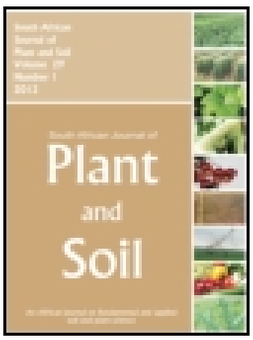

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Phenotypic characterisation of potato (*Solanum tuberosum*) genotypes in Uganda

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Identification of genetic variation and interrelationships among germplasm collections is essential for parental selection and trait identification among parents for use in breeding programmes. The aim of this study was to characterise 48 potato genotypes to identify suitable parents for crop improvement purposes. Genotypes were evaluated in the field using an alpha lattice design with three replications at the Kachwekano and Karengyere research stations in Uganda. Site had significant effects on genotype performance for all measured parameters. Genotypic effects were significant ($p < 0.01$) for total tuber yield, main stem number and plant height. The mean tuber yield for the two sites was 29.8 t ha^{-1} and tuber yield was higher in Kachwekano than Karengyere. The highest-yielding genotype in Kachwekano was 396038.105 (54.5 t ha^{-1}) and in Karengyere was NAKPOT5 (50.9 t ha^{-1}). Significant positive correlations ($p \leq 0.001$) were observed between tuber yield and plant height; duration of flowering, and days to flowering and plant height. The most stable genotypes with regard to tuber yield were Rutuku, 395112.32, 395017.14 and 393220.54. Cluster analysis revealed three principal clusters with nine subclusters. Variation for the different traits exhibited by genotypes in this study should be exploited in crop improvement programmes.

Keywords: agromorphological, genetic diversity, genotype, phenotypic traits, potato

Introduction

Globally, potato (*Solanum tuberosum* L.) is the fourth most important crop after maize, rice and wheat with more than 320 million t produced from 20 million ha (CIP 2016). Potato is a major food and cash crop in the highland regions of many African countries, and is mainly grown by small-scale farmers. Uganda is the ninth-largest producer of potato in Africa with an annual production of 188 000 t harvested from about 39 000 ha y^{-1} (FAOSTAT 2016).

The identification of suitable genotypes with complementary traits is key in crop improvement (Tseng et al. 2002; Elameen et al. 2011). Knowledge of genetic interrelationships among pools of germplasm enables plant breeders to select possible parents with desired traits for cultivar development (Yoshida 2004). Proper management and utilisation of plant genetic resources entirely depends on the extensive understanding of their genetic variability (Rukundo et al. 2015). Genetic variability is the basis of plant breeding and as a result it is a prerequisite before initiation of a breeding programme (Simmonds 1962).

Several methods have been used to measure genetic variation among plant genetic resources. These include data based on plant morphology, agronomical performance, biochemical and molecular markers (Mohammadi and Prasanna 2003). Morphological characterisation is the first step in description and classification of genetic resources (Arslanoglu et al. 2011). Phenotyping is usually done to determine the genetic variation among genotypes (Yoshida 2004). Phenotypic markers are comparatively cheap and easy to use (Elameen et al. 2011). Potato is a clonally propagated crop that exhibits a high degree of incompatibility and inbreeding depression (Muthoni et al. 2012). This makes parental selection vital if breeding progress is to be made (Hirut 2015). It is also imperative that genotypes with superior agronomical properties are selected for crop improvement studies (Pandey et al. 2005; Sandhu and Gopal 2006). It is against this background that this study was undertaken to determine the phenotypic diversity among 48 potato genotypes and to identify superior parents for breeding purposes.

Materials and methods

Genetic material

The germplasm used in this study consisted of 48 potato genotypes, which included advanced clones from the International Potato Center (CIP), commercial and farmers' cutivars. The details of the genotypes are presented in Table 1.

Planting sites

The field trials were established at the Kachwekano and Karengyere research stations of the National Agricultural

Research Organisation (NARO). Kachwekano is located at 01°16′ S, 29°57′ E in south-western Uganda at an altitude of 2 200 m above sea level (asl). The soil type at this location is isomeric typic palehumult (Kakuhenzire et al. 2013). Karegyere research station is located at 01°13.2′ S, 29°47.8′ E in south-western Uganda at 2 450 m asl. Both sites have a bimodal rainfall pattern separated by a dry spell ranging from 30 to 60 d.

Experimental design and trial establishment

Experiments were established during the season of 2015 (September to December) using an 8 × 6 alpha lattice design with three replications at both locations. The Karengyere trial was planted on 15 September 2015 and harvested on 8 January 2016. The trial in Kachwekano was planted on 18 September 2015 and harvested on 14 January 2016. The plot size was 4.5 m long by 3.0 m wide. Four rows of 15 tubers each were spaced at 75 cm between rows and 30 cm between plants. Planting was by hand. At the time of planting N:P:K 17:17:17 fertiliser was applied at the rate of 100 kg ha^{-1}. Pest and disease control was done and late blight was controlled using recommended fungicides. Hand weeding and ridging were carried out as recommended.

