Small genome size of *Utricularia gibba* problematic for evolution but not creation

Jean O'Micks

The carnivorous bladderwort, *Utricularia gibba* (see fig. 1), lives in low-nutrient ecosystems like marshes and bogs. It has a reduced leaf and root system. What makes *U. gibba* so unique is its highly specialized bladders, which employ biomechanics to suck in the plant's prey. Cells in the bladder are capable of storing protons in the intermembrane space of the mitochondrion, thereby making ATP-catalysis possible, which can be used to drive water out of the bladder after use. Bristles on the bladder also make them resemble microcrustaceans, which also help them attract prey. This specialized anatomical structure in this plant species is an example of irreducible complexity.

Evolutionists recently analyzed the compact small-scale genome of the carnivorous bladderwort species *Utricularia gibba*, which is about 82 Mbp (million base pairs) in size, and contains only around 3% non-protein-coding DNA.[1,2] This species counts as a sort of minimal flowering plant with its very small genome. By comparison, the species *Genlisea hispidula* from the same family of *Lentibulariaceae* has a genome of 1.51 Gbp (billion base pairs). It is postulated that *U. gibba* has undergone an extreme reduction in genome size. However, it contains about the same number of genes (about 28,500) as other plant species. Evolutionists speculated that intergenic, non-coding DNA that is much more abundant in other plants is not needed for normal physiological functioning (because *U. gibba* seems to function without it). According to Victor Albert, biologist at the University of Buffalo and a member of the team that analyzed the *U. gibba* genome, biological activity doesn't necessarily mean there is a function.[2] In this manner evolutionists are trying to resuscitate the old junk DNA hypothesis that non-coding intergenic material really doesn't have any function despite decades of research proving the opposite. However, upon closer inspection of this organism, we can see that a smaller genome size doesn't mean that non-coding DNA in other plants is really functionless. Furthermore, the small size of the *Utricularia* genome may point to a loss of genetic material, which would be *devolution*, not evolution.

Genomic contraction in *U. gibba*

U. gibba supposedly diverged from other *Utricularia* species about 5–15 Ma. It is notable that this species supposedly resulted from a loss of genes, some of which are related to its unusual embryogenesis, lack of distinction between shoot and leaf, and its lack of true roots—that is, its relatively simple structure. A list of *Arabidopsis* homolog genes involved in these processes that are not present or reduced in number in *U. gibba* can be seen in table 1. Furthermore, promoter regions and introns have also been compacted in *U. gibba*, along with fewer exons and numerous solo LTR (long terminal repeat) elements, giving evidence that numerous large-scale recombinations have taken place. It is interesting, however, that the plastid and mitochondrial intergenic regions were not affected by the contraction, despite a highly increased nucleotide substitution rate.[4] This is what we would expect if they also contained little to no functionless genetic elements. The plastid and mitochondrial genomes of *U. gibba* are also similar to that of *Arabidopsis*. Gene loss due to reduced function is something that would be expected based on creation, which predicts loss of genetic information due to the effects of entropy in genomes.[5] Consistent with this idea, the lack of roots may be due to missing developmental programs needed for the expression of genes in root formation.[4] Again, this would be more in line with creation, which would predict such a loss of genetic information through degenerative mutations.

Figure 1. *Utricularia gibba* (from *Britton and Brown*[3]).

It is significant that not only does *U. gibba* have a reduced genome, but also a somewhat reduced body plan to go along with it. As mentioned earlier, the plant doesn't even have a root system. Furthermore, it lives in nutrient-poor environments, and has to acquire much of its organic nitrogen, phosphorus and carbon from carnivory, since the plant lacks the genes to assimilate these minerals. The plant secretes sugars into its environment that attract microbes

Table 1. Some *Arabidopsis* homolog genes missing or in reduced numbers in *U. gibba.*

Gene symbol	Function
AT1G68170	Nodulin MtN21 transporter
PEI1	embryo-specific zinc finger transcription factor required for heart-stage embryo formation
FD	involved in flowering but also expressed in embryos and cotyledons
CASP	Casparian Strip Membrane Domain Protein
WAK	a cell-wall-associated Ser/Thr kinase involved in cell elongation and lateral root development
NAXT1	a nitrate efflux transporter mainly expressed in the cortex of adult roots
MYB48/59	nitrogen-responsive genes involved in the regulation of cell cycle progression and root growth
ANR1, XAL1	MADS box proteins

which in turn secrete allelochemicals that attract microcrustaceans, which serve as the plant's prey.[6]

