# Relationship among yield components of eight introduced yellow and orange fleshed sweetpotato in Rwanda

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Sweetpotato (*Ipomea batatas*) is a staple food grown and consumed through Rwanda. It is considered a food security crop for its ability to be harvested continuously for home consumption and its ability to grow in soils where cereals and some leguminous crop fail due to poor growth conditions. As in most Sub-Saharan countries, yields are generally low due to poor adaptability of the available sweetpotato varieties. Orange-fleshed sweetpotatoes have high total carotenoids and are seen as a cheaper and complementary source of vitamin A for the rural poor families who are the most vulnerable to vitamin A deficiency. This study therefore was conducted to evaluate the relationship of yield components existing among 8 yellow and orange fleshed introduced sweetpotato genotypes namely Cacearpedo that was considered as a control, Naspot-5, Carrot-C, Gueri, Kazinga, K 118, K135, and Ukerewe in terms of resistance to sweetpotato virus diseases, *alternaria*, yields, in mid altitudes conditions of Rwanda for 2 consecutive seasons 2008A and 2008B. Genotype Kazinga was very susceptible to the attack of *alternaria* and virus, also had a low capacity to sprout and to reach the maturity stage safely. Whereas varieties Ukerewe, Carrot-c, K135 and K118 respectively showed a considerable resistance against SPVD and alternaria diseases. Variety Carrot-c responded positively in terms of yield comparatively to Cacearpedo with 14.05T/ha while Cacearpedo had 12.76 T/ha. Varieties like Carrot-c, Cacearpedo, Ukerewe and Gueri were respectively the first fourth in marketable roots. Varieties Carrot-c, Cacearpedo, K118 and Naspot-5 yielded high in term of total number of roots. A comparison for yielding components of these 8 sweetpotato genotypes showed a negative correlation between biomass and total roots yield, total dry matter and total roots yield. While, a positive correlation was found between number of marketable roots and total yield roots. This study shows that Ukerewe, Carrot-C, Cacearpedo, and Gueri are like to be adopted since they showed good agronomic performance.

**Keywords**: Yield components, orange fleshed sweetpotato, biomass, dry matter.

## Introduction

The importance of sweetpotato in daily Rwandan diets has to be underlined. According to Tardif (1993 et *al)* and Ndirigwe (2006), the sweetpotato is one among the two most crops (common beans and sweetpotato) which help so much in the traditional alimentation of many Rwandese.

The crop is cultivated throughout the country mainly by peasant farmers, and is especially important in densely populated areas of the plateau central of Rwanda (Mid altitude) ( Ferris *et al*., 2002). It is a flexible source of food as it can be grown on soils of limited fertility and is relatively drought tolerant. Also, planting and harvest periods are more flexible than those of maize and other cereals. Provided the importance of sweetpotato in Rwandan society, our study aimed at improving our farmer's varieties which are known to be low yielding, no resistant to a big range of pests and diseases varieties and poor in beta carotene a precursor of vitamin A. Eight exotic varieties already tested in sub Saharan countries, which are high nutrient value (yellow and orange-fleshed sweet potato varieties enriched in beta –carotene: a precursor of vitamin A which intervenes in eye-sight) were introduced in Rwanda for yield performance evaluation. Therefore, this study was conducted to evaluate the relationship of yield components existing among 8 introduced sweetpotato which namely *Cacearpedo that* was considered as a control, *Naspot-5, Carrot-C, Gueri, Kazinga, K 118, K135, and Ukerewe* in terms of resistance to virus, *alternaria* sweetpotato diseases, yields, in mid altitude conditions of Rwanda.

