Supplementary text

Sequencing statistics

In total, 460,981 high-quality sequences were assigned to ITS2 and 1,054,333 to *rbcL*. There was considerable variation in the number of reads per sample, with the total number of high quality *rbcL* sequences varying from 3 to 56,981 and the number of ITS2 sequences ranging from 260 to 10,180 (excluding a single sample that contained zero sequences following quality control).

Excluding control samples, ITS2 reads included 179,450 grass sequences (Poaceae), assigned to 13 genera. Whilst not the focus of our study, the remaining 162,540 sequences consisted of 33 families and 31 genera of terrestrial plants. Of these families, 17 contained only a single genus and four contained reads which could not be identified confidently to genus level. Within the *rbcL* marker, 179,330 grass reads were assigned to 13 grass genera and the remaining 867,823 reads belonged to 68 families and 84 genera of terrestrial plants. Of these families, 33 contained only a single genus and 13 contained reads which could not be identified confidently to genus level.

ITS2 and *rbcL* detect different grass species

The contrasting characteristics of the ITS2 and *rbcL* markers makes them an ideal pairing. The ITS2 marker shows high specificity between species but cannot detect all plants [38], whereas *rbcL* primers are highly universal but the marker shows lower resolution between closely related plants [39].

Of the grass genera identified, only four were present in both ITS2 and *rbcL* datasets: *Dactylis*, *Lolium*/*Festuca*, *Anthoxanthum*, and *Avena*. While the proportion of reads assigned to *Lolium*/*Festuca* and *Anthoxanthum* were correlated between the two markers (*Lolium*/*Festuca* (*Lolium*/*Festuca*: t_{72}= 8.6, adjusted p-value < 0.001, r^2 = 0.5, S4A Fig; *Anthoxanthum*: t_{72}=2.9, adjusted p-value = 0.006, r^2 = 0.09, S4B Fig), this was not the case for *Dactylis* or *Avena* (S4C Fig; S4D Fig). However, both of the latter species were detected at

relatively low levels in both datasets, potentially increasing the degree of stochasticity introduced by library preparation [40].

Positive and negative controls

Negative controls, with all reagents and no DNA were used to identify any cross-contamination. Of the six negative controls, four contained no reads following quality control filtering, one contained a single read and one contained nine reads in the *rbcL* database. None of the negative controls in the ITS2 dataset contained any reads.

Two positive control samples were also included, a grass positive control and an exotic plant positive control. Both sets of positive controls were diluted to 0.3 ng μl^{-1}, similar to that of the aerial eDNA samples.

The grass positive control contained a mixture of fifty-two species of grass from herbarium collections held at the National Botanic Garden of Wales. The mixture of grasses contained thirty-three genera, with twenty-four of these genera represented by a single species and the remaining nine genera represented by between two and five species (S1 Table). Of the thirty-three genera in the grass positive control sample, four were detected across both markers, eight were detected by the *rbcL* marker and twelve by the ITS2 marker. The remaining sequences were too similar to be identified to genus level (27% and 37% of reads in the grass positive control samples could not be reliably assigned to genus level, using ITS2 and *rbcL* markers respectively). However, three of the genera not detected the positive control samples, despite being included, were detected in airborne samples (*Agrostis*, *Anthoxanthum*, *Alopecurus*), likely reflecting higher local abundances of airborne pollen (S2 Table). The number of species in the grass positive control is much higher than the number of species predicted to contribute to airborne pollen concentrations according to phenological studies [41, 42]. Differences in taxon diversity between the grass positive control and the airborne samples will likely lead to differences in taxonomic assignment due to taxon-specific PCR amplification biases [43-45]. While sample coverage (i.e. number of reads) obtained for

59 the grass positive control samples was comparable to the airborne samples, the high diversity
60 of the positive control and variation in the number of species between genera may have led
61 to a higher likelihood of amplification for certain genera.

