Phylogenetic relationships of Australian *Poa* (Poaceae: Poinae), including molecular evidence for two new genera, *Saxipoa* and *Sylvipoa*

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Abstract. Phylogenetic relationships among Australian species of *Poa* and other subtribe Poinae genera were studied on the basis of plastid *trn*T–*trn*L–*trn*F and nuclear ribosomal ITS and ETS DNA sequence data. Molecular evidence is provided for two new monotypic endemic Australian genera, *Sylvipoa* and *Saxipoa*, on the basis of two species formerly included in *Poa*, *P. queenslandica* and *P. saxicola*, respectively. Both new genera resolved in a clade with three subtribe Poinae genera, the Australian genus *Hookerochloa*, the South American genus *Nicoraepoa*, and the arctic genus *Arctagrostis*. *Sylvipoa* and *Nicoraepoa* are sister taxa. *Saxipoa* resolved as sister to these plus *Arctagrostis*, but also shares DNA sequence characters with *Hookerochloa*, suggesting a possible hybrid origin. All other Australian *Poa* species studied resolved in a subclade within the *P.* subgenus *Poa* supersection *Homalopoa* clade, supporting their classification together in an expanded *P.* section *Brizoides*. Five New Zealand and one New Guinea species also resolved in this subclade, supporting their membership in this section. We postulate a minimum of two dispersal events into Australia, one for *Poa* and one for other Poinae genera, and a minimum of three into New Zealand and two into New Guinea for *Poa*.

Introduction

The grass genus *Poa*, with some 500 species worldwide, is species-rich in the Australia–New Zealand–Malesian region (Australasia). In recent treatments, *Poa* included 43 endemic species from Australia (Walsh *et al.* 2009), 32 from New Zealand, with one coastal species native to both Australia and New Zealand (Edgar and Connor 2000), and 35 in the Malesian flora, with the majority endemic to New Guinea (Veldkamp 1994). The relationships of the majority of these species are poorly known and, up to now, very few have been placed in infrageneric classifications of the genus (Tzvelev 1976; Edmondson 1980; Soreng 1998, 2007; Soreng *et al.* 2003; Gillespie and Soreng 2005; Zhu *et al.* 2006; Gillespie *et al.* 2007, 2008; Soreng and Gillespie 2007). Soreng *et al.* (2009) provided a review of the taxonomic history of the Australian *Poa* species.

Poa is a member of subtribe Poinae (including Cinninae), which comprises 21 currently recognised genera (*Agrostopoa*, *Aniselytron*, *Apera*, *Arctagrostis*, *Arctophila*, *Arctopoa*, *Bellardiochloa*, *Cinna*, *Cyathopus*, *Dupontia*, *Gaudiniopsis*, *Hookerochloa*, *Libyella*, *Limnodea*, *Lindbergella*, *Nephelochloa*, *Nicoraepoa*, *Saxipoa*, *Sylvipoa*, *Ventenata*) (Soreng *et al.* 2000; Gillespie *et al.* 2008, in press; Davidse *et al.* 2009), plus two genera likely to belong in Poinae on the basis

of a recent molecular study (*Parvotrisetum*, *Simplicia*) (Döring 2009). An additional 13 Poinae genera were previously recognised, and are now mostly synonymised under *Poa* (Gillespie and Soreng 2005; Gillespie *et al.* 2007, 2008, in press; Soreng *et al.* 2007); included here are *Aphanelytrum*, *Dissanthelium* and *Tovarochloa*, which belong within *Poa*, but have yet to be transferred (Refulio-Rodriguez 2007; Gillespie *et al.* 2008). All the Poinae genera grow in temperate to cold climatic zones. In Australia, this subtribe includes three endemic genera, *Hookerochloa*, *Saxipoa* and *Sylvipoa*, in addition to the widespread genus *Poa*. The previously recognised Australian genera *Austrofestuca* (shared with New Zealand) and *Neuropoa* have recently been merged into *Poa* (Gillespie and Soreng 2005; Gillespie *et al.* 2008), and *Festucella* has been merged into *Hookerochloa* (Jacobs *et al.* 2008). All other Poinae genera from the southern hemisphere (*Anthochloa*, *Aphanelytrum*, *Dasypoa*, *Dissanthelium*, *Parodiochloa*, and *Tovarochloa* from South America, and *Tzvelevia* from Heard and Kerguelen islands in the southern Indian Ocean) are phylogenetically nested within *Poa* (Gillespie and Soreng 2005; Gillespie *et al.* 2007, 2008), with the exception of the recently described South American genus *Nicoraepoa* (Soreng and Gillespie 2007; Gillespie *et al.*

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2008), and the New Zealand endemic genus *Simplicia* (Döring 2009).

Relationships within the genus *Poa* have been examined in molecular phylogenetic studies, initially with plastid restriction-site data (Soreng 1990; Gillespie and Boles 2001; Gillespie and Soreng 2005), and subsequently with plastid *trn*T–*trn*L–*trn*F (TLF) sequence data (Gillespie *et al.* 2007), plus nuclear rDNA (nrDNA) internal transcribed spacer (ITS) sequence data (Gillespie *et al.* 2008; Soreng *et al.* in press), and most recently with nrDNA external transcribed spacer (ETS) data (Gillespie *et al.* in press). All previously sampled Australian *Poa* (nine species, including the following *Austrofestuca s.s.* and *Neuropoa* species: *Austrofestuca littoralis* = *P. billardierei*, *Austrofestuca pubinervis*, *P. drummondiana*, *P. fawcettiae*, *P. fax*, *P. labillardierei*, *P. poiformis*, *P. porphyroclados* and *P. sieberiana*; Soreng 1990; Hunter *et al.* 2004; Gillespie and Soreng 2005; Patterson *et al.* 2005; Gillespie *et al.* 2007, 2008) were determined to belong in the same major *Poa* clade, *P.* subgenus *Poa* supersection *Homalopoa* (Dumort.) Soreng & L.J.Gillespie (HAMBADD clade *sensu* Gillespie and Soreng 2005; Gillespie *et al.* 2007, 2008). Nosov and Rodionov (2008) published an ITS study of *Poa* that included 17 sequences of New Zealand *Poa* species (provided by Richard Gardner, Jeanette Keeling, Peter de Lange, Shane Wright and Ewen Cameron – see Acknowledgements).

Two new monotypic genera, *Saxipoa* and *Sylvipoa*, are published in a companion paper in this issue (Soreng *et al.* 2009), to accommodate two morphologically divergent and unusual Australian species formerly placed in *Poa*, namely, *P. saxicola* and *P. queenslandica*. The two genera differ considerably in habit and habitat; *Saxipoa* is a short plant with narrow panicles of rocky alpine or subalpine habitats, whereas *Sylvipoa* is a tall plant with large open panicles of temperate rainforest margins and openings. In the same paper, a new infrageneric classification is proposed for the remaining Australian *Poa* species. *Poa* section *Brizoides* Pilg. ex Potztal (in *P.* subgenus *Poa* supersection *Homalopoa*) was expanded to encompass all the Australian species, and six New Zealand and one New Guinean species. Four subsections were established to accommodate most of these species: *Australopoa* Soreng, L.J.Gillespie & S.W.L.Jacobs; *Austrofestuca* (Tzvelev) Soreng, L.J.Gillespie & S.W.L.Jacobs; *Brizoides* (Pilg. ex Potztal) Soreng, L.J.Gillespie & S.W.L.Jacobs; and *Neuropoa* (Clayton) Soreng, L.J.Gillespie & S.W.L.Jacobs.

Here, we provide molecular evidence for the recognition of *Saxipoa* and *Sylvipoa* and for their phylogenetic relationships within subtribe Poinae. We place the remaining Australian *Poa* species in a phylogenetic context, and provide molecular support for the new infrageneric classification. Biogeographic connections among Australasian Poinae are discussed.

Materials and methods

Taxon sampling

The sampling of taxa used here builds on our earlier molecular phylogenetic studies of *Poa* and subtribe Poinae (Gillespie and Boles 2001; Gillespie and Soreng 2005; Gillespie *et al.* 2007, 2008, in press; Soreng *et al.* in press). For *Poa*, we sampled 122 individuals representing 100 species (Appendix 1), including

26 of the 41 species of Australian *Poa* (including species formerly included in *Austrofestuca* and *Neuropoa*), 20 species from New Zealand and one from New Guinea. The analysis also included a broad taxonomically and geographically representative sample of 53 additional *Poa* species, including three of *Dissanthelium* (combinations pending in *Poa*). Our sampling within *Poa* includes elements of every major lineage within the genus resolved in our previous molecular phylogenetic studies (Gillespie and Boles 2001; Gillespie and Soreng 2005; Gillespie *et al.* 2007, 2008, in press); we sampled most extensively in the major clade (subgenus *Poa*) in which the Australian species resolved. Outside of *Poa* in subtribe Poinae (including Cinninae), we sampled 11 genera and 17 species, including the Australian genus *Hookerochloa* (including *Festucella*), and the two new monotypic endemic genera, *Saxipoa* and *Sylvipoa*. Taxa of putative hybrid origins (e.g. *Arctopoa*, *Nicoraepoa pugionifolia*, *P. abbreviata* and *P. annua*; see Gillespie *et al.* in press; Soreng *et al.* in press) and two South American genera (*Aphanelytrum*, *Tovarochloa*) that resolve on long branches within *Poa* (Gillespie *et al.* 2008) were not included in the analyses because they do not contribute to the understanding of the Australian lineages.

The following taxa representative of the four other subtribes of the large clade comprising Poinae and related subtribes (PPAM clade, Gillespie *et al.* 2008) were also included: Alopecurinae (2 genera: *Alopecurus*, *Beckmannia*; 3 species), Miliinae (1 genus: *Milium*; 2 species), Phleinae (1 genus: *Phleum*; 1 species) and Puccinelliinae (2 genera: *Catabrosa*, *Puccinellia*; 3 species) (Appendix 1). The classification of tribe Poeae *s.l.* followed here is that of Soreng *et al.* (2000 [version 27 Oct. 2008]), with modifications for these four subtribes based on Gillespie *et al.* (2008, in press; Döring 2009). Five outgroup genera were included as representatives of the other two major tribe Poeae *s.l.* clades (see Gillespie *et al.* 2008), namely, *Anthoxanthum* (subtribe Phalaridinae *s.l.*), *Agrostis* (Agrostidinae), *Deschampsia* (Airinae *s.l.*), *Festuca* (Loliinae), and *Helictotrichon s.s.* (Aveninae). New sequence data for the Australian genus *Dryopoa* (subtribe uncertain) were also included.

DNA sequences and data matrix

The majority of sequences were generated at the Canadian Museum of Nature, with 68 plastid, 80 ITS and 144 ETS sequences newly generated for the present study (Appendix 1) (~20% of these new sequences were also used in two studies submitted just before the present study, namely, Gillespie *et al.* in press, Soreng *et al.* in press). Two plastid and 13 ITS sequences were downloaded from GenBank; all other sequence data were first published in our previous studies based on plastid and ITS sequence data (Gillespie *et al.* 2007, 2008). Our methods of DNA extraction, amplification and direct sequencing of TLF and ITS are outlined in Gillespie *et al.* (2008). A region of ~460–500 base pairs (bp) at the 3′ end of the nrDNA external transcribed spacer (ETS) was amplified and sequenced by using the same reaction conditions as for ITS and primers 18S-R (Starr *et al.* 2004) and RETS4-F, a primer newly designed in our laboratory (5′-TGGCTACGCGAGCGCATGAG-3′). Although designed specifically for use in *Poa*, the RETS4-F primer also

successfully amplified all other genera in subtribe Poinae and many other tribe Poeae taxa.

Sequence assembly and editing, automated alignment and manual alignment editing were performed with Sequencher vers. 4.7 (Gene Codes Corp., Ann Arbor, MI, USA), ClustalX ver. 1.83 (Jeanmougin *et al.* 1998) and BioEdit ver. 5.0.9 (Hall 1999), respectively, as outlined in Gillespie *et al.* (2008). Obvious and unambiguous nucleotide variants within a sequence (i.e. double peaks of approximately equal strength on electropherogram traces, or at least unambiguous double peaks in an otherwise clean sequence) were coded as polymorphisms by using standard IUB ambiguity codes.

TLF, ITS, and ETS sequence alignments were merged into a single nexus format data matrix (data matrix available from the authors on request). The majority of samples had complete or near complete sequence data for all three regions. For 22 samples, sequence data for only one or two of the three data partitions were available as follows: three samples with only ITS and ETS data (*Bellardiochloa polychroa*, *Milium effusum*, *Poa hybrida*), two with TLF and ITS data (*Anthoxanthum monticola*, *Dryopoa dives*), 13 with only ITS data (all GenBank samples from New Zealand) and four (*Milium effusum*, *Poa hybrida*, *P. meionectes G7348*, *P. sieberiana AY589145*) with only TLF data (Appendix 1). Sixteen of these samples were downloaded from GenBank; the other six samples did not successfully amplify or sequence. For each terminal taxon in the combined data matrix, TLF, ITS and ETS sequences were from the same collection and individual, except for *Milium effusum* and *Poa hybrida* (Appendix 1).

