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Evaluation of Acceptable Yield for Potato Tuber Genotypes Based on Specific Processing Traits

Raphael Butler Chepken

Kachwekano Zonal Agricultural Research and Development Institute, National Agricultural Research Organization, Kabale, Uganda

ABSTRACT

In Uganda few studies have characterized processing attributes on dry matter content and other morphological attributes among genotype sets, and limited reports on reducing sugars as Nuwamanya et al., only quantified reducing sugars on only 3 released potato varieties. The limited research focus on tuber processing qualities has led to a demand deficit for potato varieties to serve the potato industry. It's against this background, that this study was undertaken to determine the phenotypic variation among 30 potato genotypes on the basis of desirable tuber processing attributes (dry matter content and reducing sugars) so as to characterize and identify potential parental genotypes for future breeding purposes.

KEYWORDS

Dry matter content; Reducing Sugars; Potato; Uganda.

1. Introduction

Potato (Solanum tuberosum) is an important staple crop, and globally it's the fourth after maize, rice and wheat [1]. Potato in the highland regions of many African countries is a major food and cash crop which is mainly grown by smallscale farmers. In Uganda the crop is mainly grown in the highland areas 1500 - 3000 meters above sea level (masl) in the districts of Kabale, Kisoro and Mbale [2, 3]. Kabale and Kisoro account for over 60% of the country potato production [3, 4]. In the year of 2017, Uganda had an annual potato production of 173,244 tons harvested from an area of 39,374 ha [5].

The consumer demand for potato in Uganda is increasing [6]. This is mainly due to the ever expanding potato processing value chain, where by the potato is processed into chips/French fries and crisps [6]. Despite the processing demand, the biggest bottle neck to the expansion of the Ugandan potato processing industry is the unavailability of adequate stocks of good quality tubers from the potato farmers that have desirable internal processing attributes. To be sustainable, the potato processing industry requires varieties with superior attributes in high dry matter content and low reducing sugars. But such varieties are limited in Uganda.

The basic starting point in improving economically important traits in a crop like potato is characterizing or phenotyping for those traits in a set of genotypes to assess the levels of genetic variations that can be used in the crop improvement program [7]. The genetic variation of a population is a prerequisite for an effective plant breeding program to meet its diversified goals [8, 9]. Genetic variation is a useful and essential factor in crop improvement especially when choosing suitable parents with complimentary traits for a hybridization strategy to develop better potential cultivars [9, 10]. Different methods have been deployed to carry out phenotyping and these methods have based data on plant morphology, agronomical performance, biochemical and molecular markers [7, 11, 12]. Phenotyping of tuber processing attributes especially dry matter content and reducing sugars usually involves some biochemical analytical tools [13, 14].

2. Materials and Methods

2.1 Study Site

The study was carried out at Kachwekano Zonal Agricultural Research and Development Institute (KAZARDI) located at 1° 15′07.04′′S 29°56′25.06′′, 2,204 meters above sea level (m.a.s.l). The soils are classified as typicpalehumult [18], with bi-modal rainfall pattern separated by a dry spell ranging from 30 to 60 days.

2.1.1 Germplasm material

Table 1. Characteristics of germplasm used in the study.

Genotype	Tuber shape	Skin colour	Eye depth	Yield
391046.14	Oval	Cream	shallow	HY
391919.3	long-oval	Purple	medium	LY
392657.8	Oval	Pink	shallow	HY
393077.54	Globe	White	medium	HY
393220.54	Globe	White, pink points	shallow	HY
394895.7	long-oval	White	shallow	MY
395011.2	Oval	White	deep	MY
395015.6	Oval	Red	shallow	HY
395017.14	Oval	White	shallow	LY
395077.12	Globe	White, pink points	shallow	MY
395096.2	Globe	White, pink points	medium	HY
395109.34	short-oval	White, pink points	medium	LY
395112.32	Globe	Pink	shallow	HY
395438.1	short-oval	Red	shallow	MY
396077.159	n/a	n/a	n/a	MY
395017. 229	n/a	n/a	n/a	MY
CRUZA	short-oval	White	shallow	MY
KINIGI	Globe	Purple	deep	MY
NAKPOT1	Globe	White	shallow	MY
NAKPOT5	Oval	White	shallow	HY
NAROPOT 1	Globe	Pink	medium	HY
NAROPOT 3	Globe	Red	medium	HY
nkrk19.10	Globe	Pink	shallow	HY
nkrk19.17	short-oval	Pink	deep	HY
nkrn59.41	Oval	White	shallow	LY
nkrn59.48	Oval	Pink	shallow	MY
nkrn59.58	Oval	Pink	shallow	MY
RUTUKU	Oval	Red	shallow	HY
RWANGUME	Globe	Red	medium	MY
RWASHAKI	Globe	Pink	deep	MY

