

## SUPPLEMENTARY DATA

**TABLE S1.** *Herbarium accession number, geographic details and regions amplified for all individuals used in microsatellite and/or sequence analysis.* 1 = successful amplification (and successful sequencing for the gene regions). 0 = unsuccessful amplification and/or sequencing. Untested marker/individual combinations are shaded grey. Marker/individual combinations in bold indicate sequences gained using 454 sequencing.

Individual	Species	Accession no.	State	Lat	Long	Microsatellite					Nuclear				Chloroplast							
						CA1F4	AES	HO1HO6	CA1D4	M16B	waxy A	waxy B	DMC1 A	DMC1 B	trx A	trx B	CDO504 A	CDO504 B	trnH-psbA	rpoB-trnC	rpl32-trnL	
Pan_ACT_97	<i>Poa annua</i>	CANB 312513	ACT	-35.283	149.117						1	1	1	1	0	0	1	1	1	1	1	1
Pan_NSW_92	<i>Poa annua</i>	CANB 407148	NSW	-36.250	150.233						1	1	1	1	0	0	0	0	1	1	1	1
Pan_NSW_93	<i>Poa annua</i>	CANB 343723	NSW	-36.450	148.283						1	1	1	1	0	0	1	1	1	1	1	1
Pcl_ACT_102	<i>Poa clivicola</i>	CANB 438760	ACT	-35.567	148.783						1	1	1	1	1	1	1	1	1	1	1	1
Pcl_ACT_103	<i>Poa clivicola</i>	CANB 228786	ACT	-35.533	148.917						1	1	1	1	1	1	1	1	1	1	1	1
Pcl_ACT_104	<i>Poa clivicola</i>	CANB 8906309	ACT	-35.689	148.842						1	1	1	1	1	0	1	1	1	1	1	1
Pcl_ACT_105	<i>Poa clivicola</i>	CANB 8702739	ACT	-35.542	148.950						1	1	1	1	1	0	1	1	1	1	1	1
Pcl_ACT_44	<i>Poa clivicola</i>	MEL 650412A	ACT	-35.533	148.900	1	1	1	1	1	0	0	1	1							0	1
Pcl_ACT_45	<i>Poa clivicola</i>	MEL 1617342A	ACT	-35.575	148.783	1	1	1	1	1	1	0	1	1							1	1
Pcl_NSW_100	<i>Poa clivicola</i>	CANB 329728	NSW	-36.500	148.333						1	1	1	1	1	1	1	0	1	1	1	1
Pcl_NSW_101	<i>Poa clivicola</i>	CANB 228805	NSW	-35.550	148.667						1	1	1	1	1	0	1	1	1	1	1	1
Pcl_NSW_99	<i>Poa clivicola</i>	CANB 647153	NSW	-35.783	149.350						1	1	1	1	1	1	1	1	1	1	1	1
Pcl_Vic_46	<i>Poa clivicola</i>	MEL 2011778A	Vic	-37.017	147.233	1	1	1	1	1	1	1	1	1							1	1
Pco_NSW_1	<i>Poa costiniana</i>	MEL 302832A	NSW	-36.450	148.250	1	1	1	1	1	0	1	0	0							0	1
Pco_NSW_107	<i>Poa costiniana</i>	CANB 619578	NSW	-34.575	149.736						1	1	1	1	1	0	1	1	1	1	1	1
Pco_NSW_108	<i>Poa costiniana</i>	CANB 619540	NSW	-34.374	149.545						1	1	1	1	1	0	1	1	1	0	1	1
Pco_NSW_110	<i>Poa costiniana</i>	CANB 505348	NSW	-36.450	148.267						1	1	1	1	1	1	1	1	1	1	1	1
Pco_NSW_117	<i>Poa costiniana</i>	CANB 9707880	NSW	-36.456	148.278						1	1	1	1	1	0	1	1	1	1	1	1