Data collection

Data were recorded on different agromorphological characters. Qualitative traits recorded were flower colour, tuber shape, skin texture, skin colour, flesh colour, eye colour and depth as described by Arslanoglu et al. (2013) (Table 2). Quantitative data collected comprised plant height, main stem number, days to flowering and duration of flowering. Measurements for plant height and main stem number were done on 10 randomly selected plants in each plot and replication. Plant height (cm) was measured using a metre ruler as the distance between the top point of the plant and the ground surface after flowering. Main stem number, recorded as the number of main stems per plant, was counted at 50% flowering. Days to flowering was recorded as number of days from planting to 50% flowering of the plants in a plot. Duration of flowering was recorded as the difference between number of days from 50% flowering of the plants in a plot to 50% flower senescence. At harvest, data were recorded for number of plants in the two central rows, number of tubers and total tuber weght. Tuber yield was calculated as a function of number of plants per plot and total tuber weight (TTW). This was expressed in tonnes per hectare (t ha^{-1}). Genotypes with yields greater than 30 t ha^{-1} were classified as high yielding (HY), as moderate yielding (MY) when the yields ranged between 15 and 30 t ha^{-1}, and low yielding (LY) genotypes yielded less than 15 t ha^{-1}.

Data analysis

Data were analysed using the GenStat 14th Edition (Payne et al. 2011) software package. When significant differences were detected, means were separated using the least significant difference (LSD) test at the 5% significance level, using Fisher's protected LSD. Correlations between quantitative traits were determined using parametric tests. Spearman correlation coefficient values were calculated to determine trait associations among qualitative traits using

Table 2: Description of qualitative traits of potato genotypes used in the study

Character	Description
Flower colour	(1) White, (2) Violet, (3) Blue, (4) Pink
Eye colour	(1) White, (2) Red, (3) Pink, (4) Purple
Skin colour	(1) White, (2) White with pink points, (3) Red, (4) Purple, (5) Pink, (6) Cream
Flesh colour	(1) White, (2) Cream, (3) Light yellow, (4) Yellow, (5) Dark yellow)
Eye depth	(1) Very deep, (3) Deep, (5) Medium, (7) Shallow, (9) Very shallow
Skin texture	(1) Very rough, (3) Rough, (5) Intermediate, (7) Smooth, (9) Very smooth
Tuber shape	(1) Globe, (2) Short-oval, (3) Oval, (4) Long-oval, (5) Long, (6) Very long
Flower frequency	(1) Very high, (2) High, (3) Moderate, (4) Rare
Pollen production	(1) Present, (2) Absent

Table 1: Source of the 48 potato genotypes used in the study. CIP = International Potato Center, NARO = National Agriculture Research Organisation

No.	Genotype	Source	No.	Genotype	Source	No.	Genotype	Source
1	395017.14	CIP	17	396031.108	CIP	33	Rutuku	NARO
2	391919.3	CIP	18	391046.14	CIP	34	NKRK19.10	NARO
3	395109.34	CIP	19	396038.105	CIP	35	NKRN59.124	NARO
4	394905.8	CIP	20	395011.2	CIP	36	396026.103	NARO
5	395077.12	CIP	21	393220.54	CIP	37	NKR159.41	NARO
6	391580.3	CIP	22	392633.64	CIP	38	NAKPOT1	NARO
7	395096.2	CIP	23	394895.7	CIP	39	Cruza	NARO
8	392657.8	CIP	24	396034.268	CIP	40	NKRN59.48	NARO
9	393077.54	CIP	25	Kimuri	Farmer	41	Victoria	NARO
10	392661.18	CIP	26	Petero	Farmer	42	NKRN59.61	NARO
11	391002.6	CIP	27	Mabondo	Farmer	43	Rwashaki	NARO
12	395438.1	CIP	28	NKRN59.11	NARO	44	Rwangume	NARO
13	396038.101	CIP	29	NKRN59.58	NARO	45	NKRN59.29	NARO
14	395015.6	CIP	30	396034.103	NARO	46	Kinigi	NARO
15	392797.22	CIP	31	396038.107	NARO	47	Kachpot1	NARO
16	395112.32	CIP	32	NKRK19.17	NARO	48	NAKPOT5	NARO

IBM SPSS Statistics for Windows 19 (IBM Corporation, Armonk, NY, USA, 2010). A cluster analysis was carried out using 15 morphological traits to determine genetic relationships among genotypes.

Results

Flower and tuber characteristics

Qualitative characteristics of the 48 tested genotypes are presented in Table 3. There were marked differences in the flowering ability of genotypes ranging from rare to very high. With regard to pollen production, 85% of the genotypes produced pollen. Genotypes had different flower colours ranging from pink (14 genotypes), purple (12 genotypes), white (10 genotypes), violet (10 genotypes) to blue (two genotypes). The tuber shape was globe (27 genotypes), oval (12 genotypes), short-oval (six genotypes) or long-oval (three genotypes). The skin colour of the tubers varied from white (16 genotypes) to pink (12 genotypes), red (11 genotypes), white with pink points (four genotypes),

Table 3: Qualitative characteristics of the 48 potato genotypes used in the study

