

Coffea Genome Structure and Relationship with Evolution

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SUMMARY

Among the numerous species constituting the *Coffea* genus, only one, *C. arabica* is tetraploid ($2n=4X=44$) all the others are diploid but their DNA content is quite variable. Originating from East Africa and Mascarene Islands, coffee trees are found all along the forest belt that crosses the continent. Interestingly, the genome of the species found closely to the origin center have the lowest amount of DNA and oppositely, the species that “migrated” have a much bigger genome in terms of DNA content. The main reason to explain this difference can be attributed to the nature and amount of repeated sequences. It has been shown that, as all the plants so far analyzed, coffee contains many different retrotransposons. It is assumed that the movement of some of these elements and the multiplication of copies in the genome can be related to the migration of the coffee trees and the stresses encountered. The augmentation of the DNA content also define new genetic barriers as the level of sterility in F1 hybrids issued from interspecific crosses is higher when the two parental species have bigger difference in DNA content. This sterility level is tightly related to the presence of univalent chromosomes during meiosis in the gamete precursor cells.