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DNA barcode data accurately identify higher taxa

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Abstract

The use of unique DNA sequences as a method for taxonomic identification is no longer fundamentally controversial, even though debate continues on the best markers, methods, and technology to use. Although both existing databanks such as GenBank and BOLD, as well as reference taxonomies, are imperfect, in best case scenarios “barcodes” (whether single or multiple, organelle or nuclear, loci) clearly are an increasingly fast and inexpensive method of identification, especially as compared to manual identification of unknowns by increasingly rare expert taxonomists. Because most species on Earth are undescribed, a complete reference database at the species level is impractical in the near term. The question therefore arises whether unidentified species can, using DNA barcodes, be accurately assigned to more inclusive groups such as genera and families—taxonomic ranks of putatively monophyletic groups for which the global inventory is more complete and stable. We used a carefully chosen test library of CO1 sequences from 49 families, 313 genera, and 816 species of spiders to assess the accuracy of genus and family-level identifications. We used BLAST queries of each sequence against the entire library and got the top ten hits resulting in 8160 hits. The percent sequence identity was reported from these hits (PIdent, range 75-100%). Accurate identification (PIdent above which errors totaled less than 5%) occurred for genera at PIdent values > 95 and families at PIdent values ≥ 91, suggesting these as heuristic thresholds for generic and familial identifications in spiders. Accuracy of identification increases with numbers of species/genus and genera/family in the library; above five genera per family and fifteen species per genus all identifications were correct. We propose that using percent sequence identity between conventional barcode sequences may be a feasible and reasonably accurate method to identify animals to family/genus. However, the quality of the underlying database impacts accuracy of results; many outliers in our dataset could be attributed to taxonomic and/or sequencing errors in BOLD and GenBank. It seems that an accurate and complete reference library of families and genera of life *could* provide accurate higher level taxonomic identifications cheaply and accessibly, within years rather than decades.

Introduction

Accurate identification of biological specimens has always limited the application of biological data to important societal problems. Obstacles are well-known and difficult: the vast majority of species are undescribed scientifically (Erwin 1982; May 1992; Mora et al. 2011); some unknown but large fraction of higher taxa are not monophyletic (Goloboff et al. 2009; Pyron & Wiens 2011); many species can only be identified if certain life stages are available (e.g. adults (Coddington & Levi 1991)), classical data sources such as morphology imperfectly track species identity; the discipline of taxonomy continues to dwindle; the classical taxonomic process of identification is mostly manual and cannot scale to provide the amounts of data required for real-time decisions such as environmental monitoring, invasive species, climate change, etc.

DNA sequence data potentially can eliminate most of these obstacles. DNA barcoding uses a fragment of the mitochondrial gene cytochrome *c* oxidase subunit I (CO1) as a unique species diagnosis/identification tool in the animal kingdom (Hebert et al. 2003), with analogous single to several locus protocols applied for vascular plants, ferns, mosses, algae and fungi (Chase & Fay 2009; Kress & Erickson 2007; Liu et al. 2010; Nitta 2008; Saunders 2005), protists (Scicluna et al. 2006), and prokaryotes (Barraclough et al. 2009). Due to relative ease and inexpensive sequencing, DNA barcoding is a popular tool in species identification and taxonomic applications (e.g. Doña et al. 2015; Xu et al. 2015), and the method is no longer fundamentally controversial at the species level (Čandek & Kuntner 2015; Anslan & Tedersoo 2015; Pentinsaari et al. 2014; Wang et al. 2015).

While most species remain undescribed the situation is not so dire for larger monophyletic groups such as clades accorded the Linnean ranks of genus or family. In assessing the state of knowledge about biodiversity, it is important to distinguish between the first scientific discovery of an exemplar of a lineage, and phylogenetic understanding of that lineage. Phylogenetic understanding—both tree topology and consequent taxonomic changes, are research programs with no clear end in sight. Linnean rank is partially arbitrary, and one expects that the number of higher taxa will probably increase over time as understanding improves. Discovery, however, can have an objective definition: the year of the earliest formal taxonomic description of a member of the lineage or taxonomic group in which it is currently included. By this definition the earliest possible discovery of an animal lineage is 1758 (Linné 1758), or in the case of spiders, 1757 (Clerck 1757).

More illuminating are the latest discoveries of lineages with the rank of family within larger clades, because the data tell us something about progress towards broad scale knowledge of biodiversity. The most recent discovery of a family of birds, for example is the Broad-billed Sapayoa, *Sapayoa aenigma* Hunt, 1903 (Sapayoaidae). The most recently discovered mammal family is Kitti's hog-nosed bat, *Craseonycteris thonglongyai* Hill, 1974 (Craseonycteridae). For flowering plants, it is *Gomortega keule* (Molina) Baill, 1972 (Gomertegaceae). For bees, it is *Stenotritus elegans* Smith, 1853 (Stenotritidae). For spiders, a megadiverse and poorly known group, it is *Trogloraptor marchingtoni* Griswold, Audisio & Ledford, 2012 (Trogloraptoridae), but the second most recent discovery of an unambiguously new spider family was in 1955 (Gradungulidae). Figure 1 illustrates the tempo of first discovery of families for these five well-known clades. At the family level, these curves are essentially asymptotic, implying that science is close to completing the inventory of clades ranked as families for these large lineages. On the other hand, for Bacteria and Archaea (Figure 1), as one would expect, the curve is not asymptotic at all but sharply increasing; prokaryote discovery and understanding is obviously just beginning.

In fact, although many new eukaryote families are named every year, the vast majority of these new names result from advances in phylogenetic understanding, not biological discovery of major new forms of life. The last ten years of Zoological Record suggests that roughly 5-10 truly new families are discovered per year.

In the context of the above question—approximate taxonomic identification of organisms using DNA sequences—these data suggest that our knowledge of major clades of life is approaching completion. The Global Genome Initiative (GGI; http://www.mnh.si.edu/ggi/) of the Smithsonian Institution via the GGI Knowledge Portal (http://ggi.eol.org/) has tabulated a complete list of families of life, which total 9,642—on the whole a surprisingly small number. 10,000 barcodes, more or less, seems like a feasible goal. If we were able to assemble a complete database of DNA sequences at the family level, would it suffice to identify any eukaryote on Earth to the family level?

While the literature on species identification success of DNA barcodes comprises thousands of studies, only a few have tested their effectiveness at the level of higher taxonomic units. In the seminal paper on DNA barcodes Hebert et al. (2003) established that animal CO1 sequences can roughly assign taxa to phyla (96% success) or orders (100% success). However, their test was based on a neighbor joining tree-building approach, and it remained unknown if sequence data itself, i.e. percent identity among taxa, can be used in this way. Similarly, Nagy et al. (2012) showed that DNA barcoding in reptiles usually correctly assigned barcodes to species, genus and family. Their approach was phylogenetic: they tested whether including a sequence in tree building rendered the higher group non-monophyletic, which would imply failure. Finally, Wilson et al. (2011) provided a similar tree based test in sphingid moths, and established reliabilities of correct generic and subfamily taxonomic assignments between 74 and 90% using a liberal, and only 66-84% using a strict, tree-based criterion. These authors argued that tree-based methods perform better than sequence comparison methods, but that reliability, of course, depends on the library completeness.

Our project not only contributes original DNA barcode data for Central European spiders, but also works in synergy with the GGI towards a permanent preservation of genomic biodiversity: the formation of a collection of deeply frozen spider tissues and their DNA. We provide: 1) tissues of reliably identified species of Central European spiders permanently frozen in ethanol, and their vouchers photographed and deposited in public museums; 2) permanently frozen genomic DNA of these species; 3) publicly accessible DNA barcodes for these species (genetic sequence of cytochrome oxidase I – CO1) as public identification tool (Hebert et al. 2003), freely available to facilitate organism identification, taxonomy, ecology and conservation.

In addition, this project addresses to what extent higher level taxonomic units such as the Linnean family can be reliably identified using barcodes of unknown spiders, and specifically asks what percent sequence identity in BLAST results is necessary to correctly identify unknown taxa to genus and/or family. We ask what is the percent sequence identity value above which 5% or less of higher level (genus/family) taxonomic identifications are incorrect and if the frequency of correct identifications correlated with the number of taxa in the database.

Materials & Methods

Specimen processing and imaging

We used automated and manual sampling methods for collecting spiders in the field in numerous localities in Slovenia and Switzerland. Faunistic and sampling details are published elsewhere (Čandek et al. 2013; see also 2015 corrigendum). Collected spiders were fixed in absolute ethanol immediately after being caught and the ethanol was replaced on the following day. Spiders were frozen at -80°C, same day, or as soon as possible. In the laboratory they were expertly identified, labeled, photographed and processed for DNA extraction and sequencing. Voucher specimens (voucher codes starting with 0078) are deposited at National Museum of Natural History, Smithsonian Institution (Washington D.C., USA), with duplicates (voucher codes starting with ARA) at Naturhistorisches Museum der Burgergemeinde Bern (Switzerland) and EZ LAB, ZRC SAZU (Ljubljana, Slovenia).

Voucher images are published along with their barcodes (see Table 1) at http://ezlab.zrc-sazu.si/dna (Supplemental Figure 1).

Tissues

After specimen identification and processing, up to four legs (or in the case of very small individuals the whole prosoma) of a spider were removed and stored in fresh absolute ethanol in cryovials. Part of the tissue was used for DNA isolation while the other part remains permanently frozen at -80 °C at GGI facilities. The maintenance and use of these materials abides by the international legal standards and conventions of the biological genetic heritage (The Access and Benefit Sharing agreement as part of the 2010 Nagoya protocol).

Molecular procedures

At Laboratories of Analytical Biology (National Museum of Natural History, Smithsonian Institution, hereafter LAB), specimens were extracted using the AutoGenPrep phenol-chloroform automated extractor (AutoGen). Samples were digested overnight in buffer containing proteinase-k before extraction. At EZ Lab, specimens (codes starting with ARA) were extracted using the Mag MAX^{TM} Express magnetic particle processor Type 700 with DNA Multisample kit (Applied Biosystems, Foster City, CA) following the manufacturer's protocols.

