O-37 *The –omic technologies*

PEPTIDOMICS OF THE ZEBRAFISH: IDENTIFICATION OF NEUROPEPTIDES BY LC-MS

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(Neuro)peptides are small messenger molecules that are derived from larger, inactive precursor proteins by the highly controlled action of processing enzymes. These biologically active peptides can be found in all metazoan species where they orchestrate a wide variety of physiological processes. Obviously, detailed knowledge on the actual peptide sequences, including the potential existence of truncated versions or presence of post-translation modifications is of high importance when studying respective signaling cascades. A peptidomics approach therefore aims to identify and characterize the endogenously present peptide complement of a defined tissue or organism using liquid chromatography and mass spectrometry (LC-MS). While the zebrafish *Danio rerio* is considered as an important aquatic model, either in the domain of ecotoxicology or rather as general vertebrate model in a medical context, very little is known about their peptidergic signaling cascades. We therefore set out to biochemically characterize endogenously present (neuro)peptides from the zebrafish. The brain region of adult zebrafishes were carefully dissected and (neuro)peptides were extracted using a specific extraction protocol. Resulting peptide samples were analyzed using a nanoLC instrument that is directly coupled with an LTQ-Orbitrap mass spectrometer to yield biochemical identifications of about 100 peptides including several shortened forms (aminoterminally or carboxyterminally truncated) of the presumed biologically active peptides. These peptide variants may result from further *in vivo* processing in the vesicles or might be the result of extracellular (in vivo) peptide processing by specific peptidases. Alternatively, they can also occur from in vitro degradation during sample processing. Obtained sequence data from these first zebrafish peptidomics experiments are likely to pave the way for further functional studies concerning peptidergic signaling in fish.