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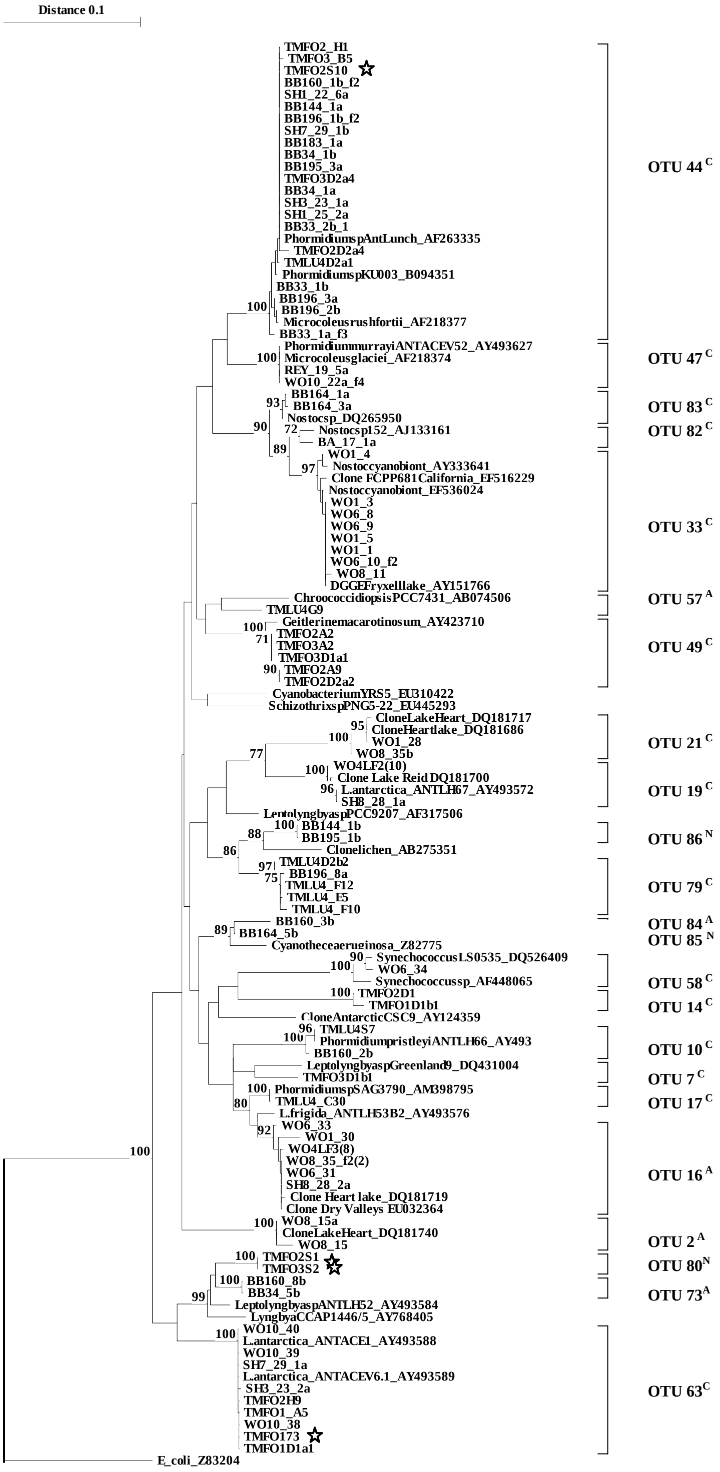

Fig. 1. A phylogenetic tree based on cyanobacterial partial 16S rRNA gene sequences constructed with the TREECON software. Clones and DGGE sequences from different Antarctic samples are grouped into OTUs. A: Antarctic, C: cosmopolitan and N: new. The Neighbor joining method was used, bootstrap values equal or higher than 70 % are indicated besides the nodes.

