Project Papers – The Correlation of Genome Size and Life Form

Jakob, S.S., A. Meister, F. R. Blattner. (2004). *The Considerable Genome Size Variation of Hordeum Species (Poaceae) Is Linked to Phylogeny, Life Form, Ecology, and Speciation Rates*. Molecular Biology and Evolution, Volume 21, Issue 5, 1 May 2004, Pages 860–869, <https://academic.oup.com/mbe/article/21/5/860/1014084>

Abstract:

Genome size variation in plants is thought to be correlated with cytological, physiological, or ecological characters. However, conclusions drawn in several studies were often contradictory. To analyze nuclear genome size evolution in a phylogenetic framework, DNA contents of 134 accessions, representing all but one species of the barley genus Hordeum L., were measured by flow cytometry. The 2C DNA contents were in a range from 6.85 to 10.67 pg in diploids (2n = 14) and reached up to 29.85 pg in hexaploid species (2n = 42). The smallest genomes were found in taxa from the New World, which became secondarily annual, whereas the largest diploid genomes occur in Eurasian annuals. Genome sizes of polyploid taxa equaled mostly the added sizes of their proposed progenitors or were slightly (1% to 5%) smaller. The analysis of ancestral genome sizes on the base of the phylogeny of the genus revealed lineages with decreasing and with increasing genome sizes. Correlations of intraspecific genome size variation with the length of vegetation period were found in H. marinum populations from Western Europe but were not significant within two species from South America. On a higher taxonomical level (i.e., for species groups or the entire genus), environmental correlations were absent. This could mostly be attributed to the superimposition of life-form changes and phylogenetic constraints, which conceal ecogeographical correlations.

Grotkopp, E, M. Rejmánek, M. J. Sanderson, and T. L. Rost. *Evolution of Genome Size In Pines (Pinus) And Its Life-History Correlates: Supertree Analyses. Evolution 58(8):1705-1729. 2004.* [*http://www.bioone.org/doi/abs/10.1554/03-545*](http://www.bioone.org/doi/abs/10.1554/03-545)

Abstract:

Genome size has been suggested to be a fundamental biological attribute in determining life-history traits in many groups of organisms. We examined the relationships between pine genome sizes and pine phylogeny, environmental factors (latitude, elevation, annual rainfall), and biological traits (latitudinal and elevational ranges, seed mass, minimum generation time, interval between large seed crops, seed dispersal mode, relative growth rate, measures of potential and actual invasiveness, and level of rarity). Genome sizes were determined for 60 pine taxa and then combined with published values to make a dataset encompassing 85 species, or 70% of species in the genus. Supertrees were constructed using 20 published source phylogenies. Ancestral genome size was estimated as 32 pg. Genome size has apparently remained stable or increased over evolutionary time in subgenus *Strobus*, while it has decreased in most subsections in subgenus *Pinus*. We analyzed relationships between genome size and life-history variables using cross-species correlations and phylogenetically independent contrasts derived from supertree constructions. The generally assumed positive relation between genome size and minimum generation time could not be confirmed in phylogenetically controlled analyses. We found that the strongest correlation was between genome size and seed mass. Because the growth quantities specific leaf area and leaf area ratio (and to a lesser extent relative growth rate) are strongly negatively related to seed mass, they were also negatively correlated with genome size. Northern latitudinal limit was negatively correlated with genome size. Invasiveness, particularly of wind-dispersed species, was negatively associated with both genome size and seed mass. Seed mass and its relationships with seed number, dispersal mode, and growth rate contribute greatly to the differences in life-history strategies of pines. Many life-history patterns are therefore indirectly, but consistently, associated with genome size.

Mechanisms of Recent Genome Size Variation in Flowering Plants <https://academic.oup.com/aob/article/95/1/127/198516>

Abstract

• Background and Aims Plant nuclear genomes vary tremendously in DNA content, mostly due to differences in ancestral ploidy and variation in the degree of transposon amplification. These processes can increase genome size, but little is known about mechanisms of genome shrinkage and the degree to which these can attenuate or reverse genome expansion. This research focuses on characterizing DNA removal from the rice and Arabidopsis genomes, and discusses whether loss of DNA has effectively competed with amplification in these species.

• Methods Retrotransposons were analyzed for sequence variation within several element families in rice and Arabidopsis. Nucleotide sequence changes in the two termini of individual retrotransposons were used to date their time of insertion.

• Key Results An accumulation of small deletions was found in both species, caused by unequal homologous recombination and illegitimate recombination. The relative contribution of unequal homologous recombination compared to illegitimate recombination was higher in rice than in Arabidopsis. However, retrotransposons are rapidly removed in both species, as evidenced by the similar apparent ages of intact elements (most less than 3 million years old) in these two plants and all other investigated plant species.

• Conclusions Differences in the activity of mechanisms for retrotransposon regulation or deletion generation between species could explain current genome size variation without any requirement for natural selection to act on this trait, although the results do not preclude selection as a contributing factor. The simplest model suggests that significant genome size variation is generated by lineage-specific differences in the molecular mechanisms of DNA amplification and removal, creating major variation in nuclear DNA content that can then serve as the substrate for fitness-based selection.

Genome Size Variation and Plant Systematics. <https://academic.oup.com/aob/article/82/suppl_1/75/211192>

Abstract: The importance of genome size, as a useful taxonomic marker, has been stressed in many studies based on different groups. A critical appraisal of intraspecific variability reported in various species so far shows that the plant genome is fairly stable (taking a narrow species concept) and is one of the salient features defining a biological species. Large differences in DNA amounts may exist at the infrageneric level which may be correlated with various adaptive traits at nuclear, cellular, tissue and organismic levels. Therefore, being an adaptive character, a comparison of nuclear C-values in conjunction with other characters may provide a natural way to elucidate evolutionary relationships. In a number of cases it is possible to study whether gain or loss of DNA has occurred during speciation which may coincide with the existing taxonomic treatment and presumed evolutionary relationships within a narrow taxonomic group. The present account deals with many recent examples which highlight the importance of genome size in microsystematics.

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