A6.8 QUANTITATION AND COMPREHENSION OF OSMOTIC EFFECTS ON PROTEOME DYNAMICS INEURYHALINE FISH

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Organismal physiology, morphology, and behavior are based on the function of structural proteins and enzymes. Proteins represent the central regulatory plane in the genome to phenome continuum. The protein complement of cells and tissues (the proteome) is highly dynamic and mirrors environmental and developmental influences on organismal phenotypes. Therefore, dynamic proteomes are excellent bioindicators of environmental exposure. Comprehensive blueprints of environmental exposures are reflected in specific proteome states and capturing those states is achieved by quantitative proteomics. We have developed quantitative proteomics workflows to characterize environmental influences on proteome states and proteome dynamics of euryhaline and euryhthermal fish populations in coastal areas. These workflows utilize tissue- and cell-specific assay libraries for data-independent acquisition (DIA) or Sequentially Windowed Acquisition of all THeoretically possible MSMS spectra (SWATH) mass spectrometry. Qunatitative proteome datasets generated with these workflows are highly accurate and they consistently cover precisely defined sets of proteomes. This consistent coverage renders systematic and long-term network and topological data analysis (TDA) approaches feasible. These workflows and approaches are explained and their application to coastal fish biology is discussed using selected datasets as examples. The data presented illustrate that habitat differences such as salinity and temperature changes are readily captured in state changes of tissue-specific proteomes. The overall topology of proteome states is indicative of particular tissues, species, and environmental contexts and is therefore suitable for deducing functional and phenotypic consequences of environmental changes on coastal organisms.