# Things fall apart: biological species form unconnected parsimony networks

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## Electronic Supplementary Material

## Statistical parsimony methods

TCS uses coalescent theory (Hudson 1989; Templeton *et al.* 1992) to evaluate the probability that two DNA sequences share a parsimonious relationship without multiple substitutions underlying any single nucleotide difference. This probability is a function of the sequence length, the number of sequence differences between individuals, *j*, and the probability of nucleotide changes, *q*. The software uses an iterative Bayesian method to estimate $q_j$ for incremental increases in *j,* with priors bounded by a function of the number of haplotypes in the sample and of $\theta$ (estimated from the data). These iterations end at the largest value of *j* – the connection limit – for which the probability of parsimony is greater than some selected prior standard. Individual DNA sequences that differ by no more than the connection limit are grouped together into a subnetwork. Sequences that are more divergent than this connection limit are isolated in separate subnetworks whose relationships to each other are deemed to be unknowable – due to homoplasy – except at some lower level of statistical confidence. These subnetworks are isolated from each other without graphical connections in the TCS output. The breakdown of sequence variation among individuals from different species into discrete subnetworks at the connection limit reflects the accumulated effects of mutation, selection, and genetic drift between species. Other algorithms and software can estimate networks from

haplotype data (Cassens *et al.* 2003) but without an objective standard for separating haplotypes into unconnected subnetworks.

Inferences from this method depend on the chosen probability of parsimony. The published studies we reviewed (663 analyses in 517 papers; some studies included multiple independent analyses of different taxa or of different unlinked loci for the same population samples) used a probability of parsimony of 0.95 (a 95% connection limit or $L_{95}$; this is the default value in all versions of TCS). In our analyses of butterfly and cowrie data we chose 0.95 as a widely accepted standard analogous to $\alpha = 0.05$ from statistical hypothesis testing (Cowles & Davis 1982). We also explored the consequences of varying this standard to a higher (0.99) or lower (0.90; these are the extremes permitted by TCS 1.21) probability of parsimony or by fixing the connection limit to a specific number of steps as a kind of sensitivity analysis to explore the resolution of false positives or false negatives (see below), and to illustrate the robust or weak nature of the conclusions based on the 95% connection limit.

Because sequence ambiguities (including missing nucleotides and gaps) can be interpreted in favor of sequence identity between two samples, and because the resolution of sequence ambiguities can depend on the order in which sequences are input as data (Clement *et al.* 2000), we pruned sequences and nucleotide sites from each alignment to remove all ambiguities while preserving large numbers of individuals (N) and characters (n). In each case we note the differences between the original alignment (N, n) and our pruned alignment (*N, n*). For example, in the *Astraptes* mtDNA sequence alignment N = 484, n = 648; *N* = 426, *n* = 610.

The cowrie mtDNA sequence alignment posed some particular difficulties. The large sequence alignment (N = 2036, n = 614; *N* = 1988, *n* = 412; $L_{95} = 8$) involved a very large number of potential network connections that could not be analyzed together in TCS. We subdivided the problem by analyzing data separately for each of 19 genera for which there were many ESUs (3-23) or sequences (*N* = 18-

252). We analyzed an additional 20th data set consisting of all sequences for 27 other small or less-well-sampled genera (*N* = 206). We compared resulting network structures to the on-line list of cowrie ESUs (http://www.flmnh.ufl.edu/cowries/taxon_list.htm). The sensitivity analysis (table 1 of the main text) focused on 15 of these 19 well-sampled genera in which we found one or more false positive subnetworks or false negative taxa.

We characterized the reliability of the parsimony network method as an operational species definition by application of receiver operating characteristic analysis. This method uses counts of true and false positive and negative diagnoses of signals (in our case, species and subnetworks) to characterize diagnostic accuracy. We counted false positives as the number of subnetworks for a given taxon minus one; and false negatives as the number of network connections between different taxa grouped together in a single subnetwork. True positives were then defined as the number of taxa minus the number of false positives minus 1; and true negatives were defined as the number of unique haplotypes minus the number of subnetworks minus the number of false negatives. The true positive rate was then calculated as the number of true positives divided by the sum of true positives plus false negatives; and the false positive rate was calculated as the number of false positives divided by the sum of false positives and true negatives.

## Analysis of errors: false positive snakes (*Popeia* spp.)

We illustrate two likely sources of false positive and false negative errors in network analyses. First, under-sampling of haplotype diversity from species that are rare or difficult to collect might strand some sequences in separate subnetworks as an artifact that mimics the effect of real lineage sorting. Sanders *et al.* (2006) sampled genetic, morphological, and ecological similarities among individuals in the *Popeia popeiorum* species complex along latitudinal and altitudinal gradients across

southeast Asia. On the basis of a relatively small (32) sample of individual mtDNA sequences from these rare snakes, Sanders *et al.* argued for a conservative organization of this complex into three species. Does a network analysis support this result?

Because many or all nucleotides were missing for many individuals at three of the four mitochondrial genes in the original analysis, we analyzed just the cytochrome b sequences for which some data were available for most individuals ($N$ = 29, $n$ = 286; $L_{95}$ = 7). We found six subnetworks (figure S1). Three of these included 26 individuals in total and corresponded approximately to the species identified by Sanders *et al.* as *P. popeiorum* s. s. (northern Thailand, Laos, and a single haplotype from southern Thailand), *P. nebularis* (Cameron Highlands of Malaysia, plus a haplotype from Myanmar), and *P. sabahi* (southern Thailand, Sumatra, Borneo). The remaining subnetworks each consisted of a single haplotype from western Thailand and Myanmar (*P. popeiorum* s. s.) or Malaysia (*P. sabahi*).

These three stranded haplotypes might be unrecognized *Popeia* species, or they might be false positives caused by undersampling of mtDNA diversity within the three distinctive morphological and ecological phenotypes. We found the same three singleton false positives at a slightly less stringent connection limit ($L_{94}$ = 7, the same number of steps as $L_{95}$). We could resolve these false positives at the next-lower connection limit ($L_{93}$ = 8 steps), but at this lower connection limit we also introduced an unintended false negative: haplotypes of *P. popeiorum* s. s. and *P. sabahi* formed a single subnetwork with each other and the three false positives and separate only from the haplotypes characteristic of *P. nebularis* in a second subnetwork. The quality of this inference and the strong dependence on selection of a probability of parsimony suggest that considerably more data are needed to test *Popeia* species identities using this network method, and that operational species definitions based on parsimony subnetworks might often be unreliable when based on small samples.

## Analysis of errors: false negative whelks (*Nucella* spp.)

Network methods (and other methods based on divergence of DNA sequences) might fail to correctly identify recently diverged species with modest genetic differences or shared ancestral polymorphisms by lumping them together in a false negative (Verheyen *et al.* 2003). Marko (1998) analyzed the phylogeography of a sister species pair of northeast Pacific whelks, *Nucella emarginata* and *N. ostrina*, that have broad geographic ranges overlapping in central California but are reproductively isolated and morphologically distinct. He showed that *N. ostrina* mtDNA sequences are paraphyletic with respect to *N. emarginata*, which probably diverged from closely related southern *N. ostrina* populations in allopatry. Marko noted that the *N. emarginata* shell phenotype appeared in the fossil record much more recently (about 0.12 Mya) than the *N. ostrina* phenotype. Does this late Pleistocene divergence of *N. ostrina* and *N. emarginata*, and the limited opportunities for mutation and lineage sorting, prevent these two biological species from being distinguished as separate parsimony subnetworks?

Analysis of the unedited sequence alignment (N = 55, n = 589; $L_{95}$ = 10), including five outgroup sequences from two other northeast Pacific *Nucella* species (*N. canaliculata*, *N. lima*), produced three subnetworks (figure S2). The outgroups formed a pair of subnetworks separate from *N. ostrina* and *N. emarginata*, which suggests that the data could differentiate *Nucella* species from each other using network methods as in other examples we analyzed. However, all *N. ostrina* and *N. emarginata* sequences were lumped together in a single subnetwork in which haplotypes of the two species were separated by as little as one step. For such close similarities, no connection limit >1 step would differentiate these two species. The close similarities and paraphyletic relationships among most sequences from these two biological species are probably caused by their recent divergence and limited opportunities for mutation and lineage sorting. In addition, the occurrence of two

deeply nested *N. emarginata* haplotypes among *N. ostrina* phenotypes from the zone of sympatry in central California suggests some continuing introgression as an additional source of genetic similarity (see Marko 1998). In either case, the failure to differentiate these two species at the 95% (or any other meaningful) connection limit suggests that these late Pleistocene speciation events might generally be difficult to identify using network methods and similar genetic markers.

## Supplementary references

Cassens, I., van Waerebeek, K., Best, P. B., Crespo, E. A., Reyes, J. & Milinkovitch, M. C. 2003 The phylogeography of dusky dolphins (*Lagenorhynchus obscurus*): a critical examination of network methods and rooting procedures. *Mol. Ecol.* **12**: 1781-1792.

Clement, M., Posada, D. & Crandall, K. A. 2000 TCS: a computer program to estimate gene genealogies. *Mol. Ecol.* **9**: 1657-1660.

Cowles, S. M. & Davis, C. 1982 On the origins of the .05 level of statistical significance. *Amer. Psychol.* **37**: 553-558.

Hudson, R. R. 1989 How often are polymorphic restriction sites due to a single mutation. *Theor. Pop. Biol.* **36**: 23-33.

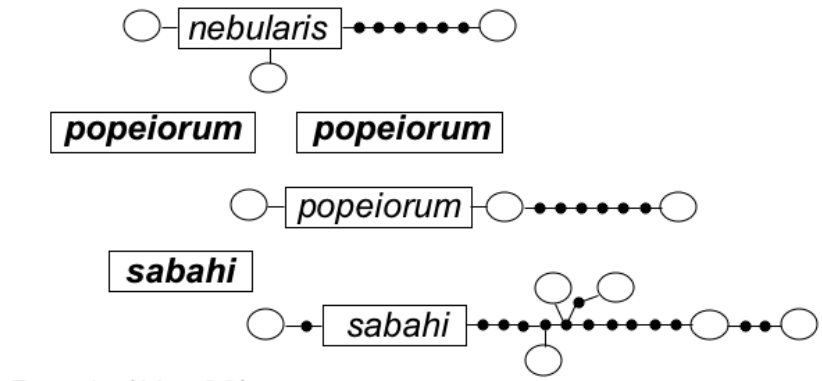
Marko, P. B. 1998 Historical allopatry and the biogeography of speciation in the prosobranch snail genus *Nucella. Evolution* **52**: 757-774.

Sanders, K. L., Malhotra, A. & Thorpe, R. S. 2006 Combining molecular, morphological, and ecological data to infer species boundaries in a cryptic tropical pitviper. *Biol. J. Linn. Soc.* **87**: 343-364.

Templeton, A. R., Crandall, K. A. & Sing, C. F. 1992 A cladistic analysis of phenotypic associations with haplotypes inferred from restriction endonuclease mapping and DNA sequence data. III. Cladogram estimation. *Genetics* **132**: 619-633.

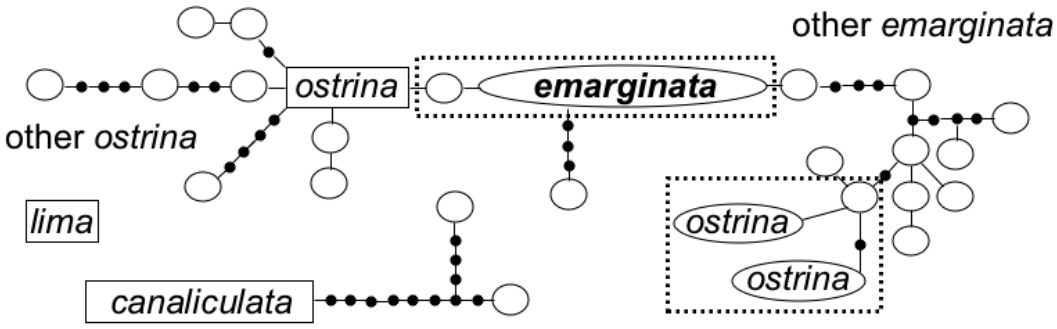
Verheyen, E., Salzburger, W., Snoeks, J. & Meyer, A. 2003 Origin of the superflock of cichlid fishes from Lake Victoria, East Africa. *Science* **300**: 325-329.

**Supplementary Figure S1.** 95% parsimony subnetworks for *Popeia* species (Sanders *et al.* 2006). Open symbols are sampled haplotypes (square = root haplotype); small filled symbols are unsampled intermediate haplotypes; lines indicate single sequence differences (mutations) joining haplotypes.




*Popeia* (*N* = 29)
6 subnetworks ($L_{95}$ = 7 steps), **3 false positives** (0.50)
3 species, 1 correct identification (0.33)

**Supplementary Figure S2.** 95% parsimony subnetworks (as in figure S1) for *Nucella* species (Marko 1998). Broken lines enclose haplotypes from *N. ostrina* and *N. emarginata* individuals that differed by just one or two nucleotides.




*Nucella* (*N* = 50)
3 subnetworks ($L_{95}$ = 10 steps)
4 species, 2 correct identifications (0.500), **1 false negative** (0.333)

**Supplementary Table S1.** Abbreviated reference, taxon, genetic marker, number of taxa and networks, and number of errors for 517 publications containing 663 statistical parsimony network analyses of species identification. These studies used different taxa (algae, plants, animals), genetic markers (coding and non-coding regions of the mitochondrial, nuclear, and chloroplast genomes), and versions of the TCS software. False positives or false negatives in parentheses (h) denote instances of hybridization identified as such by the original authors (and not counted as errors in our review).

| Reference | Taxon/taxa | DNA type | Locus | Species or ESUs | Networks | False negatives | False positives |
|---|---|---|---|---|---|---|---|
| Abbot P & Moran NA (2002) Mol Ecol 11:2649 | *Buchnera sp.* | endosymbiont DNA | leuBC | 1 | 1 | | |
| Abbot P & Moran NA (2002) Mol Ecol 11:2649 | *Buchnera sp.* | endosymbiont DNA | atpAHFE | 1 | 1 | | |
| Abbot P & Moran NA (2002) Mol Ecol 11:2649 | *Pemphigus obesinymphae* | mtDNA | COI, COII | 1 | 1 | | |
| Abbott CL & Double MC (2003) Mol Ecol 12:2747 | *Thalassarche cauta, T. steadi* | mtDNA | CR | 2 | 1 | 1 | |
| Abbott RJ & Comes HP (2004) New Phytol 161:211 | *Saxifraga oppositifolia* | cpDNA | RFLPs | 1 | 1 | | |
| Abila R et al. (2004) Mol Ecol 13:2589 | *cichlid species flock* | mtDNA | CR | 38 | 1 | 37 | |
| Aboim MA et al. (2005) Mol Ecol 14:1343 | *Helicolenus dactylopterus* | mtDNA | cyt b | 1 | 1 | | |
| Addison JA & Hart MW (2005) Evolution 59:532 | *Strongylocentrotus droebachiensis* | mtDNA | COI | 1 | 2 | | (1h) |
| Aleixo A (2006) Biol J Linn Soc Lond 89:383 | *Xiphorhynchus kienerii* | mtDNA | cyt b | 1 | 1 | | |
| Aleixo A (2006) Biol J Linn Soc Lond 89:383 | *Xiphorhynchus obsoletus* | mtDNA | cyt b | 1 | 1 | | |
| Alexander MP & Burns KJ (2006) Condor 108:489 | *Picoides albolarvatus* | mtDNA | cyt b, ATPase6 | 1 | 1 | | |

