**Toward introgression and molecular dissection of QTLs for tolerance of flooding during germination in rice**

Endang M. Septiningsih1,Sudip Biswas1, Dipak Khanal 1, Maria Cristina C. Heredia2, Fergie Quilloy2, Dmytro Chebotarov2, Shalabh Dixit2

1 Department of Soil and Crop Sciences, Texas A&M University, College Station, TX 77843, USA

2 International Rice Research Institute, DAPO Box 7777, Metro Manila 1301, Philippines

Most rice production in the U.S. is direct-seeded and addressing constraints in this system is essential to providing robust crop establishment leading to higher yields. At the same time, direct-seeded rice (DSR) is being rapidly adopted across many rainfed and irrigated ecosystems in traditionally transplanted areas in South and Southeast Asia. One of the key traits to improve DSR production is tolerance of flooding during germination or anaerobic germination (AG). AG tolerance is needed to prevent poor crop emergence and establishment due to frequent rainfall, unleveled fields, and poor drainage. Together with our collaborator from the International Rice Research Institute (IRRI), Philippines, we recently identified three major AG QTLs (qSUR7.1, qSUR6.1 and qSUR3.1), from the rice landrace Kalarata, which were detected in two related mapping populations. We aim to introduce the three QTLs into a Texas popular cultivar and molecularly dissect at least one of the major QTLs using comparative whole genome sequence, transcriptome analysis and transgenics. We also aim to combine the three AG QTLs with a previously characterized anaerobic germination QTL, AG1, where the underlying gene has been identified as trehalose-6-phosphate phosphatase (*OsTPP7*), and the well-known Sub1 QTL for tolerance to complete submergence during vegetative stage. Three major sets of crosses were developed to achieve this goal. Simultaneously, we have performed RNAseq and whole genome sequencing to assist in identifying candidate genes underlying the AG QTLs from Kalarata. We have selected the most promising candidate gene for one of the QTLs for further characterization.