

Appendix:

Figure 1



Figure 1: Vegetable sheep

Top: *Haastia pulvinaris* (Photo credit: Craig Phillips).

Bottom: *Raoulia mammillaris* (Photo credit: Murray Dawson)



Figure 2



Figure 2:

Left: *Haastia recurva* (Photo credit: Mellissa Hutchinson). Right: *Haastia sinclairii* (Photo credit: John Barkla).

Figure 3

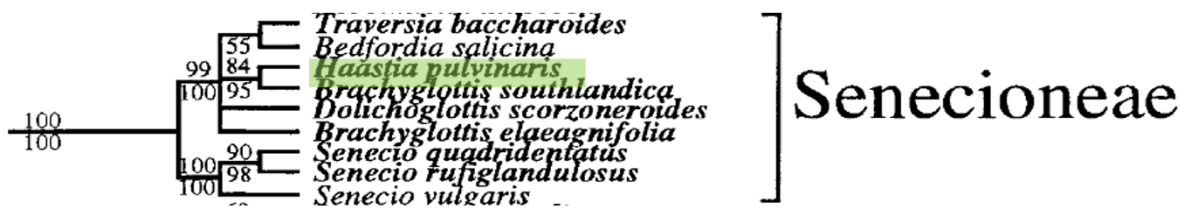


Figure 3: The Senecioneae clade of a phylogenetic tree produced by Wagstaff and Breitwieser (2002) with *Haastia pulvinaris* highlighted in green and bootstrap values are indicated above branches with jackknife values below.

Figure 4

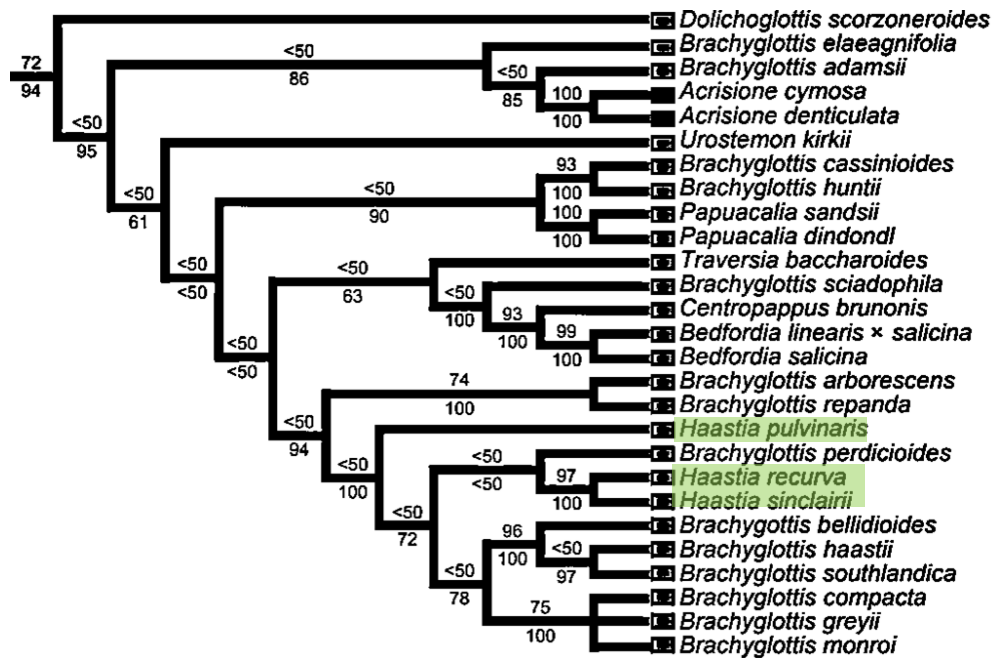


Figure 4: Phylogeny of most Brachyglottidinae using the ITS region with *Haastia* species highlighted green, and bootstrap values indicated above branches and posterior probabilities indicated below branches (Pelser *et al.* 2007).

