

IN BRIEF

A Transcriptomic Approach to Evolutionary Genetics of Giant Horsetail

Homosporous ferns and their relatives have surprisingly large chromosome numbers—a fact that has both stimulated and discouraged research into their genetics (reviewed in Hauffer, 2014). Among the outstanding questions about these species is how they came to contain so many chromosomes, including what role polyploidization played in the process and how it might have affected their evolutionary fitness. Members of the genus *Equisetum* (horsetail) serve as excellent representatives of these issues: The 15 living *Equisetum* species each have a chromosome number of 108 and together comprise what might be the oldest genus among extant vascular plants. *Equisetum* species are able to grow in waterlogged soil and efficiently accumulate nutrients. These factors have likely been key to the evolutionary longevity of horsetails, and the possible role of polyploidy in conferring the capacity for adaptation has been a matter of debate (reviewed in Van de Peer et al., 2009; Soltis et al., 2014; Vanneste et al., 2014).

Now, **Vanneste et al. (2015)** have revisited the issue of *Equisetum* evolution using modern genomic techniques. The authors sequenced and assembled the transcriptome of *Equisetum giganteum* (giant horsetail; see figure), generating a catalog of expressed genes that provided good coverage of the protein-coding *E. giganteum* genome. The age distribution of duplicated genes supported the conclusion that there was a single, ancient, whole-genome duplication in the *E. giganteum* lineage. This paleopolyploidy likely occurred in the Late Cretaceous period, possibly near the time when a number of other lineages underwent whole-genome duplication (Vanneste et al., 2014).

To examine whether this polyploidization might have influenced the capacity for adaptation, Vanneste et al. analyzed the



Equisetum giganteum. (Photo courtesy of E. Mizrachi and M. Ranik, 2010.)

putative functions of homoeologous genes. Among those enriched were regulation and development-related genes, consistent with results from other species and kingdoms showing that these functions are preferentially retained after whole-genome duplication. Interestingly, homoeologous genes were also enriched for functions related to nutrient metabolism and abiotic stress responses. These findings are particularly intriguing given the fact that horsetails are well adapted to grow in waterlogged conditions, in which soil is low in nutrients and oxygen. Thus, this pattern of retained gene expression is consistent with the idea that whole-genome duplication provided variation that could confer increased adaptability.

Together, this work addresses several outstanding questions. First, it appears that multiple rounds of polyploidy did not cause the high chromosome numbers in *Equisetum*, as had been proposed in the past. Instead, Vanneste et al. found evidence for only one polyploidization event. In addition, this study shows that, at least in this case, whole-genome duplication may have promoted evolutionary success. The surviving members of this genus have experienced great variation in environmental conditions. Based on the type of genes retained, the whole-genome duplication may have improved the lineage's ability to adapt to new environments and ecological niches.

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