Pen_Vic_78	<i>Poa ensiformis</i>	MEL 2023602A	Vic	-37.500	145.867	1	1	1	0	1	0	0									
Pfa_ACT_16	<i>Poa fawcettiae</i>	MEL 2138088A	ACT	-35.567	148.767	1	1	1	1	1	1	1	0	0							
Pfa_ACT_9	<i>Poa fawcettiae</i>	MEL 596118A	ACT	-37.817	146.294	1	1	1	1	1	0	0									
Pfa_NSW_11	<i>Poa fawcettiae</i>	MEL 1518741A	NSW	-37.350	146.783	1	0	1	1	1	0	0									
Pfa_NSW_131	<i>Poa fawcettiae</i>	CANB 505356	NSW	-36.450	148.250						1	1	1	1	1	1	0	0	1	1	1
Pfa_NSW_132	<i>Poa fawcettiae</i>	CANB 505353	NSW	-36.450	148.283						1	1	1	1	1	0	1	1	1	1	1
Pfa_NSW_133	<i>Poa fawcettiae</i>	CANB 505340	NSW	-36.450	148.283						1	1	1	1	1	1	0	0	1	1	1
Pfa_NSW_134	<i>Poa fawcettiae</i>	CANB 228865	NSW	-36.350	148.417						1	1	1	1	1	1	0	0	1	1	1
Pfa_NSW_135	<i>Poa fawcettiae</i>	CANB 345640	NSW	-36.400	148.350						1	1	1	1	1	1	1	1	1	1	1
Pfa_NSW_136	<i>Poa fawcettiae</i>	CANB 228879	NSW	-36.417	148.417						1	1	1	1	1	0	1	1	1	1	1
Pfa_NSW_137	<i>Poa fawcettiae</i>	CANB 230925	NSW	-36.450	148.283						1	1	1	1	1	1	1	1	1	1	1
Pfa_NSW_15	<i>Poa fawcettiae</i>	MEL 649620A	NSW	-36.450	148.267	1	1	1	1	1	1	1	0	0							
Pfa_NSW_17	<i>Poa fawcettiae</i>	MEL 652850A	NSW	-36.350	148.417	1	1	1	1	1	0	0	0	0							
Pfa_NSW_18	<i>Poa fawcettiae</i>	MEL 286299A	NSW	-36.450	148.250	0	0	1	1	0	0	0									
Pfa_Tas_13	<i>Poa fawcettiae</i>	MEL 695201A	Tas	-41.533	147.650	1	1	1	1	1	1	1	1	1							
Pfa_Tas_14	<i>Poa fawcettiae</i>	MEL 2138673A	Tas	-41.750	147.500	1	1	1	1	1	1	1	0	0							
Pfa_Vic_10	<i>Poa fawcettiae</i>	MEL 619714A	Vic	-37.840	146.274	1	1	1	1	1	1	1	0	1							
Pfa_Vic_12	<i>Poa fawcettiae</i>	MEL 2013073A	Vic	-37.125	147.117	1	1	1	1	1	0	0	0	0							
Pfa_Vic_146	<i>Poa fawcettiae</i>	CANB 488116	Vic	-37.160	146.427						1	1	1	1	1	0	1	1	1	1	1
Pfa_Vic_147	<i>Poa fawcettiae</i>	CANB 67067	Vic	-37.317	142.333						1	1	1	1	1	0	1	1	1	1	1
Pfa_Vic_148	<i>Poa fawcettiae</i>	CANB 9501151	Vic	-36.892	147.138						1	1	1	1	1	1	1	1	1	1	1
Pfa_Vic_43	<i>Poa fawcettiae</i>	MELU M10771	Vic	-37.504	145.883	1	1	1	1	1	0	0									
Pfa_Vic_f1	<i>Poa fawcettiae</i> field collection 2005, Mt Nelse, Bogong High Plains, Alpine National Park. Alpine grassland. Coll: S. Byars. Det: N. Walsh		Vic	-36.825	147.342						1	0	1	1							
Pgu_Tas_149	<i>Poa gunnii</i>	CANB 8904303	Tas	-42.678	146.503						1	1	1	1	1	0	1	1	1	0	1
Pgu_Tas_150	<i>Poa gunnii</i>	CANB 195943	Tas	-42.650	146.517						1	1	1	1	1	0	1	1	1	1	1
Pgu_Tas_151	<i>Poa gunnii</i>	CANB 341316	Tas	-41.533	147.667						0	1	0	0	1	0	1	1	1	0	1
Pgu_Tas_152	<i>Poa gunnii</i>	CANB 402406	Tas	-42.950	146.400						1	1	1	0	1	0	1	1	1	0	1
Pgu_Tas_153	<i>Poa gunnii</i>	CANB 9215410	Tas	-41.508	147.667						1	1	1	0	1	0	0	1	1	0	1



