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# Proteomic responses to nanoparticulate and ionic silver in fungi from metal-polluted and non-polluted streams

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## Abstract

Enhanced production and usage of silver nanoparticles (AgNPs) raise concerns about their potential impacts in aquatic ecosystems. Effects of AgNPs and Ag<sup>+</sup> were assessed based on the variations in the overall proteome and the activities of selected antioxidant enzymes in two fungal strains of *Articulospora tetracladia*, one isolated from a non-polluted stream (At72) and the other from a metal-polluted stream (At61). For that, fungi were exposed to concentrations of AgNPs and Ag<sup>+</sup> affecting 20% of growth (EC20). A total of 432 proteins were identified, of which 172 belonged to At72 and 260 to At61; 71 were expressed in both strains. At72 had 58% and 52% of the proteins induced by AgNPs and Ag<sup>+</sup>, respectively. For At61, the percentages were higher (~77%). The higher percentages of proteins suppressed by either Ag forms suggest higher stress in At72 than in At61, which is consistent with the background of this fungal strain. Major groups of proteins were related to carbohydrate metabolism, amino-acid and protein biosynthesis. Both Ag forms also induced stress-responsive proteins, including catalase and superoxide dismutase which remained consistent with the profile of their enzymatic activities. These results supported the ability of these fungi in initiating an efficient antioxidant response to cope with Ag-induced toxicity. Overall, the functional proteomic approach can be useful to get a mechanistic insight on the stress induced by AgNPs or Ag<sup>+</sup> in aquatic fungi that play a key role in plant litter decomposition in streams.

**Keywords:** AgNPs and Ag<sup>+</sup>, stress response, functional proteomics, antioxidant enzymes, aquatic fungi.

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