## Materials and methods

Eight new genotypes of sweetpotato which names are as follows*: Cacearpedo, Carrot-c, Naspot-5, Gueri, K118, K135, Kazinga* and *Ukerewe* were used in the study and were compared to *Cacearpedo* as check. The experiment was set up in a randomized complete block design with four replications at Rubona Station. The experiment was carried out at ISAR Rubona Station during 2008A and 2008B (lat. 2°29′ S, Long. 29° 46′E, and 1650masl) with the average temperature of 19°C and the annual rainfall average of 1271mm (ISAR, 2008). Trials were established at the beginning of the rainy season. The inter-row spacing was 80cm and spacing between ridges 30cm. Apical cuttings were planted on 4 ridges measuring 4.5 m long formed a single plot, resulting in plant population of 16 plants/ridge (64 plants/ plot). Cuttings were planted at a depth of ± 15 cm with at least 2 nodes underground in random completed block design (RCBD) with 4 replicates. Weeding and hilling up took place about one month after planting. At harvesting time, foliage weight was recorded and used to evaluate cultivars potential for providing planting material. Plants in the two central ridges of each plot were uprooted and used to estimate the marketable and unmarketable roots. Fresh roots were counted, weighted and graded into marketable (≥3cm of diameter) and unmarketable yield less than 3cm. ANOVA was performed using Genstat and Excel software was used to draw different graphs.

## Results and discussions

### *Yield of marketable roots (large roots)*

Results (Table 1) showed significant difference among genotypes at P>0.05 with 3 homogenous groups. Yield of marketable roots varied from 14.05 to 4.14 T/ha. Variety *Gueri, K118* and *Ukerewe* had recorded high weight of marketable roots than the control. Genotype *Kazinga* was the lowest variety in weight of marketable roots during the 2 seasons, implying that is no adapted.

**Table 1. Mean yield performance in T/ha of the 8 genotypes at Rubona during 2008A and 2008B**

| Genotypes | Yield T/ha | Homogeneous Groups |
|---|---|---|
| Carrot-c | 14.05 | A |
| Cacearpedo | 12.76 | ABC |
| Ukerewe | 12.20 | ABC |
| Gueri | 12.00 | ABC |
| Naspot-5 | 10.82 | ABC |
| K118 | 8.18 | BC |
| K135 | 7.43 | BC |
| Kazinga | 4.14 | C |

Lsd: 2,11

Results (not shown) showed that 96.8% of variation in total number of roots was explained by variation in roots weight. Considering the biomass of eight sweetpotato genotypes, the analysis of variance for biomass showed that genotypes varied highly among them at (p< 0.001). The mean separation showed that there are six homogenous groups. There is a highly significant difference among those genotypes. The variety *K118* ranked first in biomass yield and *Kazinga* ranked last (results not shown). The difference between the first three varieties and the check was highly significant. Different genotypes differ in number of roots and aptitude to yield (Mwanga *et al*., 2004) which all have a inheritance of genetic pool (Huaman, 1992). Different studies showed that genotypes with higher number of roots, generally provide at harvest time high yield (Ndolo *et al*., 2001; ATDT, 2002 and Ndirigwe, 2006).

Figure 1 shows that 93.09 % of variation in biomass was explained by variation in yield that was expressed in ton per hectare. Varieties which had a big number of biomass came last in yielding performance. *K118* recorded high biomass yield but was the third last in root yield .This also verifies for *K135*. A net negative correlation between biomass and yield was obvious. Those eight sweetpotato genotypes showed higher vigor of plants during growing period and remarkable resistance to virus and *alternaria* diseases. Varieties, *Carrot-c, Cacearpedo, Ukerewe, and Gueri,* showed excellent potential in terms of yield ton per hectare 14.05, 12.76, 12.20, and 12.00 respectively. The variety *Naspot-5* and *Kazinga* revealed higher sensibility to virus attack compared to *Cacearpedo (*check). The variety *Carrot-c* ranked first in terms of total number of roots, but it ranked last in terms of yield; this implies that *Carrot-c* has a big number of non marketable roots. The variety *Ukerewe* has performed well in all parameters. This study shows that *Ukerewe, Carrot-C, Cacearpedo, and Gueri* are like to be adopted since they showed good agronomic performance .They were also positive correlation between yield components.