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<a href="#">Dendrosenecio elgonensis chloroplast_complete genome</a>	<a href="#">Dendrosenecio elgonensis</a>	50523	2.520e+05	94%	0.0	99.59%	150548	<a href="#">KY434194.1</a>
<a href="#">Dendrosenecio erici-rosenii subsp. alticola chloroplast_complete genome</a>	<a href="#">Dendrosenecio erici-rosenii subsp. alticola</a>	50523	2.499e+05	93%	0.0	99.59%	150551	<a href="#">MK778421.1</a>
<a href="#">Dendrosenecio elgonensis chloroplast_complete genome</a>	<a href="#">Dendrosenecio elgonensis</a>	50523	2.510e+05	93%	0.0	99.59%	150553	<a href="#">MK756018.1</a>
<a href="#">Dendrosenecio elgonensis subsp. barbatipes chloroplast_complete genome</a>	<a href="#">Dendrosenecio elgonensis subsp. barbatipes</a>	50523	2.510e+05	93%	0.0	99.59%	150554	<a href="#">MK756017.1</a>
<a href="#">Dendrosenecio elgonensis chloroplast_complete genome</a>	<a href="#">Dendrosenecio elgonensis</a>	50523	2.572e+05	96%	0.0	99.59%	150551	<a href="#">MN250334.1</a>
<a href="#">Dendrosenecio elgonensis subsp. barbatipes chloroplast_complete genome</a>	<a href="#">Dendrosenecio elgonensis subsp. barbatipes</a>	50523	2.572e+05	96%	0.0	99.59%	150615	<a href="#">MN250330.1</a>
<a href="#">Dendrosenecio erici-rosenii subsp. alticola chloroplast_complete genome</a>	<a href="#">Dendrosenecio erici-rosenii subsp. alticola</a>	50523	2.569e+05	96%	0.0	99.59%	150552	<a href="#">MK483214.1</a>
<a href="#">Dendrosenecio elgonensis subsp. barbatipes chloroplast_complete genome</a>	<a href="#">Dendrosenecio elgonensis subsp. barbatipes</a>	50518	2.520e+05	94%	0.0	99.59%	150614	<a href="#">MG560047.1</a>
<a href="#">Dendrosenecio erici-rosenii chloroplast_complete genome</a>	<a href="#">Dendrosenecio erici-rosenii</a>	50518	2.498e+05	93%	0.0	99.59%	150545	<a href="#">MK778420.1</a>
<a href="#">Dendrosenecio elgonensis voucher J9 chloroplast_complete genome</a>	<a href="#">Dendrosenecio elgonensis</a>	50518	2.572e+05	96%	0.0	99.59%	150551	<a href="#">NC_058824.1</a>

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<a href="#">Senecio otites isolate 729 clone 2 18S ribosomal RNA gene, partial sequence: internal transcribed spacer 1, 5.8S ri...</a>	<a href="#">Senecio otites</a>	795	1202	100%	0.0	99.77%	753	<a href="#">GU818666.1</a>
<a href="#">Senecio otites isolate 729 clone 3 18S ribosomal RNA gene, partial sequence: internal transcribed spacer 1, 5.8S ri...</a>	<a href="#">Senecio otites</a>	789	1197	100%	0.0	99.54%	753	<a href="#">GU818667.1</a>
<a href="#">Senecio otites isolate 729 clone 1 18S ribosomal RNA gene, partial sequence: internal transcribed spacer 1, 5.8S ri...</a>	<a href="#">Senecio otites</a>	789	1202	100%	0.0	99.54%	753	<a href="#">GU818665.1</a>
<a href="#">Senecio otites isolate 729 clone 6 18S ribosomal RNA gene, partial sequence: internal transcribed spacer 1, 5.8S ri...</a>	<a href="#">Senecio otites</a>	778	1191	100%	0.0	99.07%	753	<a href="#">GU818670.1</a>
<a href="#">Senecio otites isolate 729 clone 4 18S ribosomal RNA gene, partial sequence: internal transcribed spacer 1, 5.8S ri...</a>	<a href="#">Senecio otites</a>	778	1185	100%	0.0	99.07%	753	<a href="#">GU818668.1</a>
<a href="#">Senecio otites isolate 729 voucher T. Plowman 2627 18S ribosomal RNA gene, partial sequence: internal transcribe...</a>	<a href="#">Senecio otites</a>	778	1191	100%	0.0	99.07%	740	<a href="#">EF538363.1</a>
<a href="#">Senecio otites isolate 729 clone 5 18S ribosomal RNA gene, partial sequence: internal transcribed spacer 1, 5.8S ri...</a>	<a href="#">Senecio otites</a>	773	1185	100%	0.0	98.84%	753	<a href="#">GU818669.1</a>
<a href="#">Monticalia myrsinites isolate 898 voucher F. Hekker &amp; W.H.A. Hekking 10.183 18S ribosomal RNA gene, partial seq...</a>	<a href="#">Monticalia myrsin...</a>	728	1058	100%	0.0	97.00%	754	<a href="#">EF538261.1</a>
<a href="#">Monticalia arbutifolia isolate KAD302 voucher B. Nordenstam 9436 18S ribosomal RNA gene, partial sequence: inte...</a>	<a href="#">Monticalia arbutif...</a>	728	1058	100%	0.0	97.00%	753	<a href="#">EF538257.1</a>
<a href="#">Elekmania buchii isolate 1007 voucher B. Nordenstam &amp; R. Lundin 506 internal transcribed spacer 1, partial sequen...</a>	<a href="#">Elekmania buchii</a>	706	1004	94%	0.0	96.07%	693	<a href="#">EF538191.1</a>

