Electronic Appendix 1. – Explanation of used traits. Source: 1) Kubát et al. (2002), 2) Fitter & Peat (1994), Royal Botanic Gardens Kew (2008), Moles et al. (2005), Institute of Botany of the ASCR (2010), 3) Klotz et al. (2002), 4) Klimešová & Klimeš (2006, 2008), Klimešová & de Bello (2009).

Plant traits	Source	Explanation
Maximum height	1	maximum species height
Minimum height	1	minimum species height
Seed mass	2	weight of seeds
Flowering phenology	3	values 0-10 according to vegetation period
Fruit type	3	berry
		lomentum
		legume
		capsule
		nut
		aggregate follicles
		aggregate nutlets
		siliqua
		schizocarp
		vegetative
Pollen vectors	3	pollination by wind
		selfing by a neighbouring flower
		pollination by insects
		pollination by slugs
		spontaneous pollination within a flower
		selfing in unopened, rudimentary flower
		selfing in unopened flower
Clonal growth organs	4	stem tuber
		turion
		plantlet (pseudovivipary)
		plant fragment of stem origin
		epigeogenous stem (rhizome)
		hypogeogenous stem (rhizome)
		stem tuber
		bulb
		root-splitter
		roots with adventitious buds
		root tuber
		offspring tuber at distal end of above-ground stem
Branching type	4	monopodial
		sympodial
		dichotomous
Leaf distribution	4	no rosette
		semi-rosette
		rosette
Lateral spread (m/yr)	4	<0.01
		0.01-0.25
		>0.25
		dispersable

Electronic Appendix 2. – A summary of the mean percentage of species in each plot for which data on each trait was missing. For presence-absence data, this was calculated as the number of species missing trait data for a given plot divided by the total number of species in that plot (i.e. plot richness); the mean of this plot-level value across plots is presented below. For abundance data, the same measure was calculated, but weighted by abundance.

	Average data missing per plot			
	Presence-absence		Abundance	
Plot size (cm)	25 × 25	75 × 75	25 × 25	75 × 75
Maximum height	0.9%	0.7%	0.9%	0.7%
Minimum height	0.9%	0.7%	0.9%	0.7%
Seed mass	2.9%	2.9%	2.2%	2.3%
Flowering phenology	4.5%	4.6%	5.5%	5.3%
Fruit type	0.9%	0.8%	0.9%	0.8%
Pollen vectors	0.9%	0.9%	1.0%	0.9%
Clonal growth organs	1.6%	1.6%	1.6%	1.5%
Branching type	4.1%	4.3%	1.5%	2.0%
Leaf distribution	1.0%	0.8%	1.0%	0.9%
Lateral spread	1.9%	2.4%	1.7%	2.1%

Electronic Appendix 3. – Results from a sensitivity analysis investigating the impact of missing trait data on results. This test was conducted using flowering phenology, the trait with the highest proportion of missing trait data. This analysis used only plots that contained species for which flowering phenology is known (25x25 cm: 68 plots; 75x75 cm: 38 plots).

			Presence-absence		Abundance	
Plot size	No. plots	Test statistic	Obs>Exp	Obs<Exp	Obs>Exp	Obs<Exp
25 × 25 cm	68	Richness	0.880		0.908	
		Evenness	0.121		0.179	
75 × 75 cm	38	Richness	0.512		0.517	
		Evenness	0.774		0.632	

Electronic Appendix 4. – Results from trait dispersion analysis on three continuous species-level traits: maximum height, minimum height (minimum size at reproduction), and seed mass. These analyses focused only on 51 dry grassland plots; analyses used presence-absence and abundance data from 126 plots for each of two plot sizes (25 × 25cm, 75 × 75cm). P-values indicate whether plots are overdispersed (Obs>Exp), or underdispersed (Obs<Exp) for the trait of interest. Bold values signify type-1 error rates at $\alpha<0.05$ (i.e. P-values).

		Presence-absence				Abundance			
	Test statistic	Obs>Exp		Obs<Exp		Obs>Exp		Obs<Exp	
	Plot size (cm)	25 × 25	75 × 75	25 × 25	75 × 75	25 × 25	75 × 75	25 × 25	75 × 75
Maximum height	Mean	0.882	0.750			0.736	0.569		
	Range			0.657	0.840			0.678	0.866
	Mean NTD		0.865	0.660		0.886			0.838
	Var NTD			0.608	0.687			0.678	0.982
Minimum height	Mean	0.343	0.560			0.154	0.179		
	Range	0.242	0.356			0.225	0.352		
	Mean NTD	0.201	0.342			0.720	0.907		
	Var NTD	0.834	0.980			0.245	0.840		
Seed mass	Mean			0.606ψ	0.414ψ			0.648ψ	0.602ψ
	Range	0.668ψ			0.466ψ			0.694ψ	0.493ψ
	Mean NTD	0.737ψ			0.742ψ	0.278	0.660		
	Var NTD			0.279ψ	0.698ψ	0.592	0.595		

ψ change in significance from full analysis

Electronic Appendix 5. – Results from trait dispersion analysis on three continuous species-level traits: maximum height, minimum height (minimum size at reproduction), and seed mass. These analyses focused only on 52 wet grassland plots; analyses used presence-absence and abundance data from 126 plots for each of two plot sizes (25x25cm, 75x75cm). P-values indicate whether plots are overdispersed (Obs>Exp), or underdispersed (Obs<Exp) for the trait of interest. Bold values signify type-1 error rates at $\alpha<0.05$ (i.e. P-values).