	Qualitative characteristic								
Genotype	Flower colour	Flower frequency	Tuber shape	Skin colour	Skin texture	Flesh colour	Eye colour	Eye depth	Pollen production
395017.14	Pink	Very high	Oval	White	Smooth	White	White	Shallow	Present
391919.3	Violet	Very high	Long-oval	Purple	Smooth	Cream	Purple	Medium	Absent
395109.34	Pink	Moderate	Short-oval	White, pink points	Smooth	Cream	Pink	Medium	Present
NKR159.41	Pink	Moderate	Oval	White	Smooth	Cream	White	Shallow	Present
395077.12	Violet	Moderate	Globe	White, pink points	Smooth	Cream	Pink	Shallow	Present
NAKPOT1	Blue	Rare	Globe	White	Smooth	White	White	Shallow	Present
Kimuri	White	Rare	Globe	White	Rough	White	White	Shallow	Present
Cruza	Violet	Very high	Short-oval	White	Smooth	White, purple	Purple	Shallow	Absent
391580.3	White	Very high	Globe	White	Intermediate	Cream	White	Shallow	Present
Petero	Pink	High	Globe	Red	Smooth	White, purple	Purple	Deep	Present
Rwashaki	Purple	Very high	Globe	Pink	Smooth	Cream	Pink	Deep	Present
395438.1	Pink	Moderate	Short-oval	Red	Smooth	Cream	Red	Shallow	Present
Rwangume	Purple	Moderate	Globe	Red	Smooth	Cream	Red	Medium	Present
NKRN59.29	Violet	Very high	Globe	Pink	Intermediate	Cream	Pink	Shallow	Present
392797.22	Violet	Moderate	Long-oval	Purple	Intermediate	White	White	Deep	Absent
Kinigi	Blue	Rare	Globe	Purple	Intermediate	Cream	Purple	Deep	Present
396038.105	Purple	Very high	Short-oval	Pink	Intermediate	White	Red	Shallow	Present
395011.2	Purple	High	Oval	White	Intermediate	Cream	White	Deep	Present
Kachpot1	Violet	Very high	Globe	Red	Rough	Cream	Red	Medium	Absent
392633.64	White	Moderate	Globe	White	Smooth	Cream	White	Shallow	Present
394895.7	Violet	Moderate	Long-oval	White	Rough	White	White	Shallow	Present
395096.2	Pink	Rare	Globe	White, pink points	Smooth	White	Red	Medium	Present
NKRN59.48	Pink	Moderate	Oval	Pink	Smooth	Cream	Red	Shallow	Present
Victoria	Pink	Rare	Globe	Red	Smooth	White	Red	Shallow	Present
NKRN59.61	White	Rare	Globe	Red	Rough	Cream	Red	Shallow	Present
396038.101	Violet	Moderate	Globe	Red	Rough	White	Red	Shallow	Present
Mabondo	Purple	High	Globe	White	Smooth	White	Red	Shallow	Absent
395015.6	White	Moderate	Oval	Red	Smooth	Cream	White	Shallow	Present
NKRN59.11	Purple	Moderate	Short-oval	Pink	Smooth	Cream	Red	Medium	Absent
NKRN59.58	White	Very high	Oval	Pink	Intermediate	Cream	White	Shallow	Present
396031.108	White	Moderate	Globe	White	Rough	Cream	White	Shallow	Present
396026.103	Purple	Moderate	Globe	Red	Rough	Cream	Red	Shallow	Present
396034.103	Purple	Very high	Globe	Red	Rough	Cream	Red	Medium	Present
396038.107	Purple	Very high	Globe	Pink	Intermediate	Cream	Red	Medium	Present
392661.18	Pink	Very high	Oval	White	Smooth	White	White	Shallow	Present
391002.6	White	Very high	Globe	White	Smooth	White	White	Shallow	Present
395112.32	Pink	High	Globe	Pink	Smooth	Cream	White	Shallow	Present
393220.54	Violet	High	Globe	White, pink points	Smooth	Cream	Red	Shallow	Present
396034.268	Pink	High	Globe	Red	Intermediate	Cream	Red	Shallow	Present
NAKPOT5	Violet	Moderate	Oval	White	Smooth	White	White	Shallow	Present
391046.14	White	Very high	Oval	Cream	Smooth	Cream	White	Shallow	Present
NKRK19.17	Purple	High	Short-oval	Pink	Smooth	Cream	Red	Deep	Present
392657.8	Purple	Very high	Oval	Pink	Smooth	Cream	Pink	Shallow	Present
393077.54	Pink	High	Globe	White	Intermediate	Cream	White	Medium	Present
Rutuku	Purple	Moderate	Oval	Red	Smooth	Cream	Red	Shallow	Present
NKRK19.10	Pink	Moderate	Globe	Pink	Smooth	Cream	White	Shallow	Absent
NKRN59.124	White	Moderate	Oval	Cream	Smooth	Cream	White	Shallow	Present
394905.8	White	High	Globe	White	Intermediate	White	White	Shallow	Present

purple (three genotypes) and cream (two genotypes). The skin texture of the tubers was predominantly smooth, whereas a few genotypes had an intermediate (11 genotypes) or rough texture (eight genotypes). The majority of the genotypes had a cream tuber flesh (32 genotypes), but two genotypes (Cruza and Petero) produced white-fleshed tubers with a purple ring and the remainder of genotypes had white-fleshed tubers. The eye colour of the tubers was largely white (22 genotypes) or red (17 genotypes). With regard to eye depth of the tubers, 33 genotypes had shallow eyes, six genotypes medium-depth eyes and the remaining genotypes had deep eyes.

The results of analysis of variance for tuber yield, main stem number, plant height, days to flowering and duration of flowering are presented in Table 4. Site had significant effects on all measured parameters ($p < 0.01$). Genotype effects were significant ($p < 0.01$) for yield, main stem number and plant height. Genotype and site interactions were only significant for the main stem number ($p < 0.01$).

