

fields with the physiological. To isolate the parameters of the experiments the flow that is set to be investigated is the flow of blood out of the aortic valve into the aortic root. This is an area of flow with non-uniform shear rates which should have a pronounced effect on the velocity profile of a Newtonian versus non Newtonian fluid. This experiment has been completed before in literature to allow for comparison to data of previous works. The focus here is the comparison of shear dependent fluids and the fact that the fluid is tunable and controlled based on its computational model and the flow apparatus, the aorta, is made from open source patient-specific data that can be used to recreate that specific aorta. The valve for these experiments will be a tilting disc valve, which allows for known flow characteristics. The goal will be to conduct a statistical comparison that will give a non-dimensional score of the flow field to allow for a quantitative analysis of the device in the flow field.

Botany

QUANTITATIVE ANALYSIS OF ANTIOXIDANTS IN SPECIALTY WINES. Alexandra C. Heil, Hannah E. Wines, & Michael H. Renfroe, Dept. of Biol., James Madison University, Harrisonburg VA 22801. Wines are sources of antioxidants such as procyanidins and resveratrol along with polyphenolics that provide important health benefits and help protect against hypertension, arteriosclerosis, cancer, and other diseases. Most commercial wines are made from the domesticated European grape (*Vitis vinifera*). However, there are specialty wines that are made from native American grapes (*Vitis labrusca*), and wines that are fruit based or blended with fruit extracts. Our research compared the antioxidant levels found in muscadine and scuppernong wines to those found in fruit-based or fruit-flavored wines. Antioxidants were measured using the trolox equivalent antioxidant capacity assay (TEAC) and results were reported in μmol trolox equivalents (TE) per mL. Muscadine and scuppernong wines from a single vineyard were compared and antioxidant concentrations ranged from 2.2-5.5 μmol TE/mL wine. Four fruit wines were compared from a single vineyard and the raspberry and peach were low in antioxidants (2.0 and 1.7 μmol TE/mL, respectively), whereas the blackberry and chocolate-flavored wines were very high in antioxidants (10.7 and 12.6 μmol TE/mL, respectively). Other fruit wines were tested and fell either within this range or slightly below it. These results indicate that wines can vary significantly in their antioxidant content, and that scuppernong and muscadine wines were comparable to some reported values of European grape-based wines.

QUANTITATIVE ANALYSIS OF ANTIOXIDANT ACTIVITIES IN TOMATOES AND PROCESSED TOMATO PRODUCTS. Anna T. Dinh & Michael H. Renfroe, Dept. of Biol., James Madison University, Harrisonburg VA 22801. The amount of antioxidants present in food varies depending on environmental conditions in which produce was grown and how products were processed prior to consumption. This study focused on quantitative analysis of antioxidant activities in commercially produced whole tomatoes and processed tomato products (paste, sauce, juice, diced, and soup) and fresh tomatoes grown experimentally in different light intensities. Variations and significant differences were observed between different types of whole tomatoes,

different types of processed tomatoes, different batches of the same brand and type of processed tomatoes. These variations could be attributed to the different locales tomatoes were grown, type of tomatoes used for processed tomato products, or additives such as herbs and spices used for flavoring. Data also indicated statistical differences between tomatoes grown under the same as well as different light intensities, on fw basis. Tomatoes grown in 100% light had TAA ranging from 1.898 to 3.565 mmol TE/g fw (7.73 to 13.405 mmol TE/g dw), 2.375 to 2.523 mmol TE/g fw (8.558 to 13.223 mmol TE/g dw) in 50% light, and 1.623 to 1.958 mmol TE/g fw (8.068 to 13.073 mmol TE/g dw) in 25% light. While small differences in data proved to be statistically significant, some of these differences may be too small to be of biological consequence. Data from this study, along with currently available data on antioxidants in foods, can provide useful information to consumers interested in purchasing products that are most beneficial to their health and to dietitians when making dietary recommendations to patients.

USING THE FLORISTIC QUALITY ASSESSMENT INDEX (FQAI) AT THE ABRAMS CREEK WETLANDS, A CALCAREOUS WETLAND COMPLEX IN WINCHESTER AND FREDERICK COUNTY VIRGINIA. Daniel F. Cooper & Woodward S. Bousquet, Environmental Studies Program, Shenandoah University, Winchester, VA 22601. The Abrams Creek Wetlands consist of more than 50 acres that are underlain by limestone bedrock and straddle the boundary between Winchester City and Frederick County, Virginia. The wetlands were divided into ten sites based on community types and property boundaries. Each site was visited twice during the 2013 growing season to record its vascular plant species. Unknown specimens were reviewed and identified by Gary Fleming of the Virginia Natural Heritage Program. A total of 227 species from 63 families were found and identified. Two species, *Symphotrichum praealtum* var. *angustior* (Willowleaf Aster) and *Scutellaria galericulata* (Hooded Skullcap), have not been found at any other site in Virginia. After a final species list was compiled for each site, as well as the wetlands as a whole, floristic quality calculations were performed. Through the Floristic Quality Assessment Index (FQAI), the Abrams Creek Wetlands achieved a score of 51.9, which signifies high floristic quality. Scores calculated for each of the ten sites permit numerical, not subjective, evaluations of these different portions of the wetlands. The FQAI will allow researchers to assess the impacts of any future disturbances. Furthermore, this approach will permit managers of natural areas to set priorities for preservation and restoration.