		Presence-absence				Abundance			
	Test statistic	Obs>Exp		Obs<Exp		Obs>Exp		Obs<Exp	
	Plot size (cm)	25 × 25	75 × 75	25 × 25	75 × 75	25 × 25	75 × 75	25 × 25	75 × 75
Maximum height	Mean			0.271	0.357			0.276	0.368
	Range			0.776	0.692			0.794	0.668
	Mean NTD	0.611	0.712				0.465	0.850	
	Var NTD	0.562	0.544					0.815	0.926
Minimum height	Mean			0.090	0.130			0.154	0.189
	Range	0.890			0.959	0.866			0.942
	Mean NTD	0.491	0.773			0.910	0.714		
	Var NTD	0.507	0.487					0.756	0.578
Seed mass	Mean			**0.032**	**0.005**			0.084ψ	0.034ψ
	Range			**0.023**	**0.002**			0.022ψ	0.007ψ
	Mean NTD			**0.013**	**0.006**		0.707	0.398	
	Var NTD			**0.045**	0.114ψ			0.542	0.913

Electronic Appendix 6. – Results from trait dispersion analysis on seven nominal traits for only dry grassland plots (51 plots). P-values indicate whether plots are richer (Richness: Obs>Exp), or poorer (Richness: Obs<Exp) in terms of variation in these traits, and whether these traits are more evenly (Evenness: Obs>Exp), or less evenly (Evenness: Obs<Exp) distributed within plots. Studied traits include flowering phenology (month of flowering), fruit type, pollen vector, leaf distribution, clonal growth organ and branching type. The last four of these traits are unique in that a single species can have multiple values; for example, a species may be both insect and wind pollinated. This was incorporated into the analysis. Bold values signify type-1 error rates at $\alpha<0.05$ (i.e. P-values).

		Presence-absence				Abundance			
	Test Statistic	Obs>Exp		Obs<Exp		Obs>Exp		Obs<Exp	
	Plot size (cm)	25 × 25	75 × 75	25 × 25	75 × 75	25 × 25	75 × 75	25 × 25	75 × 75
Flowering phenology	Richness			0.102	0.552			0.094	0.567
	Evenness	0.265			0.836	0.114			0.619
Fruit type	Richness			0.470	0.729			0.480	0.714
	Evenness			0.064ψ	0.507			**0.005**	0.217ψ
Pollen vectors	Richness	0.682			0.753	0.742			0.761
	Evenness	0.789			0.770	0.642			0.628
Clonal growth organ	Richness			0.627	0.728			0.646	0.722
	Evenness			0.487ψ	0.491ψ			0.145ψ	0.206ψ
Branching type	Richness	0.296			0.168ψ		0.260	0.257	
	Evenness		0.847ψ	0.112ψ		**0.046ψ**			**0.038ψ**
Leaf distribution	Richness			**0.016**	**0.001**			**0.016ψ**	**0.001**
	Evenness	**0.002**	**0.001**			**0.002**	**0.001**		
Lateral spread	Richness			0.442	0.096			0.437	0.101
	Evenness			0.171	0.130			0.118	0.148

ψ change in significance from full analysis

Electronic Appendix 7. – Results from trait dispersion analysis on seven nominal traits for wet grassland plots (52 plots). P-values indicate whether plots are richer (Richness: Obs>Exp), or poorer (Richness: Obs<Exp) in terms of variation in these traits, and whether these traits are more evenly (Evenness: Obs>Exp), or less evenly (Evenness: Obs<Exp) distributed within plots. Studied traits include flowering phenology (month of flowering), fruit type, pollen vector, leaf distribution, clonal growth organ and branching type. The last four of these traits are unique in that a single species can have multiple values; for example, a species may be both insect and wind pollinated. This was incorporated into the analysis. Bold values signify type-1 error rates at $\alpha<0.05$ (i.e. P-values).

		Presence-absence				Abundance			
	Test Statistic	Obs>Exp		Obs<Exp		Obs>Exp		Obs<Exp	
	Plot size (cm)	25 × 25	75 × 75	25 × 25	75 × 75	25 × 25	75 × 75	25 × 25	75 × 75
Flowering phenology	Richness	0.415	0.577			0.410	0.581		
	Evenness	0.055	0.092			0.111	0.130		
Fruit type	Richness			0.333	0.220			0.354	0.148
	Evenness			0.060	0.197			**0.037**	0.196ψ
Pollen vectors	Richness		0.940	0.436ψ			0.927	0.439	
	Evenness	0.990			0.897			0.711ψ	0.464
Clonal growth organ	Richness		0.735	0.624			0.723	0.640	
	Evenness			**0.020**	**0.023**			**0.007**	**0.005**
Branching type	Richness	0.180	0.173ψ			0.201	0.171		
	Evenness			0.256ψ	0.287ψ			0.312	0.363
Leaf distribution	Richness			0.230ψ	0.188ψ			0.217	0.182ψ
	Evenness	**0.025**	**0.045**			**0.013**	0.060ψ		
Lateral spread	Richness			0.933	IV*			0.955	IV*
	Evenness			0.776	0.770			0.657	0.601

*Insufficient variation to test; ψ change in significance from full analysis