Phi_Vic_f2	<i>Poa hiemata</i> field collection 2005, Mt Nelse, Bogong High Plains, Alpine National Park. Alpine grassland. Coll: S. Byars. Det: N. Walsh		Vic	-36.825	147.342						0	1	1	1					1	1
Phi_Vic_f3	<i>Poa hiemata</i> field collection 2005, Mt Nelse, Bogong High Plains, Alpine National Park. Alpine grassland. Coll: S. Byars. Det: N. Walsh		Vic	-36.825	147.342	1	1	1	1	1	0	0								
Pho_Vic_191	<i>Poa hothamensis</i> <i>var. hothamensis</i>	CANB 409990	Vic	-36.867	147.267						1	1	1	1	1	0	1	1	1	1
Pho_Vic_192	<i>Poa hothamensis</i> <i>var. hothamensis</i>	CANB 67341	Vic	-36.983	147.150						1	1	1	1	1	0	1	1	1	1
Pho_Vic_198	<i>Poa hothamensis</i> <i>var. hothamensis</i>	CANB 207886	Vic	-36.933	147.283						1	1	1	0	1	0	1	1	1	1
Pho_Vic_199	<i>Poa hothamensis</i> <i>var. hothamensis</i>	CANB 207893	Vic	-37.833	146.283						1	1	0	0	1	0	0	1	1	0
Pho_Vic_41	<i>Poa hothamensis</i> <i>var. hothamensis</i>	MELU M102595	Vic	-36.893	147.214	1	1	1	1	1	0	0	0	0					0	1
Pho_Vic_42	<i>Poa hothamensis</i> <i>var. hothamensis</i>	MELU M102597	Vic	-36.875	147.249	0	0	1	0	1	0	0								
Pho_Vic_65	<i>Poa hothamensis</i> <i>var. hothamensis</i>	MEL 1592155A	Vic	-36.867	147.267	1	0	1	1	1	0	0								
Pho_Vic_67	<i>Poa hothamensis</i> <i>var. hothamensis</i>	MEL 252256A	Vic	-36.883	147.317	1	1	1	1	1	1	0	1	1					0	0
Pho_Vic_68	<i>Poa hothamensis</i> <i>var. hothamensis</i>	MEL 1592158A	Vic	-36.750	146.783	0	1	1	1	1	0	0								
Pho_Vic_69	<i>Poa hothamensis</i> <i>var. hothamensis</i>	MEL 1542253A	Vic	-36.746	147.537	1	1	1	1	0	0	0								
Pho_Vic_70	<i>Poa hothamensis</i> <i>var. hothamensis</i>	MEL 2275845A	Vic	-36.958	147.333	1	0	1	0	0	0	0								
Pho_Vic_71	<i>Poa hothamensis</i> <i>var. hothamensis</i>	MEL 717823A	Vic	-37.000	147.150	1	0	1	1	1	0	0								
Pho_Vic_89	<i>Poa hothamensis</i> <i>var. hothamensis</i>	CANB 207890	Vic	-36.933	147.283						1	1	1	1	1	0	1	1	1	1
Pho_Vic_f1	<i>Poa hothamensis</i> <i>var. hothamensis</i> field collection 2005, Mt Nelse, Bogong High Plains, Alpine National		Vic	-36.825	147.342						1	1	1	1						1



	<i>var. sieberiana</i>																				
	<i>Poa sieberiana</i>																				
Psi_Vic_29	<i>var. sieberiana</i>	MEL 1056947A	Vic	-37.217	145.900	1	1	1	1	1	0	0	0	0					0	1	
Psi_Vic_30	<i>Poa sieberiana</i>																				
Psi_Vic_30	<i>var. sieberiana</i>	MEL 519545A	Vic	-37.167	146.617	1	0	1	1	1	0	0									
Psi_Vic_31	<i>Poa sieberiana</i>																				
Psi_Vic_31	<i>var. sieberiana</i>	MEL 2268838A	Vic	-37.053	148.084	1	1	1	1	1	1	0	1	1					1	1	
Psi_Vic_32	<i>Poa sieberiana</i>																				
Psi_Vic_32	<i>var. sieberiana</i>	MEL 2269869A	Vic	-35.848	143.572	1	1	1	1	1	1	1	1	1					1	1	
Psi_Vic_35	<i>Poa sieberiana</i>																				
Psi_Vic_35	<i>var. sieberiana</i>	MEL 1537323A	Vic	-37.353	149.938	1	0	1	1	0	0	0									
TOTAL						65	53	69	63	60	82	78	78	73	57	16	52	53	56	60	102

**TABLE S2.** PCR annealing temperature, size range and total number of alleles detected across the 10 species surveyed for each microsatellite marker.