HYis high yield (above 30 tha-1), MY is moderarate yield (15 – 30 tha-1), LY is low yield (below 15 tha-1), R is resistant, MR is moderate resistant and n/a is not available [11, 19].

Thirty potato genotypes were used in this study. The germplasm was sourced from the potato breeding program at KAZARDI as summarized in Table 1.

2.1.2 Experimental design and trial establishment

The field experiment was planted on a strip terrace under a 5×6 alpha lattice experimental design comprising of thirty potato genotypes that were replicated three times.

Randomization was generated from breeding management long and 1.4 meters wide with 1 meter spacing between plots and about 2 meter spacing between replications. Two row plots of ten tubers each were furrow drilled for planting at a spacing of 75×30 cm. At planting, NPK compound fertilizer (composed of; 17% nitrogen: 17% phosphorus: 17% potassium) was applied in the planting furrows at a rate of 100 kg ha-1. All agronomic practices, pest and disease management were done as recommended.

2.1.3 Data collection

Data were collected on yield parameters, dry matter content and reducing sugars. Yield parameters collected included counting number of tubers per plant, tuber weight per plant and consequently total tuber yield in tons per hectare (tha-1) per genotype was calculated as a function of number of total tubers per plot, total weight of tubers per plot and converted to tons per hectare on an adjusted model of plant population per hectare according to plant spacing used per plot in the experiment. The average weight per tuber was got from a function of the number of tubers per plant, tuber weight per plant. Using a method as reported by Esuma et al., [20], dry matter content was quantified were by 400 g of potato sample of each genotype per plot was weighed, washed under running water and dried with a cloth towel. The dried potato tubers were cut and chopped into smaller pieces and mixed manually to get a homogeneous sample. Approximately 200 gm of each homogenous sample were taken in duplicates for measurement of dry matter content by drying the sample in an oven to constant weight at a temperature of 105°C. The dried samples were reweighed and the dry matter content was calculated by the formula; (Dry weight of sample/fresh weight of sample) X 100. The average calculation from the duplicate samples was taken as dry matter content per genotype per plot. The 2, 4dinitrophenol solution method as described by Bisognin et al., [14] was used to estimate reducing sugars. Approximately two potato tubers per genotype per plot were washed under running water, dried with a cloth towel and the tubers peeled. Then the peeled tubers were chopped into smaller pieces and mixed manually to create a homogenous sample. This chopped sample of each genotype per plot was oven dried at 60°C to constant weight. The dried sample was milled into flour using a seed grinder. For reducing sugars 1 g of each milled sample per genotype was weighed into a test tube as duplicates, 5ml of distilled water was added to the sample. The samples were then vortexed to mix thoroughly and centrifuged at 5000 revolutions per minute (rpm). From the supernatant 2 ml was added to 0.5 ml of 2, 4-dinitrophenol solution (0.038M). The samples were incubated at 70°C in a water bath for 6 minutes then cooled off under tap running water. Then reducing sugar absorbencies were read at 600 nm spectrophotometrically. To estimate the concentrations of the reducing sugars a glucose standard curve was used. The procedure to getting the standard curve was gotten by weighing 0.2 g of pure glucose into a test tube and dissolving it in 4 ml of distilled water. From this solution 2 ml was pipetted into a fresh test tube and topped with 2 ml distilled water to make 4 ml of solution. Subsequently the procedure was repeated for up to 9 dilutions.1 ml of each diluted solution was picked off in duplicate and 3 ml of distilled water was added consequently. For each dilution 0.5 ml of 2, 4-dinitrophenol solution (0.038M) was added, centrifuged and absorbencies were read at 600nm spectrophotometrically. From the corresponding glucose concentrations to absorbencies a standard glucose curve was generated.