Figure 5: BLAST results, with plastome results (top) and ITS results (bottom).

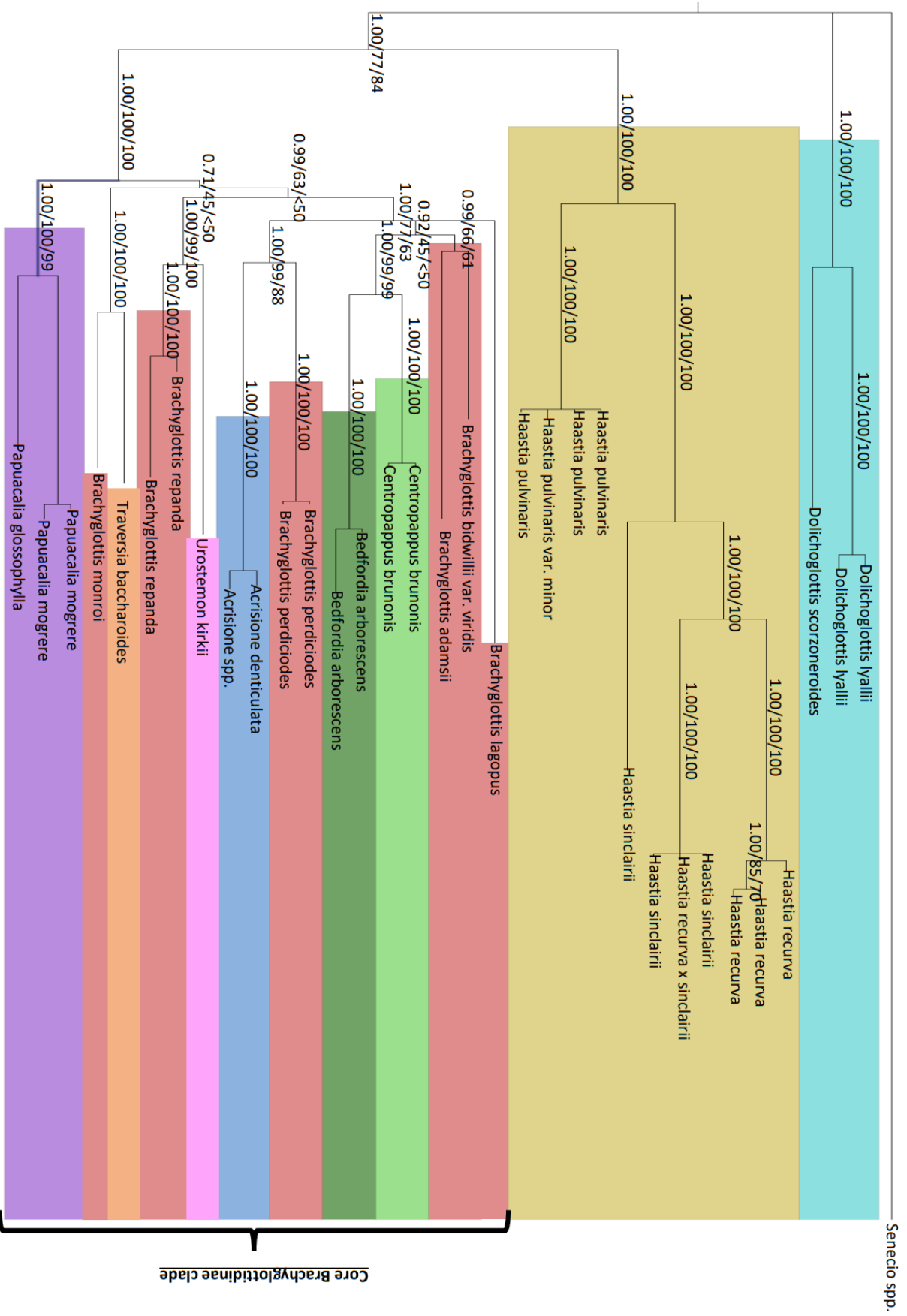


Figure 6: Phylogeny of Brachyglottidinae using the plastome. Values on branches show Bayesian Posterior probability/Maximum likelihood bootstrap support (%)/Parsimony bootstrap support (%). Each genus is distinguished by a different colour. Branch length indicates sequence divergence.