At EZ Lab PCR was carried out using mainly primers LCO1490 and HCO2198 (Folmer et al. 1994). Standard reaction volume was 35 µL containing 2.3 mM $MgCl_2$ (Promega), 0.15 mM each dNTP (Biotools), 0.4 µM of each primer, 0.2 µL 10 mg/mL BSA (Promega), 0.2 µL GoTaqFlexi polymerase (Promega) and 2 µL DNA. PCR cycling conditions were as follows: an initial denaturation step of 2 min at 94° C followed by 35 cycles of 40 sec at 94° C, 1 min at 48°-52° C, 1 min at 72° C, with final extension at 72° C for 3 min. Additional primers were used for PCR for a few problematic specimens: dgLCO1490 and dgHCO2198 (Meyer & Paulay 2005) and the reverse primer Chelicerate-R2 (Barrett & Hebert 2005). Cycling parameters for difficult specimens were: 20 cycles of usual cycling protocol (above) followed by 15 cycles of 1.5 min at 94° C, 1.5 min at 52° C and 2 min at 72° Cm version 5.6.6 (Kearse et al. 2012). EZ Lab PCR products were sequenced at Macrogen Inc. (Amsterdam, Netherlands), and the sequences were edited and processed in Geneious Pro version 5.6.6 (Kearse et al. 2012).

At LAB, PCR was carried out using the primer pair LCO1490 (Folmer et al. 1994) and Chelicerate R-2 (Barrett & Herbert 2005). A 10 µL reaction mix contained 2.5 mM $MgCl_2$, 0.3 µM of each primer, 0.5 mM dNTPs, and 5 units of Biolase DNA polymerase (Bioline). PCR cycling conditions were as follows: 35 cycles of 30 sec at 95° C, 30 sec at 48° C, 45 sec at 72° C. PCR products were cleaned with ExoSAP-IT (Affymetrix), sequenced using Big

Dyes (Life Technologies) and run on a 3730xl DNA sequencer (Applied Biosystems). Sequences were examined using Sequencher 5.01 (Gene Codes).

Barcode library

While we targeted 649 bp long DNA barcodes we also submitted (Table 1) 18 shorter fragments (>570 bp) as per requirements of The Barcode of Life Data System BOLD systems (Ratnasingham & Hebert 2007). We combined the 298 species barcodes from this study with publically available Araneae sequences from BOLD retrieved 4 December 2013, for a total of 816 species sequences, which formed the test library for this study. Sequences from BOLD were initially included if the sequence length was at least 600 bases and identification was to species. We further filtered and curated the data to exclude sequences whose identification was anonymous or by non-arachnologists, diverged dramatically from all other spider sequences, or for other reasons the sequences were not deemed to be reliable. We did not, however, assess the accuracy of every sequence, as it is well known that both BOLD and GenBank contain errors of various kinds, and we wanted our test library to reflect real world conditions. A single sequence was used per species, resulting in 816 species representing 313 genera and 49 families. Eighteen sequences were singletons at the family level; the maximum number of species per family was 224. 157 sequences were singletons at the genus level; the maximum number of species per genus was 34.

The standalone BLAST+ suite 2.2.28 (Altschul et al. 1990; Zhang et al. 2000) was used to create a custom BLAST database from these sequences. Each sequence was then queried against the full set using blastn (MegaBLAST task, minimum e value of 1e-10, maximum of top ten hits other than the hit of the query to itself). For each hit the percent of identical nucleotides in the aligned region (PIdent) was calculated by BLAST. Custom Python scripts (GitHub https://github.com/mkweskin/spider-blast) were used to parse the results, removing the match of the query to itself and to score whether hits matched the genus and family of the query sequence or not. Obviously, if the generic identification matched, the family identification also matched; families therefore always match more often than genera.

On the other hand, singleton generic sequences cannot match correctly at the genus level, and, likewise, singleton family sequences cannot match correctly at the family level. We included singletons as targets in order to model more realistically BLAST searches against the BOLD database (many sequences in BOLD are higher level singletons), and also to test more strongly the ability of sequences with two or more species per either genus or family to match correctly. Including 18 singleton family sequences and 157 singleton genus sequences, therefore, increases the probability of misidentification at either ranks and more strongly tests the usefulness of barcodes as supraspecific identification aids.

However, because the 18 unique family sequences must fail at both the family and genus levels, and the 157 unique genus level sequences must fail at the genus level, these necessary failures were not included in the overall assessments of the ability of barcode sequences to provide accurate identifications at supraspecific levels.

Results

The 816 query sequences returned 8160 total hits (Supplemental Table 1). PIdent scores ranged from 75% to 100%. Figure 2 shows the frequency distributions of PIdent values of correct and incorrect identifications at the genus and family rank.

1. 95% of incorrect genus identifications were below PIdent = 95 when all hits for all queries are included, which suggests the latter value as a heuristic threshold to delimit incorrect from correct identifications (for these data). For only the highest rank hits whose PIdent ≥ 95, 98% of genus identifications were correct.
2. 95% of incorrect family identifications were below PIdent = 91 when all hits for all queries are included, which suggests the latter value as a heuristic threshold to delimit incorrect from correct identifications (for these data). For only the highest rank hits whose PIdent ≥ 91, 97% of family identifications were correct.
3. Library accuracy is crucial, but sequencing, labelling, and identification errors are difficult to detect *a priori*. The highest ranked incorrect family identification was *Steatoda grossa* (Theridiidae) to *Meta menardi* (Tetragnathidae), at PIdent = 96. Further study of the *M. menardi* sequence shows that the BOLD record is probably a mislabeled *Steatoda*. The first true incorrect family identification occurs at a PIdent value of 88; the best hit for *Octonoba* (Uloboridae) is *Amaurobius* (Amaurobiidae).
4. For the 136 genera with at least two species in the library, 76% (n=103) best matched congeners. Thirty-three failed, perhaps because sequences were incorrectly identified taxonomically, or the sequence itself may be erroneous.
5. The distributions of PIdents for correct family and genus identifications differ significantly from the distributions of incorrect identifications (Figure 2).
6. Plotted against increasing numbers of species/genus, and genera/family, the proportion of top ten PIdent values that exceed the above suggested threshold values increases. Roughly speaking, 15 species per genus, and 5 genera per family, are sufficient to ensure that best hits represent correct identifications (Figure 3).

Discussion

We show that standard DNA barcodes can accurately identify unknown specimens to genus and family level given sufficient sequence identity and sufficient taxonomic representation in the database. Accurate identification (PIdent above which less than 5% of identifications were incorrect) occurred for genera at PIdent values > 95 and families at PIdent values ≥ 91, suggesting these as heuristic thresholds for generic and familial identifications in spiders (shaded in Figure 2). Accuracy of identification increases with numbers of species/genus and genera/family; above five genera per family and 15 species per genus all identifications were correct (Figure 3).

The accurate identification of specimens remains a critical challenge for megadiverse groups such as arthropods, most other invertebrates, plants, fungi, protists etc. Morphological identification to species, or even more inclusive taxonomic ranks like genera and families, in many cases requires extensive training, and for most groups taxonomic expertise is limited and dwindling—the so called ‘taxonomic impediment’ (Rodman & Cody 2003). DNA barcodes have been proposed as convenient tools to overcome this impediment by making identification a purely technical procedure available to any interested researcher or even ‘citizen scientists’. However, the accuracy of such a tool strongly depends on the scope and quality of the barcode library (Smit et al. 2013). Currently available data on databanks like BOLD and GenBank are extensive for some groups, yet the vast majority of species on earth have not yet been barcoded, much less discovered and described taxonomically—each of these tasks is enormous. Even for existing barcoding data, the majority of sequences lack taxonomic identification, limiting their utility (e.g. only 58% of Araneae in BOLD are identified to species, and of those many are not correctly identified, as shown in our results; see also Shen et al. 2013). Therefore, the identification of unknown specimens through blasting against BOLD or GenBank will be inaccurate if the databases lack close hits or contain errors. While the ideal database would allow species-level identification by containing barcodes from expertly identified and vouchered specimens of all species, we hypothesized that rapid surveys of well-known biotas can help quickly to build valuable tools allowing identification of larger clades such as genera and families.

Although we were careful to screen available barcode sequences from BOLD to produce a test library with as few errors as possible, it is certainly possible that errors remained, either due to mistakes in the lab or taxonomic identifications of vouchers. For example, *Meta menardi* (Tetragnathidae) blasted to *Steatoda grossa* (Theridiidae) at PIdent = 96, and BLAST searches on GenBank suggest this *Meta* sequence is actually a *Steatoda*. Likewise, the linyphiids *Agyneta orites* and *Incestophantes frigidus* sequences were identical; one of these records is probably wrong. These sorts of errors bias identifications and limit utility of barcodes. Other examples of identical barcode sequences were all congeners, and therefore are less likely to involve errors but could indicate faults in taxonomy: *Arctosa maculata* and *A. fulvolineata*, *Bolyphantes luteolus* and *B. alticeps*, *Pardosa alacris* and *P. trifrons*, and *Pityohyphantes tacoma* and *P. cristatus*. Likewise the genus *Neriene* (Linyphiidae) seems non-monophyletic and identifications were thus not accurate.

Conclusions

These results suggest that accurate identification of unknown taxa to the genus and family level is feasible through DNA barcoding. Database quality is crucial. Numbers of potential matches at generic and familial ranks also affect the probability that an unknown sequence will blast best to the correct family or genus. Unlike the inventory of species, discovery of family-level clades of life also seems far advanced—few eukaryotic families, apparently, remain to be discovered. Taken together, these results suggest that barcode-targeted sequencing of exemplars from all families of life (and most genera, if possible) should be an important scientific priority. It would enable approximate taxonomic identification of any organism anywhere on Earth by rapid, cheap, purely technical procedures requiring no specialist knowledge—certainly an important milestone in the on-going attempt to discover, classify, and understand the Earth's biota.