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|---|---|---|---|---|---|---|---|
| Alexandrino J et al. (2002) Heredity 88:66 | *Chioglossa lusitanica* | mtDNA | cyt b | 1 | 1 | | |
| Alpers DL et al. (2004) Mol Ecol 13:1771 | *Hippotragus equinus* | mtDNA | CR | 2 | 4 | | 2 |
| Alsos IG et al. (2005) Mol Ecol 14:2739 | *Vaccinium uliginosum* | cpDNA | IGS | 1 | 1 | | |
| Althoff DM & Pellmyr O (2002) Evolution 56:1632 | *Prodoxus decipiens* | mtDNA | COI, Leu tRNA | 1 | 1 | | |
| Antunes A et al. (2002) Mol Biol Evol 19:1272 | *Salmo trutta* | nuclear | transferrin (TF) | 1 | 1 | | |
| Apte S & Gardner JPA (2002) Mol Ecol 11:1617 | *Perna canaliculus* | mtDNA | ND-4 | 1 | 1 | | |
| Arnason E (2004) Genetica 166:1871 | *Gadus morhua* | mtDNA | cyt b | 1 | 1 | | |
| Asai S et al. (2006) Bird Conserv Int 16:113 | *Spizaetus nipalensis* | mtDNA | CR | 1 | 1 | | |
| Astolfi L et al. (2005) Mar Ecol Prog Ser 297:233 | *Atherina boyeri* | mtDNA | CR | 1 | 3 | | 2 |
| Audzijonyte A & Vainola R (2006) Mol Ecol 15:3287 | *Mysis salemaai* | mtDNA | COI | 1 | 1 | | |
| Audzijonyte A & Vainola R (2006) Mol Ecol 15:3287 | *Mysis segerstralei* | mtDNA | COI | 1 | 1 | | |
| Audzijonyte A et al. (2006) Mol Ecol 15:2969 | *Limnomysis benedeni* | mtDNA | COI | 1 | 1 | | |
| Audzijonyte A et al. (2006) Mol Ecol 15:2969 | *Paramysis ullskyi* | mtDNA | COI | 1 | 1 | | |
| Audzijonyte A et al. (2006) Mol Ecol 15:2969 | *Paramysis kessleri* | mtDNA | COI | 1 | 1 | | |

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|---|---|---|---|---|---|---|---|---|
| Audzijonyte A et al. (2006) Mol Ecol 15:2969 | *Paramysis sowinskii* | mtDNA | COI | 1 | 1 | | | |
| Audzijonyte A et al. (2006) Mol Ecol 15:2969 | *Paramysis intermedia* | mtDNA | COI | 1 | 1 | | | |
| Audzijonyte A et al. (2006) Mol Ecol 15:2969 | *Paramysis baeri sensu lato* | mtDNA | COI | 2 | 2 | | | |
| Audzijonyte A et al. (2006) Mol Ecol 15:2969 | *Paramysis lacustris* | mtDNA | COI | 1 | 2 | | | 1 |
| Austin JD et al. (2004) Mol Phylogenet Evol 32:799 | *Pseudacris crucifer* | mtDNA | cyt b | 1 | 3 | | | 2 |
| Austin JD et al. (2004) Mol Phylogenet Evol 32:799 | *Rana catesbeiana* | mtDNA | cyt b | 1 | 1 | | | |
| Austin JJ et al. (2004) Mol Phylogenet Evol 31:109 | *Phelsuma cepediana* | mtDNA | cyt b | 3 | 3 | | | |
| Austin JJ et al. (2004) Mol Phylogenet Evol 31:109 | *Phelsuma ornata ornata* | mtDNA | cyt b | 1 | 1 | | | |
| Avila LJ et al. (2006) Biol J Linn Soc Lond 89:241 | *Liolaemus boulengeri* | mtDNA | cyt b | 5 | 1 | (4h) | | |
| Ayoub NA & Riechert SE (2004) Mol Ecol 13:3453 | *Agelenopsis aperta* | mtDNA | COI | 1 | 4 | | | 3 |
| Babik W et al. (2004) Mol Ecol 13:1469 | *Rana arvalis* | mtDNA | cyt b | 1 | 2 | | | 1 |
| Baer CF et al. (2004) Mol Ecol 13:1859 | *Diaeretiella rapae* | mtDNA | COI, COII | 1 | 1 | | | |
| Baker AM et al. (2003) Mol Ecol 12:3313 | *Cheumatopsyche sp. AV1* | mtDNA | COI | 1 | 1 | | | |

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|---|---|---|---|---|---|---|---|
| Baratti M et al. (2005) J Exp Mar Biol Ecol 315:225 | *Sphaeroma terebrans* | mtDNA | COI | 3 | 3 | | |
| Baudry E et al. (2003) Mol Ecol 12:1843 | *Pimelia granulicollis, P. estevezi, P. fernandezlopezi* | mtDNA | COII | 3 | 1 | (2h) | |
| Baudry E et al. (2003) Mol Ecol 12:1843 | *Pimelia sparsa* | mtDNA | COII | 1 | 3 | | 2 |
| Bay LK et al. (2004) Mar Biol 144:757 | *Chlorurus sordidus* | mtDNA | CR | 1 | 1 | | |
| Beheregaray LB & Sunnucks P (2001) Mol Ecol 10:2849 | *Odontesthes argentinensis* | mtDNA | CR | 1 | 1 | | |
| Beheregaray LB et al. (2002) Proc R Soc Lond, B, Biol Sci 269:65 | *Odontesthes perugiae* | mtDNA | CR | 5 | 1 | 4 | |
| Beheregaray LB et al. (2003) Conserv Genet 4:31 | *Geochelone nigra* | mtDNA | CR | 4 | 4 | | |
| Behrmann-Godel J et al. (2004) Mol Ecol 13:491 | *Perca fluviatilis* | mtDNA | CR | 1 | 1 | | |
| Belahbib N et al. (2001) Mol Ecol 10:2003 | *Quercus suber, Quercus ilex* | cpDNA and mtDNA | cpDNA: DT, TF, CD, AS, VL mtDNA: ND7 | 2 | 1 | (1h) | |
| Berlin S et al. (2004) J Mol Evol 58:163 | *Parus caeruleus* | mtDNA | CR | 1 | 1 | | |
| Bittkau C & Comes HP (2005) Mol Ecol 14:4065 | *Nigella arvensis* | cpDNA | cpDNA | 4 | 2 | (2h) | |
| Blatter RHE et al. (2004) Theor Appl Genet 108:360 | *Triticum spelta, T. aestivum, T.durum* | nuclear | glutenin B1-1 subunit gene | 3 | 1 | 2 | |
| Blatter RHE et al. (2004) Theor Appl Genet 108:360 | *Triticum spelta, T. aestivum, T.durum* | nuclear | glutenin A1-2 subunit gene | 3 | 1 | 2 | |

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|---|---|---|---|---|---|---|---|---|
| Bohlen J et al. (2006) Mol Phylogenet Evol 40:856 | *Rhodeus colchicus, R. sericeus, R. amarus, R. meridionalis* | mtDNA | cyt b | 4 | 4 | | | |
| Bollmer JL et al. (2006) Mol Phylogenet Evol 39:237 | *Buteo galapagoensis, B. swainsoni* | mtDNA | cyt b, CR, ND2, COI | 2 | 1 | 1 | | |
| Bos DH & Sites JW (2001) Mol Ecol 10:1499 | *Rana luteiventris* | mtDNA | cyt b | 1 | 3 | | | 2 |
| Boulet M et al. (2005) Conserv Genet 6:539 | *Podiceps auritus* | mtDNA | ND3 | 1 | 1 | | | |
| Bowen BW et al. (2006) J Hered 97:1 | *Centropyge spp.* | mtDNA | CR | 1 | 1 | | | |
| Bowen BW et al. (2006) Mar Biol 149:899 | *Holocentrus ascensionis* | mtDNA | cyt b | 1 | 1 | | | |
| Bowen BW et al. (2006) Mar Biol 149:899 | *Myripristis jacobus* | mtDNA | cyt b | 1 | 1 | | | |
| Bowie RC et al. (2004) Mol Phylogenet Evol 33:56 | *Nectarinia olivacea, N. obscura* | mtDNA | ND3 | 2 | 1 | 1 | | |
| Bowie RCK et al. (2006) Mol Phylogenet Evol 38:171 | *Pogonocichla stellata* | mtDNA | ND3 | 1 | 1 | | | |
| Brant SV & Orti G (2003) Mol Ecol 12:1435 | *Blarina brevicauda* | mtDNA | cyt b | 2 | 2 | | | |
| Brehm A et al. (2003) Mol Phylogenet Evol 26:222 | *Lacerta dugesii* | mtDNA | cyt b, 12S rRNA | 1 | 4 | | | 3 |
| Brisson JA et al. (2004) Genetica 168:1999 | *Drosophila polymorpha* | nuclear | Omb | 1 | 1 | | | |
| Brisson JA et al. (2005) Evolution 59:1046 | *Drosophila melanogaster* | mtDNA | cyt b, ND1, tRNA-ser | 1 | 1 | | | |
| Brisson JA et al. (2005) Evolution 59:1046 | *Drosophila melanogaster* | nuclear | 6-PGD | 1 | 1 | | | |
| Broderick D et al. (2003) Conserv Genet 4:793 | *Otis tarda* | mtDNA | CR, cyt b | 1 | 1 | | | |

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|---|---|---|---|---|---|---|
| Brown RP et al. (2002) Mol Phylogenet Evol 24:324 | *Agama impalearis* | mtDNA | 16S rRNA, ND2 | 2 | 2 | |
| Brumfield RT (2005) Auk 122:414 | *Thamnophilus caerulescens* | mtDNA | cyt b | 1 | 1 | |
| Brunner PC et al. (2004) Heredity 93:364 | *Thrips tabaci* | mtDNA | COII | 3 | 3 | |
| Brunsfeld SJ & Sullivan J (2005) Conserv Genet 6:895 | *Cardamine constancei* | cpDNA | matK, trnK, trnL, trnF | 1 | 1 | |
| Buhay JE & Crandall KA (2005) Mol Ecol 14:4259 | *Orconectes australis packardi, Orconectes incomptus, Orconectes sp. nov., Orconectes australis australis* | mtDNA | 16S rRNA | 4 | 2 | 2 |
| Bunje PME (2005) Mol Ecol 14:4323 | *Theodoxus fluviatilis* | mtDNA | COI | 2 | 2 | |
| Burban C & Petit RJ (2003) Mol Ecol 12:1487 | *Pinus pinaster, P. thunbergii* | cpDNA | psaA-trnS | 2 | 1 | 1 |
| Burg TM & Croxall JP (2004) Mol Ecol 13:2345 | *Diomedea spp.* | mtDNA | CR | 3 | 3 | |
| Burns KJ & Barhoum DN (2006) Mol Phylogenet Evol 38:117 | *Chamaea fasciata* | mtDNA | cyt b, ATPase6, ATPase8 | 1 | 1 | |
| Burridge CP et al. (2006) Evolution 60:1038 | *Galaxias divergens* | mtDNA | cyt b, CR | 1 | 1 | |
| Burridge CP et al. (2006) Evolution 60:1038 | *Galaxias vulgaris* | mtDNA | cyt b, CR | 1 | 1 | |
| Caesar RM et al. (2005) Ann Entomol Soc Am 98:931 | *Acrotrichis xanthocera* | mtDNA | COI | 1 | 1 | |
| Cagnon C et al. (2004) Mar Biol 145:1257 | *Hydrobates pelagicus* | mtDNA | cyt b | 1 | 1 | |

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|---|---|---|---|---|---|---|
| Caicedo AL & Schaal BA (2004) Mol Ecol 13:1871 | *Solanum pimpinellifolium* | nuclear | fruit vacuolar invertase | 1 | 1 | |
| Caicedo AL & Schaal BA (2004) Proc Natl Acad Sci USA 101:17444 | *Solanum pimpinellifolium* | nuclear | Cf-2 genes | 1 | 1 | |
| Campos JL et al. (2006) Conserv Genet 7:515 | *Salmo trutta* | mtDNA | ND1 | 1 | 1 | |
| Cantanhede AM et al. (2005) Mol Ecol 14:401 | *Trichechus inunguis* | mtDNA | CR | 1 | 1 | |
| Capelli C et al. (2006) Mol Phylogenet Evol 40:620 | *Loxondonta cyclotis, L. africana, Mammuthus primigenius* | nuclear | BGN, CHRNA1, GBA, LEPR and VWF | 4 | 1 | 3 |
| Cardoso A & Vogler AP (2005) Mol Ecol 14:3531 | *Cicindela hybrida* | mtDNA | COI, ND1, cyt b | 4 | 4 | |
| Carini G & Hughes JM (2004) Heredity 93:350 | *Macrobrachium australiense* | mtDNA | COI | 1 | 1 | |
| Carini G & Hughes JM (2006) Biol J Linn Soc Lond 88:1 | *Notopala sublineata* | mtDNA | COI | 1 | 1 | |
| Carisio L et al. (2004) J Biogeogr 31:1149 | subspecies of *Trypocopris fulgidus, T. amedei, T. inermis* | mtDNA | COI | 10 | 8 | 2 |
| Carranza S et al. (2006) Mol Phylogenet Evol 40:532 | *Malpolon monspessulanus* | mtDNA | cyt b, 12S rRNA | 1 | 1 | |
| Carson EW & Dowling TE (2006) Mol Ecol 15:667 | *Cyprinodon atrorus, C. bifasciatus* | mtDNA | cyt b | 2 | 1 | (1h) |
| Carstens BC et al. (2004) Syst Biol 53:781 | *Plethodon idahoensis* | mtDNA | cyt b | 1 | 1 | |
| Carstens BC et al. (2005) Mol Ecol 14:255 | *Dicamptodon aterrimus* | mtDNA | cyt b | 1 | 1 | |
| Cassens I et al. (2003) Mol Ecol 12:1781 | *Lagenorhynchus obscurus* | mtDNA | cyt b | 1 | 1 | |

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|---|---|---|---|---|---|---|---|---|
| Cassone BJ & Boulding EG (2006) Mar Biol 149:213 | *Pachygrapsus crassipes* | mtDNA | COI | 1 | 1 | | | |
| Chappell DE et al. (2004) Conserv Genet 5:759 | *Gulo gulo* | mtDNA | CR | 1 | 1 | | | |
| Charrier G et al. (2006) Mol Phylogenet Evol 38:742 | *Lophius budegassa* | mtDNA | CR | 1 | 1 | | | |
| Charrier G et al. (2006) Mol Phylogenet Evol 38:742 | *Lophius piscatorius* | mtDNA | CR | 1 | 1 | | | |
| Chen B et al. (2004) Mol Ecol 13:3051 | *Anopheles jeyporiensis* | mtDNA | COII | 1 | 1 | | | |
| Chen SF et al. (2006) Mol Ecol 15:1643 | *Rhinolophus monoceros* | mtDNA | mtDNA hypervariable domain | 1 | 1 | | | |
| Cheviron ZA et al. (2005) Mol Phylogenet Evol 36:338 | *Lepidothrix coronata* | mtDNA | cyt b, ND2, ND3 | 1 | 3 | | | 2 |
| Chiari Y et al. (2004) Mol Ecol 13:3763 | *Mantella aurantiaca, M. milotympanum, Mantella crocea* | mtDNA | cyt b | 3 | 2 | 1 | | |
| Chiari Y et al. (2005) Conserv Genet 6:1041 | *Mantella cowani, M. baroni* | mtDNA | cyt b | 2 | 2 | | | |
| Chiari Y et al. (2006) Conserv Genet 7:473 | *Dyscophus antongilii, D, guineti* | mtDNA | cyt b | 2 | 1 | 1 | | |
| Chung KF et al. (2005) Am J Bot 92:2054 | *Oreomyrrhis spp.* | nuclear | ITS | 22 | 1 | 21 | | |
| Cognato AI et al. (2003) Environ Entomol 32:1262 | *Ips confusus* | mtDNA | COI | 1 | 1 | | | |
| Cognato AI et al. (2005) Agric For Entomol 7:87 | *Dendroctonus valens* | mtDNA | COI | 1 | 1 | | | |

