

Table S1. Sample resources are used in this study

Speices	Sample ID	Topology	Accession Number	Reference
<i>Endochironomus albipennis</i>	XL1630	Linear	OP950227	This study
<i>Endochironomus pekanus</i>	XL2023	Circle	OP950219	This study
<i>Endochironomus tendens</i>	XL1631	Linear	OP950228	This study
<i>Phaenopsectra flavipes</i>	LGS279	Circle	OP950216	This study
<i>Polypedilum heberti</i>	XL821	Linear	OP950225	This study
<i>Polypedilum</i> sp.1	NAM06	Circle	OP950217	This study
<i>Polypedilum nubifer</i>	/	Circle	MZ747090	[1]
<i>Polypedilum vanderplanki</i>	/	Circle	KT251040	[2]
<i>Polypedilum yongsanensis</i>	HHLY216	Linear	OP950222	This study
<i>Polypedilum unifascium</i>	/	Circle	MW677959	[3]
<i>Polypedilum masudai</i>	XL2759	Linear	OK513041	This study
<i>Sergentia baueri</i>	XL2656	Circle	OP950220	This study
<i>Stictochironomus akizukii</i>	XL1229	Circle	OP950218	This study
<i>Stictochironomus juncaii</i>	XL1582	Linear	OP950226	This study
<i>Stictochironomus rosenschoeldi</i>	XL552	Linear	OP950224	This study
<i>Synendotendipes impar</i>	ITA1	Linear	OP950223	This study
<i>Synendotendipes</i> sp.1	XL3845	Circle	OP950221	This study
<i>Stenochironomus baishanzenensis</i>	NLCH802	Linear	OL742441	[4]
<i>Stenochironomus okialbus</i>	ZJ761	Circle	OL753645	[4]

Reference

1. Xiao, Y.L.; Xu, Z.G.; Wang, J.X.; Fang, X.L.; Fu, Y. Complete mitochondrial genome of a Eurytopic midge, *Polypedilum nubifer* (Diptera: Chironomidae). *Mitochondr. DNA Part B Resour.* **2022**, *7*, 1936–1938. <https://doi.org/10.1080/23802359.2022.2122746>
2. Deviatiiarov, R.; Kikawada, T.; Gusev, O. The complete mitochondrial genome of an anhydrobiotic midge *Polypedilum vanderplanki* (Chironomidae, Diptera). *Mitochondrial DNA Part A* **2017**, *2*, 218–220. <https://doi.org/10.3109/19401736.2015.1115849>
3. Zheng, C.G.; Liu, Z.; Zhao, Y.M.; Wang, Y.; Bu, W.J.; Wang, X.H.; Lin, X.L. First report on mitochondrial gene rearrangement in non-biting midges, revealing a synapomorphy in *Stenochironomus* Kieffer (Diptera: Chironomidae). *Insects* **2022**, *13*, 115. <https://doi.org/10.3390/insects13020115>
4. Zheng, C.G.; Liu, Z.; Zhao, Y.M.; Wang, Y.; Bu, W.J.; Wang, X.H.; Lin, X.L. First report on mitochondrial gene rearrangement in non-biting midges, revealing a synapomorphy in *Stenochironomus* Kieffer (Diptera: Chironomidae). *Insects* **2022**, *13*, 115. <https://doi.org/10.3390/insects13020115>.

