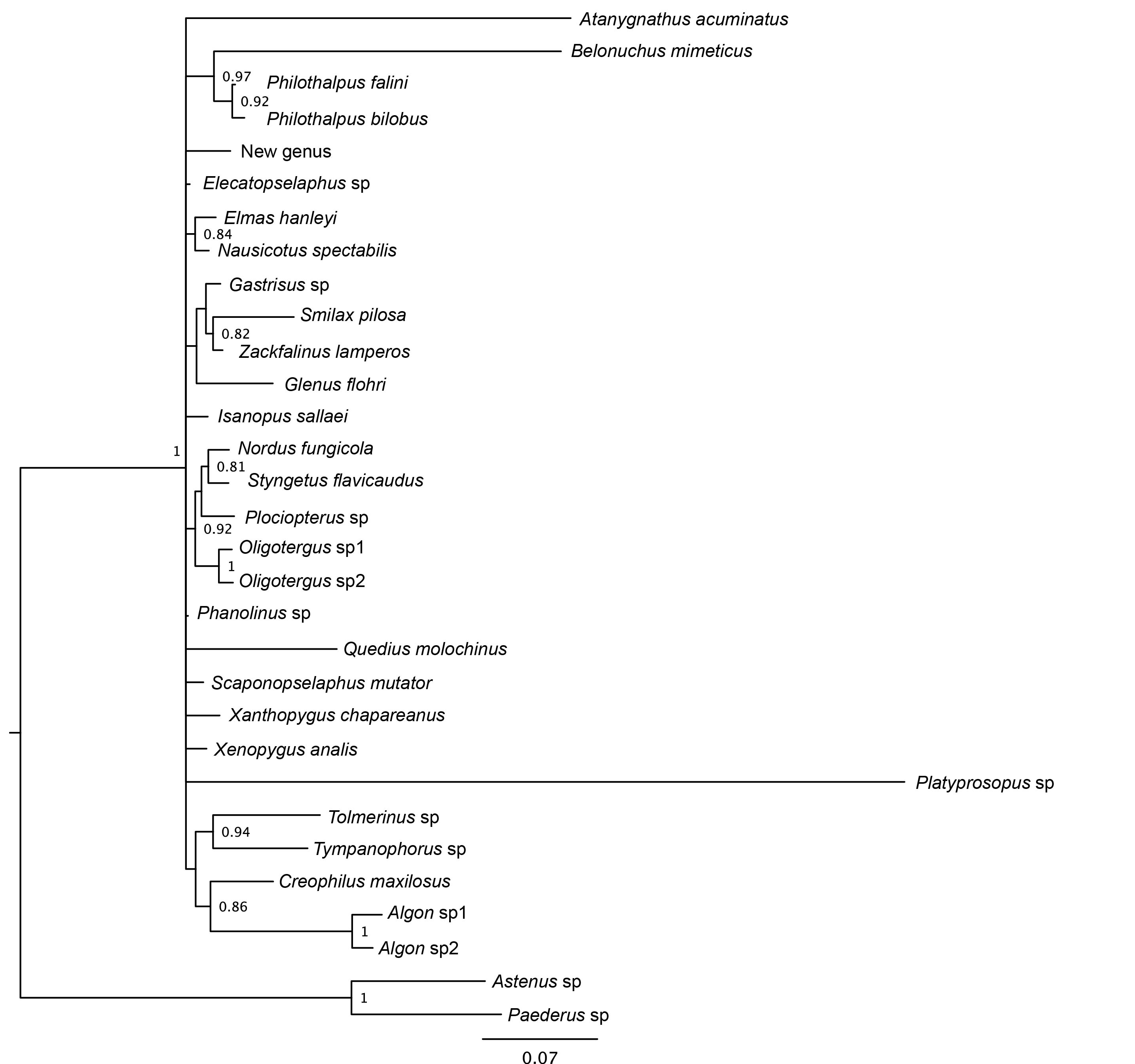
**Table S1**. GenBank numbers for the species used in this study. Novel GenBank accessions are **bold**. Vouchers are deposited at the following institutions: SBMNH: Santa Barbara Museum of Natural History; ZMUC: Zoological Museum, University of Copenhagen; UTCI: University of Tennessee at Chattanooga Insect Collection. With the exception of *Astenus* and *Paederus* all taxa belong in Staphylininae.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Species | Higher Taxon | Country | Voucher | Extract | COI | Wingless | TP I | 28S rDNA | ArgK | CAD |
| *Astenus* sp*.* | Paederinae | USA | SBMNH | SC-0103 | GU377362 | GU377463 | GU377412 | GU377318 | **KF178775** | **KF178807** |
| *Paederus* sp*.* | Paederinae | Denamrk | ZMUC | PAE01 | GU377386 | GU377488 | GU377437 | GU377340 | **KF178776** | **KF178808** |
| *Platyprosopus* sp*.* | Platyprosopini | S. Africa | ZMUC | PLsp01 | GU377391 | GU377493 | GU377442 | GU377344 | **KF178777** | **KF178809** |
| *Tolmerinus* sp*.* | Anisolinina | Laos | ZMUC | AIsp01 | GU377360 | GU377461 | GU377410 | GU377317 | **KF178778** | **KF178810** |
| *Tympanophorus* sp*.* | Anisolinina | Laos | ZMUC | TYsp01 | GU377401 | GU377503 | GU377452 | GU377351 | **KF178779** | **KF178811** |
| *Belonuchus mimeticus* Sharp, 1885 | Philonthina | Costa Rica | UTCI | SC-0014 | GU377366 | GU377467 | GU377416 | GU377322 | **KF178780** | - |
| *Cafius seminitens* Horn, 1884 | Philonthina | USA | UTCI | SC-0002 | GU377368 | GU377469 | GU377418 | - | **KF178781** | **KF178812** |
| *Philonthus splendens* (F., 1793) | Philonthina | Denmark | ZMUC | PHspl01 | GU377387 | GU377489 | GU377438 | - | **KF178782** | **KF178813** |
| *Quedius molochinus* (Grav., 1806) | Quediina | Denmark | ZMUC | QUmol01 | GU377396 | GU377498 | GU377447 | GU377348 | **KF178783** | **KF178814** |
| *Creophilus maxilosus* (L., 1758) | Staphylinina | USA | UTCI | SC-0235 | **KF178714** | **KF178730** | **KF178746** | **KF178760** | **KF178784** | **KF178815** |
| *Emus hirtus* (L., 1758) | Staphylinina | Denmark | ZMUK | EMhir01 | **KF178715** | **KF178731** | **KF178747** | - | **KF178785** | **KF178816** |
| *Atanygnathus acuminatus* (Casey, 1915) | Tanygnathina |  | SBMNH | MSC-1455 | GU377363 | GU377464 | GU377413 | GU377319 | **KF178786** | **KF178817** |
| *Algon* sp*.*1 | Incertae sedis | Laos | ZMUC | ALsp01 | GU377356 | GU377457 | GU377406 | GU377314 | **KF178787** | **KF178818** |
| *Algon* sp. 2 | Incertae sedis | Laos | ZMUC | RIsp01 | **KF178716** | **KF178732** | **KF178748** | **KF178761** | **KF178788** | **KF178819** |
| *Philothalpus bilobus* Chatzimanolis & Ashe, 2005 | Incertae sedis | Guyana | UTCI | SC-0086 | **KF178717** | **KF178733** | - | **KF178762** | **-** | **KF178820** |
| *Philothalpus falini* Chatzimanolis & Ashe, 2005 | Incertae sedis | Costa Rica | UTCI | SC-0008 | **KF178718** | **KF178734** | **KF178749** | **KF178763** | **KF178789** | **KF178821** |
| *Elecatopselaphus* sp*.* | Xanthopygina | Bolivia | ZMUC | ELsp01 | GU377371 | GU377472 | GU377421 | GU377326 | **KF178790** | **KF178822** |
| *Elmas hanleyi* Ashe & Chatzimanolis 2003 | Xanthopygina | Costa Rica | UTCI | SC-0007 | **KF178719** | **KF178735** | - | **KF178764** | **-** | **KF178823** |
| *Gastrisus* sp*.* | Xanthopygina | Costa Rica | UTCI | SC-0085 | GU377372 | GU377473 | GU377422 | GU377327 | **KF178791** | **KF178824** |
| *Glenus flohri* Sharp, 1884 | Xanthopygina | Guatemala | UTCI | SC-0172 | **KF178720** | **KF178736** | **KF178750** | **KF178765** | **KF178792** | **KF178825** |
| *Isanopus sallaei* Sharp, 1884 | Xanthopygina | Guatemala | UTCI | SC-0202 | **KF178721** | **KF178737** | **KF178751** | **KF178766** | **KF178793** | **KF178826** |
| *Nausicotus spectabilis* Sharp, 1884 | Xanthopygina | Costa Rica | UTCI | SC-0010 | GU377378 | GU377480 | GU377429 | GU377333 | **KF178794** | **KF178827** |
| *Nordus fungicola* Sharp, 1884 | Xanthopygina | Panama | UTCI | SC-0006 | GU377380 | GU377482 | GU377431 | GU377334 | **KF178795** | **KF178828** |
| *Oligotergus* sp. 1 | Xanthopygina | Costa Rica | UTCI | SC-0009 | GU377383 | GU377485 | GU377434 | GU377337 | **KF178796** | **KF178829** |
| *Oligotergus* sp. 2 | Xanthopygina | Guatemala | UTCI | SC-0199 | **KF178722** | **KF178738** | **KF178752** | **KF178767** | **KF178797** | **KF178830** |
| *Phanolinus* sp. | Xanthopygina | Costa Rica | UTCI | SC-0195 | **KF178723** | **KF178739** | **KF178753** | **KF178768** | **KF178798** | **KF178831** |
| *Plociopterus* sp. | Xanthopygina | Costa Rica | UTCI | SC-0197 | **KF178724** | **KF178740** | **KF178754** | **KF178769** | **KF178799** | **KF178832** |
| *Scaponopselaphus mutator* (Sharp, 1876) | Xanthopygina | Suriname | UTCI | SC-0230 | **KF178725** | **KF178741** | **KF178755** | **KF178770** | **KF178800** | - |
| *Smilax pilosa* (F., 1787) | Xanthopygina | Costa Rica | UTCI | SC-0222 | **KF178726** | **KF178742** | **KF178756** | **KF178771** | **KF178801** | **KF178833** |
| *Styngetus flavicaudus* Sharp, 1884 | Xanthopygina | Guatemala | UTCI | SC-0173 | **KF178727** | **KF178743** | **KF178757** | **KF178772** | **KF178802** | **KF178834** |
| *Xanthopygus* chapareanus Scheerpeltz, 1969*.* | Xanthopygina | Bolivia | UTCI | SC-0102 | GU377403 | GU377505 | GU377454 | GU377353 | **KF178803** | **KF178835** |
| *Xenopygus analis* (Er., 1840) | Xanthopygina | Panama | UTCI | SC-0011 | GU377404 | GU377506 | GU377455 | GU377354 | **KF178804** | **KF178836** |
| *Zackfalinus lamperos* Chatzimanolis, 2012 | Xanthopygina | Guatemala | UTCI | SC-0168 | **KF178728** | **KF178744** | **KF178758** | **KF178773** | **KF178805** | - |
| New Genus | Xanthopygina | Bolivia | ZMUK | DYsp01 | **KF178729** | **KF178745** | **KF178759** | **KF178774** | **KF178806** | **KF178837** |

