The thioredoxin system of the filamentous fungus *Aspergillus nidulans*: impact on development and oxidative stress response.

Thön M, Al-Abdallah Q, Hortschansky P, Brakhage AA (2007) The thioredoxin system of the filamentous fungus *Aspergillus nidulans*: impact on development and oxidative stress response. *J Biol Chem* 282(37), 27259-27269.

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PubMed

Abstract

Redox regulation has been shown to be of increasing importance for many cellular processes. Here, redox homeostasis was addressed in Aspergillus nidulans, an important model organism for fundamental biological questions such as development, gene regulation or the regulation of the production of secondary metabolites. We describe the characterization of a thioredoxin system from the filamentous fungus A. nidulans. The A. nidulans thioredoxin A (AnTrxA) is an 11.6-kDa protein with a characteristic thioredoxin active site motif (WCGPC) encoded by the trxA gene. The corresponding thioredoxin reductase (AnTrxR), encoded by the trxR gene, represents a homodimeric flavoprotein with a native molecular mass of 72.2 kDa. When combined in vitro, the in Escherichia coli overproduced recombinant proteins AnTrxA and AnTrxR were able to reduce insulin and oxidized glutathione in an NADPH-dependent manner indicating that this in vitro redox system is functional. Moreover, we have created a thioredoxin A deletion strain that shows decreased growth, an increased catalase activity, and the inability to form reproductive structures

like conidiophores or cleistothecia when cultivated under standard conditions. However, addition of GSH at low concentrations led to the development of sexual cleistothecia, whereas high GSH levels resulted in the formation of asexual conidiophores. Furthermore, by applying the principle of thioredoxin-affinity chromatography we identified several novel putative targets of thioredoxin A, including a hypothetical protein with peroxidase activity and an aldehyde dehydrogenase.

Beteiligte Forschungseinheiten

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PMID: 17631497