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|---|---|---|---|---|---|---|---|---|
| Colgan DJ et al. (2005) Mar Biol 146:263 | *Patiriella exigua* | mtDNA | COI, COII, tRNA-Trp (part), tRNA-Ala, tRNA-Leu, tRNA-Asn, tRNA-Gln, tRNA-Pro, tRNA-Arg, ND4 | 1 | 1 | | | |
| Connelly HM et al. (2006) Southeast Nat 5:85 | *Cyprinella gibbsi* | mtDNA | ND4 | 1 | 1 | | | |
| Contreras-Diaz HG et al. (2003) Mol Ecol 12:2131 | *Pimelia granulicollis, P. estevezi, P. fernandezlopezi* | mtDNA | COII | 3 | 1 | 2 | | |
| Contreras-Diaz HG et al. (2003) Mol Ecol 12:2131 | *Pimelia sparsa* | mtDNA | COII | 3 | 3 | | | |
| Correia AT et al. (2006) Fish Sci 72:20 | *Conger conger* | mtDNA | CR | 1 | 1 | | | |
| Cosson JF et al. (2005) Mol Ecol 14:1151 | *Crocidura russula* | mtDNA | cyt b | 1 | 2 | | | 1 |
| Costedoat C et al. (2005) Biol J Linn Soc Lond 85:135 | *Chondrostoma nasus nasus* | mtDNA | cyt b | 1 | 1 | | | |
| Costedoat C et al. (2005) Biol J Linn Soc Lond 85:135 | *Chondrostoma toxostoma toxostoma* | mtDNA | cyt b | 1 | 1 | | | |
| Couch BC et al. (2005) Genetics 170:613 | *Magnaporthe oryzae* | nuclear | 21 SSCP loci | 1 | 1 | | | |
| Craig MT et al. (2006) J Biogeogr 33:969 | *Epinephelus labriformis, E. clippertonensis* | mtDNA | cyt b | 2 | 1 | 1 | | |
| Criscione CD & Blouin MS (2004) Evolution 58:198 | *Deropegus aspina* | mtDNA | ND2 | 2 | 2 | | | |
| Criscione CD & Blouin MS (2004) Evolution 58:198 | *Nanophyetus salmincola* | mtDNA | ND3 | 1 | 1 | | | |

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|---|---|---|---|---|---|---|---|---|
| Criscione CD & Blouin MS (2004) Evolution 58:198 | *Plagioporus shawi* | mtDNA | ND4 | 1 | 1 | | | |
| Culling MA et al. (2006) Mol Ecol 15:173 | *Cobitis taenia* | mtDNA | cyt b | 1 | 1 | | | |
| Cunha HA et al. (2005) Mar Biol 148:449 | *Sotalia fluviatilis, Sotalia guianensis* | mtDNA | CR | 2 | 1 | 1 | | |
| Dabrowski A et al. (2005) Conserv Genet 6:843 | *Vermivora chrysoptera, V.opinus* | mtDNA | ND2 | 2 | 2 | (2h) | | |
| Daniels SR et al. (2006) J Biogeogr 33:1538 | *Potamonautes perlatus* | mtDNA | 16S rRNA | 1 | 1 | | | |
| Davis LA et al. (2006) Mol Ecol 15:2141 | *Dendroica caerulescens* | mtDNA | CR | 1 | 1 | | | |
| de Bruyn M et al. (2005) Heredity 94:370 | *Macrobrachium rosenbergii* | mtDNA | COI | 1 | 1 | | | |
| De Gelas K & De Meester L (2005) Mol Ecol 14:753 | *Daphnia magna* | mtDNA | COI | 1 | 1 | | | |
| de la Fuente J et al. (2005) Exp Parasitol 109:16 | *Dermacentor andersoni* | nuclear | ITS | 1 | 1 | | | |
| de la Fuente J et al. (2005) Exp Parasitol 109:16 | *Dermacentor andersoni* | mtDNA | 16S rRNA | 1 | 1 | | | |
| de Moraes-Barros N et al. (2006) Genetica 126:189 | *Bradypus torquatus* | mtDNA | CR | 1 | 2 | | | 1 |
| de Moraes-Barros N et al. (2006) Genetica 126:189 | *Bradypus variegatus* | mtDNA | CR | 1 | 1 | | | |

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|---|---|---|---|---|---|---|
| Dean MD et al. (2003) Genetics 165:1959 | *Drosophila simulans* | mtDNA | ND2, COI, COII, ND5, ND4 genes, the transfer RNAs for Trp, Cys, Tyr, Asp, His, four intervening spacer regions | 1 | 2 | 1 |
| DeChaine EG & Martin AP (2004) Evolution 58:113 | *Parnassius smintheus* | mtDNA | COI | 1 | 1 | |
| DeChaine EG & Martin AP (2005) Am J Bot 92:477 | *Sedum lanceolatum* | cpDNA | tRNA-L to tRNA-F, tRNA-S to tRNA-G | 1 | 1 | |
| DeChaine EG & Martin AP (2005) J Biogeogr 32:1943 | *Colias meadii* | mtDNA | COI | 1 | 1 | |
| DeChaine EG & Martin AP (2005) J Biogeogr 32:1943 | *Parnassius smintheus* | mtDNA | COI | 1 | 1 | |
| DeJong RJ et al. (2003) Mol Ecol 12:3041 | *Biomphalaria glabrata* | mtDNA | 16S rRNA | 1 | 1 | |
| DeJong RJ et al. (2003) Mol Ecol 12:3041 | *Biomphalaria pfeifferi* | mtDNA | ND1 | 1 | 2 | 1 |
| DeJong RJ et al. (2003) Mol Ecol 12:3041 | *Biomphalaria pfeifferi* | mtDNA | 16S rRNA | 1 | 1 | |
| Demboski JR & Sullivan J (2003) Mol Phylogenet Evol 26:389 | *Tamias amoenus* | mtDNA | cyt b | 2 | 6 | (4h) |
| Devi KU et al. (2006) Genome 49:495 | *Beauveria bassiana* | mtDNA | S rRNA | 1 | 1 | |
| Devi KU et al. (2006) Genome 49:495 | *Beauveria bassiana* | nuclear | 7 beta-tubulin | 1 | 1 | |
| Diegisser T et al. (2004) J Evol Biol 17:83 | *Tephritis bardanae* | mtDNA | COI and COII | 1 | 1 | |
| Diegisser T et al. (2006) Mol Ecol 15:681 | *Tephritis conura* | mtDNA | COI, COII, 16S rRNA, ND1 | 1 | 1 | |

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|---|---|---|---|---|---|---|---|---|
| Dietzen C et al. (2006) J Ornithol 147:485 | *Serinus canaria* | mtDNA | cyt b | 1 | 1 | | | |
| Dobes CH et al. (2004) Mol Ecol 13:349 | *Arabis holboellii* | cpDNA | rnL intron, trnL/F IGS | 3 | 2 | 1 | | |
| Domingues VS et al. (2006) Mol Phylogenet Evol 40:139 | *Chromis limbata* | mtDNA | CR | 1 | 16 | | | |
| Donnelly MJ et al. (2004) Heredity 92:61 | *Anopheles gambiae, A. arabiensis* | mtDNA | ND5 | 2 | 1 | (1h) | | |
| Dowling TE et al. (2002) Mol Biol Evol 19:446 | *Astyanax mexicanus* | mtDNA | ND2 | 1 | 1 | | | |
| Downie DA (2002) Mol Ecol 11:2013 | *Daktulosphaira vitifoliae* | mtDNA | COI | 1 | 3 | | 2 | |
| Downie DA (2004) J Biogeogr 31:1759 | *Daktulosphaira vitifoliae* | mtDNA | COI | 1 | 2 | | 1 | |
| Doyle JJ et al. (2002) Evolution 56:1388 | *Glycine tomentella* | nuclear | H3-D | 1 | 1 | | | |
| Driscoll DA & Hardy CM (2005) Mol Ecol 14:1613 | *Amphibolurus nobbi* | mtDNA | ND3, ND4 | 2 | 2 | | | |
| Duftner N et al. (2006) Mol Ecol 15:2381 | *Varibilichromis moorii* | mtDNA | CR | 1 | 2 | | 1 | |
| Duncan KM et al. (2006) Mol Ecol 15:2239 | *Sphyrna lewini* | mtDNA | CR | 1 | 1 | | | |
| Duran S & Rutzler K (2006) Mol Phylogenet Evol 40:292 | *Chondrilla cf. nucula* | mtDNA | COI | 1 | 1 | | | |
| Duran S et al. (2004) Mol Ecol 13:109 | *Crambe crambe* | nuclear | ITS I & II | 1 | 1 | | | |
| Duran S et al. (2004) Mol Ecol 13:3317 | *Paracentrotus lividus* | mtDNA | COI | 1 | 1 | | | |
| Eastwood R & Hughes JM (2003) Aust J Zool 51:331 | *Acrodipsas cuprea* | mtDNA | COI | 1 | 1 | | | |
| Eastwood R et al. (2006) Ann Entomol Soc Am 99:164 | *Papilio demoleus* | mtDNA | COI | 1 | 1 | | | |

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| Eastwood R et al. (2006) Evolution 60:315 | *Jalmenus evagoras* | mtDNA | COI | 1 | 1 | | | |
| Eggert C et al. (2006) Conserv Genet 7:185 | *Palobates fuscus* | mtDNA | cyt b | 1 | 1 | | | |
| Ehrich D & Stenseth NC (2001) Heredity 86:716 | *Lemmus sibiricus* | mtDNA | CR | 1 | 2 | | | 1 |
| Elnaiem DEA et al. (2005) Insect Mol Biol 14:145 | *Phlebotomus papatasi* | nuclear | SP-15 | 1 | 1 | | | |
| Emerson BC et al. (2006) Mol Ecol 15:449 | *Brachyderes rugatus rugatus* | mtDNA | COII | 1 | 1 | | | |
| Eriksson R et al. (2006) Org Divers Evol 6:71 | *Flabellina verrucosa* | mtDNA | COI | 1 | 1 | | | |
| Etter RJ et al. (2005) Evolution 59:1479 | *Deminucula atacellana* | mtDNA | 16S rRNA | 1 | 1 | | | |
| Etter RJ et al. (2005) Evolution 59:1479 | *Ledella ultima* | mtDNA | 16S rRNA | 1 | 1 | | | |
| Etter RJ et al. (2005) Evolution 59:1479 | *Malletia abyssorum* | mtDNA | 16S rRNA | 1 | 1 | | | |
| Etter RJ et al. (2005) Evolution 59:1479 | *Nuculoma similis* | mtDNA | 16S rRNA | 1 | 1 | | | |
| Evans BJ et al. (2003) Evolution 57:1436 | *Bufo celebensis* | mtDNA | 12S rRNA | 1 | 3 | | | 2 |
| Evans BJ et al. (2003) Evolution 57:1931 | *Macaca maura, M. tonkeana, M. ochreata, M. brunnescens, M. hecki, M. nigrescens, M. nigra* | mtDNA | 12S rRNA | 7 | 1 | (6h) | | |
| Farias IP et al. (2004) Anim Conserv 7:265 | *Caiman crocodilus* | mtDNA | cyt b | 1 | 1 | | | |
| Farias IP et al. (2004) Anim Conserv 7:265 | *Melanosuchus niger* | mtDNA | cyt b | 1 | 1 | | | |
| Fenart S et al. (2006) Proc R Soc Lond, B, Biol Sci 273:1391 | *Beta vulgaris ssp. maritima* | cpDNA | trnK intron, trnD-trnT and trnL-trnF IGS | 1 | 1 | | | |
| Fet V et al. (2006) J Arachnol 34:248 | *Euscorpius italicus* | mtNDA | 16S rRNA | 1 | 1 | | | |

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| Fetzner JW & Crandall KA (2003) Evolution 57:2101 | *Orconectes luteus* | mtDNA | 16S rRNA | 1 | 1 | | | |
| Feulner PGD et al. (2006) Mol Phylogenet Evol 39:198 | *Campylomormyrus numenius* | mtDNA | cyt b | 1 | 1 | | | |
| Fineschi S et al. (2003) Can J For Res 33:2503 | *Tilia cordata* | cpDNA | TF, CD, DT, HK, K1K2, VL | 1 | 1 | | | |
| Fineschi S et al. (2005) Plant Syst Evol 250:187 | *Crataegus monogyna, C. laevigata* | cpDNA | TF, CD, CS, DT, HK, K1K2, VL | 2 | 1 | (1h) | | |
| Fjeldsa J et al. (2006) J Ornithol 147:578 | *Batis mixta, B. crypta* | mtDNA | ND2 | 2 | 2 | | | |
| Flagstad O & Roed KH (2003) Evolution 57:658 | *Rangifer tarandus* | mtDNA | CR | 1 | 1 | | | |
| Fordyce JA & Nice CC (2003) Evolution 57:1089 | *Battus philenor* | mtDNA | COII | 1 | 1 | | | |
| Forister ML et al. (2004) Mol Ecol 13:3489 | *Hesperia comma* | nuclear | wingless | 2 | 1 | 1 | | |
| Forister ML et al. (2004) Mol Ecol 13:3489 | *Hesperia comma* | mtDNA | COII | 2 | 2 | | | |
| Formia A et al. (2006) Conserv Genet 7:353 | *Chelonia mydas* | mtDNA | CR | 2 | 2 | | | |
| Francisco SM et al. (2006) Est Coast Shelf Sci 69:655 | *Atherina presbyter* | mtDNA | CR | 1 | 1 | | | |
| Francisco SM et al. (2006) Mol Phylogenet Evol 39:288 | *Lipophrys pholis* | mtDNA | CR | 1 | 3 | | | 2 |
| Fredsted T et al. (2004) Behav Ecol Sociobiol 56:393 | *Microcebus murinus* | mtDNA | CR | 1 | 1 | | | |
| Freeland JR et al. (2003) Ecol Entomol 28:413 | *Anax junius* | mtDNA | COI | 1 | 1 | | | |

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| Friesen VL et al. (2005) Conserv Genet 6:607 | *Brachyramphus marmoratus* | mtDNA | CR | 1 | 1 | | | |
| Fritz U et al. (2006) Zool Scr 35:531 | *Testudo hermanni* | mtDNA | cyt b | 1 | 1 | | | |
| Fritz U et al. (2006) Zool Scr 35:97 | *Mauremys leprosa* | mtDNA | cyt b | 1 | 1 | | | |
| Froufe E et al. (2003) Divers Distrib 9:269 | *Brachymystax lenok* | mtDNA | CR | 1 | 1 | | | |
| Froufe E et al. (2003) Divers Distrib 9:269 | *Thymallus grubii, Thymallus arcticus* | mtDNA | CR | 2 | 4 | | | 2 |
| Froufe E et al. (2005) J Fish Biol 67:1040 | *Hucho taimen* | mtDNA | CR, ATPase 6, ND1 | 1 | 1 | | | |
| Fuerst GS & Austin CC (2004) J Herpetol 38:257 | *Eumeces septentrionalis* | mtDNA | CR, ND4 | 2 | 2 | | | |
| Gabrielsen TM et al. (2002) Mol Ecol 11:2083 | *Ceramium tenuicorne* | mtDNA | COII, COIII | 1 | 2 | | | 1 |
| Garcia-Machado E et al. (2004) Mar Biol 144:147 | *Hypoplectrus spp* | mtDNA | cyt b | 6 | 1 | 5 | | |
| Garcia-Moreno J et al. (2004) Mol Phylogenet Evol 33:186 | *Chlorospingus ophthalmicus* | | COII, tRNA-lysine, ATPase6, ATPase8 | 5 | 7 | | | 2 |
| Garcia-Paris M et al. (2003) Evolution 57:129 | *Salamandra salamandra* | mtDNA | cyt b | 2 | 2 | | | |
| Garrick RC & Sunnucks P (2006) BMC Genet 7: | *Acanthanura n. sp.* | nuclear | UcEF-1a | 1 | 1 | | | |
| Garrick RC & Sunnucks P (2006) BMC Genet 7: | *Acanthanura n. sp.* | nuclear | Uc3 | 1 | 3 | | | 2 |
| Garrick RC & Sunnucks P (2006) BMC Genet 7: | *Acanthanura n. sp.* | nuclear | Uc180 | 1 | 2 | | | 1 |
| Garrick RC & Sunnucks P (2006) BMC Genet 7: | *Pseudachorutinae n sp.* | nuclear | SmEF-1a | 1 | 1 | | | |
| Garrick RC & Sunnucks P (2006) BMC Genet 7: | *Pseudachorutinae n sp.* | nuclear | Sm8 | 1 | 2 | | | 1 |