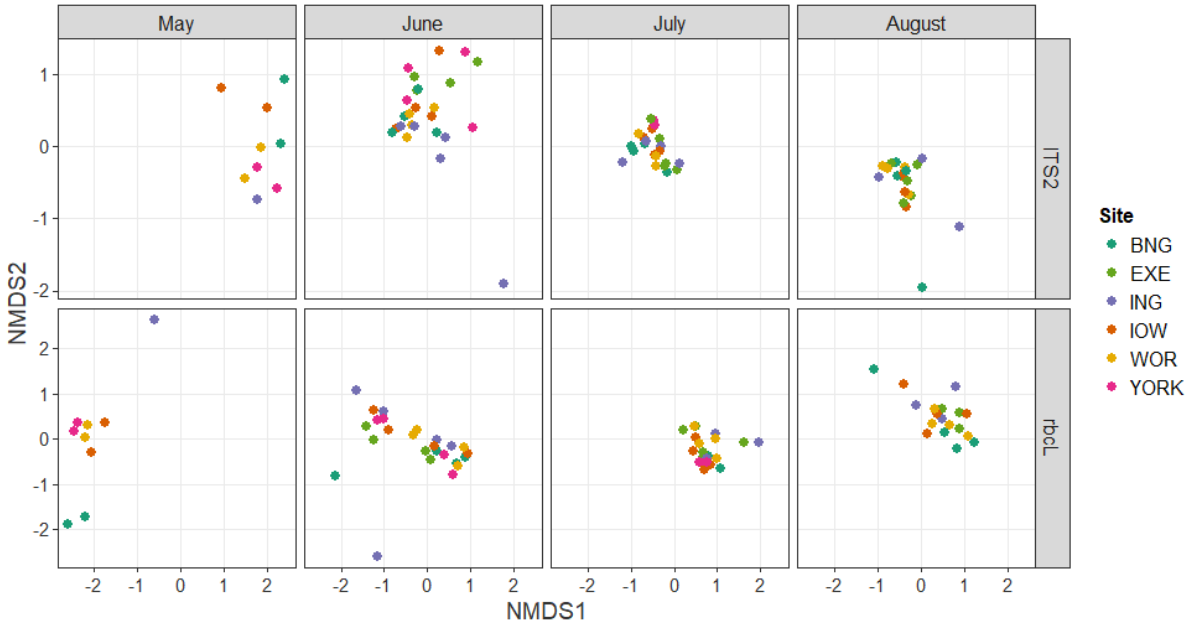
62

63 In order to check for cross-contamination between samples, an exotic plant positive control
64 sample was used containing DNA extracted from twenty-one tropical tree species samples
65 held at the National Botanic Garden of Wales. None of the genera identified in this positive
66 control were present in the experimental samples.

