

Metabolic fingerprinting: Using proteomics to identify proteins in gymnosperm pollination drops

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Proteins are vital parts of living organisms, performing a variety of essential functions such as DNA replication, catabolizing reactions, and responding to stimuli. The complete set of proteins expressed in an organism at a given time, under defined conditions, is known as the proteome. While the genome of an organism remains relatively stable, the proteome is remarkably dynamic, varying from cell to cell and even within a single cell and changing rapidly in response to developmental and environmental cues.

Proteomics is a powerful technique for examining the structure and function of the [proteome](#). For some organisms, proteomics can uncover the relationship between DNA, RNA, and the production of proteins—enabling the comparison of the genome to the proteome. For those organisms that have not yet been sequenced, proteomics facilitates the discovery and identification of proteins. In a new study published in the April issue of *Applications in Plant Sciences*, graduate student Natalie Prior and her colleagues demonstrate the suitability of proteomics in determining the composition of gymnosperm pollination drops.

"The biggest limitation in what we are doing is that there is no published gymnosperm genome," says Prior. "Most of the work on gymnosperms has been anatomical, histological, or morphological. The biochemical perspective is really lacking."

Mediating signaling between the pollen and the ovule, one role of the pollination drop is to provide a germination medium, which can be species specific. Additionally, in some species, anti-microbial proteins have been identified, suggesting that pollination drops provide protection in addition to acting as a landing spot for pollen grains.

"The proteins we are finding are really starting points for other research," says Prior. "We can identify these proteins, but there is a lot more research that can be done once we know what proteins are there."

Identification of the proteins found in [pollination](#) drops provides a metabolic fingerprint and thereby informs understanding of seed plant evolution. Comparing the proteomes of different species allows for identification of proteins, elucidating pollen-ovule interactions in gymnosperms.

"We are using proteomics to examine the biological relevance of the proteins that the [pollen grain](#) is exposed to in the drop," comments Prior. "It's fascinating to know if any of those proteins are consistent among groups of [gymnosperms](#) and what we can learn from that."

More information: The paper is available for free viewing at <http://www.bioone.org/doi/pdf/10.3732/apps.1300008>

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