

# Bad seeds: How the parental lineage may determine viability in tomato hybrids

September 6 2016

---



Representative seeds for each of the four cross types, obtained 60 days after pollination. From left to right, the bars quantify the average number of seeds per fruit in crosses among 'sib' plants of LA4329 (*S. chilense*), hybrid crosses with LA1616 plants (*S. peruvianum*) as pollen donors, hybrid crosses with LA4329 plants as pollen donors, and among 'sib' plants of LA1616. White bar proportions correspond to viable seeds, whereas gray proportions indicate shriveled, empty seeds. Note the coiled embryos in normal seeds from within-population crosses (4329 sib and 1616 sib) and the flat, inviable seeds (aborted embryos) from hybrid crosses, which are much smaller when LA4329 acts as pollen donor. Scale bar, 3 mm. Credit: Thomas Städler, Institute of Integrative Biology & Zurich-Basel Plant Science Center

Hybrid seeds have dramatically boosted yield for industrial scale crops such as corn, alfalfa and wheat. But for backyard tomato growers, sometimes the fruits of their labor can lie fallow as interbreeding among species of wild tomatoes often yields unviable seeds.

Now a group led by Thomas Städler at the Swiss Federal Institute of Technology (ETH Zurich), in collaboration with researchers at the University of Zurich, has performed the first study to investigate the genome-wide changes from interbreeding among closely related species of [wild tomatoes](#). They wanted to explore the molecular culprits responsible for the failure of the majority of hybrid seeds to grow from crosses between two closely related South American wild tomato species, *S. peruvianum* (found in southwestern Peru) and *S. chilense* (from northern Chile).

The new study by Ana Florez-Rueda et al., published in the advance online edition of the journal *Molecular Biology and Evolution*, has evaluated whether the fascinating and complex phenomenon of epigenetic genomic imprinting (a parental maternal or paternal bias as to whether or not a gene is turned on or off in the offspring) could be

contributing to the seed deaths. Genomic imprinting is known to be important for normal seed development in flowering plants and primarily occurs inside the nourishing endosperm compartment of the seed, which contains a triploid genome with a 2:1 ratio of maternal to paternal genomes.

Using next-generation sequencing tools and laser-microdissected seeds, they indeed found misregulated imprinting at play. Genome-wide shifts occurred that almost completely eliminated strongly paternally biased gene expression in seeds from the *S. peruvianum* cross with *S. chilense* (mom x dad, and less pronounced in the other direction of the hybrid cross), affecting core gene regulation and possibly contributing to hybrid seed failure. The relative dominance of the maternal expression may be a reflection of processes posited by the "kinship" theory that states that there should be genetic conflicts at work between maternally and paternally derived genes over the allocation of resources from mother to offspring.



Histological sections of developing seeds; one a "normal" within-species seed and the other a failing hybrid seed. Credit: Thomas Städler

The researchers observed a strong shift in the hybrid endosperm towards expression of the maternally-derived genes. The authors hypothesize that there has been divergence between species in gene expression machinery and that the bias in favor of the maternal transcriptional machinery will favor transcription of maternal transcripts. This hypothesis should be widely applicable to plant hybrids and could be an important factor in explaining differences in seed viability of interspecific crosses.

The findings provide new insights into factors affecting barriers to hybridization in flowering plants, as well as new insights into the molecular evolutionary forces at work that may promote reproductive isolation in recently diverged species.

"Our work should be seen as a "pilot" study uncovering somewhat novel phenomena in need of both mechanistic and evolutionary explanations, and not as providing clear-cut answers to a well-formulated problem," said Städler. "From the outset, however, we knew we would have to develop new (but simple) statistical tools to make full use of the subtle, often heterozygous nucleotide differences between parental plants to allow assignment of maternal and paternal expression proportions in their fertilization products, specifically, the endosperm compartment of the seed. Hence, there is also a practical aspect to our work that is likely to be useful for other researchers."

**More information:** *Molecular Biology and Evolution*, [DOI: 10.1093/molbev/msw175](https://doi.org/10.1093/molbev/msw175)

Provided by Oxford University Press

Citation: Bad seeds: How the parental lineage may determine viability in tomato hybrids (2016, September 6) retrieved 5 May 2024 from <https://phys.org/news/2016-09-bad-seeds-parental-lineage-viability.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.