



**Figure 1.** Phylogenetic position of *Chorisodontium aciphyllum* determined using the Maximum-Likelihood method based on combined analysis with amino acid sequences of 36 mitochondrial genes common in all taxa. The bootstrap values (>70) are presented near the corresponding branch. Sequences from liverworts were used as outgroup. GenBank accession number of mitogenomes used are *Aneura pinguis* (NC\_026901), *Anomodon attenuatus* (NC\_021931), *Atrichum angustatum* (NC\_024520), *Bartramia pomiformis* (NC\_024519), *Brachythecium rivulare* (NC\_031212), *Bucklandiella orthotrichacea* (NC\_026974), *Buxbaumia aphylla* (NC\_024518), *Callicladium imponens* (NC\_024516), *Calypogeia arguta* (NC\_035978), *Climacium americanum* (NC\_024515), *Codriophorus laevigatus* (NC\_025931), *Funaria hygrometrica* (NC\_024523), *Lewinskya speciosa* (NC\_026121), *Marchantia polymorpha* (NC\_037508), *Mielichhoferia elongata* (NC\_036945), *Niphotrichum elongatum* (NC\_026890), *Orthotrichum diaphanum* (NC\_029356), *Orthotrichum macrocephalum* (NC\_029355), *Physcomitrella patens* (NC\_007945), *Ptychomnion cygnisetum* (NC\_024514), *Sanionia uncinata* (NC\_027974), *Sphagnum palustre* (NC\_024521), *Stoneobryum bunyaense* (NC\_031392), *Syntrichia filaris* (NC\_027515), *Tetraphis pellucida* (NC\_024290), *Tetraplodon fuegianus* (NC\_028191), and *Ulota crispa* (NC\_031393).