XPRESS PRESENTATION - SYSTEMS BIOLOGY AND MODELING

COMPARATIVE TRANSCRIPTOMICS BETWEEN XYLOSE FERMENTING YEASTS THROUGH INTERACTION NETWORKS

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The use of fossil fuels to obtain energy is responsible for a large part of greenhouse gas emissions into the atmosphere. Second generation bioethanol (2G ethanol) appears as a great option because it is a cleaner and renewable source and does not compromise food security, as it uses lignocellulosic biomass and not food inputs as raw material. However, there are still several bottlenecks that limit the efficiency of 2G ethanol production. Through the use of bioinformatics tools, such as differential expression analysis and gene interaction networks of previously generated RNA-Seq and microarray transcriptomic data, we compared the metabolism of xylose fermenting yeasts with the insertion of the XR/XDH and XI pathways under contrasting conditions of 2G ethanol fermentation (glucose vs xylose). As a result, interaction networks were generated from the differentially expressed genes (glucose vs xylose) of both pathways. The XR/XDH interactome, which has a total of 485 nodes (degree >=1), 1416 edges and a density of 0.023, we identified biological processes related to metabolism, oxide reduction process and generation of metabolites and energy, such as oxoacid metabolic process (GO:0043436), carboxylic acid metabolic process (GO:0019752) and oxidation-reduction process (GO:0055114), showing that yeast suffers from the reuse of cofactors.

The XI interactome, which has 571 nodes (degree >=1), 9573 edges and a density of 0.078, we identified differentially biological processes related to cell metabolism, as others related to oxidation and amino acid base processes, such as the oxidation-reduction (GO:0055114), organic acid metabolic (GO:0006082), nucleotide biosynthetic process (GO:0009165) and ribose phosphate metabolic process (GO:0019693), indicating a more abrupt change in the base metabolism of the yeast. In addition, we identify unique submodules in each interactome and, by analyzing the expression of genes in each of them, we identify those that are uniquely expressed at each stage of fermentation. For example, we identified an uniquely expressed submodule in XR/XDH related to process cell division (GO: 0051301) exclusive in glucose, and an uniquely expressed submodule related to DNA metabolic process (GO:0006259) in xylose. We also identified an uniquely expressed submodule in XI interactome related to response to stress (GO:0006950) exclusive in glucose, and uniquely expressed submodules related to oxidation-reduction process (GO:0055114), glucose 6-phosphate metabolic process (GO:0051156) and cellular amino acid biosynthetic process (GO:0008652) exclusive in xylose. These results can be used to understand the role of each group of genes in each 2G ethanol fermentation step through XI and XR/XDH pathways.