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FIGURES

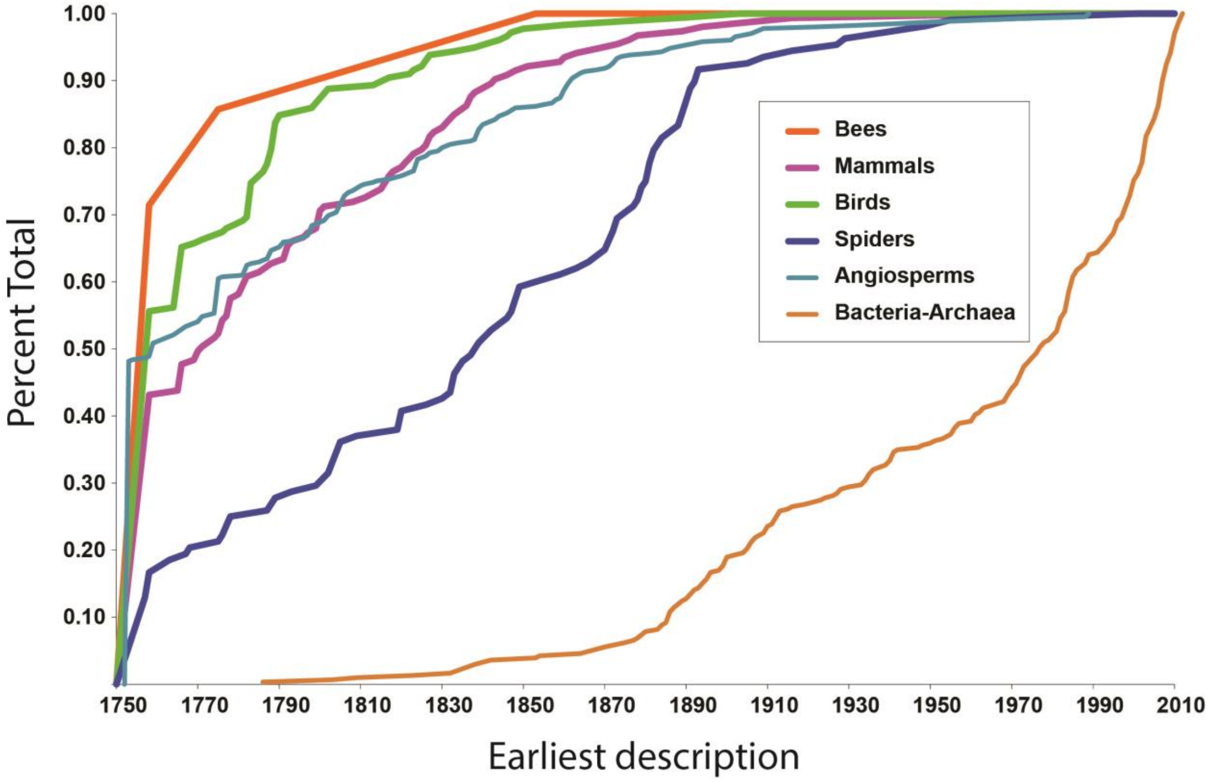

Figure 1. Accumulation curve of dates of first discovery (year of first description of a contained species) of families for six major clades of life, 1758-2010.

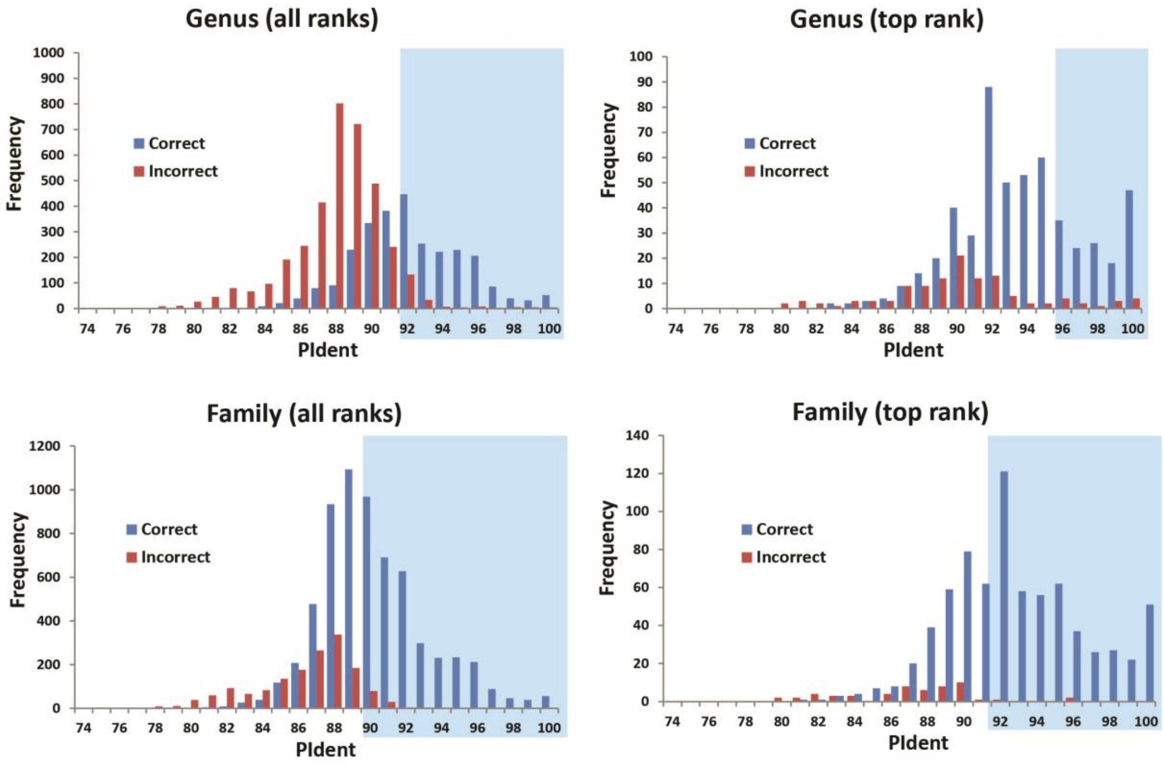

Figure 2. Frequency distributions of correct and incorrect identifications by percent sequence identity (PIdent) for the top ten and/or best hits at the genus and family level. Shaded areas include hits where no more than 5% of identifications were incorrect.

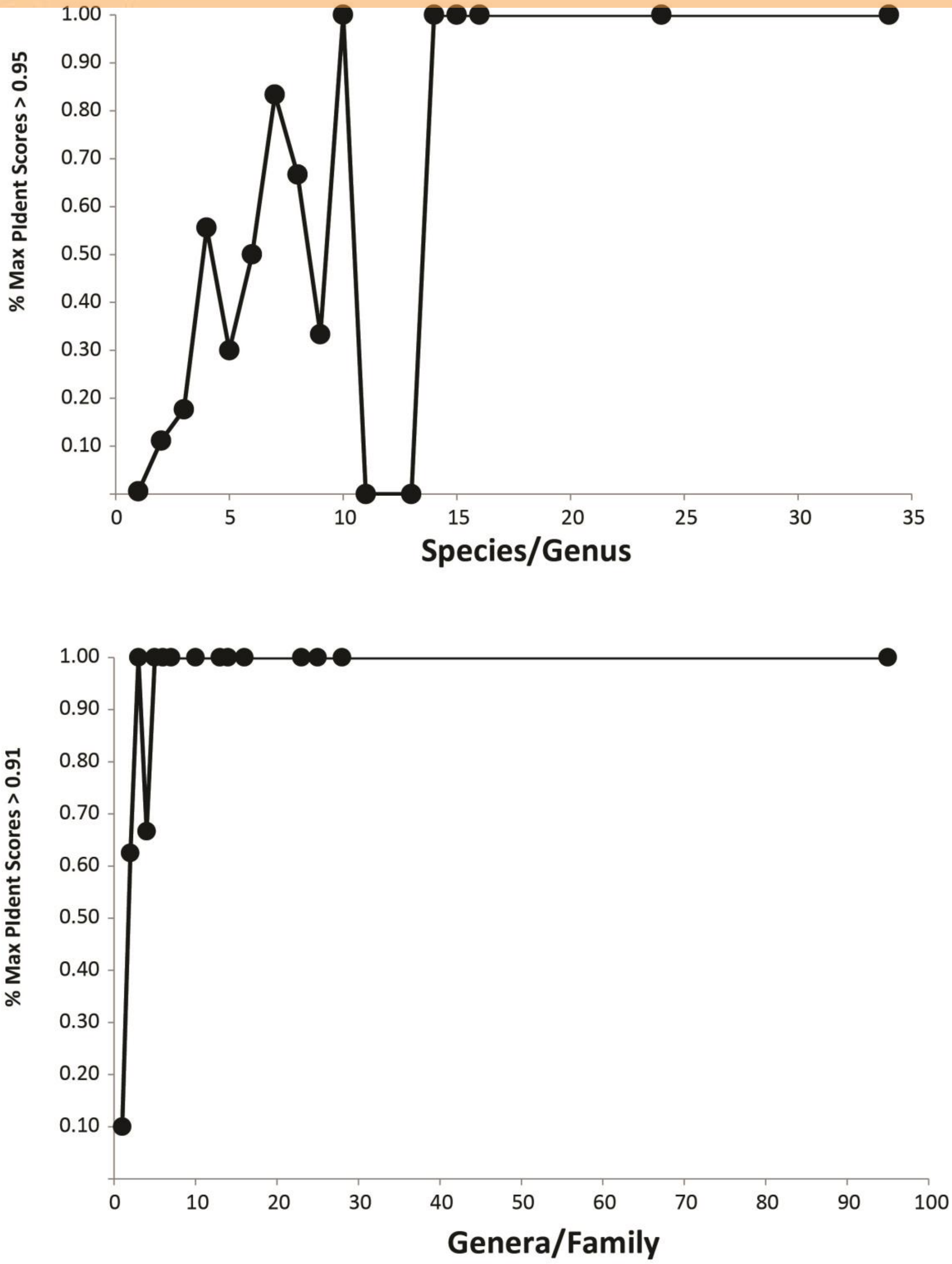

Figure 3. Relation between proportion of best sequence identity and numbers of species per genus, and genera per family (thresholds 95 and 91 respectively).

TABLES

Table 1. Original sequences this project submitted to BOLD. Legend: MNH, SI = National Museum of Natural History, Smithsonian Institution; EZ LAB = Evolutionary Zoology Lab, ZRC SAZU; NMBE = Naturhistorisches Museum der Burgergemeinde Bern; SVN = Slovenia; CHE = Switzerland; MYS = Malaysia.

