

Phosphoproteomics profiling of Malpighian Tubules during blood meal processing reveals dramatic transition in function in *Aedes aegypti*

Yashoda Kandel¹, Matthew Pinch¹, Mahesh Lamsal¹, Nathan Martinez¹, Immo A. Hansen^{1,2}

¹ *Department of Biology, New Mexico State University, Las Cruces, NM 88003, U.S.A.*

² *Institute of Applied Biosciences, New Mexico State University, Las Cruces, NM 88003, U.S.A.*

Malpighian tubules, the renal organs of mosquitoes, facilitate the rapid dehydration of blood meals through aquaporin-mediated osmosis. We performed phosphoproteomics analysis of three Malpighian tubule protein-libraries from unfed female mosquitoes as well as one and 24 hours after a blood meal. We identified 4663 putative phosphorylation sites in 1955 different proteins. We observed bloodmeal-induced changes in phosphorylation patterns in many subunits of V-ATPase, proteins of the target of rapamycin signaling pathway, vesicle-mediated protein transport proteins, proteins involved in monocarboxylate transport, and aquaporins. Our phosphoproteomics data suggest the involvement of a variety of new pathways including nutrient-signaling, membrane protein shuttling, and paracellular water flow in the regulation of urine excretion. Together with immunofluorescence analysis data of mosquito aquaporin 1 our results support a model in which aquaporin channels translocate from intracellular vesicles to the cell membrane of stellate cells and the brush border membrane of principal cells upon blood feeding.