



# Large-scale detection and application of expressed sequence tag single nucleotide polymorphisms in *Nicotiana*

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**ABSTRACT.** Single nucleotide polymorphisms (SNPs) are widespread in the *Nicotiana* genome. Using an alignment and variation detection method, we developed 20,607,973 SNPs, based on the expressed sequence tag sequences of 10 *Nicotiana* species. The replacement rate was much higher than the transversion rate in the SNPs, and SNPs widely exist in the *Nicotiana*. *In vitro* verification indicated that all of the SNPs were high quality and accurate. Evolutionary relationships between 15 varieties were investigated by polymerase chain reaction with a special primer; the specific 302 locus of these sequence results clearly indicated the origin of Zhongyan 100. A database of *Nicotiana* SNPs (NSNP) was developed to store and search for SNPs in *Nicotiana*. NSNP is a tool for researchers to develop SNP markers of sequence data.

**Key words:** *Nicotiana*; Single nucleotide polymorphism; EST; Database; Evolution; Primer