

Nuclear DNA C-values of multicellular eukaryotic algae

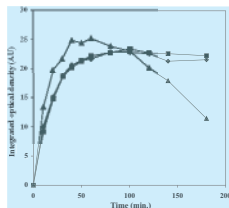
C-values have been published for less than 1 % of the described species of multicellular eukaryotic algae.

Kapraun (pp. 7–44) doubles the number of taxa investigated and compares known nuclear DNA contents with emerging molecular phylogenies.



DNA amounts (C-values) for 804 angiosperm species

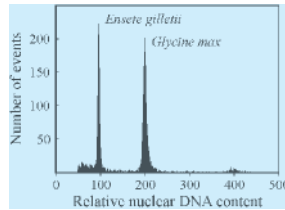
Increasing the availability of C-value data is a key goal for plant genome size research. **Bennett and Leitch (pp. 45–90)** contribute to this by collating C-values for 804 species taken from 88 original references, including values for 628 species not listed in any of the six previous compilations by Bennett and colleagues.



Intraspecific variation in genome size in angiosperms – identifying intraspecific variation and best practice

In the face of accumulating genome size data, more critical investigations of methods and rules for best practice are urgently needed. **Greilhuber (pp. 91–98)** reviews case studies on intraspecific variation and investigates the critical

steps of the Feulgen reaction for estimating nuclear DNA in plants.



Plant DNA flow cytometry and estimation of nuclear genome size

Flow cytometry is a popular method for estimating the absolute amounts of nuclear DNA in plants. **Doležel and Bartos (pp. 99–110)** review current procedures. They discuss methodological pitfalls encountered in estimating intraspecific variation in genome size and problems linked to the use of DNA flow cytometry for fieldwork.



Temperature-induced errors in estimating genome size

Noirot et al. (pp. 111–118) show that, in two coffee species and *Petunia hybrida*, nuclear DNA measurements by flow cytometry are affected by the temperature in which extracted nuclei are suspended (range 21–84 °C). The authors discuss the consequences of these observations on data interpretation, propose stoichiometric error detection methods and suggest approaches for minimizing these errors.



Review of impact of variation in nuclear DNA C-values

The existence and significance of intraspecific DNA C-value variation

remain controversial, because of possible measuring artefacts.

However, examples continue to be reported that are generated using best practice methodology. **Murray (pp. 119–125)** reviews whether this variation affects phenotype or contributes to population divergence. Both are key issues for speciation and taxonomy.



Competing increases and decreases in nuclear genome size

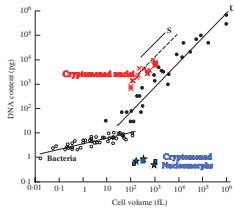
Dramatic plant genome growth by polyploidy and transposon amplification is well documented. However, comparably effective mechanisms of genome shrinkage remain to be demonstrated.

Bennetzen et al. (pp. 127–132) use sequence variation in retrotransposons to show that small deletions induced by illegitimate recombination and unequal homologous recombination are active in removing DNA from plant nuclear genomes.



The C-value enigma in plants and animals

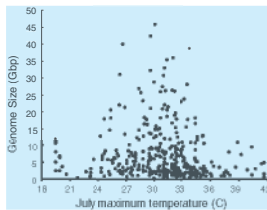
For over 50 years, variation in nuclear DNA contents (the ‘C-value enigma’) has remained a central puzzle of molecular biology. Plants and animals represent the best-studied groups from this perspective, and each has provided many important insights. However, **Gregory (pp. 133–146)** notes that the enigma transcends taxonomic boundaries, making it time for increased talk across the trenches.



Co-evolution of nuclear and cell volumes

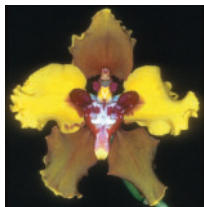
Amounts of nuclear DNA and its degree of unfolding determine nuclear volumes while selection for efficient balanced growth favours a constant karyoplasmic ratio. Therefore, nuclear volume and genome sizes necessarily co-evolve with adaptively significant changes in cell volume, itself genetically determined by cell cycle controls.

