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Examining the utility of DNA barcodes for the identification of tallgrass prairie flora

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Manuscript received 7 August 2020; revision accepted 1 November 2020.

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Citation: Herzog, S. A., and M. Latvis. 2021. Examining the utility of DNA barcodes for the identification of tallgrass prairie flora. *Applications in Plant Sciences* 9(1): e11405.

doi:10.1002/aps3.11405

PREMISE: The tallgrass prairies of North America are one of the most threatened ecosystems in the world, making efficient species identification essential for understanding and managing diversity. Here, we assess DNA barcoding with high-throughput sequencing as a method for rapid plant species identification.

METHODS: Using herbarium collections representing the tallgrass prairie flora of Oak Lake Field Station, South Dakota, USA, we amplified and examined four common nuclear and plastid barcode regions (ITS, *matK*, *psbA-trnH*, and *rbcl*), individually and in combination, to test their success in identifying samples to family, genus, and species levels using BLAST searches of three databases of varying size.

RESULTS: Concatenated barcodes increased performance, although none were significantly different than single-region barcodes. The plastid region *psbA-trnH* performed significantly more poorly than the others, while barcodes containing ITS performed best. Database size significantly affected identification success at all three taxonomic levels. Confident species-level identification ranged from 8–44% for the global database, 13–56% for the regional database, and 21–80% for the sampled species database, depending on the barcode used.

DISCUSSION: Barcoding was generally successful in identifying tallgrass prairie genera and families, but was of limited use in species-level identifications. Database size was an important factor in successful plant identification. We discuss future directions and considerations for improving the performance of DNA barcoding in tallgrass prairies.

KEY WORDS DNA barcode; grassland; high-throughput sequencing; Northern Great Plains; prairie.

Rapid species identification is vital for understanding the continuing losses in threatened communities (Raven and Miller, 2020). Many monitoring programs have sacrificed identification accuracy due to the time it takes for correct taxa assignment, but in doing so are failing to capture critical information that can be used in further research. Compounding the problem of species identification is the decreasing number of taxonomists in the field (Drew, 2011). Morphological plasticity in populations, cryptic species, and dependency on life stage also hinder efficient species identification (Hebert et al., 2003; Hollingsworth et al., 2016). Although morphology and anatomy are extremely important for species identification, it takes time to assess these plant features and requires an increasingly rare level of expertise. DNA barcoding offers one potential solution, as all that is needed is a small amount of tissue, regardless of developmental stage, to identify the plant.

DNA barcoding uses small segments of DNA to identify species and has been effectively used for species-level identification

in many animal and plant groups (Hebert et al., 2003; CBOL Plant Working Group, 2009), invasive species control (Floyd et al., 2010), forensics (Savolainen and Lundeberg, 1999), and regulatory enforcement (Parveen et al., 2016). Although DNA barcoding is unlikely to replace the field identification of species, it is another tool for when morphological features are not available, whether due to disturbance (e.g., grazing or burning), for the analysis of fecal material (Goldberg et al., 2020), or for the verification of morphology-based identification. Whereas animals have a recognized barcoding region (mitochondrial *CO1*), a universal barcode for plants has remained elusive. The most effective methods use a combination of gene regions, such as a selection of plastid (*matK*, *rbcl*, *rpoC1*, *rpoB*, *psbA-trnH*, and *trnL*) and nuclear (internal transcribed spacer [ITS]) regions; however, many of these regions are not universally usable across all plant groups (Kress et al., 2005; Chase et al., 2007; CBOL Plant Working Group, 2009; Hollingsworth et al., 2009). The advent of high-throughput

sequencing (HTS) has opened up even more potential for the application of DNA barcodes. HTS methods result in shorter read lengths (~300 bp) compared with Sanger sequencing, potentially leading to insufficient variation in sequences to correctly classify closely related species and species with unresolved boundaries (Seberg and Petersen, 2009); however, the advantage of HTS is the ability to sequence numerous regions and individuals at once, reducing time and cost inputs.

Temperate grasslands are one of the most threatened ecosystems globally (Hoekstra et al., 2005) and could benefit from DNA barcoding as a tool for the rapid identification of taxa. Within the United States, the grasslands of the Great Plains have seen large reductions in area and are continuing to be lost at a relatively higher rate than the Brazilian Amazon Rainforest (World Wildlife Fund, 2018). The tallgrass prairie ecosystems of the Great Plains have been particularly hard hit, with over 99% of pre-settlement tallgrass prairie having been lost, primarily to row-crop agriculture and non-native species planted for grazing (Wright and Wimberly, 2013; Lark et al., 2015; Wright et al., 2017). The rate of loss is especially severe in the Northern Great Plains, with South Dakota having the highest rate of grassland conversion (Wright and Wimberly, 2013; Larkin et al., 2015; Wright et al., 2017). The morphological identification of plant species in tallgrass prairies can be difficult due to disturbance (e.g., grazing or burning), inadequate developmental stage at the time of sampling (e.g., not yet at or past anthesis), and the existence of closely related species that require a taxonomic key and magnification to distinguish (e.g., species in Poaceae, Cyperaceae, and Asteraceae). These challenges have led to observer discrepancies in identification of 10–30% of species in grassland systems compared with a 2–10% error rate in other habitat types (Morrison, 2016). Accelerating the pace of accurate species identification within this ecosystem has the potential to hasten subsequent studies of ecosystem function and biodiversity.

As morphological identification is not always feasible or accurate, HTS could be an alternative method allowing many samples to be identified in parallel to remove some of the identification error; however, the high number of closely related species in grasslands of the Northern Great Plains, including many with uncertain boundaries, may render HTS methods ineffective as an identification tool. This study aims to examine the effectiveness of using commonly proposed DNA barcodes as a potential service to identify tallgrass prairie species using HTS methods. Previous studies have found moderate success in grasslands (31–85% species resolution) when using Sanger sequencing to obtain barcode sequences (Braukmann et al., 2017). If HTS approaches can provide confident species identifications, DNA barcoding could be

a rapid and cost-effective tool for the identification of regional flora.

METHODS

Sampling

Leaf material was removed from 286 herbarium samples (C. A. Taylor Herbarium [SDC], South Dakota State University, Brookings, South Dakota, and Oak Lake Field Station herbarium [OLFS], Astoria, South Dakota) based on the OLFS species inventory list (see Appendix 1 for voucher information). Herbarium tissue was used, rather than fresh samples, in an effort to begin documenting historical specimen genetic data for long-term preservation (as discussed in Raven and Miller, 2020). The OLFS species list consists of 269 species in 63 families, with nearly half of the species in four angiosperm families: Asteraceae, Poaceae, Cyperaceae, and Fabaceae (18%, 13%, 10%, and 8% of the total list, respectively).

We prioritized voucher specimens collected at OLFS, choosing the most recent collections for DNA extraction to reduce the amount of degraded DNA and improve sequence amplification (Adams and Sharma, 2010; Staats et al., 2011). For inventoried species lacking vouchers from the OLFS property, we sampled herbarium vouchers from localities near OLFS.

DNA extraction, amplification, and sequencing

From each sample, 0.02–0.03 mg of tissue was used for total genomic DNA extraction using a modified 2× cetyltrimethylammonium bromide (CTAB) approach (Doyle and Doyle, 1987). The DNA extractions were then visualized on agarose gel to assess DNA quality and concentration. Four DNA regions were selected for this study due to their prominence as “universal” plant barcodes: nuclear ITS2, and plastid *rbcLa*, *matK*, and *psbA-trnH* (see Table 1 for primer sequences and references; *psbA-trnH* abbreviated in figures and tables as *trnH*). These primers were selected due to their ability to amplify across angiosperm families and produce amplicon lengths compatible with the Illumina MiSeq (San Diego, California, USA) HTS platform limit of 300-bp paired-end reads (CBOL Plant Working Group, 2009; China Plant BOL Group, 2011; Braukmann et al., 2017).

We followed a modified 16S Illumina library construction protocol (Illumina, 2013) and optimized the annealing temperatures for each primer set using the OligoAnalyzer Tool (Owczarzy et al., 2008). This process consisted of an initial amplification of

TABLE 1. Selected DNA barcoding regions and their primer pairs compatible for high-throughput sequencing.

Region	Primer	Primer sequence from 5' end	Amplicon length (bp)	References
ITS2 (nuclear)	UniPlantF (5')	TGTGAATTGCARRATYCMG	300	Moorhouse-Gann et al., 2018
	UniPlantR (3')	CCCGHYTGAYYTRGGTCDC		
<i>matK</i> (chloroplast)	matK-1F (5')	ACTGTATCGCACTATGTATCA	400–600	Bremer et al., 2002
	matK-4R (3')	GCATCTTTTACCARTAGCGAAG		
<i>rbcLa</i> (chloroplast)	rbcLa-F (5')	ATGTCACCACAAACAGAGACTAAAGC	550	Kress and Erickson, 2007
	rbcLa-R (3')	GTAATAATCAAGTCCACCRGC		
<i>psbA-trnH</i> (chloroplast)	psbA3_f (5')	GTTATGCATGAACGTAATGCTC	500	Sang et al., 1997; Tate and Simpson, 2003
	trnHf_05 (3')	CGCGCATGGTGGATTCAATCC		

target regions using site-specific primers (“PCR 1”), with an additional adapter sequence tag added to the 5′ end of the synthesized oligonucleotide. These tags acted as a binding site for an additional pair of primers to add an 8-bp index sequence in a second round of PCR (“PCR 2”; see Appendix 2 for sequences), allowing for the identification of samples after the amplicons were pooled. To construct the library, Phusion Hot Start II High-Fidelity PCR Master Mix (Thermo Fisher Scientific, Waltham, Massachusetts, USA) and the Nextera XT Index Kit v2 (Illumina) were used. All four amplicons for each specimen were pooled after PCR 1, which gave each individual the same index for later identification while still allowing each region to be identified by primer sequence. Bead cleanup was conducted after PCR 2 to remove unwanted reaction components (e.g., fragments shorter than 50 bp) using HighPrep PCR Clean-up System magnetic beads (MAGBIO, Gaithersburg, Maryland, USA) in an IntegenX Apollo 324 automated library preparation system (Thermo Fisher Scientific). All samples were pooled after PCR 2 to a concentration of 4 nM based on the concentration values determined using a Qubit 3 Fluorometer (Thermo Fisher Scientific). The pooled library was then sequenced in one run with the Illumina MiSeq platform using 300-bp paired-end reads.

The data were received through BaseSpace (cloud-based Illumina software; <https://basespace.illumina.com>), pre-demultiplexed to individual sample, and the index sequences were removed. Raw sequence files were deposited in the National Center for Biotechnology Information (NCBI) Sequence Read Archive database (BioProject accession PRJNA649768). Pooled reads for each individual were run through Fluidigm2PURC (Blischak et al., 2018) using default settings, which trims the sequences and combines paired reads. Because the data were pre-demultiplexed using the Illumina software based on the index sequences, we used a custom script to further group sequences by amplicon based on the primer sequences and then remove primers (locus_assigner; F.-W. Li, Cornell University, personal communication). Consensus sequences were generated and chimeric sequences removed using `purc_recluster2` in Fluidigm2PURC, with clustering values of 0.92 and 0.93, and the largest consensus cluster was used for downstream analysis. Sequences identified as fungal contaminants were removed. Cleaned sequences were then concatenated in all possible combinations between the four single-locus barcodes in Geneious Prime version 2019.2.3 (<https://www.geneious.com>).

BLAST

In order to evaluate the performance of individual regions and concatenated regions (both hereafter referred to as “barcodes”), we constructed three different sequence databases: (1) the entirety of GenBank sequence data, representing a broad range of species (accessed 4 October 2020; Clark et al., 2016); (2) a regional database using South Dakota and regional tallgrass prairie species occurrence data from the Great Plains Regional Herbarium Network (<https://ngpherbaria.org/>) and vouchered sequences from GenBank to create a more realistic scenario for the use of DNA barcodes (i.e., no knowledge of species identity a priori) (accessed 4 October 2020); and (3) only species sampled from OLFs, creating a “best-case scenario” to reduce the amount of closely related species (accessed 4 October 2020). Basic Local Alignment Search Tool (BLAST) (Altschul et al., 1990; Camacho et al., 2009)

was used to find the sequences that best match the generated DNA barcode sequences in each of the databases.

BLAST processing

We retrieved each top hit with the highest *E*-value from the BLAST searches against our three databases and compared them against our vouchered specimens. If multiple top hits were returned, they were filtered to use the ones with highest percentage identity and bitscore. “Confident” successful identification was recorded for species that were always correctly identified by the top results, “ambiguous” identification was assigned when results contained both correct and incorrect species, and an “incorrect” identification was assigned when none of the top hits contained the correct species. Success was determined for family-, genus-, and species-level identification. Family names were generated and species names updated using the Catalogue of Life: 2019 Annual Checklist (Roskov et al., 2019) with `taxize` (Chamberlain and Szocs, 2013; Chamberlain et al., 2020) in R (version 0.9.92; R Core Team, 2018) for both BLAST results and the original OLFs species list. To evaluate the confident identification success between barcodes, we used `prop.test` in the base R package `stats` (version 3.5.1) to run a pairwise Pearson’s chi-squared test statistic (Holm [1979] correction method) on the mean confident correct identification levels for each barcode ($\alpha = 0.05$).

RESULTS

After updating the taxonomic names in `taxize`, we identified 266 distinct species for our 286 samples, as some taxa were combined under the same name and four samples failed to amplify. The *rbclLa* region had the highest amplification success, with 249 retrieved sequences, while *matK* amplification was worst, with only 112 sequences retrieved (Fig. 1). We retrieved 178 sequences of ITS2 and

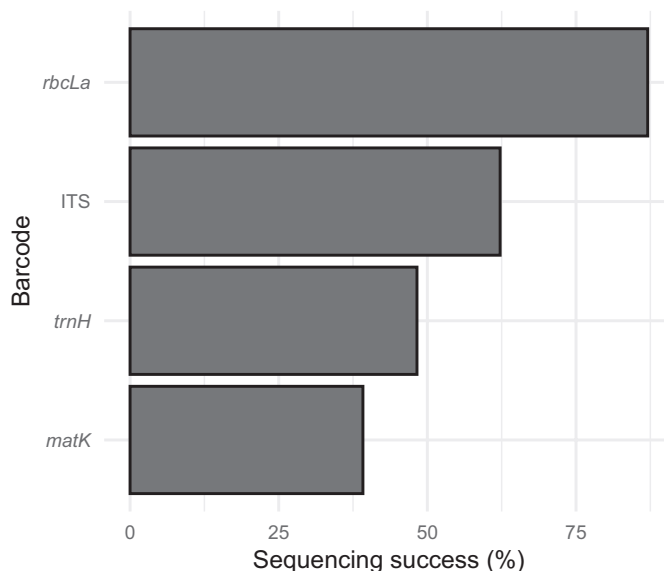


FIGURE 1. Sequence retrieval success of amplicons for 286 tallgrass prairie plant herbarium specimens sampled. *psbA-trnH* is listed as *trnH* on the figure.

138 sequences of *psbA-trnH*. Of our 266 taxa, nine species were not represented in GenBank. Additionally, the coverage of the tested regions in GenBank varied, with 253 of the 266 species represented for the *rbcLa* region (97%), 246 species covered by ITS2 (94%), 239 by *matK* (91%), and 123 by *psbA-trnH* (47%). Species not in databases were still included in the results because we were looking for an overall view of barcoding success for the identification of the regional flora in the context of a potential barcoding service for regional stakeholders.

The GenBank database resulted in 79–98% confident and 0–12% ambiguous family identifications (Fig. 2, Appendix 3). Genus identification rates ranged from 54–78% confident and 0–40% ambiguous. Species identification when using GenBank was the lowest of the three databases, with confident identification rates of 8–44% and ambiguous identification rates of 7–65%. No barcodes yielded a significantly different level of confidence in genus or species identification, but *matK* and ITS2 gave significantly

different rates of confidence in family identification (Figs. 2, 3; see Appendix S1 for table of chi-squared test results). The *matK* and *rbcLa* gene regions were the least successful individual regions for confident species-level identification (10% and 8%, respectively) using the GenBank database as a reference, followed by *psbA-trnH* (23%). The ITS2 region had the highest success (30%) of the single-region barcodes. The concatenation of ITS2, *matK*, and *psbA-trnH* proved to yield the most successful confident species discrimination at 44%.