Comparison with the *Arabidopsis* genome

A similar genomic contraction phenomenon supposedly occurred between two *Arabidopsis* species; namely *A. lyrata* and *A. thaliana*, which are 207 and 125 Mbp, respectively, and contain 32,670 and 27,025 genes, respectively. These two species supposedly diverged 10 Ma ago,[7] a similar time-frame to the supposed divergence of *U. gibba* from other *Utricularia* species. According to the evolutionists' logic, this would therefore mean that the 5,645-gene difference between the two *Arabidopsis* species means that the extra genes in *A. lyrata* are also functionless, just like the 'missing' non-coding intergenic elements in the genome of *U. gibba*. This however, clearly does not follow. It is highly unlikely that *A. thaliana* is the result of a deletion process from *A. lyrata* since more than 50% of the *A. lyrata* genome doesn't match up with the *A. thaliana* genome. Only a small percent of the *A. thaliana* genome is made up of pseudogenes, which we would have expected to have accumulated from the *A. lyrata* genome if it was truly derived from this species. Hu *et al.* state that 90% of the size difference between the two genomes is due to hundreds of thousands of smaller insertions or deletions, mainly in intergenic regions.[7]

Whole genome duplications in *U. gibba* and other plants

One of the great paradoxes of the *U. gibba* genome is that the authors propose that this species had undergone three whole genome duplications (WGD) before it reached its present state.[2] Species belonging to the genus *Utricularia* have genomes varying from 88 Mbp to 401 Mbp (see table 2, taken from Greilhuber [8]). Thus, despite differences of hundreds of millions of base pairs in genetic material, evolution is not capable of anything more than variation within the *Utricularia* genus.

WGDs, as polyploidy events are, are admitted by some evolutionists to be unimportant evolutionary dead ends, even though they are very common (happening in about 35% of plant species[9]). They are subsequently followed by a stabilizing phase called diploidization. Instability attributed to WGDs is associated with pathological conditions such as cancer and gall formation in plants.[10] Furthermore, newly polyploid cells generally have a smaller surface-to-volume ratio, causing lower growth rates, and changes in protein concentrations affecting cellular kinetics, as well as changes in genetic and epigenetic gene expression. Furthermore, polyploid speciation rates are significantly lower than those of diploids, and are not significantly differentiated from their diploid relatives.[11] According to evolution, polyploidization would create large chunks of raw genetic material, making it possible for a great many genes to evolve, thus making large-scale speciation possible, yet practically this is not the case.

Table 2. Genome sizes of different *Utricularia* species.

***Utricularia* species name**	**Genome size in Mbp**
australis	175
blanchetii	135
gibba	88.3
humboldtii	232
livida	252
microcalyx	214
parthenopipes	140
praelonga	158
prehensilis	401
pubescens	216
quelchii	157
reniformis	328
sandersonii	235
subulata	247

Evolutionists speculate that different plant genomes arose from each other due to WGDs. It is noteworthy that even though there are large-scale similarities between different plant genomes when compared to each other, colinearity between species is disrupted at the microlevel by small inversions, tandem duplications, multiple gene insertions and/or deletions and translocations.[12]

Contrary to evolutionary speculations, plants may have genes in duplicate copies simply because they need them. As we have seen, loss of genetic material due to devolutionary processes is widespread, thus having duplicate copies of genes would help the plant buffer against the loss of such genes.

Retention of conserved non-coding sequences during gene fractionation

Furthermore, a specific post-WGD event also suggests that non-coding genetic elements do have functions: gene fractionation. Following a WGD, each gene *as well as its regulatory sequences* are present in two copies. Over time, different groups of genes are either retained or lost in different numbers. Schnable *et al*.[13] showed that certain groups of genes, such as transcription factors, which are associated with a large number of conserved non-coding sequences (CNSs), are preferentially retained during this fractionation process, along with their relatively higher number of CNSs. High-level upstream transcription factors tend to be under tight regulation themselves, containing a large number of transcription factor binding sites. It is because of the functionality of these regulatory sites within CNSs that evolutionists think these sites are conserved.

Conclusion

To deny the functionality of non-coding genetic elements based on the single case of *U. gibba* is superficial, and denies decades of thorough scientific work proving that at least many non-coding genetic elements have function. Biological activity doesn't *necessarily* equate to function, but scientific progress may discover functions later, as has been proven and is proving to be the case. This plant species seems to have undergone a set of WGDs, after which it lost a lot of its unnecessary genetic material due to its relatively simple morphology (such as its missing root system). If compared to two *Arabidopsis* species, by similar logic we would come to the faulty conclusion that neither do (protein-coding) genes carry any meaningful information.

