strand selection by Argonaute (AGO) proteins from small RNA duplexes (21-nt dsRNAs) by using this protoplast RNAi system.

Transcriptional and Post-Transcriptional Gene Silencing
Chanseok Shin - Poster-G158

Abstract Title: SMALL RNA SEQUENCING PROVIDES INSIGHTS INTO DIVERGENCE OF microRNAs AND THEIR TARGETS IN HIBISCUS SYRIACUS

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Abstract

AIM: MicroRNAs (miRNAs) are essential small RNA molecules that regulate the expression of target mRNAs in plants and animals. Here, we aimed to identify miRNAs and their putative targets in Hibiscus syriacus, the national flower of South Korea. METHODS: We employed high-throughput sequencing of small RNAs from four different tissues (i.e., leaf, root, flower and ovary) and identified 33 conserved and 30 novel miRNA families. Targets of miRNAs were computationally predicted and experimentally validated using 5' rapid amplification of cDNA ends analysis. RESULTS: Many of miRNAs showed differential tissue-specific expression. The validated novel target of miR477 was a terpene synthase, the primary gene for the formation of disease-resistant terpene metabolites, such as sterols and phytoalexins. In addition, NB-LRR is the target of conserved miRNAs, miR482, which is involved in effector-triggered immunity. We also identified the target of miR396, SHORT VEGETATIVE PHASE, in flower initiation in Hibiscus syriacus. The genome of Hibiscus syriacus was duplicated in twice after speciation and duplication of genome is associated with divergence of miRNAs. We further investigated the impact of genome duplication on miRNAs of Hibiscus syriacus. This work was supported by the Next-Generation BioGreen 21 Program (No. PJ01332501), Rural Development Administration, Republic of Korea.

Tropical and Mediteranean Plants
Fabienne Micheli - Poster-B186

Abstract Title: ALTERNATIVE OXIDASE (AOX) CONSTITUTES A SMALL FAMILY OF PROTEINS IN CITRUS CLEMENTINA AND CITRUS SINENSIS L. OSB

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Abstract

The alternative oxidase (AOX) protein is present in plants, fungi and some invertebrates. It is involved in the mitochondrial respiratory chain, providing an alternative route for the transport of electrons, leading to the reduction of oxygen to form water. The present study aimed to characterize the family of AOX genes in mandarin and sweet orange. Four AOX genes were identified in each citrus species. The 1500 bp-upstream region of each AOX gene contained regulatory cis-elements related to internal and external response factors. CsAOX genes showed a differential expression in citrus tissues. AOX proteins

contained conserved motifs as well as several putative post-translational modification sites. The CcAOXd protein was modeled by homology and its 3-D structure showed two hydrophobic helices probably involved in the anchoring in the inner mitochondrial membrane. The active site of the protein is located in a hydrophobic environment deep inside the AOX structure and contains a diiron center. The molecular docking of CcAOXd with ubiquinone showed that the binding site is a recessed pocket formed by the helices and submerged in the membrane. These data are important for future functional studies of citrus AOX, as well as for biotechnological approaches leading to AOX inhibition using ubiquinone homologs.

Tropical and Mediteranean Plants
Ching-Ping Lin - Poster-P239

Abstract Title: BARCODE DISCOVERY FROM CHLOROPLAST GENOMES OF AGARWOOD TREES

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Abstract

Agarwood can only come from a resin produced in the heartwood of a couple of species of fungus-infected agarwood trees in tropical. Owing to the long-term overexploitation of agarwood trees, the trees are critically endangered in the wild. To detect and avoid illegal logging of agarwood trees, an accurate identification method is essential. We used PacBio and Illumina sequencing to complete the chloroplast genomes of two genera representatives, Aquilaria agallocha (174,836 bp in size) and Gyrinops versteegii (174,812 bp in size). Only rpl32 and most of the ndhF are in the small single copy region (SSC). In addition, this extremely short SSC is conserved in A . agallocha (3,346 bp), A . yunnanensis (3,351 bp), G . versteegii (3,246 bp), Daphne kiusiana (2,681 bp), A . beccariana , A . crassna , A . malaccensis , A . microcarpa , and G . cf. caudate , whereas the latter five are verified by PCR. Sequence variation analyses revealed 500 single nucleotide polymorphisms and 130 indels among A . agallocha , A . sinensis , A . yunnanensis and G . versteegii cp genomes, excluding one copy of inverted repeat. These genetic variations might be considered as candidates for barcode development to improve the resolution during identification of agarwood trees.