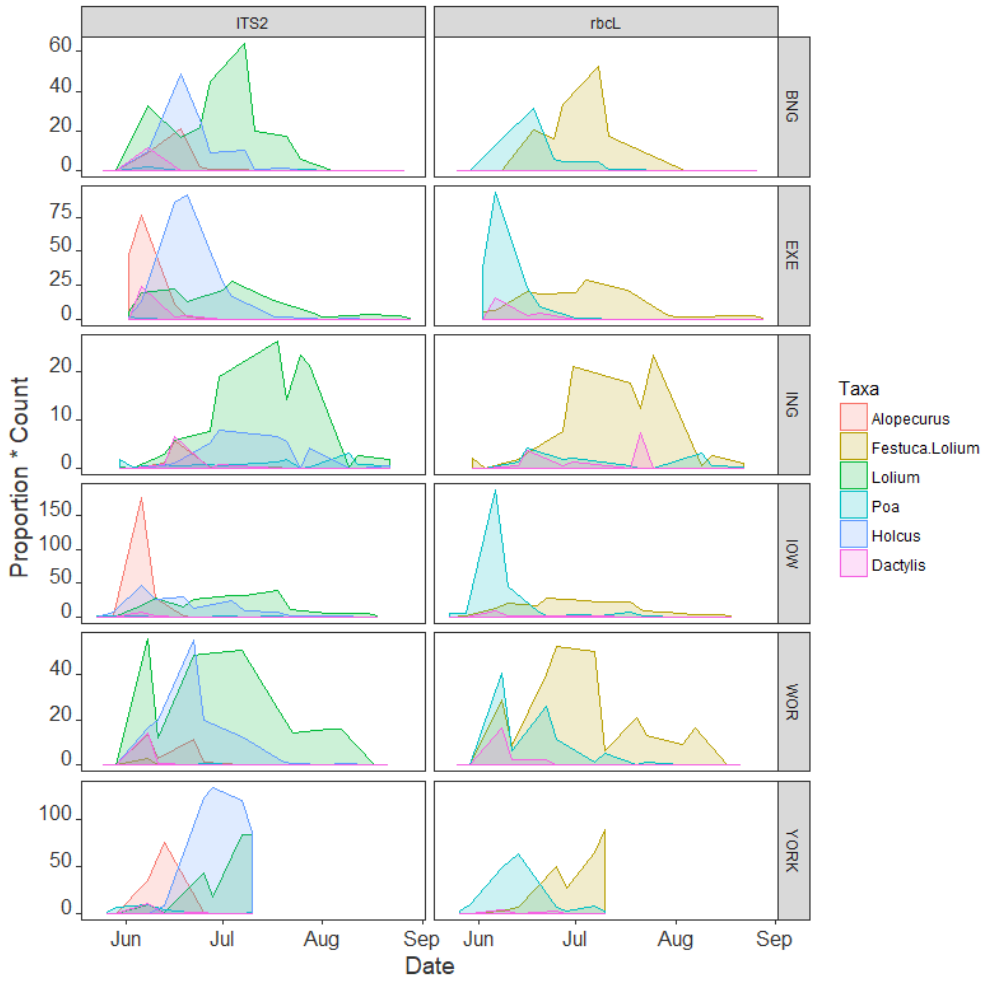
67

68

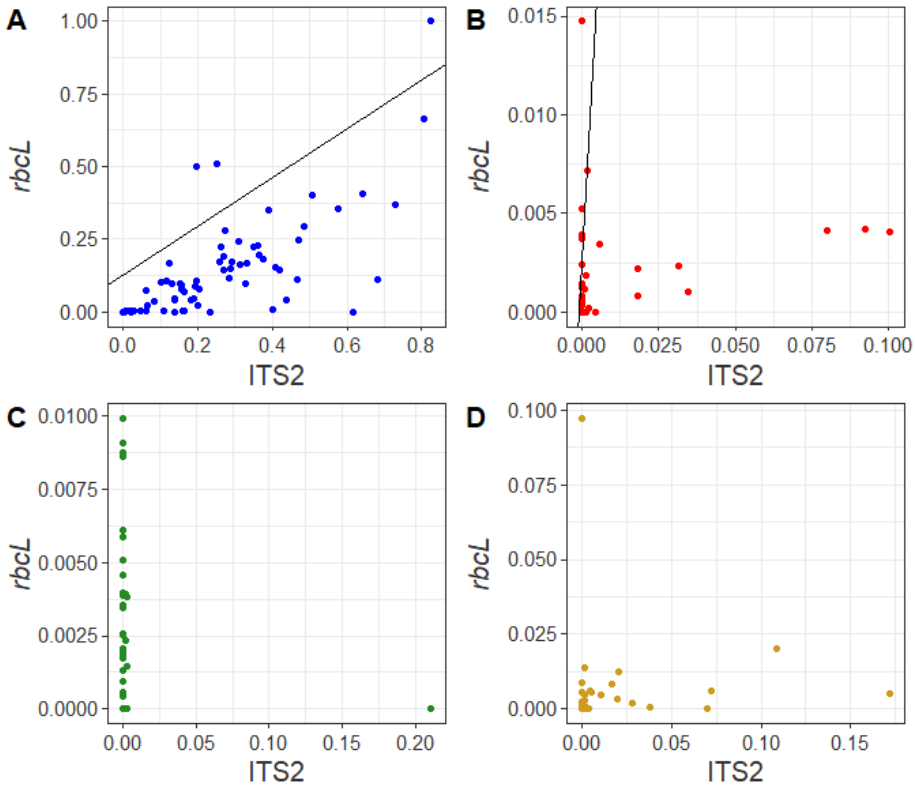
S1 Fig. Map showing position of the six sampling sites. Contains OS data Crown copyright and database right (2018). Image Crown Copyright, 2018, The Met Office.



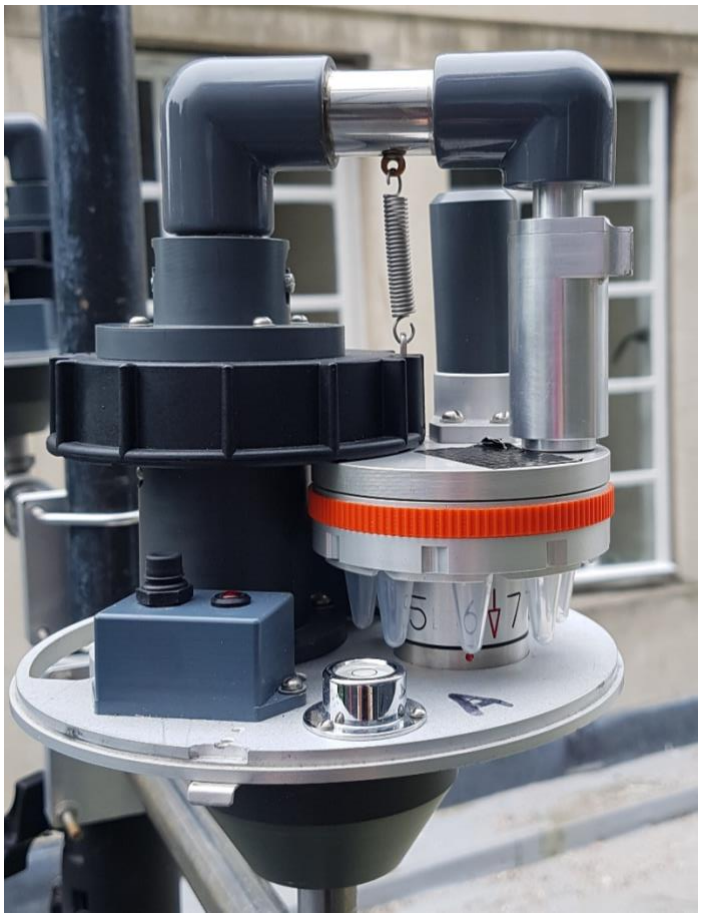
S2 Fig. Non-metric multidimensional scaling (NMDS) ordination of grass community similarity shows a strong effect of time on the overall community composition. Coloured circles indicate sampling sites. **Site** labels are abbreviated as follows: BNG = Bangor; EXE = Exeter; ING = Invergowrie; IOW = Isle of Wight; WOR = Worcester; YORK = York. Coloured circles indicate samples sites. Site labels abbreviated as follows: BNG = Bangor; EXE = Exeter; ING = Invergowrie; IOW = Isle of Wight; WOR = Worcester; YORK = York.



S3 Fig. Relative abundance of the five most abundant grasses at genus level, normalized according to airborne pollen concentration data. Relative abundances were calculated as a proportion of reads assigned to Poaceae, rather than of reads as a whole, then multiplied by mean pollen concentration across the three pooled days. Markers used to identify grass pollen are stated in the top panel label. Due to errors in sampling equipment, only 4 weeks of samples were collected at the York sampling site. Sampling sites are indicated in the right panel label abbreviated as follows: BNG = Bangor; EXE = Exeter; ING = Invergowrie; IOW = Isle of Wight; WOR = Worcester; YORK = York.

