Genome doubling, cell size and novelty

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In the 2019 Coulter Review, "Polyploidy, the Nucleotype, and Novelty: The Impact of Genome Doubling on the Biology of the Cell," published in the *International Journal of Plant Sciences* (180:1-52), Jeff J. Doyle and Jeremy E. Coate examine the effects of genome doubling on cell biology and the generation of novelty in plants.

Polyploidy, or the presence of more than two chromosomes in a cell, is common across many plant species. This "genome doubling" generates evolutionary novelty and is a prime facilitator of new species. How polyploidy alters cells to generate novelty, however, is complex, and, as Doyle and Coate illustrate, not well understood even on a fundamental level. Rapidly developing technology, however, will enable researchers to shed light not only on this integral part of plant evolution and biology, but also on the function of cells in general.

Many of the documented effects of genome doubling on cells, such as increases in cell size, nuclear volume and cell cycle duration, are hypothesized to be "nucleotypic—effects induced by changes in bulk DNA amount irrespective of genotype. Doyle and Coate update our understanding of the nucleotype and other mechanisms by which genome doubling can alter cell biology, hightlighting insights gained from studies of synthetic autopolyploids and relating these to the current state of knowledge in the field of cell biology.

Cell size in particular was of great interest to the authors, since it is strongly associated with genome doubling. Though it has long been known that genome size and cell size correlate, recent work shows that

this correlation is cell type-specific, and the factors that control cell size, polyploidy or otherwise, remain mysterious.

Doyle and Coate write that they had hoped the long running literature of cell biology would hold the answers to how polyploidy operates at the cellular level. "Instead, we discovered that these questions, as well as a host of other issues needed to address the question of what polyploidy "does," have yet to be answered satisfactorily," they write. "In many cases, there are competing theories, and often there exists a dearth of compelling data even in mature model systems, such as human and yeast, or in the best plant models, such as Arabidopsis and maize, let alone in non-model plant species."

The authors go on to suggest that in order to understand polyploidy, as well as cellular function in general, researchers must shift their focus to quantitative data, such as time resolution, rate constants, and local molecule concentrations, when analyzing polyploids against their diploid progenitors.

Doyle and Coate outline questions on polyploidy research going forward. These include how nuclear crowdedness varies with nuclear size across cell types and species, whether protein stability is affected by polyploidy, and whether changes in transcriptome size associated with polyploidy is a response to increased nuclear volume or vice versa.

"The technology exists to address such questions quantitatively, with ever-increasing precision and at ever-decreasing scales down to individual cells and molecules," they write. "We are now poised to address these questions and to understand what polyploidy 'does.'"