The regional database resulted in identifications with a significantly higher rate of confidence (average 34%) than GenBank (average 23%). Family identification rates ranged from 75–98% confident, while 0–2% were ambiguous (Fig. 2, Appendix 3). Genus-level identification rates ranged from 42–90% confident, while 1–20% were ambiguous. Using the regional database, ITS2 was again the best-performing single-locus barcode at 48% confident species identifications, followed by *matK* and *rbcLa* at 18% and

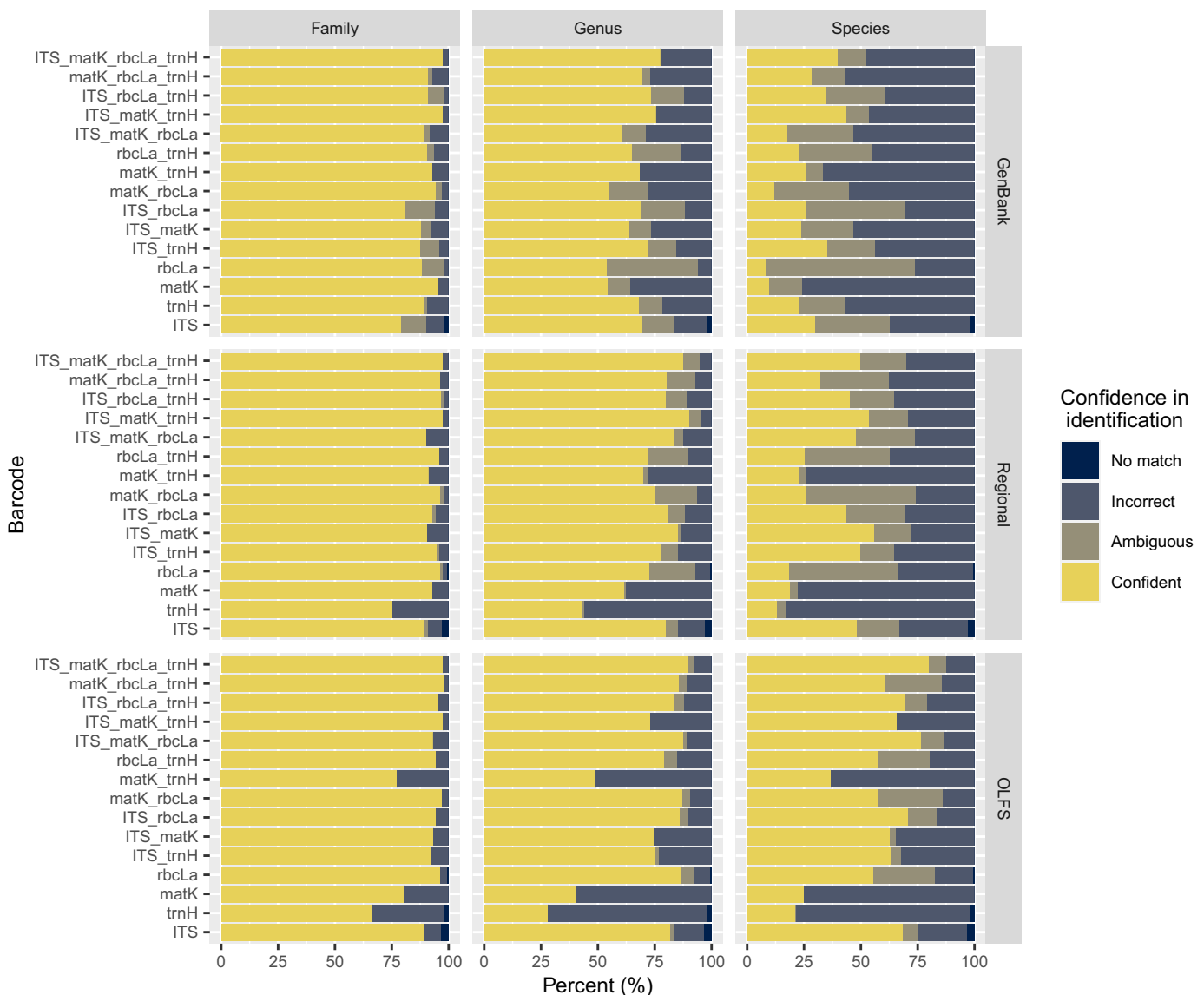


FIGURE 2. Success of identification to family, genus, and species using various barcodes. Barcode names linked with an underscore indicate multi-region barcodes. OLFs, database of species sampled from Oak Lake Field Station.

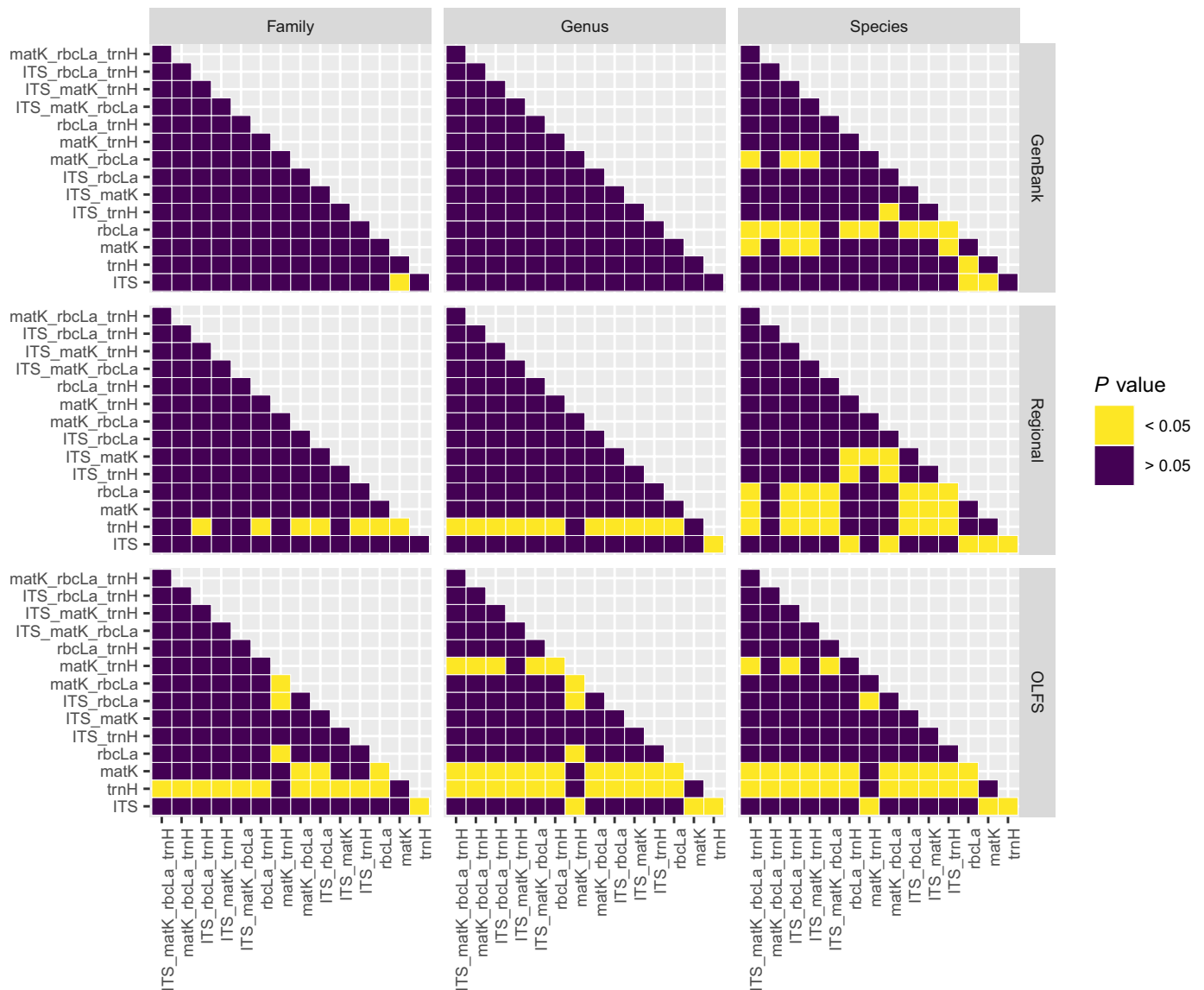


FIGURE 3. Pairwise proportion tests indicate significant differences in the rate of confident identification at the species, genus, and family taxonomic levels for the three tested databases. OLFS, database of species sampled from Oak Lake Field Station.

psbA-trnH at 13%. The ITS2 and *matK* barcodes performed the best, at 56% each. At the family-, genus-, and species-level identification, *psbA-trnH* performed significantly more poorly than the other barcodes (Figs. 2, 3).

When using the smallest database containing only sampled species (average confident identification = 57%), we found confident family identification rates of 66–98%, while none were ambiguous (Fig. 2, Appendix 3). Genus identifications ranged from 28–90% confident and 0–6% ambiguous. As in the other databases, ITS2 performed the best as a single-locus barcode (69% confident species identifications), followed by *rbcLa* (55%), *matK* (25%), and *psb-trnH* (21%). Combining all four barcodes resulted in the highest confident species identification (80%). Barcodes *psbA-trnH* and *matK* were significantly poorer for making confident identifications than the other barcodes across the three taxonomic levels (Figs. 2, 3). The use of the OLFS database resulted in significantly

better confident species identifications than GenBank and the regional database.

Breaking down the results by the four most speciose families in our tallgrass prairie community (Asteraceae, Poaceae, Cyperaceae, and Fabaceae, with 49, 35, 25, and 22 specimens, respectively), we found ITS2 and *rbcLa* had the highest levels of sequence retrieval. The *rbcLa* barcode was most successful for identifying the Asteraceae (30/49), Fabaceae (20/22), and Cyperaceae (23/25), while ITS2 and *psbA-trnH* were most useful for the Poaceae (25/35). The barcode that performed best for confident identifications varied for each family; however, concatenated barcodes containing ITS2 generally performed best (Figs. 4–6, Appendix 4). Identification success was low (<25%) for these families when using GenBank (except when using ITS2 for Fabaceae). Reducing the database size improved the taxonomic resolution for all four families.

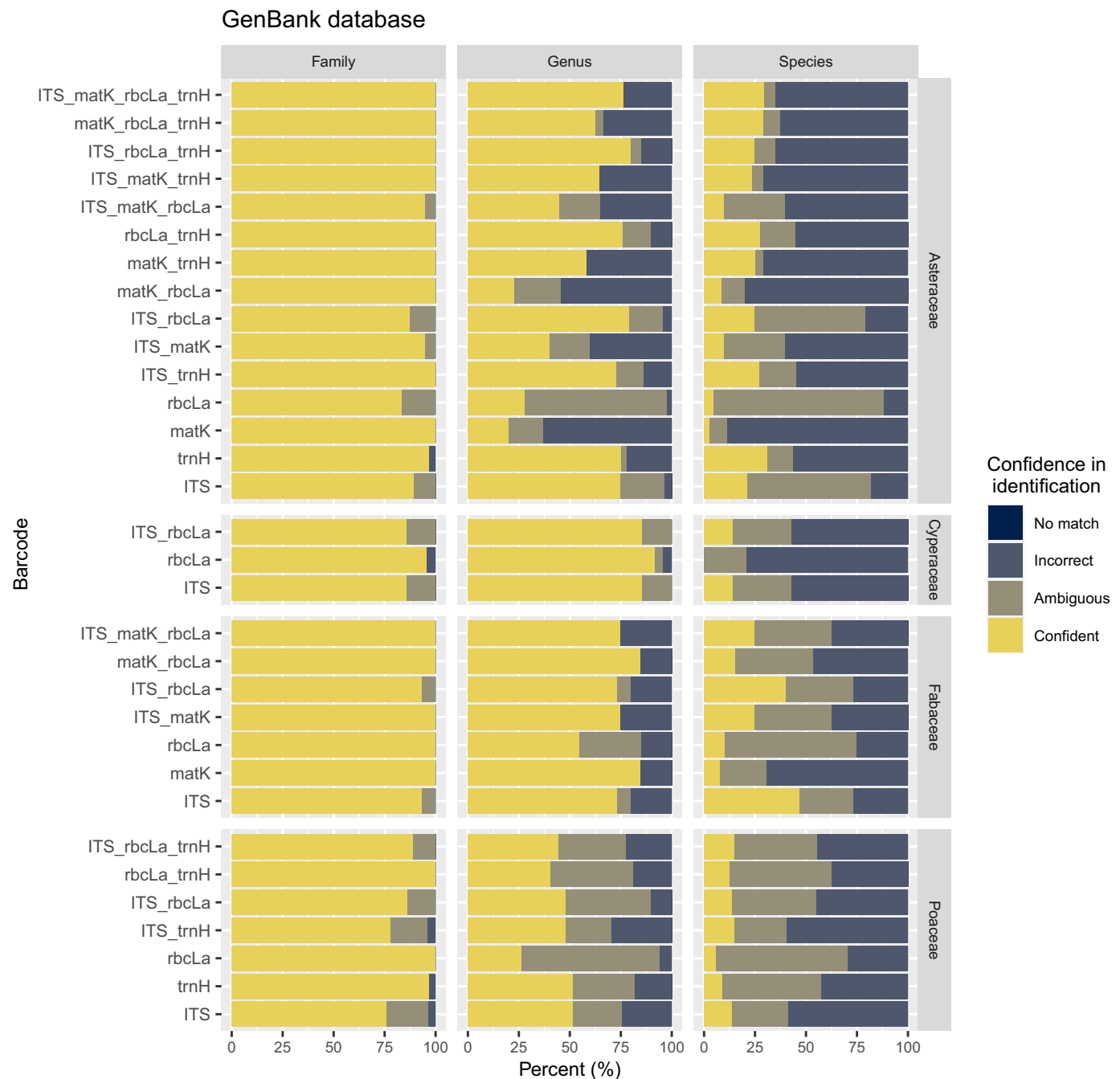


FIGURE 4. Barcode success for the four most diverse families when using GenBank as the reference database (see Figs. 5 and 6 for other databases and Appendix 4 for more information). Only barcodes for which more than five sequences were obtained are shown. [Color figure can be viewed at wileyonlinelibrary.com]

DISCUSSION

Our results indicate DNA barcoding is useful for the identification of taxa at the ranks of genus and family across the tested barcodes but demonstrated only low to moderate success at the species level. We found higher success when using smaller, more focused databases, as was expected due to the presence of more closely related species in larger databases than are found regionally, lowering species resolution, which was also reported by

Parmentier et al. (2013). Reducing database size is especially helpful when identifying closely related species, such as members of the Asteraceae, Poaceae, Fabaceae, and Cyperaceae, as our identifications greatly improved when using smaller databases for our identification of these families (Figs. 4–6). We did see reductions in taxa discrimination at the higher taxonomic levels for some barcodes when using the smaller databases, likely due to removal of closely related species (i.e., congeners). Here, we were particularly interested in the ability of DNA barcodes to differentiate

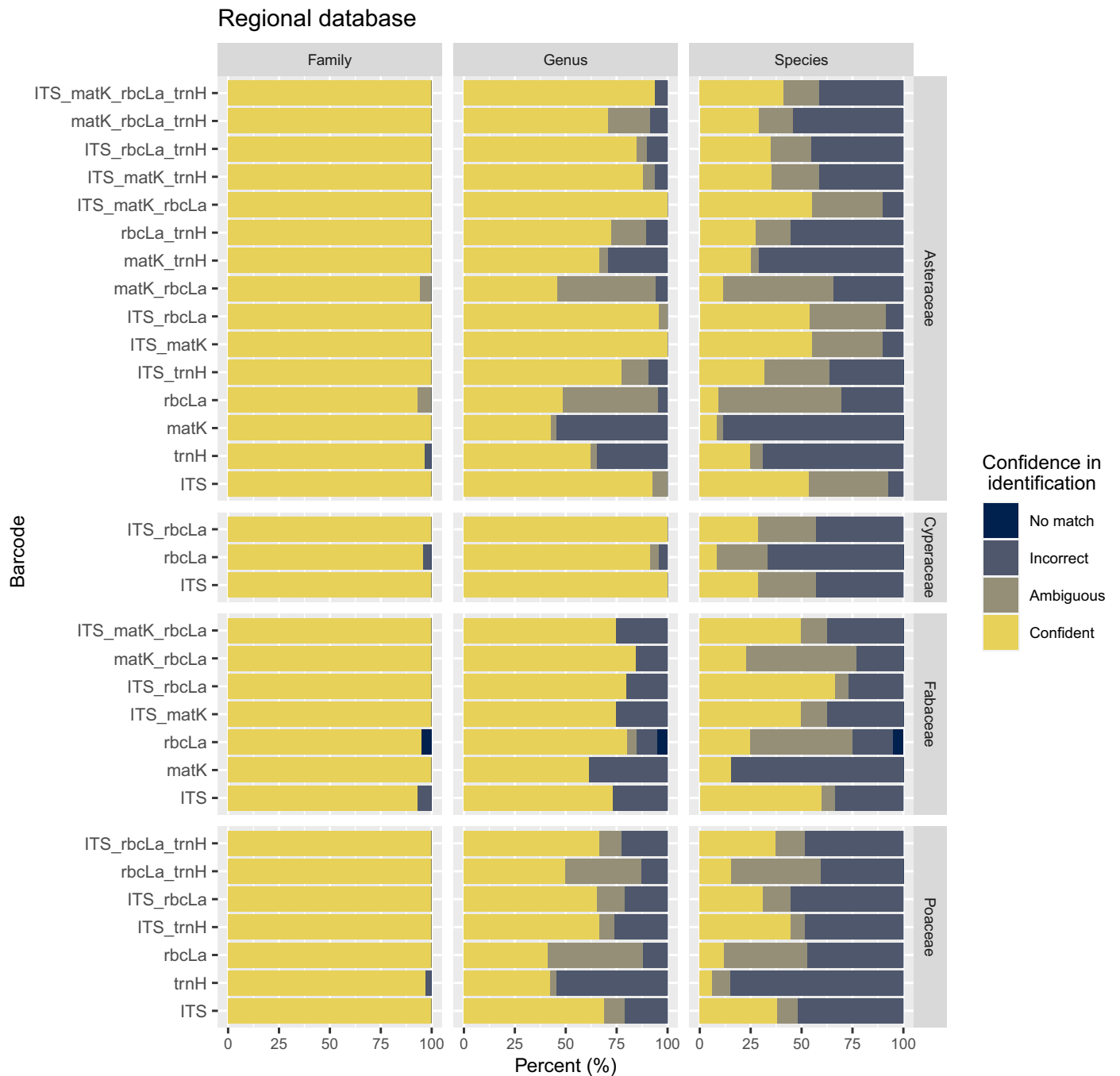


FIGURE 5. Barcode success for the four most diverse families when using a regional database as the reference (see Figs. 4 and 6 for other databases and Appendix 4 for more information). Only barcodes for which more than five sequences were obtained are shown. [Color figure can be viewed at wileyonlinelibrary.com]

plant taxa of the tallgrass prairies of the Northern Great Plains as a possible identification service. As such, using a focused database of only sampled species (as shown in our OLFS-specific database) would require a priori knowledge of species identity; however, we included it to examine the barcode success rates under a “best-case” scenario. Our findings indicate that reducing a regional database of state-wide and regional plant species to a smaller, more focused database would be beneficial if using DNA barcodes as an

identification service. Using a regional database is preferable over a large-scale database such as GenBank.