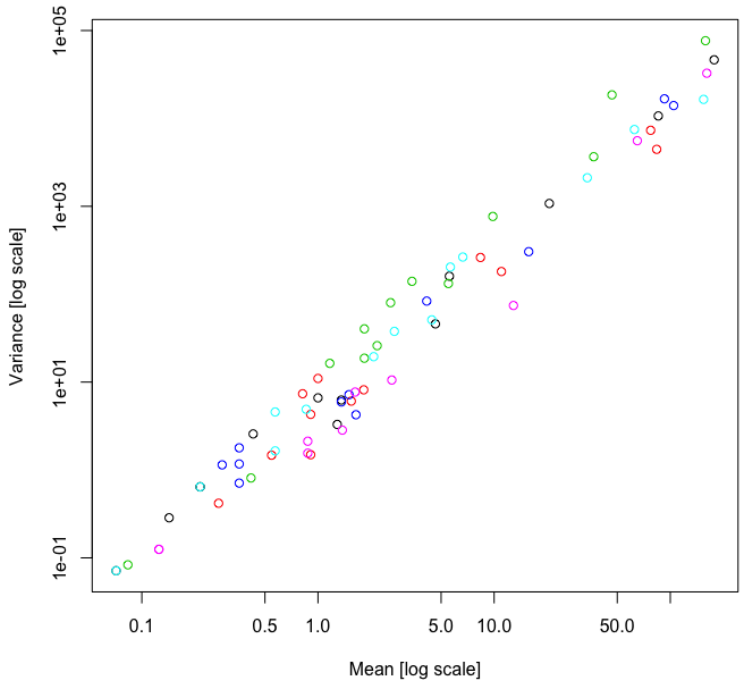


S4 Fig. Correlations between proportions of reads made up by the same genus in the two marker gene datasets. All four genera present in both datasets are shown: (A) *Lolium*/*Festuca*, (B) *Anthoxanthum*, (C) *Avena*, and (D) *Dactylis*. For cases where there was a significant relationship between relative abundances in both datasets, black lines show the intercept and slope.

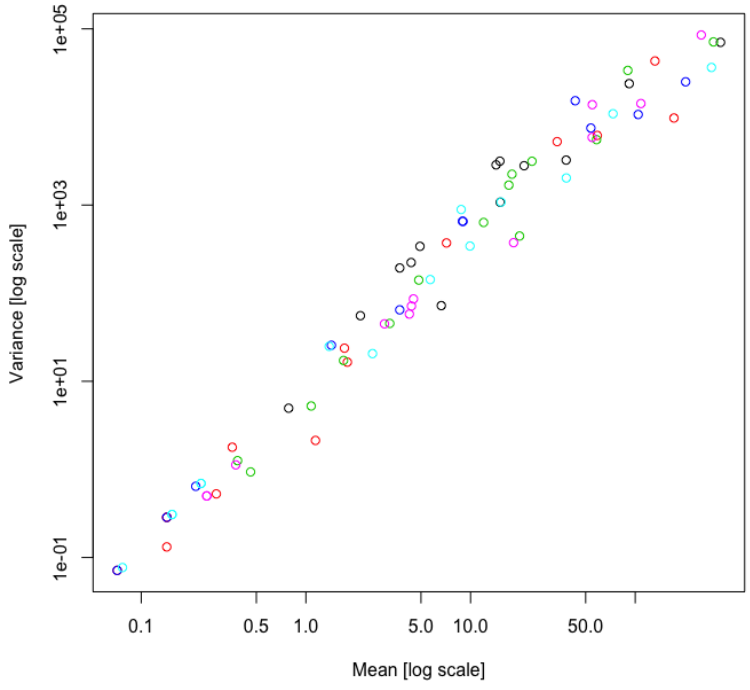


S5 Fig. Photograph of 1.5 ml microcentrifuge tubes mounted onto carousel on Burkard Automatic Multi-Vial Cyclone Sampler. Author provided.

A)

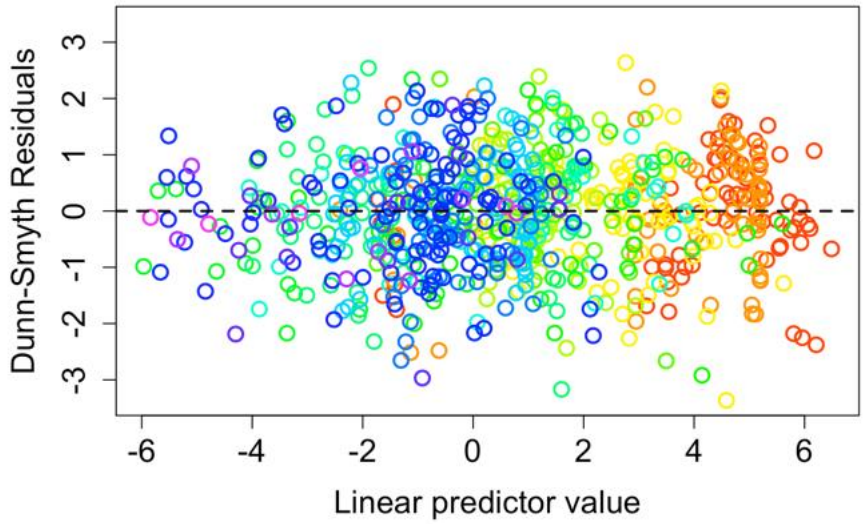


B)

