Table 1. Sequence information used in phylogenetic analysis

Locus	Species	Character	Length range	Mean	Standard Deviation	Divergence (%)	Variable (%)	Informative (%)
rps16	78	817	774	742,7	74,6	1,8	19,8	9,5
trnL-F	78	370	363	351	8,7	1,5	17,6	9,2

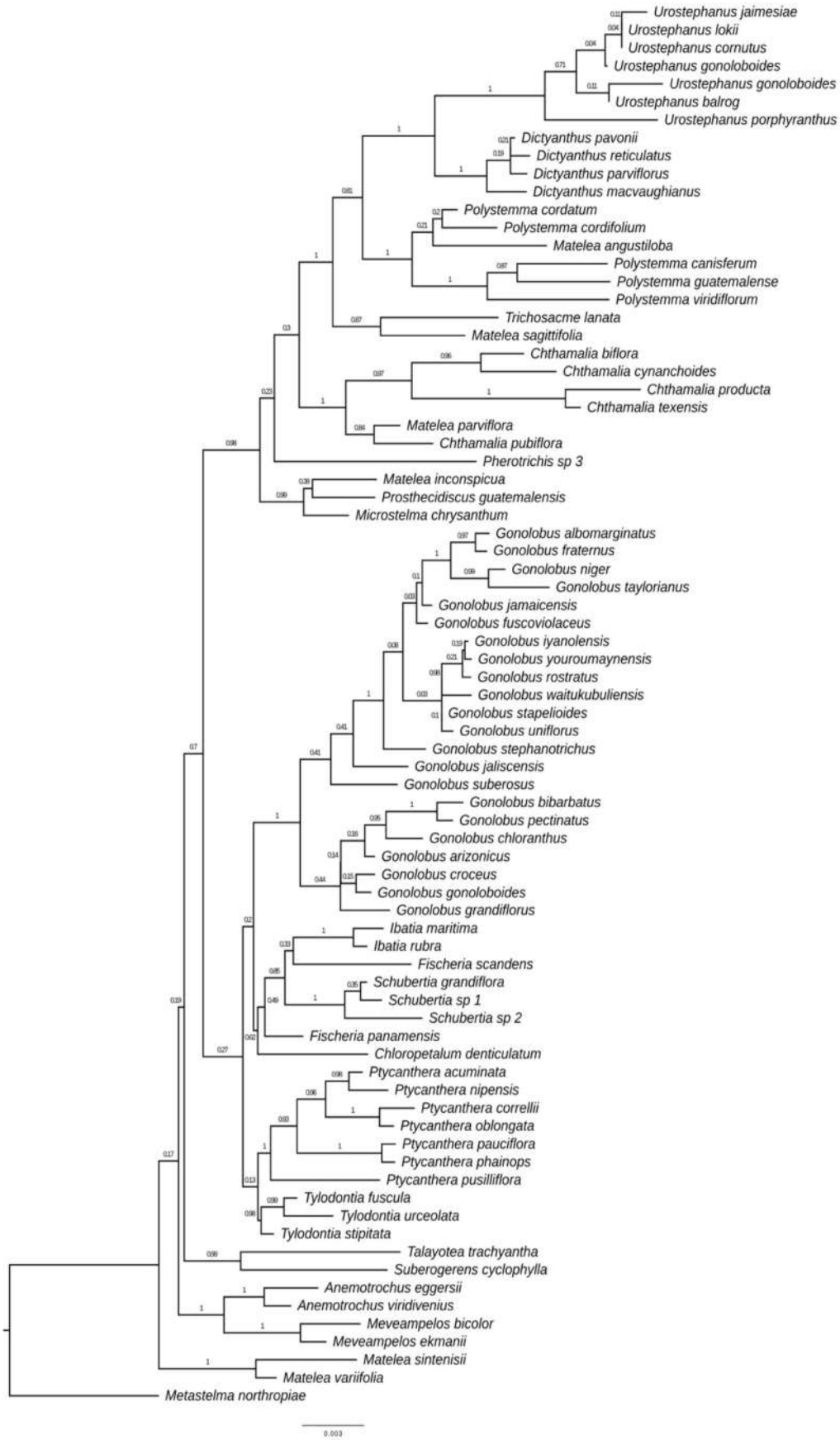


Figure 1. Maximum clade credibility tree obtained from the phylogenetic analysis with two loci.