Generally, single-region barcodes had lower success at species-level identification than multi-region barcodes, in accordance with previous studies (Chase et al., 2007; CBOL Plant Working Group, 2009; China Plant BOL Group, 2011). We found significant variation in the ability of a barcode to successfully identify individuals at the species, genus, and family levels. The nuclear ITS2 region consistently

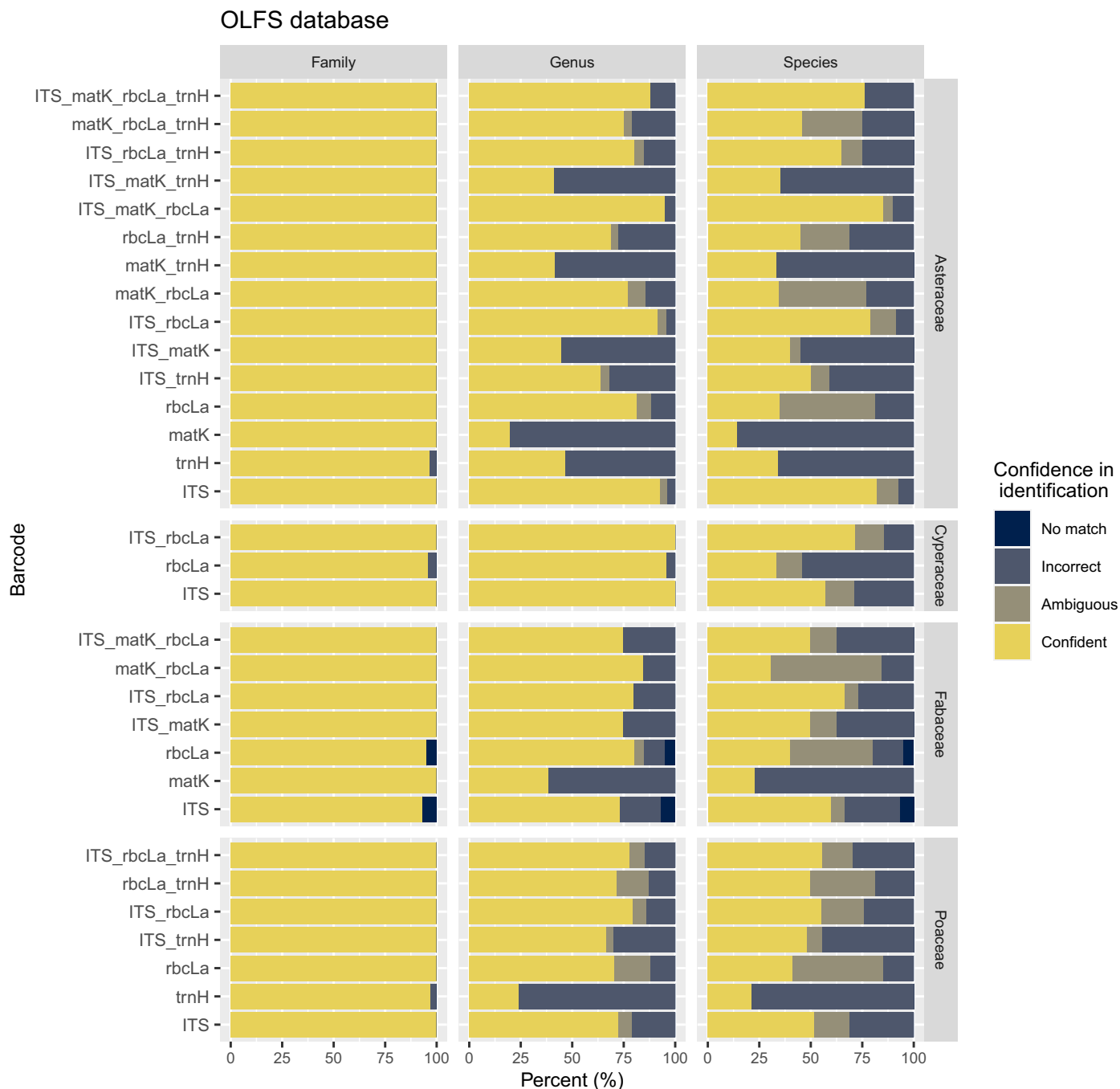


FIGURE 6. Barcode success for the four most diverse families when using the database of species sampled from Oak Lake Field Station (OLFS) (see Figs. 4 and 5 for other databases and Appendix 4 for more information). Only barcodes for which more than five sequences were obtained are shown.

performed best in terms of confident species identification, both as a single-locus barcode and as a member of the top-performing concatenated barcodes. Plastid regions *matK* and *psbA-trnH* were particularly poor at identifying species when used as single-region barcodes.

The low success rate in species discrimination when using *matK* contrasts with other studies, where *matK* was one of the most successful barcoding regions for plant identification (Lahaye et al., 2008; CBOL Plant Working Group, 2009; Braukmann et al., 2017). A major limitation in using *matK* is the difficulty of finding universal primer pairs (CBOL Plant Working Group, 2009; Hollingsworth

et al., 2011). In contrast, although *rbcL* only has moderate identification success, it amplifies well across taxa, in our study and others, which has led to it being promoted as a good candidate for inclusion in a multi-region barcode (CBOL Plant Working Group, 2009; China Plant BOL Group, 2011; Hollingsworth et al., 2011). The combination of *matK* and *rbcL* has been promoted as one of the most promising universal two-region plant barcodes (CBOL Plant Working Group, 2009). The failure of this two-region barcode for species identification in some systems, particularly for closely related taxa (Seberg and Petersen, 2009; Roy et al., 2010; Parmentier

et al., 2013), has resulted in the recommendation to include a nuclear-encoded ribosomal internal transcribed spacer, ITS2 (Chen et al., 2010; China Plant BOL Group, 2011; Hollingsworth et al., 2011). The universal presence of ITS2 across plant taxa and its short length (~350 bp) make it a promising barcode for use in community assessments and HTS approaches for DNA barcoding. Our results correspond with previous studies that ITS performs well at both amplification and taxon discrimination.

It is possible to increase identification success for tallgrass prairie species. Likely the best methodology for DNA barcoding of these species would be through the creation of a specific probe set suited for this plant community to increase the amplification success of some taxonomic groups, particularly for regions such as *matK* as was done by Heckenhauer et al. (2016). A concentrated effort to supplement molecular data from species missing from the database will be beneficial, as will continued effort to collect the genetic information of regional species. Creating a smaller database based on verified voucher specimens, as we have started to do through our sequencing efforts in this project, will result in fewer potential identification errors than occur when using GenBank (although misidentification levels appear to be low in GenBank, as noted by Leray et al. [2019]). Additionally, HTS makes it more feasible to increase the number of sequenced regions to offset the lower identification success created by using shorter reads, leading to the proposal of whole plastid genome sequencing for species discrimination (Parks et al., 2009; Nock et al., 2011; Steele and Pires, 2011; Kane et al., 2012). Nuclear probe sets such as Angiosperms353, which targets 353 nuclear single protein-coding regions, might be promising, as these amplified regions are variable at shallow taxonomic levels (Johnson et al., 2018; Larridon et al., 2020). The increased number of regions returned with HTS also allows for the inclusion of chloroplast regions, in addition to nuclear, potentially increasing the resolution of species identification. This could be particularly helpful for species with ambiguous species boundaries or historical hybridization events, as chloroplast genomes are generally inherited maternally and nuclear genomes are inherited biparentally (Rieseberg and Soltis, 1991; Soltis and Kuzoff, 1995).

Our results indicate there is potential for the use of DNA barcoding to identify tallgrass prairie plant species of the Northern Great Plains using HTS methods, particularly at the family and genus levels; however, species-level identification with these barcoding regions could be limiting, depending on the resolution needed. The optimization of primers for prairie species and the addition of missing species in a regional database are promising future directions that will likely increase successful identification at these shallow taxonomic scales.

ACKNOWLEDGMENTS

The authors thank the South Dakota State University (SDSU) Genomics Sequencing Facility and SDSU Research Computing Group for genomics and computational expertise. We thank SDSU Oak Lake Field Station and C. A. Taylor Herbarium for the destructive sampling of herbarium specimens. We thank F.-W. Li (Cornell University), C. Rothfels (University of California, Berkeley), and D. Tank (University of Idaho) for advice regarding Fluidigm2PURC and PURC. Financial support was provided by a U.S. Department of Agriculture National Institute of Food and Agriculture grant (NIFA 1016764).

AUTHOR CONTRIBUTION

M.L. conceived of the study. S.A.H. performed sample preparation, analyzed the data, and wrote the manuscript with assistance from M.L. All authors approved the final manuscript.

DATA AVAILABILITY

The raw Illumina output files have been uploaded to the National Center for Biotechnology Information Sequence Read Archive database (BioProject accession PRJNA649768).

SUPPORTING INFORMATION

Additional Supporting Information may be found online in the supporting information tab for this article.

APPENDIX S1. *P* values from pairwise chi-squared tests between each barcode's confident correct species identification. Barcodes were compared within each database.

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APPENDIX 1. Herbarium voucher information of sampled tallgrass prairie plants.

Family	Species	Collection	Herbarium	BioSample accession
Amaryllidaceae	<i>Allium stellatum</i>	Mixon s.n.	OLFS	SAMN15679782
Anacardiaceae	<i>Rhus glabra</i>	Larson 6925	OLFS	SAMN15679923
Anacardiaceae	<i>Toxicodendron rydbergii</i>	Larson 11716	OLFS	SAMN15679861
Apiaceae	<i>Cicuta bulbifera</i>	Beauzay 323	OLFS	SAMN15679813
Apiaceae	<i>Cicuta maculata</i>	Beauzay 332	SDC	SAMN15679650
Apiaceae	<i>Cryptotaenia canadensis</i>	Ode 84-102	OLFS	SAMN15679770
Apiaceae	<i>Osmorhiza longistylis</i>	Stahnke s.n.	SDC	SAMN15679651
Apiaceae	<i>Osmorhiza longistylis</i>	Larson 8724	OLFS	SAMN15679888
Apiaceae	<i>Sium suave</i>	Beauzay 322	SDC	SAMN15679727
Apiaceae	<i>Zizia aptera</i>	Troelstrup s.n.	SDC	SAMN15679726
Apiaceae	<i>Zizia aurea</i>	Jensen s.n.	SDC	SAMN15679725
Apocynaceae	<i>Apocynum cannabinum</i>	King 94	OLFS	SAMN15679798
Apocynaceae	<i>Apocynum cannabinum</i>	Stahnke s.n.	SDC	SAMN15679724
Apocynaceae	<i>Apocynum cannabinum</i>	Jensen s.n.	SDC	SAMN15679723
Apocynaceae	<i>Asclepias incarnata</i>	Stahnke s.n.	SDC	SAMN15679722
Apocynaceae	<i>Asclepias incarnata</i>	Beauzay 327	SDC	SAMN15679721
Apocynaceae	<i>Asclepias syriaca</i>	Mixon s.n.	OLFS	SAMN15679797
Apocynaceae	<i>Asclepias verticillata</i>	Jensen s.n.	SDC	SAMN15679720
Apocynaceae	<i>Asclepias verticillata</i>	Troelstrup s.n.	SDC	SAMN15679719
Araceae	<i>Lemna trisulca</i>	Larson 9016	OLFS	SAMN15679835
Araceae	<i>Lemna turionifera</i>	Fredrickson s.n.	OLFS	SAMN15679834
Asparagaceae	<i>Maianthemum stellatum</i>	Larson 8750	OLFS	SAMN15679873
Asteraceae	<i>Achillea millefolium</i>	Beauzay 296	OLFS	SAMN15679781
Asteraceae	<i>Agoseris glauca</i>	Pooler 173	OLFS	SAMN15679779
Asteraceae	<i>Ambrosia artemisiifolia</i>	Larson 9917	OLFS	SAMN15679778
Asteraceae	<i>Ambrosia psilostachya</i>	Larson 9922	OLFS	SAMN15679777
Asteraceae	<i>Artemisia frigida</i>	Roemmich 114	OLFS	SAMN15679776
Asteraceae	<i>Artemisia ludoviciana</i>	Taylor 7506	OLFS	SAMN15679774
Asteraceae	<i>Artemisia ludoviciana</i>	Buckert s.n.	SDC	SAMN15679775
Asteraceae	<i>Bidens frondosa</i>	Sargent s.n.	OLFS	SAMN15679795
Asteraceae	<i>Carduus nutans</i>	Johnson 419	OLFS	SAMN15679773
Asteraceae	<i>Cirsium arvense</i>	Mixon s.n.	OLFS	SAMN15679772
Asteraceae	<i>Cronquistianthus bulliferus</i>	Bauer 042	OLFS	FAILED
Asteraceae	<i>Echinacea angustifolia</i>	Jensen s.n.	SDC	SAMN15679715
Asteraceae	<i>Echinacea angustifolia</i>	Jensen s.n.	SDC	SAMN15679716
Asteraceae	<i>Erigeron canadensis</i>	Law 105	OLFS	SAMN15679771
Asteraceae	<i>Erigeron philadelphicus</i>	Larson 8980	OLFS	SAMN15679791
Asteraceae	<i>Erigeron strigosus</i>	Taylor s.n.	OLFS	SAMN15679790
Asteraceae	<i>Eupatorium perfoliatum</i>	Anders 24	OLFS	SAMN15679759
Asteraceae	<i>Euthamia graminifolia</i>	Ode s.n.	OLFS	SAMN15679758
Asteraceae	<i>Eutrochium maculatum</i>	Beauzay 326	SDC	SAMN15679714
Asteraceae	<i>Grindelia squarrosa</i>	Mixon s.n.	OLFS	SAMN15679789
Asteraceae	<i>Helenium autumnale</i>	Stahnke s.n.	SDC	SAMN15679713
Asteraceae	<i>Helianthus grosseserratus</i>	Larson s.n.	OLFS	SAMN15679787
Asteraceae	<i>Helianthus maximiliani</i>	Jensen s.n.	SDC	SAMN15679712
Asteraceae	<i>Helianthus maximiliani</i>	Law 73	OLFS	SAMN15679786
Asteraceae	<i>Helianthus nuttallii</i>	Larson 11732	OLFS	SAMN15679788
Asteraceae	<i>Heliopsis helianthoides</i>	Jensen s.n.	SDC	SAMN15679711
Asteraceae	<i>Liatris aspera</i>	Stahnke s.n.	SDC	SAMN15679709
Asteraceae	<i>Liatris punctata</i>	Mixon s.n.	OLFS	SAMN15679785
Asteraceae	<i>Lygodesmia juncea</i>	Troelstrup s.n.	SDC	SAMN15679708
Asteraceae	<i>Matricaria discoidea</i>	Anderson 09	OLFS	SAMN15679898
Asteraceae	<i>Packera paupercula</i>	Larson 8920	OLFS	SAMN15679906
Asteraceae	<i>Packera plattensis</i>	Jensen s.n.	SDC	SAMN15679705
Asteraceae	<i>Packera pseud aurea</i>	Larson 9967	OLFS	FAILED
Asteraceae	<i>Ratibida columnifera</i>	Stahnke s.n.	SDC	SAMN15679707
Asteraceae	<i>Ratibida columnifera</i>	Jensen s.n.	SDC	SAMN15679706
Asteraceae	<i>Ratibida columnifera</i>	Mixon s.n.	OLFS	SAMN15679925
Asteraceae	<i>Rudbeckia laciniata</i>	Larson 6912	OLFS	SAMN15679924
Asteraceae	<i>Silphium perfoliatum</i>	Mixon s.n.	OLFS	SAMN15679876
Asteraceae	<i>Solidago canadensis</i>	Jensen s.n.	SDC	SAMN15679704
Asteraceae	<i>Solidago gigantea</i>	Beauzay 337	SDC	SAMN15679703