Phylogenetic analyses

The decision to combine the plastid and the two nuclear ribosomal data partitions was based on examination and comparison of the separate preliminary maximum parsimony analyses of the three data partitions, and taking into account the results of incongruence length difference (ILD) tests (Farris *et al.* 1994) performed previously on a comparable Poinae dataset (Gillespie *et al.* in press). In the current dataset, the positions of Australian species did not conflict among the three data partitions when each partition was analysed separately. Although the ILD tests performed previously on similar datasets indicated that both ITS + ETS and TLF + ITS + ETS partitions were incongruent, this incongruence was primarily due to the conflicting positions of several species groups within *Poa*. These data partitions were not significantly incompatible for other Poinae genera, apart from several putative hybrid genera and species that were excluded from analyses here. Therefore, given our focus on the Australian taxa, combining data partitions is justified for the purposes of the present paper. Conflict in the *Poa* clade will be explored and described in a future paper.

Following exploratory parsimony analyses of TLF, ITS, ETS, ITS + ETS and TLF + ITS + ETS data partitions, the following three final parsimony analyses were run: TLF (plastid), ITS + ETS (nrDNA), and TLF + ITS + ETS (combined) analyses (Table 1). The number of terminals was 144 in the TLF analysis, 158 in the ITS + ETS analysis and 137 in the TLF + ITS + ETS analysis. Missing data represented <1% of each of the three data partitions. In the TLF partition, apart from missing bases in

conserved primer regions and at the ends of some sequences, three samples were incomplete, missing either the *trn*T–*trn*L spacer or the *trn*L–*trn*F spacer (Appendix 1); two of these were excluded from the TLF analysis because the missing data appeared to result in a clade collapse; however, they were included in the combined analysis (*P. cita*, *P. clelandii*). Terminal taxa were complete for all data partitions in the ITS + ETS and TLF + ITS + ETS analyses, with the exception of 13 samples in the nrDNA analysis that included only ITS data (sequences downloaded from GenBank), and two samples (*Anthoxanthum monticola*, *Dryopoa dives*) included in both analyses that were missing the ETS data partition. We excluded from the TLF + ITS + ETS analysis 15 species of *P.* subgenus *Poa* that resolved in the 'X clade' in the ITS + ETS tree (see Results) because the positions they resolve in are incongruent between the TLF and ITS + ETS trees.

Maximum parsimony (MP) and bootstrap analyses were performed in PAUP* 4.0b10 (Swofford 2002) as outlined in Gillespie *et al.* (2008). Insertion–deletion (indel) characters were not included in these analyses. Two heuristic search strategies were used, including (1) maximum tree setting of 90 000, no replication and (2) 100 random addition replicates, 900 trees saved per replicate (both search strategies gave the same results). Bootstrap analyses were performed with 1000 replicates, with 10 random addition sequences per replicate, TBR swapping, and the 'MULTREES' setting turned off because of long search times (DeBry and Olmstead 2000). Following the suggestion of Starr *et al.* (2004), bootstrap support (BS) for clades is characterised as very poor (<55%), poor (55–64%), moderate (65–74%), good (75–84%), very good (85–94%) or strong (95–100%).

Results

Sequence characteristics

Summary characteristics of the TLF, ITS and ETS data partitions, both separate and combined, are given in Table 1. The combined TLF + ITS + ETS aligned data matrix comprised 3930 characters, of which 722 positions (explained below) were deleted for a total of 3208 characters in the final analysed

Table 1. Summary statistics for maximum parsimony analyses of separate TLF, ITS and ETS datasets, and combined datasets

Total bases, total number of aligned bases; Char, no. of characters included in each analysis; PI char, no. of parsimony-informative characters; %PI char, percentage parsimony-informative characters; L, length of most parsimonious trees; CI, consistency index; CIexcPU, CI excluding parsimony-uninformative characters; and RI, retention index

Parameter	TLF (Fig. 1)	ITS	ETS	ITS + ETS (Fig. 2)	TLF + ITS + ETS (Fig. 3)
No. of terminals	144	158	142	158	137
Total bases	2053	654	680	1334	3930
Char	1972	654	582	1236	3208
PI char	196	189	223	413	626
%PI char	9.9	28.9	38.3	33.4	19.5
L	666	815	921	1776	2414
CI	0.751	0.481	0.555	0.510	0.569
CIexcPU	0.634	0.408	0.470	0.430	0.470
RI	0.923	0.817	0.855	0.832	0.850

data matrix. The TLF data partition was by far the longest, but with the lowest percentage of parsimony-informative characters, whereas the ETS partition was the shortest, but contained the most parsimony-informative characters. Detailed characteristics of TLF and ITS sequences were described in Gillespie *et al.* (2007, 2008). In the aligned TLF data matrix, an 81-bp region of ambiguous alignment in the *trn*T–*trn*L spacer was deleted before analysis; no positions were deleted from the ITS data matrix. In the ITS data, there was no evidence for the presence of pseudogenes in the 5.8S coding region; the 5.8S gene was highly conserved in all ITS sequences except for one 9-bp region (percentage parsimony-informative characters was 9% in the 5.8S region *v.* 36% in ITS1 and 35% in ITS2, and indels were absent from all 5.8S sequences).

The aligned ETS data matrix comprised a total of 680 characters, of which 98 base positions were excluded from the analysis for a total of 582 analysed characters. One 12-bp region of ambiguous alignment was excluded. Also excluded were 86 positions corresponding to four insertions; all of these insertions lacked variable nucleotide characters, two were unique to a single sample, including a 64-bp insertion in *P. infirma*, and two were shared by two samples. For individual samples, the length of the ETS region that was sequenced and included in the data matrix ranged from ~500 bp (numerous species) to 567 bp (*P. infirma*).

In the TLF data matrix, four indels were shared among Australasian taxa, and two were shared by samples within a species. *Saxipoa* and *Hookerochloa* (both species) shared a 20-bp insertion. All three samples of *Saxipoa* shared a 20-bp duplication (adjacent to and repeating the latter 20-bp insertion) and a 10-bp duplication. *Poa affinis* and *P. poiformis* (*S5911*) shared a unique 20-bp insertion. An 8-bp insertion was shared by the following 15 Australian samples: *P. amplexicaulis*, *P. billardierei*, *P. clelandii*, *P. drummondiana*, *P. fax*, *P. ensiformis*, *P. fawcettiae* (*MEL2323765*), *P. fordeana* (*G7326*), *P. homomalla*, *P. meionectes* (*G7348*), *P. porphyroclados*, *P. orba*, *P. orthoclada*, *P. pubinervis* and *P. sallacustris*; and the following three New Zealand samples: *P. cita*, *P. cockayneana* and *P. sieberiana* (AY589145). *Poa fax*, *P. fordeana* (*G7326*), *P. lowanensis* and *P. poiformis* (*G7381*) shared a 4-bp deletion. Only one informative indel was present among Australasian taxa in the ETS data matrix, namely, a 2-bp duplication shared by *P. orba* and *P. sallacustris*. There were no indels among Australasian taxa in the ITS data matrix. Although indels were not coded and included in the analysis, those that support multi-species clades are indicated on the phylograms (Figs 1–3).

Within-individual (i.e. intra-accession) variation was detected in some nrDNA sequences by using the direct sequencing approach, suggesting the presence of two (or possibly more) variant or paralagous sequences within a sample. Single nucleotide variants ('polymorphisms') were detected in about

7% of the ITS sequences (in the ITS1 and ITS2 regions, none found in the 5.8S region) and 16% of the ETS sequences for the samples sequenced in our lab (i.e. excluding those downloaded from GenBank, Appendix 1). Insertion–deletion (indel) variants were detected in about 4% of the ITS sequences and 10% of the ETS sequences; these variants were detected within a single sequencing reaction and resulted in a difficult to read chromatogram trace downstream from indel sites. To interpret this indel variation, sequences from multiple reverse- and forward-sequencing reactions, plus those from internal primers in the case of ITS, were used to form a consensus sequence. Base variants were coded with standard IUB ambiguity codes. For indel variants, the dominant variant was coded, or where peaks were equal in size, the longest variant; in examples cited below the variant coded is given first. Only variants in Australian species are described here; none were found in New Zealand species sequenced for the present study, only minor nucleotide variation was found in the New Guinean species sampled, and variants in other species are described in Gillespie *et al.* (2008, in press). Taxa from outside the Australasian region included in the present study did not have infra-sample indel variants or extensive nucleotide variants, except for *Catabrosa* and *Aniselytron* (in the latter case, only the ITS variant that was not incongruent with the TLF and ETS data was included here).

ITS sequences of all three samples of *Saxipoa saxicola* shared three insertion/deletion (indel) variants and seven base variants. Table 2 lists these 10 variants and gives the Poinae taxa that shared each variant. *Sylvipoa queenslandica* had one ITS indel variant (ITS2, Position 590: –/CGTA), the insertion being a duplication unique to this sample.

One position in the aligned ETS matrix (Characters 342, 343) was highly variable among and within Australian *Poa* samples. Both samples of *P. helmsii* and one sample of *P. phillipsiana* (*G7346*) had an indel variant at this position, with the variant being G/AC, G/AC and AC/C, respectively. These three samples shared one variant (AC) not found in any other sample or taxon analysed. The *P. helmsii* samples shared their other variant (G) with *P. orba* and *P. sallacustris* (and samples given below polymorphic for this site), whereas the second variant of *P. phillipsiana* (C) was common to all other Australian *Poa*. Several other Australian species and samples exhibited C/G nucleotide variation at this site, e.g. *P. costiniana* (*G7356-1*), *P. ensiformis*, *P. phillipsiana* (*G7369*) and *P. poiformis* (*G7381*), whereas *P. porphyroclados* showed C/A base variation at this site. Two other positions in the ETS data matrix (Characters 286 and 551) were also highly variable among Australian *Poa* species and samples, and also exhibited some within individual nucleotide variation.

Poa homomalla (for which we obtained sequence data after completion of analyses) has TLF sequences identical to *P. sallacustris* and *P. orba*, and ITS and ETS identical (apart

Fig. 1. Phylogram of subtribes Poinae, Alopecurinae, Miliinae and Puccinelliinae (PPAM clade), resulting from maximum parsimony analysis of the plastid TLF sequence data (length = 663 steps; CI excluding uninformative characters = 0.63). The strict consensus tree is indicated by bold lines on one of the 90 000 most parsimonious trees. Bootstrap values of ≥50% are given on the branches. Informative indels are indicated to the left of the tree. Species represented by more than one sample are followed by abbreviated collection information (or GenBank accession number when downloaded from GenBank). Australian species are indicated in bold; New Zealand species of *Poa* are indicated by 'NZ', followed by a letter corresponding to one of the species groups (A–C and E) outlined by Edgar (1986); 'X' refers to species that are members of the X clade in the nrDNA analysis; members of subtribe Alopecurinae are indicated by 'A'. One sample containing only *trn*T–*trn*L and *trn*L intron data is noted as 'TLL'. Major clades and subclades are indicated on the right; species assemblages that resolve as clades in the nrDNA and combined analyses are noted by dashed lines.

P cheelii
P helmsii G7339
63 P hookeri
P helmsii S5921
P meionectes G7316
P sieberiana J8482
P costiniana G7356
P costiniana G7367
P hiemata
P phillipsiana G7369
P sieberiana G7374
20 bp insertion
63 P fawcettiae S5919
P phillipsiana G7346
P poiformis G7381
P affinis
P poiformis S5911
P sieberiana G7319
P iowanensis
64 P labillardierei
P keysseri DS4925
P keysseri DS4935   New Guinea
P fordeana G7321
P fawcettiae MEL2323765
P meionectes G7348
P fax   subsect. Neuropoa
P sallacustris
8 bp insertion * P drummondiana   subsect. Brizoides
P porphyrroclados
P fordeana G7326
P amplexicaulis
P orba
P pubinervis
P billardierei G7382   subsect. Austrofestuca
P ensiformis
P orthoclada

sect. Brizoides

subsect. Homalopoa
subgenus Poa

P hesperia   NZ B - X
87 P chaixii S4677
P chaixii S7524
91 P arachnifera
63 P holciformis
P stuckertii
P colensoi   NZ B - X
51 P reflexa
P sieberiana AY589145   **sect. Brizoides**
Diss calycinum
63 Dissanthelium peruvianum
P mathewsii   **NZ E - X**
8 bp insertion * Dissanthelium brevifolium
P atropidiformis
P hybrida
P cockayneana   **NZ C - sect. Brizoides**
P scaberula
P gymnantha
P kurtzii
P astonii   **NZ B - X**
100 P polycolea
95 P lepidula P15604
P lepidula P18138
P subvestita   **NZ A2 - X**
63 P cusickii pallida
P fendleriana
76 P macrantha
P nervosa
P wheeleri
P porsildii
63 P pratensis irrigata
P pratensis pratensis
86 P arctica   **sect. Malacanthae - X**
87 P smirnowii mariae
P ircutica
98 P pratensis alpigena
P pratensis angustifolia
P remota

supersect. Poa
supersect. Poa

99

58 P sibirica
63 P compressa
P glauca
87 P pseudoabbreviata
P laxa flexuosa
98 P nemoralis
P lettermanii
95 P trivialis

subg. Stenopoa

63 P media H17
P media H04-11
P dolosa
64 P trichophylla

"N" clade

P diaphora   subg. Pseudopoa

99 P flabellata W4NCD
63 P flabellata W9NSG
P kerguelensis HGEN5
55 P kerguelensis HGEN6
96 P cookii HGEN1
P cookii HGEN8   **NZ A1**
77 100 P supina
99 P infirma

subg. Ochlopoa

95

63 P alpina
P molinerii
98 P badensis
P bulbosa S5814
P thessala
100 P ligulata TLL
54 P bulbosa C13-2000

74

62 P alsodes
61 P wolfii
P saltuensis
66 99 P autumnalis
P sylvestris

subg. Sylvestres

91 Nicoraepoa chonotica
Nicoraepoa robusta
Saxipoa saxicola MEL2323764
Hookerochloa eriopoda J9128
Hookerochloa eriopoda J9129
59 **Saxipoa saxicola 7353-4**
Saxipoa saxicola 7353-1
99 Arctagrostis latifolia G6586
Arctagrostis latifolia A157a
Nicoraepoa andina
Hookeropoa hookeriana J9127
Nicoraepoa subenervis spegazziniana P19186
Nicoraepoa subenervis spegazziniana S7155
Nicoraepoa subenervis subenervis S7334
Sylvipoa queenslandica
Aniselytron treutleri
Cinna arundinacea