Cavalier-Smith (pp. 147–175) proposes that this co-evolution explains the huge variation in genome size whereas neutral/selfish DNA theories do not.



Selection pressure against species with large genomes

While there is 1000-fold variation in plant genome sizes, most genomes are small. **Knight et al. (pp. 177–190)** present evidence for selection pressures operating against species with large genomes and attempt to pinpoint mechanisms involved. These could include a negative correlation between genome size and photosynthetic rate.



Genome sizes and rapid cycling neotropical orchids

Species in the subtribe Oncidiinae (Orchidaceae) include several with

particularly fast rates of development (6 months from seed to flower).

Chase et al. (pp. 191–199) find these species to have notably small genomes. Generally, epiphytic species have smaller genomes than terrestrial species, and the closest relatives of the rapid cycling species also have similarly small genomes, although they are more typical long-lived perennials.



Adaptive changes to the genome of stressed flax

Flax can respond to stressful environments by altering its genome at a large number of specific sites.

Cullis (pp. 201–206) suggests that these reproducible modifications provide adaptive variation on which selection can act and result in new genetic types after a single generation. The labile regions involved are shown to be frequently polymorphic in natural populations.



Genome size evolution across land plants (Embryophyta)

There is an approx. 1000-fold range of C-values in land plants.

By superimposing C-value data for 4538 species onto robust phylogenetic trees, **Leitch et al. (pp. 207–217)** reveal an evolutionary distribution of C-values and the dynamic nature of genome size evolution.

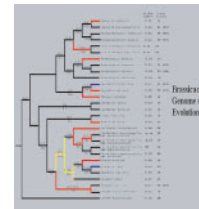
Key nodal points within the phylogenies are identified where independent evolutionary increases and decreases in C-values have taken place.



Genomic obesity is not irreversible

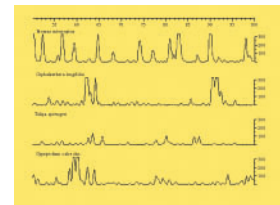
Plants may have a 'one way ticket to genomic obesity' due to polyploidy and the accumulation of retrotransposons.

This 'increase-only' hypothesis of genome size evolution is tested by **Price et al. (pp. 219–227)** who analyse the DNA content of 21 of the 25 species of *Sorghum* from a phylogenetic perspective. The authors conclude that DNA content evolution in *Sorghum* does not fit an 'increase-only' hypothesis.



Evolution of genome size in the Brassicaceae

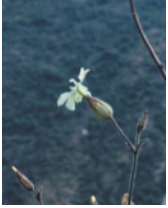
To examine genome size evolution in Brassicaceae, **Johnston et al. (pp. 229–235)** superimpose genome size and chromosome numbers onto an ITS sequence phylogeny. An ancestral genome size of $1C = 0.2 \text{ pg}$ is proposed. Increases and decreases in genome size are observed in clades with diploid species and in a clade containing *Brassica*, where two ploidy events are identified.



Large genomes make fingerprinting difficult

Amplified fragment length polymorphisms (AFLP) are applicable to species with a wide range of genome size. However, with large genome sizes ($1C > 15 \text{ pg}$), **Fay et al. (pp. 237–246)**

demonstrate that AFLP are suboptimal, partly due to large numbers of retrotransposons in these large genomes. The effect of different ploidy levels is also discussed.



DNA content underlies flower size variation

Flower size in *Silene latifolia* is characterized by quantitative genetics models but is also correlated with

nuclear DNA content. **Meagher *et al.* (pp. 247–254)** show that quantitative trait loci (QTL) for flower size and DNA content are correlated and conclude that these QTL include structural as well as regulatory genetic factors.

GENOME SIZE	
Monoploid genome size:	Holoploid genome size:
C _x -value	C-value

Genome size terminology revised
Usage of the term ‘genome size’ has not stabilized and is currently applied with

different meanings. **Greilhuber *et al.* (pp. 255–260)** propose a new unifying terminology that describes nuclear DNA contents with ease and without ambiguity.