

**Background:** Dipterocarpaceae is a pantropical tree family that plays an important role in our understanding of the ecology of Asian tropical rain forests. However, genome sizes for members of the Dipterocarpaceae are still poorly known.

**Aims:** To report the genome size of 115 dipterocarp species and examine the variation and evolution of genome size in this family.

**Methods:** Genome size was estimated using flow cytometry. Both the *rpoB* and *trnL* intron were sequenced to uncover the evolution of genome size within a phylogenetic framework.

**Results:** The 1C genome size varied between 0.267 and 0.705 pg in *Shorea hemsleyana* and *Shorea ovalis*, respectively, a 2.64-fold variation across the family. Most dipterocarps are characterised by very small genomes with a mean 1C value of 0.416 pg (sd = 0.075) and five polyploids are recorded. The ancestral genome size for dipterocarps was reconstructed as  $1Cx = 0.481$  pg (95% CI = 0.433–0.534).

**Conclusions:** Genome size variation in dipterocarps was characterised by very small values with a narrow range. Overall, genome size reduction from the ancestral state is a general trend in Dipterocarpaceae.