

TRANSPOSITION MEDIATED DECONSTRUCTION OF A (PALEO)POLYPLOID GENOME

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Plants have followed a reticulate type of evolution and taxa have frequently merged via allopolyploidization. The polyploid structure of sequenced genomes has been frequently proposed, but the chromosomes belonging to putative component genomes are difficult to identify. The grapevine chromosomes are, evolutionary, stable structures, existing in triplicate copies.

We focused our investigation on the grapevine *Nucleotide Binding Site (NBS)* gene family in order to better understand mechanisms underlying the evolution of the grapevine genome.

We show that, in grapevine, i) helitrons have significantly contributed to *NBS* genes transposition; ii) *NBS* gene cluster similarity indicates the existence of two groups of chromosomes that may have evolved independently.

Time estimation indicates that grapevine component genomes may have fused around 60 mya, having had at least 40-60 mya to evolve independently. Chromosome triplets consist of two Va and one Vc chromosomes, as expected from tetraploid and diploid conditions of two component genomes. The hexaploid state could be derived from allopolyploidy, or the Va and Vc component genomes were separated in the same nucleus before fusion, as known for Rosaceae species. Chromosome number variation in the Vitaceae and related families, and the gap between the time of eudicot radiation and the age of Vitaceae fossils, are accommodated in the frame of our hypothesis.

In conclusion, two groups of grapevine chromosomes seem to have evolved independently, opening the possibility that a tetraploid and a diploid genomes merged to generate the extant hexaploidy state of grapevine.