

Coffee Tree Genome Size Variation: Its Relation with Retrotransposons Copy Number

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SUMMARY

Coffea genus contains over 80 species and taxons among which only *C. arabica* is an allotetraploid. The genome size varies from $2C=1.03$ pg to $2C = 1.76$ pg with a constant chromosome number, $2n = 22$. The genome size varies globally from East Africa, with the smallest genomes, towards Central and West Africa where the bigger genomes are found. *Coffea* species supposedly originated in East Africa. A hypothesis states that genome size differences resulted from an increase due to the presence of different types and copy numbers of repeated sequences among which retrotransposons. Gene duplication is also to consider but it may not be responsible for such a wide difference among species. Duplication of long chromosomal regions, instead of single genes, are also possible. Reduction of genome size cannot be discarded but it is a more complicated phenomena and with more dramatic consequences which can hardly be accounted for the present situation within *Coffea* genus.

Changes in genomic size were certainly accompanied by speciation as the success of interspecific crosses is correlated to the difference in the genome size of the parental species. We are presently analysing repeated sequences present in these genomes. We are estimating the copy numbers of different retrotransposons already identified. Paradoxically, one of the biggest genome, *C.heterocalyx* ($2C = 1.73$ pg) has apparently a low copy number of gypsy/Ty3 retrotransposon type, lower than *C. pseudozanguebariae*, which has a small genome ($2C = 1,13$ pg). Copia/Ty1 retrotransposon type seems to be more frequent than gypsy/Ty3 type in *Coffea* genomes. Nevertheless, increase of genomic sizes may depend not only on the copy number of retrotransposons but also on their genomic ubiquitous presence which might be at the origin of non reciprocal recombination due to the recognition of homologous sequences dispersed all over the genome.