Family	**Genus**	**Species**	**BOLD specimen page**	**BOLD sequence page**	**Voucher stored at**	**Collected in**
Theridiidae	*Sardinidion*	*blackwalli*	00786271	SPSLO321-13	MNH, SI	SVN
Philodromidae	*Philodromus*	*albidus*	00786272	SPSLO312-13	MNH, SI	SVN
Gnaphosidae	*Drassodes*	*pubescens*	00786273	SPSLO291-13	MNH, SI	SVN
Gnaphosidae	*Micaria*	*pulicaria*	00786274	SPSLO293-13	MNH, SI	SVN
Thomisidae	*Xysticus*	*erraticus*	00786275	SPSLO322-13	MNH, SI	SVN
Gnaphosidae	*Gnaphosa*	*bicolor*	00786276	SPSLO292-13	MNH, SI	SVN
Linyphiidae	*Agyneta*	*saxatilis*	00786277	SPSLO298-13	MNH, SI	SVN
Gnaphosidae	*Zelotes*	*apricorum*	00786278	SPSLO295-13	MNH, SI	SVN
Gnaphosidae	*Trachyzelotes*	*pedestris*	00786279	SPSLO294-13	MNH, SI	SVN
Salticidae	*Pseudeuophrys*	*lanigera*	00786280	SPSLO316-13	MNH, SI	SVN
Segestriidae	*Segestria*	*senoculata*	00786281	SPSLO317-13	MNH, SI	SVN
Salticidae	*Heliophanus*	*auratus*	00786282	SPSLO315-13	MNH, SI	SVN
Dictynidae	*Argenna*	*subnigra*	00786283	SPSLO288-13	MNH, SI	SVN
Clubionidae	*Clubiona*	*pseudoneglecta*	00786286	SPSLO286-13	MNH, SI	SVN
Dysderidae	*Dysdera*	*adriatica*	00786287	SPSLO289-13	MNH, SI	SVN
Theridiidae	*Paidiscura*	*pallens*	00786288	SPSLO319-13	MNH, SI	SVN
Lycosidae	*Pardosa*	*hortensis*	00786289	SPSLO307-13	MNH, SI	SVN
Theridiidae	*Robertus*	*scoticus*	00786290	SPSLO320-13	MNH, SI	SVN
Linyphiidae	*Porrhomma*	*pygmaeum*	00786292	SPSLO301-13	MNH, SI	SVN
Salticidae	*Heliophanus*	*aeneus*	00786293	SPSLO314-13	MNH, SI	SVN
Linyphiidae	*Diplocephalus*	*crassilobus*	00786294	SPSLO296-13	MNH, SI	SVN
Linyphiidae	*Agyneta*	*simplicitarsis*	00786295	SPSLO299-13	MNH, SI	SVN
Dysderidae	*Dysdera*	*adriatica*	00786296	SPSLO290-13	MNH, SI	SVN
Titanoecidae	*Titanoeca*	*tristis*	00786297	SPSLO324-13	MNH, SI	SVN
Tetragnathidae	*Metellina*	*merianae*	00786298	SPSLO318-13	MNH, SI	CHE
Linyphiidae	*Tenuiphantes*	*mengei*	00786301	SPSLO300-13	MNH, SI	CHE
Thomisidae	*Xysticus*	*kochi*	00786303	SPSLO323-13	MNH, SI	SVN
Agelenidae	*Malthonica*	*silvestris*	00786304	SPSLO283-13	MNH, SI	SVN
Linyphiidae	*Tenuiphantes*	*cristatus*	00786305	SPSLO302-13	MNH, SI	CHE
Amaurobiidae	*Amaurobius*	*ferox*	00786307	SPSLO284-13	MNH, SI	SVN
Lycosidae	*Pardosa*	*ferruginea*	00786309	SPSLO306-13	MNH, SI	CHE
Lycosidae	*Pardosa*	*oreophila*	00786310	SPSLO308-13	MNH, SI	CHE
Lycosidae	*Pardosa*	*proxima*	00786311	SPSLO309-13	MNH, SI	SVN
Lycosidae	*Arctosa*	*maculata*	00786312	SPSLO305-13	MNH, SI	SVN
Salticidae	*Evarcha*	*michailovi*	00786313	SPSLO313-13	MNH, SI	SVN
Araneidae	*Hypsosinga*	*sanguinea*	00786314	SPSLO285-13	MNH, SI	SVN
Lycosidae	*Pardosa*	*riparia*	00786315	SPSLO310-13	MNH, SI	SVN
Linyphiidae	*Pityohyphantes*	*phrygianus*	00786316	SPSLO236-12	MNH, SI	CHE
Linyphiidae	*Ceratinella*	*brevipes*	00786317	SPSLO234-12	MNH, SI	CHE
Linyphiidae	*Gonatium*	*rubellum*	00786318	SPSLO212-12	MNH, SI	CHE
Linyphiidae	*Mughiphantes*	*mughi*	00786319	SPSLO227-12	MNH, SI	CHE
Liocranidae	*Agroeca*	*brunnea*	00786320	SPSLO247-12	MNH, SI	SVN
Lycosidae	*Pardosa*	*oreophila*	00786321	SPSLO254-12	MNH, SI	CHE
Linyphiidae	*Mughiphantes*	*mughi*	00786322	SPSLO217-12	MNH, SI	CHE
Araneidae	*Hypsosinga*	*albovittata*	00786323	SPSLO191-12	MNH, SI	CHE
Uloboridae	*Uloborus*	*walckenaerius*	00786324	SPSLO282-12	MNH, SI	SVN
Theridiidae	*Steatoda*	*bipunctata*	00786325	SPSLO276-12	MNH, SI	CHE
Araneidae	*Zygiella*	*x-notata*	00786326	SPSLO193-12	MNH, SI	CHE
Theridiidae	*Episinus*	*truncatus*	00786327	SPSLO270-12	MNH, SI	CHE

Linyphiidae	*Agnyphantes*	*expunctus*	00786328	SPSLO203-12	MNH, SI	CHE
Theridiidae	*Enoplognatha*	*latimana*	00786329	SPSLO269-12	MNH, SI	CHE
Araneidae	*Neoscona*	*adianta*	00786330	SPSLO192-12	MNH, SI	SVN
Linyphiidae	*Gonatium*	*rubens*	00786331	SPSLO213-12	MNH, SI	CHE
Salticidae	*Evarcha*	*arcuata*	00786332	SPSLO259-12	MNH, SI	CHE
Nemesiidae	*Nemesia*	*pannonica*	00786333	SPSLO311-13	MNH, SI	SVN
Theridiidae	*Robertus*	*mediterraneus*	00786334	SPSLO275-12	MNH, SI	CHE
Lycosidae	*Arctosa*	*fulvolineata*	00786336	SPSLO250-12	MNH, SI	SVN
Lycosidae	*Pardosa*	*amentata*	00786337	SPSLO251-12	MNH, SI	SVN
Salticidae	*Macaroeris*	*nidicolens*	00786338	SPSLO262-12	MNH, SI	SVN
Linyphiidae	*Ostearius*	*melanopygius*	00786339	SPSLO122-12	MNH, SI	SVN
Theridiidae	*Theridion*	*betteni*	00786340	SPSLO277-12	MNH, SI	CHE
Linyphiidae	*Palliduphantes*	*pallidus*	00786341	SPSLO233-12	MNH, SI	CHE
Linyphiidae	*Lepthyphantes*	*leprosus*	00786342	SPSLO214-12	MNH, SI	SVN
Linyphiidae	*Tenuiphantes*	*alacris*	00786343	SPSLO241-12	MNH, SI	CHE
Lycosidae	*Trochosa*	*spinipalpis*	00786344	SPSLO137-12	MNH, SI	SVN
Dictynidae	*Dictyna*	*uncinata*	00786345	SPSLO197-12	MNH, SI	SVN
Theridiidae	*Asagena*	*phalerata*	00786346	SPSLO156-12	MNH, SI	SVN
Thomisidae	*Xysticus*	*audax*	00786347	SPSLO180-12	MNH, SI	SVN
Salticidae	*Hasarius*	*adansoni*	00786348	SPSLO261-12	MNH, SI	SVN
Linyphiidae	*Microlinyphia*	*impigra*	00786350	SPSLO228-12	MNH, SI	CHE
Linyphiidae	*Tiso*	*vagans*	00786351	SPSLO246-12	MNH, SI	CHE
Linyphiidae	*Obscuriphantes*	*obscurus*	00786354	SPSLO231-12	MNH, SI	CHE
Miturgidae	*Cheiracanthium*	*mildei*	00786355	SPSLO139-12	MNH, SI	SVN
Linyphiidae	*Tenuiphantes*	*jacksoni*	00786356	SPSLO242-12	MNH, SI	CHE
Tetragnathidae	*Metellina*	*segmentata*	00786357	SPSLO152-12	MNH, SI	SVN
Lycosidae	*Pardosa*	*blanda*	00786358	SPSLO253-12	MNH, SI	CHE
Thomisidae	*Diaea*	*livens*	00786359	SPSLO174-12	MNH, SI	SVN
Tetragnathidae	*Tetragnatha*	*pinicola*	00786361	SPSLO267-12	MNH, SI	CHE
Salticidae	*Salticus*	*scenicus*	00786362	SPSLO265-12	MNH, SI	CHE
Hahniidae	*Hahnia*	*difficilis*	00786363	SPSLO202-12	MNH, SI	CHE
Theridiidae	*Phylloneta*	*sisyphia*	00786364	SPSLO274-12	MNH, SI	CHE
Lycosidae	*Alopecosa*	*accentuata*	00786365	SPSLO248-12	MNH, SI	CHE
Philodromidae	*Philodromus*	*vagulus*	00786366	SPSLO257-12	MNH, SI	CHE
Miturgidae	*Cheiracanthium*	*erraticum*	00786367	SPSLO138-12	MNH, SI	SVN
Araneidae	*Agalenatea*	*redii*	00786368	SPSLO095-12	MNH, SI	SVN
Dictynidae	*Dictyna*	*arundinacea*	00786369	SPSLO196-12	MNH, SI	CHE
Salticidae	*Neon*	*reticulatus*	00786370	SPSLO150-12	MNH, SI	SVN
Linyphiidae	*Minicia*	*marginella*	00786371	SPSLO120-12	MNH, SI	SVN
Thomisidae	*Xysticus*	*desidiosus*	00786372	SPSLO183-12	MNH, SI	SVN
Theridiidae	*Theridion*	*varians*	00786374	SPSLO173-12	MNH, SI	SVN
Lycosidae	*Pirata*	*piraticus*	00786375	SPSLO255-12	MNH, SI	CHE
Thomisidae	*Xysticus*	*macedonicus*	00786376	SPSLO281-12	MNH, SI	CHE
Salticidae	*Sibianor*	*aurocinctus*	00786377	SPSLO266-12	MNH, SI	CHE
Clubionidae	*Clubiona*	*reclusa*	00786378	SPSLO195-12	MNH, SI	CHE
Theridiidae	*Platnickina*	*tincta*	00786380	SPSLO167-12	MNH, SI	SVN
Salticidae	*Icius*	*subinermis*	00786381	SPSLO148-12	MNH, SI	SVN
Araneidae	*Larinioides*	*sclopetarius*	00786382	SPSLO096-12	MNH, SI	SVN
Linyphiidae	*Tenuiphantes*	*tenuis*	00786383	SPSLO129-12	MNH, SI	SVN
Gnaphosidae	*Micaria*	*aenea*	00786384	SPSLO200-12	MNH, SI	CHE
Lycosidae	*Pardosa*	*agrestis*	00786385	SPSLO134-12	MNH, SI	SVN
Theridiidae	*Episinus*	*angulatus*	00786386	SPSLO159-12	MNH, SI	SVN
Thomisidae	*Misumena*	*vatia*	00786387	SPSLO175-12	MNH, SI	SVN
Lycosidae	*Piratula*	*hygrophila*	00786388	SPSLO135-12	MNH, SI	SVN
Amaurobiidae	*Amaurobius*	*fenestralis*	00786389	SPSLO189-12	MNH, SI	CHE
Mimetidae	*Ero*	*furcata*	00786390	SPSLO256-12	MNH, SI	CHE
Linyphiidae	*Agyneta*	*innotabilis*	00786393	SPSLO220-12	MNH, SI	CHE
Linyphiidae	*Mermessus*	*trilobatus*	00786395	SPSLO118-12	MNH, SI	SVN
Linyphiidae	*Oedothorax*	*gibbifer*	00786396	SPSLO232-12	MNH, SI	CHE
Linyphiidae	*Bolyphantes*	*luteolus*	00786397	SPSLO101-12	MNH, SI	CHE