Marker	Primers from	Annealing temp. (°C)	Size (bp)	Plants genotyped	Total no. alleles	Alleles found by Byars <i>et al.</i> (2009)	H <sub>o</sub>
AE5	(Albertini et al., 2003)	48	239–305	53	21	6	0.94
CA1D4	(Maurer et al., 2005)	57.5	294–336	65	21	13	0.74
MI6-B	(Kindiger, 2006)	56	127–182	60	24	14	0.73
H01H06	(Kindiger, 2006)	59.5	166–182	69	13	10	0.83
CA1F4	(Maurer et al., 2005)	60	171–229	64	22	35	0.70
GAC1	(Maurer et al., 2005)	57	79–106	Marker excluded	19 (unreliable)	17	---

H<sub>o</sub> = observed heterozygosity (proportion of heterozygotes).

**TABLE S3.** Chloroplast and nuclear regions: PCR annealing temperature, size range and total number of alleles detected. The primers and conditions reported here are those used for the initial Sanger sequencing (for the chloroplast regions, and the nuclear regions *waxy* and *DMC1*); and those used for the 454 sequencing that were not reported in Griffin et al. (2011): *trx* and *CDO504*.

Region	Sequencing method	Primers from	PCR conditions	No. individuals sequenced	Gene Copy	Length (bp)	Base changes	Indels
<i>rpl32-trnL</i>	Sanger	(Shaw et al., 2007)	80°C (5 min); 30 × 95°C (60 s), 54°C (60 s), 65°C (4 min); 65°C (5 min)	40		838–850	2	3 (2–8 bp)
<i>rpoB-trnC</i>	Sanger	(Shaw et al., 2005)	80°C (5 min); 35 × 96°C (60 s), 52°C (30 s), 72°C (30 s); 72°C (5 min)	13		1176–1177	3	2 (1 bp)
<i>trnH-psbA</i>	Sanger	(Tate and Simpson, 2003), (Sang et al., 1997)	95°C (5 min); 35 × 95°C (45 s), 56°C (60 s), 72°C (30 s); 72°C (3 min)	0		Approx. 800	Poor sequence*	Poor sequence*
<i>DMC1</i>	Sanger	(Petersen and Seberg, 2000)	95°C (2 min); 40 × 95°C (60 s), 55°C (60 s), 72°C (2 min); 72°C (10 min). [MgCl <sub>2</sub> ] = 2.5 mM	19	Copy A	1047	17	0
				17	Copy B	1017	29	0
<i>waxy</i>	Sanger	(Petersen and Seberg, 2000)	94°C (2 min); 35 × 94°C (60 s), 65°C (60 s), 72°C (2 min); 72°C (10 min). [MgCl <sub>2</sub> ] = 2.0 mM	26	Copy A	511–519	41	1 (8 bp)
				20	Copy B	519–535	22	5 (1–14 bp)
<i>trx</i>	454	(for) 5'- TGATGTTGATGACCTGA	96°C (2 min); 40 × 96°C (40 s), 50°C (60 s), 72°C (40 s); 72°C	57	Copy A	338-381	113	8 (1-12 bp)



		TGGT-3'	(5 min). [MgCl <sub>2</sub> ] = 2.0 mM						
		(rev) 5'-		18		Copy B**	387-393	29	0
		AGCACACTCCACACAG							
		TTTCA-3'							
<b>waxy</b>	454	(for) 5'-	96°C (2 min); 40 × 96°C (40 s),	56		Copy A	362-412	75	7 (2-13 bp)
		ATTGCCGTCAACTACGA	50°C (60 s), 72°C (40 s); 72°C						
		TGC-3'	(5 min). [MgCl <sub>2</sub> ] = 2.0 mM						
		(rev) 5'-		58		Copy B	379-408	87	5 (2-13 bp)
		GGCCATGATCTGGTGA							
		GC-3'							

For the multiple-gene analysis described in the text, the Sanger-sequenced results were aligned with the consensus 454 results and trimmed to match their shorter length. The final alignment was used to create input for \*BEAST.

The *trx* Copy A dataset included two *Poa annua* sequences from GenBank (accession numbers 51702653 and 51702654).

*Trx* Copy A and *waxy* Copy A and B 454 results include *Poa annua* sequences, hence the higher number of SNPs and indels.

\* These primers produced poor products for *trnH-psbA* but the primers used for later sequencing (Griffin et al., 2011) produced shorter, clean products

\*\* *trx* Copy B amplified poorly in most individuals and was excluded from further analysis

## References

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