Genotype means

Genotype means for tuber yield, main stem number, plant height, days to flowering and duration of flowering are presented in Table 5. The mean tuber yield across the two locations was 29.8 t ha^{-1}. The average yield was higher at Kackwekano (31.9 t ha^{-1}) than at Karengyere (27.7 t ha^{-1}). Genotypes were assigned to yield classes where genotypes with yields above 30 t ha^{-1} were classified as high yielding (HY), moderate yielding (MY) when the yields ranged between 15 and 30 t ha^{-1}, and low yielding (LY) if yields were less than 15 t ha^{-1}. On the basis of yield classes, 52% of the genotypes were high yielding (30 t ha^{-1} and above), 8% were low yielding, and the remainder were average yielding (between 15 and 30 t ha^{-1}). The highest-yielding genotype across sites was 397038.105 with 46.0 t ha^{-1}, whereas the genotype 392633.64 produced the lowest yield (12.9 t ha^{-1}). On average, genotypes produced a greater number of stems at Kachwekano and required more days to flower. At Karengyere, genotypes were taller and had a longer flowering duration. The tallest genotype was NAKPOT5 (68.4 cm), whereas the genotype Kimuri was the shortest (33.4 cm).

Correlations between qualitative and quantitative traits

Correlations between morphological traits are presented in Table 6. For qualitative traits the following correlations were positive and significant: eye colour with flesh colour and skin colour ($p \leq 0.001$); flower colour with flower frequency ($p \leq 0.01$) and foliage cover ($p \leq 0.05$); and flower frequency and foliage cover ($p \leq 0.05$). Tuber shape and eye depth were positively correlated. Eye depth was negatively correlated with eye colour ($p \leq 0.001$), flesh colour ($p \leq 0.01$), flower colour ($p \leq 0.05$) and skin colour ($p \leq 0.05$). In addition, a significant negative correlation was observed between growth habit and skin texture ($p \leq 0.05$). Correlations between duration of flowering, and days to flowering and plant height were positive and significant ($p \leq 0.001$). On the other hand, a significant ($p \leq 0.01$) negative correlation was observed between days to flowering and main stem number. Significant positive correlations were also observed between duration of flowering and tuber yield ($p \leq 0.01$). The correlation between plant height and main stem number was negative and significant ($p \leq 0.05$). A significant positive correlation ($p \leq 0.001$) was observed between tuber yield and plant height.

Level of genotypic diversity between genotypes

The level of genotypic diversity between the 48 genotypes is shown in Figure 1. Cluster analysis grouped the genotypes into three major clusters, consisting of 33, eight and seven genotypes, respectively. At the secondary level, major cluster 1 had five subclusters, major clusters 2 and 3 had two and three subclusters, respectively. Among these nine subclusters, the genotypes were randomly grouped. Subcluster C2 consisted of only one genotype (Rwashaki) and all genotypes from subclusters 8 and 9 were obtained from the International Potato Center. From major cluster 1, 16 genotypes were identified as potential parents. These were 395017.14, NAKPOT5, NAKPOT1, NKRN59.41, 391046.14, NKRN59.58, 393077.54, 396026.103, 396034.103, 391919.3, NKRK 19.17, 396038.107, Rwangume, Rutuku, NkRN59.48 and 392657.8. Three genotypes (393220.54, Kinigi and Kimuli) were potential parents from major cluster 2. All of the selected genotypes possessed different desirable traits necessary for crop improvement. These ranged from high yields, early maturity and resistance to diseases, mainly late blight among others. The similarity distance varied from 0.5 to 1.

Discussion

Genotypes with good foliage cover showed a higher flower frequency. Genotypes with high to very high flower frequency and pollen production were chosen to be used as parents. Genotypes with pink, purple and blue flowers had good foliage cover compared with those with white flowers.

Table 4: Analysis of variance showing mean squares and significance of tuber yield, main stem number, plant height, days to flowering and duration of flowering of 48 potato genotypes evaluated at the Kachwekano and Karengyere research stations, Uganda in 2015. MSN = main stem number, PH = plant height, DAF = days to flowering, DOF = duration of flowering

Source of variation	df	Mean squares				
		Tuber yield	MSN	PH	DAF	DOF
Site	1	1 341.60**	274.37**	1 655.79**	775.97**	2 783.13**
Genotype	47	591.01**	6.95**	327.82**	40.59	66.32
Site.Genotype	47	76.86	2.66**	86.92	37.77	13.12
Residual	188	68.36	1.29	76.06	32.95	68.64
Total	287					

* $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$

Table 5: Tuber yield, main stem number, plant height, days to flowering and duration of flowering for 48 genotypes evaluated at Kachwekano and Karengyere research stations, Uganda. Means within a column followed by the same superscript letter are not significantly different (P = 0.05). HY = high yield, MY = medium yield, LY = low yield, PH = plant height, MSN = main stem number, DAF = days to flowering, DOF = duration of flowering, MKach = mean Kachwekano, MKar = mean Karengyere, GM = grand mean, SED = standard error of difference, LSD = least significant difference