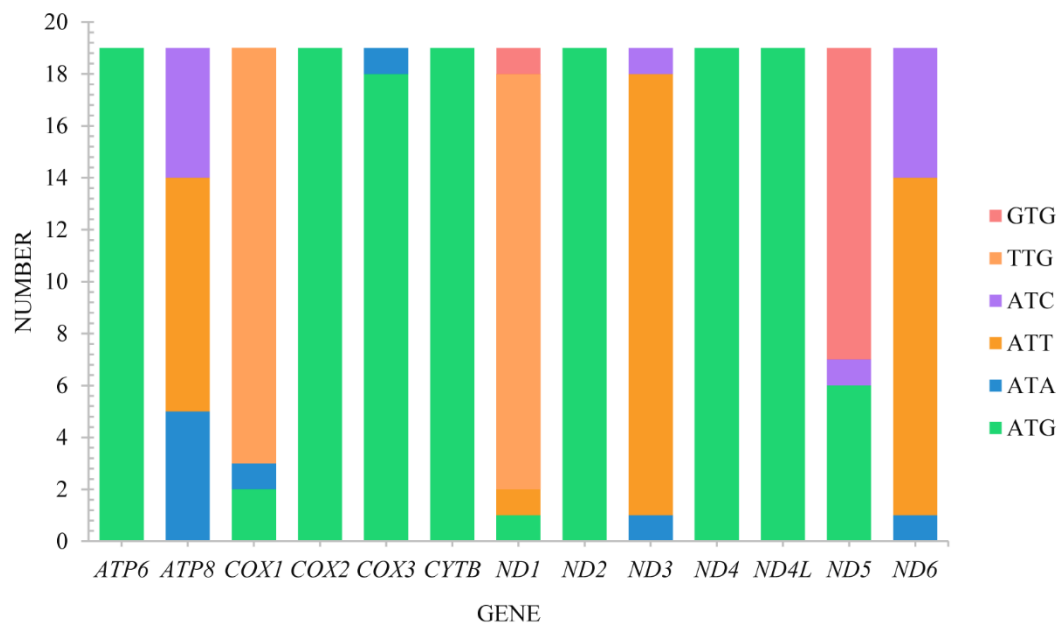


Figure S1. Start codons of protein-coding genes among *Polypedilum* generic complex mitogenomes

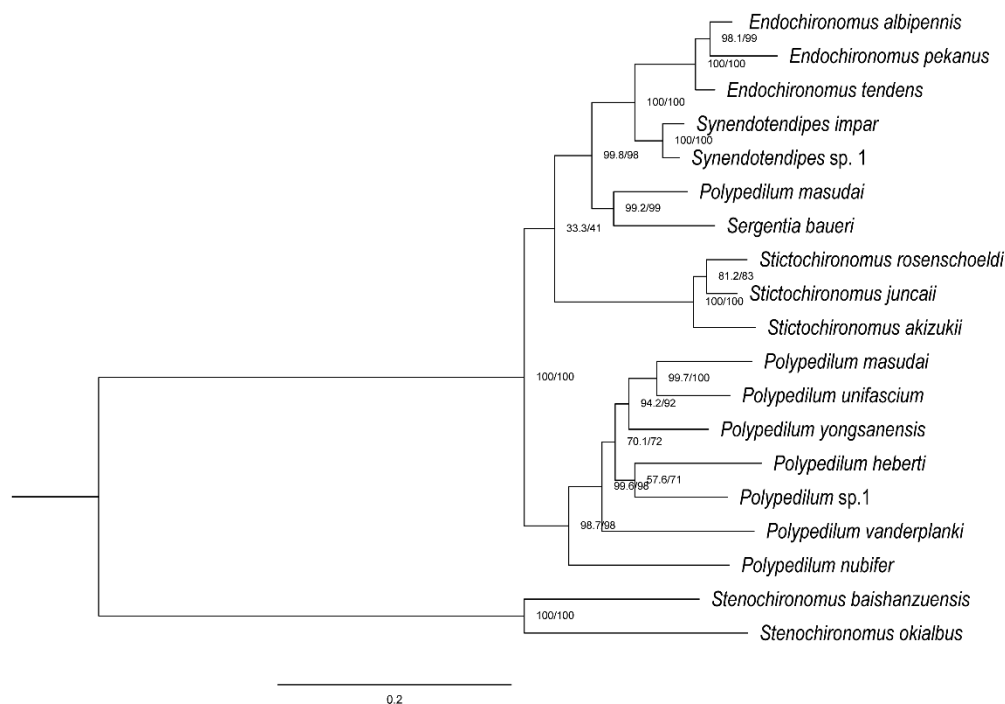


Figure S2. ML phylogenetic tree of *Polypedilum* generic complex based on the analysis of cds_faa with Partition model in IQTREE. Support values on nodes indicate SH-aLRT/UFBoot2, respectively.

