GENE REGULATION IN THE *NUC-2* MUTANT STRAIN OF *NEUROSPORA CRASSA* GROWN UNDER PHOSPHATE STARVATION.

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Microorganisms have evolved complex signal transduction networks that enable them to make optimal use of the nutrient sources available. The phosphorus acquisition system in *Neurospora crassa* includes four regulatory genes: *nuc*-2$^+$, *preg*$^+$, *pgov*$^+$, and *nuc*-1$^+$. In an attempt to identify genes involved in metabolic responses to exogenous Pi sensing, we employed suppression subtractive hybridization (SSH) between RNA isolated from the wild type and *nuc*-2A (FGSC#1996) grown under Pi starvation, pH 5.4. Following SSH, expression of clones was examined using dot-blot macro-arrays. Of the 900 clones arrayed, approximately 21% were differentially regulated. A total of 66 differentially up-regulated and 124 down-regulated clones were identified and sequenced. Virtual and Northern blot analyses of selected genes confirmed the differential genic expression. Genes encoding proteins involved in the initiation of mRNA translation were identified among the up-regulated sequences, including the translation initiation factor eIF3, 40S ribosomal proteins S13, S16, and the ubiquitin-ribosomal protein S27a fusion protein. The up-regulation of these genes may result in the recruitment of the cellular translation machinery responsible for translation initiation of a subpopulation of mRNAs. Among the genes found to be down-regulated in *nuc*-2A, six were involved in gluconeogenesis and oxidative phosphorylation. Thus, the identification of differentially-regulated genes in *nuc*-2A is relevant to a further understanding of the molecular events involved in phosphorus sensing.