Department of Biological Sciences

Ph.D. Open Seminar

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Date & Time: **April 20th, 2018 at 3:00 PM** Venue: **L-3, LHC**

Evolutionary conservation and emerging functional diversity of the cytosolic Hsp70: J protein chaperone network in plants

Being sessile, plants have to deal with complex environmental cues including a variety of stresses. The Hsp70: J protein machines play important role in fine tuning the cellular protein quality control in all organisms under normal as well as stress conditions. Cytoplasm is the hub for most diverse cellular processes, thus requires efficient chaperone surveillance systems for the maintenance of the functional proteome. Consistent with this, the Hsp70: J protein network is most complex in the cytosol. The function of Hsp70 is dictated by J proteins, thus J proteins are the drivers of Hsp70: J protein chaperone machine. The number of J proteins has dramatically increased in plants which underline the requirement of highly complex and robust Hsp70: J protein networks. Although ubiquitous, the functional specificity and complexity of the plant Hsp70: J protein network has not been studied.

We attempted to dissect the J protein network in the cytosol of *Arabidopsis thaliana* by using yeast as a genetic tool. We show that although the functional specificities of most plant J proteins are maintained across long evolutionary timescales, the Hsp70: J protein network in the *A. thaliana* cytosol is incredibly complex. Detailed phylogenetic and functional analysis revealed that the higher number of J proteins is contributing only partly to the expansion of the Hsp70: J protein network in plants. Above that; regulatory differences, sub-functionalization, neo-functionalization, along with combinatorial interactions among these chaperones are creating unprecedented functional diversity of the Hsp70: J protein network in higher plants. Based on our study, we propose that higher plants have orchestrated their "chaperome", especially their J protein complement, according to their specialized cellular and physiological stipulations.

References:

1. Verma, A. K., Diwan, D., Raut, S., Dobriyal, N., Brown, R. E., Gowda, V., Hines J.K., Sahi, C. (2017). *G3: Genes|Genomes|Genetics*; *7*(6):1941–1954.
2. Craig E. A., Marszalek J. (2017). *Trends Biochem Sci*.; 42(5):355-368.