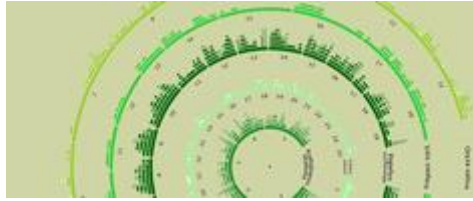


Evolution of plant genomes: a tale of duplications



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Genomes form the blueprints of life and decoding them provide insights into the lifestyle, evolution, and adaptation of their hosts. Genomes of plants are highly dynamic entities that, during their evolutionary past, have been rearranged extensively, often as a result of duplications due to ancient polyploidy events (where entire genomes are being duplicated).

The figure shows part of a so-called circle plot representing chromosomes or parts of chromosomes for *Arabidopsis thaliana*, papaya (*Carica papaya*), poplar (*Populus trichocarpa*), grapevine (*Vitis vinifera*) and rice (*Oryza sativa*).

Stacks (containing at least 30 genes) denote duplicated (homologous) segments that have been identified with bioinformatics and computational tools. Parts from a stack that are shown as being hollow represent duplicated segments that could only be uncovered through the use of sophisticated methodology, while filled boxes represent segments for which the homology is rather obvious.

Identifying such 'stacks of duplicated segments' is important for unveiling the number of genome duplications a genome (species) has undergone during evolution, and provide information about which genes could potentially give rise to novel gene functions.