Genotype	Tuber yield (t ha^{-1})			Class	MSN	PH (cm)	DAF	DOF
	Kachwekano	Karengyere	Mean across sites					
395017.14	13.1^{a}	12.6^{abc}	12.9	LY	1.9	46.1	48.8	33.3
391919.3	14.7^{ab}	11.3^{ab}	13.0	LY	2.7	62.0	44.0	38.8
395109.34	15.8^{abc}	10.9^{a}	13.4	LY	1.4	65.5	50.0	29.8
NKR159.41	16.5^{abc}	12.6^{abc}	14.6	LY	1.0	46.8	44.5	27.0
395077.12	18.6$^{a–d}$	20.1$^{a–h}$	19.4	MY	2.6	51.3	44.5	35.3
NAKPOT1	18.9$^{a–d}$	18.9$^{a–g}$	19.0	MY	3.2	50.7	51.5	34.0
Kimuri	19.3$^{a–d}$	14.9$^{a–d}$	17.1	MY	3.2	53.1	52.5	35.8
Cruza	20.3$^{a–e}$	20.3$^{a–h}$	20.3	MY	1.3	52.2	51.0	33.5
391580.3	20.3$^{a–e}$	20.3$^{a–h}$	20.3	MY	2.5	52.4	50.3	27.3
Petero	20.4$^{a–e}$	17.8$^{a–g}$	19.1	MY	2.6	33.4	41.0	29.0
Rwashaki	20.5$^{a–e}$	17.3$^{a–f}$	18.9	MY	3.4	39.5	46.3	28.0
395438.1	20.7$^{a–f}$	15.4$^{a–e}$	18.1	MY	1.0	50.4	43.5	17.8
Rwangume	21.2$^{a–g}$	21.2$^{a–i}$	21.2	MY	2.7	48.3	50.3	31.5
NKRN59.29	22.6$^{a–h}$	24.9$^{c–l}$	23.8	MY	2.8	44.3	41.5	32.0
392797.22	22.7$^{a–h}$	22.7$^{a–i}$	22.7	MY	2.0	52.9	47.0	35.5
Kinigi	24.0$^{a–i}$	24.0$^{a–j}$	24.0	MY	2.5	51.8	46.3	34.3
396038.105	24.5$^{a–j}$	24.5$^{b–k}$	24.5	MY	2.3	58.6	47.5	32.5
395011.2	25.5$^{a–k}$	25.5$^{c–l}$	25.5	MY	2.8	53.3	47.0	31.3
Kachpot1	28.8$^{b–l}$	22.1$^{a–i}$	25.4	MY	3.2	57.4	39.5	39.0
392633.64	28.9$^{b–l}$	24.6$^{b–k}$	26.8	MY	4.0	52.8	41.5	30.5
394895.7	30.3$^{c–l}$	25.7$^{c–l}$	28.0	MY	3.6	59.3	43.3	23.0
395096.2	32.1$^{d–m}$	50.9^{o}	41.5	HY	3.3	68.4	45.3	36.0
NKRN59.48	32.3$^{d–n}$	27.7$^{d–n}$	30.0	MY	4.0	51.2	41.8	31.0
Victoria	32.7$^{d–n}$	21.3$^{a–i}$	27.0	MY	2.7	55.3	42.0	35.0
NKRN59.61	34.2$^{e–n}$	30.4$^{f–n}$	32.2	HY	1.5	40.7	47.5	35.8
396038.101	35.3$^{f–n}$	27.4$^{d–m}$	31.3	HY	4.4	50.9	48.3	30.5
Mabondo	35.7$^{g–n}$	28.2$^{d–n}$	31.9	HY	1.6	48.4	46.3	32.5
395015.6	35.9$^{h–n}$	37.7$^{k–o}$	36.8	HY	4.6	62.7	46.8	29.8
NKRN59.11	35.9$^{h–n}$	27.5$^{d–n}$	31.7	HY	4.8	59.2	43.0	30.3
NKRN59.58	36.0$^{h–n}$	24.1$^{a–j}$	30.0	HY	3.7	48.9	42.8	32.0
396031.108	36.0$^{h–n}$	23.8$^{a–i}$	29.9	MY	3.8	54.0	45.0	33.5
396026.103	36.6$^{h–n}$	29.6$^{f–n}$	33.1	HY	4.3	62.0	44.0	34.0
396034.103	36.8$^{h–n}$	34.1$^{i–n}$	35.4	HY	3.0	56.6	40.8	33.3
396038.107	37.8$^{i–n}$	47.7^{o}	42.8	HY	4.7	66.9	45.0	30.5
392661.18	38.6$^{j–o}$	37.7$^{k–o}$	38.1	HY	5.1	64.8	42.0	28.0
391002.6	39.4$^{k–p}$	40.7^{mno}	40.3	HY	3.9	58.8	47.8	32.8
395112.32	40.0$^{k–q}$	31.0$^{g–n}$	35.5	HY	4.4	58.2	45.0	34.8
393220.54	40.3$^{l–q}$	40.3^{mno}	40.3	HY	3.0	54.3	44.0	40.8
396034.268	40.8$^{l–q}$	28.4$^{d–n}$	34.6	HY	4.5	61.0	47.3	39.3
NAKPOT5	41.7$^{l–q}$	28.6$^{d–n}$	35.1	HY	3.0	64.8	42.3	34.8
391046.14	42.5$^{l–q}$	50.1^{o}	46.3	HY	1.6	49.9	48.8	36.8
NKRK19.17	45.2$^{m–q}$	28.8$^{e–n}$	37.0	HY	4.1	64.8	46.3	35.5
392657.8	46.4$^{m–q}$	41.1^{no}	43.7	HY	2.2	53.5	45.5	33.3
393077.54	46.5$^{m–q}$	39.9^{mno}	43.2	HY	3.4	62.3	48.0	35.3
Rutuku	46.7$^{n–q}$	32.7$^{h–n}$	39.7	HY	4.5	65.2	45.8	34.3
NKRK19.10	52.9^{opq}	38.5$^{l–o}$	45.7	HY	3.5	63.4	47.3	34.0
NKRN59.124	54.1^{pq}	34.0$^{i–n}$	44.1	HY	3.5	53.9	41.8	36.0
394905.8	54.5^{q}	37.6$^{j–o}$	46.0	HY	2.1	55.4	40.3	31.8
Mean	32.0	27.7	29.8	MKach	4.0	52.6	47.4	28.9
SED	7.3	6.8	5.0	MKar	2.0	57.4	43.4	36.5
LSD	14.6	13.6	9.9	GM	4.0	55.0	45.4	32.7
CV (%)	28.1	30.0	29.1	SED	0.9	7.1	4.1	5.8
				LSD	1.8	13.9	8.1	11.6
				CV (%)	36.9	15.7	12.6	25.3

