



Architecture and evolution of a minute plant genome

Abstract:

It has been argued that the evolution of plant genome size is principally unidirectional and increasing owing to the varied action of whole-genome duplications (WGDs) and mobile element proliferation. However, extreme genome size reductions have been reported in the angiosperm family tree. Here we report the sequence of the 82-megabase genome of the carnivorous bladderwort plant *Utricularia gibba*. Despite its tiny size, the *U. gibba* genome accommodates a typical number of genes for a plant, with the main difference from other plant genomes arising from a drastic reduction in non-genic DNA. Unexpectedly, we identified at least three rounds of WGD in *U. gibba* since common ancestry with tomato (*Solanum*) and grape (*Vitis*). The compressed architecture of the *U. gibba* genome indicates that a small fraction of intergenic DNA, with few or no active retrotransposons, is sufficient to regulate and integrate all the processes required for the development and reproduction of a complex organism.