**Thomas Work Plan 24-07-2015**

**Aim: Identify all SNPs on rice miRNA precursor sequences and mature sequences.**

560 miRNAs in total, excluding those either having no genome coordination in miRBase, or having failed in genome lifting (MSU7 lifted to MSU6.1 to match RiceVarMap). Some of the coordination can be manually added. For example, miR444 family.

**Plan:** 1. Classify all miRNAs into conserved and non-conserved groups; compare the SNP frequencies between them: a. Frequencies in the mature region; b. Overall frequencies in the whole precursor region. Controls for miRNA SNP frequencies are required. (Compare to flanking region of precursors? Compare to other highly conserved, non-coding genes (Relatively low priority).

2. SNPs on mature miRNAs: classify to conserved and non-conserved groups. Analyse: A. SNPs’ pattern/distribution; B. Potential free energy changes between miRNA and miRNA\* which may impact AGO loading;

3. Haplotype analysis: A. Haplotypes in highly conserved miRNAs with higher SNP numbers and higher population number. B. Check the impact of haplotypes on secondary structure of precursors.

MUST READ ASAP: Genome-wide identification and analysis of miRNA-related single nucleotide polymorphisms (SNPs) in rice.

Bioinformatic resources: <http://omicslab.genetics.ac.cn/psRobot/>

<http://www.comgen.pl/mirex2>