

Origins, variation and domestication of vanilla: the case of *Vanilla tahitensis* J.W. Moore.
(Oral Presentation)

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Introduction

Vanilla Swartz [Orchidaceae] is a pan-tropical genus of more than 100 species of hemi-epiphytic and saprophytic herbs. While the source of over 95% of natural vanilla is the cured fruit of *Vanilla planifolia* G. Jacks. in Andrews, a rare, Mexico/Central America endemic, an important niche market also exists for *Vanilla tahitensis* J.W. Moore, coveted for its thicker, more oil-rich fruits and distinct flavor notes. Having never been found in the wild, *V. tahitensis* is overall most similar morphologically to neotropical *Vanilla*, and is unique in at least one respect: it is the only polyploid reported in the genus. On the basis of morphological characteristics, it has been hypothesized to be a recent hybrid between *V. planifolia* and either *Vanilla pompona* Schiede or *Vanilla odorata* Presl., two occasionally sympatric species. In order to test the hybrid origin(s) of *V. tahitensis*, sequence data from the ITS region of nrDNA and psbA-trnH non-coding region of cpDNA were generated to discern patterns of paternity, kinship, additivity, and overall phylogenetic signal. Non-congruence of the ITS and psbA-trnH topologies suggests genetic contributions from different species, with *V. planifolia* acting as the maternal donor. The mixed ploidy levels observed in *V. tahitensis*, and historical geography of vanilla domestication will be discussed.

Objectives

Determine evolutionary origin(s) of *Vanilla tahitensis* J.W. Moore. Specifically, test putative hybrid origin hypotheses, as well as determine whether mixed ploidy levels observed in *V. tahitensis* are best explained as part of an allo- or auto-polyploidization process.

Methods

Use of a combination of DNA sequence markers from nrDNA (ITS region) and cpDNA (psbA-trnH) to generate relationships between 15 neotropical taxa and *V. tahitensis*. Data analysis performed with PAUP to perform Neighbor Joining, Maximum Parsimony, and Maximum Likelihood analyses.

Results

V. tahitensis is most closely related to *V. planifolia* in cpDNA across all analyses. The ITS phylogeny shows a closer relationship of *V. tahitensis* to *V. odorata*. *V. odorata* and *V. planifolia* are quite divergent in both trees. Additivity of *V. tahitensis* between *V. odorata* and *V. planifolia* in ITS tree is low.

Conclusion

V. tahitensis is of hybrid origin. The overall lack of additivity observed in the sequence data, though, does not support F1 hybrid status. Preliminary results of an AFLP survey looking at genome-wide patterns of additivity will be presented.

Keywords: hybridization, polyploidy, spices, neotropics

Selected References

1. Besse, P., et al. 2004. RAPD genetic diversity in cultivated vanilla: *Vanilla planifolia*, and relationships with *V. tahitensis* and *V. pompona*. *Plant Science* 167:379-385.

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