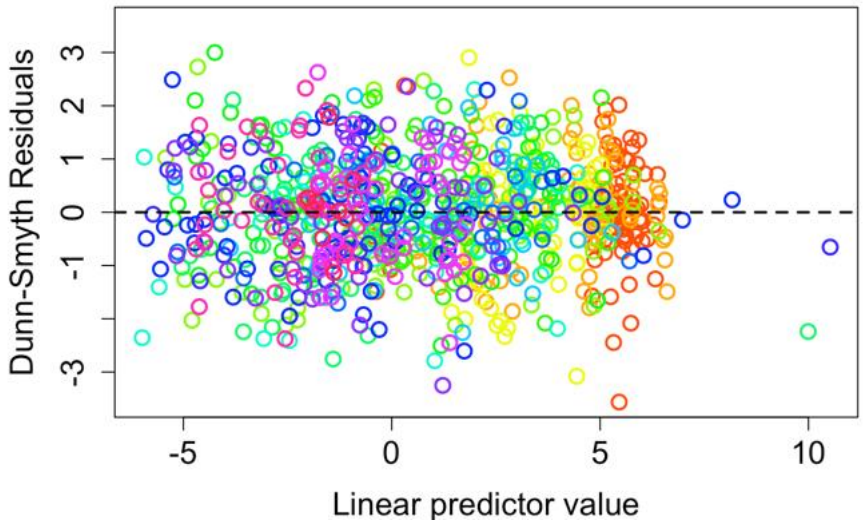


S6 Fig. There is a strong relationship between the mean proportion of sequences and the variance of the proportion of sequences from each sampling site using both A) *rbcL* and B) ITS2 markers. Coloured circles denote sampling site. The plots were produced using the meanvar.plot function in the mvabund package in R (*21*).

A)



B)



S7 Fig. Scatter plot of linear predictor values and the residuals output from the models selected to analyse the abundance data produced by the A) *rbcL* marker and B) ITS2 marker. Little pattern suggests that the models selected are plausible and the mean-variance assumption of the negative binomial regression is correct. Coloured circles denote different genera in the abundance data. The plots were produced using the plot.manyglm function in the mvabund package in R (*21*).

S1 List Borneo plant taxa pooled for the exotic plant positive control.

Aglaia sp.
Antidesma sp.
Baccaurea stipulata
Cynometra sp.
Dalbergia sp.
Dehaasia sp.
Dillenia excelsa
Diospryos sp.
Kleinhovia hospita
Lagerstroemia sp.
Lophopyxis sp.
Madhuca dubardii
Mallotus muticus
Microcos crassifolia
Pternandra sp.
Pterospermum macrocarpum
Syzygium sp.
Uncaria sp.
Urophyllum sp.
Vatica sp.
Xylosma sp.

146 S1 Table. Grass species pooled for the Grass Positive Control at equal volumes.

Grass positive control	Concentration of DNA (ng/µl)
Agrostis canina	0.121
Agrostis capillaris	1.29
Agrostis gigantea	9.48
Agrostis stolonifera	3.7
Agrostis vinealis	1.03
Aira praecox	0.8
Alopecurus geniculatus	1.18
Alopecurus pratensis	1.42
Anisantha sterilis	0.848
Anthoxanthum odoratum	0.804
Arrhenatherum elatius	1.36
Brachypodium sylvaticum	0.804
Briza media	2
Bromopsis ramosa	0.35
Bromus hordeaceus	0.098
Catapodium rigidum	3.96
Cynosurus cristatus	0.0736
Dactylis glomerata	13.8
Danthonia decumbens	1.34
Deschampsia cespitosa	2.52
Deschampsia flexuosa	0.648
Elymus caninus	1.62
Elytrigia repens	3.47
Festuca arundinacea	1.21
Festuca gigantea	1.32
Festuca ovina	0.592
Festuca pratensis	1.34
Festuca rubra	2.68
Glyceria declinata	0.226
Glyceria fluitans	0.892
Glyceria maxima	8.32
Glyceria notata	0.992
Holcus lanatus	0.42
Holcus mollis	below detection limit*
Hordeum murinum	0.476
Hordeum secalinum	0.416
Lolium perenne	0.452
Milium effusum	0.524
Molinia caerulea	2.24
Nardus stricta	0.246
Phalaris arundinacea	below detection limit*

Phleum bertolonii	0.444
Phleum pratense	18
Phragmites australis	13.2
Poa annua	0.0844
Poa humilis	2.37
Poa pratensis	1.13
Poa trivialis	below detection limit*
Puccinellia distans	11.1
Trisetum flavescens	0.736
Triticum aestivum	1.47
Vulpia myuros	0.199

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148 * note these samples successfully amplified using *rbcL* and ITS2 primers shown in S5 Table.

S2 Table. Genera included in the grass positive control, and genera detected using metabarcoding of both marker genes in both the positive control and in actual aerial DNA extracts. Genera with a grey background were detected by at least one marker gene; genera with a white background were not.