HSAQN

Poa
Clade I

PPAM clade

96

85 80 Dupontia fisheri G6589
89 Dupontia fisheri G6699
Arctophila fulva
Cinna latifolia
Beckmannia syzigachne   **A**
89 Alopecurus borealis   **A**
83 Alopecurus gerardii   **A**
100 Bellardiochloa variegata
Apera interrupta
69 97 Milium vernale
Milium effusum

Phleum pratense

66 86 Catabrosa aquatica
Catabrosa werdermmannii
100 Puccinellia vahliana

Deschampsia brevifolia

100 **Dryopoa dives**
33 steps Festuca baffinensis
Anthoxanthum monticola
Helictotrichon sempervirens
Agrostis mertensii

Milinae
Phleinae

Puccinelliinae

OUTGROUPS

5 steps

from minor base polymorphisms) to *P. clelandii*, *P. costiniana*, *P. fawcettiae* (*S5919*), *P. keysseri*, *P. phillipsiana* and *P. poiformis* (*S5911*).

Parsimony analyses

Results given here focus on the Australasian species of *Poa* and subtribe Poinae. Positions and relationships of other *Poa*, Poinae and PPAM clade species are mostly described in previous papers (Gillespie *et al.* 2007, 2008, in press; Soreng *et al.* in press).

Plastid analysis

Maximum parsimony analysis of the TLF data matrix resulted in 90 000 trees (the maximum saved), 666 steps long (Table 1). Figure 1 illustrates one of the most parsimonious trees, with the strict consensus tree indicated by bold lines.

The PPAM clade is moderately supported (BS = 69%), with subtribe Puccinelliinae strongly supported (BS = 96%) as sister to all other members (subtribes Alopecurinae, Miliinae, Phleinae, and Poinae). The sister clade is divided into two main clades with moderate to good support, namely, *Poa* (BS = 74%) and a clade comprising all sampled Poinae genera except *Poa* and including *Alopecurus* and *Beckmannia* (subtribe Alopecurinae) (Clade 1; BS = 85%). Two additional lineages, *Milium* and *Phleum*, resolve together in a clade in the bootstrap tree (BS = 66%), but not in the strict consensus tree. Five genera for which multiple species were included resolved as monophyletic; these include *Alopecurus* (BS = 89%), *Catabrosa* (BS = 86%), *Dupontia* (BS = 80%), *Milium* (BS = 97%) and *Poa* (including *Dissanthelium* for which combinations in *Poa* are pending; BS = 74%). The two samples of *Arctagrostis latifolia* also resolved as monophyletic (BS = 99%). *Cinna*, *Hookerochloa*, *Nicoraepoa* and *Saxipoa* did not resolve as monophyletic; relationships among their species and samples were not or poorly resolved, and there was little sequence divergence among the latter three genera. The three samples of *Saxipoa* shared two unique insertions (a 10-bp duplication and a 20-bp duplication) providing some TLF evidence for the monophyly of the genus.

The two new Australian genera, *Saxipoa* and *Sylvipoa*, resolved within Clade 1. Relationships within the part of Clade 1 that included these genera (Fig. 1: HSAQN group) were not or poorly resolved. Both genera had sequences most similar to, and in one case (*Saxipoa saxicola* MEL2323764) identical to, samples of *Hookerochloa* and *Nicoraepoa* (except for two duplications in *Saxipoa*, and one insertion shared with *Hookerochloa*). All other Australian taxa of Poinae were included within *Poa*, in a very well supported supersection *Homalopoa* clade (BS = 91%) within *P.* subgenus *Poa* (BS = 100%). Included in the supersection *Homalopoa* clade were all sampled Australian species of *Poa*, including species sometimes previously treated under *Austrofestuca* (*P. billardierei*, *P. pubinervis*) and *Neuropoa* (*P. fax*), and all New Zealand *Poa* (except Edgar's (1986) Group A1 species, *P. cookii*, from the Sub-Antarctic

Islands). Relationships within this large clade were poorly resolved as a result of very low levels of sequence divergence. Six Australian *Poa* samples (*P. cheelii*, *P. helmsii* (2 collections), *P. hookeri*, *P. meionectes* (one of two collections: *G7316*) and *P. sieberiana* (one of three collections: *J8482*)) form a subclade, with poor bootstrap support (BS = 63%) based on a single shared character. Two Australian samples, *P. affinis* and *P. poiformis* (one of two collections: *S5911*), formed a subclade (BS = 63%), which was further supported by a unique 20-bp insertion. A group of 13 Australian samples resolved as a clade in some of the most parsimonious trees, and was further supported by a shared 8-bp insertion (Fig. 1); two New Zealand samples, *P. cockayneana* and *P. sieberiana* (AY589145, cultivated sample native to Australia), also shared this insertion, but did not resolve in this clade.

Nuclear ribosomal analysis

Maximum parsimony analysis of the combined ITS and ETS data matrix resulted in 90 000 trees (the maximum saved), 815 steps long (Table 1; Fig. 2).

In this nrDNA analysis, a clade of all PPAM members (BS = 93%) resolved into the following three main clades: Puccinelliinae (BS = 100%), *Poa* (BS = 87%) and Clade 1 (BS = 84%) comprising all Poinae taxa, except *Poa*, and including *Alopecurus* and *Beckmannia* (Alopecurinae). Relationships among these three clades and the two separate lineages, *Phleum* and *Milium*, were poorly resolved. All genera for which multiple species were included resolved as monophyletic; these include *Alopecurus* (BS = 99%), *Bellardiochloa* (BS = 86%), *Catabrosa* (BS = 100%), *Cinna* (BS = 89%), *Hookerochloa* (BS = 93%), *Milium* (BS = 100%), *Nicoraepoa* (BS = 94%) and *Poa* (including *Dissanthelium* for which combinations in *Poa* are pending; BS = 87%). All genera in which multiple samples of the same species were included also resolved as monophyletic: *Arctagrostis* (BS = 99%), *Dupontia* (BS = 85%) and *Saxipoa* (91%).

Both *Saxipoa* and *Sylvipoa* resolved in Clade 1, in a very strongly supported subclade with *Arctagrostis*, *Hookerochloa* and *Nicoraepoa* (HSAQN clade; BS = 100%). *Sylvipoa* resolved as sister to *Nicoraepoa* (BS = 68%), in a strongly supported clade with *Arctagrostis* (AQN; BS = 96%). *Saxipoa* resolved as sister to this clade, with moderate support (BS = 73%).

All Australian *Poa* species sampled, including those sometimes previously placed in *Austrofestuca* and *Neuropoa* (Fig. 2: subsections *Austrofestuca* and *Neuropoa*), resolved together in a subclade (section *Brizoides*; BS = 67%) within a large clade comprising the majority of *Poa* subgenus *Poa* species (BS = 91%), but not including those belonging to the X clade (Fig. 2, see below). Also included in the section *Brizoides* subclade were five New Zealand *Poa* species (all sampled species of Edgar's (1986) Group C) and one from New Guinea. Phylogenetic structure within section *Brizoides* was

Fig. 2. Phylogram of subtribes Poinae, Alopecurinae, Miliinae and Puccinelliinae (PPAM clade), resulting from maximum parsimony analysis of the nuclear ribosomal ITS and ETS sequences (length = 1776 steps; CI excluding uninformative characters = 0.43); the strict consensus tree is indicated by bold lines; labelling conventions and abbreviations follow those for Fig. 1. Samples with only ITS data (i.e. missing ETS data) are indicated by 'ITS'. Major clades and subclades are indicated on the right; taxa not corresponding to clades in this analysis, but that do resolve as clades in the plastid (Fig. 1) and combined analyses (Fig. 2), are noted by dashed lines.

Table 2.   Intra-accession indel and base variants in ITS sequences of *Saxipoa saxicola*

Variants were identical in sequences of all three accessions sampled (except for one minor difference in one variant in the ITS2 region). Position in the aligned ITS data matrix, and other Poinae taxa sharing each variant are given. Genera belonging to the same subclade as *Saxipoa saxicola* are given first: A = *Arctagrostis*; H = *Hookerochloa*; N = *Nicoraepoa*; Q = *Sylvipoa queenslandica*; followed by other Poinae genera. For indel variants, the first variant given was the one coded; base variants were coded with base ambiguity codes

Position	ITS region	Variants	Variant 1	Variant 2
70	ITS1	C/T	C: HAQN, most Poinae	T: N, many *Poa*
88	ITS1	G/A	G: HAQN, most Poinae	A: some *Poa* (subg. *Stenopoa*; *P. diaphora*)
130	ITS1	–/C	C: HAN, most Poinae (T: N, *Poa flabellata*; G: Q)	–: unique to *Saxicola*
216	ITS1	C/T	C: HAQN, most Poinae	T: *Poa* subg. *Ochlopoa, Cinna arundinacea*
234	ITS1	C/T	C: HAQN, most Poinae	T: most *Poa, Cinna latifolia*
446, 449	ITS2	AC/–, ACC/–[A]	AC, ACC: H, most Poinae	–: AQN
465–467	ITS2	CAG/AT	CAG: H, most Poinae	AT: AN (CT: Q)
483	ITS2	T/G	T: H, *Cinna*	G: AQN, most Poinae
495	ITS2	A/C	A: H, *Cinna*	C: AQN, most Poinae
584	ITS2	T/A	T: H, most Poinae	A: AQN

[A]AC/– in accessions *G7353-1* and *G7353-4*; ACC/– in MEL2323764.

poorly resolved, with only two small clades supported, namely, subsection *Austrofestuca* (both species and all three collections sampled; BS = 65%) and the two collections sampled of *P. fordeana* (BS = 97%). Two of the New Zealand species (*P. cita* and *P. cockayneana*) formed a clade in the bootstrap analysis (BS = 70%), but not in the MP strict consensus tree. One ETS indel provides additional support for a clade comprising *P. orba* and *P. sallacustris*, which resolved in some of the most parsimonious trees (Fig. 2). The majority of species in the primarily Australian section *Brizoides* clade showed little sequence divergence, and collections of the same species often did not resolve together. Much of the sequence variation can be accounted for by several hypervariable characters in the ETS data matrix (Positions 286, 342, 343 and 551, described above under Sequence characteristics), which vary within species, both between and within samples, as well as between species.

Although the majority of *P.* subgenus *Poa* species formed a large clade in the ITS + ETS analysis, 15 species that resolved within the *P.* subgenus *Poa* clade in the TLF analysis (Fig. 1) resolved outside of this clade. These species resolved as a subclade (Fig. 2: X clade) of the sister clade to this large clade that includes most subgenus *Poa* species. The X clade includes 13 species from New Zealand (Groups A2, B, D–F; Edgar 1986) and two species of *P.* subgenus *Poa* supersection *Poa* section *Malacanthae* (Roshev.) Olon. (*P. smirnowii* from Asia and the circumarctic species *P. arctica*). Sister to the X clade is a clade of three diploid species belonging to three European sections of *Poa* that are not considered members of *P.* subgenus *Poa* (Figs 1–3: N clade).

Combined plastid and nuclear ribosomal analysis

Maximum parsimony analysis of the combined TLF, ITS and ETS data matrix resulted in 90 000 trees (the maximum saved), 2414 steps long (Table 1, Fig. 3).

The PPAM clade and three major internal clades, Puccinelliinae, *Poa* and Clade 1, resolved with strong support (BS = 98–100%). Both *Phleum* and *Milium* resolved with *Poa* in a moderately supported clade (BS = 65%); this clade and Clade 1 resolved together as the sister clade to subtribe Puccinelliinae, with good support (BS = 82%). All genera for which multiple species or samples were included resolved as monophyletic, including *Alopecurus* (BS = 100%), *Arctagrostis* (BS = 100%), *Catabrosa* (BS = 100%), *Cinna* (BS = 77%), *Dupontia* (BS = 95%), *Hookerochloa* (BS = 92%), *Milium* (BS = 100%), *Nicoraepoa* (BS = 94%), *Poa* (including *Dissanthelium*; BS = 100%) and *Saxipoa* (BS = 91%).

