

Whole genome transcription profile of *Saccharomyces cerevisiae* in response to silver nanoparticles

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Silver nanoparticles (AgNPs) exhibit a broad size and morphologies with highly reactive facets. They are widely applicable in real-life, but not verified for biosafety. Here we studied global gene response in yeast cells exposed to AgNPs and silver ions using DNA microarray. We have identified that a large number of genes affected by AgNPs and silver ions, which amount for ~3 and 5% of genome, respectively. Strongly up-regulated genes are those that mediate high resistance to metals, such as copper and iron. A total of 17 unique genes were found to be the most dominantly induced genes at 120 min of AgNP exposure. Toxicity of AgNPs was severe at early growth stages targeted genes engaged in metabolism, stress response and cell rescue. Silver ions also induced a significant number of genes that are unique. Ninety-genes have found commonly induced to AgNPs and Ag-ions. Our toxicogenomic studies indicate that AgNPs/ions affected cell-wall integrity, transporter proteins, heat shock and stress-related genes. Prolonged exposure of AgNPs resulted in a response similar to that of silver ions, which induced genes involved in metal ion transport, cell-division, and stress responses.