Expected	rbcL- Control	ITS2- Control	rbcL- Samples	ITS2- Samples
Agrostis				*Agrostis*
Aira				
Alopecurus				*Alopecurus*
Anisantha				
Anthoxanthum			*Anthoxanthum*	*Anthoxanthum*
Arrhenatherum		*Arrhenatherum*		*Arrhenatherum*
Avena	*Avena*		*Avena*	*Avena*
Brachypodium				
Briza	*Briza*	*Briza/Bromus*	*Briza*	
Bromopsis				
Bromus		*Briza/Bromus*		
Catapodium				
Cynosurus		*Cynosurus*		*Cynosurus*
Dactylis	*Dactylis*	*Dactylis*	*Dactylis*	
Danthonia				
Deschampsia		*Deschampsia*		*Deschampsia*
Elymus				
Elytrigia				
Festuca	*Festuca/Lolium*	*Festuca/Lolium*	*Festuca/Lolium*	*Festuca/Lolium*
Glyceria		*Glyceria*		
Holcus				*Holcus*
Hordeum		*Hordeum*		*Hordeum*
Lolium		*Lolium*		*Lolium*
Milium				
Molinia	*Molinia*		*Molinia*	
Nardus				
Phalaris				
Phleum	*Phleum*		*Phleum*	
Phragmites				
Poa	*Poa*	*Poa*	*Poa*	*Poa*
Puccinellia				
Trisetum				
Triticum	*Poa*			
Vulpia				

154 **S3 Table.** Latitude and longitude of each pollen sampling site.

Site Name	Abbreviation	Latitude	Longitude
Bangor	BNG	53.2300	-4.1300
Exeter	EXE	50.7365	-3.5322
Invergowrie	ING	56.4576	-3.0687
Isle of Wight	IOW	50.7111	-1.3009
Worcestershire	WORK	52.1976	-2.2430
York	YORK	53.9484	-1.0535

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S4 Table. Sample collection dates of each sequenced air sample. Three consecutive days of air samples were pooled during DNA extraction (note that sample ING_w2_p2, three consecutive samples were unavailable due to sampling error and the next sampling day was selected for pooling). The mean pollen concentration for the three pooled days and the index i5 and i7 sequence for demultiplexing is shown here.

Sample	Index i5 and i7 Sequence	Week	Pool	Site	Collection date (2016)	Mean pollen conc. (grains m^{-3})
BNG_w1_p1	CAAGTCGT	1	1	BNG	25 May - 28 May	61.7
BNG_w1_p2	TAACGTCG	1	2	BNG	29 May - 01 Jun	27
BNG_w2_p1	CTGTATGC	2	1	BNG	08 Jun - 11 Jun	NA
BNG_w2_p2	TGCTTGCT	2	2	BNG	18 Jun - 21 Jun	NA
BNG_w3_p1	GTAGTACC	3	1	BNG	24 Jun - 27 Jun	NA
BNG_w3_p2	AAGTCCTC	3	2	BNG	27 Jun - 30 Jun	NA
BNG_w4_p1	GCATAACG	4	1	BNG	08 Jul - 11 Jul	35.3
BNG_w4_p2	ATAGTCGG	4	2	BNG	11 Jul - 14 Jul	18.3
BNG_w5_p1	TAGGAGCT	5	1	BNG	21 Jul - 24 Jul	5.7
BNG_w5_p2	AGGTGTTG	5	2	BNG	25 Jul - 28 Jul	2
BNG_w6_p1	CATTGACG	6	1	BNG	04 Aug - 07 Aug	4.3
BNG_w6_p2	CCACAACA	6	2	BNG	08 Aug - 11 Aug	1.3
BNG_w7_p1	TCTAGGAG	7	1	BNG	22 Aug - 25 Aug	3.3
BNG_w7_p2	TTGCTTGG	7	2	BNG	26 Aug - 29 Aug	2.3
EXE_w1_p1	TGATCACG	1	1	EXE	02 Jun - 05 Jun	63
EXE_w1_p2	TCTGGACA	1	2	EXE	06 Jun - 09 Jun	139.3
EXE_w2_p1	CAGTGCTT	2	1	EXE	16 Jun - 19 Jun	126
EXE_w2_p2	ATAGGTCC	2	2	EXE	20 Jun - 23 Jun	124.7
EXE_w3_p1	CTGTACCA	3	1	EXE	01 Jul - 04 Jul	52.3
EXE_w3_p2	AAGCATCG	3	2	EXE	04 Jul - 07 Jul	61.3
EXE_w4_p1	CCTGTCAA	4	1	EXE	14 Jul - 17 Jul	56
EXE_w4_p2	AATGGTCG	4	2	EXE	17 Jul - 20 Jul	21.7
EXE_w5_p1	CTCCTGAA	5	1	EXE	29 Jul - 01 Aug	7
EXE_w5_p2	GACGAACT	5	2	EXE	01 Aug - 04 Aug	2.7
EXE_w6_p1	GGTCGTAT	6	1	EXE	11 Aug - 14 Aug	2.3
EXE_w6_p2	AAGTGCAG	6	2	EXE	14 Aug - 17 Aug	3.3
EXE_w7_p1	CCATGAAC	7	1	EXE	25 Aug - 28 Aug	3
EXE_w7_p2	TACTAGCG	7	2	EXE	28 Aug - 31 Aug	0.7
ING_w1_p1	GTGATCCA	1	1	ING	30 May - 02 Jun	2
ING_w1_p2	ATAACGCC	1	2	ING	03 Jun - 06 Jun	1
ING_w2_p1	ACCATAGG	2	1	ING	13 Jun - 16 Jun	7
ING_w2_p2	AGTTCGCA	2	2	ING	16 Jun, 19 Jun, 20 Jun	19.3
ING_w3_p1	CAACTTGG	3	1	ING	27 Jun - 30 Jun	19

