A Proteomic approach of Immune Responses and *O*-GlcNAc in *Drosophila melanogaster*

Ji-ae Lee, Su-jin Park and Jin-won Cho

Department of biology, School of biological science, Yonsei University

In response to microbial infections, *Drosophila* turns on a multifaceted immune response involving humoral reactions that leads to the destruction of invading organisms by lytic peptides. These defense mechanisms are activated *via* two distinct signaling pathways. One of these, the Imd pathway is responsible for defense against Gram-negative bacterial infections. This response occurs through a tightly organized, complex signal transduction pathway, yet the components appertaining to it is not fully revealed. We sought to find proteins that are not previously reported to be involved in Imd pathway using proteomic techniques. We gave immune induction with Gram-negative bacteria to *Drosophila* SL2 cells, separated its total lysate with 2-DE, and compared with control group. We were able to identify manifold proteins using MALDI-TOF Mass Spectrometry. These proteins were analyzed to be associated with many cellular events: translational elongation, protein folding, protein modification, cAMP-mediated signaling, stress response, etc. Also, we found *O*-GlcNAc modification in these proteomes showed altered levels, by using specific anti-*O*-GlcNAc monoclonal antibody, CTD110.6. Knock-out of the *O*-GlcNAc transferase result in stem cell and embryonic lethality so *O*-GlcNAc metabolism in Drosophila will likely provide important clues to the cellular functions of *O*-GlcNAc modification. We found novel *O*-GlcNAcylated proteins including ATP synthase beta subunit. Also, we are eagerly intending to identify the position of these proteins in Imd signal transduction pathway, and ultimately, find the functional role of these proteins involved in innate immune response.