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APPENDIX 1. Continued

Family	Species	Collection	Herbarium	BioSample accession
Asteraceae	<i>Solidago missouriensis</i>	Bortem 102	OLFS	SAMN15679875
Asteraceae	<i>Solidago mollis</i>	Stahnke s.n.	SDC	SAMN15679702
Asteraceae	<i>Solidago rigida</i>	Larson 9926	SDC	SAMN15679701
Asteraceae	<i>Symphyotrichum ericoides</i>	Bortnem 110	SDC	SAMN15679718
Asteraceae	<i>Symphyotrichum laeve</i>	Stahnke s.n.	SDC	SAMN15679717
Asteraceae	<i>Taraxacum officinale</i>	Monteith s.n.	OLFS	SAMN15679863
Asteraceae	<i>Tragopogon dubius</i>	Jensen s.n.	SDC	SAMN15679700
Asteraceae	<i>Vernonia fasciculata</i>	Larson 11538	OLFS	SAMN15679848
Asteraceae	<i>Vernonia fasciculata</i>	Jensen s.n.	SDC	SAMN15679699
Balsaminaceae	<i>Impatiens capensis</i>	Beauzay 335	SDC	SAMN15679676
Boraginaceae	<i>Lithospermum canescens</i>	Stahnke s.n.	SDC	SAMN15679678
Boraginaceae	<i>Lithospermum canescens</i>	Troelstrup s.n.	SDC	SAMN15679679
Boraginaceae	<i>Lithospermum incisum</i>	Jensen s.n.	SDC	SAMN15679680
Boraginaceae	<i>Lithospermum incisum</i>	Stahnke s.n.	SDC	SAMN15679677
Boraginaceae	<i>Lithospermum onosmodium</i>	Beauzay 282	OLFS	SAMN15679889
Brassicaceae	<i>Capsella bursa-pastoris</i>	Taylor 11799	OLFS	SAMN15679833
Brassicaceae	<i>Cardamine bulbosa</i>	Steinauer s.n.	OLFS	SAMN15679832
Brassicaceae	<i>Erysimum cheiranthoides</i>	Larson 11335	OLFS	SAMN15679760
Brassicaceae	<i>Lepidium densiflorum</i>	Law 93	OLFS	SAMN15679836
Brassicaceae	<i>Rorippa palustris</i>	McLead s.n.	OLFS	SAMN15679918
Campanulaceae	<i>Lobelia siphilitica</i>	Beauzay 330	OLFS	SAMN15679698
Campanulaceae	<i>Lobelia siphilitica</i>	Beauzay 330	SDC	SAMN15679904
Campanulaceae	<i>Lobelia spicata</i>	Larson s.n.	OLFS	SAMN15679903
Cannabaceae	<i>Celtis occidentalis</i>	Ode 12-27	OLFS	SAMN15679815
Caprifoliaceae	<i>Lonicera tatarica</i>	Stahnke s.n.	SDC	SAMN15679696
Caprifoliaceae	<i>Symphoricarpos occidentalis</i>	Stahnke s.n.	SDC	SAMN15679697
Caryophyllaceae	<i>Callitriche brutia</i>	Larson s.n.	OLFS	SAMN15679865
Caryophyllaceae	<i>Stellaria media</i>	Bortem 2	OLFS	SAMN15679866
Celastraceae	<i>Celastrus scandens</i>	Larson 11227	OLFS	SAMN15679816
Ceratophyllaceae	<i>Ceratophyllum demersum</i>	Larson 6963	OLFS	SAMN15679814
Comandraceae	<i>Comandra umbellata</i>	Jensen s.n.	SDC	SAMN15679684
Commelinaceae	<i>Tradescantia bracteata</i>	Roberts 72-5-28:6	OLFS	SAMN15679860
Convolvulaceae	<i>Calystegia macounii</i>	Larson 11358	OLFS	SAMN15679793
Convolvulaceae	<i>Calystegia sepium</i>	Pooler 84996	OLFS	SAMN15679792
Convolvulaceae	<i>Convolvulus sepium</i>	Jensen s.n.	SDC	SAMN15679695
Cornaceae	<i>Cornus sericea</i>	Larson 11240	OLFS	SAMN15679812
Cupressaceae	<i>Juniperus virginiana</i>	Taylor s.n.	OLFS	FAILED
Cyperaceae	<i>Carex aquatilis</i>	Ode 82-11	OLFS	SAMN15679830
Cyperaceae	<i>Carex blanda</i>	Larson 11215	OLFS	SAMN15679829
Cyperaceae	<i>Carex brevior</i>	Larson 11132	OLFS	SAMN15679828
Cyperaceae	<i>Carex cristatella</i>	Larson 11330	SDC	SAMN15679694
Cyperaceae	<i>Carex emoryi</i>	Larson 6393	OLFS	SAMN15679827
Cyperaceae	<i>Carex granularis</i>	Larson 11346	OLFS	SAMN15679826
Cyperaceae	<i>Carex grvida</i>	Larson 6395	OLFS	SAMN15679825
Cyperaceae	<i>Carex hystericina</i>	Larson 11337	SDC	SAMN15679693
Cyperaceae	<i>Carex meadii</i>	Ode 83-57	OLFS	SAMN15679824
Cyperaceae	<i>Carex molesta</i>	Larson 9365	OLFS	SAMN15679822
Cyperaceae	<i>Carex pellita</i>	Larson 9270	OLFS	SAMN15679823
Cyperaceae	<i>Carex praegracilis</i>	Peterson s.n.	SDC	SAMN15679692
Cyperaceae	<i>Carex sartwellii</i>	Larson s.n.	OLFS	SAMN15679821
Cyperaceae	<i>Carex sprengelii</i>	Larson 11216	OLFS	SAMN15679820
Cyperaceae	<i>Carex stricta</i>	Larson 11329	SDC	SAMN15679690
Cyperaceae	<i>Carex tenera</i>	Larson 6396	OLFS	SAMN15679819
Cyperaceae	<i>Carex tetanica</i>	Larson s.n.	OLFS	SAMN15679818
Cyperaceae	<i>Carex utriculata</i>	Larson 9165	OLFS	SAMN15679817
Cyperaceae	<i>Carex vulpinoidea</i>	Larson 11345	SDC	SAMN15679691
Cyperaceae	<i>Cyperus odoratus</i>	Beauzay 341	SDC	SAMN15679689
Cyperaceae	<i>Eleocharis erythropoda</i>	Larson 11639	OLFS	SAMN15679766
Cyperaceae	<i>Eleocharis palustris</i>	Sletten 169	OLFS	SAMN15679765
Cyperaceae	<i>Eriophorum angustifolium</i>	Larson 11340	OLFS	SAMN15679761
Cyperaceae	<i>Scirpus microcarpus</i>	Larson s.n.	OLFS	SAMN15679910
Cyperaceae	<i>Scirpus pallidus</i>	Beauzay 257	OLFS	SAMN15679909

(Continues)

APPENDIX 1. Continued

Family	Species	Collection	Herbarium	BioSample accession
Elaeagnaceae	<i>Elaeagnus angustifolia</i>	Johnson 420	OLFS	SAMN15679767
Equisetaceae	<i>Equisetum arvense</i>	Jensen s.n.	SDC	SAMN15679688
Fabaceae	<i>Amorpha canescens</i>	Jensen s.n.	SDC	SAMN15679675
Fabaceae	<i>Amorpha fruticosa</i>	Beauzay 317	SDC	SAMN15679674
Fabaceae	<i>Amphicarpa bracteata</i>	Larson 6680	OLFS	SAMN15679811
Fabaceae	<i>Astragalus crassicaarpus</i>	Pooler 186	OLFS	SAMN15679796
Fabaceae	<i>Caragana arborescens</i>	Fairlee 54	OLFS	SAMN15679831
Fabaceae	<i>Dalea candida</i>	Stahnke s.n.	SDC	SAMN15679667
Fabaceae	<i>Dalea purpurea</i>	Stahnke s.n.	SDC	SAMN15679666
Fabaceae	<i>Gleditsia triacanthos</i>	Purinton s.n.	OLFS	SAMN15679841
Fabaceae	<i>Lathyrus palustris</i>	Pengra P-16-17	OLFS	SAMN15679838
Fabaceae	<i>Lathyrus polymorphus</i>	Troelstrup s.n.	SDC	SAMN15679665
Fabaceae	<i>Lathyrus venosus</i>	Mixon s.n.	OLFS	SAMN15679837
Fabaceae	<i>Medicago lupulina</i>	Anderson 17	OLFS	SAMN15679897
Fabaceae	<i>Medicago sativa</i>	Larson 11421	OLFS	SAMN15679896
Fabaceae	<i>Melilotus officinalis</i>	Johnson s.n.	SDC	SAMN15679673
Fabaceae	<i>Melilotus officinalis</i>	Johnson s.n.	SDC	SAMN15679672
Fabaceae	<i>Melilotus officinalis</i>	Larson 9041	OLFS	SAMN15679895
Fabaceae	<i>Psoralea argophylla</i>	Stahnke s.n.	SDC	SAMN15679671
Fabaceae	<i>Psoralea esculenta</i>	Jensen s.n.	SDC	SAMN15679670
Fabaceae	<i>Trifolium pratense</i>	Jensen s.n.	SDC	SAMN15679669
Fabaceae	<i>Trifolium pratense</i>	Beauzay 276	OLFS	SAMN15679859
Fabaceae	<i>Vicia americana</i>	Jensen s.n.	SDC	SAMN15679668
Fabaceae	<i>Dalea purpurea</i>	Jensen s.n.	SDC	SAMN15679664
Fagaceae	<i>Quercus macrocarpa</i>	Stahnke s.n.	OLFS	SAMN15679927
Gentianaceae	<i>Gentiana andrewsii</i>	Troelstrup s.n.	SDC	SAMN15679687
Gentianaceae	<i>Gentiana puberulenta</i>	Roemmich 98	OLFS	SAMN15679842
Grossulariaceae	<i>Ribes americanum</i>	Larson 8885	OLFS	SAMN15679922
Grossulariaceae	<i>Ribes americanum</i>	Pooler 84045	OLFS	SAMN15679921
Hydrophyllaceae	<i>Hydrophyllum virginianum</i>	Taylor 7540	OLFS	SAMN15679840
Iridaceae	<i>Sisyrinchium campestre</i>	Larson 8733	OLFS	SAMN15679874
Juncaceae	<i>Juncus dudleyi</i>	Bettross 51	OLFS	SAMN15679839
Juncaceae	<i>Juncus nodosus</i>	Larson 11334	SDC	SAMN15679657
Lamiaceae	<i>Lycopus americanus</i>	Beauzay 346	SDC	SAMN15679663
Lamiaceae	<i>Lycopus asper</i>	Beauzay 342	SDC	SAMN15679662
Lamiaceae	<i>Lycopus uniflorus</i>	Larson 11426	OLFS	SAMN15679901
Lamiaceae	<i>Mentha arvensis</i>	Troelstrup s.n.	SDC	SAMN15679660
Lamiaceae	<i>Monarda fistulosa</i>	Stahnke s.n.	SDC	SAMN15679661
Lamiaceae	<i>Scutellaria lateriflora</i>	Roemmich 259	OLFS	SAMN15679907
Lamiaceae	<i>Stachys palustris</i>	Stahnke s.n.	SDC	SAMN15679659
Lamiaceae	<i>Stachys palustris</i>	Larson 11508	OLFS	SAMN15679867
Liliaceae	<i>Lilium philadelphicum</i>	Jensen s.n.	SDC	SAMN15679658
Mazocraeidae	<i>Brickellia eupatorioides</i>	Stahnke s.n.	SDC	SAMN15679710
Melanthiaceae	<i>Anticlea elegans</i>	Mixon s.n.	OLFS	SAMN15679843
Nyctaginaceae	<i>Mirabilis nyctaginea</i>	Bortem 23	OLFS	SAMN15679894
Oleaceae	<i>Fraxinus pennsylvanica</i>	Ode s.n.	OLFS	SAMN15679757
Onagraceae	<i>Epilobium leptophyllum</i>	Millar 37	OLFS	SAMN15679764
Onagraceae	<i>Oenothera biennis</i>	Beauzay 334	SDC	SAMN15679686
Onagraceae	<i>Oenothera serrulata</i>	Larson 11247	OLFS	SAMN15679794
Orchidaceae	<i>Cypripedium candidum</i>	Leoschke 1531	OLFS	SAMN15679769
Orchidaceae	<i>Liparis loeselii</i>	Larson 11327	OLFS	SAMN15679905
Orchidaceae	<i>Platanthera aquilonis</i>	Larson 11328	OLFS	SAMN15679878
Orchidaceae	<i>Platanthera hyperborea</i>	Larson 9140	OLFS	SAMN15679877
Orobanchaceae	<i>Pedicularis lanceolata</i>	Ode 00-21	OLFS	SAMN15679885
Oxalidaceae	<i>Oxalis corniculata</i>	Mixon s.n.	OLFS	SAMN15679887
Oxalidaceae	<i>Oxalis violacea</i>	Larson 11212	OLFS	SAMN15679886
Papaveraceae	<i>Dicentra cucullaria</i>	Larson 6380	OLFS	SAMN15679768
Phrymaceae	<i>Erythranthe glabrata</i>	Larson 11325	SDC	SAMN15679683
Phrymaceae	<i>Mimulus ringens</i>	Beauzay 351	SDC	SAMN15679682
Phrymaceae	<i>Phryma leptostachya</i>	Ode 84-97	OLFS	SAMN15679883
Pinaceae	<i>Picea glauca</i>	Taylor s.n.	OLFS	SAMN15679881
Pinaceae	<i>Pinus ponderosa</i>	Lehman 38	OLFS	SAMN15679880

(Continues)

APPENDIX 1. Continued

Family	Species	Collection	Herbarium	BioSample accession
Plantaginaceae	<i>Penstemon albidus</i>	Larson 11234	OLFS	SAMN15679884
Plantaginaceae	<i>Plantago major</i>	Beauzay 303	OLFS	SAMN15679879
Plantaginaceae	<i>Veronica anagallis-aquatica</i>	Larson 10785	OLFS	SAMN15679851
Plantaginaceae	<i>Veronica peregrina</i>	Larson 9999	OLFS	SAMN15679850
Poaceae	<i>Agropyron cristatum</i>	Pooler 84027	OLFS	SAMN15679784
Poaceae	<i>Agrostis stolonifera</i>	Ode s.n.	OLFS	SAMN15679783
Poaceae	<i>Andropogon gerardii</i>	Roemmich 81	OLFS	SAMN15679810
Poaceae	<i>Bouteloua curtipendula</i>	Jensen s.n.	SDC	SAMN15679656
Poaceae	<i>Bromus inermis</i>	Peterson s.n.	SDC	SAMN15679655
Poaceae	<i>Calamagrostis canadensis</i>	Sletten 305	OLFS	SAMN15679809
Poaceae	<i>Calamagrostis stricta</i>	Hansen 852	OLFS	SAMN15679808
Poaceae	<i>Cenchrus americanus</i>	Beauzay 257	OLFS	SAMN15679912
Poaceae	<i>Echinochloa muricata</i>	Beauzay 347	SDC	SAMN15679653
Poaceae	<i>Elymus repens</i>	Kanoute 033	OLFS	SAMN15679803
Poaceae	<i>Elymus villosus</i>	Genereux s.n.	OLFS	SAMN15679804
Poaceae	<i>Elymus virginicus</i>	VanSickle 586	OLFS	SAMN15679805
Poaceae	<i>Glyceria grandis</i>	Sletten 303	OLFS	SAMN15679802
Poaceae	<i>Glyceria striata</i>	Kjellsen 35	OLFS	SAMN15679801
Poaceae	<i>Hordeum jubatum</i>	Orth s.n.	OLFS	SAMN15679800
Poaceae	<i>Koeleria macrantha</i>	Kopp 225	OLFS	SAMN15679799
Poaceae	<i>Muhlenbergia cuspidata</i>	Kanoute 092	OLFS	SAMN15679893
Poaceae	<i>Nassella viridula</i>	Lehmon 179	OLFS	SAMN15679864
Poaceae	<i>Panicum acuminatum</i>	Larson 11060	OLFS	SAMN15679807
Poaceae	<i>Panicum oligosanthes</i>	Bortnem s.n.	SDC	SAMN15679654
Poaceae	<i>Panicum virgatum</i>	King 103	OLFS	SAMN15679892
Poaceae	<i>Panicum wilcoxianum</i>	Larson 10982	OLFS	SAMN15679806
Poaceae	<i>Phalaris arundinacea</i>	Sletten 136	OLFS	FAILED
Poaceae	<i>Phleum pratense</i>	Christner s.n.	OLFS	SAMN15679891
Poaceae	<i>Poa palustris</i>	Ode 84-107	OLFS	SAMN15679890
Poaceae	<i>Poa pratensis</i>	Larson 6850	SDC	SAMN15679652
Poaceae	<i>Schizachyrium scoparium</i>	VanSickle 536	OLFS	SAMN15679913
Poaceae	<i>Setaria viridis</i>	Roemmich 82	OLFS	SAMN15679911
Poaceae	<i>Sorghastrum nutans</i>	Larson s.n.	SDC	SAMN15679728
Poaceae	<i>Sphenopholis intermedia</i>	Larson 11341	OLFS	SAMN15679730
Poaceae	<i>Sphenopholis intermedia</i>	Larson 11341	SDC	SAMN15679871
Poaceae	<i>Sphenopholis obtusata</i>	Sletten 379	OLFS	SAMN15679870
Poaceae	<i>Sporobolus compositus</i>	Dirks s.n.	OLFS	SAMN15679869
Poaceae	<i>Sporobolus heterolepis</i>	Pauly s.n.	OLFS	SAMN15679868
Poaceae	<i>Sporobolus michauxianus</i>	Beauzay 325	SDC	SAMN15679729
Polemoniaceae	<i>Phlox pilosa</i>	Troelstrup s.n.	SDC	SAMN15679731
Polygonaceae	<i>Persicaria amphibia</i>	Beauzay 321	SDC	SAMN15679732
Polygonaceae	<i>Persicaria amphibia</i>	Ode s.n.	OLFS	SAMN15679929
Polygonaceae	<i>Persicaria lapathifolia</i>	Beauzay 320	SDC	SAMN15679733
Polygonaceae	<i>Persicaria punctata</i>	Beauzay 339	SDC	SAMN15679734
Polygonaceae	<i>Polygonum aviculare</i>	Larson 11565	OLFS	SAMN15679930
Polygonaceae	<i>Polygonatum biflorum</i>	Pooler 84029	OLFS	SAMN15679931
Polygonaceae	<i>Rumex crispus</i>	Unkenholz s.n.	OLFS	SAMN15679920
Polygonaceae	<i>Rumex orbiculatus</i>	Roberts 73-8-19:1	OLFS	SAMN15679919
Primulaceae	<i>Lysimachia ciliata</i>	Beauzay 352	OLFS	SAMN15679900
Primulaceae	<i>Lysimachia thyrsoflora</i>	Sletten 273	OLFS	SAMN15679899
Ranunculaceae	<i>Anemonastrum canadense</i>	Troelstrup s.n.	SDC	SAMN15679735
Ranunculaceae	<i>Anemone cylindrica</i>	Stahnke s.n.	SDC	SAMN15679736
Ranunculaceae	<i>Aquilegia canadensis</i>	Jensen s.n.	SDC	SAMN15679738
Ranunculaceae	<i>Caltha palustris</i>	Troelstrup s.n.	SDC	SAMN15679739
Ranunculaceae	<i>Delphinium carolinianum</i>	Jensen s.n.	SDC	SAMN15679740
Ranunculaceae	<i>Pulsatilla patens</i>	Stahnke s.n.	SDC	SAMN15679737
Ranunculaceae	<i>Ranunculus hispidus</i>	Ode 02-7	OLFS	SAMN15679926
Ranunculaceae	<i>Ranunculus macounii</i>	Jensen s.n.	SDC	SAMN15679741
Ranunculaceae	<i>Thalictrum dasycarpum</i>	Larson 6651	OLFS	SAMN15679862
Rhamnaceae	<i>Rhamnus cathartica</i>	Stahnke s.n.	SDC	SAMN15679742
Rosaceae	<i>Agrimonia striata</i>	Beauzay 349	SDC	SAMN15679743
Rosaceae	<i>Amelanchier alnifolia</i>	Stahnke s.n.	SDC	SAMN15679744

(Continues)