ING_w3_p2	CGCAATGT	3	2	ING	30 Jun - 03 Jul	38
ING_w4_p1	GGCTCAAT	4	1	ING	18 Jul - 21 Jul	67.7
ING_w4_p2	GACTTGTG	4	2	ING	21 Jul - 24 Jul	22.7
ING_w5_p1	GCTACAAC	5	1	ING	25 Jul - 28 Jul	19.7
ING_w5_p2	GGTACGAA	5	2	ING	28 Jul - 31 Jul	27.3
ING_w6_p1	ACGAACGA	6	1	ING	09 Aug - 12 Aug	3.3
ING_w6_p2	AACACTGG	6	2	ING	12 Aug - 15 Aug	3.3
ING_w7_p1	TGGATGGT	7	1	ING	22 Aug - 25 Aug	3
IOW_w1_p1	TACTGCTC	1	1	IOW	23 May - 26 May	7.3
IOW_w1_p2	CTTCGCAA	1	2	IOW	28 May - 31 May	13.7
IOW_w2_p1	GATCAAGG	2	1	IOW	06 Jun - 09 Jun	253
IOW_w2_p2	GGCGAATA	2	2	IOW	10 Jun - 13 Jun	84
IOW_w3_p1	CAACGAGT	3	1	IOW	19 Jun - 22 Jun	57.7
IOW_w3_p2	ATCGGAGA	3	2	IOW	22 Jun - 25 Jun	39.7
IOW_w4_p1	TGTTCCGT	4	1	IOW	04 Jul - 07 Jul	86
IOW_w4_p2	ATCCACGA	4	2	IOW	08 Jul - 11 Jul	52.3
IOW_w5_p1	TCACCTAG	5	1	IOW	18 Jul - 21 Jul	64.3
IOW_w5_p2	AGGATAGC	5	2	IOW	22 Jul - 25 Jul	13
IOW_w6_p1	ATGACAGG	6	1	IOW	03 Aug - 06 Aug	5
IOW_w6_p2	CCGTTATG	6	2	IOW	06 Aug - 09 Aug	6.7
IOW_w7_p1	ACCTCTTC	7	1	IOW	15 Aug - 18 Aug	4.3
IOW_w7_p2	ACAGAGGT	7	2	IOW	18 Aug - 21 Aug	2
WOR_w1_p1	CGCTACAT	1	1	WOR	25 May - 28 May	0
WOR_w1_p2	AACCAGAG	1	2	WOR	29 May - 01 Jun	0
WOR_w2_p1	GCAATTCC	2	1	WOR	08 Jun - 11 Jun	114.7
WOR_w2_p2	AGCCGTAA	2	2	WOR	11 Jun - 14 Jun	40.7
WOR_w3_p1	AACAAGGC	3	1	WOR	22 Jun - 25 Jun	131
WOR_w3_p2	GAGCAATC	3	2	WOR	25 Jun - 28 Jun	78.7
WOR_w4_p1	AGTATGCC	4	1	WOR	07 Jul - 10 Jul	76
WOR_w4_p2	TCGATGAC	4	2	WOR	10 Jul - 13 Jul	16
WOR_w5_p1	GATACCTG	5	1	WOR	20 Jul - 23 Jul	26.3
WOR_w5_p2	ACCGACAA	5	2	WOR	23 Jul - 26 Jul	16
WOR_w6_p1	ACGAATCC	6	1	WOR	03 Aug - 06 Aug	0
WOR_w6_p2	TCGAGAGT	6	2	WOR	07 Aug - 10 Aug	0
WOR_w7_p1	GTTCTTCG	7	1	WOR	17 Aug - 20 Aug	0
WOR_w7_p2	CCTTCCAT	7	2	WOR	21 Aug - 24 Aug	0
YORK_w1_p1	TCCACGTT	1	1	YORK	26 May - 29 May	3
YORK_w1_p2	TTACCGAC	1	2	YORK	29 May - 01 Jun	9.7
YORK_w2_p1	TTCGCCAT	2	1	YORK	08 Jun - 11 Jun	84.7
YORK_w2_p2	TATGGCAC	2	2	YORK	13 Jun - 16 Jun	96.7
YORK_w3_p1	CGCGTATT	3	1	YORK	25 Jun - 28 Jun	178
YORK_w3_p2	AGCCTATC	3	2	YORK	28 Jun - 01 Jul	157
YORK_w4_p1	GACACAGT	4	1	YORK	07 Jul - 10 Jul	234.3

YORK_w4_p2	GAGAGTAC	4	2	YORK	10 Jul - 13 Jul	245.3
Negative control 1	CCACTAAG	-	-	-	-	-
Negative control 2	CCACATTG	-	-	-	-	-
Negative control 3	CCGATGTA	-	-	-	-	-
Negative control 4	CTCGGTAA	-	-	-	-	-
Negative control 5	AACCGTGT	-	-	-	-	-
Negative control 6	CGGTTGTT	-	-	-	-	-
Negative control 7	CTAGCAGT	-	-	-	-	-
Negative control 8	ACAACAGC	-	-	-	-	-
Negative control 9	GATTGTCC	-	-	-	-	-
Exotic positive control	ACAGGCAT	-	-	-	-	-
Grass positive control	TTCGTACG	-	-	-	-	-

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S5 Table. Primer sequences used in library preparation. Round 1 PCR primer sequences contain forward or reverse template primer, the forward primer sequence contains a series of N's in order to improve clustering and cluster detection on MiSeq sequencing. Round 1 and round 2 sequences contain complementary universal tails. Round 2 PRC primers sequences also contain the P5 or P7 Illumina adaptors and an 8 bp unique index on both the forward and reverse primers used for demultiplexing samples (see S4 Table for index i5 and i7 sequence).