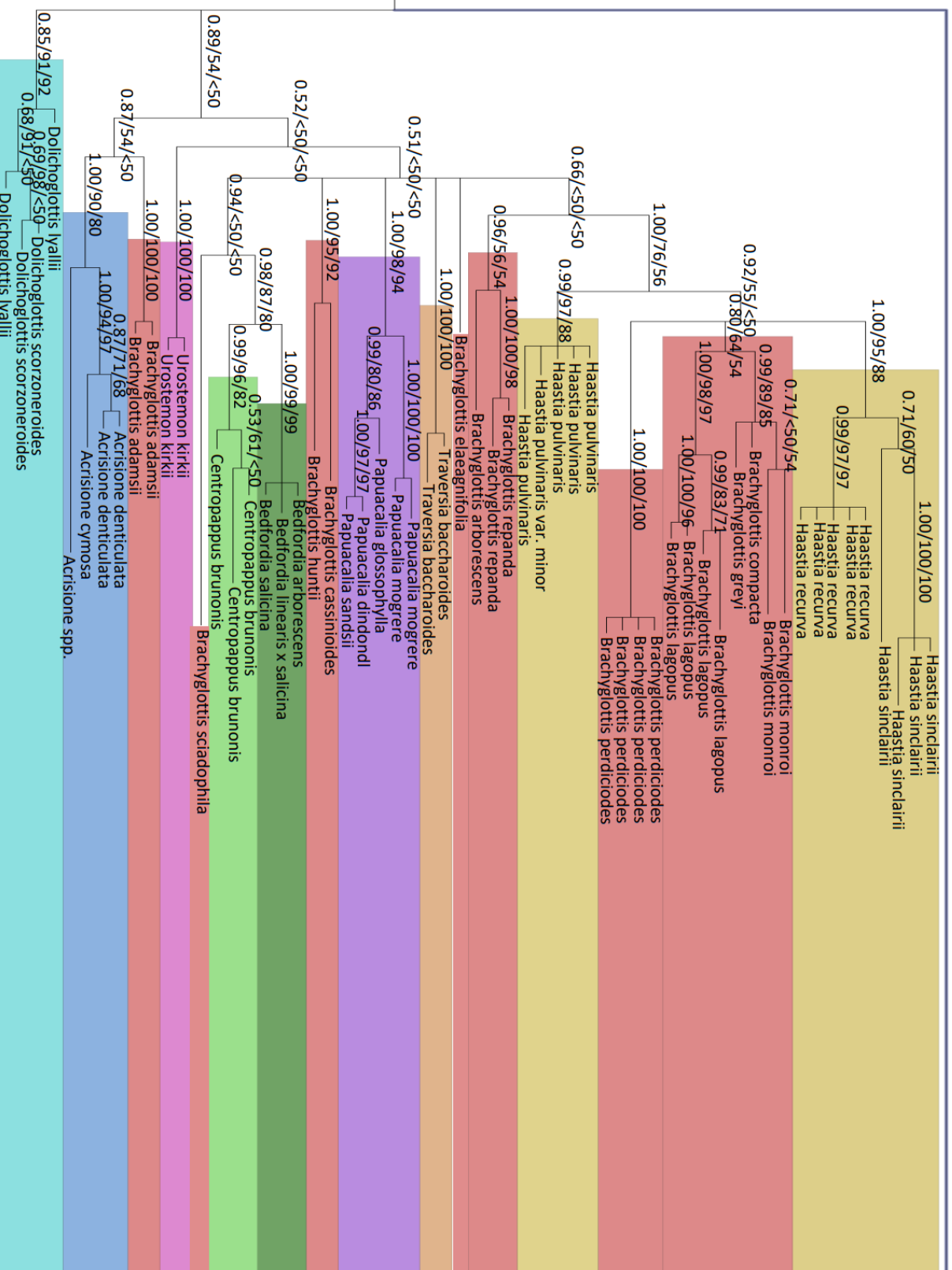


Figure 7: Phylogeny of Brachyglottidiinae using the ITS region. Values on branches show Bayesian Posterior probability/Maximum likelihood bootstrap support (%)/Parimony bootstrap support (%). Each genus is distinguished by a different colour. Branch length indicates sequence divergence.