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| Garrick RC & Sunnucks P (2006) BMC Genet 7: | *Pseudachorutinae n sp.* | nuclear | Sm2 | 1 | 2 | 1 |
| Garrick RC et al. (2004) Mol Ecol 13:3329 | not named yet | mtDNA | COII | 1 | 2 | 1 |
| Gaskin JF et al. (2005) Mol Ecol 14:2331 | *L. draba, L. appelianum, L. propinquum* | cpDNA | IGS region | 3 | 3 | |
| Gelembiuk GW et al. (2006) Mol Ecol 15:1033 | *Dreissena caputlacus* | mtDNA | COI | 1 | 1 | |
| Gelembiuk GW et al. (2006) Mol Ecol 15:1033 | *Dreissena polymorpha* | mtDNA | COI | 1 | 1 | |
| Gelembiuk GW et al. (2006) Mol Ecol 15:1033 | *Dreissena stankovici* | mtDNA | COI | 1 | 1 | |
| Gentile G et al. (2002) Genetics 161:1561 | *Anopheles gambiae, A. arabiensis* | nuclear | ITS region | 2 | 2 | |
| Gentile G et al. (2004) Insect Mol Biol 13:371 | *Anopheles gambiae* | nuclear | intron 1 of voltage-gated sodium channel gene | 1 | 1 | |
| Gergus EWA et al. (2004) Copeia :758 | *Hyla wrightorum* | mtDNA | cyt b | 1 | 1 | |
| Gifford ME et al. (2004) Mol Phylogenet Evol 32:735 | *Ameiva chrysolaema* | mtDNA | ND2, Trp tRNA | 1 | 2 | 1 |
| Glover AG et al. (2005) Mar Ecol 26:223 | *Bathykurila guaymasensis* | mtDNA | COI | 2 | 2 | |
| Goldstien SJ et al. (2006) Mol Ecol 15:3259 | *Cellana flava* | mtDNA | cyt b | 1 | 1 | |
| Goldstien SJ et al. (2006) Mol Ecol 15:3259 | *Cellana ornata* | mtDNA | cyt b | 1 | 1 | |
| Goldstien SJ et al. (2006) Mol Ecol 15:3259 | *Cellana radians* | mtDNA | cyt b | 1 | 1 | |

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| Gomez-Zurita J & Vogler AP (2006) J Mol Evol 62:421 | *Timarcha goettingensis complex* | mtDNA and nuclear | COII, ITS-2 | 13 | 4 | 9 |
| Gompert Z et al. (2006) Mol Ecol 15:1759 | *Lycaeides melissa melissa, Lycaeides melissa samuelis* | mtDNA | COI, COII | 2 | 1 | 1 |
| Gonzalez MA et al. (2003) Condor 105:228 | *Thryothorus nigricapillus* | mtDNA | ATPase 6, 8 | 1 | 1 | |
| Good JM & Sullivan J (2001) Mol Ecol 10:2683 | *Odontesthes argentinensis* | mtDNA | CR | 1 | 1 | |
| Good JM et al. (2003) Evolution 57:1900 | *Tamias ruficaudus, T. r. ruficaudus, T. r. simulans* | mtDNA | cyt b | 3 | 2 | (2h) |
| Gottelli D et al. (2004) Mol Ecol 13:2275 | *Canis simensis* | mtDNA | CR | 1 | 1 | |
| Grant WS (2005) Genetica 125:293 | *Engraulis encrasicolus* | mtDNA | RFLPs | 1 | 1 | |
| Grant WS & Bowen BW (2006) Biol J Linn Soc Lond 88:673 | *Engraulis japonicus, E. australis, E. capensis, E. encrasicolus* | mtDNA | cyt b | 1 | 1 | |
| Grapputo A et al. (2005) Mol Ecol 14:4207 | *Leptinotarsa decemlineata* | mtDNA | COI, COII | 1 | 1 | |
| Grobler JP et al. (2005) Mammal Biol 70:291 | *Tragelaphus angasii* | mtDNA | CR | 1 | 1 | |
| Gruning CR et al. (2004) Fungal Genet Biol 41:676 | *Phialocephala fortinii* | nuclear | ITS1, 5.8S, ITS2 rDNA | 4 | 1 | (3h) |
| Guarniero I et al. (2002) J Fish Biol 60:1459 | *Solea vulgaris* | mtDNA | CR | 1 | 1 | |
| Gum B et al. (2005) Mol Ecol 14:1707 | *Thymallus thymallus* | mtDNA | ND5 | 4 | 2 | 2 |
| Gurgel CFD et al. (2004) J Phycol 40:748 | *Gracilaria tikvahiae* | cpDNA | rbcL | 1 | 1 | |
| Gurgel CFD et al. (2004) J Phycol 40:748 | *Gracilaria tikvahiae* | nuclear | ITS | 1 | 1 | |
| Haase M (2005) J Evol Biol 18:1076 | *P. antipodarum, P. doci, P. oppidanus, P. troglodytes* | mtDNA | 16S rDNA | 4 | 1 | 3 |

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| Hadly EA et al. (2004) Plos Biology 2:1600 | *Microtus montanus* | mtDNA | cyt b | 1 | 1 | | | |
| Hadly EA et al. (2004) Plos Biology 2:1600 | *Thomomys talpoides* | mtDNA | cyt b | 1 | 1 | | | |
| Haig SM et al. (2004) Conserv Genet 5:683 | *Strix occidentalis caurina, occidentalis, lucida* | mtDNA | CR | 2 | 2 | | | |
| Hampe A et al. (2003) Mol Ecol 12:3415 | *Frangula alnus* | cpDNA | RFLP haplotypes | 1 | 1 | | | |
| Harlin-Cognato A et al. (2006) J Evol Biol 19:955 | *Eumetopias jubatus* | mtDNA | CR and cyt b | 1 | 1 | | | |
| Hart MW et al. (2006) Biol Cons 210:158 | *Parvulastra exigua* | mtDNA | COI, 12S rDNA, tRNA, CR | 4 | 4 | | | |
| Hedin M & Wood DA (2002) Mol Ecol 11:1975 | *Hypochilus thorelli* | mtDNA | COI | 1 | 1 | | | |
| Heilveil JS et al. (2006) Mol Ecol 15:1627 | *Nigronia serricornis* | mtDNA | COI | 1 | 1 | | | |
| Herron MD et al. (2005) Mol Ecol 14:2773 | *Xerus inauris* | mtDNA | cyt b | 1 | 3 | | | 2 |
| Heuertz M et al. (2006) Mol Ecol 15:2131 | *Fraxinus angustifolia, Fraxinus excelsior, Fraxinus ornus* | cpDNA | chloroplast microsatellites | 3 | 1 | 1(1h) | | |
| Hickerson MJ & Cunningham CW (2005) Evolution 59:344 | *Xiphister atropurpureus* | mtDNA | CR | 1 | 1 | | | |
| Hickerson MJ & Cunningham CW (2005) Evolution 59:344 | *Xiphister atropurpureus* | nuclear | alpha-tropomyosin intron | 1 | 1 | | | |
| Hickerson MJ & Cunningham CW (2005) Evolution 59:344 | *Xiphister atropurpureus* | nuclear | alpha-enolase intron | 1 | 1 | | | |
| Hickerson MJ & Cunningham CW (2005) Evolution 59:344 | *Xiphister mucosus* | mtDNA | CR | 1 | 1 | | | |

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| Hickerson MJ & Cunningham CW (2005) Evolution 59:344 | *Xiphister mucosus* | nuclear | alpha-tropomyosin intron | 1 | 1 | | |
| Hickerson MJ & Cunningham CW (2005) Evolution 59:344 | *Xiphister mucosus* | nuclear | alpha-enolase intron | 1 | 1 | | |
| Hoarau G et al. (2004) J Sea Res 51:183 | *Pleuronectes platessa* | mtDNA | CR | 1 | 1 | | |
| Hoffman EA & Blouin MS (2004) Evolution 58:145 | *Rana pipiens* | mtDNA | ND1 | 1 | 2 | | 1 |
| Hoffmann FG et al. (2003) Mol Ecol 12:2981 | *Uroderma bilobatum* | mtDNA | cyt b | 1 | 4 | | 3 |
| Holder K et al. (2004) Can J Zool 82:564 | *Lagopus mutus* | mtDNA | CR | 1 | 1 | | |
| Horn A et al. (2006) Mol Ecol 15:1603 | *Tomicus destruens* | mtDNA | COI, COII | 1 | 1 | | |
| Horning ME & Cronn RC (2006) Genome 49:134 | *Purshia tridentata* | cpDNA | trnH(GUG)-psbA, trnT(UGU)-trnL(UAA), trnL(UAA)-trnF(GAA), trnK, accD-psaI spacers, rp116 intron | 1 | 1 | | |
| Howes BJ et al. (2006) Mol Phylogenet Evol 40:183 | *Eumeces fasciatus* | mtDNA | cyt b | 1 | 6 | | 5 |
| Hu J et al. (2006) Biochem Genet 44:161 | *Hydropotes inermis* | mtDNA | CR | 1 | 1 | | |
| Huang SF et al. (2004) J Biogeogr 31:1251 | *Trochodendron aralioides* | cpDNA | intergenic spacer of petG-trnP and petA-psbJ | 1 | 1 | | |

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| Huey JA et al. (2006) Biol J Linn Soc Lond 87:457 | *Neosilurus hyrtlii* | mtDNA | CR | 1 | 1 |
| Huey JA et al. (2006) Biol J Linn Soc Lond 87:457 | *Porochilus argenteus* | mtDNA | CR | 1 | 1 |
| Hufbauer RA et al. (2004) Mol Ecol 13:337 | *Aphidius ervi* | mtDNA | COI, COII | 1 | 1 |
| Hughes J et al. (2004) Mol Ecol 13:3197 | *Velesunio sp. A* | mtDNA | COI | 1 | 1 |
| Hughes J et al. (2004) Mol Ecol 13:3197 | *Velesunio sp. B* | mtDNA | COI | 1 | 1 |
| Hughes J et al. (2004) Mol Ecol 13:3197 | *Velesunio sp. C* | mtDNA | COI | 1 | 1 |
| Hughes J et al. (2004) Mol Ecol 13:3197 | *Velesunio sp. D* | mtDNA | COI | 1 | 1 |
| Hughes JM & Hillyer MJ (2003) Mar Freshw Res 54:587 | *Cherax destructor* | mtDNA | COI | 1 | 1 |
| Hughes JM & Hillyer MJ (2006) J Fish Biol 68:270 | *Nematalosa erebi* | mtDNA | ATPase 6, 8 | 1 | 1 |
| Hughes JM et al. (2003) Freshw Biol 48:2149 | *Baetis bicaudatus* | mtDNA | COI | 1 | 1 |
| Hughes JM et al. (2003) Freshw Biol 48:709 | *Bungona narilla* | mtDNA | COI | 1 | 1 |
| Hurtado LA et al. (2004) Mol Ecol 13:1365 | *Drosophila mettleri* | mtDNA | COI | 1 | 1 |
| Hurtado LA et al. (2004) Mol Ecol 13:1365 | *Drosophila nigrospiracula* | mtDNA | COI | 1 | 1 |
| Hurtado LA et al. (2004) Mol Ecol 13:1365 | *Drosophila pachea* | mtDNA | COI | 1 | 1 |
| Hurtado LA et al. (2004) Mol Ecol 13:2603 | *Alvinella pompejana* | mtDNA | COI | 1 | 1 |
| Hurtado LA et al. (2004) Mol Ecol 13:2603 | *Branchipolynoe symmytilida* | mtDNA | COI | 1 | 1 |

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| Hurtado LA et al. (2004) Mol Ecol 13:2603 | *Oasisia alvinae* | mtDNA | COI | 1 | 1 | | |
| Hurtado LA et al. (2004) Mol Ecol 13:2603 | *Riftia pachyptila* | mtDNA | COI | 1 | 1 | | |
| Hurtado LA et al. (2004) Mol Ecol 13:2603 | *Tevnia jerichonana* | mtDNA | COI | 1 | 1 | | |
| Hurwood DA & Hughes JM (2001) Mol Ecol 10:113 | *Caridina zebra* | mtDNA | COI | 1 | 3 | | 2 |
| Hurwood DA et al. (2005) Mar Freshw Res 56:1099 | *Ostrea angasi* | mtDNA | COI | 1 | 1 | | |
| Idaghdour Y et al. (2004) Mol Ecol 13:43 | *Chlamydotis undulata* | mtDNA | CR | 3 | 2 | (1h) | |
| Ikeda H & Setoguchi H (2006) J Plant Res 119:489 | *Arcterica nana* | cpDNA | trnT–trnL, psbB–psbF spacers | 1 | 1 | | |
| Jaarola M & Searle JB (2004) Heredity 92:228 | *Microtus agrestis* | mtDNA | cyt b | 1 | 1 | | |
| Jakob SS & Blattner FR (2006) Mol Biol Evol 23:1602 | *Hordeum spp.* | cpDNA | trnL–trnF spacer | 6 | 1 | 5 | |
| Janko K et al. (2003) J Evol Biol 16:1280 | *Cobitis elongatoides, C. taenia, C. tanaitica* | mtDNA | cyt b | 3 | 2 | 1 | |
| Jaramillo-Correa JP & Bousquet J (2005) Genetics 171:1951 | *Picea mariana, P. rubens* | mtDNA | ND1, ND5, ND7 | 2 | 1 | (1h) | |
| Jaramillo-Correa JP et al. (2004) Mol Ecol 13:2735 | *Picea mariana* | mtDNA | SSU rRNA V1 region, nad1 intron b/c, nad5 intron 1 | 1 | 1 | | |
| Jaramillo-Correa JP et al. (2006) Mol Ecol 15:2787 | *P. chihuahuana, P. martinezii* | mtDNA | SNPS | 2 | 1 | 1 | |
| Jaramillo-Correa JP et al. (2006) Mol Ecol 15:2787 | *P. martinezii* | cpDNA | SNPS | 1 | 1 | | |