APPENDIX 1. Continued

Family	Species	Collection	Herbarium	BioSample accession
Rosaceae	<i>Amelanchier ovalis</i>	Reese s.n.	SDC	SAMN15679745
Rosaceae	<i>Fragaria virginiana</i>	Monteith s.n.	OLFS	SAMN15679763
Rosaceae	<i>Geum aleppicum</i>	Larson 11332	SDC	SAMN15679746
Rosaceae	<i>Geum canadense</i>	Larson 11336	OLFS	SAMN15679762
Rosaceae	<i>Geum rossii</i>	Jensen s.n.	SDC	SAMN15679747
Rosaceae	<i>Prunus americana</i>	Stahnke s.n.	SDC	SAMN15679748
Rosaceae	<i>Prunus serotina</i>	Stahnke s.n.	SDC	SAMN15679749
Rosaceae	<i>Rosa arkansana</i>	Stahnke s.n.	SDC	SAMN15679750
Rosaceae	<i>Rubus occidentalis</i>	Larson 10437	OLFS	SAMN15679917
Rubiaceae	<i>Galium aparine</i>	Anderson 02	OLFS	SAMN15679756
Rubiaceae	<i>Galium boreale</i>	Jensen s.n.	SDC	SAMN15679751
Rubiaceae	<i>Galium trifidum</i>	Larson 9213	OLFS	SAMN15679754
Rubiaceae	<i>Galium triflorum</i>	Larson 6882	OLFS	SAMN15679755
Salicaceae	<i>Populus tremuloides</i>	Larson 11227	OLFS	SAMN15679928
Salicaceae	<i>Populus xjackii</i>	Larson 1131	SDC	SAMN15679685
Salicaceae	<i>Salix alba</i>	Millar 011	OLFS	SAMN15679916
Salicaceae	<i>Salix amygdaloides</i>	Larson 7023	OLFS	SAMN15679915
Salicaceae	<i>Salix interior</i>	Larson 11264	OLFS	SAMN15679914
Sapindaceae	<i>Aesculus glabra</i>	Taylor s.n.	OLFS	SAMN15679780
Scrophulariaceae	<i>Scrophularia lanceolata</i>	Mixon s.n.	OLFS	SAMN15679908
Solanaceae	<i>Lycium barbarum</i>	Taylor 11723	OLFS	SAMN15679902
Solanaceae	<i>Physalis virginiana</i>	Roberts s.n.	OLFS	SAMN15679882
Typhaceae	<i>Sparganium eurycarpum</i>	Sletten 210	OLFS	SAMN15679872
Typhaceae	<i>Typha angustifolia</i>	Stahnke s.n.	SDC	SAMN15679681
Typhaceae	<i>Typha latifolia</i>	Larson 9117	OLFS	SAMN15679857
Typhaceae	<i>Typha xglauca</i>	Larson 11386	OLFS	SAMN15679858
Ulmaceae	<i>Ulmus americana</i>	Riley 51	OLFS	SAMN15679856
Ulmaceae	<i>Ulmus pumila</i>	Larson 11559	OLFS	SAMN15679855
Urticaceae	<i>Urtica dioica</i>	Mixon s.n.	OLFS	SAMN15679854
Verbenaceae	<i>Verbena bracteata</i>	Law 103	OLFS	SAMN15679853
Verbenaceae	<i>Verbena hastata</i>	Beauzay 319	SDC	SAMN15679753
Verbenaceae	<i>Verbena stricta</i>	Jensen s.n.	SDC	SAMN15679752
Verbenaceae	<i>Verbena stricta</i>	Pooler 84028	OLFS	SAMN15679852
Violaceae	<i>Viola canadensis</i>	Larson 11214	OLFS	SAMN15679847
Violaceae	<i>Viola nephrophylla</i>	Larson 9985	OLFS	SAMN15679846
Violaceae	<i>Viola pedatifida</i>	Larson 11219	OLFS	SAMN15679845
Violaceae	<i>Viola sororia</i>	Larson 7019	OLFS	SAMN15679844
Vitaceae	<i>Vitis riparia</i>	Sletten 175	OLFS	SAMN15679849

Note: OLFS = Oak Lake Field Station at South Dakota State University; SDC = C. A. Taylor Herbarium at South Dakota State University.

APPENDIX 2. The dual-indexing strategy uses two 8-base indices, Index 1 (i7) and Index 2 (i5), which provides unique sequences at the ends of amplicons. The following indices and sequences are from the 24-sample Nextera XT Index Kit (Illumina).

Index	Index adapter	Primer sequence
Index 1 (i7)	N701	TAAGGCGA
	N702	CGTACTAG
	N703	AGGCAGAA
	N704	TCCTGAGC
	N705	GGACTCCT
	N706	TAGGCATG
	N707	CTCTCTAC
	N708	CAGAGAGG
	N709	GCTACGCT
	N710	CGAGGCTG
	N711	AAGAGGCA
	N712	GTAGAGGA
Index 2 (i5)	S501	TAGATCGC
	S502	CTCTCTAT
	S503	TATCCTCT
	S504	AGAGTAGA
	S505	GTAAGGAG
	S506	ACTGCATA
	S507	AAGGAGTA
S508	CTAAGCCT	

APPENDIX 3. Identification success for tested barcodes (individual and concatenated regions) of tallgrass prairie plant species, listing the number of retrieved sequences and the number of correctly identified sequences at the family, genus, and species levels for the three tested databases.

Locus ^a	Taxon level	Database	Sequences	Confident	Ambiguous	Incorrect	No match
ITS	Family	GenBank	178	141 (79.21%)	20 (11.24%)	13 (7.3%)	4 (2.25%)
ITS	Family	Regional	178	159 (89.33%)	3 (1.69%)	11 (6.18%)	5 (2.81%)
ITS	Family	OLFS	178	159 (89.33%)	0	13 (7.3%)	6 (3.37%)
ITS	Genus	GenBank	178	124 (69.66%)	25 (14.04%)	25 (14.04%)	4 (2.25%)
ITS	Genus	Regional	178	142 (79.78%)	10 (5.62%)	21 (11.8%)	5 (2.81%)
ITS	Genus	OLFS	178	146 (82.02%)	3 (1.69%)	23 (12.92%)	6 (3.37%)
ITS	Species	GenBank	178	53 (29.78%)	59 (33.15%)	62 (34.83%)	4 (2.25%)
ITS	Species	Regional	178	86 (48.31%)	33 (18.54%)	54 (30.34%)	5 (2.81%)
ITS	Species	OLFS	178	122 (68.54%)	12 (6.74%)	38 (21.35%)	6 (3.37%)
trnH	Family	GenBank	138	123 (89.13%)	2 (1.45%)	13 (9.42%)	0
trnH	Family	Regional	138	104 (75.36%)	0	34 (24.64%)	0
trnH	Family	OLFS	138	92 (66.67%)	0	43 (31.16%)	3 (2.17%)
trnH	Genus	GenBank	138	94 (68.12%)	14 (10.14%)	30 (21.74%)	0
trnH	Genus	Regional	138	59 (42.75%)	2 (1.45%)	77 (55.8%)	0
trnH	Genus	OLFS	138	39 (28.26%)	0	96 (69.57%)	3 (2.17%)
trnH	Species	GenBank	138	32 (23.19%)	27 (19.57%)	79 (57.25%)	0
trnH	Species	Regional	138	18 (13.04%)	6 (4.35%)	114 (82.61%)	0
trnH	Species	OLFS	138	29 (21.01%)	1 (0.72%)	105 (76.09%)	3 (2.17%)
matK	Family	GenBank	112	107 (95.54%)	0	5 (4.46%)	0
matK	Family	Regional	112	104 (92.86%)	0	8 (7.14%)	0
matK	Family	OLFS	112	90 (80.36%)	0	22 (19.64%)	0
matK	Genus	GenBank	112	61 (54.46%)	11 (9.82%)	40 (35.71%)	0
matK	Genus	Regional	112	69 (61.61%)	1 (0.89%)	42 (37.5%)	0
matK	Genus	OLFS	112	45 (40.18%)	0	67 (59.82%)	0
matK	Species	GenBank	112	11 (9.82%)	16 (14.29%)	85 (75.89%)	0
matK	Species	Regional	112	21 (18.75%)	4 (3.57%)	87 (77.68%)	0
matK	Species	OLFS	112	28 (25.00%)	0	84 (75.00%)	0
rbcLa	Family	GenBank	249	220 (88.35%)	24 (9.64%)	5 (2.01%)	0
rbcLa	Family	Regional	249	240 (96.39%)	3 (1.20%)	5 (2.01%)	1 (0.4%)
rbcLa	Family	OLFS	249	240 (96.39%)	0	8 (3.21%)	1 (0.4%)
rbcLa	Genus	GenBank	249	135 (54.22%)	99 (39.76%)	15 (6.02%)	0
rbcLa	Genus	Regional	249	181 (72.69%)	50 (20.08%)	17 (6.83%)	1 (0.4%)
rbcLa	Genus	OLFS	249	215 (86.35%)	14 (5.62%)	19 (7.63%)	1 (0.4%)
rbcLa	Species	GenBank	249	20 (8.03%)	164 (65.86%)	65 (26.1%)	0
rbcLa	Species	Regional	249	46 (18.47%)	120 (48.19%)	82 (32.93%)	1 (0.4%)
rbcLa	Species	OLFS	249	138 (55.42%)	68 (27.31%)	42 (16.87%)	1 (0.4%)
ITS_trnH	Family	GenBank	96	84 (87.5%)	8 (8.33%)	4 (4.17%)	0
ITS_trnH	Family	Regional	96	91 (94.79%)	1 (1.04%)	4 (4.17%)	0
ITS_trnH	Family	OLFS	96	89 (92.71%)	0	7 (7.29%)	0
ITS_trnH	Genus	GenBank	96	69 (71.88%)	12 (12.5%)	15 (15.62%)	0
ITS_trnH	Genus	Regional	96	75 (78.12%)	7 (7.29%)	14 (14.58%)	0
ITS_trnH	Genus	OLFS	96	72 (75%)	2 (2.08%)	22 (22.92%)	0
ITS_trnH	Species	GenBank	96	34 (35.42%)	20 (20.83%)	42 (43.75%)	0
ITS_trnH	Species	Regional	96	48 (50%)	14 (14.58%)	34 (35.42%)	0
ITS_trnH	Species	OLFS	96	61 (63.54%)	4 (4.17%)	31 (32.29%)	0
ITS_matK	Family	GenBank	75	66 (88%)	3 (4%)	6 (8%)	0
ITS_matK	Family	Regional	75	68 (90.67%)	0	7 (9.33%)	0
ITS_matK	Family	OLFS	75	70 (93.33%)	0	5 (6.67%)	0
ITS_matK	Genus	GenBank	75	48 (64%)	7 (9.33%)	20 (26.67%)	0
ITS_matK	Genus	Regional	75	64 (85.33%)	1 (1.33%)	10 (13.33%)	0
ITS_matK	Genus	OLFS	75	56 (74.67%)	0	19 (25.33%)	0
ITS_matK	Species	GenBank	75	18 (24%)	17 (22.67%)	40 (53.33%)	0
ITS_matK	Species	Regional	75	42 (56%)	12 (16%)	21 (28%)	0
ITS_matK	Species	OLFS	75	47 (62.67%)	2 (2.67%)	26 (34.67%)	0
ITS_rbcLa	Family	GenBank	164	133 (81.1%)	21 (12.8%)	10 (6.1%)	0
ITS_rbcLa	Family	Regional	164	152 (92.68%)	3 (1.83%)	9 (5.49%)	0
ITS_rbcLa	Family	OLFS	164	155 (94.51%)	0	9 (5.49%)	0
ITS_rbcLa	Genus	GenBank	164	113 (68.9%)	32 (19.51%)	19 (11.59%)	0
ITS_rbcLa	Genus	Regional	164	133 (81.1%)	12 (7.32%)	19 (11.59%)	0
ITS_rbcLa	Genus	OLFS	164	141 (85.98%)	6 (3.66%)	17 (10.37%)	0
ITS_rbcLa	Species	GenBank	164	43 (26.22%)	71 (43.29%)	50 (30.49%)	0

(Continues)

APPENDIX 3. Continued

Locus ^a	Taxon level	Database	Sequences	Confident	Ambiguous	Incorrect	No match
ITS_rbcLa	Species	Regional	164	72 (43.9%)	42 (25.61%)	50 (30.49%)	0
ITS_rbcLa	Species	OLFS	164	116 (70.73%)	21 (12.8%)	27 (16.46%)	0
matK_rbcLa	Family	GenBank	109	103 (94.5%)	3 (2.75%)	3 (2.75%)	0
matK_rbcLa	Family	Regional	109	105 (96.33%)	2 (1.83%)	2 (1.83%)	0
matK_rbcLa	Family	OLFS	109	106 (97.25%)	0	3 (2.75%)	0
matK_rbcLa	Genus	GenBank	109	60 (55.05%)	19 (17.43%)	30 (27.52%)	0
matK_rbcLa	Genus	Regional	109	82 (75.23%)	20 (18.35%)	7 (6.42%)	0
matK_rbcLa	Genus	OLFS	109	95 (87.16%)	4 (3.67%)	10 (9.17%)	0
matK_rbcLa	Species	GenBank	109	13 (11.93%)	36 (33.03%)	60 (55.05%)	0
matK_rbcLa	Species	Regional	109	28 (25.69%)	53 (48.62%)	28 (25.69%)	0
matK_rbcLa	Species	OLFS	109	63 (57.8%)	31 (28.44%)	15 (13.76%)	0
matK_trnH	Family	GenBank	57	53 (92.98%)	0	4 (7.02%)	0
matK_trnH	Family	Regional	57	52 (91.23%)	0	5 (8.77%)	0
matK_trnH	Family	OLFS	57	44 (77.19%)	0	13 (22.81%)	0
matK_trnH	Genus	GenBank	57	39 (68.42%)	0	18 (31.58%)	0
matK_trnH	Genus	Regional	57	40 (70.18%)	1 (1.75%)	16 (28.07%)	0
matK_trnH	Genus	OLFS	57	28 (49.12%)	0	29 (50.88%)	0
matK_trnH	Species	GenBank	57	15 (26.32%)	4 (7.02%)	38 (66.67%)	0
matK_trnH	Species	Regional	57	13 (22.81%)	2 (3.51%)	42 (73.68%)	0
matK_trnH	Species	OLFS	57	21 (36.84%)	0	36 (63.16%)	0
rbcLa_trnH	Family	GenBank	126	114 (90.48%)	4 (3.17%)	8 (6.35%)	0
rbcLa_trnH	Family	Regional	126	121 (96.03%)	0	5 (3.97%)	0
rbcLa_trnH	Family	OLFS	126	119 (94.44%)	0	7 (5.56%)	0
rbcLa_trnH	Genus	GenBank	126	82 (65.08%)	27 (21.43%)	17 (13.49%)	0
rbcLa_trnH	Genus	Regional	126	91 (72.22%)	22 (17.46%)	13 (10.32%)	0
rbcLa_trnH	Genus	OLFS	126	100 (79.37%)	7 (5.56%)	19 (15.08%)	0
rbcLa_trnH	Species	GenBank	126	29 (23.02%)	40 (31.75%)	57 (45.24%)	0
rbcLa_trnH	Species	Regional	126	32 (25.4%)	47 (37.3%)	47 (37.3%)	0
rbcLa_trnH	Species	OLFS	126	73 (57.94%)	28 (22.22%)	25 (19.84%)	0
ITS_matK_rbcLa	Family	GenBank	73	65 (89.04%)	2 (2.74%)	6 (8.22%)	0
ITS_matK_rbcLa	Family	Regional	73	66 (90.41%)	0	7 (9.59%)	0
ITS_matK_rbcLa	Family	OLFS	73	68 (93.15%)	0	5 (6.85%)	0
ITS_matK_rbcLa	Genus	GenBank	73	44 (60.27%)	8 (10.96%)	21 (28.77%)	0
ITS_matK_rbcLa	Genus	Regional	73	61 (83.56%)	3 (4.11%)	9 (12.33%)	0
ITS_matK_rbcLa	Genus	OLFS	73	64 (87.67%)	1 (1.37%)	8 (10.96%)	0
ITS_matK_rbcLa	Species	GenBank	73	13 (17.81%)	21 (28.77%)	39 (53.42%)	0
ITS_matK_rbcLa	Species	Regional	73	35 (47.95%)	19 (26.03%)	19 (26.03%)	0
ITS_matK_rbcLa	Species	OLFS	73	56 (76.71%)	7 (9.59%)	10 (13.7%)	0
ITS_matK_trnH	Family	GenBank	41	40 (97.56%)	0	1 (2.44%)	0
ITS_matK_trnH	Family	Regional	41	40 (97.56%)	0	1 (2.44%)	0
ITS_matK_trnH	Family	OLFS	41	40 (97.56%)	0	1 (2.44%)	0
ITS_matK_trnH	Genus	GenBank	41	31 (75.61%)	0	10 (24.39%)	0
ITS_matK_trnH	Genus	Regional	41	37 (90.24%)	2 (4.88%)	2 (4.88%)	0
ITS_matK_trnH	Genus	OLFS	41	30 (73.17%)	0	11 (26.83%)	0
ITS_matK_trnH	Species	GenBank	41	18 (43.9%)	4 (9.76%)	19 (46.34%)	0
ITS_matK_trnH	Species	Regional	41	22 (53.66%)	7 (17.07%)	12 (29.27%)	0
ITS_matK_trnH	Species	OLFS	41	27 (65.85%)	0	14 (34.15%)	0
ITS_rbcLa_trnH	Family	GenBank	91	83 (91.21%)	6 (6.59%)	2 (2.2%)	0
ITS_rbcLa_trnH	Family	Regional	91	88 (96.7%)	1 (1.1%)	2 (2.2%)	0
ITS_rbcLa_trnH	Family	OLFS	91	87 (95.6%)	0	4 (4.4%)	0
ITS_rbcLa_trnH	Genus	GenBank	91	67 (73.63%)	13 (14.29%)	11 (12.09%)	0
ITS_rbcLa_trnH	Genus	Regional	91	73 (80.22%)	8 (8.79%)	10 (10.99%)	0
ITS_rbcLa_trnH	Genus	OLFS	91	76 (83.52%)	4 (4.4%)	11 (12.09%)	0
ITS_rbcLa_trnH	Species	GenBank	91	32 (35.16%)	23 (25.27%)	36 (39.56%)	0
ITS_rbcLa_trnH	Species	Regional	91	41 (45.05%)	18 (19.78%)	32 (35.16%)	0
ITS_rbcLa_trnH	Species	OLFS	91	63 (69.23%)	9 (9.89%)	19 (20.88%)	0
matK_rbcLa_trnH	Family	GenBank	56	51 (91.07%)	1 (1.79%)	4 (7.14%)	0
matK_rbcLa_trnH	Family	Regional	56	54 (96.43%)	0	2 (3.57%)	0
matK_rbcLa_trnH	Family	OLFS	56	55 (98.21%)	0	1 (1.79%)	0
matK_rbcLa_trnH	Genus	GenBank	56	39 (69.64%)	2 (3.57%)	15 (26.79%)	0
matK_rbcLa_trnH	Genus	Regional	56	45 (80.36%)	7 (12.5%)	4 (7.14%)	0
matK_rbcLa_trnH	Genus	OLFS	56	48 (85.71%)	2 (3.57%)	6 (10.71%)	0