Tetragnathidae	*Pachygnatha*	*degeeri*	00786399	SPSLO153-12	MNH, SI	SVN
Linyphiidae	*Maso*	*sundevalli*	00786400	SPSLO216-12	MNH, SI	CHE
Theridiidae	*Phylloneta*	*impressa*	00786401	SPSLO273-12	MNH, SI	CHE
Lycosidae	*Piratula*	*knorri*	00786402	SPSLO136-12	MNH, SI	SVN
Clubionidae	*Clubiona*	*kulczynskii*	00786404	SPSLO194-12	MNH, SI	CHE
Hahniidae	*Antistea*	*elegans*	00786405	SPSLO201-12	MNH, SI	CHE
Linyphiidae	*Tapinocyba*	*affinis*	00786406	SPSLO127-12	MNH, SI	CHE
Lycosidae	*Arctosa*	*lutetiana*	00786407	SPSLO132-12	MNH, SI	SVN
Salticidae	*Evarcha*	*falcata*	00786408	SPSLO145-12	MNH, SI	SVN
Linyphiidae	*Silometopus*	*elegans*	00786409	SPSLO126-12	MNH, SI	CHE
Linyphiidae	*Porrhomma*	*pallidum*	00786410	SPSLO239-12	MNH, SI	CHE
Linyphiidae	*Agyneta*	*rurestris*	00786411	SPSLO117-12	MNH, SI	CHE
Linyphiidae	*Centromerus*	*subalpinus*	00786412	SPSLO208-12	MNH, SI	CHE
Linyphiidae	*Tenuiphantes*	*mengei*	00786413	SPSLO243-12	MNH, SI	CHE
Linyphiidae	*Mansuphantes*	*fragilis*	00786415	SPSLO114-12	MNH, SI	CHE
Linyphiidae	*Erigone*	*remota*	00786416	SPSLO107-12	MNH, SI	CHE
Linyphiidae	*Microlinyphia*	*pusilla*	00786417	SPSLO225-12	MNH, SI	CHE
Linyphiidae	*Tenuiphantes*	*tenebricola*	00786418	SPSLO244-12	MNH, SI	CHE
Linyphiidae	*Agyneta*	*orites*	00786419	SPSLO221-12	MNH, SI	CHE
Linyphiidae	*Scotinotylus*	*clavatus*	00786420	SPSLO240-12	MNH, SI	CHE
Linyphiidae	*Pocadicnemis*	*juncea*	00786421	SPSLO237-12	MNH, SI	CHE
Linyphiidae	*Pocadicnemis*	*pumila*	00786422	SPSLO238-12	MNH, SI	CHE
Linyphiidae	*Agyneta*	*fuscipalpa*	00786425	SPSLO218-12	MNH, SI	CHE
Linyphiidae	*Agyneta*	*cauta*	00786426	SPSLO204-12	MNH, SI	CHE
Theridiidae	*Neottiura*	*suaveolens*	00786427	SPSLO164-12	MNH, SI	SVN
Linyphiidae	*Walckenaeria*	*antica*	00786429	SPSLO130-12	MNH, SI	CHE
Linyphiidae	*Tenuiphantes*	*jacksoni*	00786430	SPSLO128-12	MNH, SI	CHE
Linyphiidae	*Walckenaeria*	*furcillata*	00786431	SPSLO131-12	MNH, SI	CHE
Salticidae	*Myrmarachne*	*formicaria*	00786432	SPSLO149-12	MNH, SI	SVN
Theridiidae	*Robertus*	*mediterraneus*	00786433	SPSLO168-12	MNH, SI	CHE
Theridiidae	*Robertus*	*truncorum*	00786435	SPSLO169-12	MNH, SI	CHE
Linyphiidae	*Metopobactrus*	*prominulus*	00786437	SPSLO119-12	MNH, SI	CHE
Linyphiidae	*Agyneta*	*affinis*	00786439	SPSLO115-12	MNH, SI	CHE
Linyphiidae	*Caracladus*	*zamoniensis*	00786441	SPSLO102-12	MNH, SI	CHE
Linyphiidae	*Agyneta*	*alpica*	00786443	SPSLO116-12	MNH, SI	CHE
Linyphiidae	*Scotinotylus*	*alpigena*	00786444	SPSLO125-12	MNH, SI	CHE
Theridiidae	*Neottiura*	*bimaculata*	00786445	SPSLO163-12	MNH, SI	SVN
Linyphiidae	*Agyneta*	*conigera*	00786448	SPSLO100-12	MNH, SI	CHE
Linyphiidae	*Improphantes*	*nitidus*	00786449	SPSLO109-12	MNH, SI	CHE
Linyphiidae	*Ceratinella*	*brevipes*	00786450	SPSLO103-12	MNH, SI	CHE
Linyphiidae	*Centromerus*	*pabulator*	00786451	SPSLO207-12	MNH, SI	CHE
Lycosidae	*Alopecosa*	*sulzeri*	00786452	SPSLO249-12	MNH, SI	SVN
Lycosidae	*Pardosa*	*bifasciata*	00786453	SPSLO252-12	MNH, SI	SVN
Theridiidae	*Crustulina*	*guttata*	00786454	SPSLO268-12	MNH, SI	SVN
Thomisidae	*Thomisus*	*onustus*	00786455	SPSLO280-12	MNH, SI	SVN
Clubionidae	*Clubiona*	*terrestris*	00786457	SPSLO098-12	MNH, SI	SVN
Salticidae	*Evarcha*	*michailovi*	00786458	SPSLO260-12	MNH, SI	SVN
Linyphiidae	*Entelecara*	*acuminata*	00786460	SPSLO210-12	MNH, SI	CHE
Linyphiidae	*Diplocephalus*	*latifrons*	00786461	SPSLO209-12	MNH, SI	CHE
Salticidae	*Pellenes*	*seriatus*	00786462	SPSLO263-12	MNH, SI	SVN
Linyphiidae	*Microctenonyx*	*subitaneus*	00786463	SPSLO224-12	MNH, SI	CHE
Linyphiidae	*Agyneta*	*gulosa*	00786464	SPSLO219-12	MNH, SI	CHE
Linyphiidae	*Bolyphantes*	*alticeps*	00786465	SPSLO205-12	MNH, SI	CHE
Linyphiidae	*Micrargus*	*herbigradus*	00786466	SPSLO223-12	MNH, SI	CHE
Theridiidae	*Neottiura*	*herbigrada*	00786467	SPSLO272-12	MNH, SI	SVN
Theridiidae	*Euryopis*	*flavomaculata*	00786468	SPSLO271-12	MNH, SI	SVN
Thomisidae	*Heriaeus*	*hirtus*	00786469	SPSLO278-12	MNH, SI	SVN
Gnaphosidae	*Aphantaulax*	*cincta*	00786470	SPSLO199-12	MNH, SI	SVN
Linyphiidae	*Neriene*	*furtiva*	00786471	SPSLO229-12	MNH, SI	SVN
Salticidae	*Philaeus*	*chrysops*	00786472	SPSLO264-12	MNH, SI	SVN

