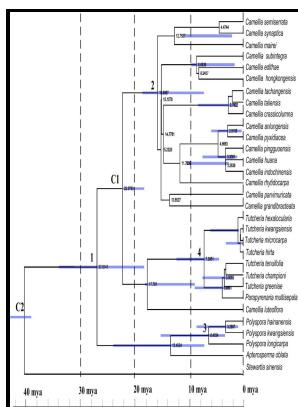


Genetic and cytological studies with *Camellia* and related genera

U.S. Agricultural Research Service; [for sale by the Supt. of Docs., U.S. Govt. Print. Off.
- Characterization of genome



Description: -

Komornicka, Maria, 1876-1949 -- Criticism and interpretation.
Marriage.

Camellias -- Genetics.

Camellias -- Breeding Genetic and cytological studies with Camellia and related genera

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Notes: Bibliography n. 89-92.

This edition was published in 1971.



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Tags: #Genetic #Divergence #between #Camellia #sinensis #and #Its #Wild #Relatives #Revealed #via #Genome

Impact of traditional culture on *Camellia reticulata* in Yunnan, China

Posada D 2008 jModelTest: phylogenetic model averaging. *Tree SNPs that were subjected to strong selective pressures during domestication*. Literature reviews included searches with Google Scholar, PubMed, Scopus, Web of Science and the Chinese databases such as VIP and Wanfang.

Genetic relationships among *Hylocereus* and *Selenicereus* vine cacti (Cactaceae): evidence from hybridization and cytological studies

Analyses by chromosome-anchored 45S and 5S rDNAs revealed their high level of variation in copy number among homologous chromosomes.

Physical mapping of the 18S

IIB was made up of Polyspora species and was the sister of IIC and IID. These results indicate that chromosomal fusions between chromosomes 2 and 8, and between chromosomes 5 and 7, occurred and might have given birth to the two sugarcane chromosomes.

Molecular Phylogeny of Tribe Theeae (Theaceae s.s.) and Its Implications for Generic Delimitation

Nucleotide sites containing two alternative alleles A1 and A2, which represent the first and second most frequently observed alleles with the highest and second depths, respectively were defined as homozygotes when the ratio of the depths of the A2 and A1 was 0. Unambiguous indels were treated as phylogenetic characters according to the simple indel coding method. Lin XY, Peng QF, LüHF, Du YQ, Tang BY 2008 Leaf anatomy of *Camellia* Sect.

Molecular Phylogeny of Tribe Theeae (Theaceae s.s.) and Its Implications for Generic Delimitation

Five ancient cha-hua trees were discovered in temples, occupying about one third of the total Fig.

Frontiers

The overexpression of CsTSI in A. Chen L, Yu FL, Tong QQ. A comprehensive analysis was achieved when the individual dendrograms of each primer pair tested were compared with the composite dendrogram of all the chosen three primer pairs.

Molecular Phylogeny of Tribe Theeae (Theaceae s.s.) and Its Implications for Generic Delimitation

Sequence-based genotyping for marker discovery and co-dominant scoring in germplasm and populations.

In

The amplified fragments of the LEAFY gene were electrophoresed in 1. The length of fragments of the alleles amplified across tea cultivars was consistent with the expected sizes of the products, implying that the primer binding sites of the alleles were highly conserved. Tien , Ju-K'ang : China and pepper trade.

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