(Continues)

APPENDIX 3. Continued

Locus ^a	Taxon level	Database	Sequences	Confident	Ambiguous	Incorrect	No match
matK_rbcLa_trnH	Species	GenBank	56	16 (28.57%)	8 (14.29%)	32 (57.14%)	0
matK_rbcLa_trnH	Species	Regional	56	18 (32.14%)	17 (30.36%)	21 (37.5%)	0
matK_rbcLa_trnH	Species	OLFS	56	34 (60.71%)	14 (25%)	8 (14.29%)	0
ITS_matK_rbcLa_trnH	Family	GenBank	40	39 (97.5%)	0	1 (2.5%)	0
ITS_matK_rbcLa_trnH	Family	Regional	40	39 (97.5%)	0	1 (2.5%)	0
ITS_matK_rbcLa_trnH	Family	OLFS	40	39 (97.5%)	0	1 (2.5%)	0
ITS_matK_rbcLa_trnH	Genus	GenBank	40	31 (77.5%)	0	9 (22.5%)	0
ITS_matK_rbcLa_trnH	Genus	Regional	40	35 (87.5%)	3 (7.5%)	2 (5%)	0
ITS_matK_rbcLa_trnH	Genus	OLFS	40	36 (90%)	1 (2.5%)	3 (7.5%)	0
ITS_matK_rbcLa_trnH	Species	GenBank	40	16 (40%)	5 (12.5%)	19 (47.5%)	0
ITS_matK_rbcLa_trnH	Species	Regional	40	20 (50%)	8 (20%)	12 (30%)	0
ITS_matK_rbcLa_trnH	Species	OLFS	40	32 (80%)	3 (7.5%)	5 (12.5%)	0

Note: OLFS = database of species sampled from Oak Lake Field Station.

^aMulti-region barcodes are indicated by an underscore.

APPENDIX 4. Identification success for tested barcodes (individual and concatenated regions) for tallgrass prairie plant species in Asteraceae, Cyperaceae, Fabaceae, and Poaceae, listing the number of retrieved sequences and the number of correctly identified sequences at the family, genus, and species levels for the three tested databases.

Family	Locus ^a	Taxon level	Database	Sequences	Confident	Ambiguous	Incorrect	No match
Asteraceae	ITS	Family	GenBank	28	25 (89.29%)	3 (10.71%)	0	0
Asteraceae	ITS	Family	Regional	28	28 (100%)	0	0	0
Asteraceae	ITS	Family	OLFS	28	28 (100%)	0	0	0
Asteraceae	ITS	Genus	GenBank	28	21 (75%)	6 (21.43%)	1 (3.57%)	0
Asteraceae	ITS	Genus	Regional	28	26 (92.86%)	2 (7.14%)	0	0
Asteraceae	ITS	Genus	OLFS	28	26 (92.86%)	1 (3.57%)	1 (3.57%)	0
Asteraceae	ITS	Species	GenBank	28	6 (21.43%)	17 (60.71%)	5 (17.86%)	0
Asteraceae	ITS	Species	Regional	28	15 (53.57%)	11 (39.29%)	2 (7.14%)	0
Asteraceae	ITS	Species	OLFS	28	23 (82.14%)	3 (10.71%)	2 (7.14%)	0
Asteraceae	trnH	Family	GenBank	32	31 (96.88%)	0	1 (3.12%)	0
Asteraceae	trnH	Family	Regional	32	31 (96.88%)	0	1 (3.12%)	0
Asteraceae	trnH	Family	OLFS	32	31 (96.88%)	0	1 (3.12%)	0
Asteraceae	trnH	Genus	GenBank	32	24 (75%)	1 (3.12%)	7 (21.88%)	0
Asteraceae	trnH	Genus	Regional	32	20 (62.5%)	1 (3.12%)	11 (34.38%)	0
Asteraceae	trnH	Genus	OLFS	32	15 (46.88%)	0	17 (53.12%)	0
Asteraceae	trnH	Species	GenBank	32	10 (31.25%)	4 (12.5%)	18 (56.25%)	0
Asteraceae	trnH	Species	Regional	32	8 (25%)	2 (6.25%)	22 (68.75%)	0
Asteraceae	trnH	Species	OLFS	32	11 (34.38%)	0	21 (65.62%)	0
Asteraceae	matK	Family	GenBank	35	35 (100%)	0	0	0
Asteraceae	matK	Family	Regional	35	35 (100%)	0	0	0
Asteraceae	matK	Family	OLFS	35	35 (100%)	0	0	0
Asteraceae	matK	Genus	GenBank	35	7 (20%)	6 (17.14%)	22 (62.86%)	0
Asteraceae	matK	Genus	Regional	35	15 (42.86%)	1 (2.86%)	19 (54.29%)	0
Asteraceae	matK	Genus	OLFS	35	7 (20%)	0	28 (80%)	0
Asteraceae	matK	Species	GenBank	35	1 (2.86%)	3 (8.57%)	31 (88.57%)	0
Asteraceae	matK	Species	Regional	35	3 (8.57%)	1 (2.86%)	31 (88.57%)	0
Asteraceae	matK	Species	OLFS	35	5 (14.29%)	0	30 (85.71%)	0
Asteraceae	rbcLa	Family	GenBank	43	36 (83.72%)	7 (16.28%)	0	0
Asteraceae	rbcLa	Family	Regional	43	40 (93.02%)	3 (6.98%)	0	0
Asteraceae	rbcLa	Family	OLFS	43	43 (100%)	0	0	0
Asteraceae	rbcLa	Genus	GenBank	43	12 (27.91%)	30 (69.77%)	1 (2.33%)	0
Asteraceae	rbcLa	Genus	Regional	43	21 (48.84%)	20 (46.51%)	2 (4.65%)	0
Asteraceae	rbcLa	Genus	OLFS	43	35 (81.4%)	3 (6.98%)	5 (11.63%)	0
Asteraceae	rbcLa	Species	GenBank	43	2 (4.65%)	36 (83.72%)	5 (11.63%)	0
Asteraceae	rbcLa	Species	Regional	43	4 (9.3%)	26 (60.47%)	13 (30.23%)	0
Asteraceae	rbcLa	Species	OLFS	43	15 (34.88%)	20 (46.51%)	8 (18.6%)	0
Asteraceae	ITS_trnH	Family	GenBank	22	22 (100%)	0	0	0
Asteraceae	ITS_trnH	Family	Regional	22	22 (100%)	0	0	0
Asteraceae	ITS_trnH	Family	OLFS	22	22 (100%)	0	0	0
Asteraceae	ITS_trnH	Genus	GenBank	22	16 (72.73%)	3 (13.64%)	3 (13.64%)	0
Asteraceae	ITS_trnH	Genus	Regional	22	17 (77.27%)	3 (13.64%)	2 (9.09%)	0
Asteraceae	ITS_trnH	Genus	OLFS	22	14 (63.64%)	1 (4.55%)	7 (31.82%)	0

(Continues)

APPENDIX 4. Continued

Family	Locus ^a	Taxon level	Database	Sequences	Confident	Ambiguous	Incorrect	No match
Asteraceae	ITS_trnH	Species	GenBank	22	6 (27.27%)	4 (18.18%)	12 (54.55%)	0
Asteraceae	ITS_trnH	Species	Regional	22	7 (31.82%)	7 (31.82%)	8 (36.36%)	0
Asteraceae	ITS_trnH	Species	OLFS	22	11 (50%)	2 (9.09%)	9 (40.91%)	0
Asteraceae	ITS_matK	Family	GenBank	20	19 (95%)	1 (5%)	0	0
Asteraceae	ITS_matK	Family	Regional	20	20 (100%)	0	0	0
Asteraceae	ITS_matK	Family	OLFS	20	20 (100%)	0	0	0
Asteraceae	ITS_matK	Genus	GenBank	20	8 (40%)	4 (20%)	8 (40%)	0
Asteraceae	ITS_matK	Genus	Regional	20	20 (100%)	0	0	0
Asteraceae	ITS_matK	Genus	OLFS	20	9 (45%)	0	11 (55%)	0
Asteraceae	ITS_matK	Species	GenBank	20	2 (10%)	6 (30%)	12 (60%)	0
Asteraceae	ITS_matK	Species	Regional	20	11 (55%)	7 (35%)	2 (10%)	0
Asteraceae	ITS_matK	Species	OLFS	20	8 (40%)	1 (5%)	11 (55%)	0
Asteraceae	ITS_rbcLa	Family	GenBank	24	21 (87.5%)	3 (12.5%)	0	0
Asteraceae	ITS_rbcLa	Family	Regional	24	24 (100%)	0	0	0
Asteraceae	ITS_rbcLa	Family	OLFS	24	24 (100%)	0	0	0
Asteraceae	ITS_rbcLa	Genus	GenBank	24	19 (79.17%)	4 (16.67%)	1 (4.17%)	0
Asteraceae	ITS_rbcLa	Genus	Regional	24	23 (95.83%)	1 (4.17%)	0	0
Asteraceae	ITS_rbcLa	Genus	OLFS	24	22 (91.67%)	1 (4.17%)	1 (4.17%)	0
Asteraceae	ITS_rbcLa	Species	GenBank	24	6 (25%)	13 (54.17%)	5 (20.83%)	0
Asteraceae	ITS_rbcLa	Species	Regional	24	13 (54.17%)	9 (37.5%)	2 (8.33%)	0
Asteraceae	ITS_rbcLa	Species	OLFS	24	19 (79.17%)	3 (12.5%)	2 (8.33%)	0
Asteraceae	matK_rbcLa	Family	GenBank	35	35 (100%)	0	0	0
Asteraceae	matK_rbcLa	Family	Regional	35	33 (94.29%)	2 (5.71%)	0	0
Asteraceae	matK_rbcLa	Family	OLFS	35	35 (100%)	0	0	0
Asteraceae	matK_rbcLa	Genus	GenBank	35	8 (22.86%)	8 (22.86%)	19 (54.29%)	0
Asteraceae	matK_rbcLa	Genus	Regional	35	16 (45.71%)	17 (48.57%)	2 (5.71%)	0
Asteraceae	matK_rbcLa	Genus	OLFS	35	27 (77.14%)	3 (8.57%)	5 (14.29%)	0
Asteraceae	matK_rbcLa	Species	GenBank	35	3 (8.57%)	4 (11.43%)	28 (80%)	0
Asteraceae	matK_rbcLa	Species	Regional	35	4 (11.43%)	19 (54.29%)	12 (34.29%)	0
Asteraceae	matK_rbcLa	Species	OLFS	35	12 (34.29%)	15 (42.86%)	8 (22.86%)	0
Asteraceae	matK_trnH	Family	GenBank	24	24 (100%)	0	0	0
Asteraceae	matK_trnH	Family	Regional	24	24 (100%)	0	0	0
Asteraceae	matK_trnH	Family	OLFS	24	24 (100%)	0	0	0
Asteraceae	matK_trnH	Genus	GenBank	24	14 (58.33%)	0	10 (41.67%)	0
Asteraceae	matK_trnH	Genus	Regional	24	16 (66.67%)	1 (4.17%)	7 (29.17%)	0
Asteraceae	matK_trnH	Genus	OLFS	24	10 (41.67%)	0	14 (58.33%)	0
Asteraceae	matK_trnH	Species	GenBank	24	6 (25%)	1 (4.17%)	17 (70.83%)	0
Asteraceae	matK_trnH	Species	Regional	24	6 (25%)	1 (4.17%)	17 (70.83%)	0
Asteraceae	matK_trnH	Species	OLFS	24	8 (33.33%)	0	16 (66.67%)	0
Asteraceae	rbcLa_trnH	Family	GenBank	29	29 (100%)	0	0	0
Asteraceae	rbcLa_trnH	Family	Regional	29	29 (100%)	0	0	0
Asteraceae	rbcLa_trnH	Family	OLFS	29	29 (100%)	0	0	0
Asteraceae	rbcLa_trnH	Genus	GenBank	29	22 (75.86%)	4 (13.79%)	3 (10.34%)	0
Asteraceae	rbcLa_trnH	Genus	Regional	29	21 (72.41%)	5 (17.24%)	3 (10.34%)	0
Asteraceae	rbcLa_trnH	Genus	OLFS	29	20 (68.97%)	1 (3.45%)	8 (27.59%)	0
Asteraceae	rbcLa_trnH	Species	GenBank	29	8 (27.59%)	5 (17.24%)	16 (55.17%)	0
Asteraceae	rbcLa_trnH	Species	Regional	29	8 (27.59%)	5 (17.24%)	16 (55.17%)	0
Asteraceae	rbcLa_trnH	Species	OLFS	29	13 (44.83%)	7 (24.14%)	9 (31.03%)	0
Asteraceae	ITS_matK_rbcLa	Family	GenBank	20	19 (95%)	1 (5%)	0	0
Asteraceae	ITS_matK_rbcLa	Family	Regional	20	20 (100%)	0	0	0
Asteraceae	ITS_matK_rbcLa	Family	OLFS	20	20 (100%)	0	0	0
Asteraceae	ITS_matK_rbcLa	Genus	GenBank	20	9 (45%)	4 (20%)	7 (35%)	0
Asteraceae	ITS_matK_rbcLa	Genus	Regional	20	20 (100%)	0	0	0
Asteraceae	ITS_matK_rbcLa	Genus	OLFS	20	19 (95%)	0	1 (5%)	0
Asteraceae	ITS_matK_rbcLa	Species	GenBank	20	2 (10%)	6 (30%)	12 (60%)	0
Asteraceae	ITS_matK_rbcLa	Species	Regional	20	11 (55%)	7 (35%)	2 (10%)	0
Asteraceae	ITS_matK_rbcLa	Species	OLFS	20	17 (85%)	1 (5%)	2 (10%)	0
Asteraceae	ITS_matK_trnH	Family	GenBank	17	17 (100%)	0	0	0
Asteraceae	ITS_matK_trnH	Family	Regional	17	17 (100%)	0	0	0
Asteraceae	ITS_matK_trnH	Family	OLFS	17	17 (100%)	0	0	0
Asteraceae	ITS_matK_trnH	Genus	GenBank	17	11 (64.71%)	0	6 (35.29%)	0
Asteraceae	ITS_matK_trnH	Genus	Regional	17	15 (88.24%)	1 (5.88%)	1 (5.88%)	0

(Continues)