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|---|---|---|---|---|---|---|
| Jesus J et al. (2005) Mol Phylogenet Evol 37:503 | *Mabuya maculilabris* | mtDNA | 12S rRNA, 16S rRNA, cyt b | 1 | 1 | |
| Johannesen J et al. (2005) Biol J Linn Soc Lond 84:739 | *Stegodyphus lineatus* | mtDNA | ND1, 16S rRNA, tRNA | 1 | 1 | |
| Johannesen J et al. (2005) Biol J Linn Soc Lond 86:1 | *Eresus walckenaeri* | mtDNA | 16S rRNA, ND1 | 2 | 2 | |
| Johnson JA & Dunn PO (2006) Conserv Genet 7:37 | *Tympanuchus cupido pinnatus, T. cupido cupido, T. cupido attwateri, T. pallidicinctus* | mtDNA | CR | 2 | 1 | (1h) |
| Johnson JA et al. (2005) Proc R Soc Lond, B, Biol Sci 272:1365 | *Milvus milvus, Milvus migrans* | mtDNA | CR | 2 | 1 | 1 |
| Johnson JB (2002) Evolution 56:948 | *Gila atraria* | mtDNA | CR | 1 | 1 | |
| Johnson KP et al. (2002) Mol Ecol 11:25 | *Columbicola gracilicapitis* | mtDNA | COI | 1 | 1 | |
| Johnson KP et al. (2002) Mol Ecol 11:25 | *Columbicola macrourae* | mtDNA | COI | 1 | 1 | |
| Johnson KP et al. (2002) Mol Ecol 11:25 | *Columbicola passerinae* | mtDNA | COI | 1 | 1 | |
| Johnson KP et al. (2002) Mol Ecol 11:25 | *Physconelloides ceratoceps* | mtDNA | COI | 1 | 1 | |
| Johnson KP et al. (2002) Mol Ecol 11:25 | *Physconelloides eurysema* | mtDNA | COI | 1 | 1 | |
| Johnson SB et al. (2006) Biol Bull 210:140 | *Lepetodrilus fucensis, L. gordensis* | nuclear | Pgm-i | 2 | 1 | 1 |
| Johnson SB et al. (2006) Biol Bull 210:140 | *Lepetodrilus fucensis, L. gordensis* | mtDNA | COI | 2 | 2 | |
| Johnson SG (2005) Mol Ecol 14:2299 | *Mexipyrgus churinceanus* | mtDNA | cyt b | 1 | 1 | |
| Jolly MT et al. (2006) Mol Ecol 15:1841 | *Owenia fusiformis* | mtDNA | COI | 3 | 3 | |

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|---|---|---|---|---|---|---|---|---|
| Jolly MT et al. (2006) Mol Ecol 15:1841 | *Pectinaria koreni* | mtDNA | COI | 2 | 2 | | | |
| Joly S & Bruneau A (2004) Evolution 58:284 | *Apios americana, A. priceana* | nuclear | H3-D region | 2 | 2 | | | |
| Jones ME et al. (2006) Conserv Genet 7:691 | *Eucalyptis grandis* | cpDNA | JLA | 1 | 1 | | | |
| Jones RC et al. (2005) Aust JBot 53:367 | *Eucalyptus morrisbyi* | cpDNA | JLA | 1 | 1 | | | |
| Jordal BH et al. (2006) Mol Ecol 15:2935 | *Aphanarthrum glabrum* | nuclear | enolase | 2 | 1 | 1 | | |
| Jordan S et al. (2005) Mol Ecol 14:3457 | *Megalagrion xanthomelas, M. pacificum* | mtDNA | COII | 2 | 2 | | | |
| Kasapidis P et al. (2005) Mol Phylogenet Evol 34:55 | *Lepus europaeus* | mtDNA | CR | 2 | 2 | | | |
| Kawai M et al. (2006) Environ Entomol 35:569 | *Monochamus alternatus* | mtDNA | COII | 1 | 2 | | | (1h) |
| Kawamura K et al. (2006) Mol Ecol 15:613 | *Lepomis macrochirus* | mtDNA | cyt b, CR | 1 | 1 | | | |
| Kawane M et al. (2005) J Nat Hist 39:3903 | *Deiratonotus japonicus* | mtDNA | COI | 1 | 1 | | | |
| Keller GP et al. (2004) Mol Ecol 13:2405 | *Chelymorpha alternans* | mtDNA | COI | 1 | 1 | | | |
| Ketmaier V & Bernardini C (2005) J Hered 96:318 | *Lutra lutra* | mtDNA | CR | 1 | 1 | | | |
| Ketmaier V et al. (2005) J Zool 266:401 | *Tanymastix stagnalis* | mtDNA | 16S rRNA, COI | 1 | 9 | | | 8 |
| Kim SJ et al. (2003) Hydrobiologia 505:41 | *Littorina brevicula* | mtDNA | cyt b, ND6 | 1 | 1 | | | |
| Kim SJ et al. (2003) Mar Pollut Bull 46:74 | *Littorina brevicula* | mtDNA | ND6 | 1 | 1 | | | |
| Kim SJ et al. (2003) Mar Pollut Bull 46:74 | *Littorina brevicula* | mtDNA | cyt b | 1 | 1 | | | |
| Knowles JD et al. (2005) Mar Ecol 26:216 | *Paralvinella pandorae* | mtDNA | COI | 1 | 1 | | | |

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|---|---|---|---|---|---|---|---|
| Koch MA et al. (2006) Mol Ecol 15:825 | *Arabis alpina* | nuclear | ITS region | 1 | 4 | | 3 |
| Koch MA et al. (2006) Mol Ecol 15:825 | *Arabis alpina* | cpDNA | cpDNA | 1 | 1 | | |
| Kojima S et al. (2004) Mar Ecol Prog Ser 276:161 | *Batillaria cumingi* | mtDNA | COI | 1 | 1 | | |
| Kojima S et al. (2005) Ecol Res 20:686 | *Batillaria zonalis* | mtDNA | COI | 1 | 1 | | |
| Kotlik P & Berrebi P (2001) Mol Ecol 10:2177 | *Barbus barbus* | mtDNA | cyt b | 1 | 1 | | |
| Kuchta SR & Tan AM (2005) Mol Ecol 14:225 | *Taricha granulosa* | mtDNA | cyt b | 1 | 1 | | |
| Kulikova IV et al. (2004) Auk 121:930 | *Anas zonorhyncha, A. platyrhynchos, A. fulvigula, A. rubripes, A. diazi* | mtDNA | CR | 5 | 1 | 3(1h) | |
| Kulikova IV et al. (2005) Auk 122:949 | *Anas platyrhynchos* | mtDNA | CR | 1 | 1 | | |
| Kvist L et al. (2005) Mol Phylogenet Evol 34:501 | *Parus caeruleus* | mtDNA | CR | 2 | 3 | | 1 |
| Larena BG et al. (2002) Mol Ecol 11:1965 | *Armeria filicaulis, A. villosa* | cpDNA | trnL-F | 2 | 1 | (1h) | |
| Lauga B et al. (2005) J Ornithol 146:257 | *Cinclus cinclus* | mtDNA | cyt b | 1 | 1 | | |
| Law JH & Crespi BJ (2002) Mol Ecol 11:1471 | *Timema spp.* | mtDNA | COI | 19 | 3 | 16 | |
| Lebarbenchon C et al. (2006) Mammal Biol 71:164 | *Mustela nivalis* | mtDNA | CR | 1 | 1 | | |
| Lecomte F et al. (2004) Mol Ecol 13:2169 | *Engraulis mordax* | mtDNA | cyt b | 1 | 1 | | |
| Lecomte F et al. (2004) Mol Ecol 13:2169 | *Sardinops sagax* | mtDNA | cyt b | 1 | 1 | | |
| Lee J et al. (2006) J Hered 97:290 | *Melanoplus femurrubrum* | nuclear | ITS | 1 | 1 | | |

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|---|---|---|---|---|---|---|
| Lee J et al. (2006) J Hered 97:290 | *Melanoplus femurrubrum* | mtDNA | COI | 1 | 1 | |
| Lee T & Foighil DO (2005) Evolution 59:2139 | *Brachidontes exustus Antiles clade* | mtDNA | COI | 2 | 2 | |
| Lee T & Foighil DO (2005) Evolution 59:2139 | *Brachidontes exustus Atlantic clade* | mtDNA | COI | 1 | 1 | |
| Lee T & Foighil DO (2005) Evolution 59:2139 | *Brachidontes exustus Bahamas clade* | mtDNA | COI | 3 | 3 | |
| Lee T & Foighil DO (2005) Evolution 59:2139 | *Brachidontes exustus Gulf clade* | mtDNA | COI | 1 | 1 | |
| Lee T & Foighil DO (2005) Evolution 59:2139 | *Brachidontes exustus W. Caribbean clade* | mtDNA | COI | 3 | 3 | |
| Leebens-Mack J & Pellmyr O (2004) J Hered 95:127 | *Tegeticula yuccasella* | mtDNA | COI | 1 | 1 | |
| Lefebure T et al. (2006) Mol Ecol 15:1797 | *Niphargus virei* | mtDNA | COI | 1 | 11 | 10 |
| Lesia MGA et al. (2003) Afr Zool 38:109 | *Chersina ungulata* | mtDNA | cyt b | 1 | 1 | |
| Leskinen E et al. (2004) Mol Ecol 13:2257 | *Ulva compressa* | nuclear | ITS region | 1 | 1 | |
| Leskinen E et al. (2004) Mol Ecol 13:2257 | *Ulva intestinalis* | nuclear | ITS region | 1 | 1 | |
| Lessios HA & Robertson DR (2006) Proc R Soc Lond, B, Biol Sci 273:2201 | *Acanthurus nigricans* | mtDNA | ATPase8, ATPase6 | 1 | 1 | |
| Lessios HA & Robertson DR (2006) Proc R Soc Lond, B, Biol Sci 273:2201 | *Acanthurus triostegus* | mtDNA | ATPase8, ATPase6 | 2 | 2 | |

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| Lessios HA & Robertson DR (2006) Proc R Soc Lond, B, Biol Sci 273:2201 | *Arothron meleagris* | mtDNA | ATPase8, ATPase6 | 1 | 1 | |
| Lessios HA & Robertson DR (2006) Proc R Soc Lond, B, Biol Sci 273:2201 | *Atherina boyeri* | mtDNA | CR | 1 | 1 | |
| Lessios HA & Robertson DR (2006) Proc R Soc Lond, B, Biol Sci 273:2201 | *Calotomus carolinus* | mtDNA | ATPase8, ATPase6 | 1 | 1 | |
| Lessios HA & Robertson DR (2006) Proc R Soc Lond, B, Biol Sci 273:2201 | *Cantherhinus dumerilii* | mtDNA | ATPase8, ATPase6 | 1 | 1 | |
| Lessios HA & Robertson DR (2006) Proc R Soc Lond, B, Biol Sci 273:2201 | *Cirrhitichthys oxycephalus* | mtDNA | ATPase8, ATPase6 | 2 | 1 | 1 |
| Lessios HA & Robertson DR (2006) Proc R Soc Lond, B, Biol Sci 273:2201 | *Ctenochaetus marginatus* | mtDNA | ATPase8, ATPase6 | 1 | 1 | |
| Lessios HA & Robertson DR (2006) Proc R Soc Lond, B, Biol Sci 273:2201 | *Diodon holocanthus* | mtDNA | ATPase8, ATPase6 | 1 | 1 | |
| Lessios HA & Robertson DR (2006) Proc R Soc Lond, B, Biol Sci 273:2201 | *Doryrhamphus excisus* | mtDNA | ATPase8, ATPase6 | 5 | 5 | |
| Lessios HA & Robertson DR (2006) Proc R Soc Lond, B, Biol Sci 273:2201 | *Forcipiger flavissimus* | mtDNA | ATPase8, ATPase6 | 1 | 1 | |

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| Lessios HA & Robertson DR (2006) Proc R Soc Lond, B, Biol Sci 273:2201 | *Heterepriacanthus cruentatus* | mtDNA | ATPase8, ATPase6 | 1 | 1 |
| Lessios HA & Robertson DR (2006) Proc R Soc Lond, B, Biol Sci 273:2201 | *Mulloidichthys vanicolensis* | mtDNA | ATPase8, ATPase6 | 1 | 1 |
| Lessios HA & Robertson DR (2006) Proc R Soc Lond, B, Biol Sci 273:2201 | *Myripristus berntdi* | mtDNA | ATPase8, ATPase6 | 1 | 1 |
| Lessios HA & Robertson DR (2006) Proc R Soc Lond, B, Biol Sci 273:2201 | *Novaculichthys taeniourus* | mtDNA | ATPase8, ATPase6 | 1 | 1 |
| Lessios HA & Robertson DR (2006) Proc R Soc Lond, B, Biol Sci 273:2201 | *Ostracion meleagris* | mtDNA | ATPase8, ATPase6 | 1 | 1 |
| Lessios HA & Robertson DR (2006) Proc R Soc Lond, B, Biol Sci 273:2201 | *Scarus ghobban* | mtDNA | ATPase8, ATPase6 | 1 | 1 |
| Lessios HA & Robertson DR (2006) Proc R Soc Lond, B, Biol Sci 273:2201 | *Scarus rubroviolaceus* | mtDNA | ATPase8, ATPase6 | 1 | 1 |
| Lessios HA & Robertson DR (2006) Proc R Soc Lond, B, Biol Sci 273:2201 | *Sectator ocyurus* | mtDNA | ATPase8, ATPase6 | 1 | 1 |
| Lessios HA & Robertson DR (2006) Proc R Soc Lond, B, Biol Sci 273:2201 | *Stethojulis bandanensis* | mtDNA | ATPase8, ATPase6 | 1 | 1 |

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| Lessios HA & Robertson DR (2006) Proc R Soc Lond, B, Biol Sci 273:2201 | *Zanclus cornutus* | mtDNA | ATPase8, ATPase6 | 1 | 1 | |
| Lewter JA et al. (2006) Fla Entomol 89:63 | *Spodoptera frugiperda* | mtDNA | COI, tRNA leucine, COII | 1 | 1 | |
| Li M et al. (2005) Mol Phylogenet Evol 36:78 | *Ailurus fulgens* | mtDNA | cyt b, CR | 1 | 1 | |
| Lihova J et al. (2004) Am J Bot 91:1231 | *Cardamine amporitana* | cpDNA | trnL-trnF | 8 | 1 | 7 |
| Lin JZ et al. (2002) Genetics 162:2007 | *Hordeum vulgare ssp. spontaneum* | nuclear | adh2 | 1 | 1 | |
| Lin JZ et al. (2002) Genetics 162:2007 | *Hordeum vulgare ssp. spontaneum* | nuclear | adh1 | 1 | 1 | |
| Lindblom L & Ekman S (2005) Mycol Res 109:187 | *Xanthoria parietina, X. aureola, X. calcicola* | nuclear | ITS | 3 | 2 | 1 |
| Lindblom L & Ekman S (2005) Mycol Res 109:187 | *Xanthoria parietina, X. aureola, X. calcicola* | nuclear | IGS | 3 | 1 | 2 |
| Lindblom L & Ekman S (2006) Mol Ecol 15:1545 | *Xanthoria parietina* | nuclear | ITS region | 1 | 1 | |
| Lindblom L & Ekman S (2006) Mol Ecol 15:1545 | *Xanthoria parietina* | nuclear | IGS region | 1 | 1 | |
| Lloyd BD (2003) Mol Ecol 12:1895 | *Mystacina tuberculata* | mtDNA | CR, ND2, partial 12S,16S rRNA | 1 | 1 | |
| Lloyd CJ et al. (2005) Biol Invasions 33:153 | *Spurgia capitigena* | mtDNA | 16S rRNA | 1 | 1 | |
| Lopez-Castro MC & Rocha-Olivares A (2005) Mol Ecol 14:3325 | *Lepidochelys olivacea* | mtDNA | CR | 1 | 1 | |