2.1.4 Data processing and statistical analysis

Data for number of tubers per plant, tuber weight per plant, average weight per tuber, total tuber yield, dry matter content and reducing sugars was subjected to analysis using Restricted Maximal Likelihood (ReML) and generalized analysis of variance (ANOVA) approaches in Genstat 18th edition. Genotypes were

considered as fixed, and replication, blocks nested in replication were random factors. The predicted genotype mean performance under each traits found significant from the analysis was separated with Lease Significant Difference (LSD's) at an alpha level of 0.05.

3. Results

3.1 Analysis of Variance Source of variation

Average weight per tuber, and Total tuber yield is :

The performance of different genotypes for dry matter presented. Dry matter content had an overall mean. The analysis of variance revealed highly significant effects (P<0.001), of the genotype for, reducing sugars, number of tubers, tuber weight per plant, average weight per tuber and total tuber yield while dry matter content was significant (p<0.01) among the genotypes.

Of 19.19% among the experimental genotypes and the genotypes with the required dry matter content threshold were 395438.1 (21.85%), 395096.2 (20.99%), 3950077.12 (20.97%), 395015.6 (20.87%), NAROPOT 3 (20.57%), Kinigi (20.26%) and 393220.54 (20.19%), while the genotype with the lowest dry matter content was 395109.34 at 16.49%. Reducing sugars had an overall mean of 3.9 (mg/g/db) with 73% of the genotypes evaluated being below 5 (mg/g) and genotype 395438.1 had the lowest reducing sugars value of 0.4 (mg/g/db), while nkrk19.17 with 11.3 (mg/g/db) was the highest. Among the experimental genotypes, the overall mean number of tubers per plant was 8 tubers and Cruza had the highest number of tubers at 14 tubers. The genotype with the lowest number of tubers was nkrn59.41 with 6 tubers. The overall mean of tuber weight per plant was 0.64 kg and among the experimental genotypes, 392657.8 had the highest weight per plant of 1.02 kg and 391046.14 with 0.35 kg was the genotype with lowest tuber weight per plant. Average weight per tuber had an overall mean of 82.8 g among the experimental genotypes and 395109.34 with the highest average weight per tuber at 133.1g. The genotype with the lowest average weight per tuber was 391046.14 (35.5 g). Total tuber yield had a mean of 31.7 tha-1 among the experimental genotypes and 392657.8 was the highest yielder at a total tuber yield of 50.4tha-1. The genotype with the lowest total tuber yield was 391046.14 (17.1 tha-1)

Table 2. Performance of the genotypes for reducing sugars, dry matter content, number of tubers, tuber weight per plant, average weight per tuber, and total tuber yield, evaluated at Kachwekano from January –May 2018.

Table 4. Phenotypic correlation between average weight per tuber, number of tubers per plant, tuber weight per plant, total tuber yield

Genotype	RS (mg/g/db)	DMC (%)	NT	TTY (tha-1)
391046.14	3.7	19.46	9	17.1
391919.3	3.7	18.64	12	35.7
392657.8	3.1	19.28	9	50.4
393077.54	1.8	18.49	7	20.3
393220.54	4.9	20.19	12	49.5
394895.7	4.2	18.75	6	26.8
395011.2	6.1	19.74	8	27.3
395015.6	1.8	20.87	9	38.5
395017.14	3.1	19.06	9	47.3
395017.229	8.1	19.49	9	42.4
395077.12	2.1	20.97	12	38.6
395096.2	2.0	20.99	10	30.8
395109.34	2.2	16.49	7	39.7
395112.32	5.2	19.02	7	43.7
395438.1	0.4	21.85	7	24.9
396077.159	1.6	18.89	6	27.6
CRUZA	2.4	19.54	14	41.5

