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Assessment of New Yacon (*Smallanthus sonchifolius*) Genotypes Obtained via Indirect Somatic Embryogenesis

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Abstract

Yacon [*Smallanthus sonchifolius* (Poepp. and Endl.) Robinson] is a perennial root crop belonging to the *Asteraceae* family, and originating in the Andean regions. It is cultivated for its edible roots that contain fructooligosaccharides (FOS) of inulin type with low caloric value. The aim of this study was to evaluate morphologically and chemically four new yacon genotypes, obtained via indirect somatic embryogenesis within a previous research carried out by Viehmannova et al. (2014). These new somaclones were classified as B8, E1, E9 and F5, and were obtained from an octoploid plant classified as ECU 41, which was also used as the control plant in our study. Five plants from each genotype were transferred *ex vitro*. After acclimation of plants in the greenhouse, the plants were planted to the trial plots. At the end of the vegetation, plant height, number of nodes, tuberous root production, weight of rhizomes and the content of fructooligosaccharides were evaluated. Significant differences among genotypes were found for some morphological characteristics and FOS content in tuberous roots. Overall, the most promising results provided genotypes E1 and F5 producing plants comparably high as control, with similar number of nodes and yields, however with significantly higher FOS content in tuberous roots. On the contrary, genotypes B8 and E9 provided in most characteristics the lowest values of all studied genotypes. Surprisingly, all the new genotypes produced rhizomes with higher weight than the control plant. Based on these results can be concluded that genotypes E1 and F5 demonstrated promising improvements when compared to the control plant and they might be used for further breeding of yacon. Moreover, mass production of new somaclones followed by thorough selection might represent an effective tool for breeding of yacon.

Keywords: Fructooligosaccharides, plant morphology, regenerants, *Smallanthus sonchifolius*, somaclonal variation

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