RADIAL GROWTH DYNAMICS OF A RARE WHITE CEDAR (*THUJA OCCIDENTALIS* L.) FOREST IN THE SHENANDOAH VALLEY, VIRGINIA. Angela N. Felicio¹, Joshua A. Kincaid², & Cory M. Miller², ¹Department of Biology, Shenandoah University and ²Environmental Studies Program, Shenandoah University Winchester VA. 22601. Northern White Cedar (*Thuja occidentalis* L.) is a boreal coniferous tree species found from Quebec to Manitoba, Canada. Smaller disjunct populations occur southward along the Appalachian Mountains extending to Tennessee and western North Carolina. During the summers of 2011 and 2012 Shenandoah University researchers gathered samples by increment borer to document the growth-climate relationships of a disjunct Northern White Cedar forest in the Shenandoah

Valley. A total of 37 cores were collected and analyzed. Correlation analysis was used to determine the ring width response to climate from 1919-2012. There was a positive relationship with precipitation in the months of June and July ($p < 0.05$). Discharge in the Shenandoah River was positively correlated from June-September ($p < 0.05$). The Palmer drought severity index (PDSI) showed positive correlations during June-December and February-March ($p < 0.05$). Given that only five stands of this species have been studied in Virginia, analysis of growth dynamics is instrumental in understanding this species.

COMMELINA BENGHALENSIS, NEW TO VIRGINIA. W. John Hayden, Department of Biology, University of Richmond, Richmond, VA 23173. *Commelina benghalensis* L. (Benghal dayflower) was discovered growing spontaneously among ornamental landscape plants on the University of Richmond campus on 19 October 2012. This federally listed noxious weed can be distinguished from other species of *Commelina* found in Virginia by the combination of spathes bearing chasmogamous flowers at aerial stem tips and nearly closed spathes bearing cleistogamous flowers from proximal, often subterranean, lateral branches. The population consisted of three mature plants bearing numerous aerial and subterranean spathes and nine non-reproductive seedlings. All individuals found were removed and used to make specimens for anatomical study and herbarium vouchers; vouchers will be distributed from URV to other major herbaria in Virginia. Searches of other landscape plantings in the vicinity failed to reveal additional occurrences of the plant. Benghal dayflower has spread progressively northward from its discovery in Florida in 1928. Given the setting of the population discovered, these plants may have been dispersed coincidentally with landscape plants. This is the first record of *Commelina benghalensis* to occur in Virginia where its status should be considered a non-native waif.

THE FLORA OF VIRGINIA HAS BEEN PUBLISHED: THE FUTURE OF THE FOUNDATION OF THE FLORA OF VIRGINIA PROJECT. Marion B. Lobstein, Professor Emeritus, Northern Virginia Community College, Manassas, VA 20109. Virginia, for its landmass, has the most diversity of vascular plant species of any state in the United States. The Colony of Virginia had the first colonial flora, *Flora Virginica*, which was last updated in 1762. Since 1926, the Virginia Academy of Science has supported efforts to produce a modern *Flora of Virginia*. The Foundation of the *Flora of Virginia*, Inc, was formed in 2001 to realize this goal. The *Flora of Virginia* was published in December 2012. The Foundation of the *Flora of Virginia* project will continue to function to accomplish future goal of the Project. One of those goals is the development of teaching and learning modules. Marion Lobstein shared details of her efforts to develop workshops and materials to facilitate the use of the new *Flora of Virginia* by interested adult groups. Botany section members were also encouraged to share their ideas to begin to implement this goal.

THE FLORA OF VIRGINIA, A MANUAL TO THE MANUAL AND THE FUTURE OF THE PROJECT. J. Christopher Ludwig, Virginia Department of Conservation and Recreation, Division of Natural Heritage, Richmond, VA 23102. The 1554-page *Flora of Virginia* was published in November, 2012. This manual to the vascular plants of

Virginia treats 3164 native and naturalized taxa. Many conventions and shortcuts that are used in the Flora of Virginia will be presented which will make the manual easier and more useful to use. All information within the Flora of Virginia has been maintained in a database for eventual digital presentation in combination with other databases that have additional information on the distribution and habitats of Virginia plants. This digital presentation will likely take the form of an app for handheld devices. The app will be designed for use in the field and will link to an image library. These and other future plans will be detailed.