**Table S2**. Primers and genes used in this study. Data for COI, wingless, topoisomerase I and 28srDNA are from Chatzimanolis *et al*., (2010). For CAD primers, **bold** indicate most widely used primers.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Genes | Bps | Strategy | Primers | Sequence (5’-3’) | Source |
| COI | 798 | C1-J-2183(Jerry) /L2-N-3014(Pat) | C1-J-2183(Jerry)  L2-N-3014(Pat) | CAACATTTATTTTGATTTTTTGG  TCCAATGCACTAATCTGCCATATTA | Simon *et al*., (1994)  Simon *et al*., (1994) |
| Wingless | 368–380 | Wg550F/WgABRZ; then nested PCR using internal primers Wg578F/WgABR | Wg550F  Wg578F  WgABRZ  WgABR | ATGCGTCAGGARTGYAARTGYCAYGGYATGTC  TGCACNGTGAARACYTGCTGGATG  CACTTNACYTCRCARCACCARTG  ACYTCGCAGCACCARTGGAA | Wild & Maddison (2008)  Ward & Downie (2005)  Wild & Maddison (2008)  Abouheif & Wray (2002) |
| Topoisomerase I | 712 | TP643F/TP932R; then nested PCR using primers TP675F/TP932R or TP675/TP919R | TP643F  TP675F  TP919R  TP932R | GACGATTGGAARTCNAARGARATG  GAGGACCAAGCNGAYACNGTDGGTTGTTG  GTCTCTTTGCGTYTTRTTRTADATYTTYTC  GGWCCDGCATCDATDGCCCA | Wild & Maddison (2008)  Wild & Maddison (2008)  Wild & Maddison (2008)  Wild & Maddison (2008) |
| 28S rDNA | 678–1174 | NFL184-21/  LS1041R; for difficult taxa added 5μl Q solution | NFL184-21/ LS1041R | ACCCGCTGAAYTTAAGCATAT  TACGGACRTCCATCAGGGTTTCCCCTGACTTC | Van der Auwera *et al* (1994)  Maddison (2008) |
| Arginine kinase | 723 | AK168F/AK939R then semi-nested PCR using AK183F/AK939R | AK168F  AK183F  AK939R | CAGGTTTGGARAAYCACGAYTCYGG  GATTCTGGAGTCGGNATYTAYGCNCCYGAYGC  GCCNCCYTCRGCYTCRGTGTGYTC | Wild & Maddison (2008)  Wild & Maddison (2008)  Wild & Maddison (2008 |
| CAD | 1752–  1761 | For the template:  **CD439F/CD1098R** or  CD439F**/** CD1231R orCD338F/CD1098R or CD338F/CD1231R. For CADA: **CD439F/CD688R** or  CD439F/CD668R or CD439F/CD630nR or  CD400F/CD688R.  For CADB:  **CD667F/CD851R** or  CD630F/CD851R.  For CADC:  **CD821F/CD1098R** or  CD806F3/CD1098R or  CD821F/CD1000R | CD338F  CD439F  CD400F  CD630F  CD630R  CD667F  CD668R  CD688R  CD806F3  CD821F  CD851R  CD1000R  CD1098R  CD1231R | ATGAARTAYGGYAATCGTGGHCAYAA  TTCAGTGTACARTTYCAYCCHGARCAYAC  GACTGGGARACSYTATTTTACAACG  TCTCTTGGAGGTTTRGGNTCDGGDTTYGC  GCRAAHCCHGANCCYAAACCTCCAAGAGA  GGATGGAAGGAAGTDGARTAYGARGT  ACGACTTCATAYTCNACYTCYTTCCA  TGTATACCTAGAGGATCDACRTTYTCCATRTTRCA  TTAYTGYGTTGTNAARATWCCNMGNTGGGA  AGCACGAAAATHGGNAGYTCNATGAARAG  GGATCGAAGCCATTHACATTYTCRTCHACCAT  ACNGTYTCCGGRTTGTARTTNACC  GCTATGTTGTTNGGNAGYTGDCCNCCCAT  TCCACGTGTTCNGANACNGCCATRCA | Wild (pers. comm.)  Wild & Maddison (2008)  This study  Wild & Maddison (2008)  This study  Wild & Maddison (2008)  Wild & Maddison (2008)  Wild & Maddison (2008)  Wild & Maddison (2008)  Wild & Maddison (2008)  Wild & Maddison (2008)  This study  Wild & Maddison (2008)  Wild & Maddison (2008) |