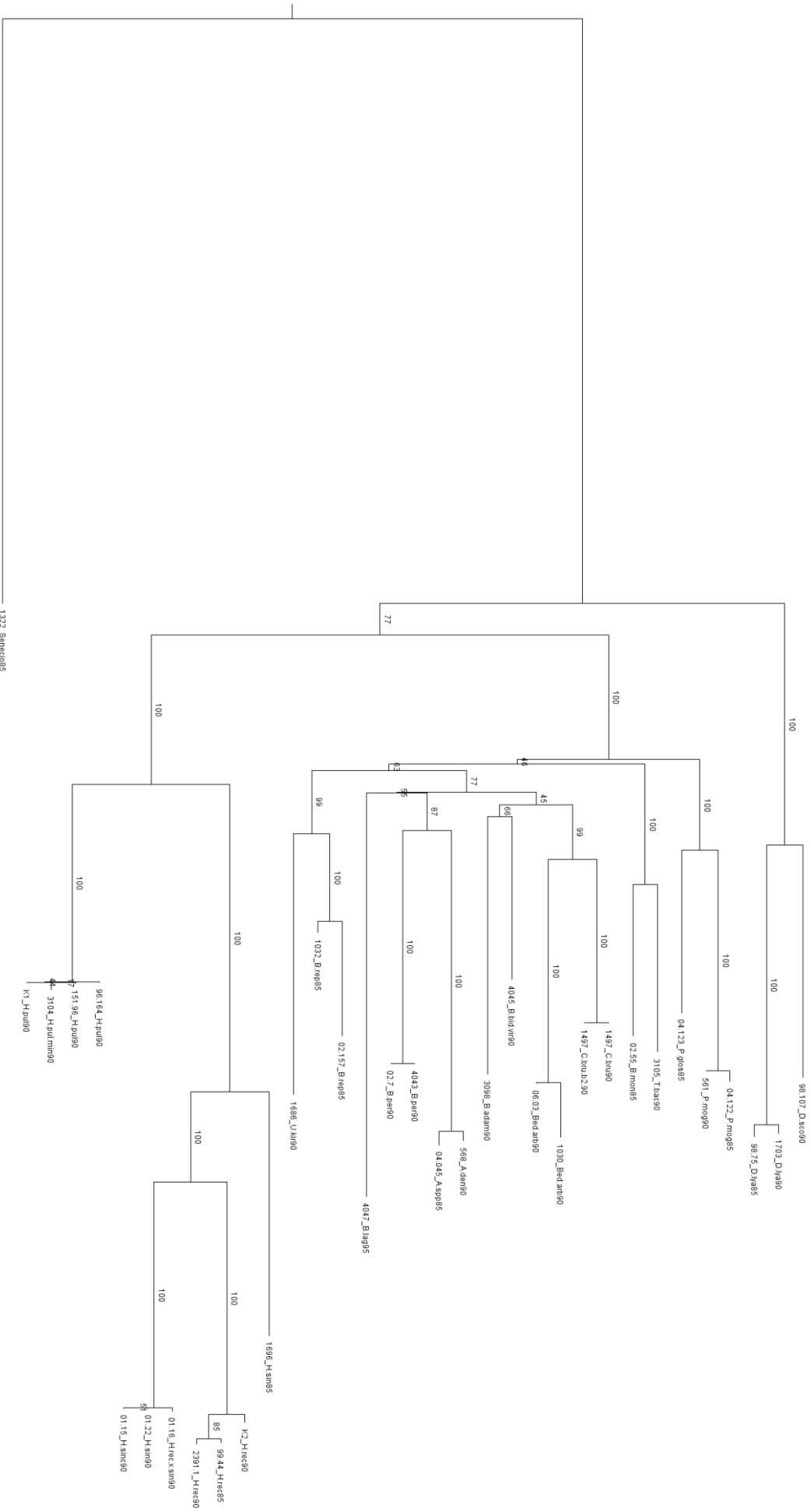


Figure 6.2: Maximum likelihood phylogeny of Brachyglottidinae using the plastome. Values on branches show bootstrap support (%). Branch length indicates sequence divergence. Numbers in front of names indicate sample number. Genus names are abbreviated to the first letter except for *Bedfordia*, which is 'Bed'. Specific epithets are abbreviated to the first three letters.