EVOLUTIONARY HISTORY OF CANARY GRASSES: PHYLOGEOGRAPHY, CYTOLOGY AND FLORET STRUCTURE. Stephanie M. Voshell & Khidir W. Hilu. Dept. of Biological Sciences, Virginia Tech, Blacksburg, VA. *Phalaris* (Poaceae) contains 21 endemic to cosmopolitan species, found throughout the temperate and subtropical regions of the world with distinct centers of diversity in the Mediterranean Basin and western North America. The species display annual or perennial habit and possess basic chromosome numbers of $x=6$ and 7, with polyploidy confined to the later cytotype. *Phalaris* presents a valuable opportunity to study long distance dispersal, historic hybridization and polyploidy events, and the impact of floret structure on natural range expansion in grasses. We present here the first phylogeographic study showing the historic events of migration, speciation and dates of divergence in the genus using Bayesian inference and dispersal-vicariance analyses. The genus emerged in the Mediterranean Basin during the Miocene epoch (23-5.3 MYA). A basal split occurred between the $x=6$ and $x=7$, with the former group (3 species) remaining as diploids in the Mediterranean region and the later group expanding into Africa and Asia and evolving various ploidy levels. Dispersal to North America via the Bering Land Bridge resulted in diversification in the Americas based on diploid speciation. The greater speciation and dispersal success of the diploid $x=7$ cytotype compared to its $x=6$ counterpart raises questions about the significance of this early chromosome rearrangement. Florets with prominent and pubescent sterile lemmas, as seen in the New World species, may be advantageous for dispersal via animal transport.

GENES VS. GENOMES IN RESOLVING DIMENSIONALITY OF THE TREE OF LIFE: CARYOPHYLLALES AS A CASE STUDY. Khidir W. Hilu & Sunny S. Crawley, Department of Biological Sciences, Virginia Tech, Blacksburg, VA 24061. Decline in sequencing costs resulted in a surge in the number of organelle genome sequences, providing an abundance of molecular characters for molecular phylogenetics. Phylogenetic reconstruction based on whole genome matrices although tending to provide robust trees, is generally strongly skewed toward relatively narrow taxon representation. In contrast, datasets based on a few genomic regions although promoting a denser taxon sampling, are construed as potentially too character-poor to accurately resolve phylogenetic histories. Using the angiosperm order Caryophyllales as a taxonomic platform, we contrast the relative efficacy in phylogenetic reconstruction of whole genome/narrow taxon representation vs. few genomic regions/denser taxon sampling, and explore the potential of combining these two types of datasets, allowing for the inherently large proportion of missing data. Our preliminary results demonstrate that a prudent selection of a limited number of genomic regions can provide a phylogenetic tree that approaches the genome-based tree with the

added benefit of considerable detail at recent histories. Combining the dataset recovered the backbone and provided valuable information on the terminal nodes despite extensive amounts of missing characters/genomic regions. This approach provides a cost- and-time-effective platform for discerning the dimensionality of the tree of life.

Posters

INVESTIGATING THE ROLE OF STP1 IN OSMOTIC BALANCE IN ARABIDOPSIS THALIANA. Janet C. Daniel, Morgan Donovan, Ji Lee, Tiffanie Le & Maria Wilkins, Department of Biology, James Madison University Harrisonburg, VA. 22807. *Arabidopsis thaliana* is a commonly used model organism in plant research and is described as a glycophytic plant. In this study, we investigated the role of sugar transport protein-1 (STP1) in salt resistant phenotype exhibited by the STP1 k/o plant by observing WT and STP1 k/o plants watered with various concentrations of NaCl. We measured plants grown in soil, using a hydroponics system and on plates. RESULTS: STP1 k/o roots grown in soil and watered with 50mM NaCl solution are significantly longer than WT plants at 2 weeks (12.1mm vs. 6.03mm, $p=2.4 \times 10^{-3}$). On average, STP1 roots (16.62 mm vs. 9.93 mm at 3 weeks) and shoot growth (3.4 mm vs. 2.77mm at 2 weeks, $p=1.29 \times 10^{-4}$) in 50 mM NaCl were longer than than WT. In order to obtain increased plant tissue to initiate gene expression studies, we have adapted a hydroponics system to grow plants in larger quantities for ease in harvesting tissues for molecular and microscopic analysis. Growing plants hydroponically results in comparable root and shoot growth to growth on soil and agar plates. WT roots grown in 50mM NaCl were significantly different than those grown in 0mM NaCl (13.07mm vs. 5.67mm, $p=5.1 \times 10^{-5}$) while STP1 k/o were not significantly different (11.89 mm vs. 9.67mm, $p=0.26$). Characterization of the mechanism of salt tolerance exhibited by the *Arabidopsis thaliana* STP1 knockout will provide further insight into role STP1 plays in osmotic regulation of the plant.

