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XAS study of selenium enriched shiitake mycelium

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Shiitake mushrooms are well known as a common component of eastern cuisine as well as an important element in Asian medicine. Recently, some efforts on producing bio-active specimens based upon selenium enriched Shiitake mycelium have been undertaken. A crucial problem for understanding its biomedical activity is determination of the form of Selenium in them, as well as its location in the molecular structures of individual species. Among useful tools for solving these problems the X-ray Absorption Spectroscopy (XAS) is the most suitable one. Therefore, in the present work XAS in the near-edge region (XANES) and in the extended range (EXAFS) of the K-absorption edge of Selenium was used.

The mycelium samples studied have been obtained from the mushrooms grown on substrates enriched in selenium. Four samples have been selected for the study: a lyophilised mycelium and three isolated polysaccharide fractions with different protein content. Additionally, four reference samples of known Selenium form have been studied. Measurements have been carried out at the X-Beamline of the synchrotron laboratory HASYLAB/DESY in Hamburg. The spectra have been measured at the temperatures of 77 K and 10 K.

XANES spectra show that the Selenium form varies between the samples from elemental form in the polysaccharide fraction with the highest Se content to Se(IV) in the sample with its lowest content. The lyophilised shows predominant content of Se(II). The Fourier transformed EXAFS spectra have been compared to the spectra simulated for the possible Selenium containing species and provided the information as to which one is the most populated in the particular sample.

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Dimerisation of *Pseudomonas syringae* efector protein HopQ1 (S51A) in solution without DTT

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Plant pathogenic bacteria use type III secrection system (TTSS) to inject proteins to the plant cell apoplasts in order to evade plant immune response and help in colonization. Many of this proteins, called effectors, are recognized by the plant immune system that triggers programed cell death to stop further pathogen colonization.

HopQ1 is an effector protein injected to the plant cell by the bacteria *Pseudomonas syringae*. Bacteria cells, producing HopQ1 protein, are able to colonize bean plants but are recognized by the tobacco plants immune system [1]. HopQ1 molecule consist of two domains: N-terminal unstructurized domain and C-terminal domain with homology to the nucleoside hydrolases. HopQ1 protein interact with the plant 14-3-3 protein [2]. Phosphorylation of serine 51 of HopQ1 is necessary for the interaction. Mutation of serine 51 to alanine leads to the changes in cellular localization from nuclear to the cytoplasmic.

In solution HopQ1 (S51A) protein exists as a monomer with elongated and unstructurized N-terminal domain. In conditions without reduction agents like dithiothreitol HopQ1 mutant (S51A) forms dimers with maximum particle dimater (D_{max}) equal to 12.8 nm. Low resolution *ab-initio* model obtained using DAMMIN program [3] is elliptical and clearly distinct from the model of monomeric HopQ1 which is bottle shaped.

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