# ASSESMENT OF NEW YACON (*SMALLANTHUS SONCHIFOLIUS*) GENOTYPES OBTAINED VIA INDIRECT SOMATIC EMBRYOGENESIS

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## INTRODUCTION

Yacon (*Smallanthus sonchifolius* (Poepp. & Endl.) H. Rob) is a perennial root crop of the *Asteraceae* family, originated in the Andean region. Yacon leaves, containing antioxidants, can be used for infusion. The plant is mainly cultivated for its succulent edible tuberous roots, that contain fructooligosaccharides of low caloric value. Yacon is vegetatively propagated and produces a reduced number of flowers and viable seeds, causing low genetic variability within the species and making conventional breeding methods difficult to perform. Nevertheless, biotechnological methods may be a valuable tool for breeding of this species. Biotechnological approaches such as induction of somaclonal variation have been employed for yacon breeding. Viehmannova et al. (2014) reported induction of somaclonal variation by somatic embryo derived plants of yacon using original explant material from Ecuador (ECU 41). The authors obtained four genetically distinct somaclones classified as B8, E1, E9 and F5, which were not evaluated in terms of morphology and chemical composition. The aim of this study was to evaluate these four new genotypes and to determine whether somaclonal variation can be used for production of plants with altered morphological and chemical traits compared to the original plant from which they were obtained. The study was carried out to determine if somaclonal variation could be an effective tool for yacon breeding.

## METHODOLOGY

Five plants of genotypes B8, E1, E9 and F5, along with five belonging to the control plant ECU 41 were transplanted from i*n vitro* conditions to greenhouse acclimatization, followed by transplantation to trial plots (Figure 1). Growth and development evaluation of the above grown parts such as height (cm), number of shoots and number of nodal segments of each individual belong to ECU 41 and the genotypes was done to determine the presence of morphological differences between newly obtained genotypes and control plant.

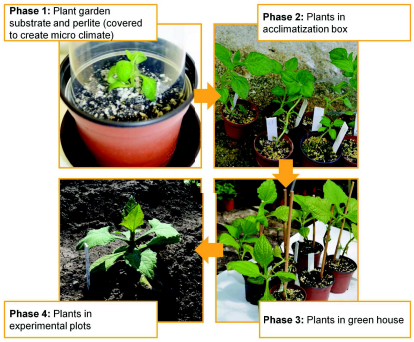


**Figure 1**. Phases of *ex vitro* transfer, plant acclimatization and transplantation to experimental plots

After a seven-month growing period, plants were harvested and the weight and number of tuberous roots along with the weight of rhizomes, were evaluated (Figure 2). This was followed by a chemical analysis of fructooligosaccharides (FOS) in tuberous roots which was done using Megazyme Fructan HK Assay Kit (Megazyme International Ireland LTD., Wicklow, Ireland) according to Kit instructions. Statistical analysis of data obtained from morphological evaluation of the above ground parts, tuberous roots and rhizomes, as well as chemical evaluation of FOS in tuberous roots of plants belonging to each genotype and control plant, was performed using one-way ANOVA and Turkey's HSD test ($P \leq 0.05$) [StatSoft STATISTICA 12.0].

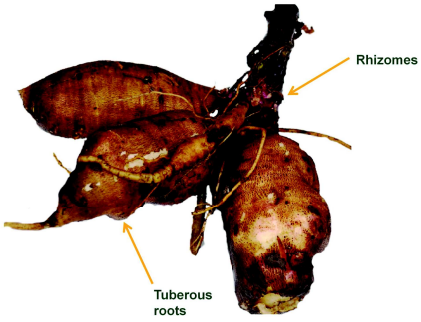


**Figure 2**. Tuberous roots and yacon rhizomes after harvesting

## RESULTS

Genotypes E1 and F5 grew at the same rate and produced comparably the same amount of nodal segments and shoots as control plant ECU 41. Genotypes B8 and E9, on the other hand, only showed improvement in the number of nodal segments and had the lowest values on other traits for the above grown plants parts (Table 1).