Both *Saxipoa* and *Sylvipoa* resolved in Clade 1, within a subclade with *Arctagrostis*, *Hookerochloa*, and *Nicoraepoa* (Fig. 3: HSAQN clade; BS = 100%). *Sylvipoa* resolved as sister to *Nicoraepoa* (BS = 71%), and these in a very well supported clade with *Arctagrostis* (BS = 93%). *Saxipoa* resolved as sister to this clade, with moderate support (BS = 65%).

Australian *Poa* species (including those sometimes previously placed in *Austrofestuca* and *Neuropoa*) resolved in the supersection *Homalopoa* clade (BS = 76%) within a very strongly supported *Poa* subgenus *Poa* clade (BS = 100%). All Australian species resolved in a subclade (BS = 87%), section *Brizoides*, together with two New Zealand species (*P. cita* and *P. cockayneana*, of Edgar's (1986) Group C) and one New Guinean species (*P. keysseri*). Relationships within this clade were mostly poorly resolved, with only the following five multi-species clades being supported: subsection *Austrofestuca* (2 species; BS = 94%); subsection *Austrofestuca*, *P. amplexicaulis*, *P. fawcettiae* (*MEL2323765*) and *P. orthoclada* (BS = 63%); *P. cita* and *P. cockayneana* (BS = 94%); *P. affinis* and *P. poiformis* (*S5911*) (BS = 63%); and *P. orba* and *P. sallacustris* (BS = 66%, clade not present in the strict consensus tree). Shared indels provided additional support for

Fig. 3. Phylogram of subtribes Poinae, Alopecurinae, Miliinae and Puccinelliinae (PPAM clade), resulting from maximum parsimony analysis of combined plastid TLF and nuclear ribosomal ITS and ETS sequences (length 2414 steps; CI excluding uninformative characters = 0.47); the strict consensus tree is indicated by bold lines; labelling conventions and abbreviations follow those for Fig. 1. Species that belong to the X Clade in the nrDNA analysis (Fig. 2) are excluded here. Two samples missing the ETS data partition are indicated by 'TI'; three samples with partial TLF data, but including ITS and ETS data, are indicated as follows: *trn*T–*trn*L and *trn*L intron = 'TLIE'; *trn*L intron and *trn*L–*trn*F spacer = 'LFIE'. The inset on left shows the *Poa* supersection *Homalopoa* clade, with horizontal branches lengthened to show the branching pattern more clearly.

the last two clades (Fig. 1). The following three species, with two samples each, also resolved as clades: *P. fordeana* (BS = 71%), *P. helmsii* (BS = 55%) and *P. keysseri* (BS = 63%). A large clade of 14 Australian and two New Zealand samples that was present in the majority of most parsimonious trees, but not in the strict consensus tree, was further supported by a shared insertion (not present in *P. fordeana G7321*) (Fig. 3). As noted in the Materials and methods, X clade species were excluded from this combined analysis because of incompatibility between TLF and ITS + ETS datasets.

Discussion

In the present paper, we focus on the relationships of Australasian *Poa* and of two Australian genera newly segregated from *Poa*, namely, *Saxipoa* and *Sylvipoa*. More detailed discussions of relationships among genera within subtribe Poinae and taxa of intergeneric hybrid origin are provided in Gillespie *et al*. (2008, in press). Gillespie and Boles (2001), Gillespie and Soreng (2005), Gillespie *et al*. (2007, 2008, in press) and Soreng *et al*. (in press) discussed phylogenetic structure within the genus *Poa*.

Saxipoa *and* Sylvipoa – *two new Australian genera*

Saxipoa and *Sylvipoa* are two newly described monotypic genera endemic to Australia, based on species formerly placed in the genus *Poa*, *P. saxicola* and *P. queenslandica*, respectively (Soreng *et al*. 2009). All analyses, plastid, nrDNA and combined, resolved *Saxipoa* and *Sylvipoa* within a well to strongly supported clade, comprising subtribe Poinae (all genera except *Poa*) and Alopecurinae *s.s.* (i.e. minus Phleinae) (Figs 1–3): Clade 1. Within Clade 1, a strongly supported subclade of *Arctagrostis*, *Hookerochloa*, *Nicoraepoa*, *Saxipoa* and *Sylvipoa* (HSAQN clade) was resolved in the nrDNA and combined plastid and nrDNA analyses (this part of Clade 1 was unresolved in the plastid analysis). Gillespie *et al*. (2008, in press) reported a similar phylogenetic structure in Clade 1 (as 'Poinae (–*Poa*)'), without the inclusion of samples from the two new genera described here, and found a subclade of *Arctagrostis*, *Hookerochloa* and *Nicoraepoa* (HAN of the HSAQN subclade). Within the HSAQN clade, all genera resolved as monophyletic (or were not resolved in the plastid analysis). *Hookerochloa* (including *Festucella*; Jacobs *et al*. 2008) was sister to the other four genera. A clade of *Arctagrostis*, *Nicoraepoa* and *Sylvipoa* had very good to strong support (Figs 2, 3: AQN clade).

Neither Clade 1 nor the HSAQN subclade has any obvious morphological synapomorphies. Geographically, HSAQN includes all the southern hemisphere genera in Clade 1 (apart from wide-ranging species of *Alopecurus* and one species of *Cinna*). However, within HSAQN, *Arctagrostis* is strictly arctic and has single-flowered spikelets, whereas the other genera are restricted to the southern hemisphere in Australia, New Zealand and South America, and have multiple-flowered spikelets. *Arctagrostis*, with its single-flowered spikelets and broad, flat, morphologically unspecialised leaf blades, has more morphological features in common with the principally northern hemisphere genera sometimes placed in subtribe Cinninae, i.e. *Cinna* (Eurasia and North America,

except *C. poiformis* which extends from Mexico to Bolivia), *Limnodea* (North America), *Aniselytron* and *Cyathopus* (South-east Asia). The latter four genera grow in warm to cool temperate habitats. Because Cinninae genera are all intermingled with Poinae genera, we included them in the subtribe Poinae (Gillespie *et al*. in press). The new genus *Agrostopoa* (endemic to Colombia) has recently been included in Poinae on the basis of morphology (Davidse *et al*. 2009), adding yet another genus with single-flowered spikelets to the subtribe.

Morphologically, *Sylvipoa* is readily differentiated from other genera of the HSAQN clade and from *Poa*. We entered into the present study anticipating that it may not belong in *Poa* and might be a new genus, possibly related to the monotypic Australian genus *Dryopoa* (both are broad-leaved forest grasses with similar blades, open sheaths and large open panicles) (Vickery 1963). *Sylvipoa* is evidently not related to *Dryopoa*, a genus with much larger spikelets that resolves outside of the PPAM clade (Figs 1–3). *Sylvipoa* resolved as sister to the southern South American genus *Nicoraepoa* in the nrDNA and combined analyses, but was on a moderately long branch (17 bp differences) in the combined analysis, was and highly differentiated from the latter genus in morphology (Soreng *et al*. 2009; *Nicoraepoa* morphology was described in detail in Soreng and Gillespie 2007), and the two genera share no apparent morphological synapomorphies.

Saxipoa is distinguishable from *Poa* by a combination of characters, including densely plumose stigmas without secondary branching, ciliate glume and lemma margins, and sheaths open to near the base (Soreng *et al*. 2009). These features make *Saxipoa* quite recognisable, but they do not, by themselves or in combination, make the genus stand out sharply from *Poa*. In this case, the DNA data provided the critical evidence that this taxon did not belong within *Poa*. *Saxipoa* is most similar to the Australian genus *Hookerochloa*, sharing several morphological characters, including densely pubescent rachillas and sheath margins fused only at base (discussed in Soreng *et al*. 2009). *Saxipoa* resolved as the sister to the AQN subclade with moderate support, but also shares some DNA sequence characteristics with *Hookerochloa*, including a 20-bp insertion in TLF sequences. All three samples of *Saxipoa* were found to have the same 10 within-individual base and within-indel variants in ITS sequences, of which five in the ITS2 region have one variant shared with *Hookerochloa* and the other with *Arctagrostis*, *Nicoraepoa* and *Sylvipoa* (AQN clade) (Table 2). These variants suggested the presence of at least two paralagous ITS copies in *Saxipoa*. The high number and pattern of within-individual variants ('polymorphisms'), low bootstrap support for its position as sister to the AQN clade, and some sequence similarity with *Hookerochloa* suggested that *Saxipoa* may be an old hybrid between *Hookerochloa* and the AQN lineage. The different affinities suggested by the variants in the ITS1 region (Table 2: one variant shared with *Arctagrostis*, *Hookerochloa*, *Nicoraepoa*, *Sylvipoa*, and most other Poinae, the second variant shared mostly with species of *Poa*) *v.* the ITS2 region may also suggest incomplete homogenisation, chimeric sequences and a possible genetic contribution from *Poa*.

Dryopoa – *not a member of the PPAM clade*

Dryopoa is a monotypic genus endemic to Australia that was considered by its author to be allied to *Poa* (Vickery 1963). The taxonomic position of *Dryopoa* remains uncertain; its single species, a tall grass of forest understorey with large panicles, was originally described in *Festuca*, then transferred to *Poa*, before being treated as a separate monotypic genus. More recently, Clayton and Renvoize (1986) suggested that *Dryopoa* is very similar to *Scolochloa*, and considered both genera to be segregates of *Festuca*. On the basis of plastid and ITS data (ETS data missing), all three analyses placed *Dryopoa* outside of the PPAM clade, with moderate (plastid) to strong support (combined plastid and nrDNA). This confirms previous results based on plastid restriction-site data that showed that the genus was not close to *Poa* (Gillespie and Soreng 2005).

The X Clade

Before discussing relationships of Australian and New Zealand *Poa* we need to introduce an anomalous clade, here called the X clade, that was detected in our nrDNA analysis (Fig. 2). Positions of X clade taxa were incongruent between the nrDNA analysis and the plastid analysis (Figs 1, 2). For this reason, and because we do not yet understand the nature of the clade in which they resolve in the nrDNA trees, this set of taxa was excluded from the combined analysis. A similar clade was also resolved by Nosov and Rodionov (2008, fig. 1 as NZ1) for a smaller set of New Zealand *Poa* species and *P. arctica* on the basis of ITS data alone. Although more than a dozen extra-New Zealand species have been resolved in the X clade in our exploratory analyses of nrDNA sequence data (L. J. Gillespie and R. J. Soreng, unpubl. data), here we included only two exemplars from the *P. arctica* complex (*P.* subgen. *Poa* supersection *Poa* section *Malacanthae*) to show that species with this nrDNA type do not exclusively grow in New Zealand. The X clade is strongly supported in both separate ITS and ETS analyses, and in the combined nrDNA analysis, and resolves as sister to the N clade (Fig. 2). The X clade has not been detected in plastid analyses; in the plastid tree presented here (Fig. 1), the taxa that resolve in the X clade in the nrDNA analysis (Fig. 2) are scattered within the strongly supported *P.* subgenus *Poa* clade. When the X clade elements are included in a combined plastid and nrDNA analysis, the X clade is still resolved and is sister to a clade of all other *P.* subgenus *Poa* species (tree not shown). Although X clade taxa collectively are morphologically and geographically heterogeneous, in plastid analyses (here and e.g. Gillespie and Soreng 2005; Gillespie *et al.* 2007) most of these taxa (including all taxa studied here) resolve in *P.* subgenus *Poa*, in each supersection clade. As shown in Fig. 1, the *P. arctica* complex resolved within supersection *Poa*, and the New Zealand species were scattered within supersection *Homalopoa*. A few X clade taxa, however, have plastid DNA undifferentiated from those in the main clade of *P.* subgenus *Stenopoa* (L. J. Gillespie and R. J. Soreng, unpubl. data). So far, the X clade taxa all come from around the Pacific Ocean basin and the Himalayas, and none is from Europe (except the circumboreal *P. arctica*). In the present study, no X clade elements were detected among sampled Australian *Poa*. All sampled New Zealand species of Edgar's

Groups A2, B, D, E and F (but not those of A1 or C) resolved in the strongly supported X clade in the nrDNA analysis.

We hypothesise that the X clade involves paralogous nrDNA copies, perhaps derived from homologous chromosomes from allopolyploid genomes (no members are diploids), or some distorted evolution of the nuclear ribosomal region (possibly duplication of the nrDNA region onto another chromosome within a single genome). Further work requires a thorough investigation of the nature of the X clade via cloning of the DNA region, and selective staining of chromosome spreads. The important result here is that the New Zealand *Poa*, except for those of Edgar's Groups A1 and C, resolved in the X clade.

