Phosphoproteomic analysis of legumain deficient mice

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T. Sever[I,II], R. Vidmar[I], T. Reinheckel[III], B. Turk[I,IV], M. Fonović[I]

[I]Jožef Stefan Institute, Department of Biochemistry and Molecular and Structural Biology, Ljubljana, Slovenia, [II]Jozef Stefan International Postgraduate School, Ljubljana, Slovenia, [III]Institute of Molecular Medicine and Cell Research, Medical Faculty, University of Freiburg, Freiburg, Germany, [IV]university of Ljubljana, Faculty of Chemistry and Chemical Technology, Ljubljana, Slovenia

Legumain, an asparaginyl specific protease, is a member of the cysteine proteinase family. Normally it is confined to the endolysosomal system, though, when specific physiological conditions arise, it can also be found in the cytoplasm, cell nucleus or extracellular space. Enzyme's primary structure is highly conserved among a wide variety of species, implying its significance in evolutionary and physiological aspects. Interestingly, legumain knock out mice exhibit a very mild phenotype. They are viable, fertile and don't display any behavioural aberrations. However, their phenotype includes lowered body mass, irregular kidney function and enhanced inflammatory response. Molecular basis for the observed phenotype is largely unknown, due to the fact, that no system-wide studies on legumain deficient mice have been published to date. It has been shown that levels of EGF receptor are significantly increased in legumain null mice. An effect which may cause global changes in cellular signalling. Apart from that, legumain could also be able to influence the function of other receptors and kinases. To reveal these possible connections, we carried out a phosphoproteomic analysis of legumain deficient mice tissue samples to elucidate changes in protein phosphorylation caused by legumain. We also immunologically validated selected targets. Obtained evidence will enable us to gain an understanding of role legumain has in the physiology of the organism and its possible involvement in pathological states.