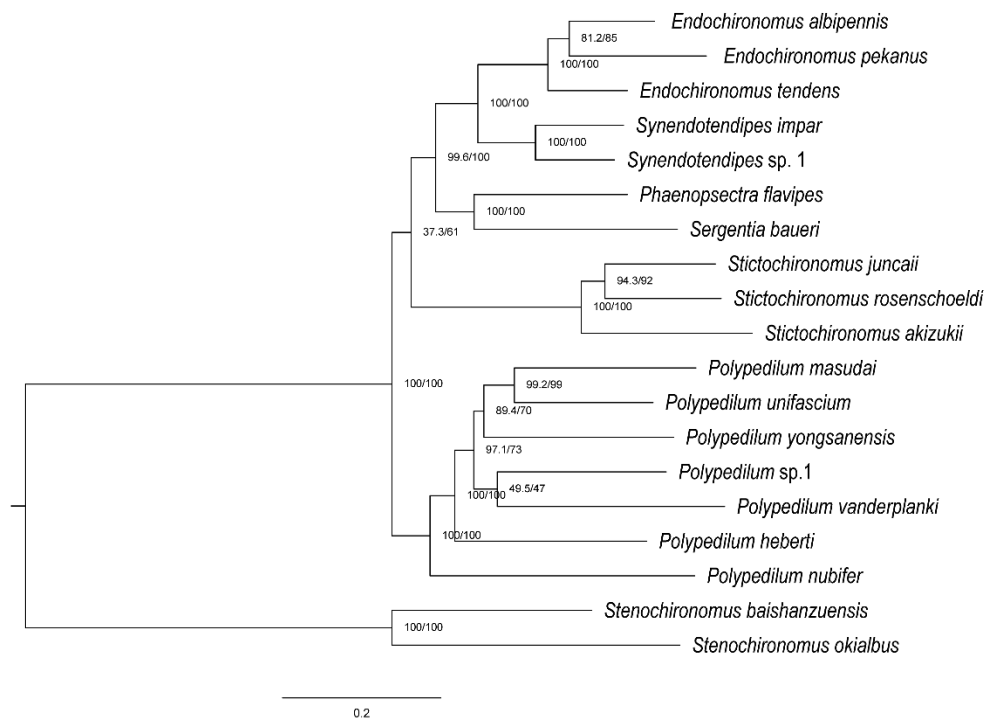


Figure S3. ML phylogenomic tree of *Polypedilum* generic complex based on the analysis *cds_fna* with Partition model in IQTREE. Support values on nodes indicate SH-aLRT/UFBoot2, respectively

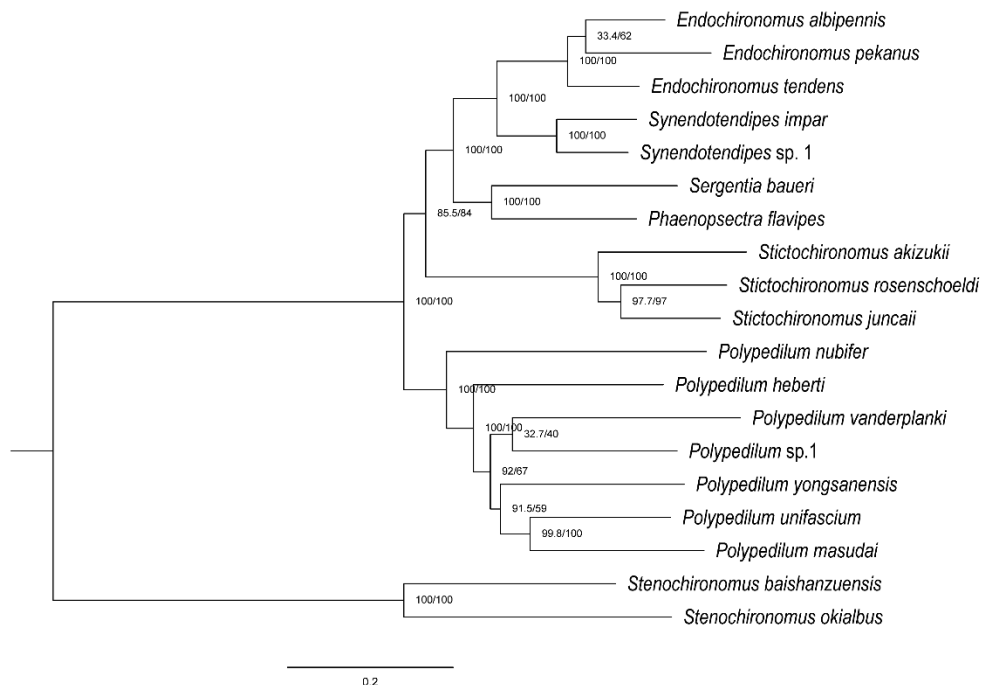


Figure S4. ML phylogenomic tree of *Polypedilum* generic complex based on the analysis *cds_rna* with Partition model in IQTREE. Support values on nodes indicate SH-aLRT/UFBoot2, respectively