KINIGI	2.6	20.26	7	28.1
NAKPOT 1	4.8	19.73	8	37.5
NAKPOT5	3.1	18.94	6	23.8
NAROPOT 1	1.9	18.41	9	25.6
NAROPOT 3	2.1	20.57	7	28.1
nkrk19.10	1.6	17.50	7	22.8
nkrk19.17	11.3	18.04	7	23.9
nkrn59.41	6.7	19.49	6	26.0
nkrn59.48	10.2	17.38	6	19.7
nkrn59.58	1.5	19.71	7	19.2
RUTUKU	5.8	17.16	6	32.4
RWANGUME	6.6	17.72	10	31.2
RWASHAKI	2.1	19.23	8	31.7
MEAN	3.9	19.19	8	31.7
SEM	0.19	0.77	0.8	3.85
LSD	0.541	2.385	2.3	11.08

4. Discussion

The study evaluated thirty potato genotypes for dry matter content, reducing sugars, yield and yield related traits for one season from a major potato growing location in the western highland region of Uganda. The evaluated genotypes varied significantly for present dry matter content, reducing sugars, number of tubers per plant, tuber weight per plant, average weight per tuber and total tuber yield. The highly significant differences observed implies that there is genetic variability amongst the materials that were used in the study. This is important since it justifies the basis for making improvements in any breeding program. Selection for the traits of interest can be done based on the mean performance of the genotype clones. The observed significant variations among the genotypes for dry matter content and reducing sugars are a good opportunity for researchers to select the genotypes for production that fit the market and processing demand. Many other researchers also reported the presence of significant differences among potato genotypes for dry matter content and reducing sugars [13, 21-23].

Genotypes with a dry matter content of ≥ 20% were justified by Abong et al., [13] as genotypes that produced acceptable fried products. This was also observed by Asmamaw and Tekalign, [22] who demonstrated that cultivars with a ≥ 20%dry matter content maintained good crisp taste. Potatoes that have a higher dry matter content ≥ 20% are preferred for frying because they result in better texture, higher yields and lower frying oil absorption in the finished product [24]. In this study, genotypes produced an average of 19.19% dry matter content but the genotypes that had ≥ 20% dry matter content were 395438.1, 395096.2, 395077.12, 395015.6, NAROPOT 3, Kinigi and 393220.54 (Table 3) and can be qualified for frying based on their dry matter content of ≥ 20% as was justified by the other studies [22, 24]. In this study out of the thirty evaluated genotypes nine were released varieties from the years of 1962 to 2016 i.e. Rutuku (1962), Rwashaki (not available), and Rwangume (2016) [19], but it's only NAROPOT 3 and Kinigi that were in the required dry matter content threshold of ≥ 20%, even Rwangume a variety reported by Namugga et al.,[3] as the most widely grown variety was below the dry matter content threshold. These finding concurs with Tesfaye et al., [6] who had reported there being few varieties that possessed desirable processing attributes in the Ugandan potato industry. But with the advanced clones performing better than released varieties in terms of dry matter content, these can be used in the improvement of processing attributes in the potato breeding program. The dry matter content differences among the genotypes can be attributed to the inherent differences among the genotypes, of which it has been reported to be genetically controlled [25-27].

Low reducing sugar is a requirement to minimize color development during the frying of potato products [24, 28]. Researchers have reported that potato tubers having low levels of reducing sugars can be used for frying [24, 28, 29]. Pedreschi, [24] reported 5 mg per gram of potato as the upper limit to have quality fried potato

