Proc. Fla. State Hort. Soc. 131:17-19. 2018.



Vanilla Conservation, Genetics, and Opportunities for Southern Florida

Alan H. Chambers \ast_1 , Elias Bassil^1, Marcio Resende², and Aureliano Bombarely 3

¹Tropical Research and Education Center, University of Florida/IFAS, 18905 SW 280th St, Homestead, FL 33030

²Horticultural Sciences Department, University of Florida/IFAS, P.O. Box 110690, Gainesville, FL 32611-0690

³Department of Horticulture, Virginia Tech University, 301 Saunders Hall #301, Blacksburg, VA 24061

ADDITIONAL INDEX WORDS. Vanilla planifolia, diversity, genomics, conservation

Florida has four native Vanilla species and naturalized V. planifolia, the major commercial species. Vanilla in southern Florida is threatened by shrinking habitats. Our conservation work includes collection and propagation of our native species to ensure their survival in the long term. Additionally, we are using molecular methods to characterize these species. This preliminary work will support future research to further characterize these species at the genetic level.

The United States is the largest importer (~1,500-2000 metric tons annually) of cured vanilla beans, but increasing costs, faltering supply, and poor quality have put the vanilla industry in crisis mode. Cured vanilla bean prices have reached excessively expensive levels in recent years, increasing from ~\$30/kg to over \$600/kg. Drought, cyclones, disease, poor infrastructure, inefficient cultural practices, cultivar limitations, underdeveloped extension activities, and theft have resulted in poor and inconsistent vanilla bean yields. Thus, our domestic vanilla-based industries are limited by serious quality and supply concerns. Additionally, increasing vanilla prices and poor regulatory oversight of international producers have increased the incentives for adulterated products that increase buyer food risks and threaten consumer confidence (Hoffman and Zapf, 2011). As the demand for natural foods increases, there will be an increasing need for a consistent supply of premium-quality vanilla beans. This paper will review our current efforts related to vanilla science. Our primary objectives include 1) conservation of our four native Vanilla species, 2) testing the genetic and genomic diversity for a living collection of diverse Vanilla accessions, and 3) describing potential opportunities for growers in southern Florida that might be interested in Vanilla cultivation. This research fills critical knowledge gaps and reduces entry barriers for domestic growers targeting vanilla agro tourism and/or local production opportunities.

Materials and Methods

DNA EXTRACTION. DNA was extracted from mature vanilla leaves using the CTAB method as previously described (Chang

et al., 1993). 0.5 to 1 g leaf tissue was used for each 5 mL extraction buffer.

rbcL CLONING. The *rbcL* locus was amplified using primers 5' CTTCACAAGCAGCAGCTAGTTC 3' and 5' ATGTCAC-CACAAACAGAAAC 3' (Cameron, 2004)2004 using Phusion High Fidelity Polymerase. Amplicons were sequenced from one direction using the first primer above sentence. Published *rbcL* sequences from Vanilla species were obtained from NCBI.

SEQUENCE ANALYSIS. Multiple alignments and the creation of phylogenetic trees were conducted using Geneious V11.1.

Results

Vanilla Conservation

Native Florida vanilla orchids are unique, beautiful, and at high risk. Some native *Vanilla* species are so rare they are thought to be extirpated in their natural settings (i.e. *Vanilla dilloniana*). Habitat destruction, over-collection, and natural disasters make the conservation of these species necessary. Many conservation areas with native *Vanilla* species are spatially restricted, and a single disruptive event could eliminate existing populations. Therefore, we have applied for and received permits to collect each of the native *Vanilla species* while working with park biologists on our conservation efforts. Our ex situ collection strategy will enable propagation and reintroduction of these native species as guided by park staff.

Vanilla Genetics

Other researchers have published limited sequence data for a number of *Vanilla* species. These sequences can be used as barcodes to identify unknown accessions. This is particularly useful for identifying *Vanilla* accessions in the absence of flowers or other diagnostic morphological traits. We have found the

^{*}Corresponding author. Email: ac@ufl.edu



Fig. 1. Vanilla planifolia, V. pompona, V. phaeantha, and V. mexicana flowers shown from left to right.

rbcL gene to be the most useful target for *Vanilla* species identification due to ease of amplification/sequencing, the number of species with published sequence information, and its presence as a single copy gene.

Opportunities for Growers in Southern Florida

The climate of southern Florida and the existence of native species suggests that commercial vanilla production could be economically viable. Commodity vanilla beans are selling for record prices that might sustain domestic growers who have higher production costs. Alternatively, non-commodity vanilla beans grown in southern Florida could leverage premium markets including locally sourced, organic, or production of specialty types including $V. \times tahitensis$. There is also potential for supplementing income using agro-tourism models and selling value added products from locally-grown, cured, and extracted vanilla.

Vanilla cultivation requires infrastructure to provide an optimal growing environment. This primarily includes shade and trellising. The highest yield typically results from monoculture production in shade houses, though cultivation on tutor trees is also prevalent. Growing vanilla on existing fruit trees could provide supplemental income and reduce barriers to entry related to high initial costs.

Conclusions

Vanilla is an interesting genus from both academic and commercial perspectives. It is surprising that so little has been done towards the genetic improvement of this species given it is the second most valuable spice globally, and probably the world's favorite flavor. This preliminary work establishes critical capabilities for conservation, identification, and the genetic improvement of this species. Future work will be guided by academic, grower, industry, and consumer interests and needs.



Fig. 2. Circular phylogenetic tree using rbcL sequences to identify native Vanilla species. Accessions marked with an asterisk (*) were generated as part of this work.

Literature Cited

- Cameron, K.M., 2004. Utility of plastid psaB gene sequences for investigating intrafamilial relationships within Orchidaceae. Molecular Phylogenetics and Evolution 31:1157–1180.
- Chang, S., Puryear, J., and Cairney, J., 1993. A simple and efficient method for isolating RNA from pine trees. Plant Molecular Biology Reporter 11:113-116.
- Hoffman, P.G. and Zapf, C.M., 2011. Flavor, Quality, and Authentication, p. 162-182. In: Havkin-Frenkel, D. and Belanger, F. C. (eds.), Handbook of Vanilla Science and Technology. Blackwell Publishing, Hoboken, NJ.