P-28

XAS study of selenium enriched shiitake mycelium

T. Strączek*, D. Zając, K. Schneider1,2, M. Sikora1, Cz. Kapusta1, and J. Turło3

1Department of Solid State Physics, Faculty of Physics and Applied Computer Science, AGH University of Science & Technology, 30-059 Krakow, Poland
2Department of Electronics, Faculty of Computer Science, Electronics and Telecommunications, AGH University of Science & Technology, 30-059 Krakow, Poland
3Department of Drug Technology and Pharmaceutical Biotechnology, Medical University of Warsaw, 02-097 Warsaw, Poland

Keywords: Selenium, bioactivity, XANES, EXAFS
*e-mail: Tomasz.Straczek@fis.agh.edu.pl

Plant pathogenic bacteria use type III secretion system (TTSS) to inject proteins to the plant cell apoplasts in order to evade plant immune response and help in colonization. Many of these 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 (Dmax) equal to 12.8 nm. Low resolution structure model obtained using DAMMIN program [3] is elliptical and clearly distinct from the model of monomeric HopQ1 which is bottle shaped.

References