Australian Poa – *a recently diversified clade*

Our molecular results support the inclusion of all sampled species of Australian *Poa*, one species of New Guinea (*P. keysseri*), the five sampled species of Edgar's Group C from New Zealand (Edgar 1986; Edgar and Connor 2000), and no other taxa, in a single lineage within *P.* subgenus *Poa* supersection *Homalopoa*. These species resolved together in a clade in the nrDNA and combined analyses, with moderate to very good support, respectively, despite the relatively low levels of sequence divergence of most species in this subgenus. Although the plastid analysis did not resolve this Australasian lineage and levels of sequence divergence were even lower, the same species did resolve together in two subclades in the majority of trees. We placed all of these species in the newly expanded and circumscribed *Poa* section *Brizoides* (Soreng *et al.* 2009). Membership in this section of all other Australian *Poa* species not tested for DNA was extrapolated on the basis of their shared morphology.

The *Poa* section *Brizoides* clade is part of a worldwide supersection *Homalopoa* clade that includes about two-thirds of the species in the genus. Phylogenetic structure within this large supersection clade is not well resolved, likely owing to the paucity of DNA characters, and also to homoplasy resulting in part from several highly variable DNA characters. Supersection *Homalopoa* contains ~300 species, presently organised in seven sections (*Homalopoa*, *Acutifoliae*, *Madropoa*, *Brizoides*, *Anthochloa*, *Dasypoa* and *Dioicopoa*; sometimes abbreviated as HAMBADD; Gillespie *et al.* 2007). Supersection *Homalopoa* also includes miscellaneous unnamed groups of species, and three genera not yet synonymised under *Poa* (*Aphanelytrum*, *Dissanthelium* and *Tovarochloa*) (Gillespie and Soreng 2005; Gillespie *et al.* 2007, 2008). As can be said of most of supersection *Homalopoa*, its position on the cladogram combined with limited DNA and morphological divergence suggests that section *Brizoides* is recent in origin. DNA variation within supersection *Homalopoa* was insufficient to resolve what group might be sister to this Australasian section.

Soreng *et al.* (2009) placed most *Poa* section *Brizoides* species within the following four subsections: *Australopoa* (with 35 spp. in Australia, six in New Zealand, and possibly one in New Guinea), *Austrofestuca* (2 spp.), *Brizoides* (1 sp.) and *Neuropoa* (1 sp.). Within section *Brizoides*, species relationships were poorly resolved and there was not sufficient DNA variation to resolve any smaller sets of taxa with good support, except for subsection *Austrofestuca*, which was strongly

supported as a clade in our nrDNA and combined analyses. Most Australian *Poa* can be placed in these four subsections on the basis of shared morphological characteristics. The majority of species appear to represent variations of the widespread *P. labillardierei–P. sieberiana* complex, and we place all of these in subsection *Australopoa* (Appendix 1). Soreng *et al.* (2009) left the following four morphologically diverse Australian species *insertae sedis* within section *Brizoides*: *P. fordeana*, *P. homomalla*, *P. orba* and *P. sallacustris*.

A unique 8-bp insertion in the plastid data matrix provided an additional synapomorphy for a clade present in the majority of the most parsimonious trees in the combined analysis (a similar but smaller clade was present in the plastid tree). The insertion was present in subsections *Austrofestuca*, *Brizoides*, *Neuropoa*, the four Australian 'insertae sedis' species, six samples of the Australian subsection *Australopoa*, and the two sampled species of subsection *Australopoa* from New Zealand (Fig. 3). The insertion was absent from most subsection *Australopoa* samples (21) and from *P. keysseri* of New Guinea. Only one of two to four samples of section *Australopoa* species, *P. fawcettiae*, *P. meionectes*, and *P. sieberiana*, had the insertion; these individuals may have gained the insertion by plastid capture. The presence of the insertion in only one of two samples of *P. fordeana* ('insertae sedis') is also likely to be the result of plastid capture; the two samples had identical nrDNA sequences and resolved as a strongly supported clade in the nrDNA tree, but resolved in separated positions in the plastid tree. In the combined analysis, these two samples formed a moderately supported subclade within the clade supported by the 8-bp insertion, which suggests that the insertion was lost in *P. fordeana G7321* through a gain of a plastid type from a subsection *Australopoa* species outside this clade (in the plastid analysis this sample resolved among section *Australopoa* members lacking the insertion in the majority of most parsimonious trees).

Species with the insertion mostly have rhizomes, stolons or at least well developed extravaginal branching systems, or have corms (*P. drummondiana*) or an annual habit (*P. fax*), and their sheaths are mostly closed between 30 and 90% of their length (except for several subsection *Australopoa* species). Species without the insertion (all of which belong to subsection *Australopoa*, excluding *P. fordeana G7321*) are mostly tufted, without rhizomes or stolons, and with sheaths closed mostly less than 35% of their length. Thus, there appears to be a correlation between the presence of the 8 bp plastid insertion and the presence of a loose habit with rhizomes or stolons and more closed sheaths, and other diverse life history traits, including annual life cycle or the presence of corms, as reflected in our subsectional taxonomy.

Among members of this clade supported by the 8-bp insertion, *P. fordeana* shares a combination of morphological features with *P. fax* and no other Australian *Poa*; these include flat flaccid leaf blades (also present in *P. drummondiana*), short branched inflorescences with crowded and elongated spikelets and lemmas with particularly dense silky appressed pubescence along the veins and sometimes between them. Both species grow in seasonal wetlands, with *P. fax* growing in subsaline soils. The two species also share a 4-bp deletion (along with

P. poiformis 7381 and *P. lowanensis*). *P. fordeana* differs in its perennial habit and thinner lemmas, and perhaps provides a link between the subsections *Neuropoa* and *Australopoa*. Apart from belonging to this clade, no other molecular support was found for Walsh's (1991) postulated link between *P. fordeana* and *P. sallacustris*. Both *P. sallacustris* and *P. orba* resemble *P. fordeana* in having a strongly rhizomatous habit and lacking truncate ciliate ligules. The first two species often resolved together in the nrDNA and combined trees (with moderate support in the latter) and shared a unique 2-bp insertion in the ETS sequence. Soreng *et al.* (2009) initially speculated that *P. orba* might be hybridogenic in origin, involving *P. pratensis*, but our new DNA data suggest the species is more likely simply a part of the diverse section *Brizoides* clade.

Although Soreng *et al.* (2009) indicated that *P. homomalla* ('insertae sedis') shares characteristics with *P.* supersection *Poa* section *Macropoa* F.Herm. ex Tzvelev, on the basis of its more closed and strongly keeled sheaths, long rhizomes, acute and smooth ligule apices, and glabrous lemmas, both plastid and nrDNA sequence data indicate that it belongs to the section *Brizoides* clade. Presence of the 8-bp TLF insertion, along with shared morphological characters (rhizomes, quite closed sheaths and aerial branching of the culm), suggests that *P. homomalla* belongs among those species that have the insertion. Certainly, the DNA data support accommodating all of the above morphologically diverse species in section *Brizoides*, but some additional or different groupings might be employed in the future.

Of the eight Australian and one New Guinean species, for which multiple samples were included, only three, namely, *P. fordeana*, *P. helmsii* and *P. keysseri*, resolved as clades, with poor to moderate support, in the combined analysis. Among the remaining species, samples of *P. costiniana* and *P. poiformis* showed little sequence divergence and resolved near each other, whereas samples of *P. phillipsiana* and *P. fawcettiae* were more divergent and separated on the tree. An 8-bp insertion was present in the TLF sequence of one of the samples of *P. fordeana* and *P. fawcettiae*, but not in the other (Fig. 1). Among samples of the morphologically variable and very common, widespread taxon *P. sieberiana*, two resolved near each other and showed little sequence divergence, whereas a third showed more divergence (all lacked the 8-bp TLF insertion, Fig. 1). A fourth sample with only TLF data, taken from a cultivated plant in New Zealand (AY589145), resolved outside of the section *Brizoides* species assemblage in the plastid analysis (and had the 8-bp insertion, Fig. 1), suggesting that it may be a misidentification (identity of this GenBank sample could not be confirmed) or that it has undergone introgression and possibly plastid capture. In the plastid analysis, two samples of *P. meionectes* also had divergent TLF sequences, each belonging to a different clade. *Poa* is renowned to be a taxonomically challenging genus (e.g. Bor 1952; Clayton and Renvoize 1986), and the Australian species are no exception (Vickery 1970). The identification of all vouchers was reconfirmed (one sample, *S5921*, initially called *P. labillardierei*, was redetermined as *P. helmsii*), so misidentification of samples is unlikely, although remains a possibility, given the difficulty of assigning specimens to species. More likely

explanations for samples of a species not resolving together include hybridisation and introgression (and possible plastid transfer), lineage sorting, and/or extensive homoplasy resulting from several hypervariable positions. More detailed studies, including those involving cloning of multiple samples per species, will be necessary to sort out relationships among Australian *Poa* species.

New Guinea Poa – an Australian connection

Poa keysseri of New Guinea is not substantially morphologically differentiated from the species of subsection *Australopoa*, because it has, like most species of the subsection, short-truncate to obtuse ciliate-rimmed ligules, sheaths closed ~12% of their length, blades folded, narrow and somewhat firm, panicles loose, with branches scabrous all over, and blunt lemma apices. This species resolved within the section *Brizoides* clade, with nrDNA sequences being identical to seven subsection *Australopoa* samples and plastid sequences with one to three autapomorphic characters.

Malesian *Poa* were revised by Veldkamp (1994) to include 38 endemic and three introduced species, 34 of these are endemic to New Guinea, one is endemic to each of Sabah and Celebes. About one-third of the endemic species are similar to *P. keysseri* in morphology, in having strongly 5-nerved lemmas (characteristic of subgenus *Poa*), whereas the remaining two-thirds of the endemics have intermediate nerves that are indistinct (characteristic of subgenus *Stenopoa*) or obsolete (otherwise unknown in *Poa*). Among the New Guinean species with strongly 5-nerved lemmas, only *P. keysseri* has truncate ciliate-rimmed ligules, characteristic of most species of subsections *Australopoa* and *Austrofestuca*. At this point, we can reasonably include *P. keysseri* in section *Brizoides*, and perhaps within subsection *Australopoa*; however, unlike other subsection *Australopoa* elements, it has a combination of a callus web and glabrous lemmas. The placement of any other Malesian *Poa* (Veldkamp 1994) in this section requires further study.

New Zealand Poa – at least three lineages

Edgar (1986) and Edgar and Connor (2000) outlined the following 10 groups and subgroups within New Zealand *Poa*: A1, A2, B, C1, C2, D, E1, E2, F1 and F2. Among these groups, we have detected three major DNA lineages corresponding to (1) A1, (2) C and (3) A2, B, D, E1, E2, F1 and F2. (1) *Poa cookii s.l.* (Edgar included *P. hamiltonii* here) and *P. ramosissima* (for which only ITS data are available) belong to Edgar's Group A1. These species resolved as members of the Sub-Antarctic Island *Parodiochloa–Tzvelevia* clade in analyses here and in Gillespie *et al*. (2008), and were placed in *P.* subgenus *Ochlopoa* section *Parodiochloa* on the basis of this DNA data, and their unusual leaf anatomy (Soreng and Gillespie 2007). Hair (1968) and Edgar (1986) anticipated their close relationship with *P. flabellata*. (2) *P. cockayneana*, *P. cita*, *P. chathamica*, *P. anceps* and *P. litorosa* (ITS data only for the last three species) of New Zealand resolved in the section *Brizoides* clade in the nrDNA and combined analyses. These species belong to Subgroups C1 and C2 (Edgar 1986; Edgar and Connor 2000), and we place them in *P.* section *Brizoides* subsection *Australopoa* (Soreng *et al*. 2009). This position is entirely consistent with

Edgar's placement of Australian species introduced into New Zealand (*P. labillardierei* and *P. sieberiana*) within her Group C1. (3) We have examined representatives of all other of Edgar's New Zealand groups by using ITS data, and representatives of A2, B and E2 for ETS, ITS and plastid data. All the sampled taxa of this set have X clade-type nrDNA (Fig. 2). Those examined for plastid DNA resolved outside of the section *Brizoides* assemblage, but within subgenus *Poa* supersection *Homalopoa*, and did not resolve into any New Zealand monophyletic subsets. Although Edgar (1986) and Edgar and Connor (2000) accepted the genus *Austrofestuca s.s.* in New Zealand, we now place it in *P.* section *Brizoides* subsection *Austrofestuca*.

Biogeography

Our phylogenetic hypothesis suggests a recent origin and diversification of the Australasian *Poa* section *Brizoides* clade and an older origin for the subtribe Poinae HSAQN clade, which includes the Australian genera *Hookerochloa* (also in New Zealand), *Saxipoa* and *Sylvipoa*. Because there are no *Poa* or Poinae fossils other than those from the late Pleistocene and Holocene, dating of these events would be highly speculative. Eurasia is postulated to be the centre of origin for *Poa* on the basis of species diversity and geographical distribution of basal lineages (Soreng 1990), and similarly the majority of Poinae genera are Eurasian or primarily so. The origin of the temperate tribe Poeae has been estimated at ~21 million years ago (time of divergence between the Triticeae and Poeae *s.l.* lineages) (Inda *et al*. 2008), well after the separation of Australia and South America from Antarctica estimated at ~37 million years ago (McLoughlin 2001). Thus, distributions of subtribe Poinae taxa in Australasia result from long-distance dispersal, and not vicariance.