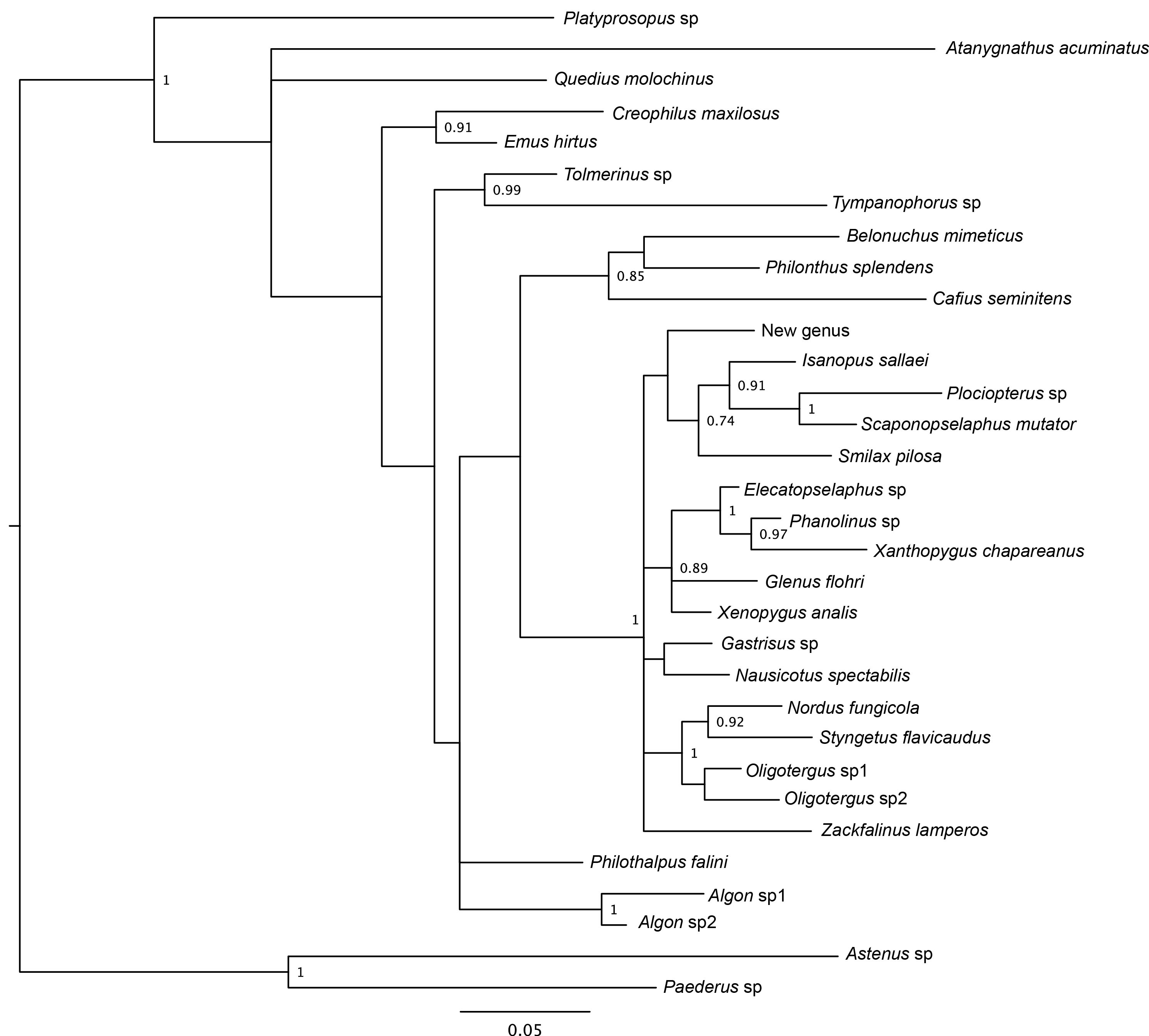
**Figure S1.** Bayesian phylogenetic tree for the 28S rDNA gene. Only posterior probabilities above 0.75 are shown.



