Comparative analyses of differentially expressed genes involved in flavonoid biosynthesis in North American native grapes: ‘Noble’ and ‘Ison’ muscadines vars., and ‘Cynthiana’ aestivalis var

S.K. Samuelian¹, C. Camps², C. Kappel², E.P. Simova¹, Serge Delrot², Violeta M. Colova (Tsolova)¹

¹Florida A&M University, CESTA, Center for Viticulture and Small Fruit Research, 6505 Mahan Drive, Tallahassee, FL 32317, USA
²UMR 1287 Ecophysiology and Grape Functional Genomics, University of Bordeaux, INRA, Institut des Sciences de la Vigne et du Vin, Domaine de la Grande Ferrade, 71 Avenue Edouard Bourlaux, 33883 Villenave d’Ornon, France

Email: Violetka.Colova@famu.edu

Background and Aims
The common Muscadinia possesses one of the highest flavonoid levels among fruits. Due to the different biological activities of plant secondary metabolites, their regular consumption may have significant consequences for human health. Study of differentially expressed genes in the flavonoid biosynthesis was carried out to generate knowledge of the production of these compounds in muscadinia and aestivalis and identify candidate genes for further functional analysis in the North American grape species.

Methods and Results
Key developmental stages – “véraison” and “physiological maturity” – were studied by the use of high throughput 70-mers microarrays in the muscadinia ‘Noble’ var. The expression profiles of 13 differentially expressed genes involved in critical steps of the flavonoid pathway were further validated in the ‘Ison’ var. and ‘Cynthiana’ aestivalis var. by real-time PCR. Six transcripts revealed similar expression patterns across the two species. From the remaining 7 genes, 5 showed significantly similar expression patterns in ‘Noble’ vs. ‘Ison’ compared to ‘Noble’ vs. ‘Cynthiana’, and for 2, the expression patterns were different in each of the varieties.

Conclusion
Out of the 13 analyzed genes involved in the flavonoid biosynthesis, 11 revealed similar expression patterns in the two muscadinia varieties and only 5 when ‘Noble’ was compared to the aestivalis variety. A high-resolution picture of the transcriptome dynamics that occur during the final developmental stages – “véraison” and “physiological maturity” of berry ripening in ‘Noble’ and ‘Ison’ provided a unique and comprehensive view of key genes involved in the flavonoid biosynthesis of the muscadines.

Significance of Study
This is the first step towards understanding the genetical enhancement of the expression of flavonoid compounds in the North American grape species during two important grape developmental stages.