—Scientific Note—

Genotyping-by-sequencing of Florida Passion Fruit Germplasm Reveals Accession Relationships

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The passion fruit genus, *Passiflora*, comprises more than 500 species that are admired for their ornate flowers and tropical-tasting fruit. The yellow or purple colored *P. edulis* Sims. is the most commercially important. Passion fruit vines are challenged by both abiotic and biotic stresses. Understanding the available genetic diversity allows breeders to combine favorable traits into elite cultivars.

Understanding diversity within a breeding germplasm is necessary for knowing how and when to use specific accessions. Molecular markers assist in breeding by enabling informed decisions related to parent selection, confirming parentage of potential hybrids, identifying mislabeled accessions and in resolving species assignments. The purpose of this study was to develop single nucleotide polymorphism (SNP) markers to characterize a passion fruit germplasm collection with an emphasis on native passion fruit species.

**Materials and Methods**

Plant DNA was extracted from 59 *Passiflora* accessions from 20 different species using a CTAB protocol. DNA samples were sequenced by the University of Minnesota Genomics Center with the restriction enzymes PstI and MspI. The resulting 78 million sequenced reads went through a bioinformatics pipeline to perform quality filtering, genome alignment, variant calling, and variant filtering, resulting in around ~5000 SNPs (single nucleotide polymorphism) available for downstream analyses.

**Results and Discussion**

The ~5k SNPs had uneven coverage across the nine chromosomes (Fig. 1). The average polymorphic information content i.e. the information value for SNPs, was 0.25. When considering *P. edulis* alone ~1300 SNPs were found to be polymorphic and could be used further in breeding and genomic studies to understand the genetic control of phenotypes. The average heterozygosity was 0.09 for *P. edulis* yellow fruited types (n = 15), 0.11 for purple-fruited types (n = 7), and 0.11 overall (n = 26, includes types with unknown fruit color). Lower values of heterozygosity indicate a smaller amount of diversity within the population analyzed.

A phylogenetic analysis based on identity by state resulted a dendrogram of groups of similar species and accessions. In the dendrogram a mislabeled accession was identified, all *P. edulis* grouped together both yellow and purple-fruit types. Eight passion fruit species native or invasive to Florida (including *P. biflora*, *P. foetida*, *P. incarnata*, *P. lutea*, *P. multiflora*, *P. pallens*, *P. sexflora*, and *P. pallida*) were well-separated as expected into subgenus (*Passiflora* and *Decaloba*) groupings. Four *P. laurifolia* seedlings showed patterns likely the resulting of a self-pollination. Interspecific hybrids between *P. edulis* and *P. incarnata* were confirmed. The resulting data can be applied to future passion fruit research and breeding both between species and within the commercial species.

![Fig. 1. SNP marker density mapped onto the nine chromosomes of the *P. edulis* genome.](image-url)