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cre. It was first described as a regulator of antibiotic, heavy metals and organic solvent resistance, and some results suggest that it could affect the redox state of the cells and carbon flow. Because of this, it is a good target for genetic manipulations to improve the synthesis of PHB. The growth of wild-type *E. coli* and a mutant lacking the *rob* regulator in aerobic and microaerobic conditions in cultures containing glucose or glycerol as a carbon source were characterized. Deletion of *rob* did not have a significant effect on growth or production of PHB in the conditions tested. On the other hand, overexpression of *rob* has been shown to confer multidrug, organic solvent and heavy metal resistance. To assess the effect of an overexpression of *rob*, we cloned the *rob* gene under an inducible promoter in a plasmid compatible with the one that carries the *pha* genes, in order to be able to maintain both plasmids in the recombinant. This plasmid permits the analysis of the effect of the overexpression of *rob* on growth and PHB synthesis in recombinant *E.coli*.

BF-P15

BIOETHANOL PRODUCTION FROM SUGAR BEET PRODUCED IN SAN JUAN: SUBMERGED AND SOLID - STATE FERMENTATION.

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Sugar beet (SB) *(Beta vulgaris)* is an appropriate crop to perform bioethanol production by direct fermentation (without previous hydrolysis) of its sugars (sucrose). In San Juan, SB has been proposed as raw material to producing bioethanol, but there is no information about performance of SB locally produced. In this work, we report laboratory scale bioethanol production by *Saccharomyces cerevisiae* PM16, in submerged fermentations (SmF) of sugar beet juice (SBJ), and solid-state fermentations (SSF) of milled sugar beet (MSB). SmF were carried out in 250 ml Erlenmeyer flasks containing 100 ml of sterile SBJ; SSF were done placing in Petri dishes about 50 g sterile MSB (particle size 1 x 10 mm, water content 0.59 g/g). Both of the fermentation media, containing 255 mg/g fermentable sugars, were inoculated with 5 x 10^7 cells/g, and incubated in anaerobic environment, at 28 ^oC, for 72 h. Results: time-courses of viable cells, carbon dioxide evolution, fermentable sugar content, and ethanol concentration are presented. Also, enzyme activities xylanase and polygalacturonase were measured. Maximum ethanol concentration was attained at 48 h of cultivation: 58 mg/g for SmF and 72 mg/g for SSF. Ethanol yield based on substrate consumed was about 0.4 g/g (78 % of the theoretic al yield) for SmF and 0.7 g/g for SSF. Polygalacturonase activity reached 6.0 U/ml for SmF, and 24,64 U/ml in the liquid contained in the SSF; while for xylanase activity, 0.38 U/ml in SmF and 6.19 U/ml in SSF were found. As a conclusion, high concentrations and yields were attained in SSF. Also, an important decrease of waste mass is achieved in SSF. Technological and economical advantages of SSF added to the results obtained in this work, are encouraging. Studies in order to optimize variables and to scale up the process are our next purpose.

BF-P16

SELECTION AND IDENTIFICATION OF ETHANOL HIPERPRODUCER YEASTS FROM SUGAR CANE MOLASSES

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The decrease of the petroliferous stock and gas in the world, coupled with environmental pollution and global warming, caused mainly by the excessive use of such fuels has generated the need for further studies to become feasible to use new energy sources. The bioethanol consumption produce lower evaporative emissions due to its higher octane concentration and vapor pressure in consequence the pollution levels are much lower than the observed with fossil fuels. The entry into force of Law 26,093 of biofuels in Argentina from 2010 will mean an opportunity for the sugar sector to expand ethanol production to supply 5% of it to all the naphthas. In that regard, Tucumán has a privileged position since its large capacity of ethanol production associated to sugar mills. Our work proposes a microbiological approach to use fermentative microorganisms with high tolerance to alcohol in order to increase ethanol concentration of 11% that is currently obtained in the factories by the alcoholic fermentation of molasses. To take up this, isolation and identification of ethanol hyper-producer strains of yeasts from sugar cane molasses was addressed. Molasses samples were taken from different sugar factories of Tucuman and used to inoculate YPS and YPD media with antibiotics. The microorganisms were inoculated in YPS medium with 50g/L sucrose, incubated at 30ºC with agitation. The fermentations assays were carried out in Erlenmeyers flasks with 200 ml of YPS with 250 g/L of sucrose and incubated at 30 ºC without aeration. Total and direct reducing sugars, biomass and ethanol concentration were determined. Three isolates were selected by your high ethanol production and named as A2, A10 and A11, which produced 11.74, 12.81 and 13.20% of ethanol, respectively. The isolates were identified by sequence analysis of their ARNr 28S intergenic spacer sequences, which allowed assigning identities of 99 and 100% to *Saccharomyces cerevisiae*. Promising results obtained with isolates A10 and A11 justify further studies leading to an optimization of bioethanol production.