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|---|---|---|---|---|---|---|---|
| Lopez-Legentil S & Turon X (2006) Biol J Linn Soc Lond 88:203 | *Cystodytes dellechiajei* | mtDNA | COI | 1 | 1 | | |
| Lourie SA et al. (2005) Mol Ecol 14:1073 | *Hippocampus barbouri* | mtDNA | cyt b | 1 | 1 | | |
| Lourie SA et al. (2005) Mol Ecol 14:1073 | *Hippocampus kuda* | mtDNA | cyt b | 2 | 2 | | |
| Lourie SA et al. (2005) Mol Ecol 14:1073 | *Hippocampus spinosissimus* | mtDNA | cyt b | 1 | 1 | | |
| Lourie SA et al. (2005) Mol Ecol 14:1073 | *Hippocampus trimaculatus* | mtDNA | cyt b | 2 | 2 | | |
| Lovette IJ et al. (2004) Conserv Biol 18:156 | *Geothlypis trichas* | mtDNA | ATPase 6, 8, tRNA-lysine | 1 | 1 | | |
| Lovette IJ et al. (2004) Conserv Biol 18:156 | *Icteria virens* | mtDNA | ATPase 6, 8, tRNA-lysine | 1 | 1 | | |
| Lovette IJ et al. (2004) Conserv Biol 18:156 | *Vermivora rugicapilla* | mtDNA | ATPase 6, 8, tRNA-lysine | 1 | 1 | | |
| Ludt CJ et al. (2004) Mol Phylogenet Evol 31:1064 | *Cervus elaphus* | mtDNA | cyt b | 2 | 5 | | 3 |
| Ludwig A et al. (2003) Mol Ecol 12:3253 | *Acipenser naccarii, Acipenser gueldenstaedtii* | mtDNA | CR | 2 | 1 | 1 | |
| Luo SJ et al. (2004) PLoS Biol 2:2275 | *Panthera tigris* | mtDNA | ND1, ND2, ND5, ND6, cyt b, CR, 12S rRNA, COI, COII, ATPase8 | 1 | 1 | | |
| Maes GE et al. (2003) J Fish Biol 63:254 | *Esox lucius* | mtDNA | CR | 1 | 1 | | |
| Mardulyn P (2001) Mol Ecol 10:1751 | *Gonioctena pallida* | mtDNA | CR | 1 | 1 | | |
| Mardulyn P & Milinkovitch MC (2005) Mol Ecol 14:1641 | *Gonioctena olivacea* | mtDNA | CR 2 | 1 | 1 | | |
| Mardulyn P & Milinkovitch MC (2005) Mol Ecol 14:1641 | *Gonioctena olivacea* | mtDNA | CR 1 | 1 | 1 | | |

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| Mardulyn P et al. (2003) J Mol Evol 56:38 | *Gonioctena olivacea* | mtDNA | CR | 1 | 1 | | |
| Mardulyn P et al. (2003) J Mol Evol 56:38 | *Gonioctena pallida* | mtDNA | CR | 1 | 1 | | |
| Maric S et al. (2006) Genet Sel Evol 38:411 | *Salmo trutta* | mtDNA | CR | 1 | 1 | | |
| Marion L & Le Gentil J (2006) Evol Ecol 20:193 | *Phalacrocorax carbo* | mtDNA | CR | 1 | 1 | | |
| Marko PB (2004) Mol Ecol 13:597 | *Nucella lamellosa* | mtDNA | COI | 1 | 1 | | |
| Marko PB (2004) Mol Ecol 13:597 | *Nucella ostrina* | mtDNA | COI | 1 | 1 | | |
| Marquez LM et al. (2002) Mol Ecol 11:1339 | *Acropora cytherea, A. hyacinthus, A. spicifera* | nuclear | Pax-C intron | 3 | 1 | (2h) | |
| Marshall JL (2004) Evolution 58:2409 | *Allonemobius socius, A. fasciatus and A. sp. nov. Tex* | mtDNA | 12S rRNA, ITS1 | 3 | 1 | 2 | |
| Martin J et al. (2002) Insect Mol Biol 11:387 | *Camptochironomus biwaprimus, C. pallidivittatus, C. tentans sensu stricto, C. dilutus* | nuclear | gb2b | 4 | 3 | 2 | |
| Martin J et al. (2002) Insect Mol Biol 11:387 | *Camptochironomus biwaprimus, C. pallidivittatus, C. tentans sensu stricto, C. dilutus* | mtDNA | cyt b, COI | 4 | 4 | (2h) | |
| Martinez-Solano I (2004) J Zoolog Syst Evol Res 42:298 | *Discoglossus galganoi, D. jeanneae* | mtDNA | cyt b, ND4 | 2 | 2 | | |
| Martinez-Solano I et al. (2004) J Biogeogr 31:603 | *Alytes obstetricans* | mtDNA | cyt b | 1 | 1 | | |
| Martinez-Solano I et al. (2006) Mol Ecol 15:3375 | *Lissotriton boscai* | mtDNA | ND4, CR | 1 | 7 | | 6 |
| Masta SE et al. (2003) Mol Ecol 12:1541 | *Bufo woodhousii* | mtDNA | 16S rRNA, tRNA, ND1 | 1 | 1 | | |

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|---|---|---|---|---|---|---|---|---|
| Matute DR et al. (2006) Mol Biol Evol 23:65 | *Paracoccidioides brasiliensis* | nuclear | 8 regions from 5 coding genes | 3 | 1 | 2 | | |
| McCartney MA et al. (2003) Mol Ecol 12:2963 | *Hypoplectrus spp.* | mtDNA | cyt b, ATPase 6/8 | 9 | 1 | 8 | | |
| McKinnon GE et al. (2004) Mol Ecol 13:3751 | *Eucalyptus cordata, E. globulus* | cpDNA | rpl2-trnH IGS, trnH gene, trnH-psbA IGS | 2 | 1 | (1h) | | |
| Mead LS et al. (2001) Evolution 55:2287 | *Desmognathus orestes* | mtDNA | cyt b | 1 | 2 | | 1 | |
| Meister J et al. (2005) Bot J Linn Soc 148:437 | *Justicia areysiana* | cpDNA | 11 loci, 5 restriction enzymes | 1 | 1 | | | |
| Mendez-Harclerode FM et al. (2005) J Mammal 86:180 | *Neotoma micropus* | mtDNA | CR | 1 | 1 | | | |
| Mesquita N et al. (2005) Mol Ecol 14:1939 | *Squalius aradensis* | mtDNA | cyt b | 1 | 1 | | | |
| Michel AP et al. (2005) Insect Mol Biol 14:375 | *Anopheles funestus* | mtDNA | ND5 | 1 | 1 | | | |
| Michel AP et al. (2005) Mol Ecol 14:4235 | *Anopheles funestus* | mtDNA | ND5 | 1 | 1 | | | |
| Miller DG & Crespi B (2003) J Evol Biol 16:731 | *Tamalia coweni, T. inquilinus* | mtDNA | COI | 2 | 7 | | 5 | |
| Mills HR et al. (2004) Anim Conserv 7:387 | *Parantechinus apicalis* | mtDNA | CR | 1 | 1 | | | |
| Mirabello L & Conn JE (2006) Heredity 96:311 | *Anopheles darlingi* | mtDNA | COI | 1 | 1 | | | |
| Mock KE & Miller MP (2005) Trans Am Fish Soc 134:267 | *Iotichthys phlegethontis* | mtDNA | cyt b | 1 | 1 | | | |
| Mock KE et al. (2006) Mol Ecol 15:2223 | Utah sucker, June sucker, Tahoe sucker | mtDNA | ND2 | 4 | 3 | 1 | | |
| Monsen KJ & Blouin MS (2003) Mol Ecol 12:3275 | *Rana cascadae* | mtDNA | CR, ND1 | 2 | 3 | | 1 | |

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|---|---|---|---|---|---|---|---|
| Monteiro FA et al. (2004) Mol Phylogenet Evol 32:46 | *Triatoma brasiliensis* | mtDNA | cyt b | 3 | 3 | | |
| Morando M et al. (2003) Syst Biol 52:159 | *Liolaemus elongatus* | mtDNA | cyt b | 4 | 4 | | |
| Morando M et al. (2004) Evolution 58:842 | *L. grosseorum, L. darwinii, L laurenti, L. sp nov* | mtDNA | cyt b | 4 | 1 | (3h) | |
| Morehouse EA et al. (2003) Mol Ecol 12:395 | *Batrachochytrium dendrobatidis,* | nuclear | 10 genes | 1 | 1 | | |
| Morrell PL et al. (2003) Proc Natl Acad Sci USA 100:10812 | *Hordeum vulgare ssp. spontaneum* | nuclear | alpha-amy1 | 1 | 1 | | |
| Morrison CL et al. (2006) Conserv Genet 7:129 | *Crystallaria asprella* | mtDNA | CR | 4 | 4 | | |
| Moya O et al. (2004) Mol Ecol 13:3153 | *Eutrichopus canariensis, E. gonzalezi* | mtDNA | COII | 2 | 1 | 1 | |
| Moya O et al. (2006) J Arid Environ 66:477 | *Pimelia laevigata* | mtDNA | COI | 4 | 4 | 1 | |
| Moyer GR et al. (2005) Evolution 59:599 | *Prochilodus magdalenae, P. mariae, P. rubrotaeniatus* | nuclear | EF 1-alpha | 3 | 1 | (2h) | |
| Moyer GR et al. (2005) Evolution 59:599 | *Prochilodus magdalenae, P. mariae, P. rubrotaeniatus* | nuclear | Cal-4 | 3 | 1 | (2h) | |
| Mu JB et al. (2005) Mol Biol Evol 22:1686 | *Plasmodium vivax* | mtDNA | whole genome | 1 | 1 | | |
| Mulcahy DG et al. (2006) Mol Ecol 15:1807 | *Phrynosoma mcallii* | mtDNA | ND4 | 1 | 1 | | |
| Mun J et al. (2003) Mol Ecol 12:2941 | *Bactrocera depressa* | nuclear | Tub Beta3 | 1 | 1 | | |
| Mun J et al. (2003) Mol Ecol 12:2941 | *Bactrocera depressa* | nuclear | EF 1alpha | 1 | 1 | | |
| Mun J et al. (2003) Mol Ecol 12:2941 | *Bactrocera depressa* | mtDNA | COI | 1 | 2 | | 1 |

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|---|---|---|---|---|---|---|---|---|
| Mundy NI et al. (2004) Science 303:1870 | *Anser spp.* | nuclear | MC1R locus for melanism | 4 | 1 | 3 | | |
| Mundy NI et al. (2004) Science 303:1870 | *Stercorarius spp.* | nuclear | MC1R locus for melanism | 3 | 1 | 2 | | |
| Munoz-Fuentes V et al. (2005) Conserv Genet 6:999 | *Oxyura leucocephala* | mtDNA | CR | 1 | 1 | | | |
| Munoz-Fuentes V et al. (2006) Mol Ecol 15:1441 | *Oxyura jamaicensis* | mtDNA | CR | 1 | 1 | | | |
| Murat C et al. (2004) New Phytol 164:401 | *Tuber melanosporum* | nuclaer | ITS | 1 | 1 | | | |
| Nardi F et al. (2005) Mol Ecol 14:2729 | *Bactrocera oleae* | mtDNA | ND1 | 1 | 1 | | | |
| Nardi F et al. (2006) Insect Biochem Mol Biol 36:593 | *Bactrocera oleae* | nuclear | ACE exon III | 1 | 1 | | | |
| Narita S et al. (2006) Mol Ecol 15:1095 | *Eurema hecabe* | nuclear | Tpi | 2 | 3 | | 1 | |
| Narita S et al. (2006) Mol Ecol 15:1095 | *Eurema hecabe* | nuclear | EF1-alpha | 2 | 1 | 1 | | |
| Narita S et al. (2006) Mol Ecol 15:1095 | *Eurema hecabe* | mtDNA | ND5 | 2 | 2 | | | |
| Narita S et al. (2006) Mol Ecol 15:1095 | *Eurema hecabe* | mtDNA | 16S rRNA | 2 | 1 | 1 | | |
| Neilson ME & Wilson RR (2005) Mar Ecol Prog Ser 296:197 | *Acanthogobius flavimanus* | mtDNA | CR | 1 | 1 | | | |
| Neumann K et al. (2004) Conserv Genet 5:181 | *Cricetus cricetus* | mtDNA | CR | 1 | 1 | | | |
| Nguyen TTT et al. (2004) Biol J Linn Soc Lond 83:539 | *Cherax destructor* | mtDNA | 16S rRNA | 2 | 2 | | | |
| Nice CC et al. (2005) Mol Ecol 14:1741 | *Lycaeides idas, Lycaeides melissa* | mtDNA | AT-rich region | 3 | 1 | 2 | | |

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|---|---|---|---|---|---|---|---|
| Nicholls JA & Austin JJ (2005) Mol Ecol 14:1485 | *Ptilonorhynchus violaceus* | mtDNA | ATPase6, ATPase 8 | 2 | 2 | | |
| Nieberding C et al. (2005) Mol Ecol 14:765 | *Heligmosomoides polygyrus* | mtDNA | cyt b | 1 | 5 | | 4 |
| Nittinger F et al. (2005) J Zoolog Syst Evol Res 43:321 | *Falco biarmicus, Falco cherrug, Falco jugger, Falco rusticolus* | mtDNA | CR | 4 | 1 | 3 | |
| Nobre T et al. (2006) Heredity 96:403 | *Reticulitermes grassei* | mtDNA | COII | 1 | 1 | | |
| Noguchi J et al. (2004) Plant Syst Evol 247:1 | *Hemerocallis middendor•i* | cpDNA | rbcL-atpB IGS, trnL (UAA) intron | 1 | 1 | | |
| Noonan BP & Gaucher P (2005) Mol Ecol 14:3017 | *Atelopus* | mtDNA | cyt b | 4 | 1 | 3 | |
| Nussey DH et al. (2006) Heredity 97:56 | *Cervus elaphus* | mtDNA | CR | 1 | 1 | | |
| Okello JBA et al. (2005) Heredity 95:206 | *Hippopotamus amphibius* | mtDNA | CR | 1 | 1 | | |
| Ostbye K et al. (2005) Mol Ecol 14:4371 | *Coregonus lavaretus* | mtDNA | cyt b, ND3 | 1 | 1 | | |
| Oyler-McCance SJ et al. (2005) Condor 107:353 | *Charadrius montanus* | mtDNA | CR | 1 | 1 | | |
| Oyler-McCance SJ et al. (2005) Mol Ecol 14:1293 | *Centrocercus urophasianus* | mtDNA | CR 1 | 2 | 2 | | |
| Palkovacs EP et al. (2004) Mol Ecol 13:1759 | *Tympanuchus cupido pinnatus, T. cupido cupido, T. cupido attwateri, T. pallidicinctus, T. phasianellus* | mtDNA | CR | 3 | 1 | (2h) | |
| Palma RE et al. (2005) J Mammal 86:191 | *Oligoryzomys longicaudatus* | mtDNA | cyt b | 1 | 1 | | |
| Palme AE & Vendramin GG (2002) Mol Ecol 11:1769 | *Corylus avellana* | cpDNA | microsatellite haplotypes | 1 | 1 | | |

