Effect of DNA Methylation on 18S rRNA Gene Sequences during Culture of *Taxus chinensis* Cells

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Cell suspension culture has rapidly become an alternative source of taxol, an anticancer compound. To investigate the role of DNA methylation in the cultural course of *Taxus chinensis* cells, analyses of 18S rRNA gene sequences of cultured *T. chinensis* cells and related species were conducted. The phylogenetic analysis of 18S rRNA gene sequences indicated that HG-1 (the cultured *T. chinensis* cells), like *T. mairei* (the natural variety of *T. chinensis*), should be a new variety of *T. chinensis*, and cell culture can change the 18S rRNA gene sequence at the level of species despite 18S rRNA is the most conserved gene. The analyses of the CpG and TpG+CpA relative abundance and GC content of the 18S rRNA gene sequences made clear that DNA methylation contributed to changes of the 18S rRNA gene sequence of HG-1 at the level of species, which can make HG-1 to become a new variety of *T. chinensis*.

Key words: 18S rRNA Gene, DNA Methylation, Taxus chinensis Cell