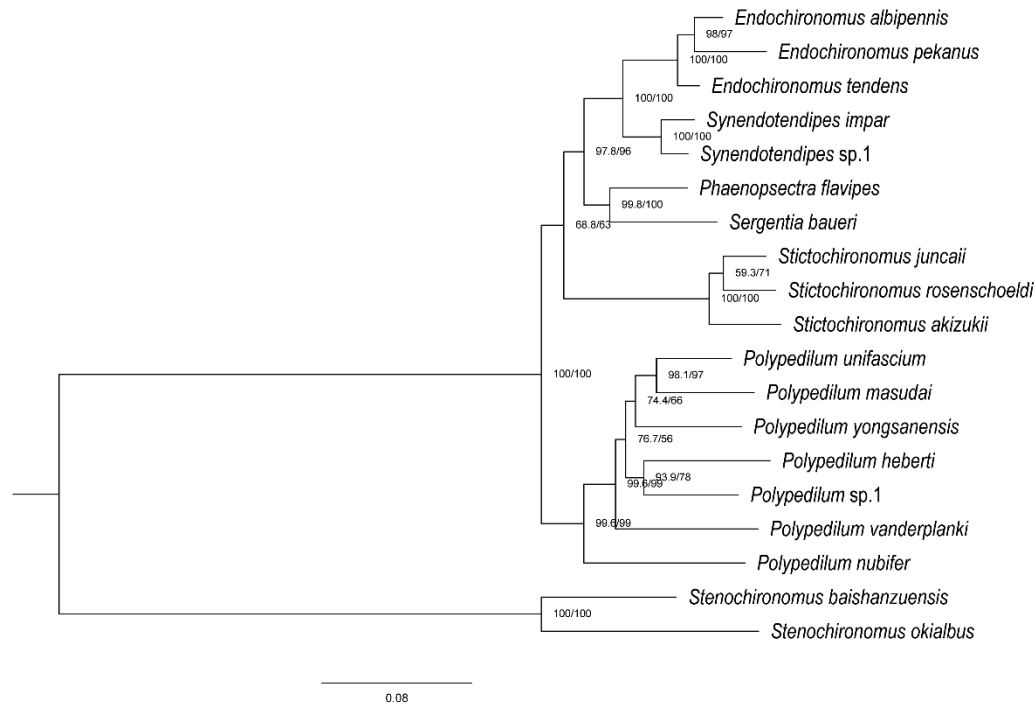


Figure S5. ML phylogenomic tree of *Polypedilum* generic complex based on the analysis *cds12_fna* with Partition model in IQTREE. Support values on nodes indicate SH-aLRT/UFBoot2, respectively

