

Natural transformants of *Camellia* section *Thea*



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Horizontal gene transfer (HGT) plays an important role in plant evolution and plant development. *Agrobacterium*-mediated gene transfer leads to the formation of crown galls or hairy roots, due to expression of transferred T-DNA genes. Spontaneous regeneration of transformed cells can produce natural transformants carrying cellular T-DNA (cT-DNA) sequences of bacterial origin. HGT from *Agrobacterium* to dicots is remarkably widespread. The production of naturally genome modified plants could play a role in plant evolution and environment.

Among these natural GMOs (nGMOs) there are the tea plants. *Camellia sinensis* var. *sinensis* cv. Shuchazao contains a single 5.5 kb cT-DNA fragment organized as imperfect inverted repeat with three inactive genes. 142 *Camellia* accessions, belonging to 10 of 11 species of the section *Thea*, were studied for the presence of cT-DNA alleles. All of them contain the cT-DNA insert, indicating that they are resulted from the single transformed event. Allele phasing showed that 82 accessions were heterozygous for T-DNA alleles, 60 others were homozygous. A phylogenetic analysis of all found alleles showed existence of two separate groups of them, further divided into subgroups. The alleles of the different *Camellia* species were distributed mosaically over groups, and different species showed very similar T-DNA alleles. This indicates that the taxonomy of *Thea* requires revision. The nucleotide divergence of the imperfect cT-DNA repeats indicates that the age of cT-DNA insertion is about 15 mya, which is earlier than emergence of section *Thea* [1]. We present a working model for the origin and evolution of nGMO plants derived from allogamous transformants.

Keywords: *Camellia*; T-DNA; nGMO.

REFERENCES

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