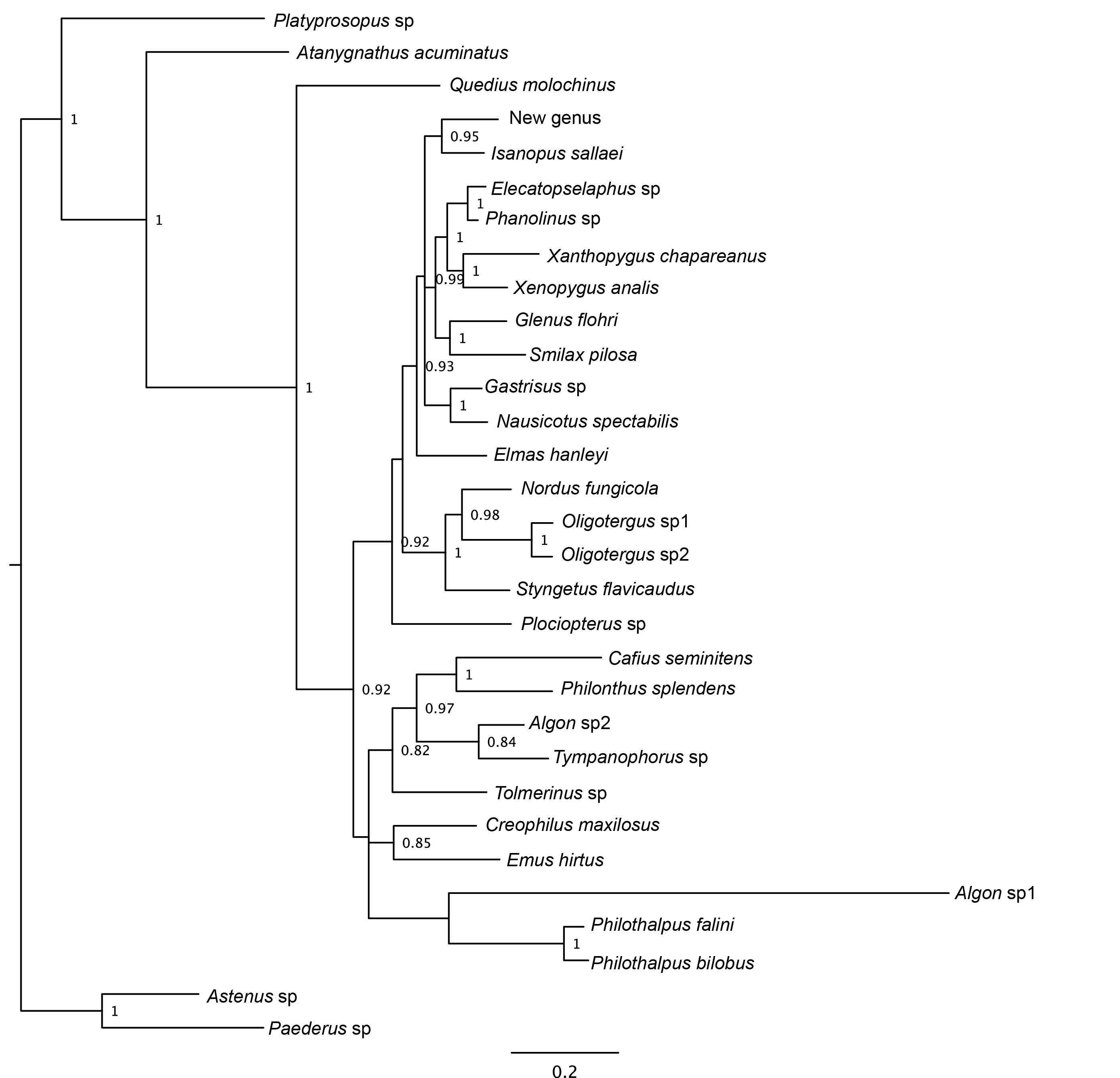
**Figure S2.** Bayesian phylogenetic tree for the COI gene. Only posterior probabilities above 0.75 are shown.



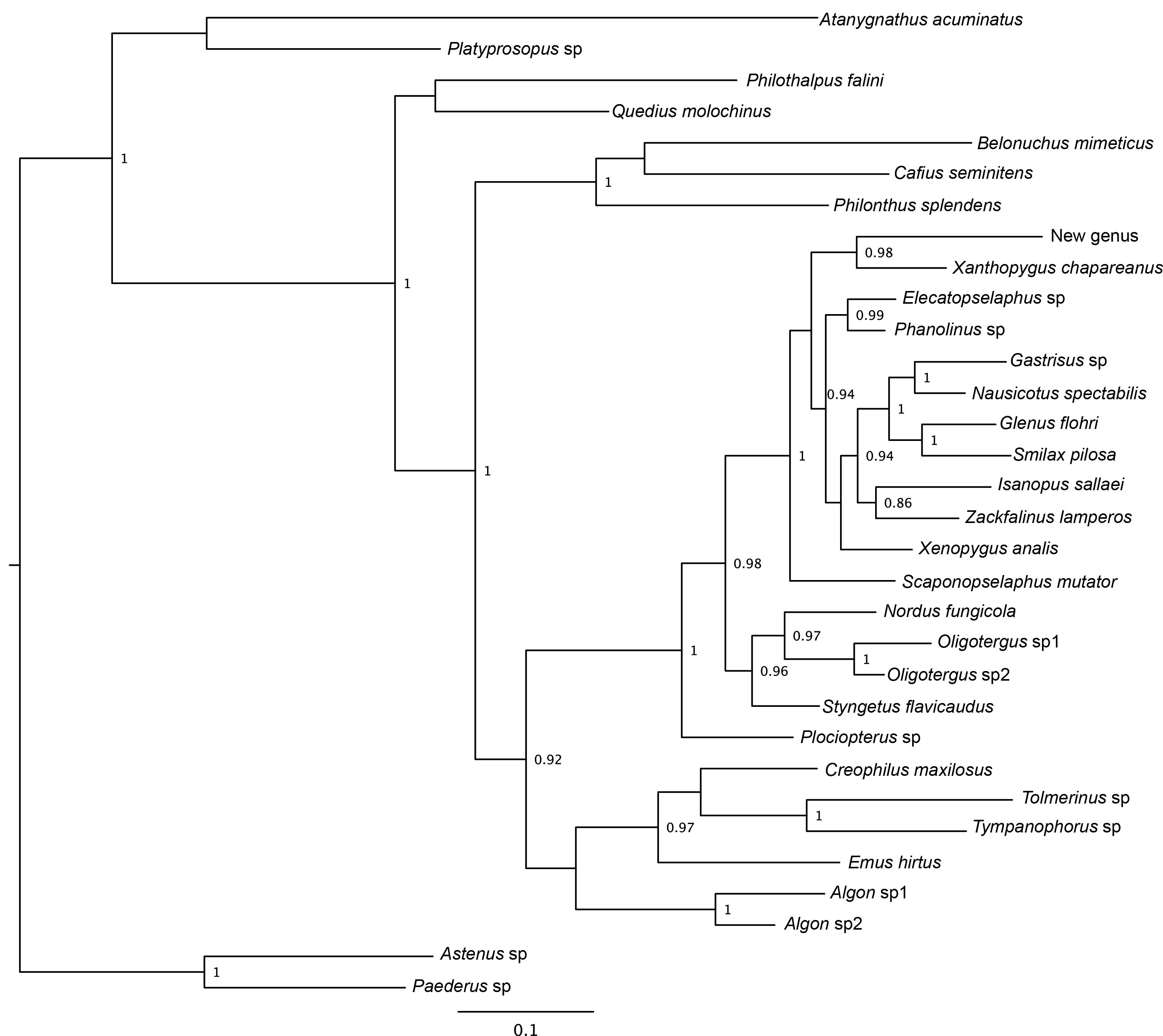
**Figure S3.** Bayesian phylogenetic tree for the arginine kinase gene. Only posterior probabilities above 0.75 are shown.