WGDs are rather common in plant species, but rarely lead to speciation events. Mayrose *et al.*[14] report that polyploid speciation rates are even lower than that of the diploids, while their extinction rates are higher. They also found that polyploidization events were found disproportionately on the tips of evolutionary phylogenetic trees, from which they deduced that polyploidy lineages fail to persist.

Furthermore, the genomes of *U. gibba* and *A. thaliana* have undergone genome contractions, which do not lend support to evolution, which demands novel genetic material to increase complexity. However, it is consistent with creation, which states that genomes lose material and information over time as part of a devolutionary process during which organisms adapt to a newer environment. This however, doesn't necessarily mean that the lost non-coding elements do not have any function. The genomes of living organisms can be seen to harbor genetic elements redundantly (sort of like the spare wheel on a car), so that an organism is buffered against the loss of these elements in case it acquires a new niche to live in where they are needed.

References

1. Sukel, K., Is noncoding DNA required for complex life? *Biotechniques,* 14 May 2013.
2. Ibarra-Laclette, E., Lyons, E., Hernández-Guzmán, G. *et al.,* Architecture and evolution of a minute plant genome, *Nature* **498**:94–98, 2013; doi: 10.1038/nature12132.
3. Britton, N.L. and Brown, A., *An illustrated flora of the northern United States, Canada and the British Possessions,* vol. 3, Charles Scribner's Sons, New York, p. 228, 1913.
4. Ibarra-Laclette, E., Albert, V.A.L., Pérez-Torres, C.A., *et al*., Transcriptomics and molecular evolutionary rate analysis of the bladderwort (*Utricularia*), a carnivorous plant with a minimal genome, *BMC Plant Biol.* 2011 Jun 3;11:101; doi: 10.1186/1471-2229-11-101.
5. Sanford, J.C., *Genetic Entropy and the Mystery of the Genome*, Ivan Press, Lima, New York, 2005.
6. Albert, V.A., Jobson, R.W., Michael, T.P. and Taylor, D.J., The carnivorous bladderwort (Utricularia, Lentibulariaceae): a system inflates, *J. Experimental Botany* **61**(1):5–9, 2010; doi: 10.1093/jxb/erp349.
7. Hu, T.T., Pattyn, P., Bakker, E.G., Cao, J. and Cheng, J.F., The *Arabidopsis lyrata* genome sequence and the basis of rapid genome size change, *Nature Genetics* **43**(5):476–81, 2011; doi: 10.1038/ng.807.
8. Greilhuber, J., Borsch, T., Müller, K., *et al*., Smallest angiosperm genomes found in lentibulariaceae, with chromosomes of bacterial size, *Plant Biology* (Stuttgart) **8**(6):770–777, 2006.
9. Wood, T.E., Takebayashi, N., Barker, M.S., *et al*., The frequency of polyploid speciation in vascular plants, *Proc. Natl. Acad. Sci. USA* **106**(33):13875–13879, 2009; doi: 10.1073/pnas.0811575106.
10. Mayfield-Jones, D., Washburn, J.D., Arias, T., *et al*., Watching the grin fade: tracing the effects of polyploidy on different evolutionary time scales, *Semin Cell Dev Biol.* **24**(4):320–331, 2013; doi: 10.1016/j.semcdb.2013.02.002.
11. Arrigo, N., Barker, M.S., Rarely successful polyploids and their legacy in plant genomes, *Current Opinions in Plant Biology* **15**(2):140–146, 2012; doi: 10.1016/j.pbi.2012.03.010.
12. Devos, K.M., Updating the 'crop circle', *Current Opinions in Plant Biology* **8**(2):155–162, 2005.
13. Schnable, J.C., Pedersen, B.S., Subramaniam, S. and Freeling, M., Dose-sensitivity, conserved non-coding sequences, and duplicate gene retention through multiple tetraploidies in the grasses, *Frontiers Plant Sci.* **2**:2, 2011; doi: 10.3389/fpls.2011.00002.
14. Mayrose, I., Zhan, S.H.I., Rothfels, C.J., *et al*., Recently formed polyploid plants diversify at lower rates, *Science* **333**(6047):1257, 2011; doi: 10.1126/science.1207205.