Table 6: Spearman correlation coefficients between qualitative traits and pair-wise correlations between quantitative traits of 48 potato genotypes tested at Kachwekano and Karengyere research stations, Uganda

Qualitative trait	Eye colour	Eye depth	Flesh colour	Flower colour	Flower frequency	Foliage cover	Growth habit	Skin colour	Skin texture	Tuber shape
Eye colour	–									
Eye depth	0.54***	–								
Flesh colour	0.49***	−0.34**	–							
Flower colour	0.26	−0.33*	0.08	–						
Flower frequency	0.15	−0.21	0.25	0.34**	–					
Foliage cover	0.11	−0.09	0.14	0.28*	0.33*	–				
Growth habit	−0.12	−0.05	−0.05	−0.17	−0.01	−0.13	–			
Skin colour	0.52***	−0.30*	0.25	0.18	−0.13	0.08	0.03	–		
Skin texture	0.15	−0.09	0.12	0.23	−0.02	0.14	−0.32*	−0.09	–	
Tuber shape	−0.16	0.31*	−0.09	−0.05	0.01	0.05	−0.13	−0.06	0.21	–

Quantitative traits	Days to flowering	Duration of flowering	Main stem number	Plant height
Days to flowering	–			
Duration of flowering	0.69***	–		
Main stem number	−0.41**	−0.09	–	
Plant height	0.76***	0.66***	−0.31*	–
Total tuber yield	0.25	0.41**	0.09	0.52***

* $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$

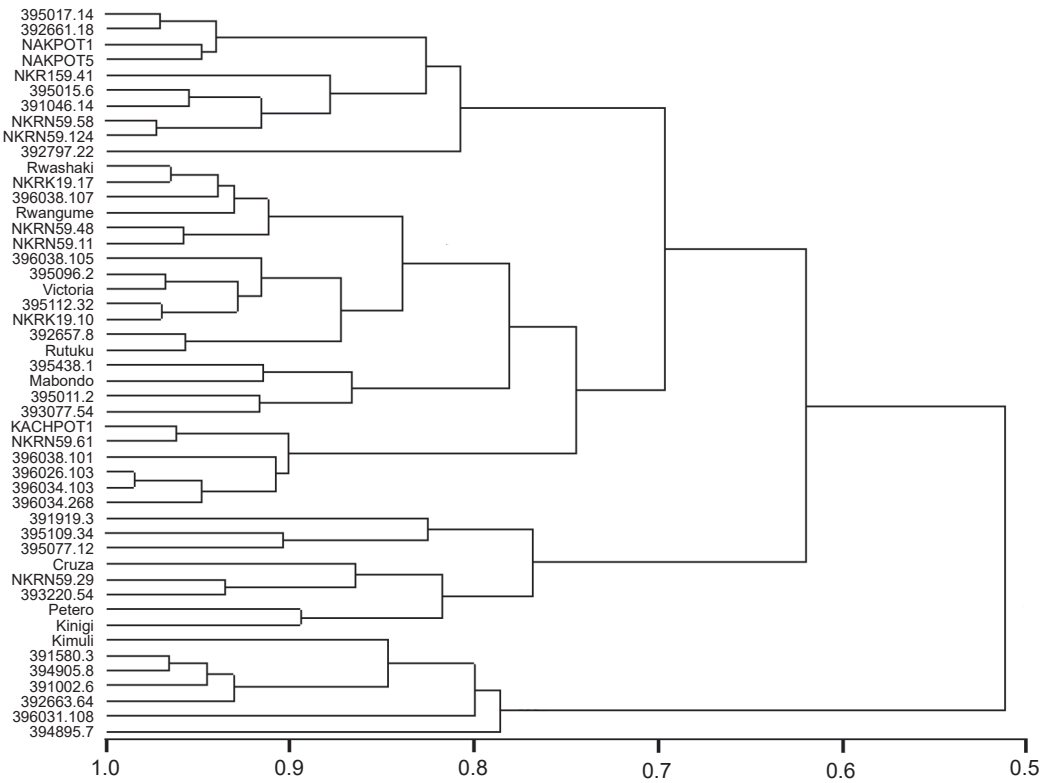

Figure 1: Dendrogram showing principal genetic clusters of 48 potato genotypes using 15 phenotypic traits

This possibly explains the positive correlation between flower colour and foliage cover. A higher percentage of the studied genotypes had a cream flesh colour (67%) and the desired tuber shape of globe to oval (81%). Eye depth also influenced tuber shape.