**Table 1. Evaluation of above grown parts of yacon cultivated in field**

| Genotypes | Final plan height (cm) (mean ± SE) | N° of nodal segments (mean ± SE) | N° of shoots (mean ± SE) |
|---|---|---|---|
| ECU 41 | 99.80 ± 6.86 a | 16.00 ± 0.31 a | 3.60 ± 0.40 a |
| E1 | 106.60 ± 4.05 a | 18.40 ± 0.81 ab | 5.20 ± 0.75 a |
| F5 | 97.40 ± 1.69 a | 17.80 ± 0.96 ab | 5.20 ± 0.48 a |
| B8 | 91.00 ± 2.72 a | 19.80 ± 0.58 b | 3.80 ± 0.48 a |
| E9 | 72.60 ± 2.24 b | 19.20 ± 0.75 b | 3.60 ± 0.24 a |

Mean values in a columns, followed by different letters, are significantly different according to the Turkey's HSD test ($P \leq 0.05$). SE=Standard error.

Results obtained from the assesment of tuberous root and rhizome showed that the control plant produced more individual tubers compared to the four genotypes evaluated. Nevertheless, the weigth of tuberous roots revealed that individual tubers belonging to the genotypes E1 and F5 were bigger than the ones produced by the control plant. All genotypes produced significantly higher amounth of rhizomes than the control plant.

Chemical analysis of fructooligosaccharides (FOS) showed that genotypes E1 and F5 had a significant increase of FOS in tuberous roots when compared to the control plant. Genotype B8 showed significant decrease of FOS, while E9 produced comparably the same amount as control plant (Table 2).

**Table 2. Evaluation of tuberous roots**

| Genotypes | N° of tuberous roots (mean ± SE) | Weight of tuberous roots (g) (mean ± SE) | Weight of rhizomes (g) (mean ± SE) | FOS content (100 g) (mean ± SE) |
|---|---|---|---|---|
| ECU 41 | 6.80 ± 1.15 a | 1,661.60 ± 158.50 a | 247.40 ± 44.87 b | 25.57 ± 1.24 b |
| E1 | 3.60 ± 0.67 b | 1,044.60 ± 219.31 ac | 436.00 ± 34.13 ab | 34.54 ± 0.57 a |
| F5 | 4.60 ± 0.40 ab | 1,554.60 ± 122.78 a | 309.20 ± 29.29 ab | 32.51 ± 1.06 a |
| B8 | 3.20 ± 0.73 b | 321.00 ± 61.35 b | 345.00 ± 38.14 ab | 16.58 ± 0.58 c |
| E9 | 3.60 ± 0.50 b | 850.20 ± 144.40 bc | 503.00 ± 98.15 a | 24.62 ± 0.92 b |

Mean values in columns, followed by different letters, are significantly different according to the Turkey's HSD test ($P \leq 0.05$). SE=Standard error.

Morphological assessment of leaves showed no significant differences in the parts of leaves belonging to each genotype compared to control plant ECU 41, however, they were slightly different in size (Figure 3).

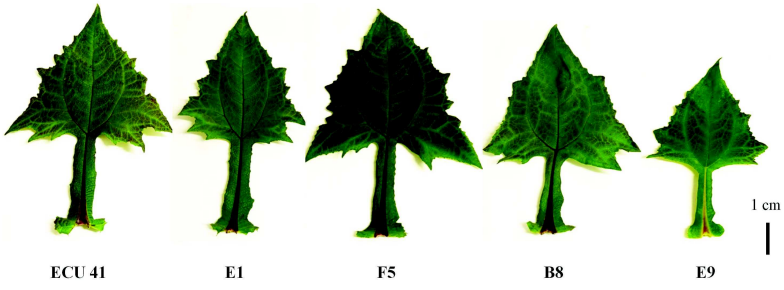


**Figure 3.** Individual control plant and genotypes leaves with visible size differences (bar=1 cm)

## CONCLUSION

The evaluation of the genetically variable genotypes revealed plants with improvements in morphological and chemical alteration when compared to the control plant from which they were obtained. Genotypes E1 and F5 revealed to be superior due to formation of larger tuberous roots, with significantly higher content of fructooligosaccharides and similarities in growth and development when compared to the control plant and other genotypes and may be used for further breeding purposes of the species. Genotypes B8 and E9, on the other hand, did not provide satisfactory results compared to the control plant and may not be used for further breading.

Due to improvements in desirable traits such as fructooligosaccharide content in tuberous roots and certain morphological characteristics of the plants, it may be concluded that induction of somaclonal variation could be a valuable tool for yacon breeding. After mass production of new genotypes and careful individual selection, superior yacon plants with highly improved desired traits may be obtained.

## ACKNOWLEDGEMENTS

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## REFERENCES

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