Round 1 PCR
Forward Universal Tail - NNNNNN - Template Specific Primer ***rbcL*aF** [ACACTCTTTCCCTACACGACGCTCTTCCGATCT]-[NNNNNN]-[ATGTCACCACAAACAGAGACTAAAGC]
Reverse Universal Tail - Template Specific Primer ***rbcL*r506** [GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT]-[AGGGGACGACCATACTTGTTCA]
Forward Universal Tail - NNNNNN - Template Specific Primer **ITS2F** [ACACTCTTTCCCTACACGACGCTCTTCCGATCT]-[NNNNNN]-[ATGCGATACTTGGTGTGAAT]
Reverse Universal Tail - Template Specific Primer **ITS3R** [GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT]- [GACGCTTCTCCAGACTACAAT]
Round 2 PCR
P5 Illumina adapter - **i5 index -** Forward Universal Tail [AATGATACGGCGACCACCGAGATCTACAC]**-[i5 index]-**[ACACTCTTTCCCTACACGACGCTC]
P7 Illumina adapter - **i7 index -** Reverse Universal Tail [CAAGCAGAAGACGGCATACGAGAT]**-[i7 index]-**[GTGACTGGAGTTCAGACGTGTGCTC]

169 **S6 Table.** Model selection based on AIC criteria. Models shown in bold were used to analyse the data
170 presented here.

Marker	Model	AIC
rbcL	**(1) Time + Time:Latitude + Latitude + Longitude + Month**	3444.949
rbcL	(2) Time + Time:Latitude + Latitude + Month	3462.208
rbcL	(3) Time + Time:Latitude + Time:Longitude + Latitude + Longitude + Month	3467.373
rbcL	(4) Latitude + Month + Longitude +	3473.788
rbcL	(5) Latitude + Month	3474.854
rbcL	(6) Time + Time:Longitude + Longitude	3479.546
rbcL	(7) Time + Time:Latitude + Time:Longitude + Latitude + Longitude + Month500_urban	3486.374
rbcL	(8) Latitude:Month + Longitude + Month	3489.559
rbcL	(9) Time + Site_ID + Time:Latitude + Month	3504.327
rbcL	(10) Time	3582.784
rbcL	(11) Time + Site_ID + Time:Site_ID + Month	3584.097
rbcL	(12) Time + Time:Latitude	3584.776
rbcL	(13) Time + Longitude +	3586.391
rbcL	(14) Time + Time:Latitude + Time:Longitude + Latitude + Longitude	3590.813
rbcL	(15) Time + Time:Longitude + Longitude	3611.398
rbcL	(16) Latitude	3614.176
rbcL	(17) Time + Site_ID + Time:Site_ID + Latitude + Month	3615.487
rbcL	(18) Time + Site_ID	3655.547
rbcL	(19) Site_ID	3688.586
rbcL	(20) Time + Site_ID + Time:Site ID	3719.946
rbcL	(21) Time + Site_ID + Time:Site_ID + Latitude	3751.946

ITS2	**(22) Time + Time:Latitude + Time:Longitude + Latitude + Longitude + Month**	**4306.795**
ITS2	(23) Time + Time:Latitude + Latitude + Longitude + Month	4312.207
ITS2	(24) Time + Time:Latitude + Time:Longitude + Latitude + Longitude + Month + 500_urban	4314.299
ITS2	(25) Time + Time:Latitude + Latitude + Month	4328.732
ITS2	(26) Latitude:Month + Longitude + Month	4345.029
ITS2	(27) Latitude + Month + Longitude	4345.197
ITS2	(28) Latitude + Month	4353.331
ITS2	(29) Time + Site_ID + Time:Latitude + Month	4362.502
ITS2	(30) Time + Site_ID + Time:Site_ID + Month	4363.541
ITS2	(31) Time + Time:Longitude + Longitude + Month	4377.7
ITS2	(32) Time + Site_ID + Time:Site_ID + Latitude + Month	4392.966
ITS2	(33) Time + Time:Latitude + Time:Longitude + Latitude + Longitude	4550.79
ITS2	(34) Time + Time:Latitude + Latitute	4569.352
ITS2	(35) Time + Time:Longitude + Longitude	4603.281
ITS2	(36) Time + Longitude	4604.212
ITS2	(37) Time	4610.119
ITS2	(38) Time + Site_ID	4625.929
ITS2	(39) Time + Site_ID + Time:Site ID	4650.117
ITS2	(40) Latitude	4675.797
ITS2	(41) Time + Site_ID + Time:Site_ID + Latitude	4680.117
ITS2	(42) Site_ID	4747.236

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