.doi.org/10.3923/ijpbg.2012.17.31

Nwangburuka, C. C., & Denton, O. A. (2012). Heritability, Character Association and Genetic Advance in Six Agronomic and Yield Related Characters in Leaf *Corchorus Olitorius*. *International Journal of Agricultural Research, 7*(7), 367-375. http://dx.doi.org/10.3923/ijar.2012.367-375

Osei-Opare, F., & Adjei-Poku, C. (1977). *Sweetpotato Processing and Utilization (Theory and Practicals)* (pp. 1-7). Home Science Department, University of Ghana, Legon.

Poole, C. F. (1955). Sweetpotato Genetic Studies. Hawaii Agricultural Experiment Station. *Technical Bulletin,*

27.

Prasad, S. R., Prakash, R., Sharma, C. M., & Haque, M. F. (1981). Genotypic and Phenotypic Variability in Quantitative Characters in Oat. *Indian Journal of Agricultural Sciience, 54*, 480-482.

Rausul, I., Khan, S. A., & Z., A. (2002). Estimation of Heterosis for Yield and Some Yield Components in Bread Wheat. *International Journal of Agriculture and Biology, 4*(2), 214-216.

Sam, J., & Dapaah, H. (2009). *West Afriican Agricultural Productiiviity Programme (WAAPP), Ghana Baseline Survey Report* (p. 133). October, 2009.

Shumbusha, D., Tusiime, G., Edema, R., Gibson, P., Adipala, E., & Mwanga, R. O. M. (2014). Inheritance of Root Dry Matter Content in Sweetpotato. *African Crop Science Journal, 22*(1), 69-78.

Warammboi, J. G., Dennien, S., Gidley, M. J., & Sopade, P. (2011). Characterization of Sweetpotato from Papua New Guinea and Australia: Physicochemical, Pasting and Gelatinisation Properties. *Food Chemistry, 126*, 1759-1770. http://dx.doi.org/10.1016/j.foodchem.2010.12.077

Wynne, J. C., Emery, D. A., & Rice, P. H. (1970). Combining Ability Estimation in *Arachis Hypogaea* L. II. Field Performance of F_1 Hybrids. *Crop Sciience, 10*, 713-715. http://dx.doi.org/10.2135/cropsci1970.0011183X001000060036x