Abstract

Hydrogen/deuterium exchange coupled to mass spectrometry (HXMS) is an increasingly popular technique in structural biology. Its spatial resolution strongly depends on the efficiency of the fragmentation or proteolytic cleavage of the studied protein. Therefore, it is desired to search for new proteases that would not only be able to digest the protein of interest under the HXMS conditions, but also to provide the best possible coverage of the protein sequence.

Finding optimal conditions for production of Oryzasin 1 aspartate protease for its potential use in HXMS experiments was done in this thesis. Selected production clones were selected from available plasmids, the identity of the produced protein was verified by peptide mapping, and optimal production conditions were found. Based on these results, large-scale protein production and inclusion body isolation were undertaken. *(In Czech)*

Keywords: Oryzasin 1, proteases, hydrogen/deuterium exchange coupled to mass spectrometry (HXMS)