

Focus	Resequencing of the NBRP collected resources intended to upgrade the genome information of <i>Lotus japonicus</i>
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Period	FY2014
Overview	<p><i>Lotus japonicus</i> has been widely used as a system to investigate the genetic background of legume-specific phenomena. The genome sequences of <i>L. japonicus</i> have been analyzed in Japan, and they have been improved by adding the sequence information generated from Illumina and 454 sequencers to transform the genomic resources of <i>L. japonicus</i> to facilitate functional genomic studies. Currently, the size of updated genome sequences reached 400 Mbp covering nearly 99% of the transcriptome sequences. However, a significant number of short contigs are still on unmapped.</p> <p>In order to upgrade the genome information on <i>L. japonicus</i>, we are going to resequence two types of RILs collected by NBRP program. By using obtained sequence information, we are going to genotype the SNP sites on the genomes of resequenced RILs. Based on the assigned genotype information, we should be able to anchor most of the unmapped contig on the pseudomolecules of the reference genome. We will also resequence wild accessions of <i>L. japonicus</i>, and SNPs between these accessions and reference Miyakojima accession will be analyzed to integrate the information into the catalog of natural variations in <i>L. japonicus</i> accessions. The information accumulated by this program will facilitate the application of information and material resources of <i>L. japonicus</i>.</p> <pre> graph TD RIL[Recombinant inbred lines] --> RIL_RS[Resequencing] RIL_RS --> RIL_SNP[SNP genotyping by read mapping] RIL_SNP --> RIL_HRQTL[High resolution QTL mapping] RIL_SNP --> RIL_AUC[Anchoring of unmapped contigs] RIL_HRQTL --> RIL_AUC RIL_AUC --> UGSI[Upgrading of genome sequence information & material resources] WCA[Newly collected Lotus japonicus wild accessions] --> WCA_RS[Resequencing] WCA_RS --> WCA_APM[Assignment of polymorphic positions by read mapping] WCA_APM --> UGSI WCA_APM --> CNV[A catalog of natural variation in Lotus japonicus] CNV --> GWAS[Application for GWAS] UGSI --- LGI[Lotus japonicus genome information] </pre>
Progress	