

Flavor Candidates through Polyploid Transcript Homogenization

1. Use GC/MS to identify presence/absence of fruit volatiles in two cultivars

		
Volatile A	present (+)	not detected(--)
Volatile B	not detected	present

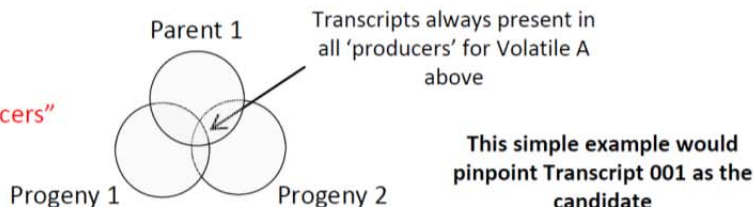
2. Cross lines exhibiting different volatile profiles, then score progeny for the volatile.

Progeny					
Volatile A	+	+	--	--	--
Volatile B	--	+	+	+	--

3. Sequence fruit RNA from individual parents and progeny

Transcript 001	+	+	--	--	--
Transcript 002	--	+	--	+	+
Transcript 003	+	--	--	--	--

4. Computationally merge transcriptome data into "producers" and "non-producers" to reveal candidates



When many plant transcriptomes are merged based on presence / absence of a volatile, the candidate list decreases rapidly, as transcripts not relevant homogenize and expose those that are related to the process.

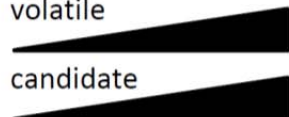
5. Validation. The previous experiments test presence / absence in genotypes and their inheritance. Where else do we see presence / absence in volatile production? Do transcript candidates match those patterns?

Accumulation with ripening



volatile

candidate



PASS!

Presence/absence with environment



+

+

PASS!

Presence/absence in other cultivars



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PASS!

CONCLUSION: The use of merged data sets between producers, comparison against non-producers, and validation by correlation through multiple developmental, environmental and genetic tests indicates a high likelihood of relevance between the candidate and the volatile.