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Dictynidae	*Lathys*	*humilis*	00786473	SPSLO198-12	MNH, SI	SVN
Linyphiidae	*Caracladus*	*avicula*	00786474	SPSLO206-12	MNH, SI	CHE
Philodromidae	*Philodromus*	*pulchellus*	00786475	SPSLO072-12	MNH, SI	SVN
Theridiidae	*Parasteatoda*	*lunata*	00786476	SPSLO165-12	MNH, SI	SVN
Thomisidae	*Xysticus*	*lanio*	00786477	SPSLO185-12	MNH, SI	SVN
Thomisidae	*Xysticus*	*tenebrosus*	00786478	SPSLO187-12	MNH, SI	SVN
Theridiidae	*Crustulina*	*scabripes*	00786479	SPSLO089-12	MNH, SI	SVN
Theridiidae	*Theridion*	*pinastri*	00786480	SPSLO172-12	MNH, SI	SVN
Araneidae	*Zilla*	*diodia*	00786481	SPSLO097-12	MNH, SI	SVN
Theridiidae	*Heterotheridion*	*nigrovariegatum*	00786482	SPSLO161-12	MNH, SI	SVN
Thomisidae	*Xysticus*	*acerbus*	00786483	SPSLO179-12	MNH, SI	SVN
Thomisidae	*Tmarus*	*piger*	00786484	SPSLO178-12	MNH, SI	SVN
Thomisidae	*Synema*	*globosum*	00786485	SPSLO177-12	MNH, SI	SVN
Thomisidae	*Xysticus*	*kempeleni*	00786486	SPSLO184-12	MNH, SI	SVN
Pisauridae	*Pisaura*	*mirabilis*	00786487	SPSLO144-12	MNH, SI	SVN
Theridiidae	*Episinus*	*maculipes*	00786488	SPSLO160-12	MNH, SI	SVN
Theridiidae	*Steatoda*	*triangulosa*	00786489	SPSLO171-12	MNH, SI	SVN
Linyphiidae	*Nematogmus*	*sanguinolentus*	00786490	SPSLO162-12	MNH, SI	SVN
Philodromidae	*Philodromus*	*dispar*	00786492	SPSLO142-12	MNH, SI	SVN
Philodromidae	*Tibellus*	*macellus*	00786493	SPSLO074-12	MNH, SI	SVN
Zoridae	*Zora*	*spinimana*	00786494	SPSLO094-12	MNH, SI	SVN
Salticidae	*Heliophanus*	*kochii*	00786495	SPSLO078-12	MNH, SI	SVN
Salticidae	*Marpissa*	*nivoyi*	00786496	SPSLO081-12	MNH, SI	SVN
Sparassidae	*Micrommata*	*virescens*	00786497	SPSLO086-12	MNH, SI	SVN
Araneidae	*Cercidia*	*prominens*	00786498	SPSLO021-12	MNH, SI	SVN
Thomisidae	*Ozyptila*	*nigrita*	00786499	SPSLO093-12	MNH, SI	SVN
Philodromidae	*Philodromus*	*praedatus*	00786500	SPSLO071-12	MNH, SI	SVN
Pholcidae	*Psilochorus*	*simoni*	00786501	SPSLO076-12	MNH, SI	SVN
Lycosidae	*Hogna*	*radiata*	00786502	SPSLO065-12	MNH, SI	SVN
Salticidae	*Evarcha*	*jucunda*	00786503	SPSLO077-12	MNH, SI	SVN
Salticidae	*Pellenes*	*seriatus*	00786504	SPSLO082-12	MNH, SI	SVN
Gnaphosidae	*Drassodes*	*lapidosus*	00786505	SPSLO099-12	MNH, SI	SVN
Theridiidae	*Dipoena*	*melanogaster*	00786506	SPSLO090-12	MNH, SI	SVN
Salticidae	*Saitis*	*barbipes*	00786507	SPSLO083-12	MNH, SI	SVN
Thomisidae	*Ebrechtella*	*tricuspidata*	00786508	SPSLO092-12	MNH, SI	SVN
Lycosidae	*Alopecosa*	*trabalis*	00786509	SPSLO064-12	MNH, SI	SVN
Salticidae	*Heliophanus*	*flavipes*	00786510	SPSLO147-12	MNH, SI	SVN
Dictynidae	*Dictyna*	*civica*	00786511	SPSLO036-12	MNH, SI	SVN
Salticidae	*Leptorchestes*	*berolinensis*	00786512	SPSLO079-12	MNH, SI	SVN
Philodromidae	*Philodromus*	*cespitum*	00786513	SPSLO070-12	MNH, SI	CHE
Lycosidae	*Pardosa*	*palustris*	00786514	SPSLO067-12	MNH, SI	SVN
Theridiidae	*Enoplognatha*	*ovata*	00786515	SPSLO158-12	MNH, SI	SVN
Liocranidae	*Liocranum*	*rupicola*	00786516	SPSLO061-12	MNH, SI	SVN
Salticidae	*Heliophanus*	*cupreus*	00786518	SPSLO146-12	MNH, SI	SVN
Miturgidae	*Cheiracanthium*	*punctorium*	00786519	SPSLO140-12	MNH, SI	SVN
Tetragnathidae	*Tetragnatha*	*pinicola*	00786520	SPSLO155-12	MNH, SI	SVN
Scytodidae	*Scytodes*	*thoracica*	00786521	SPSLO085-12	MNH, SI	SVN
Thomisidae	*Ozyptila*	*atomaria*	00786522	SPSLO176-12	MNH, SI	CHE
Salticidae	*Marpissa*	*muscosa*	00786523	SPSLO080-12	MNH, SI	SVN
Lycosidae	*Aulonia*	*albimana*	00786524	SPSLO133-12	MNH, SI	SVN
Salticidae	*Sitticus*	*rupicola*	00786525	SPSLO084-12	MNH, SI	CHE
Linyphiidae	*Linyphia*	*hortensis*	00786526	SPSLO112-12	MNH, SI	SVN
Lycosidae	*Alopecosa*	*pulverulenta*	00786527	SPSLO063-12	MNH, SI	SVN
Linyphiidae	*Tenuiphantes*	*flavipes*	00786528	SPSLO060-12	MNH, SI	SVN
Lycosidae	*Pardosa*	*cf. lugubris*	00786529	SPSLO066-12	MNH, SI	CHE
Philodromidae	*Thanatus*	*formicinus*	00786530	SPSLO073-12	MNH, SI	SVN
Theridiidae	*Parasteatoda*	*tepidariorum*	00786531	SPSLO091-12	MNH, SI	SVN
Theridiidae	*Enoplognatha*	*afrodite*	00786532	SPSLO157-12	MNH, SI	SVN
Linyphiidae	*Diplostyla*	*concolor*	00786533	SPSLO049-12	MNH, SI	SVN
Tetragnathidae	*Tetragnatha*	*nigrita*	00786534	SPSLO088-12	MNH, SI	SVN

Thomisidae	*Xysticus*	*lineatus*	00786535	SPSLO186-12	MNH, SI	SVN
Tetragnathidae	*Metellina*	*mengei*	00786536	SPSLO087-12	MNH, SI	CHE
Thomisidae	*Xysticus*	*cristatus*	00786537	SPSLO182-12	MNH, SI	SVN
Lycosidae	*Alopecosa*	*taeniata*	00786538	SPSLO062-12	MNH, SI	CHE
Philodromidae	*Philodromus*	*aureolus*	00786539	SPSLO069-12	MNH, SI	SVN
Gnaphosidae	*Zelotes*	*latreillei*	00786540	SPSLO047-12	MNH, SI	SVN
Lycosidae	*Xerolycosa*	*nemoralis*	00786541	SPSLO068-12	MNH, SI	CHE
Thomisidae	*Xysticus*	*bifasciatus*	00786543	SPSLO181-12	MNH, SI	SVN
Linyphiidae	*Floronia*	*bucculenta*	00786545	SPSLO051-12	MNH, SI	SVN
Uloboridae	*Hyptiotes*	*paradoxus*	00786546	SPSLO188-12	MNH, SI	SVN
Linyphiidae	*Linyphia*	*triangularis*	00786547	SPSLO056-12	MNH, SI	SVN
Dictynidae	*Cicurina*	*cicur*	00786548	SPSLO035-12	MNH, SI	SVN
Theridiidae	*Simitidion*	*simile*	00786549	SPSLO170-12	MNH, SI	SVN
Dictynidae	*Lathys*	*humilis*	00786550	SPSLO037-12	MNH, SI	SVN
Anyphaenidae	*Anyphaena*	*sabina*	00786551	SPSLO010-12	MNH, SI	SVN
Araneidae	*Araneus*	*angulatus*	00786552	SPSLO013-12	MNH, SI	SVN
Gnaphosidae	*Callilepis*	*schuszteri*	00786553	SPSLO041-12	MNH, SI	SVN
Araneidae	*Hypsosinga*	*pygmaea*	00786555	SPSLO024-12	MNH, SI	SVN
Gnaphosidae	*Drassyllus*	*villicus*	00786556	SPSLO042-12	MNH, SI	SVN
Agelenidae	*Allagelena*	*gracilens*	00786557	SPSLO001-12	MNH, SI	SVN
Clubionidae	*Clubiona*	*neglecta*	00786558	SPSLO033-12	MNH, SI	SVN
Corinnidae	*Phrurolithus*	*minimus*	00786559	SPSLO034-12	MNH, SI	SVN
Filistatidae	*Filistata*	*insidiatrix*	00786560	SPSLO040-12	MNH, SI	SVN
Araneidae	*Araneus*	*sturmi*	00786561	SPSLO017-12	MNH, SI	SVN
Agelenidae	*Coelotes*	*terrestris*	00786563	SPSLO003-12	MNH, SI	SVN
Gnaphosidae	*Nomisia*	*exornata*	00786564	SPSLO044-12	MNH, SI	SVN
Linyphiidae	*Gonatium*	*hilare*	00786565	SPSLO053-12	MNH, SI	SVN
Clubionidae	*Clubiona*	*germanica*	00786566	SPSLO032-12	MNH, SI	SVN
Linyphiidae	*Frontinellina*	*frutetorum*	00786567	SPSLO052-12	MNH, SI	SVN
Araneidae	*Araneus*	*alsine*	00786568	SPSLO012-12	MNH, SI	SVN
Linyphiidae	*Megalepthyphantes*	*collinus*	00786569	SPSLO057-12	MNH, SI	SVN
Araneidae	*Aculepeira*	*ceropegia*	00786570	SPSLO011-12	MNH, SI	SVN
Amaurobiidae	*Amaurobius*	*erberi*	00786571	SPSLO007-12	MNH, SI	SVN
Araneidae	*Araneus*	*quadratus*	00786572	SPSLO016-12	MNH, SI	SVN
Araneidae	*Cyclosa*	*conica*	00786573	SPSLO022-12	MNH, SI	SVN
Agelenidae	*Agelena*	*labyrinthica*	00786574	SPSLO002-12	MNH, SI	SVN
Araneidae	*Araneus*	*marmoreus*	00786575	SPSLO015-12	MNH, SI	SVN
Gnaphosidae	*Scotophaeus*	*scutulatus*	00786576	SPSLO046-12	MNH, SI	SVN
Araneidae	*Cercidia*	*prominens*	00786577	SPSLO020-12	MNH, SI	SVN
Gnaphosidae	*Haplodrassus*	*silvestris*	00786578	SPSLO043-12	MNH, SI	SVN
Araneidae	*Gibbaranea*	*bituberculata*	00786579	SPSLO023-12	MNH, SI	SVN
Atypidae	*Atypus*	*piceus*	00786580	SPSLO031-12	MNH, SI	SVN
Dysderidae	*Dasumia*	*canestrinii*	00786581	SPSLO038-12	MNH, SI	SVN
Araneidae	*Parazygiella*	*montana*	00786582	SPSLO028-12	MNH, SI	SVN
Agelenidae	*Tegenaria*	*atrica*	00786583	SPSLO006-12	MNH, SI	SVN
Anyphaenidae	*Anyphaena*	*accentuata*	00786584	SPSLO009-12	MNH, SI	SVN
Amaurobiidae	*Amaurobius*	*jugorum*	00786585	SPSLO008-12	MNH, SI	SVN
Agelenidae	*Inermocoelotes*	*anoplus*	00786586	SPSLO005-12	MNH, SI	SVN
Linyphiidae	*Drapetisca*	*socialis*	00786587	SPSLO050-12	MNH, SI	SVN
Gnaphosidae	*Zelotes*	*subterraneus*	00786588	SPSLO048-12	MNH, SI	CHE
Araneidae	*Argiope*	*bruennichi*	00786589	SPSLO019-12	MNH, SI	SVN
Araneidae	*Mangora*	*acalypha*	00786590	SPSLO026-12	MNH, SI	SVN
Araneidae	*Leviellus*	*thorelli*	00786591	SPSLO025-12	MNH, SI	SVN
Gnaphosidae	*Phaeocedus*	*braccatus*	00786592	SPSLO045-12	MNH, SI	SVN
Araneidae	*Araneus*	*diadematus*	00786593	SPSLO014-12	MNH, SI	SVN
Araneidae	*Nuctenea*	*umbratica*	00786594	SPSLO027-12	MNH, SI	SVN
Araneidae	*Araniella*	*cucurbitina*	00786596	SPSLO018-12	MNH, SI	SVN
Araneidae	*Singa*	*nitidula*	00786597	SPSLO029-12	MNH, SI	SVN
Linyphiidae	*Kaestneria*	*dorsalis*	00786598	SPSLO054-12	MNH, SI	SVN
Agelenidae	*Histopona*	*torpida*	00786599	SPSLO004-12	MNH, SI	SVN