Tuber characteristics in potato are subject to environment and genotype interactions (Abebe et al. 2013). Trait preferences by farmers are high yields, disease resistance, early maturity, marketability and good cooking quality (Low 1997; Kaguongo et al. 2008; Muthoni et al. 2012). The most preferred tuber characteristics are high dry matter, smooth red or pink skin, shallow eyes and a cream flesh colour (Tesfaye et al. 2010). In Uganda skin colour is a very important trait and greatly influences market demands and adoption (Forbes 2012). For example, cultivars such as NAKPOT1 and NAKPOT5 have had low acceptance and

marketability because of the white skin despite their high yields. Cruza, a cultivar with resistance to late blight and bacterial wilt, is not preferred by farmers because of the purple colouration of the vascular rings when fried and the tuber becomes mushy on cooking (Low 1997; Kaguongo et al. 2008). On the other hand, Victoria, a cultivar susceptible to late blight, has had wide adoption in Uganda because of the red skin, early maturity and high yields. Tuber shape is also increasingly becoming a trait of economic processing and industrial importance (Muhinyuza et al. 2015). The preferred shape is oblong and oval. In view of this, the selected parents for crosses possessed most of these traits. Tuber characteristics that may influence consumers' choice include tuber shape, eye depth, skin and flesh colour as well as skin texture.

Quantitative flower characteristics that were measured were number of days to flowering and flowering duration. The number of days to flowering and flowering period are of great importance in designing a crossing programme to ensure synchronisation in flowering and achieving hybridisation (Acquaah 2007). Duration of flowering ranged from 17 to 40 d. A longer flowering duration of 1–8 weeks was found among Indian and exotic potato cultivars (Manivel et al. 2005). Genotypes with a longer duration of flowering were mainly selected to be used as female parents for breeding purposes, whereas those with sufficient pollen production were mainly used as male parents.

The evaluated genotypes varied significantly in tuber yield and other morphological characters. Environmental differences between Kachwekano and Karengyere plus the inherent genetic variation among the test genotypes were the primary causes of the variation in tuber yield. Muhinyuza et al. (2015) reported that total tuber yield is affected by both the genotype and environment. According to Acquaah (2007), the genetic composition of a genotype influences the expression of heritable traits between and within environments.

The significant positive correlation between tuber yield and duration of flowering ($r = 0.41$) implies that those genotypes with a greater number of flowering days produced higher yields compared with the other genotypes. This may be explained by the longer vegetative growth stage, which supports the conversion of more photosynthates to yield. The long flowering duration at Karengyere can be explained by the higher-altitude conditions that could have favoured flowering over a longer period. The significant positive correlation between tuber yield and plant height observed in the present study is supported by previous studies (Luthra 2001; Mostafa and Felenji 2011; Datta et al. 2014). The negative correlation between the number of stems and plant height may be explained by the fact that genotypes with more stems have to partition the photosythates to more sinks, leading to shorter stems (Datta et al. 2014).

Knowledge on genetic distance between possible parents is essential for breeding (Acquaah 2007). Sufficient genetic diversity is required when designing a crossing program to generate new genetic recombinants. This allows selection of segregants with improved quantitative or qualitative traits such as yield (Korzun 2003). Jacoby et al. (2003) reported significant differences between genotypes and genetic distance ranging from 0.26 to 0.80 during morphological characterisation of eight genotypes of *Solanum retroflexum*. In the present study, genotypes were assembled into three major clusters and nine subclusters with genetic distance ranging from 0.5 to 1.0. The grouping of potato genotypes obtained from CIP in one cluster points to a common ancestry as some of the genotypes could be selections from a single cross (Muthoni et al. 2014).

Potato is a clonally propagated crop that exhibits a high degree of incompatibility and inbreeding depression (Muthoni et al. 2012). Kaushik et al. (2007) reported that the use of suitable parents is the most efficient way of increasing yield and controlling diseases. In the present study genotypes were selected on the basis of tuber yield and other agromorphological characteristics. The following genotypes were selected from the different clusters for possible use as parents: 396034.103, 392657.8, NKRN59.58, NKRN19.17, Kinigi, Rutuku, NAKPOT5, 396026.103, 393077.54, NKRN59.48, NKRN59.41, 396038.107, 393220.54, Rwangume, 391046.14 and 391919.3. These genotypes will be used in the development of potato cultivars that are high yielding with oblong to oval tuber shape, smooth texture, cream flesh, and red or pink skin colour.

Conclusions

The present study provided an analysis of the diversity among 48 potato genotypes evaluated at two locations in Uganda. From the studied traits, number of days to flowering, duration of flowering, pollen production, tuber shape, eye depth and flower frequency were used to select possible parents for further breeding purposes. The results of this study indicated that tuber shape, a very important trait in potato, is only associated with eye depth. Flesh and skin colour can be simultaneously improved given their relation with eye colour. Plant height and duration of flowering can be used to improve yield. Traits that were negatively correlated with yield should be independently selected for. Variation for the different traits exhibited by genotypes in this study should be exploited in breeding to obtain potato cultivars with desirable qualities. Additional studies on these genotypes should focus on other yield-related parameters, such as number of tubers per plant, average weight per tuber and number of secondary stems per plant. In addition, the processing aspects of these genotypes for quality product development should be considered.

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References

Abebe T, Wongchaochant S, Taychasinpitak T. 2013. Evaluation of specific gravity of potato varieties in Ethiopia as a criterion for determining processing quality. *Kasetsart Journal of Natural Science 47*: 30–41.

Acquaah G. 2007. *Principles of plant genetics and breeding*. Oxford: Wiley-Blackwell.

