**February 10th**

1. RNA-guided genome editing in plants using a CRISPR-Cas system

Xie and Yang (2013) Mol Plant 6:1975-1983

2. A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species

Elshire et al. (2011) PLoS ONE 6:e19379

**February 17th**

1. Switchgrass genomic diversity, ploidy, and evolution: novel insights from a network-based SNP discovery protocol

Lu et al. (2013) PLoS One 9:e1003215

2. Shared selective pressure and local genomic landscape lead to repeatable patterns of genomic divergence in sunflower

Renaut et al (2014) Mol Ecol 23:311-324

**February 24th**

1. Integration of responses within and across *Arabidopsis* natural accessions uncovers loci controlling root systems architecture

Rosas et al. (2013) PNAS 110:15133-15138

Bridging the genotyping gap: using genotyping by sequencing (GBS) to add high-density SNP markers and new value to traditional bi-parental mapping and breeding populations

Spindel et al. (2013) Theor Appl Genet 126:2699-2716

*Presentation: Alex*

*Discussion Lead: Rishi*

**March 3rd**

1. Differential expression of microRNAs in response to drought stress in maize

Li et al. (2013) J Integr Agric 12:1414-1422

2. RNA sequencing reveals the complex regulatory network in the maize kernel

Fu et al. (2013) Nature Comm 4:2832

**March 17th**

1. The tomato genome sequence provides insights into fleshy fruit evolution

Zouine et al. (2012) Nature 485:635-641

*Presentation: Alex*

*Discussion Lead: Si*

2. Synteny-based mapping-by-sequencing enabled by targeted enrichment

Galvão et al. (2012) The Plant J 71:517-526

**March 24th**

1. Population genomic and genome-wide association studies of agroclimatic traits in sorghum

Morris et al. (2013) PNAS 110:453-458

2. Next-generation mapping of Arabidopsis genes

Austin et al. (2011) The Plant J 67:715-725

**March 31st**

1. Combined sequence-based and genetic mapping analysis of complex traits in outbred rats

Rat Genome Sequencing and Mapping Consortium (2013) Nature Genet 7:767

2. Rapid genome mapping in nanochannel arrays for highly complete and accurate *de novo* sequence assembly of the complex *Aegilops tauschii* genome

Hastie et al. (2013) PLoS ONE 8:e55864

**April 7th**

1. Gene body methylation is conserved between plant orthologs and is of evolutionary consequence

Takuno and Gaut (2013) PNAS 110:1797-1802