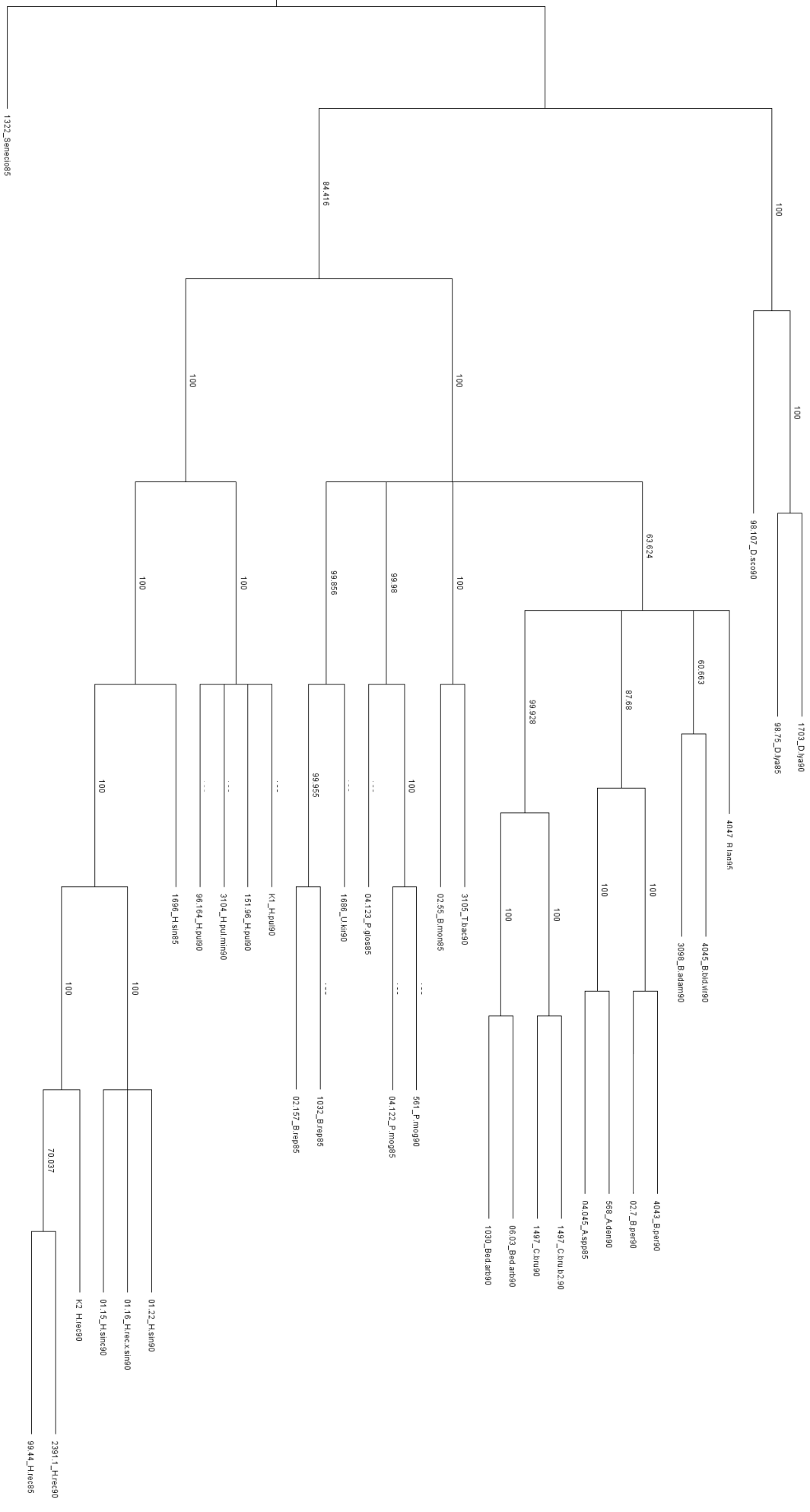