At least two dispersal events into Australia are postulated for subtribe Poinae, one for *Poa* and one for the three other Australian Poinae genera, namely, *Hookerochloa*, *Saxipoa* and *Sylvipoa*. Our phylogenetic hypothesis suggests several scenarios for the latter three genera, and from one to three dispersal events. The HSAQN clade may have diversified in Australia (following dispersal to Australia of the clade ancestor), with dispersals outward to South America (*Nicoraeopoa*) and the northern hemisphere (*Arctagrostis*). Or there may have been two dispersal events into Australia (*Hookerochloa* and *Sylvipoa*), with *Saxipoa* evolving from one of these lineages or originating from a hybridisation event between these two lineages. Alternatively, *Hookerochloa*, *Saxipoa* and *Sylvipoa* may each represent a separate dispersal event into Australia; however, given that three of five HSAQN clade genera are endemic to Australia, this seems the least likely hypothesis.

In *Poa*, there is evidence of only one DNA lineage in Australia, that which diversified into what we call *P.* section *Brizoides.* This same lineage also occurs in New Guinea and New Zealand, but is not known outside of Australasia. In New Guinea, we have evidence of at least two lineages, with one including species in section *Brizoides* (represented by *P. keysseri*) and the other including species with ITS and plastid genomes matching subgenus *Stenopoa* (L. J. Gillespie and R. J. Soreng, unpubl. data; *P. papuana* Stapf). In New Zealand, we have evidence of at

least the following three lineages: one with representatives of two subsections of section *Brizoides*, subsections *Australopoa* (Edgar's (1986) Groups C1 and C2) and *Austrofestuca*; a second lineage (A1) that has colonised the Sub-Antarctic Islands (*P.* subgen. *Ochlopoa* section *Parodiochloa*); and a third lineage with X clade-type nrDNA (A2, B, D–F). The third lineage may have heterogeneous origins in New Zealand, but further study of extra-New Zealand taxa with X clade nrDNA is needed to evaluate this possibility. Because species of subsections *Austrofestuca* (confined to coastal sand dunes) and *Brizoides* are native to both Australia and New Zealand, origin of the subsections could have taken place in either geographic region, and dispersal could have been in either direction. Given that section *Brizoides* is most diverse and speciose in Australia, the more likely scenario is that both lineages evolved in Australia and secondarily established in New Zealand. Thus, *Poa* lineages have probably colonised New Zealand at least four times.

In New Zealand, the X clade nrDNA genome is associated with plastids of *P.* subgenus *Poa* supersection *Homalopoa* in the species tested (A2, B and E), although those species do not resolve among species of section *Brizoides* (plastid data not available for species of New Zealand Groups D and F). The combination of supersection *Homalopoa* plastids and X clade nrDNA genomes is also present in South-east Asian species (e.g. in *P. acroleuca* Steud. and relatives; L. J. Gillespie and R. J. Soreng, unpubl. data). If this combination of genomes has originated only once, then this may provide a geographic connection between these South-east Asian *Poa* species and New Zealand *Poa* of the X clade.

Soreng (1990) suggested that the Australia and New Zealand 'Australopoa' group (now subsection *Australopoa*) might be derived from a South American ancestor. At this point, we cannot confirm or reject this hypothesis. Although we have included a series of representative *Poa* species from around the world, including multiple lineages from Eurasia and South America, we have not resolved a supported sister-group relationship for the *Brizoides* lineage. Asian *Poa* connections are certainly possible (Veldkamp 1994), and are hinted at in some most parsimonious nrDNA trees by the inclusion of Eurasian taxa (*P. chaixii*, *P. ircutica* and *P. polycolea*) in a polytomy with the *Brizoides* clade. In summary, it seems likely that an ancestor of *P.* section *Brizoides* entered Australia, and diversified *in situ* with two subsequent long-distance dispersals to New Zealand.

Acknowledgements

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Appendix 1.   Collections examined for plastid TLF and nrDNA ITS and ETS, with chromosome number[A] (where known for species), infrageneric classification within *Poa*, country of origin, voucher information and GenBank accession numbers

GenBank numbers in bold indicate new sequences submitted for the present paper; all other sequences are from Gillespie *et al.* (2007, 2008, in press), except for those downloaded from GenBank, which are indicated by 'GB', followed by the literature reference where first published or by the authors who submitted the sequence(s) and, where known, by the voucher information. Incomplete TLF sequences are indicated under 'TLF GenBank' as TLL = *trnT–trnL* spacer and *trnL* intron, or LLF = *trnL* intron and *trnL–trnF* spacer. Herbarium acronyms follow Thiers (continuously updated). Under 'Country of origin': ACT = Australian Capital Territory; NSW = New South Wales; WA = Western Australia

Taxon	Chromosome number	*Poa* subgenus-supersection	*Poa* section-subsection (and NZ group)	Country of origin	Voucher	TLF GenBank	ITS GenBank	ETS GenBank
Tribe Poeae – PPAM clade								
Subtribe Alopecurinae								
Alopecurus borealis Trin.	56			Canada, Nunavut	Gillespie *et al.* 6576 (CAN)	DQ353966	EU792345	**GQ324237**
A. gerardii Vill.	14			Greece	Soreng *et al.* 7494 (US)	EU792432	EU792344	**GQ324238**
Beckmannia syzigachne (Steud.) Fernald	14, 28			USA, Wyoming	Soreng 3513 (US)	DQ353965	EU792342	**GQ324255**
Subtribe Miliinae								
Milium effusum L.	14, 28			Finland	GB: Quintanar *et al.* 2007	DQ631501, DQ631435	–	–
M. effusum	14, 28			Canada, Quebec	Gillespie 7422 (CAN)	–	**GQ324477**	**GQ324273**
M. vernale M.Bieb.	14, 28			Greece	Soreng 3748 (US)[B]	DQ353963	EU792340	**GQ324274**
Subtribe Phleinae								
Phleum pratense L.	14, 28, 42, 56, 63, 70, 84			USA, cultivated	No voucher[C]	DQ353964	EU792341	**GQ324284**
Subtribe Poinae								
Aniselytron treutleri (Kuntze) Sojak				China, Yunnan	Soreng *et al.* 5229 (US)	**GQ324395**	**GQ324469**	**GQ324240**
Apera interrupta (L.) P.Beauv.	14			Argentina	Peterson *et al.* 19173 (US)	EU792439	EU792364	**GQ324242**
Arctagrostis latifolia (R.Br.) Griseb.	56			Canada, Nunavut	Archambault 157 (CAN)	EU792434	EU792353	**GQ324244**
A. latifolia	56			Canada, Nunavut	Gillespie *et al.* 6586 (CAN)	DQ353969	EU792351	**GQ324245**
Arctophila fulva (Trin.) Rupr.	42			Canada, Northwest Territories	Aiken 99-230 (CAN)	DQ354058	EU792347	**GQ324246**
Bellardiochloa polychroa (Trautv.) Roshev.				Turkey	Soreng & Guney 4191 (US)	–	EU792363	**GQ324256**
B. variegata (Lam.) Kerguelen	14			Greece	Soreng *et al.* 7519-1 (US)	EU792438	EU792361	**GQ324257**
Cinna arundinacea L.	28			USA, West Virginia	Soreng & Olonova 7462 (US)	EU792436	EU792343	**GQ324260**
C. latifolia (Trevir. ex Göpp)	28			USA, California	Peterson *et al.* 19769 (US)	**GQ324396**	**GQ324473**	**GQ324261**
Dissanthelium brevifolium Swallen & Tovar		*Poa* supersect. *Homalopoa*		Peru[E]	Peterson & Refulio 18043 (US)	EU792468	EU792424	**GQ324263**

Taxon	2n	Classification		Geographic origin	Voucher			
D. calycinum (J.Presl) Hitchc.		*P. supersect. Homalopoa*		Peru	Peterson & Refulio 1466 (US)	EU792266	EU792426	**GQ324264**
D. peruvianum (Nees & Meyen) Pilg.	44, 88	*P. supersect. Homalopoa*		Chile	Peterson & Soreng 15744 (US)	DQ354052, DQ354053	EU792415	**GQ324265**
Dupontia fisheri R.Br.				Canada, Nunavut	Gillespie et al. 6589 (CAN)	DQ353967	EU792346	**GQ324266**
D. fisheri	44, 88			Canada, Nunavut	Gillespie et al. 6699 (CAN)	DQ353968	**GQ324475**	**GQ324267**
Hookerochloa eriopoda (Vickery) S.W.L.Jacobs				Australia,[E] NSW	Jacobs 9128 (NSW)	EU792433	EU792349	**GQ324270**
H. eriopoda				Australia,[E] NSW	Jacobs 9129 (NSW)	**GQ324397**	EU792350	**GQ324271**
H. hookeriana (F.Muell. ex Hook.f.) E.B. Alexeev				Australia,[E] NSW	Jacobs 9127 (NSW)	EU792435	EU792348	**GQ324272**
Nicoraepoa andina (Trin.) Soreng & L.J.Gillespie				Chile	Soreng & Soreng 7182 (US)	DQ353971	EU792354	**GQ324275**
N. chonotica (Phil.) Soreng & L.J.Gillespie				Chile	Soreng & Soreng 7309 (US)	DQ353974	EU792355	**GQ324276**
N. robusta (Steud.) Soreng & L.J.Gillespie				Chile	Soreng & Soreng 7358 (US)	DQ353975	EU792357	**GQ324279**
N. subenervis (Hack.) Soreng & L.J.Gillespie subsp. *subenervis*				Chile	Soreng & Soreng 7334 (US)	DQ353972	EU792359	**GQ324283**
N. subenervis subsp. *spegazziniana* (Nicora) Soreng & L.J.Gillespie				Argentina	Peterson et al. 19186 (US)	EU792443	EU792358	**GQ324281**
N. subenervis subsp. *spegazziniana*				Chile	Soreng 7155 (US)	EU792442	**GQ324479**	**GQ324282**
Poa acicularifolia Buchanan	28	*P.* (X clade)	'New Zealand B'	New Zealand[E]	GB: Gardner et al. unpubl. Lange 6060 (AK-286743)	–	AY686667	–
P. affinis R.Br.		*P. supersect. Homalopoa*	*Brizoides* subsect. *Australopoa*	Australia,[E] NSW	Gillespie & Jacobs 7311-2 (US)	**GQ324399**	**GQ324482**	**GQ324285**
P. alpina L.	21–48, 56	*Ochlopoa*	*Alpinae*	USA, Colorado	Gillespie 6299 (CAN)	DQ353985	**GQ324483**	**GQ324287**
P. alsodes A.Gray		*Sylvestres*	*Sylvestres*	Canada, Quebec	Gillespie 6467 (CAN)	DQ353981	EU792374	**GQ324288**
P. amplexicaulis C.M.Weiller & G.N.Walsh		*P. supersect. Homalopoa*	*Brizoides* subsect. *Australopoa*	Australia,[E] Victoria	Walsh s.n. (MEL 2323763)	**GQ324400**	**GQ324484**	**GQ324289**
P. anceps G.Forst. subsp. *polyphylla* (Hack.) Edgar	28	*P. supersect. Homalopoa*	*Brizoides* subsect. *Australopoa* 'C2'	New Zealand[E]	GB: Gardner et al. unpubl. (AK-282943)	–	AY686666	–
P. arachnifera Torrey	32, 56, 63, 84	*P. supersect. Homalopoa*	*Dioicopoa*	USA, Oklahoma	Soreng 5801 (US)	DQ354021	**GQ324486**	**GQ324290**

(Continued next page)

Appendix 1. (*continued*)

