Poster Presentation 2

P2-46

Development and Molecular Characterization of Novel Polymorphic Genomic DNA SSR Markers in *Lentinula edodes*

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Purpose: To analyze genetic diversity and discriminate between *Lentinula edodes* varieties, we developed simple sequence repeat (SSR) markers that can complement internal genetic and external phenotypic traits.
Methods: To design reliable SSR markers from reference whole-genome sequencing data for *L. edodes*, we produced read data by re-sequencing genomic DNA extracted from 33 tested strains developed in East Asian countries (15 accessions originating from Korea, 12 accessions originating from Japan, and 6 accessions originating from China). Sequencing reads were then mapped to selected SSR motif regions of the reference genome.
Results and conclusions: Amongst all SSR motifs, 205 motifs that showed the largest conservation rate and diversity were selected, and sixteen genomic DNA SSR markers were developed. The number of alleles ranged from 3-14 and the major allele frequency was distributed from 0.17-0.96. The values of observed and expected heterozygosity ranged from 0.00-0.76 and 0.07-0.90, respectively. The polymorphic information content value ranged from 0.07-0.89. A dendrogram, based on 16 SSR markers clustered by the paired hierarchical clustering' method, showed that 33 *L. edodes* varieties could be divided into three major groups and successfully identified. These SSR markers will contribute to the efficient breeding of this species by providing diversity in *L. edodes* varieties. Furthermore, the genomic information covered by the markers can provide a valuable resource for genetic linkage map construction, molecular mapping, and marker-assisted selection in *L. edodes*.