chips or French fries. In this study 73% of the genotypes evaluated were below 5 (mg/g) and only eight of the evaluated genotypes were above this limit, these being 395112.32, Rutuku, 395011.2, Rwangume, nkrn59.41, 395011.229, nkrn59.48 and nkrk19.17 (Table 3). It has also been recommended that potato reducing sugar concentration of less than 2.5 - 3 mg/g is required to minimize colour development during frying of potato crisps [24]. The colour at frying is generated due to the non enzymaticmaillard browning reaction [30-32]. In the evaluated genotypes, fourteen of them were less than 3 mg/g of reducing sugars and of these, five were released varieties these being NAROPOT 1, Rwashaki, NAROPOT 3, Cruza, and Kinigi while nine were advanced clones, 395438.1, nkrn59.58, nkrk19.10, 396077.159, 395015.6, 393077.54, 395096.2, 395077.12 and 395109.34 (table 3). The rage of reducing sugars was from 0.4 - 11.3 (mg/g/db) (table 3), this variation could be influenced by a combination of factors but mainly due to the inherent genetic differences within the genotypes as was justified by Singh and Kumar,[30] but also the stage of maturity of the tubers has shown to influence the reducing sugar content [13].

Total tuber yield had a mean of 31.7 tha-1 and according to a classification by Namugga et al., [11] this is high yield. In general, higher total tuber yield is influenced by a both genotype and environment effect. This is true for yield related parameters [33]. The higher total tuber yield could be explained by genetic factor differences of the genotypes [19]. The high yield could also be due the fact that these genotypes in the study were selected also on the basis of there resistance to blight (Table 1), and other studies have also reported good yielding parameters of the genotypes especially due to their resistance to late blight [19, 33, 34]. But that notwithstanding also the relatively good weather growing conditions especially rainfall and the late onset of the late blight had an influence on the yield performance of these genotypes. Genotypes with the highest number of total tubers were not necessary the highest yielders implying that total tuber yield is predominantly influenced by average weight per tuber and tuber weight per plant. This same phenomenon has also been reported in other studies [19].

The significant positive correlation between average weight per tuber, number of tubers, tuber weight per plant with total fresh tuber yield indicate that they positively affect yield, and such finding have also been reported by other studies [19, 33]. Dry matter content had a significant negatively correlation with reducing sugars. This is in agreement with several other studies who found an inverse correlation between dry matter content and reducing sugars [29, 35, 36]. The differences in dry matter content and reducing sugars in each genotype are a result of the enzyme biochemical functionality of starch being hydrolyzed into reducing sugars [37]. Starch being the major component of dry matter about 65-80% [24], and is it this starch that is enzyme synthesized to reducing sugars [37].

5. Conclusion

Genotypes in this study showed significant differences for dry matter content, reducing sugars and so did yield and yield related traits. The significant differences for dry matter and reducing are a sign of genetic variability for the traits which can be utilized by the breeding program to create new varieties. There was great variation among the genotypes and the study was able to identify genotypes with good dry matter content like, 395438.1 (21.85%), 395096.2 (20.99%), 3950077.12 (20.97%), 395015.6 (20.87%), NAROPOT 3 (20.57%), Kinigi (20.26%) and 393220.54 (20.19%) (Table 3) and reducing sugars with genotypes like 395438.1, nkrn59.58, nkrk19.10, 396077.159, 395015.6, 393077.54, 395096.2, 395077.12 and 395109.34 (table 3). These finding were able to answer our objective of characterizing potato genotypes in order to identify those with desirable tuber processing attributes (dry matter content and reducing sugars). There were more advanced clones than the released varieties with recommended required levels for potato processing in terms of high dry matter content (≥20%) and reducing sugars (≤ 3 mg/g) [24]. This variation of the traits can be further studied for use in the breeding programs to improve processing abilities of potato varieties in Uganda.

From this study, genotypes 395438.1, 395096.2, 3950077.12, 395015.6, 393220.54, NAROPOT 3 and Kinigi were largely selected for possession of desirable processing tuber attributes which can be recommended for

breeding purposes and official variety release of the selected advanced clones after yield stability tests. Additional studies on these genotypes should focus on gene action, genotype by environment interaction of dry matter content and reducing sugars. Also other biochemical aspects like rapid viscoamylographic analysis (RVA) and molecular studies for quality product development should be considered.

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