**Thomas Work Progress and Plan: 26-05-2015**

**Current Progress:**

1. Checked SNPs of four conserved miRNA families in rice: miR156, miR172, miR164 and miR159. Identified several new SNPs from 3K genome.
2. Examined the expression pattern of members from those four families from <https://mpss.udel.edu/dbs/index.php?SITE=rice_sRNA2>.
3. Used psRNATarget to predict targets of those four gene families.

**Work plan:**

1. Check expression patterns of rice miRNAs with high confidence. Screen out ones which are lowly expressed in panicles. Separate those highly expressed in panicles (aka miRNAs of interest, MOI) into two groups: conserved and non-conserved. Deadline: 2015/6/14
   1. Separate MOI into 2 groups;(***MicroRNAs and Their Regulatory Roles in Plants*** Table1, along with The Conserved MicroRNAs in Plantspart**) /** *Conservation and divergence in plant microRNAs* 6days
   2. Check expression patterns; 4days
2. Design a pipeline for identifying SNPs in precursor and mature miRNAs. Identify SNPs of MOI. Examine the possible impact of SNPs identified on the secondary structure of pre-miRNAs using RNAfold server. Deadline: 2015/8/19
   1. First compare the 3 data resourses (in which, some definitions and procedures should be clarified) after literature review of SNP search; of course, first get SNPs data of the 4 conserved miRNA families, which will take 4 days.
   2. Design pipelines ---- 6 weeks
      1. Have a final view of the pipeline (the function of the pipeline)
      2. Collect data or create local database if needed
      3. Scripts of pipeline
3. Predict targets with psRNATarget and identify conserved target gene family for MOI. Check literatures for experimentally confirmed targets and also their expression patterns in RiceXPro. Identify SNPs in target genes (First focusing on the miRNA target site, and then move onto the 5’and 3’ flanking regions). Deadline: 2015/10/30
   1. Predict targets and check literatures for experimentally confirmed targets (2 week)
   2. Identify SNPs in target genes (target sites and then 5’ and 3’ flanking regions)
      1. Target sites (2 week)
      2. Flanking regions (2 week)

**Literature reviews in written format:**

1. SNP search: What methods have been utilized in the 3K Genome database? Does the default filter setting have an impact on identifying potentially important SNPs in miRNAs, as they are non-coding. (3 weeks, deadline: 2015/6/24)
   1. *Genotype and SNP calling from next-generation sequencing data (Nature reviews)*
   2. *SNP Genotyping: Technologies and Biomedical Applications (Annual Reviews)*
   3. *SNP-Seek database of SNPs derived from 3000 rice genomes*
   4. Write literature reviews
2. MiRNA genes: Biogenesis, regulatory mode and interactions with targets. (3weeks, deadline: 2015/7/1)
   1. *Biogenesis, Turnover, and Mode of Action of Plant MicroRNAs*
   2. *Effects of genetic variations on microRNA: target interactions*
   3. *MicroRNAs and Their Regulatory Roles in Plants*