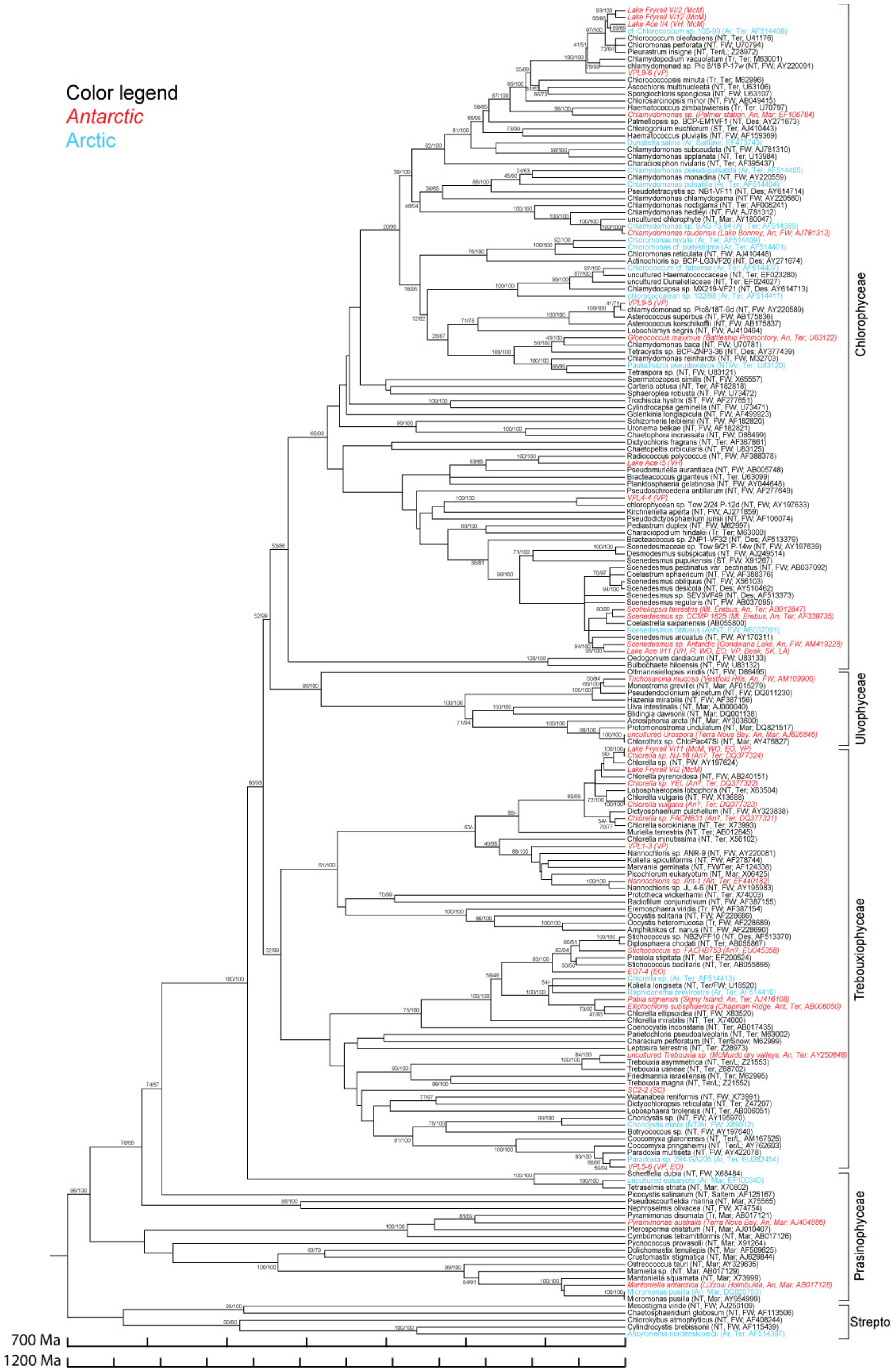

Fig. 2 App. 1 Phylogenetic tree with molecular clock. Timescale divided in 100 Ma intervals.