Araneidae	*Araneus*	*angulatus*	ARA0001	SPSLO326-13	EZ LAB	SVN
Linyphiidae	*Linyphia*	*triangularis*	ARA0004	SPSLO327-13	EZ LAB	SVN
Theridiidae	*Steatoda*	*bipunctata*	ARA0029	SPSLO328-13	EZ LAB	SVN
Araneidae	*Araneus*	*marmoreus*	ARA0030	SPSLO329-13	EZ LAB	SVN
Thomisidae	*Ebrechtella*	*tricuspidata*	ARA0033	SPSLO330-13	EZ LAB	SVN
Salticidae	*Evarcha*	*falcata*	ARA0037	SPSLO331-13	EZ LAB	SVN
Tetragnathidae	*Tetragnatha*	*nigrita*	ARA0041	SPSLO332-13	EZ LAB	SVN
Theridiidae	*Theridion*	*varians*	ARA0043	SPSLO333-13	EZ LAB	SVN
Theridiidae	*Steatoda*	*triangulosa*	ARA0046	SPSLO334-13	EZ LAB	SVN
Araneidae	*Argiope*	*bruennichi*	ARA0048	SPSLO335-13	EZ LAB	SVN
Araneidae	*Araneus*	*diadematus*	ARA0050	SPSLO336-13	EZ LAB	SVN
Miturgidae	*Cheiracanthium*	*punctorium*	ARA0056	SPSLO337-13	EZ LAB	SVN
Salticidae	*Evarcha*	*arcuata*	ARA0062	SPSLO338-13	EZ LAB	SVN
Agelenidae	*Histopona*	*torpida*	ARA0063	SPSLO339-13	EZ LAB	SVN
Lycosidae	*Pardosa*	*cf. lugubris*	ARA0065	SPSLO340-13	EZ LAB	SVN
Agelenidae	*Tegenaria*	*atrica*	ARA0076	SPSLO341-13	EZ LAB	SVN
Thomisidae	*Misumena*	*vatia*	ARA0081	SPSLO342-13	EZ LAB	SVN
Gnaphosidae	*Scotophaeus*	*scutulatus*	ARA0082	SPSLO343-13	EZ LAB	SVN
Araneidae	*Mangora*	*acalypha*	ARA0107	SPSLO344-13	EZ LAB	SVN
Araneidae	*Araneus*	*sturmi*	ARA0108	SPSLO345-13	EZ LAB	SVN
Amaurobiidae	*Amaurobius*	*erberi*	ARA0120	SPSLO347-13	EZ LAB	SVN
Filistatidae	*Filistata*	*insidiatrix*	ARA0122	SPSLO348-13	EZ LAB	SVN
Theridiidae	*Episinus*	*truncatus*	ARA0132	SPSLO349-13	EZ LAB	SVN
Theridiidae	*Enoplognatha*	*afrodite*	ARA0135	SPSLO350-13	EZ LAB	SVN
Theridiidae	*Theridion*	*pinastri*	ARA0136	SPSLO351-13	EZ LAB	SVN
Theridiidae	*Crustulina*	*scabripes*	ARA0137	SPSLO352-13	EZ LAB	SVN
Linyphiidae	*Neriene*	*furtiva*	ARA0145	SPSLO353-13	EZ LAB	SVN
Linyphiidae	*Neriene*	*radiata*	ARA0152	SPSLO354-13	NMBE	CHE
Gnaphosidae	*Zelotes*	*subterraneus*	ARA0156	SPSLO355-13	NMBE	CHE
Linyphiidae	*Scotinotylus*	*alpigena*	ARA0163	SPSLO356-13	NMBE	CHE
Linyphiidae	*Erigonella*	*ignobilis*	ARA0164	SPSLO357-13	NMBE	CHE
Araneidae	*Stroemiellus*	*stroemi*	ARA0169	SPSLO358-13	EZ LAB	SVN
Atypidae	*Atypus*	*piceus*	ARA0174	SPSLO359-13	EZ LAB	SVN
Gnaphosidae	*Zelotes*	*latreillei*	ARA0191	SPSLO360-13	EZ LAB	SVN
Zoridae	*Zora*	*spinimana*	ARA0192	SPSLO361-13	NMBE	CHE
Araneidae	*Araneus*	*quadratus*	ARA0198	SPSLO362-13	NMBE	CHE
Theridiidae	*Robertus*	*lividus*	ARA0201	SPSLO363-13	NMBE	CHE
Linyphiidae	*Incestophantes*	*frigidus*	ARA0211	SPSLO364-13	NMBE	CHE
Linyphiidae	*Macrargus*	*rufus*	ARA0213	SPSLO365-13	NMBE	CHE
Linyphiidae	*Bolyphantes*	*luteolus*	ARA0214	SPSLO366-13	NMBE	CHE
Linyphiidae	*Agyneta*	*cauta*	ARA0225	SPSLO367-13	NMBE	CHE
Linyphiidae	*Caracladus*	*avicula*	ARA0231	SPSLO368-13	NMBE	CHE
Agelenidae	*Agelena*	*labyrinthica*	ARA0239	SPSLO369-13	EZ LAB	SVN
Uloboridae	*Hyptiotes*	*paradoxus*	ARA0241	SPSLO370-13	EZ LAB	SVN
Clubionidae	*Clubiona*	*terrestris*	ARA0242	SPSLO371-13	EZ LAB	SVN
Lycosidae	*Pardosa*	*riparia*	ARA0243	SPSLO372-13	NMBE	CHE
Dysderidae	*Dysdera*	*ninnii*	ARA0244	SPSLO373-13	EZ LAB	SVN
Linyphiidae	*Agyneta*	*affinis*	ARA0245	SPSLO374-13	NMBE	CHE
Linyphiidae	*Centromerus*	*subalpinus*	ARA0250	SPSLO375-13	NMBE	CHE
Linyphiidae	*Erigone*	*dentipalpis*	ARA0256	SPSLO376-13	NMBE	CHE
Linyphiidae	*Erigone*	*atra*	ARA0257	SPSLO377-13	NMBE	CHE
Linyphiidae	*Agyneta*	*fuscipalpa*	ARA0268	SPSLO378-13	NMBE	CHE
Linyphiidae	*Micrargus*	*alpinus*	ARA0270	SPSLO379-13	NMBE	CHE
Linyphiidae	*Mansuphantes*	*fragilis*	ARA0276	SPSLO380-13	NMBE	CHE
Theridiidae	*Robertus*	*truncorum*	ARA0280	SPSLO381-13	NMBE	CHE
Linyphiidae	*Minyriolus*	*pusillus*	ARA0285	SPSLO382-13	NMBE	CHE
Thomisidae	*Xysticus*	*lineatus*	ARA0304	SPSLO383-13	EZ LAB	SVN
Theridiidae	*Parasteatoda*	*tepidariorum*	ARA0329	SPSLO384-13	EZ LAB	SVN
Thomisidae	*Xysticus*	*tenebrosus*	ARA0332	SPSLO385-13	EZ LAB	SVN
Gnaphosidae	*Callilepis*	*schuszteri*	ARA0333	SPSLO386-13	EZ LAB	SVN

