



## **ABSTRACT**

*“Of Mamiellales, the green yeasts, as models for Plant Systems Biology, and of mobile introns”*

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The interest of plant scientists for Mamiellales, comes from the assumption that the ancestor to all other Viridiplantae was part of it. Mamiellales are widespread marine picoplankters and the complete genome sequence has been obtained for six of these unicellular green algae, including *Ostreococcus* (x3) , *Micromonas* (x2) and *Bathycoccus*, all of these annotated by our group in Ghent. These genomes are small, from 13 to 22Mb, harboring from 7.500 to 10.000 genes showing no duplication in most cases. Added to easy cultivation and replacement mutation, these features makes these algae, especially the tiny *Ostreococcus tauri*, an interesting model to study gene networks for the traits which are conserved within the green lineage, bringing a frame on which to branch the duplication complexity of higher plants, in the same way yeasts are used towards animals.

The sequenced genomes of Mamiellales have a unique heterogeneity, two chromosomes having specific features compared the rest of the genome, which may be related to sex and speciation. I will also present and discuss in this talk the unexpected observation that the genomes of the two *Micromonas* species which have been sequenced harbor many invading introns which are copies of each other, and are inserted at novel positions in the genes. This was the first observation of this kind of event; it illuminates the way intron can be gained, and shakes the current assumption that introns have been acquired at the birth of eukaryotes and have essentially been lost since.