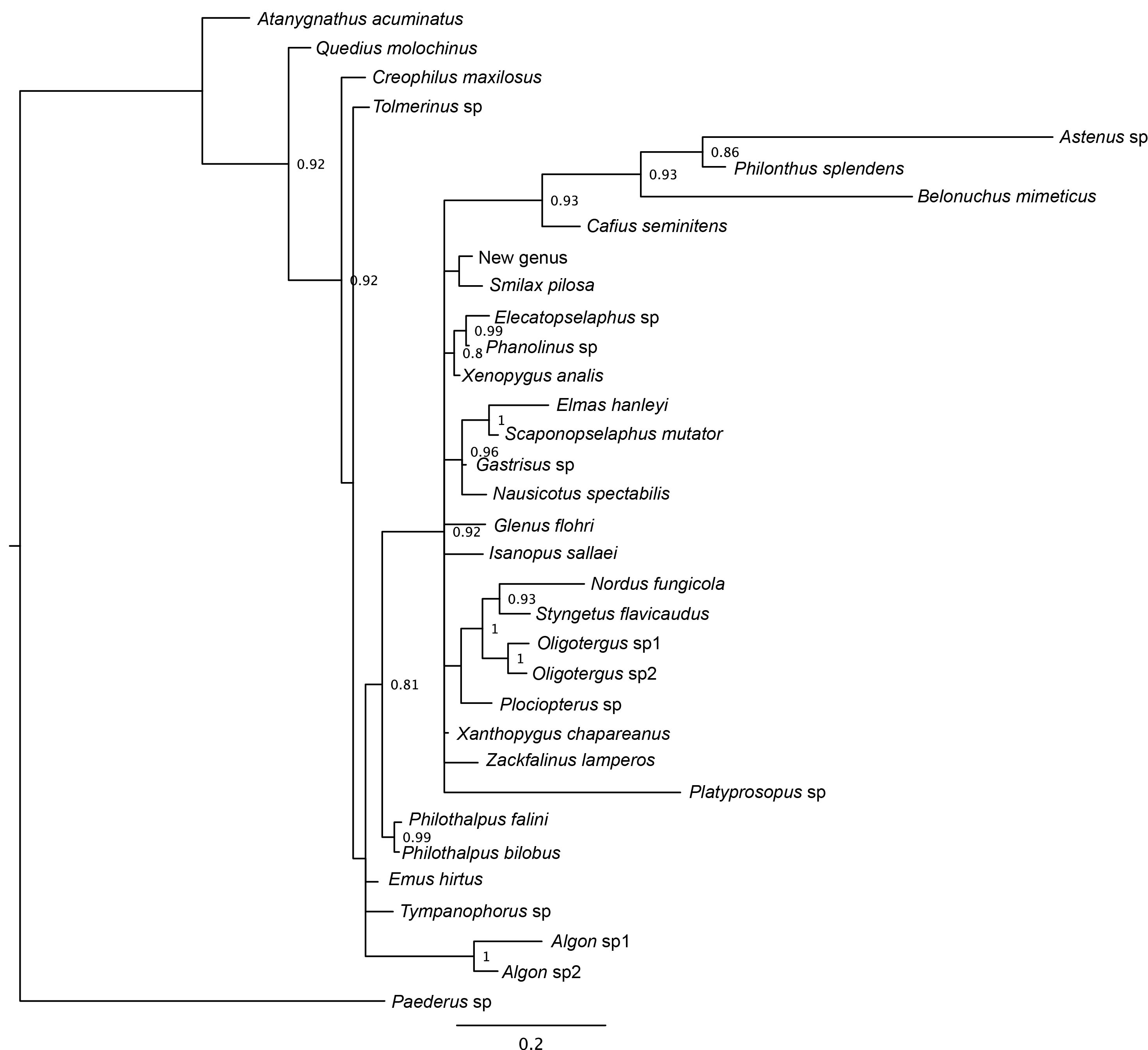
**Figure S4.** Bayesian phylogenetic tree for the CAD gene. Only posterior probabilities above 0.75 are shown.



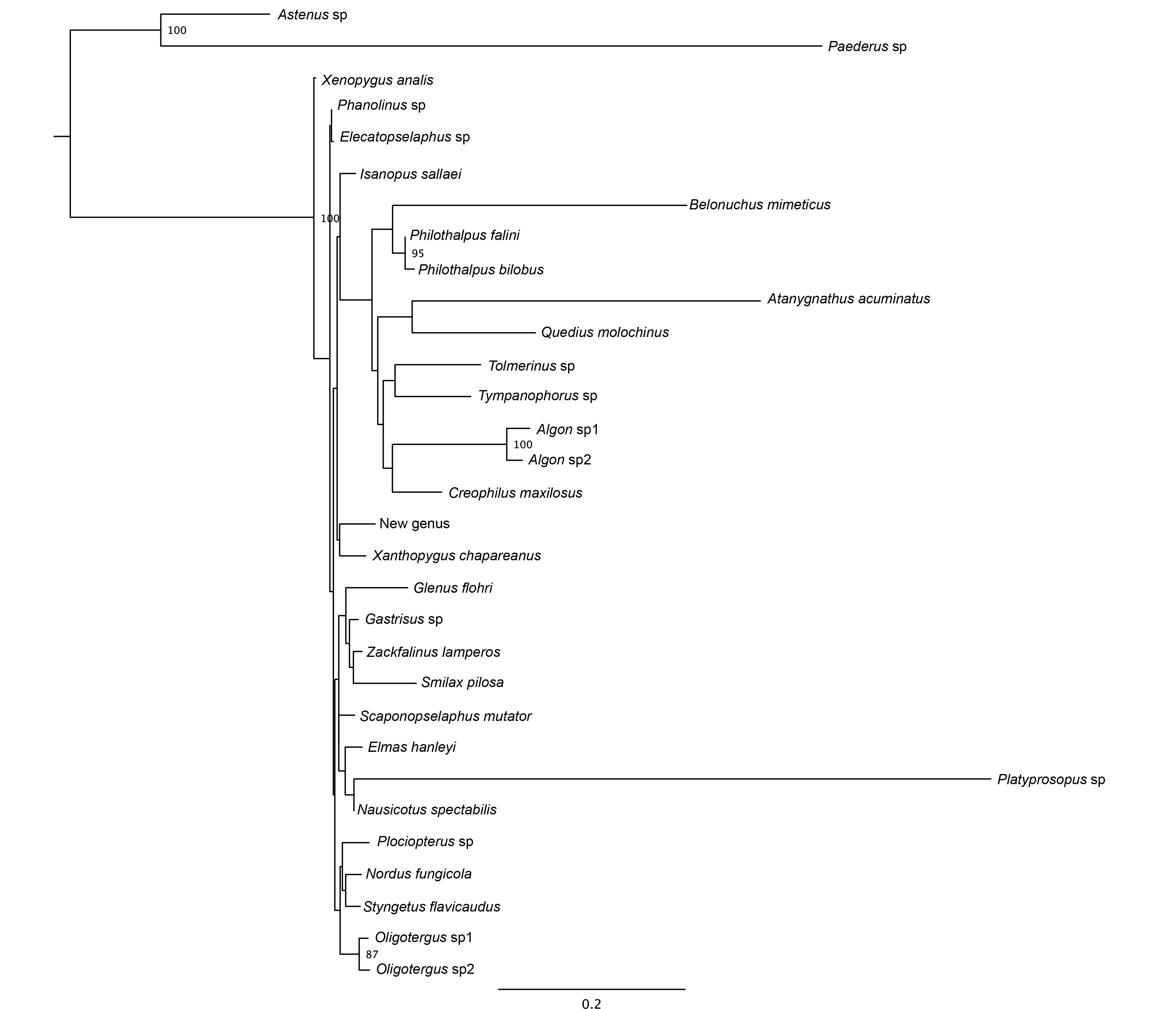
**Figure S5.** Bayesian phylogenetic tree for the topoisomerase I gene. Only posterior probabilities above 0.75 are shown.