Arslanoglu F, Aytac S, Oner K. 2011. Morphological characterization of the local potato (*Solanum tuberosum* L.) genotypes collected from the Eastern Black Sea region of

Turkey. *African Journal of Biotechnology* 10: 922–932.
CIP (Centro Internacional de la Papa). 2016. Potato facts and figures. Available at http://cipotato.org/potato/facts/ [accessed 15 July 2016].
Datta S, Das R, Singh D, Thapa U, Mundal AR. 2014. Study of correlation among various characters of different potato (*Solanum tuberosum L.*) germplasm. *Journal of Crop and Weed* 10: 186–188.
Elameen A, Larsen A, Klemsdal SS, Fjellheim S, Sundheim L, Msolla S, Masumba E, Rognli OA. 2011. Phenotypic diversity of plant morphological and root descriptor traits within a sweet potato, *Ipomoea batatas* (L.) Lam., germplasm collection from Tanzania. *Genetic Resources and Crop Evolution* 58: 397–407.
FAOSTAT. 2016. Production statistics. Available at http://faostat.fao.org [accessed 11 July 2016].
Forbes G. 2012. Using host resistance to manage potato late blight with particular reference to developing countries. *Potato Research* 55: 205–216.
Hirut GB. 2015. Genetic analyses of drought tolerance and resistance to late blight among potato genotypes. PhD Thesis. University of KwaZulu-Natal, South Africa.
Jacoby A, Labuschagne MT, Viljoen CD. 2003. Genetic relationships between southern African *Solanum retroflexum* Dun. and other related species measured by morphological and DNA markers. *Euphytica* 132: 109–113.
Kaguongo W, Gildemacher P, Demo P, Wagoire W, Kinyae P, Andrade J, Forbes G, Fuglie K. 2008. Farmer practices and adoption of improved potato varieties in Kenya and Uganda. *Social Sciences Working Paper* 2008-5. Lima: CIP.
Kakuhenzire R, Lemaga B, Kashaija IN, Ortiz O, Mateeka B. 2013. Effect of *Crotalaria falcata* in crop rotation and fallowing on potato bacterial wilt incidence, disease severity and latent infection in tubers and field soil. *Biopesticide International* 6: 182–194.
Kaushik SK, Bhardwaj V, Singh PH, Singh BP. 2007. Evaluation of potato germplasm for adaptability and resistance to late blight. *Potato Journal* 34: 43–44.
Korzun V. 2003. Molecular markers and their application in cereals breeding. *Cell and Molecular Biology Letters* 7: 811–820.
Low J. 1997. Potato in southwest Uganda: threats to sustainable production. *African Crop Science Journal* 5: 395–412.
Luthra SK. 2001. Heritability, genetic advance and character association in potato. *Journal of Indian Potato Association* 28: 1–3.
Manivel P, Kumar V, Bhardwaj V, Pandey SK, Kaushik SK. 2005. Evaluation of flowering characteristics in Indian potato varieties. *Indian Journal of Horticulture* 62: 340–345.
Mohammadi S, Prasanna B. 2003. Analysis of genetic diversity in crop plants salient statistical tools and considerations. *Crop Science* 43: 1235–1248.
Mostafa A, Felenji H. 2011. Evaluating diversity among potato cultivars using agro-morphological and yield components in fall cultivation of Jiroft area. *American-Eurasian Journal of Agriculture and Environmental Science* 11: 655–662.
Muhinyuza JB, Shimelis H, Melis R, Sibiya J, Gahakwa D, Nzaramba MN. 2015. Yield response and late blight reaction of potato genotypes in Rwanda. *American Journal of Potato Research* 92: 10–22.
Muthoni J, Shimelis H, Melis R. 2014. Study of genetic relationship among Kenyan cultivated potato clones using SSR markers. *Australian Journal of Crop Science* 8: 502–508.
Muthoni J, Shimelis H, Melis R, Kabira J. 2012. Reproductive biology and early generation's selection in conventional potato breeding. *Australian Journal of Crop Science* 6: 488–497.
Pandey SK, Singh SV, Manivel P. 2005. Genetic variability and causal relationship over seasons in potato. *Crop Research* 29: 277–281.
Payne RW, Murray DA, Harding SA, Baird DB, Soutar DM. 2011. *An introduction to GenStat for Windows (14th Edition)*. Hemel Hempstead: VSN International.
Rukundo P, Shimelis H, Laing M, Gahakwa D. 2015. Phenotypic characterization of sweetpotato genotypes grown in East and Central Africa. *South African Journal of Plant and Soil* 32: 77–86.
Sandhu SK, Gopal J. 2006. Assessment of genetic diversity in potato germplasm for spring season crop. *Crop Improvement* 33: 78–83.
Simmonds NW. 1962. Variability in crop plants its use and conservation. *Biological Reviews* 37: 422–465.
Tesfaye A, Lemaga B, Mwakasendo JA, Nzohabonayoz Z, Mutware J, Wanda KY, Kinyae PM, Ortiz O, Crissman C. 2010. Markets for fresh and frozen chips in the ASARECA region and the potential for regional trade: Ethiopia, Tanzania, Rwanda, Kenya, Burundi and Uganda. *Social Sciences Working Paper* 2010-1. Lima: CIP.
Tseng YT, Lo HF, Hwang SY. 2002. Genotyping and assessment of genetic relationships in elite polycross breeding cultivars of sweet potato in Taiwan based on SAMPL polymorphisms. *Botanical Bulletin of Academia Sinica* 43: 99–105.
Yoshida T. 2004. Sorghum diversity evaluated by simple sequence repeat (SSR) markers and phenotypic performance. *Plant Production Science* 7: 301–308.

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