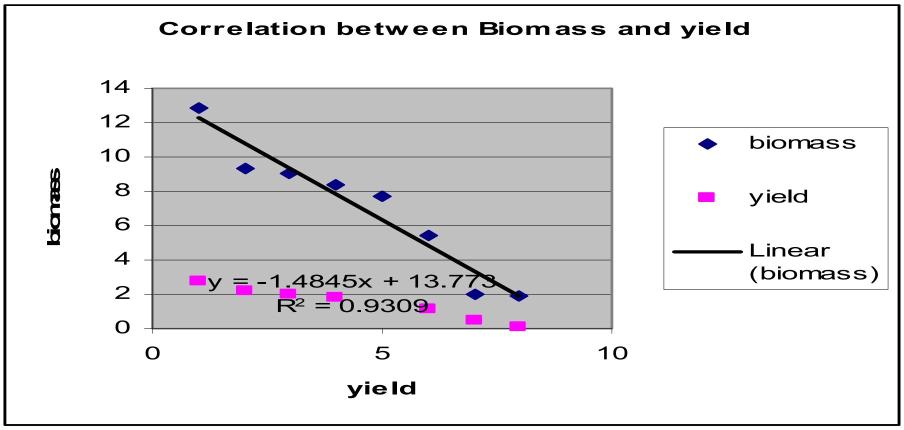


**Figure 1. Correlation between biomass and yield of 8 sweetpotato varieties**

### *Total dry matter of the 8 sweetpotato genotypes*

The analysis of variance of the total dry matter (result not shown) showed no significant difference among genotypes at P>0.05. The Total dry matter did not vary significantly among genotypes .The percentage of total dry matter rate varied from 36.8 to 28.7 %. Variety *K118* had high percentage of germination than the control. Genotype *K 118* was the lowest variety in total dry matter but in general, the exotic genotypes had high mean dry matter content compared to the check.

Figure 2 shows that 33.82 % of variation in dry matter was explained by variation in yield that was expressed in ton per hectare. Varieties with high total dry matter ranked low in yield record. This finding states that there was a negative correlation between total dry matter and yield. This is contrary with the findings made by Dixon and Nukenine (2001) and Grüneberg *et al.* (2003) who indicates respectively in cassava and sweetpotato that root dry matter content responds dynamically to changes in the environments as regards to starch deposition and mobilization which consequently increases the yield. In conclusion, a comparison for yielding components of these 8 sweetpotato genotypes showed a negative correlation between biomass and total roots yield, total dry matter and total roots yield. While, positive correlation was found between number of marketable roots and total yield roots. This study shows that Ukerewe, Carrot-C, Cacearpedo, and Gueri are like to be adopted since they showed good agronomic performance.

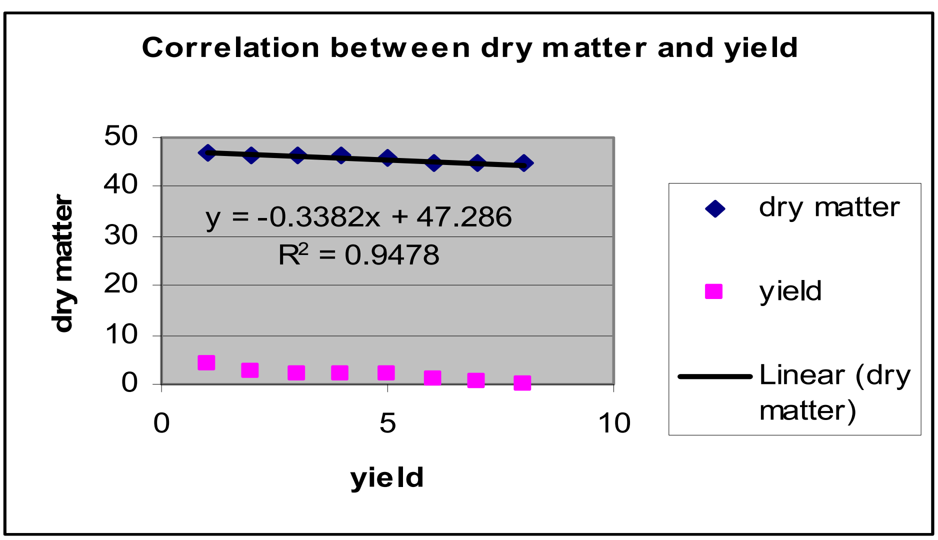


**Figure 2. Correlation between the total dry matter and yield**

Further studies are needed for orange fleshed sweetpotato varieties where high dry matter content varieties tend to give low yield compare to white fleshed sweetpotato genotypes.

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