Taxon	Chromosome number	Poa subgenus-supersection	Poa section-subsection (and NZ group)	Country of origin	Voucher	TLF GenBank	ITS GenBank	ETS GenBank
P. arctica R.Br. subsp. *arctica*	36, 38, 42, 56, 60–65, 68, 70–78, 80–86, 106	*P.* supersect. *Poa*	*Malacanthae*	Canada, Nunavut	Gillespie & Aiken 5701 (CAN)	DQ354009	**GQ324487**	**GQ324291**
P. astonii Petrie	28	*Poa* (X clade)	'New Zealand B'	New Zealand[E]	Lloyd s.n. (OTA 058919)	**GQ324401**	**GQ324488**	**GQ324292**
P. atropidiformis Hack. var. *atropidiformis*		*P.* supersect. *Homalopoa*	*Homalopoa s.l., Dissanthelium s.l.*	Chile	Soreng & Soreng 7364 (US)	DQ354020	**GQ324489**	**GQ324293**
P. autumnalis Elliott	28	*Sylvestres*	*Sylvestres*	USA, Maryland	Soreng 4680 (US)	DQ353979	EU792379	**GQ324294**
P. badensis Haenke ex Willd.	14, 18–21, 28	*Ochlopoa*	*Bolbophorum*	Bulgaria	Hajkova *et al.* 2004-12 (BRNU, US)	**GQ324402**	**GQ324490**	**GQ324295**
P. billardierei St.-Yves	28	*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Austrofestuca*	Australia, NSW	Gillespie *et al.* 7382 (CAN)	**GQ324403**	**GQ324491**	**GQ324296**
P. billardierei (as *Austrofestuca littoralis* (Labill.) Alexeev)	28	*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Austrofestuca*	New Zealand[E]	GB: Hunter *et al.* 2004		AY524824	—
P. breviglumis Hook. f.	28	*Poa* (X clade)	'New Zealand E2'	New Zealand[E]	GB: Gardner *et al.* unpubl. (AK-281888)	—	AY686656	
P. buchananii Zotov	28	*Poa* (X clade)	'New Zealand F2'	New Zealand[E]	GB: Gardner *et al.* unpubl. (AK-281045)	—	AY686654	—
P. bulbosa L.	14, 21–49, 56	*Ochlopoa*	*Bolbophorum*	Spain	Catalan 13-2000 (UZ)	DQ354034, DQ354035	EU792388	**GQ324297**
P. bulbosa subsp. *vivipara* (Koeler) Arcang.	21–49, 56	*Ochlopoa*	*Bolbophorum*	USA, Nevada (introduced from Europe)	Soreng 5814 (US)	**GQ324404**	**GQ324492**	**GQ324298**
P. chaixii Vill.	14	*P.* supersect. *Homalopoa*	*Homalopoa s.s.*	Russia	Soreng 4677 (US)	EU854590	EU792404	**GQ324299**
P. chaixii	14	*P.* supersect. *Homalopoa*	*Homalopoa s.s.*	Germany	Soreng 7524 (US)	**GQ324405**	**GQ324493**	**GQ324300**
P. chathamica Petrie	112	*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Australopoa* 'C2'	New Zealand[E]	GB: Gardner *et al.* unpubl. (CHR-562183)	—	AY686665	—
P. cheelii Vickery		*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Australopoa*	Australia,[E] NSW	Gillespie & Jacobs 7332-1 (CAN)	**GQ324406**	**GQ324494**	**GQ324301**
P. cita Edgar	84	*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Australopoa* 'C1'	New Zealand[E]	Lloyd s.n. (OTA 058916)	**GQ324407** (TLL)	**GQ324495**	**GQ324302**
P. clelandii Vickery		*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Australopoa*	Australia,[E] Victoria	Walsh s.n. (MEL2323767)	**GQ324408**(LLF)	**GQ324496**	**GQ324303**
P. cockayneana Petrie	112	*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Australopoa* 'C1'	New Zealand[E]	Lloyd s.n. (OTA 058921)	**GQ324409**	**GQ324497**	**GQ324304**

Species	2n	Supersection	Section / group	Informal group	Location	Voucher	GenBank	GenBank	GenBank
P. colensoi Hook.f.	28	*P.* (X clade)		'New Zealand B'	New Zealand[E]	Lloyd s.n. (OTA 058923)	GQ324410	GQ324498	GQ324305
P. cookii (Hook.f.) Hook.f.		*Ochlopoa*		*Parodiochloa* 'A1'	Crozet Islands (sub-Antarctic)	Hennion Gen1 (P)	EU792454	EU792383	GQ324306
P. cookii		*Ochlopoa*		*Parodiochloa* 'A1'	Kerguelen Islands (sub-Antarctic)	Hennion Gen8 (P)	EU792455	EU792382	GQ324307
P. costiniana Vickery		*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Australopoa*		Australia,[E] NSW	Gillespie *et al.* 7356-1 (CAN)	GQ324411	GQ324499	GQ324308
P. costiniana		*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Australopoa*		Australia,[E] NSW	Gillespie *et al.* 7367 (CAN)	GQ324412	GQ324500	GQ324309
P. cusickii Vasey subsp. *cusickii*	56	*P.* supersect. *Homalopoa*	*Madropoa*		USA, Nevada	Soreng 5829 (US)	DQ354029	GQ324501	GQ324310
P. diaphora Trin.	14, 28, 42	*Pseudopoa*	*Pseudopoa*		Turkey	Soreng & Güney 4165 (US)	DQ353987, DQ353988	EU792400	GQ324311
P. dipsacea Petrie	28	*Poa* (X clade)		'New Zealand D'	New Zealand	GB: Gardner *et al.* unpubl. (AK-285251)	–	AY686670	–
P. dolosa Boiss. & Heldr.	14	(N clade)		'Oreinos'	Bulgaria	Stoneberg SH18 (US)	GQ324413	GQ324503	GQ324313
P. drummondiana Nees		*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Brizoides*		Australia,[E] WA	Peterson *et al.* 14504 (US)	DQ354013	EU792411	GQ324314
P. ensiformis Vickery		*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Australopoa*		Australia,[E] NSW	Gillespie *et al.* 7379 (CAN)	GQ324415	GQ324504	GQ324315
P. fawcettiae Vickery		*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Australopoa*		Australia,[E] NSW	Soreng & Peterson 5919 (US)	GQ324416	GQ324506	GQ324317
P. fawcettiae		*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Australopoa*		Australia,[E] Victoria	Walsh s.n. (MEL2323765)	GQ324417	GQ324505	GQ324316
P. fax Willis & Court		*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Neuropoa*		Australia,[E] NSW	Jacobs 9339 (NSW)	EU792460	EU792410	GQ324318
P. fendleriana (Steud.) Vasey	56, 58–60, 64	*P.* supersect. *Homalopoa*	*Madropoa*		USA, Colorado	Gillespie 6292 (CAN)	DQ354027	EU792403	GQ324319
P. flabellata (Lam.) Raspail	28	*Ochlopoa*		*Parodiochloa*	Falkland Islands	Wright 4NCD (seed voucher US)	DQ353982	EU792380	GQ324320
P. flabellata	28	*Ochlopoa*		*Parodiochloa*	South Georgia Islands	Wright 9NSG (seed voucher US)	EU792453	EU792381	GQ324321
P. fordeana F.Muell.		*P.* supersect. *Homalopoa*		*Brizoides*	Australia,[E] NSW	Gillespie *et al.* 7321-1 (CAN)	GQ324419	GQ324507	GQ324322
P. fordeana		*P.* supersect. *Homalopoa*		*Brizoides*	Australia,[E] NSW	Gillespie & Jacobs 7326-2 (CAN)	GQ324420	GQ324508	GQ324323
P. glauca Vahl	32, 42, 50, 56–58, 64, 65, 70, 75, 78	*P.* supersect. *Homalopoa*	*Stenopoa*		Canada, Nunavut	Gillespie 5804 (CAN)	GQ324421	AY237839	GQ324324
P. gymnantha Pilg.	70	*P.* supersect. *Homalopoa*		'punapoa'	Chile	Peterson & Soreng 15656 (US)	EU792462	EU792417	GQ324325
P. helmsii Vickery		*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Australopoa*		Australia,[E] ACT	Gillespie *et al.* 7339 (CAN)	GQ324422	GQ324509	GQ324326
P. helmsii Vickery	28, 56, 84	*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Australopoa*		Australia,[E] NSW	Soreng & Peterson 5921 (US)	DQ354014 (as *P. labillardierei*)	EU792409 (as *P. labillardierei*)	GQ324327

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Appendix 1. (*continued*)

Taxon	Chromosome number	*Poa* subgenus-supersection	*Poa* section-subsection (and NZ group)	Country of origin	Voucher	TLF GenBank	ITS GenBank	ETS GenBank
P. hesperia Edgar	28	*Poa* (X clade)	'New Zealand B'	New Zealand[E]	Lloyd s.n. (OTA 058922)	**GQ324423**	**GQ324510**	**GQ324328**
P. hiemata Vickery		*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Australopoa*	Australia,[E] NSW	Gillespie *et al.* 7354 (CAN)	**GQ324424**	**GQ324511**	**GQ324329**
P. holciformis J. Presl		*P.* supersect. *Homalopoa*	*Dioicopoa*	Chile	Soreng & Soreng 7166 (US)	DQ354054, DQ354055, DQ354056	**GQ324512**	**GQ324330**
P. homomalla Nees		*P.* supersect. *Homalopoa*	*Brizoides*	Australia,[E] WA	Macfarlane 4536 (PERTH)	**GQ324425**	**GQ324513**	**GQ324331**
P. hookeri Vickery		*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Australopoa*	Australia,[E] NSW	Gillespie *et al.* 7370 (CAN)	**GQ324426**	**GQ324514**	**GQ324332**
P. hybrida Gaudin	14	*P.* supersect. *Homalopoa*	*Homalopoa s.s.*	Turkey	Soreng 4263 (US)	–	**GQ324515**	**GQ324333**
P. hybrida Gaudin	14	*P.* supersect. *Homalopoa*	*Homalopoa s.s.*	Greece	GB: Patterson *et al.* 2005 (USDA PI 249765)	AY589130	–	–
P. imbecilla Sol. ex Spreng.	28	*Poa* (X clade)	'New Zealand E2'	New Zealand[E]	GB: Gardner *et al.* unpubl. (AK-286463)	–	AY686658	–
P. infirma Kunth	14	*Ochlopoa*	*Micrantherae*	Spain	Catalan 3-2000 (UZ)	**GQ324427**	**GQ324516**	**GQ324334**
P. ircutica Roshev.	28	*P.* supersect. *Poa*	*Poa* subsect. *Nivicolae*	Russia, Irkutsk	Kasanovskiy 2002-7 (CAN)	DQ354007	EU792402	**GQ324335**
P. kerguelensis (Hook. f.) Steud		*Ochlopoa*	*Tzvelevia*	Kerguelen Islands[E] (sub-Antarctic)	Hennion Gen5 (P)	EU792457	EU792385	**GQ324336**
P. kerguelensis (Hook. f.) Steud		*Ochlopoa*	*Tzvelevia*	Kerguelen Islands[E] (sub-Antarctic)	Hennion Gen6 (P)	EU792456	EU792384	**GQ324337**
P. keysseri Pilg.	28	*P.* supersect. *Homalopoa*	*Brizoides*	New Guinea	Stančík 4925 (US)	**GQ324428**	**GQ324517**	**GQ324338**
P. keysseri	28	*P.* supersect. *Homalopoa*	*Brizoides*	New Guinea	Stančík 4935 (US)	**GQ324429**	**GQ324518**	**GQ324339**
P. kirkii Buchanan	28	*Poa* (X clade)	'New Zealand E1'	New Zealand[E]	GB: Gardner *et al.* unpubl. [de Lange 5651 (AK-282065)]	–	AY686657	–
P. kurtzii R.E.Fr.		*P.* supersect. *Homalopoa*	*Homalopoa s.l.*	Chile	Peterson & Soreng 15654 (US)	DQ354018	EU792413	**GQ324340**
P. laxa subsp. *flexuosa* (Sm.) Hyl.	42, 43, 81	*Stenopoa*	*Oreinos*	Norway	Brochmann 2000-3-1 (O)	**GQ324418**	**GQ324520**	**GQ324342**
P. labillardierei Steud.	28, 58, 84	*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Australopoa*	Australia,[E] NSW	Gillespie *et al.* 7318 (CAN)	**GQ324430**	**GQ324519**	**GQ324341**
P. lepidula (Nees & Meyen) Soreng & L.J.Gillespie		*P.* supersect. *Homalopoa*	*Anthochloa*	Chile	Peterson *et al.* 18138 (US)	EU792464	EU792422	**GQ324344**
P. lepidula		*P.* supersect. *Homalopoa*	*Anthochloa*	Chile	Peterson & Soreng 15604 (US)	EU792471	EU792416	**GQ324343**