APPENDIX 4. Continued

Family	Locus ^a	Taxon level	Database	Sequences	Confident	Ambiguous	Incorrect	No match
Asteraceae	ITS_matK_trnH	Genus	OLFS	17	7 (41.18%)	0	10 (58.82%)	0
Asteraceae	ITS_matK_trnH	Species	GenBank	17	4 (23.53%)	1 (5.88%)	12 (70.59%)	0
Asteraceae	ITS_matK_trnH	Species	Regional	17	6 (35.29%)	4 (23.53%)	7 (41.18%)	0
Asteraceae	ITS_matK_trnH	Species	OLFS	17	6 (35.29%)	0	11 (64.71%)	0
Asteraceae	ITS_rbcLa_trnH	Family	GenBank	20	20 (100%)	0	0	0
Asteraceae	ITS_rbcLa_trnH	Family	Regional	20	20 (100%)	0	0	0
Asteraceae	ITS_rbcLa_trnH	Family	OLFS	20	20 (100%)	0	0	0
Asteraceae	ITS_rbcLa_trnH	Genus	GenBank	20	16 (80%)	1 (5%)	3 (15%)	0
Asteraceae	ITS_rbcLa_trnH	Genus	Regional	20	17 (85%)	1 (5%)	2 (10%)	0
Asteraceae	ITS_rbcLa_trnH	Genus	OLFS	20	16 (80%)	1 (5%)	3 (15%)	0
Asteraceae	ITS_rbcLa_trnH	Species	GenBank	20	5 (25%)	2 (10%)	13 (65%)	0
Asteraceae	ITS_rbcLa_trnH	Species	Regional	20	7 (35%)	4 (20%)	9 (45%)	0
Asteraceae	ITS_rbcLa_trnH	Species	OLFS	20	13 (65%)	2 (10%)	5 (25%)	0
Asteraceae	matK_rbcLa_trnH	Family	GenBank	24	24 (100%)	0	0	0
Asteraceae	matK_rbcLa_trnH	Family	Regional	24	24 (100%)	0	0	0
Asteraceae	matK_rbcLa_trnH	Family	OLFS	24	24 (100%)	0	0	0
Asteraceae	matK_rbcLa_trnH	Genus	GenBank	24	15 (62.5%)	1 (4.17%)	8 (33.33%)	0
Asteraceae	matK_rbcLa_trnH	Genus	Regional	24	17 (70.83%)	5 (20.83%)	2 (8.33%)	0
Asteraceae	matK_rbcLa_trnH	Genus	OLFS	24	18 (75%)	1 (4.17%)	5 (20.83%)	0
Asteraceae	matK_rbcLa_trnH	Species	GenBank	24	7 (29.17%)	2 (8.33%)	15 (62.5%)	0
Asteraceae	matK_rbcLa_trnH	Species	Regional	24	7 (29.17%)	4 (16.67%)	13 (54.17%)	0
Asteraceae	matK_rbcLa_trnH	Species	OLFS	24	11 (45.83%)	7 (29.17%)	6 (25%)	0
Asteraceae	ITS_matK_rbcLa_trnH	Family	GenBank	17	17 (100%)	0	0	0
Asteraceae	ITS_matK_rbcLa_trnH	Family	Regional	17	17 (100%)	0	0	0
Asteraceae	ITS_matK_rbcLa_trnH	Family	OLFS	17	17 (100%)	0	0	0
Asteraceae	ITS_matK_rbcLa_trnH	Genus	GenBank	17	13 (76.47%)	0	4 (23.53%)	0
Asteraceae	ITS_matK_rbcLa_trnH	Genus	Regional	17	16 (94.12%)	0	1 (5.88%)	0
Asteraceae	ITS_matK_rbcLa_trnH	Genus	OLFS	17	15 (88.24%)	0	2 (11.76%)	0
Asteraceae	ITS_matK_rbcLa_trnH	Species	GenBank	17	5 (29.41%)	1 (5.88%)	11 (64.71%)	0
Asteraceae	ITS_matK_rbcLa_trnH	Species	Regional	17	7 (41.18%)	3 (17.65%)	7 (41.18%)	0
Asteraceae	ITS_matK_rbcLa_trnH	Species	OLFS	17	13 (76.47%)	0	4 (23.53%)	0
Cyperaceae	ITS	Family	GenBank	7	6 (85.71%)	1 (14.29%)	0	0
Cyperaceae	ITS	Family	Regional	7	7 (100%)	0	0	0
Cyperaceae	ITS	Family	OLFS	7	7 (100%)	0	0	0
Cyperaceae	ITS	Genus	GenBank	7	6 (85.71%)	1 (14.29%)	0	0
Cyperaceae	ITS	Genus	Regional	7	7 (100%)	0	0	0
Cyperaceae	ITS	Genus	OLFS	7	7 (100%)	0	0	0
Cyperaceae	ITS	Species	GenBank	7	1 (14.29%)	2 (28.57%)	4 (57.14%)	0
Cyperaceae	ITS	Species	Regional	7	2 (28.57%)	2 (28.57%)	3 (42.86%)	0
Cyperaceae	ITS	Species	OLFS	7	4 (57.14%)	1 (14.29%)	2 (28.57%)	0
Cyperaceae	trnH	Family	GenBank	5	2 (40%)	0	3 (60%)	0
Cyperaceae	trnH	Family	Regional	5	2 (40%)	0	3 (60%)	0
Cyperaceae	trnH	Family	OLFS	5	0	0	4 (80%)	1 (20%)
Cyperaceae	trnH	Genus	GenBank	5	2 (40%)	0	3 (60%)	0
Cyperaceae	trnH	Genus	Regional	5	2 (40%)	0	3 (60%)	0
Cyperaceae	trnH	Genus	OLFS	5	0	0	4 (80%)	1 (20%)
Cyperaceae	trnH	Species	GenBank	5	0	1 (20%)	4 (80%)	0
Cyperaceae	trnH	Species	Regional	5	0	0	5 (100%)	0
Cyperaceae	trnH	Species	OLFS	5	0	0	4 (80%)	1 (20%)
Cyperaceae	matK	Family	GenBank	1	0	0	1 (100%)	0
Cyperaceae	matK	Family	Regional	1	0	0	1 (100%)	0
Cyperaceae	matK	Family	OLFS	1	0	0	1 (100%)	0
Cyperaceae	matK	Genus	GenBank	1	0	0	1 (100%)	0
Cyperaceae	matK	Genus	Regional	1	0	0	1 (100%)	0
Cyperaceae	matK	Genus	OLFS	1	0	0	1 (100%)	0
Cyperaceae	matK	Species	GenBank	1	0	0	1 (100%)	0
Cyperaceae	matK	Species	Regional	1	0	0	1 (100%)	0
Cyperaceae	matK	Species	OLFS	1	0	0	1 (100%)	0
Cyperaceae	rbclLa	Family	GenBank	24	23 (95.83%)	0	1 (4.17%)	0
Cyperaceae	rbclLa	Family	Regional	24	23 (95.83%)	0	1 (4.17%)	0
Cyperaceae	rbclLa	Family	OLFS	24	23 (95.83%)	0	1 (4.17%)	0
Cyperaceae	rbclLa	Genus	GenBank	24	22 (91.67%)	1 (4.17%)	1 (4.17%)	0

(Continues)

APPENDIX 4. Continued

Family	Locus ^a	Taxon level	Database	Sequences	Confident	Ambiguous	Incorrect	No match
Cyperaceae	rbclLa	Genus	Regional	24	22 (91.67%)	1 (4.17%)	1 (4.17%)	0
Cyperaceae	rbclLa	Genus	OLFS	24	23 (95.83%)	0	1 (4.17%)	0
Cyperaceae	rbclLa	Species	GenBank	24	0	5 (20.83%)	19 (79.17%)	0
Cyperaceae	rbclLa	Species	Regional	24	2 (8.33%)	6 (25%)	16 (66.67%)	0
Cyperaceae	rbclLa	Species	OLFS	24	8 (33.33%)	3 (12.5%)	13 (54.17%)	0
Cyperaceae	ITS_trnH	Family	GenBank	1	1 (100%)	0	0	0
Cyperaceae	ITS_trnH	Family	Regional	1	1 (100%)	0	0	0
Cyperaceae	ITS_trnH	Family	OLFS	1	1 (100%)	0	0	0
Cyperaceae	ITS_trnH	Genus	GenBank	1	1 (100%)	0	0	0
Cyperaceae	ITS_trnH	Genus	Regional	1	1 (100%)	0	0	0
Cyperaceae	ITS_trnH	Genus	OLFS	1	1 (100%)	0	0	0
Cyperaceae	ITS_trnH	Species	GenBank	1	1 (100%)	0	0	0
Cyperaceae	ITS_trnH	Species	Regional	1	1 (100%)	0	0	0
Cyperaceae	ITS_trnH	Species	OLFS	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK	Family	GenBank	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK	Family	Regional	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK	Family	OLFS	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK	Genus	GenBank	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK	Genus	Regional	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK	Genus	OLFS	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK	Species	GenBank	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK	Species	Regional	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK	Species	OLFS	1	1 (100%)	0	0	0
Cyperaceae	ITS_rbcLa	Family	GenBank	7	6 (85.71%)	1 (14.29%)	0	0
Cyperaceae	ITS_rbcLa	Family	Regional	7	7 (100%)	0	0	0
Cyperaceae	ITS_rbcLa	Family	OLFS	7	7 (100%)	0	0	0
Cyperaceae	ITS_rbcLa	Genus	GenBank	7	6 (85.71%)	1 (14.29%)	0	0
Cyperaceae	ITS_rbcLa	Genus	Regional	7	7 (100%)	0	0	0
Cyperaceae	ITS_rbcLa	Genus	OLFS	7	7 (100%)	0	0	0
Cyperaceae	ITS_rbcLa	Species	GenBank	7	1 (14.29%)	2 (28.57%)	4 (57.14%)	0
Cyperaceae	ITS_rbcLa	Species	Regional	7	2 (28.57%)	2 (28.57%)	3 (42.86%)	0
Cyperaceae	ITS_rbcLa	Species	OLFS	7	5 (71.43%)	1 (14.29%)	1 (14.29%)	0
Cyperaceae	matK_rbcLa	Family	GenBank	1	0	0	1 (100%)	0
Cyperaceae	matK_rbcLa	Family	Regional	1	1 (100%)	0	0	0
Cyperaceae	matK_rbcLa	Family	OLFS	1	1 (100%)	0	0	0
Cyperaceae	matK_rbcLa	Genus	GenBank	1	0	0	1 (100%)	0
Cyperaceae	matK_rbcLa	Genus	Regional	1	1 (100%)	0	0	0
Cyperaceae	matK_rbcLa	Genus	OLFS	1	1 (100%)	0	0	0
Cyperaceae	matK_rbcLa	Species	GenBank	1	0	0	1 (100%)	0
Cyperaceae	matK_rbcLa	Species	Regional	1	0	0	1 (100%)	0
Cyperaceae	matK_rbcLa	Species	OLFS	1	0	0	1 (100%)	0
Cyperaceae	matK_trnH	Family	GenBank	1	0	0	1 (100%)	0
Cyperaceae	matK_trnH	Family	Regional	1	0	0	1 (100%)	0
Cyperaceae	matK_trnH	Family	OLFS	1	0	0	1 (100%)	0
Cyperaceae	matK_trnH	Genus	GenBank	1	0	0	1 (100%)	0
Cyperaceae	matK_trnH	Genus	Regional	1	0	0	1 (100%)	0
Cyperaceae	matK_trnH	Genus	OLFS	1	0	0	1 (100%)	0
Cyperaceae	matK_trnH	Species	GenBank	1	0	0	1 (100%)	0
Cyperaceae	matK_trnH	Species	Regional	1	0	0	1 (100%)	0
Cyperaceae	matK_trnH	Species	OLFS	1	0	0	1 (100%)	0
Cyperaceae	rbclLa_trnH	Family	GenBank	4	2 (50%)	0	2 (50%)	0
Cyperaceae	rbclLa_trnH	Family	Regional	4	3 (75%)	0	1 (25%)	0
Cyperaceae	rbclLa_trnH	Family	OLFS	4	3 (75%)	0	1 (25%)	0
Cyperaceae	rbclLa_trnH	Genus	GenBank	4	2 (50%)	0	2 (50%)	0
Cyperaceae	rbclLa_trnH	Genus	Regional	4	3 (75%)	0	1 (25%)	0
Cyperaceae	rbclLa_trnH	Genus	OLFS	4	3 (75%)	0	1 (25%)	0
Cyperaceae	rbclLa_trnH	Species	GenBank	4	0	1 (25%)	3 (75%)	0
Cyperaceae	rbclLa_trnH	Species	Regional	4	0	2 (50%)	2 (50%)	0
Cyperaceae	rbclLa_trnH	Species	OLFS	4	2 (50%)	0	2 (50%)	0
Cyperaceae	ITS_matK_rbcLa	Family	GenBank	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_rbcLa	Family	Regional	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_rbcLa	Family	OLFS	1	1 (100%)	0	0	0

(Continues)

APPENDIX 4. Continued

Family	Locus ^a	Taxon level	Database	Sequences	Confident	Ambiguous	Incorrect	No match
Cyperaceae	ITS_matK_rbcLa	Genus	GenBank	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_rbcLa	Genus	Regional	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_rbcLa	Genus	OLFS	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_rbcLa	Species	GenBank	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_rbcLa	Species	Regional	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_rbcLa	Species	OLFS	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_trnH	Family	GenBank	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_trnH	Family	Regional	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_trnH	Family	OLFS	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_trnH	Genus	GenBank	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_trnH	Genus	Regional	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_trnH	Genus	OLFS	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_trnH	Species	GenBank	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_trnH	Species	Regional	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_trnH	Species	OLFS	1	1 (100%)	0	0	0
Cyperaceae	ITS_rbcLa_trnH	Family	GenBank	1	1 (100%)	0	0	0
Cyperaceae	ITS_rbcLa_trnH	Family	Regional	1	1 (100%)	0	0	0
Cyperaceae	ITS_rbcLa_trnH	Family	OLFS	1	1 (100%)	0	0	0
Cyperaceae	ITS_rbcLa_trnH	Genus	GenBank	1	1 (100%)	0	0	0
Cyperaceae	ITS_rbcLa_trnH	Genus	Regional	1	1 (100%)	0	0	0
Cyperaceae	ITS_rbcLa_trnH	Genus	OLFS	1	1 (100%)	0	0	0
Cyperaceae	ITS_rbcLa_trnH	Species	GenBank	1	1 (100%)	0	0	0
Cyperaceae	ITS_rbcLa_trnH	Species	Regional	1	1 (100%)	0	0	0
Cyperaceae	ITS_rbcLa_trnH	Species	OLFS	1	1 (100%)	0	0	0
Cyperaceae	matK_rbcLa_trnH	Family	GenBank	1	0	0	1 (100%)	0
Cyperaceae	matK_rbcLa_trnH	Family	Regional	1	1 (100%)	0	0	0
Cyperaceae	matK_rbcLa_trnH	Family	OLFS	1	1 (100%)	0	0	0
Cyperaceae	matK_rbcLa_trnH	Genus	GenBank	1	0	0	1 (100%)	0
Cyperaceae	matK_rbcLa_trnH	Genus	Regional	1	1 (100%)	0	0	0
Cyperaceae	matK_rbcLa_trnH	Genus	OLFS	1	1 (100%)	0	0	0
Cyperaceae	matK_rbcLa_trnH	Species	GenBank	1	0	0	1 (100%)	0
Cyperaceae	matK_rbcLa_trnH	Species	Regional	1	0	0	1 (100%)	0
Cyperaceae	matK_rbcLa_trnH	Species	OLFS	1	0	0	1 (100%)	0
Cyperaceae	ITS_matK_rbcLa_trnH	Family	GenBank	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_rbcLa_trnH	Family	Regional	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_rbcLa_trnH	Family	OLFS	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_rbcLa_trnH	Genus	GenBank	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_rbcLa_trnH	Genus	Regional	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_rbcLa_trnH	Genus	OLFS	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_rbcLa_trnH	Species	GenBank	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_rbcLa_trnH	Species	Regional	1	1 (100%)	0	0	0
Cyperaceae	ITS_matK_rbcLa_trnH	Species	OLFS	1	1 (100%)	0	0	0
Fabaceae	ITS	Family	GenBank	15	14 (93.33%)	1 (6.67%)	0	0
Fabaceae	ITS	Family	Regional	15	14 (93.33%)	0	1 (6.67%)	0
Fabaceae	ITS	Family	OLFS	15	14 (93.33%)	0	0	1 (6.67%)
Fabaceae	ITS	Genus	GenBank	15	11 (73.33%)	1 (6.67%)	3 (20%)	0
Fabaceae	ITS	Genus	Regional	15	11 (73.33%)	0	4 (26.67%)	0
Fabaceae	ITS	Genus	OLFS	15	11 (73.33%)	0	3 (20%)	1 (6.67%)
Fabaceae	ITS	Species	GenBank	15	7 (46.67%)	4 (26.67%)	4 (26.67%)	0
Fabaceae	ITS	Species	Regional	15	9 (60%)	1 (6.67%)	5 (33.33%)	0
Fabaceae	ITS	Species	OLFS	15	9 (60%)	1 (6.67%)	4 (26.67%)	1 (6.67%)
Fabaceae	trnH	Family	GenBank	4	4 (100%)	0	0	0
Fabaceae	trnH	Family	Regional	4	4 (100%)	0	0	0
Fabaceae	trnH	Family	OLFS	4	4 (100%)	0	0	0
Fabaceae	trnH	Genus	GenBank	4	4 (100%)	0	0	0
Fabaceae	trnH	Genus	Regional	4	0	0	4 (100%)	0
Fabaceae	trnH	Genus	OLFS	4	0	0	4 (100%)	0
Fabaceae	trnH	Species	GenBank	4	0	0	4 (100%)	0
Fabaceae	trnH	Species	Regional	4	0	0	4 (100%)	0
Fabaceae	trnH	Species	OLFS	4	0	0	4 (100%)	0
Fabaceae	matK	Family	GenBank	13	13 (100%)	0	0	0
Fabaceae	matK	Family	Regional	13	13 (100%)	0	0	0

(Continues)