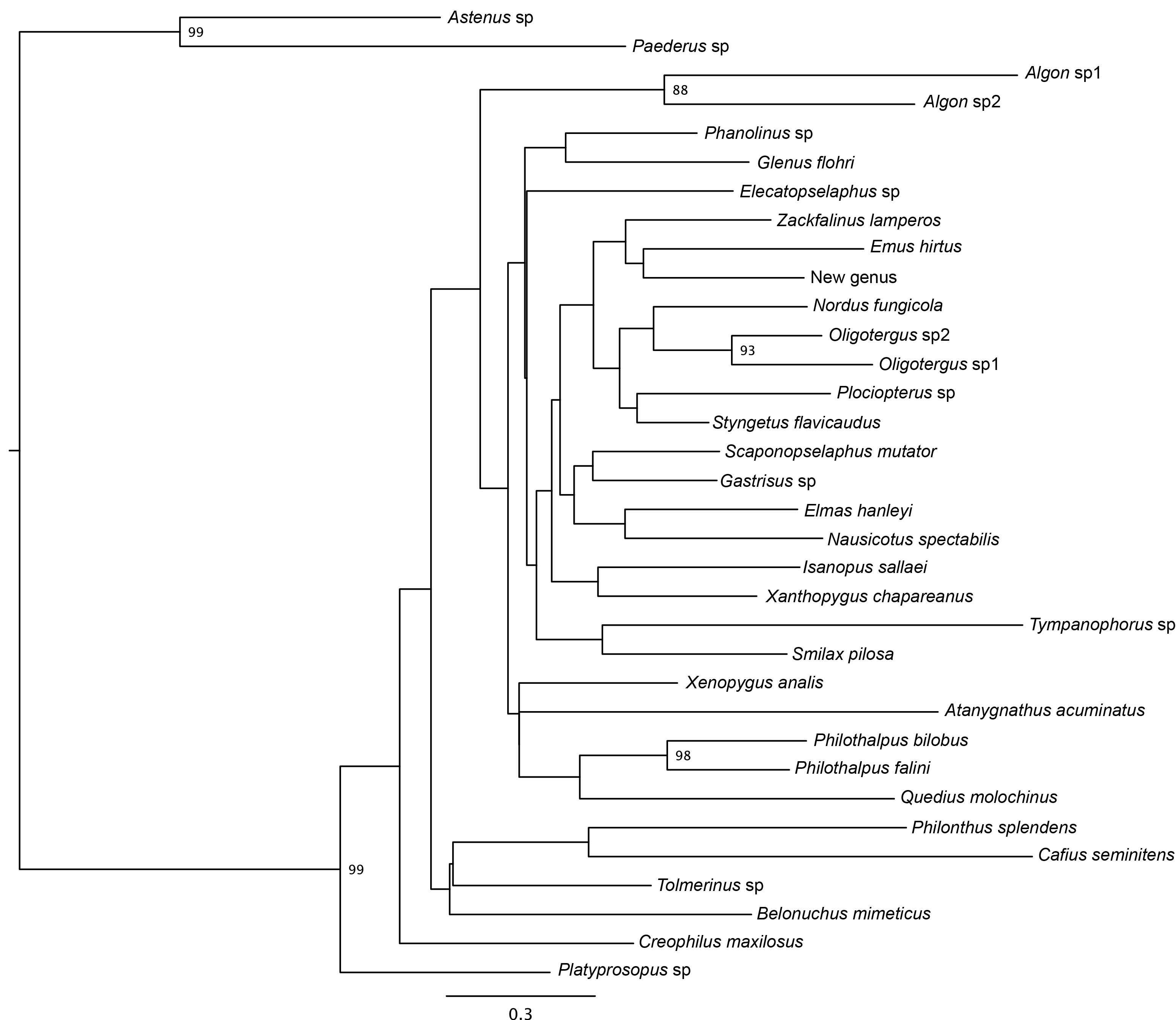
**Figure S6.** Bayesian phylogenetic tree for the wingless gene. Only posterior probabilities above 0.75 are shown.



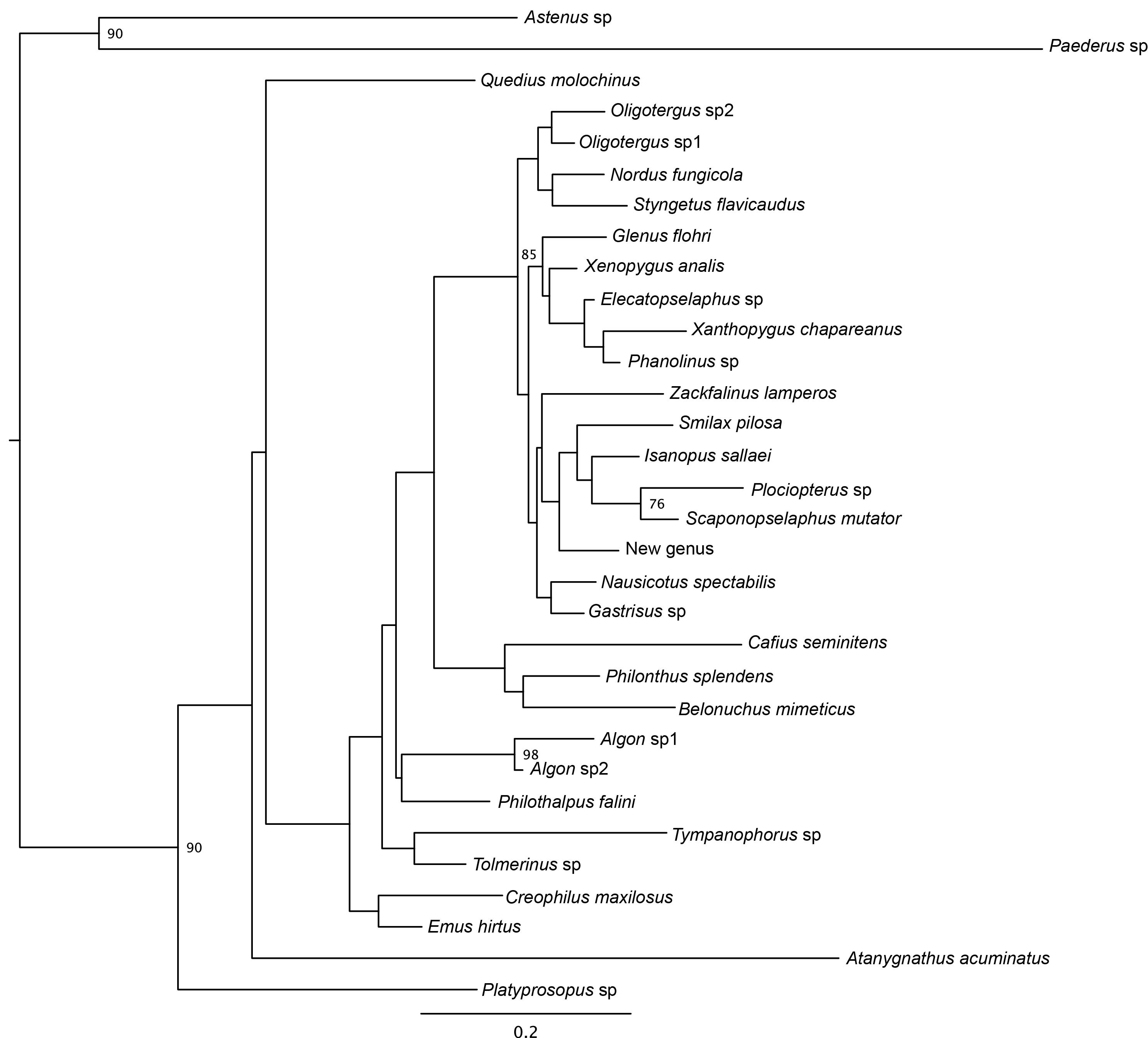
**Figure S7.** Best scoring maximum likelihood tree for the 28S rDNA gene. Only support values above 75 are shown.