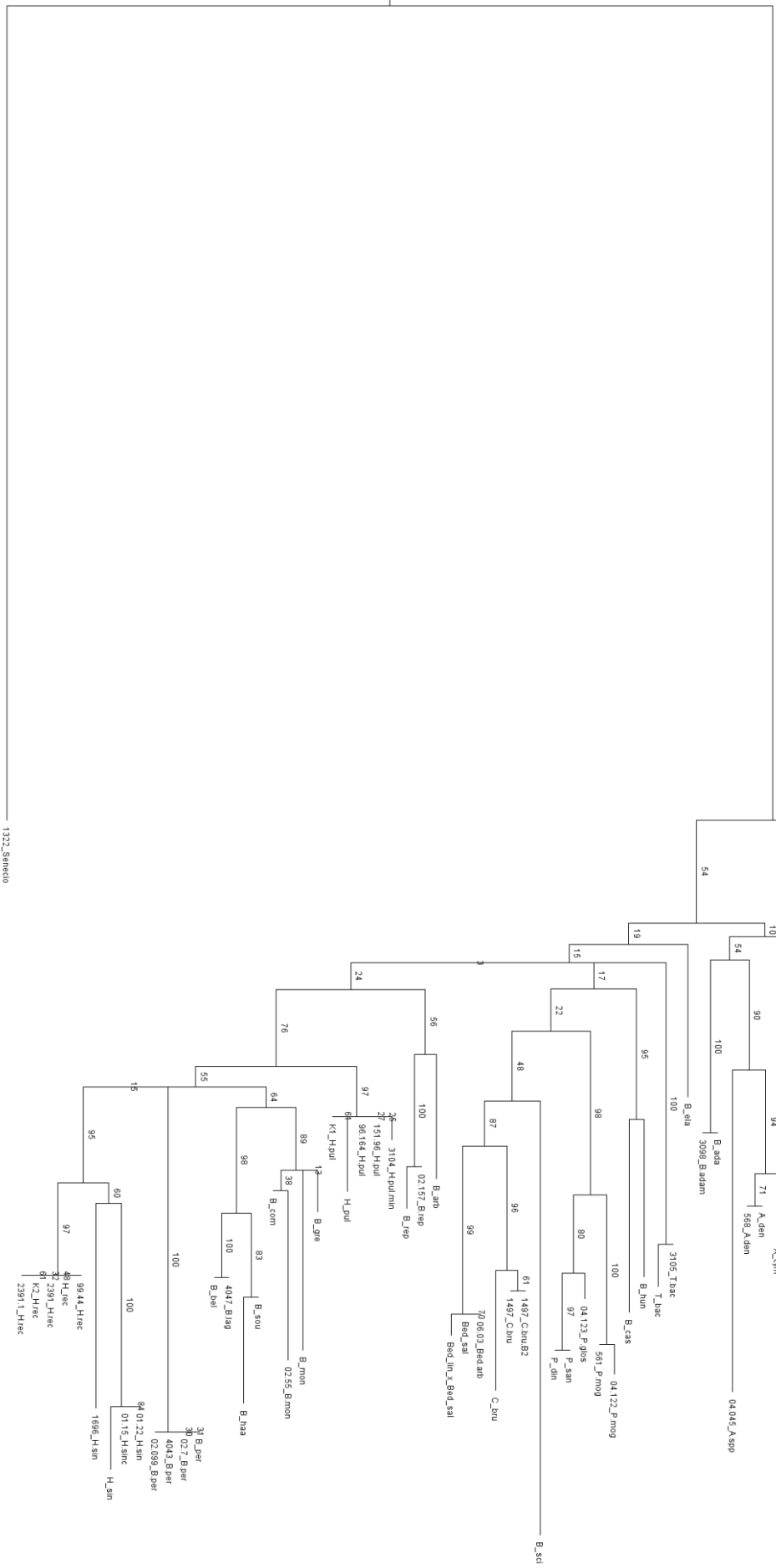


