

the unique evolutionary position of *A. trichopoda* should provide many insights into the evolution of flowering plants

Angiosperms (that is, flowering plants) are major crop plants and have a vital role as carbon sinks. Thus, analyses of their origins may give us important insights into these roles. Previous evidence strongly suggests that Amborella trichopoda is the single living species of the sister lineage to all other extant flowering plants. In three recent papers, the Amborella Genome Project team and other authors publish a new approach for sequencing non-model species such as A. trichopoda, present its genome and provide evidence that surprisingly large amounts of horizontal gene transfer events have contributed to its mitochondrial genome.

Chamala *et al.* describe a new sequencing and assembly pipeline strategy for non-model species that have large and complex genomes. They first produced a whole-genome assembly using a combination of 454, Illumina and Sanger sequencing of bacterial artificial chromosome ends. They then evaluated the accuracy of the assembly by fluorescence *in situ* hybridization — a technique that has not been exploited in this way before. Finally, to further improve the contiguity of the assembly, they carried out whole-genome mapping

(formally known as optical mapping), which allows the ordering of restriction enzyme-digested fragments of the genome, that closed up the remaining gaps in the assembly.

The Amborella Genome Project team annotated the A. trichopoda nuclear sequence and used it to analyse the evolution of angiosperms. Structural analysis confirmed a whole-genome duplication event in the common ancestor of angiosperms but revealed no further such events in the lineage that led to A. trichopoda. This nuclear genome therefore serves as an excellent reference for elucidating genome evolution in other flowering plants. For example, the authors were able to reconstruct the ancestral, pre-hexaploid gene arrangement of core eudicots, which constitute some 75% of angiosperms.

The authors' comparison of the *A. trichopoda* nuclear genome with 22 land plant genomes identified more than 1,000 genes that first appeared in angiosperms and that are probably associated with their origin. However, they found that many flowering-related genes predate the origin of angiosperms, which indicates that these genes were co-opted into floral functions.

Rice et al. present the mitochondrial genome of A. trichopoda which, at 3.9 Mb, is bigger than many bacterial genomes. As a result of horizontal gene transfer, it contains six equivalents of mitochondrial genomes that have been acquired from green algae, moss and other angiosperms. This scale of horizontal gene transfer that includes four whole-genome transfers has not been seen before. As the foreign DNA was gained in such large stretches and was derived exclusively from mitochondria of green plants, the authors posit that the transfers occurred by capture of entire mitochondria, followed by mitochondrial fusion.

The mitochondrial DNA of *A. trichopoda* is thought to be so unusual because *A. trichopoda* is more exposed to epiphytes — non-parasitic plants that grow on other plants — than most plants and because it has a propensity to sustain wounds and produce sucker sprouts that could result in mitochondrial transfer. Finally, it has an unusually low rate of mitochondrial DNA loss.

The new sequencing strategy will no doubt be useful to other non-model organisms, and the unique evolutionary position of *A. trichopoda* should provide many insights into the evolution of flowering plants. The horizontal gene transfer raises many questions about mechanisms of mitochondrial gene transfer and the evolution of mitochondrial fusion.

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ORIGINAL RESEARCH PAPERS Chamala, S. et al.
Assembly and validation of the genome of the nonmodel basal angiosperm Amborella. Science 342, 1516–1517 (2013) | Amborella Genome Project. The Amborella genome and the evolution of flowering plants. Science 342, 1241089 (2013) | Rice, D. W. et al. Horizontal transfer of entire genomes via mitochondrial fusion in the angiosperm Amborella. Science 342, 1468–1473 (2013)