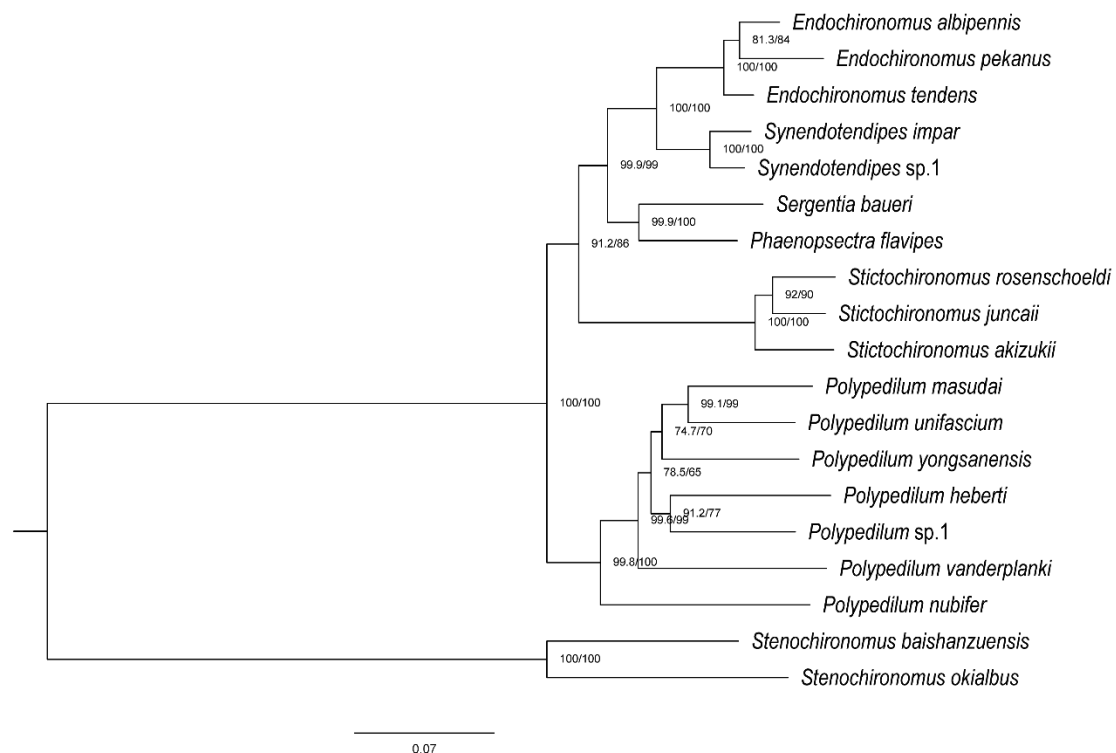


Figure S6. ML phylogenomic tree of *Polypedilum* generic complex based on the analysis *cds12_rna* with Partition model in IQTREE. Support values on nodes indicate SH-aLRT/UFBoot2, respectively

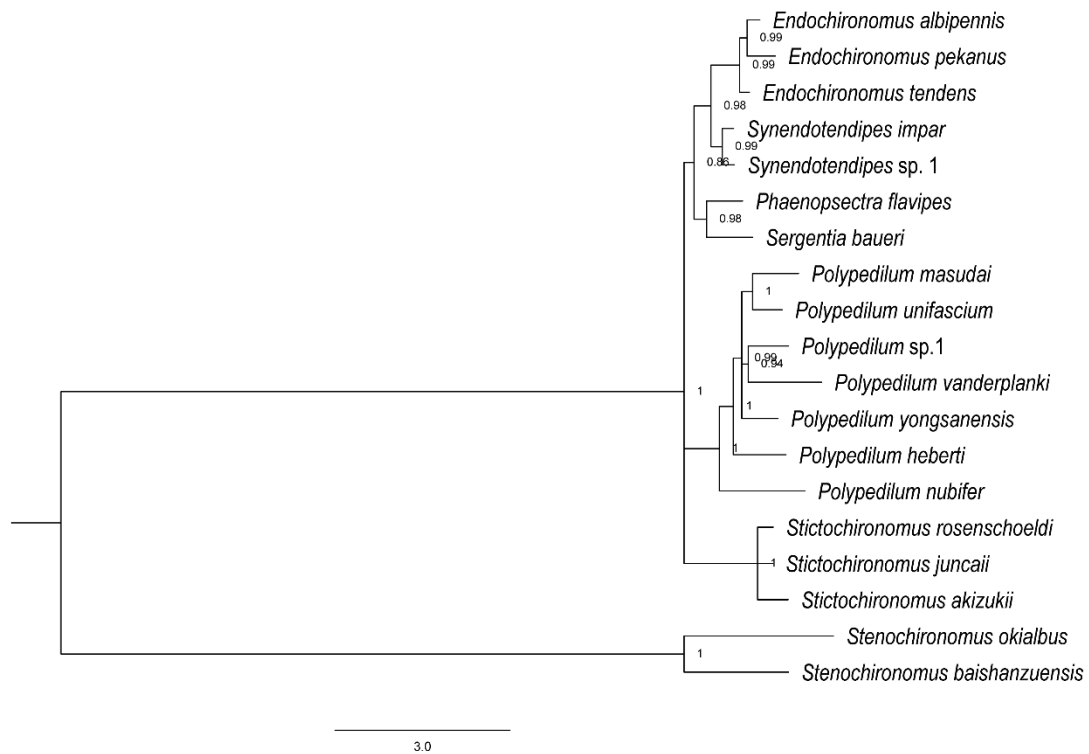


Figure S7. BI phylogenomic tree of *Polypedilum* generic complex based on the analysis cds_fna with GTR+CAT model in phylobayes. Support values on nodes indicate Bayesian posterior probabilities.