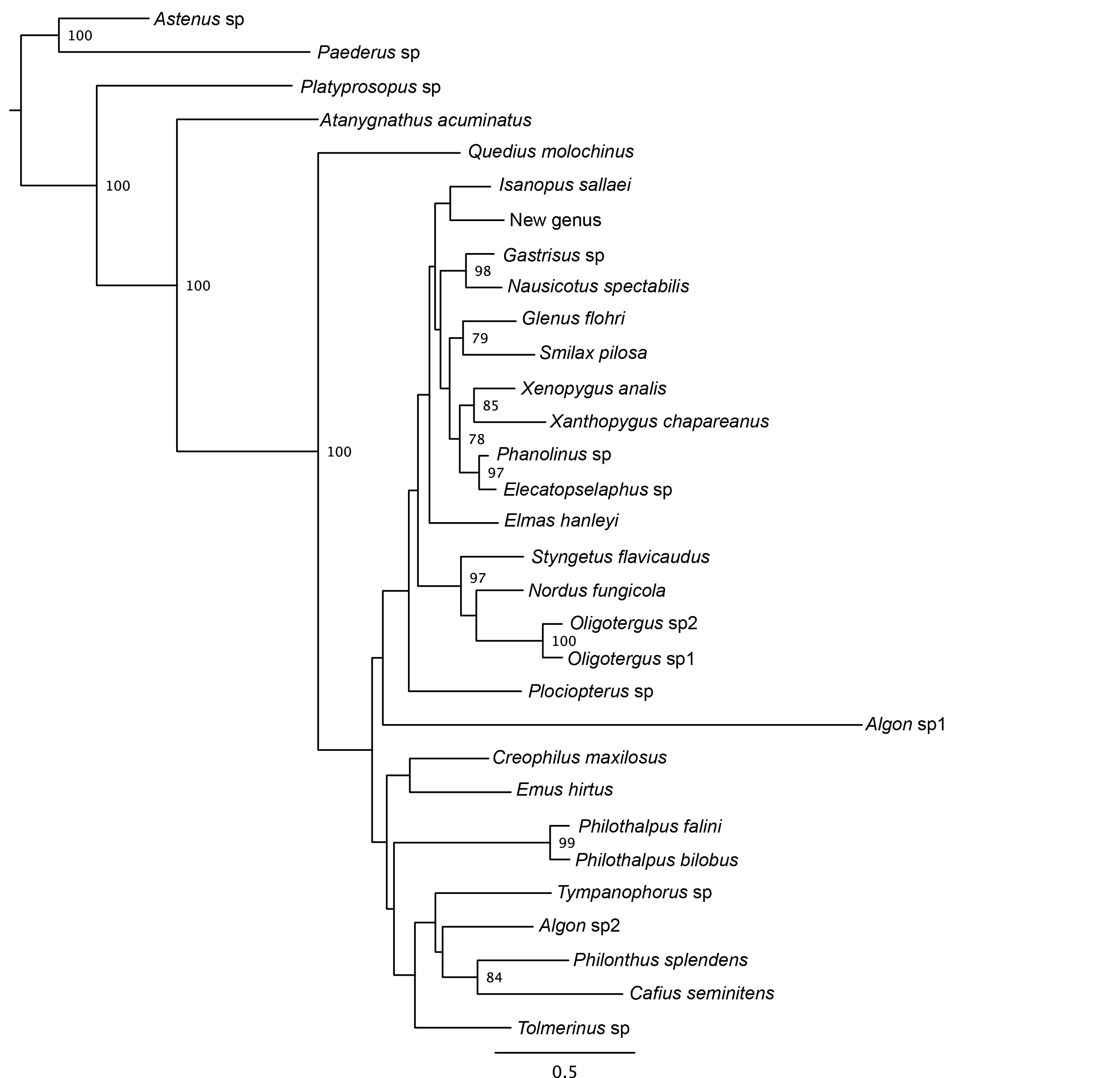
**Figure S8.** Best scoring maximum likelihood tree for the COI gene. Only support values above 75 are shown.



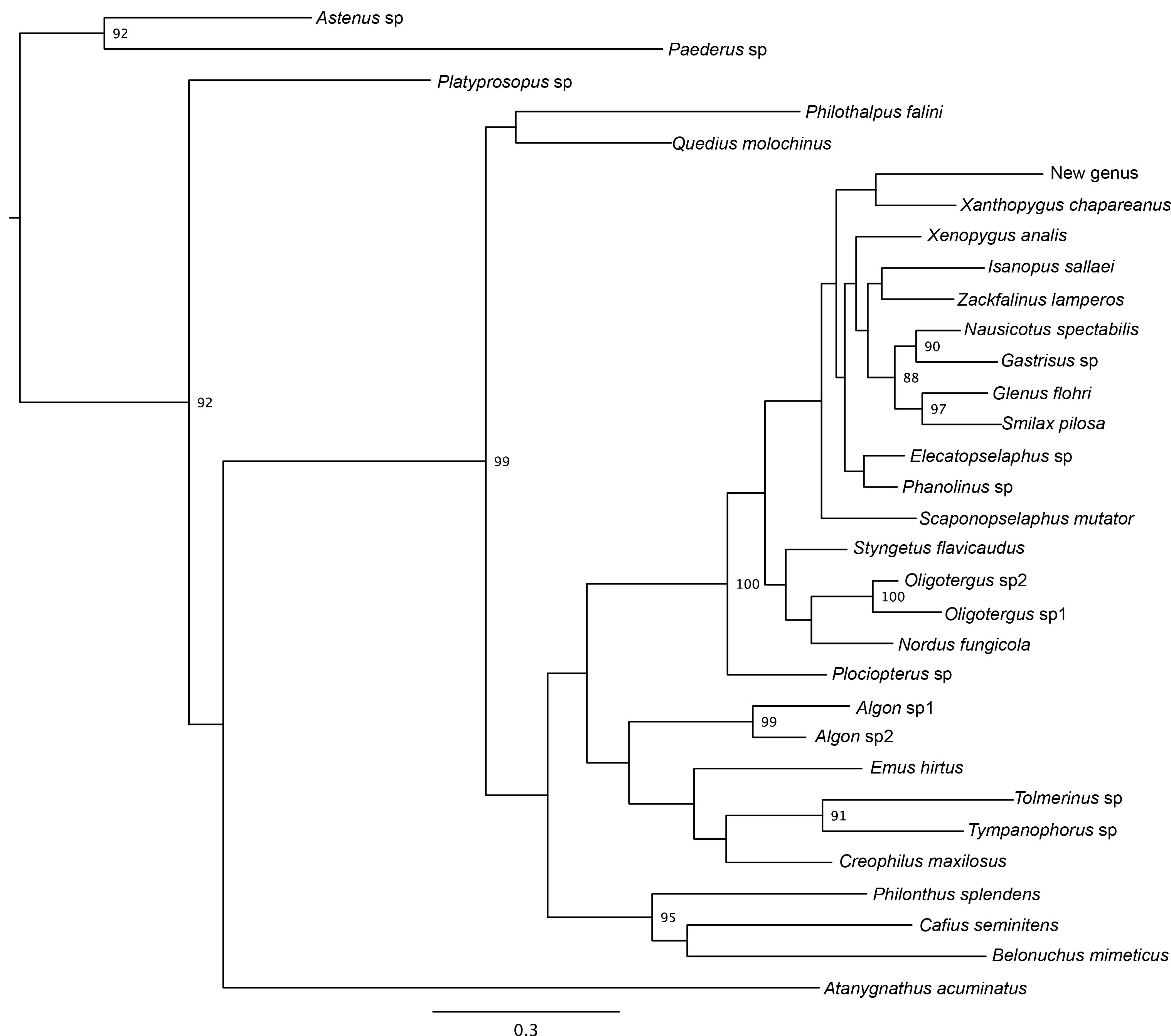
**Figure S9.** Best scoring maximum likelihood tree for the arginine kinase gene. Only support values above 75 are shown.