APPENDIX 4. Continued

Family	Locus ^a	Taxon level	Database	Sequences	Confident	Ambiguous	Incorrect	No match
Fabaceae	matK	Family	OLFS	13	13 (100%)	0	0	0
Fabaceae	matK	Genus	GenBank	13	11 (84.62%)	0	2 (15.38%)	0
Fabaceae	matK	Genus	Regional	13	8 (61.54%)	0	5 (38.46%)	0
Fabaceae	matK	Genus	OLFS	13	5 (38.46%)	0	8 (61.54%)	0
Fabaceae	matK	Species	GenBank	13	1 (7.69%)	3 (23.08%)	9 (69.23%)	0
Fabaceae	matK	Species	Regional	13	2 (15.38%)	0	11 (84.62%)	0
Fabaceae	matK	Species	OLFS	13	3 (23.08%)	0	10 (76.92%)	0
Fabaceae	rbcLa	Family	GenBank	20	20 (100%)	0	0	0
Fabaceae	rbcLa	Family	Regional	20	19 (95%)	0	0	1 (5%)
Fabaceae	rbcLa	Family	OLFS	20	19 (95%)	0	0	1 (5%)
Fabaceae	rbcLa	Genus	GenBank	20	11 (55%)	6 (30%)	3 (15%)	0
Fabaceae	rbcLa	Genus	Regional	20	16 (80%)	1 (5%)	2 (10%)	1 (5%)
Fabaceae	rbcLa	Genus	OLFS	20	16 (80%)	1 (5%)	2 (10%)	1 (5%)
Fabaceae	rbcLa	Species	GenBank	20	2 (10%)	13 (65%)	5 (25%)	0
Fabaceae	rbcLa	Species	Regional	20	5 (25%)	10 (50%)	4 (20%)	1 (5%)
Fabaceae	rbcLa	Species	OLFS	20	8 (40%)	8 (40%)	3 (15%)	1 (5%)
Fabaceae	ITS_trnH	Family	GenBank	3	3 (100%)	0	0	0
Fabaceae	ITS_trnH	Family	Regional	3	3 (100%)	0	0	0
Fabaceae	ITS_trnH	Family	OLFS	3	3 (100%)	0	0	0
Fabaceae	ITS_trnH	Genus	GenBank	3	3 (100%)	0	0	0
Fabaceae	ITS_trnH	Genus	Regional	3	3 (100%)	0	0	0
Fabaceae	ITS_trnH	Genus	OLFS	3	3 (100%)	0	0	0
Fabaceae	ITS_trnH	Species	GenBank	3	2 (66.67%)	1 (33.33%)	0	0
Fabaceae	ITS_trnH	Species	Regional	3	3 (100%)	0	0	0
Fabaceae	ITS_trnH	Species	OLFS	3	3 (100%)	0	0	0
Fabaceae	ITS_matK	Family	GenBank	8	8 (100%)	0	0	0
Fabaceae	ITS_matK	Family	Regional	8	8 (100%)	0	0	0
Fabaceae	ITS_matK	Family	OLFS	8	8 (100%)	0	0	0
Fabaceae	ITS_matK	Genus	GenBank	8	6 (75%)	0	2 (25%)	0
Fabaceae	ITS_matK	Genus	Regional	8	6 (75%)	0	2 (25%)	0
Fabaceae	ITS_matK	Genus	OLFS	8	6 (75%)	0	2 (25%)	0
Fabaceae	ITS_matK	Species	GenBank	8	2 (25%)	3 (37.5%)	3 (37.5%)	0
Fabaceae	ITS_matK	Species	Regional	8	4 (50%)	1 (12.5%)	3 (37.5%)	0
Fabaceae	ITS_matK	Species	OLFS	8	4 (50%)	1 (12.5%)	3 (37.5%)	0
Fabaceae	ITS_rbcLa	Family	GenBank	15	14 (93.33%)	1 (6.67%)	0	0
Fabaceae	ITS_rbcLa	Family	Regional	15	15 (100%)	0	0	0
Fabaceae	ITS_rbcLa	Family	OLFS	15	15 (100%)	0	0	0
Fabaceae	ITS_rbcLa	Genus	GenBank	15	11 (73.33%)	1 (6.67%)	3 (20%)	0
Fabaceae	ITS_rbcLa	Genus	Regional	15	12 (80%)	0	3 (20%)	0
Fabaceae	ITS_rbcLa	Genus	OLFS	15	12 (80%)	0	3 (20%)	0
Fabaceae	ITS_rbcLa	Species	GenBank	15	6 (40%)	5 (33.33%)	4 (26.67%)	0
Fabaceae	ITS_rbcLa	Species	Regional	15	10 (66.67%)	1 (6.67%)	4 (26.67%)	0
Fabaceae	ITS_rbcLa	Species	OLFS	15	10 (66.67%)	1 (6.67%)	4 (26.67%)	0
Fabaceae	matK_rbcLa	Family	GenBank	13	13 (100%)	0	0	0
Fabaceae	matK_rbcLa	Family	Regional	13	13 (100%)	0	0	0
Fabaceae	matK_rbcLa	Family	OLFS	13	13 (100%)	0	0	0
Fabaceae	matK_rbcLa	Genus	GenBank	13	11 (84.62%)	0	2 (15.38%)	0
Fabaceae	matK_rbcLa	Genus	Regional	13	11 (84.62%)	0	2 (15.38%)	0
Fabaceae	matK_rbcLa	Genus	OLFS	13	11 (84.62%)	0	2 (15.38%)	0
Fabaceae	matK_rbcLa	Species	GenBank	13	2 (15.38%)	5 (38.46%)	6 (46.15%)	0
Fabaceae	matK_rbcLa	Species	Regional	13	3 (23.08%)	7 (53.85%)	3 (23.08%)	0
Fabaceae	matK_rbcLa	Species	OLFS	13	4 (30.77%)	7 (53.85%)	2 (15.38%)	0
Fabaceae	matK_trnH	Family	GenBank	3	3 (100%)	0	0	0
Fabaceae	matK_trnH	Family	Regional	3	3 (100%)	0	0	0
Fabaceae	matK_trnH	Family	OLFS	3	3 (100%)	0	0	0
Fabaceae	matK_trnH	Genus	GenBank	3	3 (100%)	0	0	0
Fabaceae	matK_trnH	Genus	Regional	3	3 (100%)	0	0	0
Fabaceae	matK_trnH	Genus	OLFS	3	1 (33.33%)	0	2 (66.67%)	0
Fabaceae	matK_trnH	Species	GenBank	3	0	0	3 (100%)	0
Fabaceae	matK_trnH	Species	Regional	3	0	0	3 (100%)	0
Fabaceae	matK_trnH	Species	OLFS	3	0	0	3 (100%)	0
Fabaceae	rbcLa_trnH	Family	GenBank	4	4 (100%)	0	0	0

(Continues)

APPENDIX 4. Continued

Family	Locus ^a	Taxon level	Database	Sequences	Confident	Ambiguous	Incorrect	No match
Fabaceae	rbclLa_trnH	Family	Regional	4	4 (100%)	0	0	0
Fabaceae	rbclLa_trnH	Family	OLFS	4	4 (100%)	0	0	0
Fabaceae	rbclLa_trnH	Genus	GenBank	4	4 (100%)	0	0	0
Fabaceae	rbclLa_trnH	Genus	Regional	4	4 (100%)	0	0	0
Fabaceae	rbclLa_trnH	Genus	OLFS	4	4 (100%)	0	0	0
Fabaceae	rbclLa_trnH	Species	GenBank	4	0	0	4 (100%)	0
Fabaceae	rbclLa_trnH	Species	Regional	4	2 (50%)	2 (50%)	0	0
Fabaceae	rbclLa_trnH	Species	OLFS	4	2 (50%)	2 (50%)	0	0
Fabaceae	ITS_matK_rbcLa	Family	GenBank	8	8 (100%)	0	0	0
Fabaceae	ITS_matK_rbcLa	Family	Regional	8	8 (100%)	0	0	0
Fabaceae	ITS_matK_rbcLa	Family	OLFS	8	8 (100%)	0	0	0
Fabaceae	ITS_matK_rbcLa	Genus	GenBank	8	6 (75%)	0	2 (25%)	0
Fabaceae	ITS_matK_rbcLa	Genus	Regional	8	6 (75%)	0	2 (25%)	0
Fabaceae	ITS_matK_rbcLa	Genus	OLFS	8	6 (75%)	0	2 (25%)	0
Fabaceae	ITS_matK_rbcLa	Species	GenBank	8	2 (25%)	3 (37.5%)	3 (37.5%)	0
Fabaceae	ITS_matK_rbcLa	Species	Regional	8	4 (50%)	1 (12.5%)	3 (37.5%)	0
Fabaceae	ITS_matK_rbcLa	Species	OLFS	8	4 (50%)	1 (12.5%)	3 (37.5%)	0
Fabaceae	ITS_matK_trnH	Family	GenBank	2	2 (100%)	0	0	0
Fabaceae	ITS_matK_trnH	Family	Regional	2	2 (100%)	0	0	0
Fabaceae	ITS_matK_trnH	Family	OLFS	2	2 (100%)	0	0	0
Fabaceae	ITS_matK_trnH	Genus	GenBank	2	2 (100%)	0	0	0
Fabaceae	ITS_matK_trnH	Genus	Regional	2	2 (100%)	0	0	0
Fabaceae	ITS_matK_trnH	Genus	OLFS	2	2 (100%)	0	0	0
Fabaceae	ITS_matK_trnH	Species	GenBank	2	2 (100%)	0	0	0
Fabaceae	ITS_matK_trnH	Species	Regional	2	2 (100%)	0	0	0
Fabaceae	ITS_matK_trnH	Species	OLFS	2	2 (100%)	0	0	0
Fabaceae	ITS_rbcLa_trnH	Family	GenBank	3	3 (100%)	0	0	0
Fabaceae	ITS_rbcLa_trnH	Family	Regional	3	3 (100%)	0	0	0
Fabaceae	ITS_rbcLa_trnH	Family	OLFS	3	3 (100%)	0	0	0
Fabaceae	ITS_rbcLa_trnH	Genus	GenBank	3	3 (100%)	0	0	0
Fabaceae	ITS_rbcLa_trnH	Genus	Regional	3	3 (100%)	0	0	0
Fabaceae	ITS_rbcLa_trnH	Genus	OLFS	3	3 (100%)	0	0	0
Fabaceae	ITS_rbcLa_trnH	Species	GenBank	3	2 (66.67%)	1 (33.33%)	0	0
Fabaceae	ITS_rbcLa_trnH	Species	Regional	3	3 (100%)	0	0	0
Fabaceae	ITS_rbcLa_trnH	Species	OLFS	3	3 (100%)	0	0	0
Fabaceae	matK_rbcLa_trnH	Family	GenBank	3	3 (100%)	0	0	0
Fabaceae	matK_rbcLa_trnH	Family	Regional	3	3 (100%)	0	0	0
Fabaceae	matK_rbcLa_trnH	Family	OLFS	3	3 (100%)	0	0	0
Fabaceae	matK_rbcLa_trnH	Genus	GenBank	3	3 (100%)	0	0	0
Fabaceae	matK_rbcLa_trnH	Genus	Regional	3	3 (100%)	0	0	0
Fabaceae	matK_rbcLa_trnH	Genus	OLFS	3	3 (100%)	0	0	0
Fabaceae	matK_rbcLa_trnH	Species	GenBank	3	0	0	3 (100%)	0
Fabaceae	matK_rbcLa_trnH	Species	Regional	3	1 (33.33%)	2 (66.67%)	0	0
Fabaceae	matK_rbcLa_trnH	Species	OLFS	3	1 (33.33%)	2 (66.67%)	0	0
Fabaceae	ITS_matK_rbcLa_trnH	Family	GenBank	2	2 (100%)	0	0	0
Fabaceae	ITS_matK_rbcLa_trnH	Family	Regional	2	2 (100%)	0	0	0
Fabaceae	ITS_matK_rbcLa_trnH	Family	OLFS	2	2 (100%)	0	0	0
Fabaceae	ITS_matK_rbcLa_trnH	Genus	GenBank	2	2 (100%)	0	0	0
Fabaceae	ITS_matK_rbcLa_trnH	Genus	Regional	2	2 (100%)	0	0	0
Fabaceae	ITS_matK_rbcLa_trnH	Genus	OLFS	2	2 (100%)	0	0	0
Fabaceae	ITS_matK_rbcLa_trnH	Species	GenBank	2	2 (100%)	0	0	0
Fabaceae	ITS_matK_rbcLa_trnH	Species	Regional	2	2 (100%)	0	0	0
Fabaceae	ITS_matK_rbcLa_trnH	Species	OLFS	2	2 (100%)	0	0	0
Poaceae	ITS	Family	GenBank	29	22 (75.86%)	6 (20.69%)	1 (3.45%)	0
Poaceae	ITS	Family	Regional	29	29 (100%)	0	0	0
Poaceae	ITS	Family	OLFS	29	29 (100%)	0	0	0
Poaceae	ITS	Genus	GenBank	29	15 (51.72%)	7 (24.14%)	7 (24.14%)	0
Poaceae	ITS	Genus	Regional	29	20 (68.97%)	3 (10.34%)	6 (20.69%)	0
Poaceae	ITS	Genus	OLFS	29	21 (72.41%)	2 (6.9%)	6 (20.69%)	0
Poaceae	ITS	Species	GenBank	29	4 (13.79%)	8 (27.59%)	17 (58.62%)	0
Poaceae	ITS	Species	Regional	29	11 (37.93%)	3 (10.34%)	15 (51.72%)	0
Poaceae	ITS	Species	OLFS	29	15 (51.72%)	5 (17.24%)	9 (31.03%)	0

(Continues)

APPENDIX 4. Continued

Family	Locus ^a	Taxon level	Database	Sequences	Confident	Ambiguous	Incorrect	No match
Poaceae	trnH	Family	GenBank	33	32 (96.97%)	0	1 (3.03%)	0
Poaceae	trnH	Family	Regional	33	32 (96.97%)	0	1 (3.03%)	0
Poaceae	trnH	Family	OLFS	33	32 (96.97%)	0	1 (3.03%)	0
Poaceae	trnH	Genus	GenBank	33	17 (51.52%)	10 (30.3%)	6 (18.18%)	0
Poaceae	trnH	Genus	Regional	33	14 (42.42%)	1 (3.03%)	18 (54.55%)	0
Poaceae	trnH	Genus	OLFS	33	8 (24.24%)	0	25 (75.76%)	0
Poaceae	trnH	Species	GenBank	33	3 (9.09%)	16 (48.48%)	14 (42.42%)	0
Poaceae	trnH	Species	Regional	33	2 (6.06%)	3 (9.09%)	28 (84.85%)	0
Poaceae	trnH	Species	OLFS	33	7 (21.21%)	0	26 (78.79%)	0
Poaceae	rbcLa	Family	GenBank	34	34 (100%)	0	0	0
Poaceae	rbcLa	Family	Regional	34	34 (100%)	0	0	0
Poaceae	rbcLa	Family	OLFS	34	34 (100%)	0	0	0
Poaceae	rbcLa	Genus	GenBank	34	9 (26.47%)	23 (67.65%)	2 (5.88%)	0
Poaceae	rbcLa	Genus	Regional	34	14 (41.18%)	16 (47.06%)	4 (11.76%)	0
Poaceae	rbcLa	Genus	OLFS	34	24 (70.59%)	6 (17.65%)	4 (11.76%)	0
Poaceae	rbcLa	Species	GenBank	34	2 (5.88%)	22 (64.71%)	10 (29.41%)	0
Poaceae	rbcLa	Species	Regional	34	4 (11.76%)	14 (41.18%)	16 (47.06%)	0
Poaceae	rbcLa	Species	OLFS	34	14 (41.18%)	15 (44.12%)	5 (14.71%)	0
Poaceae	ITS_trnH	Family	GenBank	27	21 (77.78%)	5 (18.52%)	1 (3.7%)	0
Poaceae	ITS_trnH	Family	Regional	27	27 (100%)	0	0	0
Poaceae	ITS_trnH	Family	OLFS	27	27 (100%)	0	0	0
Poaceae	ITS_trnH	Genus	GenBank	27	13 (48.15%)	6 (22.22%)	8 (29.63%)	0
Poaceae	ITS_trnH	Genus	Regional	27	18 (66.67%)	2 (7.41%)	7 (25.93%)	0
Poaceae	ITS_trnH	Genus	OLFS	27	18 (66.67%)	1 (3.7%)	8 (29.63%)	0
Poaceae	ITS_trnH	Species	GenBank	27	4 (14.81%)	7 (25.93%)	16 (59.26%)	0
Poaceae	ITS_trnH	Species	Regional	27	12 (44.44%)	2 (7.41%)	13 (48.15%)	0
Poaceae	ITS_trnH	Species	OLFS	27	13 (48.15%)	2 (7.41%)	12 (44.44%)	0
Poaceae	ITS_rbcLa	Family	GenBank	29	25 (86.21%)	4 (13.79%)	0	0
Poaceae	ITS_rbcLa	Family	Regional	29	29 (100%)	0	0	0
Poaceae	ITS_rbcLa	Family	OLFS	29	29 (100%)	0	0	0
Poaceae	ITS_rbcLa	Genus	GenBank	29	14 (48.28%)	12 (41.38%)	3 (10.34%)	0
Poaceae	ITS_rbcLa	Genus	Regional	29	19 (65.52%)	4 (13.79%)	6 (20.69%)	0
Poaceae	ITS_rbcLa	Genus	OLFS	29	23 (79.31%)	2 (6.9%)	4 (13.79%)	0
Poaceae	ITS_rbcLa	Species	GenBank	29	4 (13.79%)	12 (41.38%)	13 (44.83%)	0
Poaceae	ITS_rbcLa	Species	Regional	29	9 (31.03%)	4 (13.79%)	16 (55.17%)	0
Poaceae	ITS_rbcLa	Species	OLFS	29	16 (55.17%)	6 (20.69%)	7 (24.14%)	0
Poaceae	rbcLa_trnH	Family	GenBank	32	32 (100%)	0	0	0
Poaceae	rbcLa_trnH	Family	Regional	32	32 (100%)	0	0	0
Poaceae	rbcLa_trnH	Family	OLFS	32	32 (100%)	0	0	0
Poaceae	rbcLa_trnH	Genus	GenBank	32	13 (40.62%)	13 (40.62%)	6 (18.75%)	0
Poaceae	rbcLa_trnH	Genus	Regional	32	16 (50%)	12 (37.5%)	4 (12.5%)	0
Poaceae	rbcLa_trnH	Genus	OLFS	32	23 (71.88%)	5 (15.62%)	4 (12.5%)	0
Poaceae	rbcLa_trnH	Species	GenBank	32	4 (12.5%)	16 (50%)	12 (37.5%)	0
Poaceae	rbcLa_trnH	Species	Regional	32	5 (15.62%)	14 (43.75%)	13 (40.62%)	0
Poaceae	rbcLa_trnH	Species	OLFS	32	16 (50%)	10 (31.25%)	6 (18.75%)	0
Poaceae	ITS_rbcLa_trnH	Family	GenBank	27	24 (88.89%)	3 (11.11%)	0	0
Poaceae	ITS_rbcLa_trnH	Family	Regional	27	27 (100%)	0	0	0
Poaceae	ITS_rbcLa_trnH	Family	OLFS	27	27 (100%)	0	0	0
Poaceae	ITS_rbcLa_trnH	Genus	GenBank	27	12 (44.44%)	9 (33.33%)	6 (22.22%)	0
Poaceae	ITS_rbcLa_trnH	Genus	Regional	27	18 (66.67%)	3 (11.11%)	6 (22.22%)	0
Poaceae	ITS_rbcLa_trnH	Genus	OLFS	27	21 (77.78%)	2 (7.41%)	4 (14.81%)	0
Poaceae	ITS_rbcLa_trnH	Species	GenBank	27	4 (14.81%)	11 (40.74%)	12 (44.44%)	0
Poaceae	ITS_rbcLa_trnH	Species	Regional	27	10 (37.04%)	4 (14.81%)	13 (48.15%)	0
Poaceae	ITS_rbcLa_trnH	Species	OLFS	27	15 (55.56%)	4 (14.81%)	8 (29.63%)	0

Note: OLFS = database of species sampled from Oak Lake Field Station.

^aMulti-region barcodes are indicated by underscore.