Dean's Colloquium

Dr. Herman Fennell, Assistant Professor
Department of Biological Sciences, Hampton University

When: Wednesday, March 22, 2023
Where: Turner 129
Time: 3:30 – 3:50 pm, Q&A: 10 min

Title: Receptor for Activated C Kinase and its Role in Plant Environmental Stress Signaling Pathways

BIO: Dr. Herman Fennell received his doctorate from Howard University in the area of plant molecular biology. After receiving his Ph.D. Dr. Fennell was selected as a T32 National Institute of Health Fellow in the Department of Molecular Medicine and Biochemistry at the University of California in 2012, investigating the receptor tyrosine kinases, ErbB2 in breast tumor progression and therapeutic resistance. He also conducted research on tumor suppressor deletions in ErbB2 positive breast cancer. His current lab's main interest is elucidating the scaffold protein mediated cellular signal transduction pathways in plants. His recent works span from the model plant Arabidopsis and *Oryza sativa* (Rice) response to environmental stress signaling pathways to developing small inhibitor molecules of scaffold proteins to use as a broad anti-viral and in the cancer cell metastasis processes. The scaffold protein known as the Receptor for Activated C Kinase (RACK1) is implicated in diverse signaling pathways in plants and in human diseases including cancer. His research has resulted in publications in 2021 and 2022, applications spanning from the production and application of inhibitor compounds for drought/salt stress resistance in crops, production of a broad anti-viral drug and for use in the inhibition of cancer cell metastasis. Dr. Fennell currently teaches undergraduate classes, including Cancer Biology Laboratory, Fundamentals of Cell Biology, Introduction to Biology I and one graduate class Medical Molecular Cell Biology.

ABSTRACT: The scaffold protein, Receptor for Activated C Kinase 1 (RACK1), in metazoans is known to mediate many diverse signaling transduction pathways. RACK1 interacts with more than a hundred different proteins in order to regulate these signaling pathways. This highly conserved protein is present in a diverse number of species and plays a vital role in abiotic stress resistance, root and seed pod development. A combination of molecular genetics and cell biological approaches was utilized in order to uncover plant RACK1-mediated signaling pathways.

RACK1 consensus sequences are found in a diverse array organisms including yeast, drosophila and humans. RACK1 studies in Oryza sativa allowed the investigation of the novel role of RACK1 in an agricultural crop. To test the functional conservation of RACK1 proteins, activation tagged rice plants over and under expressing one of the two RACK1 proteins were isolated. T-DNA and RACK1A specific primers were used to identify homozygous and heterozygous rice lines. Loss of function mutants in the model plant Arabidopsis thaliana showed hypersensitivity to the stress hormone abscisic acid (ABA). Water loss from knock-out mutants in Arabidopsis also was reduced when compared to the wild type after five hours of detachment from the plant. Under expression lines did not show stress related phenotypes and were resistant to oxidative stress. The homozygous over expression mutant rice line exhibited excessive developmental delay (plant and root development) when compared to the heterozygous and wild type rice plants. Over expression rice lines were extremely sensitive to oxidative and salt stress when compared to the wild-type.
Real Time PCR based assays detected 10-12 fold more RACK1A expression in the homozygous over expression line. When treated in 60mM salt wild-type rice plants had approximately 16 fold more RACK1A expression and the over expression rice (heterozygous) has approximately 58 fold more RACK1A expression. This is evidence that salt significantly induces RACK1A gene expression. After testing antioxidant enzymes CatB, MnSOD and CuZn and the salt inducible gene P5CS all genes were down-regulated when exposed to salt and contained decreased SOD enzyme activity. Photosynthetic capacity of the heterozygous over expression rice line showed decreased photosynthetic capacity when treated in salt stress. Scaffold protein RACK1A in rice, similar to Arabidopsis, potentially can regulate environmental stress signaling pathways suggesting a strategy to identify T-DNA based RACK1A under and over expression in rice plants. With the over and under expression of rice RACK1A lines, the identification of RACK1A regulated specific developmental pathways in rice was observed and documented.