

Klaas Vandepoele, Cedric Simillion, Cindy Martens and Yves Van de Peer

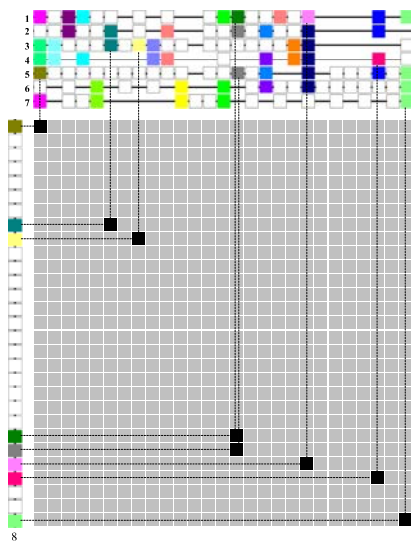
Bioinformatics & Evolutionary Genomics division, Department of Plant Systems Biology, Flanders Interuniversity Institute for Biotechnology (VIB), Ghent University, Technologiepark 927, B-9052 Ghent, Belgium, E-mail: Klaas.Vandepoele@psb.ugent.be

Introduction

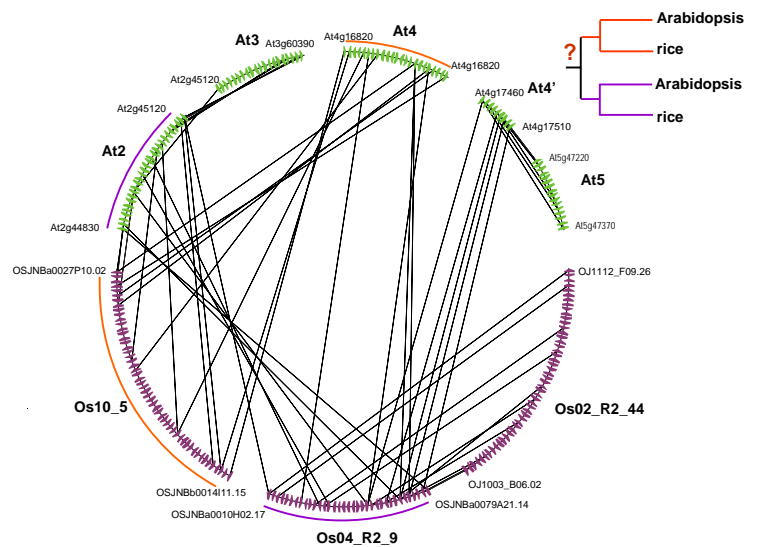
Detailed analyses of the genomes of several model organisms revealed that large-scale gene or even entire genome duplications have played a prominent role in the evolutionary history of many eukaryotes. Recently, we presented strong evidence that the genomic structure of the dicotyledonous model plant species *Arabidopsis thaliana* is the result of multiple rounds of entire genome duplications (Simillion et al., 2002). A detailed analysis of the genome of the monocotyledonous model plant rice (*Oryza sativa*) also showed that a substantial fraction of all rice genes are found in duplicated segments (Vandepoele et al., 2003). To better understand the extent to which such events influence gene and genome evolution and to identify the features that determine the heterogeneous retention/loss of gene duplicates, we are currently analyzing these duplications in more detail using data of other plants species.

Strategy & Results

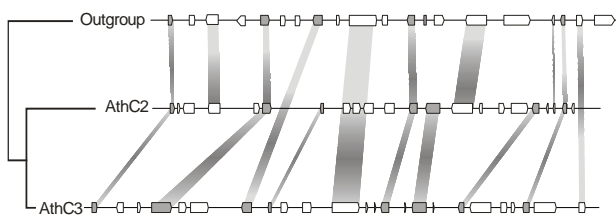
Applying colinear profiles for the detection of genomic homology



i-ADHoRe analysis on Arabidopsis and rice

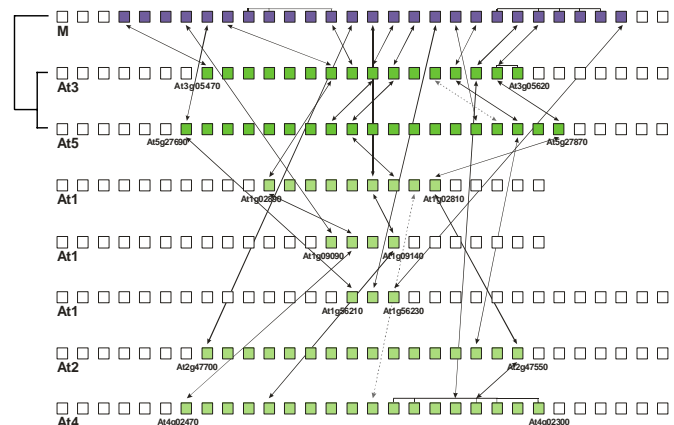


Comparative analysis of structural and functional divergence in duplicated genomic segments of Arabidopsis



- Which genes are retained after a duplication?
- How fast do genes disappear?
- Relation between the retention of genes and their position in the genome?
- Functional bias in gene retention?

Colinearity between Medicago and Arabidopsis



Conclusions

Evolutionary comparative analysis will provide new insights into the retention of gene duplicates in the context of their functional classification and gene family evolution. Moreover, detailed cross-species studies using orthologous chromosomal regions from related species should reveal patterns of gene loss, rearrangements and sub-functionalization in duplicated segments.