



Figure 1. Phylogenetic position of *Syntrichia filaris* determined by using the maximum likelihood method based on combined analysis with amino acids sequences of 72 chloroplast genes common in all taxa. The bootstrap values of 1000 replicates are presented near the corresponding branch. Sequences from hornwort and liverworts were used as outgroup. GenBank accession number of chloroplast genomes used are *Anthoceros formosae* (NC_004543), *Marchantia polymorpha* (NC_037507), *Orthotrichum rogeri* (NC_026212), *Pellia endiviifolia* (NC_019628), *Physcomitrella patens* (NC_037465), *Sanionia uncinata* (NC_025668), *Sphagnum palustre* (NC_030198), *Syntrichia filaris* (MK852705), *Syntrichia ruralis* (NC_012052), *Takakia lepidozoioides* (NC_028738), and *Tetraphis pellucida* (NC_024291).