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|---|---|---|---|---|---|---|---|---|
| Palme AE et al. (2003) Mol Ecol 12:201 | *Betula pendula* | cpDNA | RFLP haplotypes | 1 | 1 | | | |
| Papetti C et al. (2005) Mar Ecol Prog Ser 289:225 | *Meganyctiphanes norvegica* | mtDNA | ND1 | 1 | 1 | | | |
| Parducci L et al. (2005) Mol Ecol 14:2873 | *Pinus sylvestris* | plastid genome | 220 bp region | 1 | 1 | | | |
| Patarnello T et al. (2003) Mol Phylogenet Evol 28:420 | *Chionodraco hamatus, Chionodraco rastrospinosus, Chionodraco myersi* | mtDNA | CR | 3 | 2 | 1 | | |
| Patirana A et al. (2002) Conserv Genet 3:335 | *Rissa brevirostris* | mtDNA | CR | 1 | 1 | | | |
| Paulo OS et al. (2002) Mol Ecol 11:809 | *Lacerta schreiberi.* | mtDNA | cyt b | 1 | 1 | | | |
| Pauls SU et al. (2006) Mol Ecol 15:2153 | *Drusus discolor* | mtDNA | CR | 1 | 7 | | 6 | |
| Pavlova A et al. (2003) Auk 120:744 | *Motacilla flava* | mtDNA | ND3, cyt b | 1 | 1 | | | |
| Pearce JM et al. (2004) Condor 106:229 | *Somateria spectabilis* | mtDNA | cyt b | 1 | 1 | | | |
| Pearce JM et al. (2005) Conserv Genet 6:743 | *Polysticta stelleri* | mtDNA | cyt b | 1 | 1 | | | |
| Pearce RL et al. (2002) Condor 104:84 | *Synthliboramphus antiquus* | mtDNA | cyt b and CR | 1 | 1 | | | |
| Penna A et al. (2005) Mar Biol 148:13 | *Alexandrium catenella* | mtDNA | 5.8S rDNA, ITS | 1 | 1 | | | |
| Perdices A & Coelho MM (2006) J Zoolog Syst Evol Res 44:330 | *Zacco platypus* | mtDNA | cyt b | 6 | 6 | | | |
| Perdices A et al. (2004) Mol Phylogenet Evol 31:192 | *Zacco platypus* | mtDNA | cyt b | 4 | 4 | | | |
| Perdices A et al. (2005) Mol Phylogenet Evol 37:920 | *Opsariichthys bidens* | mtDNA | cyt b | 5 | 7 | | 2 | |

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|---|---|---|---|---|---|---|---|
| Perrin C et al. (2004) Mol Ecol 13:2183 | *Coscinasterias muricata* | nuclear | CR | 1 | 1 | | |
| Pestano J et al. (2003) Heredity 90:302 | *Plecotus teneriffae* | | 16S rRNA, cyt b | 1 | 1 | | |
| Pestano J et al. (2003) Mol Phylogenet Evol 26:56 | *Hypsugo savii* | mtDNA | cyt b, 16S rRNA | 1 | 1 | | |
| Pestano J et al. (2003) Mol Phylogenet Evol 26:56 | *Pipistrellus kuhlii, P. maderensis* | mtDNA | cyt b, 16S rRNA | 2 | 1 | (1h) | |
| Pestano J et al. (2003) Mol Phylogenet Evol 27:422 | *Sapromyza imitans, S. indigena* | mtDNA | 16S rRNA | 2 | 1 | 1 | |
| Pestano J et al. (2003) Mol Phylogenet Evol 27:422 | *Sapromyza laurisilvae, S. inconspicua* | mtDNA | 16S rRNA | 2 | 1 | 1 | |
| Peters JL et al. (2005) Mol Ecol 14:3407 | *Aix sponsa* | mtDNA | CR | 1 | 1 | | |
| Petersen C (2006) Biol Invas 8:565 | *Rhithropanopeus harrisi* | mtDNA | COI | 1 | 1 | | |
| Petersen SD & Stewart DT (2006) J Mammal 87:153 | *Glaucomys volans* | mtDNA | CR | 1 | 1 | | |
| Pfenninger M & Posada D (2002) Evolution 56:1776 | *Candidula unifasciata* | mtDNA | 16S rRNA | 1 | 1 | | |
| Pfenninger M et al. (2003) BMC Evol Biol 3: | *Trochoidea geyeri* | nuclear | ITS1 | 1 | 1 | | |
| Pfenninger M et al. (2003) BMC Evol Biol 3: | *Trochoidea geyeri* | mtDNA | 16S rRNA | 1 | 1 | | |
| Pinceel J et al. (2005) J Evol Biol 18:1264 | *Arion subfuscus, A. fuscus* | mtDNA | 16S rRNA | 6 | 8 | | 2 |
| Pinceel J et al. (2005) Mol Ecol 14:1133 | *Arion fuscus,* | mtDNA | COI, 16S rRNA | 2 | 2 | | |
| Pitra C et al. (2002) Mol Ecol 11:1197 | *Hippotragus niger* | mtDNA | CR | 3 | 3 | | |

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|---|---|---|---|---|---|---|---|
| Pitra C et al. (2004) Conserv Genet 5:205 | *Chlamydotis undulata macqueenii* | mtDNA | CR, cyt b | 1 | 1 | | |
| Podnar M et al. (2004) Org Divers Evol 4:307 | *Podarcis melisellensis* | mtDNA | cyt b | 3 | 3 | | |
| Pongratz N et al. (2003) BMC Evol Biol 3: 23 | *Schmidtea polychroa* | mtDNA | COI | 1 | 3 | | 2 |
| Ponniah M & Hughes JM (2006) Mar Freshw Res 57:349 | *Euastacus fleckeri* | mtDNA | COI | 1 | 1 | | |
| Ponniah M & Hughes JM (2006) Mar Freshw Res 57:349 | *Euastacus hystricosus* | mtDNA | COI | 1 | 1 | | |
| Ponniah M & Hughes JM (2006) Mar Freshw Res 57:349 | *Euastacus sulcatus* | mtDNA | COI | 1 | 1 | | |
| Ponomarev A et al. (2004) Conserv Genet 5:847 | *Grus leucogeranus* | mtDNA | CR | 1 | 1 | | |
| Pons J et al. (2006) Syst Biol 55:595 | *Rivacindela spp.* | mtDNA | cytb, COI, 16S rRNA | 47 | 25 | 22 | |
| Printzen C & Ekman S (2002) Lichenologist 34:101 | *Cavernularia hultenii* | nuclear | ITS and IGS regions | 1 | 1 | | |
| Printzen C et al. (2003) Mol Ecol 12:1473 | *Cavernularia hultenii* | nuclear | ITS region, part of IGS | 2 | 1 | 1 | |
| Pruett C et al. (2005) Mar Biol 147:593 | *Lutjanus campechanus* | mtDNA | ND4 | 1 | 1 | | |
| Qu YH et al. (2005) Mol Ecol 14:1767 | *Pyrgilauda ruficollis* | mtDNA | cyt b | 1 | 1 | | |
| Rabosky DL et al. (2004) Aust J Zool 52:531 | *Ramphotyphlops australis* | mtDNA | 16S rRNA | 1 | 2 | | 1 |
| Ramon ML et al. (2003) Mol Ecol 12:2975 | *Hypoplectrus spp* | mtDNA | part of ND5; ND6; part of tRNA-glu | 6 | 1 | (5h) | |

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| Rasgon JL et al. (2006) Proc R Soc Lond, B, Biol Sci 273:1603 | *Culex pipiens* | mtDNA | ND4 | 2 | 2 | | | |
| Rauscher JT et al. (2004) Genetics 166:987 | *Glycine tomentella* race D1/D2 | nuclear | ITS | 1 | 1 | | | |
| Rauscher JT et al. (2004) Genetics 166:987 | *Glycine tomentella* race D3 | nuclear | ITS | 1 | 1 | | | |
| Rauscher JT et al. (2004) Genetics 166:987 | *Glycine tomentella* race D4/G *clandestina* | nuclear | ITS | 1 | 1 | | | |
| Rauscher JT et al. (2004) Genetics 166:987 | *Glycine tomentella* race D5A | nuclear | ITS | 1 | 1 | | | |
| Rauscher JT et al. (2004) Genetics 166:987 | *Glycine tomentella* race D5B | nuclear | ITS | 1 | 1 | | | |
| Recuero E et al. (2006) Mol Phylogenet Evol 39:293 | *Pseudacris regilla* | mtDNA | cyt b | 3 | 3 | | | |
| Reece JS et al. (2005) Conserv Genet 6:235 | *Caretta caretta* | mtDNA | CR | 1 | 2 | | | 1 |
| Reece JS et al. (2005) Conserv Genet 6:235 | *Chelonia mydas* | mtDNA | CR | 1 | 1 | | | |
| Reece JS et al. (2005) Conserv Genet 6:235 | *Eretmochelys imbicata* | mtDNA | CR | 1 | 1 | | | |
| Rees DJ et al. (2003) Mol Phylogenet Evol 27:131 | *Hyalomma dromedarii, H. truncatum, H. marginatum rufipes* | nuclear | ITS2 | 3 | 2 | (1h) | | |
| Rendell S & Ennos RA (2002) Mol Ecol 11:69 | *Calluna vulgaris* | cpDNA | RFLP haplotypes | 1 | 1 | | | |
| Rendell S & Ennos RA (2003) Mol Ecol 12:2681 | *Ilex aquifolium* | cpDNA | RFLP and microsatellite haplotypes | 1 | 1 | | | |
| Rhymer JM et al. (2005) Auk 122:1149 | *Scolopax minor* | mtDNA | ND6 | 1 | 1 | | | |

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|---|---|---|---|---|---|---|---|
| Rhymer JM et al. (2005) Auk 122:1149 | *Scolopax minor* | mtDNA | CR | 1 | 1 | | |
| Ribera I et al. (2003) Mol Ecol 12:153 | *Melademа imbricata, M. coriacea, M. lanio* | mtDNA | COI | 4 | 4 | | |
| Ribera I et al. (2003) Mol Ecol 12:153 | *Melademа imbricata, M. coriacea, M. lanio* | mtDNA | 16s rRNA | 3 | 1 | 2 | |
| Rivera MAJ et al. (2004) Biol J Linn Soc Lond 81:449 | *Epinephelus quernus* | mtDNA | CR | 1 | 1 | | |
| Robberts FJL et al. (2004) J Clin Microbiol 42:1505 | *Pneumocystis jiroveci* | nuclear | ITS | 1 | 1 | | |
| Rocha LA et al. (2005) Mol Ecol 14:3921 | *Gnatholepis thompsoni* | mtDNA | cyt b | 2 | 1 | 1 | |
| Rodriguez RM & Ammerman LK (2004) J Mammal 85:842 | *Myotis californicus, Myotis ciliolabrum* | mtDNA | cyt b | 2 | 2 | (1h) | |
| Rodriguez-Lanetty M (2003) Mol Phylogenet Evol 28:152 | *Symbiodinium*-like dinoflagellates | nuclear | ITS1 rDNA | 12 | 23 | | 11 |
| Rodriguez-Lanetty M & Hoegh-Guldberg O (2002) Mol Ecol 11:1177 | *Plesiastrea versipora* | nuclear | ITS region | 1 | 1 | | |
| Rognon X & Guyomard R (2003) Mol Ecol 12:435 | *Oreochromis aureus, O. niloticus* | mtDNA | cyt b | 2 | 1 | (1h) | |
| Rohfritsch A & Borsa P (2005) Heredity 95:315 | *Decapterus russelli* | mtDNA | cyt b | 1 | 1 | | |
| Romo MDR et al. (2006) Fish Sci 72:556 | *Verasper moseri* | mtDNA | CR | 1 | 1 | | |
| Roy MS & Sponer R (2002) Proc R Soc Lond, B, Biol Sci 269:1017 | *Ophiactis savignyi* | mtDNA | COI | 1 | 2 | | 1 |
| Rueness EK et al. (2003) Nature 425:69 | *Lynx canadensis* | mtDNA | cyt b, CR | 1 | 1 | | |

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|---|---|---|---|---|---|---|---|---|
| Ryynanen HJ & Primmer CR (2004) Mol Ecol 13:3857 | *Salmo salar* | nuclear | GH1 | 1 | 1 | | | |
| Saavedra C & Pena JB (2005) J Exp Mar Biol Ecol 323:138 | *Pecten maximus* | mtDNA | 16s rRNA | 1 | 1 | | | |
| Salgueiro P et al. (2004) Mol Ecol 13:3357 | *Nyctalus azoreum, Nyctalus leisleri* | mtDNA | CR | 2 | 1 | 1 | | |
| Saltonstall K (2002) Proc Natl Acad Sci USA 99:2445 | *Phragmites australis* | cpDNA | rnT(UGU) "a"-trnL(UAA)5' "b" and rbcL-psaI | 1 | 1 | | | |
| Salzburger W et al. (2003) Mol Ecol 12:2371 | *Leuciscus souffia* Italian, Alpine clades | mtDNA | CR | 2 | 2 | | | |
| Salzburger W et al. (2006) Proc R Soc Lond, B, Biol Sci 273:257 | *Tropheus moorii* | mtDNA | CR | 1 | 1 | | | |
| Santos SR (2006) Mol Ecol 15:2699 | *Halocaridina rubra* | mtDNA | COI | 2 | 2 | | | |
| Sarno RJ et al. (2004) Conserv Genet 5:89 | *Vinugna vicugna* | mtDNA | CR, cyt b, 16S rRNA | 1 | 1 | | | |
| Satoh A et al. (2004) Mol Ecol 13:3057 | *Abroscelis anchoralis* | mtDNA | COI, 16S rRNA | 1 | 1 | | | |
| Satoh A et al. (2004) Mol Ecol 13:3057 | *Chaetodera laetescripta* | mtDNA | COI, 16S rRNA | 1 | 2 | | | 1 |
| Satoh A et al. (2004) Mol Ecol 13:3057 | *Cicindela lewisii* | mtDNA | COI and 16S rRNA | 1 | 1 | | | |
| Satoh A et al. (2004) Mol Ecol 13:3057 | *Lophyridia angulata* | mtDNA | COI and 16S rRNA | 1 | 1 | | | |
| Schrey NM et al. (2005) Mol Ecol 14:3317 | *Thanasimus dubius* | mtDNA | COI | 1 | 1 | | | |
| Schultheis AS et al. (2002) Mol Ecol 11:317 | *Peltoperla tarteri* | mtDNA | CR | 1 | 1 | | | |
| Scribner KT et al. (2003) Auk 120:889 | *Branta canadensis* | mtDNA | CR | 2 | 2 | | | |

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|---|---|---|---|---|---|---|---|
| Seddon JM et al. (2001) Mol Ecol 10:2187 | *Erinaceus europaeus, E. concolor* | mtDNA | cyt b, CR | 2 | 5 | | 3 |
| Segraves KA & Pellmyr O (2004) Evolution 58:2266 | *Tegeticula cassandra* | mtDNA | COI | 1 | 1 | | |
| Segraves KA & Pellmyr O (2004) Evolution 58:2266 | *Tegeticula intermedia* | mtDNA | COI | 1 | 1 | | |
| Semyenova SK et al. (2006) J Parasitol 92:525 | *Fasciola hepatica* | mtDNA | COI, ND1 | 1 | 1 | | |
| Sezonlin M et al. (2006) Mol Ecol 15:407 | *Busseola fusca* | mtDNA | cyt b | 1 | 3 | | 2 |
| Sgariglia EA & Burns KJ (2003) Auk 120:346 | *Toxostoma redivivum* | mtDNA | cyt b, COII-tRNA-ATPase8, ATPase6 | 1 | 1 | | |
| Shanker K et al. (2004) Mol Ecol 13:1899 | *Lepidochelys olivacea* | mtDNA | CR | 1 | 1 | | |
| Shaw J & Small RL (2005) Am J Bot 92:2011 | *Prunocerasus spp.* | cpDNA | rpL16 intron | 17 | 1 | 16(h) | |
| Shi W et al. (2005) Environ Entomol 34:977 | *Bactrocera dorsalis* | mtDNA | COI | 1 | 1 | | |
| Shih HT et al. (2006) J Biogeogr 33:980 | *Candidiopotamon rathbunae* | mtDNA | 16s rRNA | 1 | 1 | | |
| Shoda E et al. (2003) Appl Entomol Zool 38:339 | *Semanotus japonicus* | mtDNA | COI, tRNA leu-UUR, COII | 1 | 1 | | |
| Sinclair EA et al. (2004) Am Nat 164:396 | *Xantusia vigilis, X. sierrae* | mtDNA | cyt b | 2 | 2 | | |
| Slechtova V et al. (2004) Mol Phylogenet Evol 33:225 | *Cottus gobio, C. ferrugineous* | mtDNA | CR | 1 | 1 | | |
| Small RL & Wendel JF (2002) Mol Biol Evol 19:597 | *Gossypium hirsutum, G. barbadense* | nuclear | AdhC | 2 | 1 | 1 | |

