

Phosphoproteins in sugarcane (*Saccharum spp*) leaves

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Brazil is the world's largest producer of sugarcane and sugarcane ethanol. Growing concerns about energy supply security, particularly in the transport sector, and also the need to reduce carbon dioxide emissions, has driven the growth of the sugar-ethanol sector. In addition, we observe an increasing domestic demand for ethanol due to the growing fleet of flex fuel vehicles. Phosphorylation is one of the most important post-translational modifications of proteins, which modulate the activity of the protein, protein-protein interactions and cellular localization. So, the analysis of phosphoproteome is very important also for understanding genome regulation and function, and provides important clues to the molecular function of proteins. To study the presence of phosphoproteins in sugarcane leaves, the total protein of SP-3280 cultivar were isolated from fresh tissue of one-month-old sugarcane leaves, from plants grown in greenhouse. The proteins were digested, purified and the phosphopeptides enrichment was made with Titansphere Phos-TiO Kit (GL Sciences). The phosphopeptides were separated by MudPit (Multidimensional Protein Identification Technology), identified by mass spectrometry (LC-MS/MS), analyzed by Mascot Daemon and phosphorylations were validated in NetPhos 2.0 Server (Blom et al., 1999). The results show the presence of phosphoproteins involved in a wide variety of functional categories such as bioenergetics (C-compound and carbohydrate metabolism; photosynthesis); transport; protein metabolism (proteolysis; protein synthesis; protein targeting, sorting and translocation); nucleotide metabolism; amino-acid metabolism; lipid, fatty-acid and isoprenoid metabolism; secondary metabolism; cellular communication / signal transduction; stress response (cell rescue activities); cellular dynamics (biogenesis, organisation and structure of the cell; cell growth). These preliminary results demonstrate the importance of protein phosphorylation in different metabolic pathways and the importance of further studies for a deeper understanding of this post-translational modification mechanism, given the lack of knowledge in the area.

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