Philodromidae	*Tibellus*	*macellus*	ARA0334	SPSLO387-13	EZ LAB	SVN
Lycosidae	*Xerolycosa*	*nemoralis*	ARA0335	SPSLO388-13	NMBE	CHE
Linyphiidae	*Tenuiphantes*	*flavipes*	ARA0336	SPSLO389-13	NMBE	CHE
Gnaphosidae	*Drassyllus*	*villicus*	ARA0337	SPSLO390-13	EZ LAB	SVN
Lycosidae	*Aulonia*	*albimana*	ARA0338	SPSLO391-13	EZ LAB	SVN
Agelenidae	*Inermocoelotes*	*anoplus*	ARA0339	SPSLO392-13	EZ LAB	SVN
Araneidae	*Zilla*	*diodia*	ARA0342	SPSLO393-13	EZ LAB	SVN
Theridiidae	*Heterotheridion*	*nigrovariegatum*	ARA0343	SPSLO394-13	EZ LAB	SVN
Philodromidae	*Philodromus*	*pulchellus*	ARA0344	SPSLO395-13	EZ LAB	SVN
Lycosidae	*Pardosa*	*blanda*	ARA0345	SPSLO396-13	NMBE	CHE
Linyphiidae	*Pityohyphantes*	*phrygianus*	ARA0347	SPSLO397-13	NMBE	CHE
Lycosidae	*Pardosa*	*oreophila*	ARA0348	SPSLO398-13	NMBE	CHE
Lycosidae	*Alopecosa*	*pulverulenta*	ARA0349	SPSLO399-13	NMBE	CHE
Araneidae	*Gibbaranea*	*bituberculata*	ARA0350	SPSLO400-13	EZ LAB	SVN
Philodromidae	*Philodromus*	*vagulus*	ARA0351	SPSLO401-13	NMBE	CHE
Linyphiidae	*Neriene*	*clathrata*	ARA0352	SPSLO402-13	EZ LAB	SVN
Araneidae	*Leviellus*	*thorelli*	ARA0353	SPSLO403-13	EZ LAB	SVN
Araneidae	*Parazygiella*	*montana*	ARA0354	SPSLO404-13	NMBE	CHE
Araneidae	*Aculepeira*	*ceropegia*	ARA0355	SPSLO405-13	NMBE	CHE
Araneidae	*Cercidia*	*prominens*	ARA0356	SPSLO406-13	EZ LAB	SVN
Araneidae	*Mangora*	*acalypha*	ARA0357	SPSLO407-13	EZ LAB	SVN
Linyphiidae	*Gonatium*	*rubens*	ARA0358	SPSLO408-13	NMBE	CHE
Linyphiidae	*Nematogmus*	*sanguinolentus*	ARA0359	SPSLO409-13	NMBE	CHE
Linyphiidae	*Maso*	*sundevalli*	ARA0360	SPSLO410-13	NMBE	CHE
Linyphiidae	*Mughiphantes*	*mughi*	ARA0361	SPSLO411-13	NMBE	CHE
Linyphiidae	*Tapinocyba*	*affinis*	ARA0362	SPSLO412-13	NMBE	CHE
Linyphiidae	*Ceratinella*	*brevipes*	ARA0363	SPSLO413-13	NMBE	CHE
Sparassidae	*Micrommata*	*virescens*	ARA0365	SPSLO414-13	NMBE	CHE
Theridiidae	*Neottiura*	*bimaculata*	ARA0366	SPSLO415-13	NMBE	CHE
Theridiidae	*Enoplognatha*	*ovata*	ARA0367	SPSLO416-13	NMBE	CHE
Lycosidae	*Hogna*	*radiata*	ARA0368	SPSLO417-13	EZ LAB	SVN
Linyphiidae	*Microlinyphia*	*impigra*	ARA0369	SPSLO418-13	NMBE	CHE
Araneidae	*Hypsosinga*	*sanguinea*	ARA0370	SPSLO419-13	NMBE	CHE
Clubionidae	*Clubiona*	*reclusa*	ARA0371	SPSLO420-13	NMBE	CHE
Linyphiidae	*Mughiphantes*	*cornutus*	ARA0372	SPSLO421-13	NMBE	CHE
Tetragnathidae	*Metellina*	*mengei*	ARA0373	SPSLO422-13	NMBE	CHE
Linyphiidae	*Tenuiphantes*	*jacksonoides*	ARA0374	SPSLO423-13	NMBE	CHE
Linyphiidae	*Panamomops*	*tauricornis*	ARA0375	SPSLO424-13	NMBE	CHE
Thomisidae	*Tmarus*	*piger*	ARA0376	SPSLO425-13	EZ LAB	SVN
Salticidae	*Sitticus*	*rupicola*	ARA0378	SPSLO426-13	NMBE	CHE
Dictynidae	*Dictyna*	*arundinacea*	ARA0379	SPSLO427-13	NMBE	CHE
Araneidae	*Cyclosa*	*conica*	ARA0380	SPSLO428-13	NMBE	CHE
Araneidae	*Agalenatea*	*redii*	ARA0381	SPSLO429-13	EZ LAB	SVN
Salticidae	*Heliophanus*	*cupreus*	ARA0382	SPSLO430-13	NMBE	CHE
Pisauridae	*Pisaura*	*mirabilis*	ARA0383	SPSLO431-13	NMBE	CHE
Hahniidae	*Antistea*	*elegans*	ARA0384	SPSLO432-13	NMBE	CHE
Salticidae	*Sibianor*	*aurocinctus*	ARA0385	SPSLO433-13	NMBE	CHE
Linyphiidae	*Gonatium*	*rubellum*	ARA0386	SPSLO434-13	NMBE	CHE
Araneidae	*Nuctenea*	*umbratica*	ARA0387	SPSLO435-13	NMBE	CHE
Lycosidae	*Trochosa*	*spinipalpis*	ARA0388	SPSLO436-13	EZ LAB	SVN
Thomisidae	*Xysticus*	*cristatus*	ARA0389	SPSLO437-13	NMBE	CHE
Thomisidae	*Synema*	*globosum*	ARA0390	SPSLO438-13	NMBE	CHE
Liocranidae	*Agroeca*	*brunnea*	ARA0392	SPSLO439-13	EZ LAB	SVN
Araneidae	*Araniella*	*opisthographa*	ARA0393	SPSLO440-13	EZ LAB	SVN
Tetragnathidae	*Metellina*	*merianae*	ARA0394	SPSLO441-13	EZ LAB	SVN
Salticidae	*Heliophanus*	*flavipes*	ARA0396	SPSLO442-13	EZ LAB	SVN
Linyphiidae	*Linyphia*	*hortensis*	ARA0397	SPSLO443-13	NMBE	CHE
Linyphiidae	*Oryphantes*	*angulatus*	ARA0398	SPSLO444-13	NMBE	CHE
Hahniidae	*Hahnia*	*difficilis*	ARA0399	SPSLO445-13	NMBE	CHE
Philodromidae	*Philodromus*	*cespitum*	ARA0400	SPSLO446-13	EZ LAB	SVN

Linyphiidae	*Tiso*	*vagans*	ARA0401	SPSLO447-13	NMBE	CHE
Thomisidae	*Xysticus*	*audax*	ARA0402	SPSLO448-13	EZ LAB	SVN
Linyphiidae	*Agyneta*	*orites*	ARA0403	SPSLO449-13	NMBE	CHE
Philodromidae	*Philodromus*	*praedatus*	ARA0404	SPSLO450-13	NMBE	CHE
Linyphiidae	*Drapetisca*	*socialis*	ARA0405	SPSLO451-13	EZ LAB	SVN
Lycosidae	*Pardosa*	*palustris*	ARA0406	SPSLO452-13	NMBE	CHE
Linyphiidae	*Obscuriphantes*	*obscurus*	ARA0407	SPSLO453-13	NMBE	CHE
Linyphiidae	*Pocadicnemis*	*juncea*	ARA0409	SPSLO454-13	NMBE	CHE
Linyphiidae	*Minicia*	*marginella*	ARA0410	SPSLO455-13	NMBE	CHE
Linyphiidae	*Mughiphantes*	*mughi*	ARA0411	SPSLO456-13	NMBE	CHE
Lycosidae	*Pardosa*	*amentata*	ARA0413	SPSLO457-13	NMBE	CHE
Linyphiidae	*Tenuiphantes*	*tenebricola*	ARA0414	SPSLO458-13	NMBE	CHE
Linyphiidae	*Tenuiphantes*	*mengei*	ARA0415	SPSLO459-13	NMBE	CHE
Theridiidae	*Phylloneta*	*sisyphia*	ARA0416	SPSLO460-13	NMBE	CHE
Linyphiidae	*Tenuiphantes*	*cristatus*	ARA0418	SPSLO461-13	NMBE	CHE
Linyphiidae	*Agyneta*	*rurestris*	ARA0419	SPSLO462-13	EZ LAB	SVN
Linyphiidae	*Tenuiphantes*	*alacris*	ARA0420	SPSLO463-13	NMBE	CHE
Linyphiidae	*Centromerus*	*pabulator*	ARA0421	SPSLO464-13	NMBE	CHE
Linyphiidae	*Tiso*	*aestivus*	ARA0422	SPSLO465-13	NMBE	CHE
Dictynidae	*Dictyna*	*uncinata*	ARA0423	SPSLO466-13	EZ LAB	SVN
Thomisidae	*Thomisus*	*onustus*	ARA0426	SPSLO467-13	EZ LAB	SVN
Agelenidae	*Malthonica*	*silvestris*	ARA0427	SPSLO468-13	EZ LAB	SVN
Theridiidae	*Phylloneta*	*impressa*	ARA0428	SPSLO469-13	NMBE	CHE
Linyphiidae	*Agnyphantes*	*expunctus*	ARA0429	SPSLO470-13	NMBE	CHE
Lycosidae	*Pirata*	*piraticus*	ARA0430	SPSLO471-13	NMBE	CHE
Tetragnathidae	*Metellina*	*segmentata*	ARA0431	SPSLO472-13	EZ LAB	SVN
Linyphiidae	*Lepthyphantes*	*nodifer*	ARA0433	SPSLO473-13	NMBE	CHE
Thomisidae	*Xysticus*	*kochi*	ARA0434	SPSLO474-13	EZ LAB	SVN
Linyphiidae	*Tenuiphantes*	*jacksoni*	ARA0435	SPSLO475-13	NMBE	CHE
Salticidae	*Evarcha*	*michailovi*	ARA0436	SPSLO476-13	EZ LAB	SVN
Theridiidae	*Crustulina*	*guttata*	ARA0437	SPSLO477-13	EZ LAB	SVN
Lycosidae	*Alopecosa*	*trabalis*	ARA0438	SPSLO478-13	EZ LAB	SVN
Salticidae	*Pellenes*	*seriatus*	ARA0439	SPSLO479-13	EZ LAB	SVN
Linyphiidae	*Frontinellina*	*frutetorum*	ARA0441	SPSLO480-13	EZ LAB	SVN
Theridiidae	*Simitidion*	*simile*	ARA0442	SPSLO481-13	EZ LAB	SVN
Liphistiidae	*Liphistius*	*sp*	ARA0240	SPSLO482-15	EZ LAB	MYS

SUPPLEMENTS (AVAILABLE ONLINE)

Supplemental Figure 1. An example of a species page available online at http://ezlab.zrc-sazu.si/dna.

Supplemental Table 1. The results of the barcode matching test.