Species	2n	Section	Supersection	Origin	Voucher			
P. lettermanii Vasey	14	*Stenopoa*	*P.* supersect. *Homalopoa*	USA, Colorado	Soreng & Soreng 7434 (US)	GQ324431	GQ324521	GQ324345
P. ligulata Boiss.	14	*Ochlopoa*	*P.* supersect. *Homalopoa*	Spain	JACA 166095	GQ324432 (TLL)	GQ324522	GQ324346
P. litorosa Cheeseman	266	*Brizoides* subsect. *Australopoa* 'C1'	*P.* supersect. *Poa*	New Zealand[E]	GB: Gardner *et al.* unpubl. [de Lange 5595 (AK-281151)]	–	AY686662	–
P. lowanensis G.N. Walsh		*Brizoides* subsect. *Australopoa*	*P.* supersect. *Homalopoa*	Australia,[E] Victoria	Walsh s.n. (MEL2323766)	GQ324433	GQ324523	GQ324347
P. macrantha Vasey	28	*Madropoa*	*P.* supersect. *Homalopoa*	USA, Oregon	Soreng 5861 (US)	DQ354028	EU792407	GQ324348
P. macrocalyx Trautv. & C.A.Mey.	42–100	*Malacanthae*	*P.* supersect. *Poa*	USA, Alaska	Soreng & Soreng 6318-1 (US)	GQ324434	GQ324524	GQ324349
P. mathewsii Petrie	28	'New Zealand E2'	*Poa* (X clade)	New Zealand[E]	Lloyd s.n. (OTA 058920)	GQ324435	GQ324525	GQ324350
P. media (L.) Cav.	14	*Bolbophorum*	*Ochlopoa* (N Clade)	Bulgaria	Hajkova *et al.* 2004-11 (US)	GQ324436	GQ324526	GQ324351
P. media	14	*Bolbophorum*	*Ochlopoa* (N Clade)	Bulgaria	Stoneberg SH17 (US)	GQ324437	GQ324527	GQ324352
P. meionectes J. Vickery		*Brizoides* subsect. *Australopoa*	*P.* supersect. *Homalopoa*	Australia,[E] NSW	Gillespie & Jacobs 7316-1 (CAN)	GQ324438	GQ324528	GQ324353
P. meionectes		*Brizoides* subsect. *Australopoa*	*P.* supersect. *Homalopoa*	Australia,[E] NSW	Gillespie *et al.* 7348 (CAN)	GQ324439	–	–
P. molinerii Balb.	14, 28	*Alpinae*	*Ochlopoa*	Slovakia	Stoneberg SH13 (CAN)	DQ354036, DQ354037	EU792389	GQ324354
P. nemoralis L.	28, 33, 35, 42, 48, 56	*Stenopoa*	*Stenopoa*	Bulgaria	Hajkova *et al.* 2004-18 (BRNU)	GQ324440	GQ324529	GQ324355
P. nervosa (Hook.) Vasey	28	*Madropoa*	*P.* supersect. *Homalopoa*	USA, Oregon	Soreng 5849 (US)	DQ354025	EU792405	GQ324356
P. novae-zelandiae Hack.	28	'New Zealand A2'	*Poa* (X clade)	New Zealand[E]	GB: Gardner *et al.* unpubl. [Lange 5654 (AK-282179)]	–	AY686659	–
P. orba G.N. Walsh		*Brizoides*	*P.* supersect. *Homalopoa*	Australia,[E] Victoria	Walsh s.n. (MEL2323762)	GQ324441	GQ324530	GQ324357
P. orthoclada G.N. Walsh		*Brizoides* subsect. *Australopoa*	*P.* supersect. *Homalopoa*	Australia,[E] Victoria	Walsh s.n. (MEL2323761)	GQ324442	GQ324531	GQ324358
P. phillipsiana J. Vickery		*Brizoides* subsect. *Australopoa*	*P.* supersect. *Homalopoa*	Australia,[E] NSW	Gillespie *et al.* 7346 (CAN)	GQ324443	GQ324532	GQ324359
P. phillipsiana		*Brizoides* subsect. *Australopoa*	*P.* supersect. *Homalopoa*	Australia,[E] NSW	Gillespie *et al.* 7369 (CAN)	GQ324444	GQ324533	GQ324360
P. poiformis (Labill.) Druce	56–68	*Brizoides* subsect. *Australopoa*	*P.* supersect. *Homalopoa*	Australia,[E] NSW	Gillespie *et al.* 7381 (CAN)	GQ324445	GQ324534	GQ324361
P. poiformis		*Brizoides* subsect. *Australopoa*	*P.* supersect. *Homalopoa*	Australia,[E] NSW	Soreng & Peterson 5911 (US)	GQ324446	GQ324535	GQ324362
P. polycolea Stapf		*Poa* subsect. *Nivicolae*	*P.* supersect. *Homalopoa*	China, Yunnan	Wen *et al.* Tibet-1316 (US)	GQ324447	GQ324536	GQ324363
P. porphyroclados Nees		*Brizoides* subsect. *Australopoa*	*P.* supersect. *Homalopoa*	Australia,[E] WA	Peterson *et al.* 14476 (US)	GQ324448	GQ324537	GQ324364
P. porsildii Gjaerev.		*Madropoa*	*P.* supersect. *Homalopoa*	USA, Alaska	Soreng & Soreng 6147-1 (US)	DQ354024	GQ324538	GQ324365

Appendix 1. (*continued*)

Taxon	Chromosome number	*Poa* subgenus-supersection	*Poa* section-subsection (and NZ group)	Voucher	Country of origin	TLF GenBank	ITS GenBank	ETS GenBank
P. pratensis L. subsp. *pratensis*	25–124	*P.* supersect. *Poa*	*Poa* subsect. *Poa*	Gillespie 6291 (CAN)	USA, Colorado	DQ354010	GQ324542	GQ324369
P. pratensis subsp. *alpigena* (Lindm.) Hiitonen	28–127	*P.* supersect. *Poa*	*Poa* subsect. *Poa*	Gillespie 5801 (CAN)	Canada, Nunavut	DQ354006	GQ324539	GQ324366
P. pratensis subsp. *angustifolia* (L.) Lej.	28, 46–66, 70–72	*P.* supersect. *Poa*	*Poa* subsect. *Poa*	Catalán s.n. (UZ)	Spain	DQ354012	GQ324540	GQ324366
P. pratensis subsp. *irrigata* (Lindm.) H. Lindb.	38–117	*P.* supersect. *Poa*	*Poa* subsect. *Poa*	Soreng & Soreng 6044 (US)	USA, Alaska	GQ324449	GQ324541	GQ324368
P. pseudoabbreviata Roshev.	14	*Stenopoa*	*Abbreviatae*	Soreng & Soreng 6032-1 (US)	USA, Alaska	DQ353997	EU792398	GQ324370
P. pubinervis (Vickery) SWLJacobs, L.J.Gillespie & Soreng		*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Austrofestuca*	Peterson *et al.* 14510 (US)	Australia,[E] WA	DQ354048, DQ354049	EU792408	GQ324371
P. ramosissima Hook.f.	28	*Ochlopoa*	*Parodiochloa* (New Zealand 'Al')	GB: Gardner *et al.* unpubl. [Wright (AK-282001)]	New Zealand[E]	–	AY686655	–
P. remota Forselles	14	*P.* supersect. *Homalopoa*	*Homalopoa* s.s.	Soreng *et al.* 7540 (US)	Kyrgyz Republic	GQ324452	GQ324545	GQ324372
P. sallacustris G.N. Walsh		*P.* supersect. *Homalopoa*	*Brizoides*	Walsh s.n. (MEL2323760)	Australia,[E] Victoria	GQ324453	GQ324546	GQ324373
P. saltuensis Fernald & Wiegand	28	*P.* supersect. *Sylvestres*	*Sylvestres*	Gillespie 7043 (CAN)	Canada, Ontario	EU792451	EU792378	GQ324374
P. scaberula Hook.f.		*P.* supersect. *Homalopoa*	*Dasypoa*	Peterson & Soreng 15575 (US)	Chile	GQ324454	EU792412	GQ324375
P. sibirica Roshev. subsp. *sibirica*	14	*P.* supersect. *Poa*	*Macropoa*	Olonova 2002-1 (CAN)	Russia, Khakasia	DQ354044, DQ354045	EU792401	GQ324376
P. sieberiana Spreng.		*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Australopoa*	Gillespie *et al.* 7319 (CAN)	Australia,[E] NSW	GQ324456	GQ324548	GQ324377
P. sieberiana		*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Australopoa*	Gillespie *et al.* 7374 (CAN)	Australia,[E] NSW	GQ324457	GQ324549	GQ324378
P. sieberiana		*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Australopoa*	Jacobs 8482 (NSW)	Australia,[E] NSW	GQ324458	GQ324550	GQ324379
P. sieberiana		*P.* supersect. *Homalopoa*	*Brizoides* subsect. *Australopoa*	GB: Patterson *et al.* 2005 (USDA PI 263863)	New Zealand (cult.)	AY589145	–	–
P. smirnowii subsp. *mariae* (Reverd.) Tzvelev	[42, 70 for subsp. *smirnowii*]	*P.* supersect. *Poa*	*Malacanthae*	Olonova 2002-07 (CAN)	Russia, Khakasia	DQ354005	GQ324551	GQ324380
P. spania Edgar & Molloy		*Poa* (X clade)	'New Zealand F1'	GB: Gardner *et al.* unpubl. (AK-282077)	New Zealand[E]	–	AY686668	–

Taxon	2n	Supersection/clade	Section	Location	Voucher			
P. stuckertii (Hack.) Parodi	28		*Dioicopoa*	Chile	Soreng & Soreng 7132 (US)	DQ354022	EU792414	GQ324381
P. subvestita (Hackel.) Edgar	28	*P.* supersect. *Homalopoa* *Poa* (X clade)	'New Zealand A2'	New Zealand[E]	Lloyd s.n. (OTA 058917)	**GQ324459**	**GQ324552**	**GQ324382**
P. supina Schrad.	14	*Ochlopoa*	*Micrantherae*	USA, cult. (from Europe)	Soreng & Cayouette 5950-2 (US)	DQ353984	EU792387	GQ324383
P. sylvestris A.Gray	28		*Sylvestres*	USA, Maryland	Soreng 4678-3 (US)	DQ353980	EU792375	GQ324384
P. thessala Boiss. & Orph.	14	*Ochlopoa*	*Bolbophorum*	Greece	Soreng et al. 7522 (US)	**GQ324460**	**GQ324553**	**GQ324385**
P. trichophylla HeIDr & Sart. ex Boiss.	14	(N clade)	*Nanopoa*	Greece[E]	Soreng et al. 7508 (US)	**GQ324461**	**GQ324554**	**GQ324386**
P. trivialis L.	14	*Stenopoa*	*Pandemos*	USA, Maryland (introd.)	Soreng 4681-1 (US)	**GQ324462**	**GQ324555**	**GQ324387**
P. wheeleri Vasey	56, 61–67, 70, 75, 79–81, 87, 89, 90	*P.* supersect. *Homalopoa*	*Madropoa*	USA, Nevada	Soreng 5825 (US)	DQ354026	EU792406	**GQ324388**
P. wolfii Scribn.	28	*Sylvestres*		USA,[E] Missouri	Soreng 5800 (US)	DQ354032, DQ354033	EU792377	GQ324389
Saxipoa saxicola (R.Br.) Soreng, L.J.Gillespie, & S.W.L.Jacobs				Australia,[E] NSW	Gillespie et al. 7353-1 (CAN)	**GQ324464**	**GQ324556**	**GQ324390**
S. saxicola				Australia,[E] NSW	Gillespie et al. 7353-4 (CAN)	**GQ324463**	**GQ324557**	**GQ324391**
S. saxicola				Australia,[E] Victoria	Walsh s.n. (MEL2323764)	**GQ324465**	**GQ324558**	**GQ324392**
Sylvipoa queenslandica (C.E.Hubbard) Soreng, L.J.Gillespie, & S.W.L.Jacobs				Australia,[E] NSW	Gillespie et al. 7320 (CAN)	**GQ324466**	**GQ324559**	**GQ324393**
Subtribe Puccinelliinae								
Catabrosa aquatica (L.) P.Beauv.	20, 40			Chile	Soreng & Soreng 7150 (US)	DQ353958	EU792334	**GQ324258**
C. werdermannii (Pilg.) Nicora & Rúgolo				Argentina	Peterson et al. 19371 (US)	EU792431	EU792333	**GQ324259**
Puccinellia vahliana (Leibm.) Scribn.	14			Canada, Nunavut	Gillespie 5808 (CAN)	EU854591	EU792336	**GQ324285**
Tribe Poeae – outgroups								
Subtribe Agrostidinae								
Agrostis mertensii Trin.	56			USA, New Hampshire	Gillespie 6802 (CAN)	DQ353956	**GQ324467**	**GQ324236**
Subtribe Airinae								
Deschampsia brevifolia R.Br.	26, 27, 28, 50, 52			Canada, Northwest Territories	Gillespie & Consaul 6810b (CAN)	DQ353962	EU792328	**GQ324262**
Subtribe Aveninae								
Helictotrichon sempervirens (Vill.) Pilg.	42			USA, New York, cult.	Soreng 4622 (US)	DQ353955	EU792325	**GQ324269**
Subtribe Loliinae								
Dryopoa dives (F.Muell.) Vickery				Australia,[E] NSW	Jacobs 9239 (NSW)	EU792430	**GQ324474**	–
Festuca baffinensis Polunin	28			Canada, Northwest Territories	Gillespie & Consaul 6920 (CAN)	DQ353951, DQ353952	**GQ324476**	**GQ324268**

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Appendix 1. *(continued)*

Taxon	Chromosome number	*Poa* subgenus–supersection	*Poa* section–subsection (and NZ group)	Country of origin	Voucher	TLF GenBank	ITS GenBank	ETS GenBank
Subtribe Phalaridinae								
Anthoxanthum monticola (Bigelow) Veldkamp subsp. *alpinum* (Sw. ex Willd.) Soreng	56			Canada, Northwest Territories	Gillespie & Consaul 6859 (CAN)	DQ353953	EU792323	–

[A]Chromosome numbers are given to indicate ploidy level. Literature citations for the original counts are mostly reported in the Index to Plant Chromosome Numbers (Goldblatt and Johnson 1979–), but are also taken from secondary taxonomic literature that we believe provide reliable distillations of the primary literature (Tzvelev 1976; Moore 1982; Veldkamp 1994; Barkworth *et al.* 2007). Additional references for chromosome numbers of *Poa* are given in Soreng *et al.* (in press).
[B]Corrected from Soreng 3770, R.J. Soreng, September 2006.
[C]Contaminant in USDA PI 202208 seed accession.
[E]Refers to species endemic to the country indicated.