

Ms. Divina Kristi Discar, Department of Biology, School of Science and Engineering, Ateneo de Manila University, 1108 Katipunan Quezon City Loyola Heights, Philippines; vinakristidiscar@yahoo.com (co-author)

Moringa oleifera Lam. is an outstanding crop having seeds with a myriad of benefits including nutrition, health and phytoremediation. These benefits are attributed to the compounds present in the seeds including secondary metabolites considered as antioxidants. Exploring the transcriptome of *M. oleifera* seeds paved the way for the discovery of the expressed secondary metabolites. Although various phytochemical researchers reported the presence of secondary metabolites in the seeds of *M. oleifera*, such information is lacking at the transcriptomic level. In the present study, RNA sequencing was used to analyze the transcriptome of the mature embryo of *M. oleifera*. More than 41 million sequencing reads were generated and de novo assembled using Trinity and SOAP assemblers. Annotation was performed through the NCBI non-redundant database. Furthermore, analysis of the levels of gene expression in *M. oleifera* seeds using FPKM was performed. Trinity produced 177,417 contigs and SOAP-de novo assembly produced 49,170 contigs. Based on gene ontology functions, the highly expressed genes for secondary metabolites are mostly involved in catalytic activities, metabolic processes, and single-organism processes. Biological pathway analysis using KEGG-KAAS revealed genes encoding 18 enzymes of the phenylpropanoid pathway, 11 enzymes involved in the flavonoid pathway, and 19 enzymes in the alkaloid pathway. FPKM analysis revealed upregulated genes encoding for enzymes peroxidase and betaglucosidase suggesting that *M. oleifera* seeds have nutritional and pharmacological benefits. Hence, *M. oleifera* seeds should be incorporated in the regular diet because seeds are not often eaten as much as the leaves. This study provides the first transcriptome profile of the candidate genes involved in the biosynthesis of secondary metabolites in the *M. oleifera* seeds. This is a baseline information that may open the potentials for improving the yield of secondary metabolites in the *M. oleifera* seeds. Validation of the expression of the aforementioned genes using qRT-PCR is underway.

Keywords: Transcriptome, contigs, secondary metabolites, qRT-PCR

OS 2-10:

New sweet cherry genomic tools and their use in marker-assisted breeding

Dr. Elisabeth Dirlewanger, INRA, 71 avenue Edouard Bourlaux , 33883 Villenave d'Ornon, France; elisabeth.dirlewanger@inra.fr (presenting author)

Dr. Loick Le-Dantec , INRA, 71 avenue Edouard Bourlaux, Villenave dOrnon, France; loick.le-dantec@inra.fr (co-author)

Mathieu Fouché, INRA, 71 avenue Edouard Bourlaux, Villenave dOrnon, France; mathieu.fouche@inra.fr (co-author)

Dr. Teresa Barreneche, INRA, 71 avenue Edouard Bourlaux, Villenave dOrnon, France; teresa.barreneche@inra.fr (co-author)

