

June 20-21, 2018  
Rome, Italy

Meng-Ying Lin et al., J Plant Physiol Pathol 2018, Volume 6  
DOI: 10.4172/2329-955X-C1-015

## ALLELE SPECIFIC EXPRESSION ANALYSIS ON *MORICANDIA* HYBRIDS TO IDENTIFY FACTORS GOVERNING CO<sub>2</sub> CONCENTRATION MECHANISMS

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Plants with C<sub>3</sub>-C<sub>4</sub> photosynthesis display lower CO<sub>2</sub> compensation points than related C<sub>3</sub> species and Kranz-like anatomy. C<sub>3</sub>-C<sub>4</sub> intermediates do not have the C<sub>4</sub> photosynthetic mechanism but possess an efficient system for recycling of photorespiratory released CO<sub>2</sub> by transporting glycine into bundle sheath cells, where CO<sub>2</sub> released from mitochondria can be efficiently recaptured by numerous, adjacent chloroplasts. Within the project, we would like to investigate the importance of different biochemical and anatomical features for the function of this specific photorespiratory cycle as well as their manifestation in the genomes of the plants. In the genus *Moricandia*, species with C<sub>3</sub> and C<sub>3</sub>-C<sub>4</sub> intermediate photosynthesis exist in close phylogenetic proximity and provide suitable materials to study early evolutionary steps of C<sub>4</sub> photosynthesis. To explore Allele Specific Expression (ASE) regarding this specific CO<sub>2</sub> concentration mechanism in *Moricandia*, six interspecific *M. arvensis* x *M. moricandioides* hybrids with diverse phenotypes as well as their parental species

were selected for RNA-Seq analysis. In total, we obtained 54.97 GB of RNA-Seq data, with an average of 4.58 GB per sample. Parental species showed high aligning rate with an average of 92.33% to their own reference genome; on the other hand, reads from hybrids were about 75 to 85% mapped to each parental species. Approximately 120,000 SNP sites were examined by ASE analysis on every hybrid lines, 30% of the SNP sites were *cis*-regulatory variants, 7% of them were controlled by *trans*-acting regulators and others were with mixture of effects. Among hybrids, 3142 common *cis*-SNPs and 82 common *trans*-SNPs were found and mainly involving in cellular process (GO: 0009987) and metabolic process (GO: 0008152)..

### Biography

Meng-Ying Lin is expertise in plant genomics field and she is doing Ph.D. at Heinrich-Heine-Universität Düsseldorf, Germany.

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