Sweet potato root waste: evaluation of a culture medium to produce xylanases from *Cellulosimicrobium* sp. CO1A1

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Abstract

The development of bioprocesses using agro-industrial waste is one of the most interesting challenges in biotechnology today, as it leads to the reuse of waste in an environmentally responsible way and the development of high value-added products. In the San Pedro region, sweet potato production generates considerable volumes of waste, as approximately 40% of the total production is discarded because it does not meet the requirements for commercialisation. In this study, the ability of the strain *Cellulosimicrobium* sp. CO1A1 to produce xylanases in a medium formulated with sweet potato root residues was evaluated; xylanase being an enzyme of great industrial application.

Cellulosimicrobium sp. CO1A1 was grown in minimal saline medium containing 5 % (w/v) sweet potato root extract, at 135 rpm and 25 °C. Xylanase activity was determined using beech xylan (1%) as substrate at 50 ºC, reducing sugars released were determined by the Nelson-Somogyi method. Several assays were performed in order to evaluate xylanase activity, such as the analysis of cell fractions (supernatant -extracellular activity-, cell pellet -cell-associated activity- and cell homogenate -intracellular activity-); culture samples taken at 2, 5 and 7 days of incubation; and media formulated with different sweet potato varieties (Arapey, Beauregard, Covington, Selecta, Morada, Boni). In addition, the xylanase reaction was carried out in two buffer conditions, sodium citrate (50 mM, pH 5.2) and sodium phosphate (50 mM, pH 6.8).

The results showed that although *Cellulosimicrobium* sp. CO1A1 showed growth in the medium formulated with sweet potato root, thus proving that it has the ability to use sweet potato root as a carbon source, it did not show the ability to produce xylanases under the conditions tested, unlike other strains of the genus *Cellulosimicrobium* reported.

Keywords: Sweet potato residues, xylanases, *Cellulosimicrobium* sp.