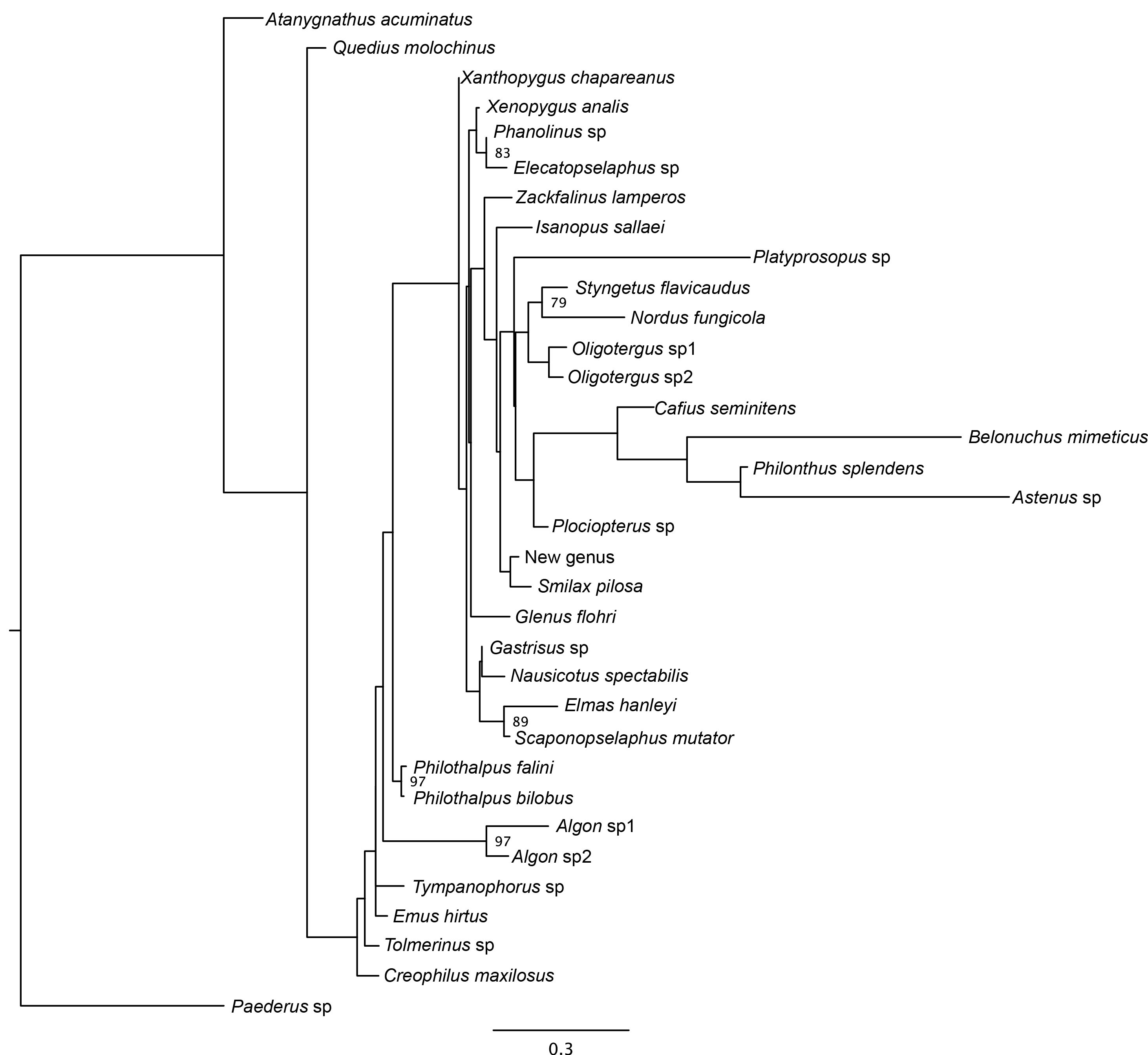
**Figure S10.** Best scoring maximum likelihood tree for the CAD gene. Only support values above 75 are shown.



**Figure S11.** Best scoring maximum likelihood tree for the topoisomerase I gene. Only support values above 75 are shown.



**Figure S12.** Best scoring maximum likelihood tree for the wingless gene. Only support values above 75 are shown.



**Supplementary References**

Abouheif, E. & Wray, G.A. (2002) Evolution of the gene network underlying wing polyphenism in

ants. *Science*, **297**, 249–252.

Maddison, D.R. (2008) Systematics of the North American beetle subgenus *Pseudoperyphus*

(Coleoptera: Carabidae: Bembidion) based upon morphological, chromosomal, and molecular data. *Annals of the Carnegie Museum of Natural History*, **77**, 147–93.

Simon, C., Frati, F., Reckenbach, A., Crespi, B., Liu, H. & Flook, P. (1994) Evolution, weighting and

phylogenetic utility of mitochondrial gene sequences and a compilation of conserved polymerase chain reaction primers. *Annals of the Entomological Society of America*, **87**, 651–701.

Van der Auwera, G., Chapelle, S. & De Wachter, R. (1994) Structure of the large ribosomal subunit

RNA of *Phytophthora megasperma*, and phylogeny of the oomycetes. *FEBS Letters*, **338**, 133–136.

Ward, P.S. & Downie, D.A. (2005) The ant subfamily Pseudomyrmecinae (Hymenoptera: Formicidae):

phylogeny and evolution of big-eyed arboreal ants. *Systematic Entomology*, **30**, 310–335.

Wild, A.L. & Maddison, D.R. (2008) Evaluating nuclear protein-coding genes for phylogenetic utility

in beetles. *Molecular Phylogenetics and Evolution*, **48**, 877–891.