Figure 6.3 Parsimony phylogeny of Brachyglottidinae using the plastome. Values on branches show bootstrap support (%). Branch length indicates sequence divergence. Numbers in front of names indicate sample number. Genus names are abbreviated to the first letter except for Bedfordia, which is 'Bed'. Specific epithets are abbreviated to the first three letters.





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Figure 7.2: Maximum likelihood phylogeny of Brachyglottidinae using the ITS region. Values on branches show bootstrap support (%). Branch length indicates sequence divergence. Numbers in front of names indicate sample number. Genus names are abbreviated to the first letter except for *Bedfordia*, which is 'Bed'. Specific epithets are abbreviated to the first three letters.

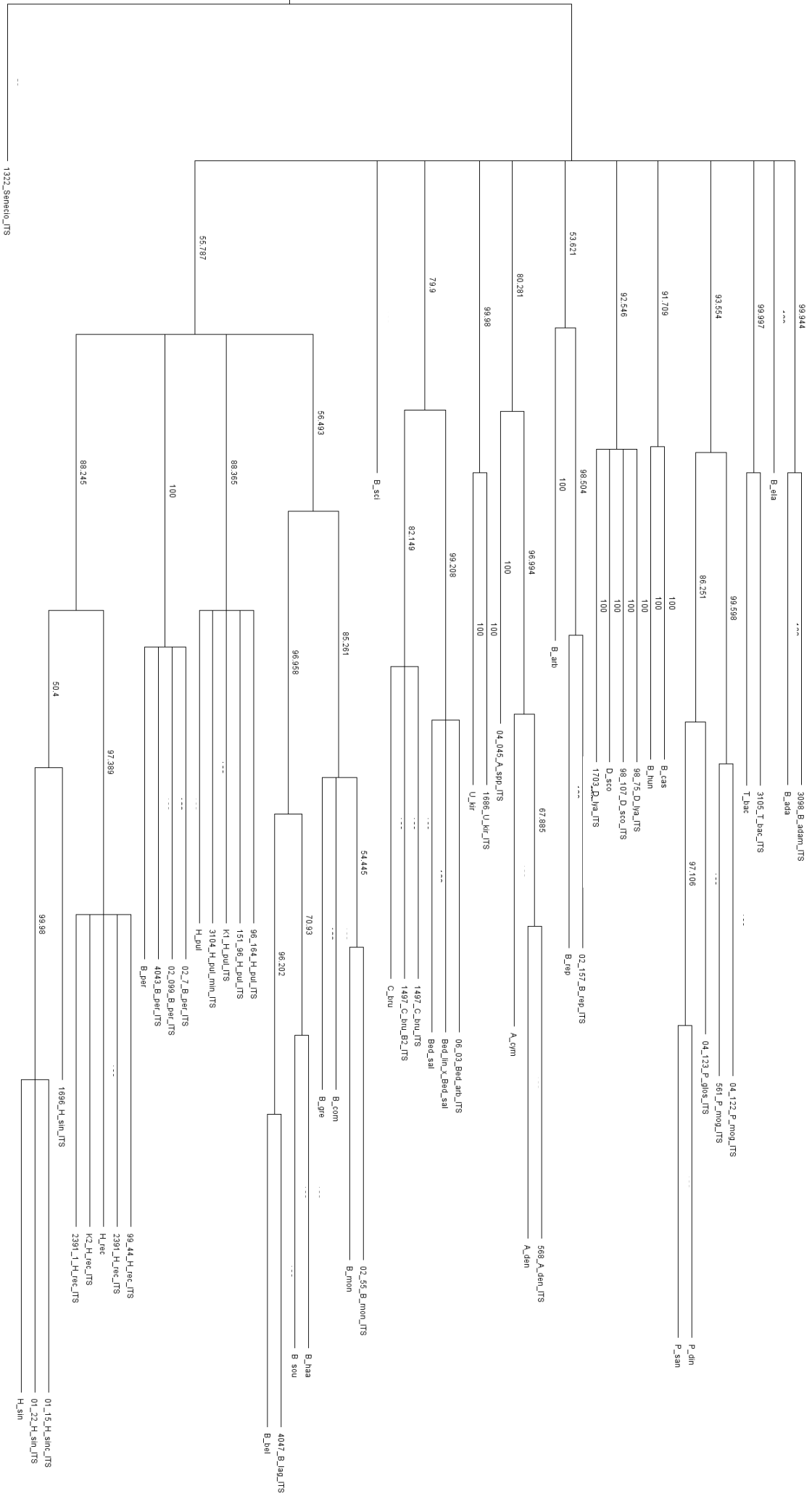


Figure 7.3 Parsimony phylogeny of Brachyglottidinae using the ITS region. Values on branches show bootstrap support (%). Branch length indicates sequence divergence. Numbers in front of names indicate sample number. Genus names are abbreviated to the first letter except for *Bedfordia*, which is 'Bed'. Specific epithets are abbreviated to the first three letters.