



Figure 1. Phylogenetic position of *Syntrichia filaris* determined by Maximum Parsimony analysis based on combined analysis with amino acids sequences of 31 mitochondrial genes common in all taxa. The bootstrap values (>50) are presented near the corresponding branch (ML/MP). Branches that were supported by above 70% bootstrap values are indicated by bold lines. Sequences from Marchantiopsida were used as outgroup. GenBank accession numbers of mitogenomes used are *Anomodon attenuatus* (NC_021931), *Anomodon rugelii* (NC_016121), *Atrichum angustatum* (NC_024520), *Bartramia pomiformis* (NC_024519), *Buxbaumia aphylla* (NC_024518), *Climacium americanum* (NC_024515), *Codriophorus laevigatus* (NC_025931), *Funaria hygrometrica* (NC_024523), *Hypnum imponens* (NC_024516), *Marchantia polymorpha* (NC_001660), *Orthotrichum speciosum* (NC_026121), *Orthotrichum stellatum* (NC_024522), *Physcomitrella patens* (NC_007945), *Pleurozia purpurea* (NC_013444), *Ptychomnion cygnisetum* (NC_024514), *Racomitrium ericoides* (NC_026540), *Sphagnum palustre* (NC_024521), *Syntrichia filaris* (KP984758), *Tetraphis pellucida* (NC_024290), *Treubia lacunosa* (NC_016122), and *Ulota hutchinsiae* (NC_024517).