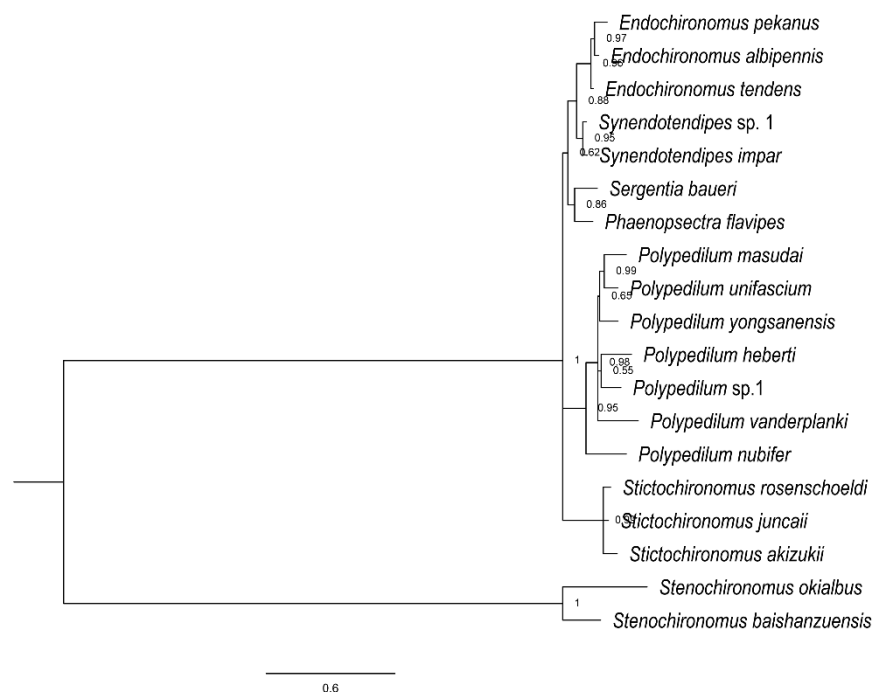


Figure S8. BI phylogenomic tree of *Polypedilum* generic complex based on the analysis cds12_fna with GTR+CAT model in phylobayes. Support values on nodes indicate Bayesian posterior probabilities.

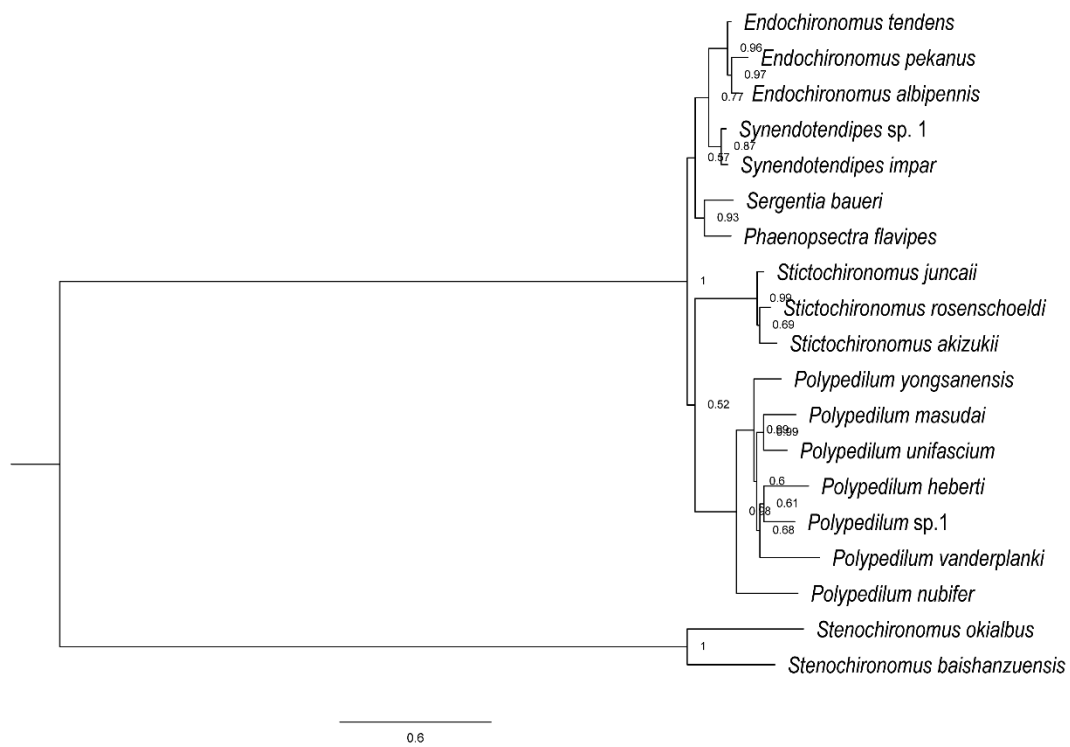


Figure S9. BI phylogenomic tree of *Polypedilum* generic complex based on the analysis cds12_rrna with GTR+CAT model in phylobayes. Support values on nodes indicate Bayesian posterior probabilities.