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cpDNA sequence variation of *Cinnamomum* species found in Sri Lanka

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Sequence variation among species of *Cinnamomum*: *Cinnamomum verum*, *C. citriodorum*, *C. capparucoronae*, *C. dubium*, *C. litseaefolium*, *C. rivulorum*, *C. sinharajense* and *C. camphora* found in Sri Lanka was studied analyzing nucleotide sequence of different chloroplast DNA (cpDNA) regions. The cpDNA regions studied were *trnL* UAA intron, intergenic spacers of *trnL-trnF* and *trnT-trnL*. The primers used in this study, successfully amplified nearly the complete sequence within the primers of chloroplast regions. The length of the amplified products of *trnL* UAA intron, intergenic spacers (IGS) of *trnL-trnF* and *trnT-trnL* were approximately 400-600 bp. The new sequences of *trnL* UAA intron, IGS regions of *trnL-trnF* and *trnT-trnL* were obtained for the first time for the cinnamon species found in Sri Lanka. One mutation was found in *trnL-trnF* and *trnT-trnL*-IGS regions while four mutation sites were in *trnL* intron. *C. camphora* found in Japan which was used as an out-group in this study had 3 polymorphic sites in *trnL* intron. *C. sinharajense* and all accessions of *Cinnamomum verum* except CRS156 had the same sequence while *C. citriodorum* and *C. camphora* had a similar type of sequence. *Cinnamomum verum* accession CRS156, *C. dubium*, *C. rivulorum* and an unidentified *Cinnamomum* species had a mutation at 130 of the sequence. Therefore, this study provides new sequencing data for the individuals from different species of *Cinnamomum* that have never been used for sequence analysis.