PROGRESS IN PHYLOGEOGRAPHIC STUDY OF NORTH AMERICAN MELAMPYRUM LINEARE (OROBANCHACEAE). Karoline Oldham & Andrea Weeks, School of Systems Biology, George Mason University, Fairfax VA 22030 & Dept. of Environmental Science and Policy, George Mason University, Fairfax VA 22030. *Melampyrum lineare* is the sole North American species of its genus, which is otherwise distributed in Europe and Asia. It is not currently known how this species migrated to North America. Current literature completely omits *M. lineare* from the taxa sampled for genus- and family-level phylogenetic studies. As a consequence, this species' relation to other members of *Melampyrum* is poorly understood. Morphology suggests a European progenitor, *M. pratense*, which implies ancestral migration across the Atlantic Ocean. However, this hypothesis has not been thoroughly investigated. Comparison of ITS sequences of *M. lineare* with 11 other species of *Melampyrum* and 21 other closely related taxa does not support a close relationship between *M. lineare* and *M. pratense*. Rather, the bootstrap 50% majority-rule consensus tree provides minimal support for a sister grouping of *M. lineare* with two Asian species, *M. klebelsbergianum* and *M. roseum*, while the 50% majority-rule consensus tree places *M. lineare* as sister to a large clade containing *M. pratense*, with *M. klebelsbergianum*

and *M. roseum* sister to this grouping. If *M. lineare* is indeed descended from Asian species of *Melampyrum*, this implies a drastically different migration history than previously hypothesized. Inclusion of another widely distributed Asian species, *M. laxum*, and phylogenetic analysis of other markers will further elucidate the relationships between *M. lineare* and other members of *Melampyrum*.

A PRELIMINARY CHECKLIST OF THE FRESH-WATER PLANKTONIC MICROALGAE OF THE NORTH LAGOON AT CROOKED TREE, BELIZE, C. A. Stephen W. Fuller, Dept. of Biol., Univ. of Mary Washington, Fredericksburg, VA 22401. Tucked in on the south end of the Yucatan peninsula, on the east side, is the small country of Belize. The northern half of the country consists of low, flat habitats, generally not exceeding 330 feet in elevation, and including lagoons, and flat plains. The lagoons vary tremendously in volume, and hence water level, with the seasonal change from the rainy to the dry season. The fresh-water algal plankton of Belize is relatively unknown, with only two studies, in 2003 and '04, reporting on plankton from two lagoons in southern Belize. In March of 2013 the North Lagoon at Crooked Tree Wildlife Sanctuary was sampled, and 31 taxa were identified. The sample was dominated by Desmids, the Chlorophyta having the most diverse representation at 15 taxa. Species of *Pediastrum* and members of the Cyanobacteria were also prevalent. But frequently, specimens of *Synura*, *Scenedesmus*, and *Dinobryon* were observed, and less frequently, specimens of diatoms and *Euglena*. A thorough investigation of the fresh-water phytoplankton throughout the country and the seasons would provide an interesting exposition of this part of the community.

A PHYLOGENETIC TREE OF THE PEANUT GENUS *ARACHIS* (FABACEAE) BASED ON *TRNT-F*/ITS VS. ALLERGEN GENES. Jenna Sackenheim, Sheena Friend, Chandra Shrestha & Khidir Hilu, Department of Biological Sciences, Virginia Tech, Blacksburg, VA 24061. The legume genus *Arachis* L. (Fabaceae) contains 80 annual and perennial, diploid and polyploid species, including the economically important crop peanut (*Arachis hypogaea*). We are exploring the usefulness of the nuclear allergen genes in *Arachis* phylogenetics. Sequence information from two allergen orthologs Ara h 2 and Ara h 6 for 17 species of *Arachis* were analyzed with RAxML to assess the phylogenetic relationships among the species. The tree based on Ara h 2 was highly congruent with the ITS/*trnT-F* tree obtained by Friend et al. (2010). In contrast, the Ara h 6 tree, although resolving some of those relationships, failed to discern others. This shortcoming might be due to either differences in amount of phylogenetic signals or varying selection pressures operating on the orthologs. Our future study will focus on addressing the issues stated above.

Chemistry

PROGRESS TOWARDS THE SYNTHESIS OF DRAGOMABIN. Michelle K. Waddell, Dept. of Chem., Hampton University, Hampton, VA 23668. Malaria is a degenerative disease caused by a parasitic infection transmitted by infected female *Anopheles* mosquitoes. Worldwide 350-500 million cases have been reported with an attributed 1 million deaths. Currently, Artemisinin is the last line of defense against