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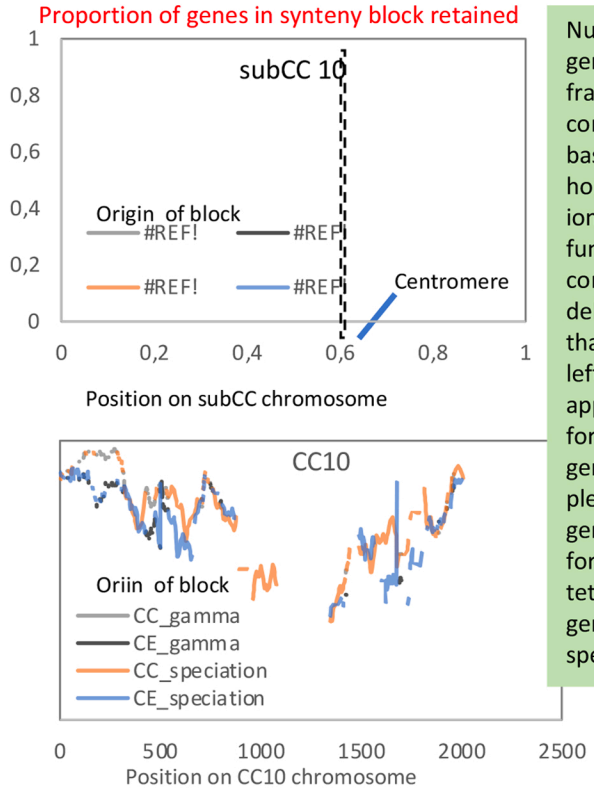
Spatial patterns of apparent fractionation on the subgenome chromosomes in *C. arabica* and gene loss in *C. canephora* and *C. eugenioides*

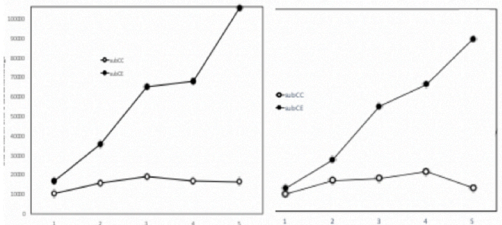
David Sankoff and Zhe Yu
University of Ottawa
Arabica Coffee Genome Consortium

We analyzed all the synteny blocks produced by SynMap in all six comparisons among the two subgenomes (subCC and subCE) of the allotetraploid *C. arabica* and the two diploid progenitor genomes *C. canephora* (CC) and *C eugenioides* (CE).

The density of retained genes after fractionation, and their spatial distribution along homeologous chromosomes is almost identical in the two subgenomes, as exemplified by two homeologous chromosomes in the figure. Indeed these tendencies reflect the same propensities in the corresponding chromosomes of the progenitor genomes. Most of the gene loss from the subgenomes actually consist of pre-existing deletions already affecting *C canephora* and C. eugenioides. The parallel distribution in these two diploids reflect in part ongoing fract-ionation, in part inheritance from their common ancestor 6-10 Mya, but more importantly contrasting propensities for gene loss in pericentromeric regions versus the rest of the chromosome,



Number of bp in inter-genic DNA in gap after fractionation, compared to number of base pairs in homeologous unfract-ionated region, as a func-tion of number of consec-utive genes deleted. This shows that there is no DNA left when a gene dis-appears: it is not trans - formed into a pseudo-gene; it is excised com-pletely from the genome. This is as true for fract-ionation after tetraploid-ization as for gene loss after speciation.



Lengths in bp of DNA segments between genes made adjacent by fractionation of intervening genes still present in the opposite subgenome. left:total. Right:lost after tetraploidization only.

The patterns of gene loss after tetraploid-ization, usually ascribed to fractionation, are statistically no different from loss as part of gene turnover in a diploid genome. This can be seem in the proportions of genes lost from paralogous synteny blocks (subCC, subCE) and from orthologous blocks (CC and CE) in the same regions of each homeologous or homologous chromosome. It also appears in the common mechanism – DNA excision – rather than pseudogenizetion.