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| Small RL & Wendel JF (2002) Mol Biol Evol 19:597 | *Gossypium hirsutum, G. barbadense* | nuclear | AdhA | 2 | 1 | 1 | |
| Smith CI & Farrell BD (2005) Mol Ecol 14:1025 | *Moneilema armatum* | mtDNA | COI | 1 | 2 | | 1 |
| Smith CI & Farrell BD (2005) Mol Ecol 14:1025 | *Moneilema gigas* | mtDNA | COI | 1 | 2 | | 1 |
| Smith PJ et al. (2006) Freshw Biol 51:12 | *Acanthophlebia cruentata* | mtDNA | cyt b | 1 | 1 | | |
| Sossai S et al. (2005) Exp Appl Acarol 37:199 | *Boophilus microplus* | nuclear | bm86 gene | 1 | 1 | | |
| Sota T & Sasabe M (2006) Syst Biol 55:329 | *Ohomopterus spp* | mtDNA | ND5 | 5 | 3 | (2h) | |
| Sota T & Sasabe M (2006) Syst Biol 55:329 | *Ohomopterus spp* | nuclear | EF-1a exon, intron | 5 | 4 | 1 | |
| Sota T et al. (2004) Entomol Sci 7:381 | *Chrysolina virgata* | mtDNA | COI | 1 | 1 | | |
| Sousa-Santos C et al. (2006) J Fish Biol 68:292 | *Retropinna semoni* | mtDNA | ATPase 6, 9 | 2 | 2 | | |
| Spaulding AW et al. (2006) Mol Ecol 15:2317 | *Tympanuchus phasianellus, Tympanuchus cupido* | mtDNA | CR | 2 | 1 | 1 | |
| Steele CA & Storfer A (2006) Mol Ecol 15:2477 | *Dicamptodon tenebrosus.* | mtDNA | cyt b | 1 | 2 | | 1 |
| Steeves TE et al. (2005) J Evol Biol 18:1000 | *Sula dactylatra* | mtDNA | CR | 1 | 3 | | 2 |
| Steeves TE et al. (2005) Mol Ecol 14:3877 | *Sula dactylatra* | mtDNA | CR | 1 | 3 | | 2 |
| Stefani F et al. (2004) Ecol Freshw Fish 13:168 | *Scardinius erythrophthalmus* | mtDNA | cyt b | 1 | 1 | | |

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|---|---|---|---|---|---|---|---|---|
| Stefani F et al. (2004) J Zoolog Syst Evol Res 42:323 | *Telestes muticellus* | mtDNA | cyt b | 1 | 1 | | | |
| Stefanni S & Thorley JL (2003) Mol Phylogenet Evol 28:601 | *Pomatoschistus minutus* | mtDNA | CR | 2 | 2 | | | |
| Stireman JO et al. (2005) Evolution 59:2573 | *Epiblema scudderiana* | mtDNA | COI | 1 | 1 | | | |
| Stireman JO et al. (2005) Evolution 59:2573 | *Procecidochares atra* | mtDNA | COI | 1 | 1 | | | |
| Stockley B et al. (2005) Mar Biol 146:793 | *Pagellus bogaraveo* | mtDNA | cyt b, CR | 1 | 1 | | | |
| Strecker U (2006) Mol Phylogenet Evol 39:865 | *Cypriodon spp* | mtDNA | CR | 7 | 1 | 6 | | |
| Strecker U et al. (2004) Mol Phylogenet Evol 33:469 | *Astyanax fasciatus* | mtDNA | cyt b | 1 | 3 | | | 2 |
| Szalanski AL et al. (2006) Ann Entomol Soc Am 99:157 | *Aedes vexans* | mtDNA | ND5 | 1 | 1 | | | |
| Takahashi H et al. (2003) Can J Fish Aquat Sci 60:421 | *Pungitius pungitius* | mtDNA | CR | 1 | 1 | | | |
| Tani N et al. (2003) Mol Ecol 12:859 | *Cryptomeria japonica* | nuclear | GapC | 1 | 1 | | | |
| Tarjuelo I et al. (2001) Mar Biol 139:455 | *Clavelina spp.* | mtDNA | COI | 4 | 4 | | | |
| Tarjuelo I et al. (2004) Mol Ecol 13:3125 | *Pseudodistoma crucigaster* | mtDNA | COI | 2 | 2 | | | |
| Teske PR et al. (2003) Mol Ecol 12:1703 | *Hippocampus capensis* | mtDNA | CR | 1 | 1 | | | |
| Tiedemann R et al. (2004) Mol Ecol 13:1481 | *Somateria mollissima* | mtDNA | CR | 1 | 1 | | | |

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|---|---|---|---|---|---|---|---|
| Timmermans MJTN et al. (2005) Mol Ecol 14:2017 | *Orchesella cincta* | mtDNA | COII | 7 | 7 | | |
| Turgeon J & McPeek MA (2002) Mol Ecol 11:1989 | *Enallagma hageni, E. ebrium, E. recurvatum, E. minusculum, E. laterale* | mtDNA | COI and COII | 5 | 1 | 4 | |
| Ursenbacher S et al. (2006) Mol Phylogenet Evol 38:546 | *Vipera aspis* | mtDNA | CR | 1 | 1 | | |
| Uthicke S & Benzie JAH (2003) Mol Ecol 12:2635 | *Holothuria nobilis* | mtDNA | COI | 2 | 2 | | |
| Uthicke S et al. (2004) Mar Freshw Res 55:837 | *Holothuria fuscogilva, H. nobilis, H. whitmaei* | mtDNA | COI | 3 | 3 | | |
| Uva P et al. (2004) Insectes Soc 51:163 | *Reticulitermes lucifugus* | mtDNA | 16S rRNA, ND1 | 2 | 2 | | |
| Uwai S et al. (2006) Hydrobiologia 553:345 | *Undaria pinnatifida* | mtDNA | CO3 | 1 | 1 | | |
| Van Houdt JK et al. (2003) Mol Phylogenet Evol 29:599 | *Lota lota* | mtDNA | cyt b | 1 | 1 | | |
| Van Houdt JKJ et al. (2005) Mol Ecol 14:2445 | *Lota lota* | mtDNA | CR | 2 | 2 | | |
| Vandergast AG et al. (2004) Mol Ecol 13:1729 | *Tetragnatha anuenue* | mtDNA | COI | 1 | 1 | | |
| Vandergast AG et al. (2004) Mol Ecol 13:1729 | *Tetragnatha brevignatha* | mtDNA | COI | 1 | 2 | | 1 |
| Vandergast AG et al. (2004) Mol Ecol 13:1729 | *Tetragnatha quasimodo* | mtDNA | COI | 1 | 3 | | 2 |
| Vasconcelos T et al. (2006) Agric For Entomol 8:103 | *Tomicus destruens* | mtDNA | COI, COII | 1 | 1 | | |

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|---|---|---|---|---|---|---|---|---|
| Veit ML et al. (2005) Conserv Genet 6:159 | *Dendroica cerulea* | mtDNA | CR | 1 | 1 | | | |
| Vences M et al. (2004) Biol J Linn Soc Lond 83:115 | *H. brooki* | mtDNA | 16S rRNA | 1 | 1 | | | |
| Vences M et al. (2004) Biol J Linn Soc Lond 83:115 | *H. mercatorius* | mtDNA | 16S rRNA | 1 | 1 | | | |
| Vences M et al. (2004) Biol J Linn Soc Lond 83:115 | *H. platycephalus* | mtDNA | 16S rRNA | 1 | 1 | | | |
| Vences M et al. (2004) Biol J Linn Soc Lond 83:115 | *Hemidactylus frenatus* | mtDNA | 16S rRNA | 1 | 1 | | | |
| Vences M et al. (2004) J Biogeogr 31:593 | *Ptychadena mascareniensis* | mtDNA | 16S rRNA | 1 | 1 | | | |
| Vences M et al. (2004) Mol Phylogenet Evol 30:295 | *Mantella aurantiaca, M. crocea, M. milotympanum, M. madagascariensis* | mtDNA | cyt b | 3 | 3 | (1h) | | |
| Verginelli F et al. (2005) Mol Biol Evol 22:2541 | *Canis familiaris, Canis lupus* | mtDNA | CR | 2 | 1 | 1 | | |
| Verheyen E et al. (2003) Science 300:325 | *Haplochromis superflock* | mtDNA | CR | 48 | 1 | 47 | | |
| Vernesi C et al. (2002) Mol Ecol 11:1285 | *Capreolus capreolus* | mtDNA | CR | 1 | 1 | | | |
| Verovnik R et al. (2004) Mol Ecol 13:1519 | *Asellus aquaticus* | mtDNA | COI | 1 | 2 | | 1 | |
| Vettori C et al. (2004) Theor Appl Genet 109:1 | *Fagus sylvatica* | cpDNA | RFLP, microsatellites | 1 | 1 | | | |
| Vieites DR et al. (2006) Mol Ecol 15:1617 | *Mantella bernhardi* | mtDNA | cyt b | 2 | 3 | | 1 | |
| Vila M & Bjorklund M (2004) Insect Mol Biol 13:213 | *Erebia palarica* | mtDNA | COI | 1 | 1 | | | |
| Vila M et al. (2005) Mol Phylogenet Evol 36:249 | *Erebia triaria* | mtDNA | CR, COI | 1 | 1 | | | |

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| Vines TH & Schluter D (2006) Proc R Soc Lond, B, Biol Sci 273:911 | *Gasterosteus aculeatus* | mtDNA | CR | 1 | 1 | | | |
| Voros J et al. (2006) Mol Phylogenet Evol 38:705 | *Bombina bombina, Bombina variegata* | mtDNA | COI, ND4 | 2 | 3 | | | 1 |
| Wagner RS et al. (2005) Can J Zool 83:396 | *Plethodon larselli* | mtDNA | cyt b | 1 | 1 | | | |
| Walker ML et al. (2006) J Hered 97:340 | *Peromyscus sejugis* | mtDNA | ND3, ND4 | 2 | 1 | 1 | | |
| Watanabe K et al. (2006) Am J Bot 93:442 | *Aristolochia kaempferi group* | cpDNA | matK gene, atpB-rbcL IGS, trnS-trnG IGS | 5 | 1 | (4h) | | |
| Waters JM et al. (2004) Mol Phylogenet Evol 32:236 | *Patiriella oriens, P. occidens, P. medius, P. gunnii* | mtDNA | COI | 4 | 4 | | | |
| Weisrock DW & Larson A (2006) Biol J Linn Soc Lond 89:25 | *Plethodon jordani* | mtDNA | ND2, tRNA-Trp, tRNA-Ala | 6 | 6 | | | |
| Weiss S et al. (2002) Mol Ecol 11:1393 | *Thymallus thymallus* | mtDNA | CR | 1 | 1 | | | |
| West JA et al. (2006) Phycol Res 54:1 | *Bostrychia radicosa* | cpDNA | RuBisCo spacer | 1 | 1 | | | |
| Wetzel JE et al. (2004) J Crust Biol 24:603 | *Orconectes placidus* | mtNDA | 16s rRNA | 1 | 1 | | | |
| Wetzel JE et al. (2004) J Crust Biol 24:603 | *Orconectes rusticus* | mtNDA | 16s rRNA | 1 | 1 | | | |
| Weyandt SE et al. (2005) J Mammal 86:1136 | *Corynorhinus townsendii ingens* | mtDNA | CR | 1 | 2 | | | 1 |
| Wilder JA & Hollocher H (2003) Evolution 57:2566 | *Drosophila dunni* | nuclear | kl-5 | 5 | 1 | 4 | | |
| Wilder JA & Hollocher H (2003) Evolution 57:2566 | *Drosophila dunni* | mtDNA | COII | 5 | 1 | 4 | | |

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| Wilke T & Pfenninger M (2002) Mol Ecol 11:1439 | *Hydrobia acuta, H. glyca* | mtDNA | COI | 2 | 2 | | |
| Williams DA et al. (2005) Mol Ecol 14:3643 | *Schinus terebinthifolius* | cpDNA | cpDNA - intergenic region | 1 | 1 | | |
| Wilson AB (2006) Mol Ecol 15:1857 | *Syngnathus leptorhynchus* | mtDNA | CR | 1 | 1 | | |
| Wilson AB (2006) Mol Ecol 15:1857 | *Syngnathus leptorhynchus* | mtDNA | 16S rRNA | 1 | 1 | | |
| Wilson GM et al. (2005) Genetica 125:141 | *Tamiasciurus hudsonicus* | mtDNA | CR | 1 | 2 | | 1 |
| Wishart MJ & Hughes JM (2003) Freshw Biol 48:28 | *Elporia barnardi* | mtDNA | COI | 2 | 2 | | |
| Worheide G et al. (2002) Mol Ecol 11:1753 | *Leucetta 'chagosensis'* | mtDNA | ITS region | 1 | 1 | | |
| Wu SH et al. (2006) J Biogeogr 33:936 | *Machilus kusanoi* | cpDNA | rnV-trnM and trnL-trnF | 1 | 1 | | |
| Wu SH et al. (2006) J Biogeogr 33:936 | *Machilus thunbergii* | cpDNA | rnV-trnM and trnL-trnF | 1 | 1 | | |
| Xie JY & Zhang ZB (2005) J Mammal 86:833 | *Cricetulus triton* | mtDNA | CR | 1 | 1 | | |
| Yamazaki Y et al. (2003) J Fish Biol 62:591 | *Lethenteron sp. N* | mtDNA | COI | 1 | 1 | | |
| Yang SJ et al. (2006) J Zool 268:187 | *Onychostruthus taczanowskii* | mtDNA | CR | 1 | 1 | | |
| Zaccara S et al. (2004) Biol Control 120:1 | *Austropotamobius pallipes, A. italicus* | mtDNA | 16S rRNA | 2 | 2 | | |
| Zaccara S et al. (2005) Freshw Biol 50:1262 | *Austropotamobius italicus* | mtDNA | COII | 1 | 2 | | 1 |
| Zamudio KR & Savage WK (2003) Evolution 57:1631 | *Ambystoma maculatum* | mtDNA | ND4, CR | 1 | 10 | | 9 |

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| Zardoya R et al. (2004) Mol Ecol 13:1785 | *Scomber japonicus* | mtDNA | CR | 1 | 1 | | | |
| Zardoya R et al. (2004) Mol Ecol 13:1785 | *Scomber scombrus* | mtDNA | CR | 1 | 1 | | | |
| Zardus JD & Hadfield MG (2005) Mol Ecol 14:3719 | *Chthamalus proteus* | mtDNA | COI | 1 | 1 | | | |
| Zardus JD et al. (2006) Mol Ecol 15:639 | *Deminucula atacellana* | mtDNA | 16S rRNA | 1 | 1 | | | |
| Zhang AB et al. (2005) Mol Ecol 14:3823 | *Coptolabrus jankowskii, Coptolabrus smaragdinus* | nuclear | PepCK | 2 | 1 | (1h) | | |
| Zhang AB et al. (2005) Mol Ecol 14:3823 | *Coptolabrus jankowskii, Coptolabrus smaragdinus* | mtDNA | COI | 2 | 2 | (2h) | | |
| Zhang JB et al. (2006) ICES J Mar Sci 63:693 | *Lutjanus erythropterus* | mtDNA | CR | 1 | 2 | | 1 | |