IN BRIEF

No Scalpel Needed: Translatome of Pollen Tubes Growing within the Flower in *Arabidopsis*

In flowering plants, pollen deposited upon the stigma of a flower germinates to produce a pollen tube that must grow through the maternal transmitting tract and into the micropyle of an ovule in order to release its two sperm cells for double fertilization with the egg and central cell. In addition to pollen tubes being useful for studying polar cell growth, the myriad interactions between the paternal and maternal tissues leading to successful double fertilization (reviewed in Dresselhaus and Franklin-Tong, 2013) are a superb model in which to study cell–cell communication. Pollen tubes can be cultured in vitro, but it has become increasingly clear that signals from maternal tissue are vital for in vivo processes, including pollen germination and pollen tube guidance. The difficulty of isolating pollen tubes growing within the flower means that many questions about the details of pollen tube growth and sperm release during double fertilization remain. Various methods have been used to get around this obstacle, including manual dissection of pollen tubes at various stages after pollination.

Now, Lin et al. (pages 602–618) describe an alternative technique to characterize the translatome of pollen tubes growing within a flower. They used transgenic *Arabidopsis thaliana* plants in which expression of a FLAG-tagged L18 ribosomal protein was driven by a pollen-specific promoter. After pollination, Lin et al. isolated polysomes from the entire flower and purified those with the FLAG epitope tag. The associated transcripts, which presumably represent those that were actively being translated, were then analyzed on microarrays, revealing the translatome of pollen-derived tissue within the flower without relying on dissection.

After demonstrating that this approach does indeed lead to enrichment of pollen-specific transcripts from among those of the entire flower, the authors compared in vivo–grown pollen tubes to in vitro–grown ones, finding fairly large differences between the translatomes of the two. This is consistent with the fact that pollen tubes grown in vitro differ from those grown in vivo and underscores the importance of communication with maternal tissues. To find pollen tube proteins that might function in late stages of pollination, Lin et al. analyzed 41 transcripts that were highly enriched in in vivo–growing pollen tubes versus in vitro–grown pollen tubes or unpollinated flowers at the same stage. They analyzed mutants for these and found 12 with seed set phenotypes. Among these, three mutants showed aberrant pollen tube behavior, such as failure to release sperm cells, failure in guidance to the micropyle, and more than one pollen tube per ovule (see figure).

Thus, this scalpel-less approach to identifying genes expressed in pollen tubes during growth within the flower successfully revealed pollen tube proteins involved fundamental processes of double fertilization. This work nicely highlights the utility of microgenomics techniques to monitor cell-type-specific expression at a genome-wide scale (Bailey-Serres, 2013).

**REFERENCES**


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Pollen genes function in late stages of pollination. Scanning electron micrographs show successful pollen tube (arrow) guidance to the micropyle (arrowhead) of the ovule in the wild type (left). Pollen from heterozygous *iv2* (middle) or *iv6* (right) mutants on wild-type gynoecia show defects including more than one pollen tube per microspore (middle) or failed targeting to the micropyle (right). (Reprinted from Lin et al. [2014], Figure 6.)