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**SOCIETY FOR INTEGRATIVE AND COMPARATIVE BIOLOGY
2021 VIRTUAL ANNUAL MEETING (VAM)
January 3 - February 28, 2021**

Meeting Abstract

P9-4 Sat Jan 2 Identification of histone post-translational modifications in three tissues of Mozambique tilapia (*Oreochromis mossambicus*) Mojica, EA*; Fu, Y; Kültz, D; University of California, Davis; University of California, Davis; University of California, Davis eajarett@ucdavis.edu

Histone post-translational modifications (PTMs) are epigenetic marks that modify the state of chromatin and lead to alterations in gene expression. Advances in mass spectrometry have enabled the high-throughput analysis of histone PTMs without the need for prior knowledge of individual PTMs of interest. In this study, the global histone PTM landscape was analyzed in the gills, kidney, and testes of Mozambique tilapia (*Oreochromis mossambicus*) through tandem mass spectrometry using data dependent acquisition (DDA-LCMS2) and PTM mapping approaches. PTM assignment to a specific amino acid was validated using A-score and localization probability scores that are based on the detection of diagnostic MSMS ions. These values signify the robustness of PTM assignment to a specific residue within the protein sequence. For PTMs that were represented by both modified and unmodified versions of the corresponding peptide, the stoichiometry was calculated and compared between tissues. We have identified multiple types of histone PTMs and assigned them to specific residues in each tissue. These PTMs include acetylation, methylation, demethylation, trimethylation, phosphorylation/ dehydration, and ubiquitination. Our results indicate that the gills, kidney, and testes each display a unique profile of histone PTMs. These data provide a strong basis for the generation of spectral libraries that enable high-throughput quantitative analyses of histone PTM stoichiometry on a global scale in tilapia exposed to diverse environmental and developmental contexts. This study is supported by NSF award 1656371.