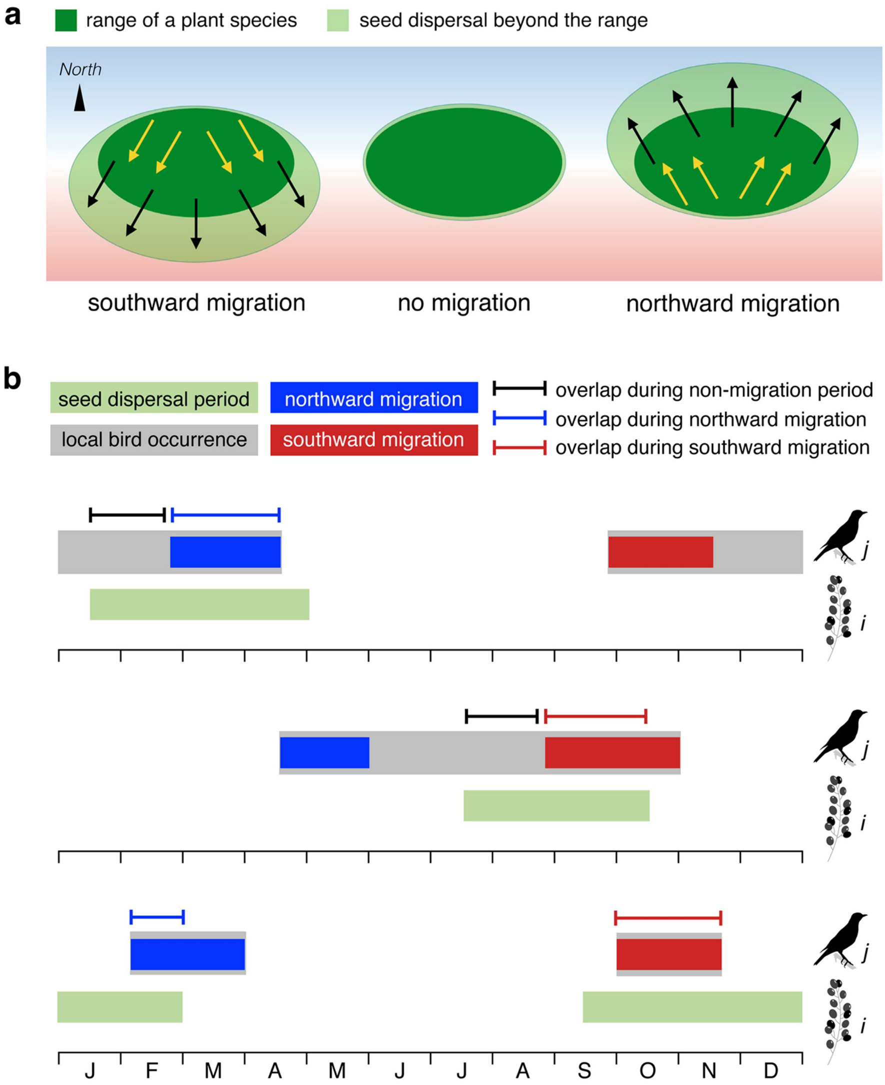
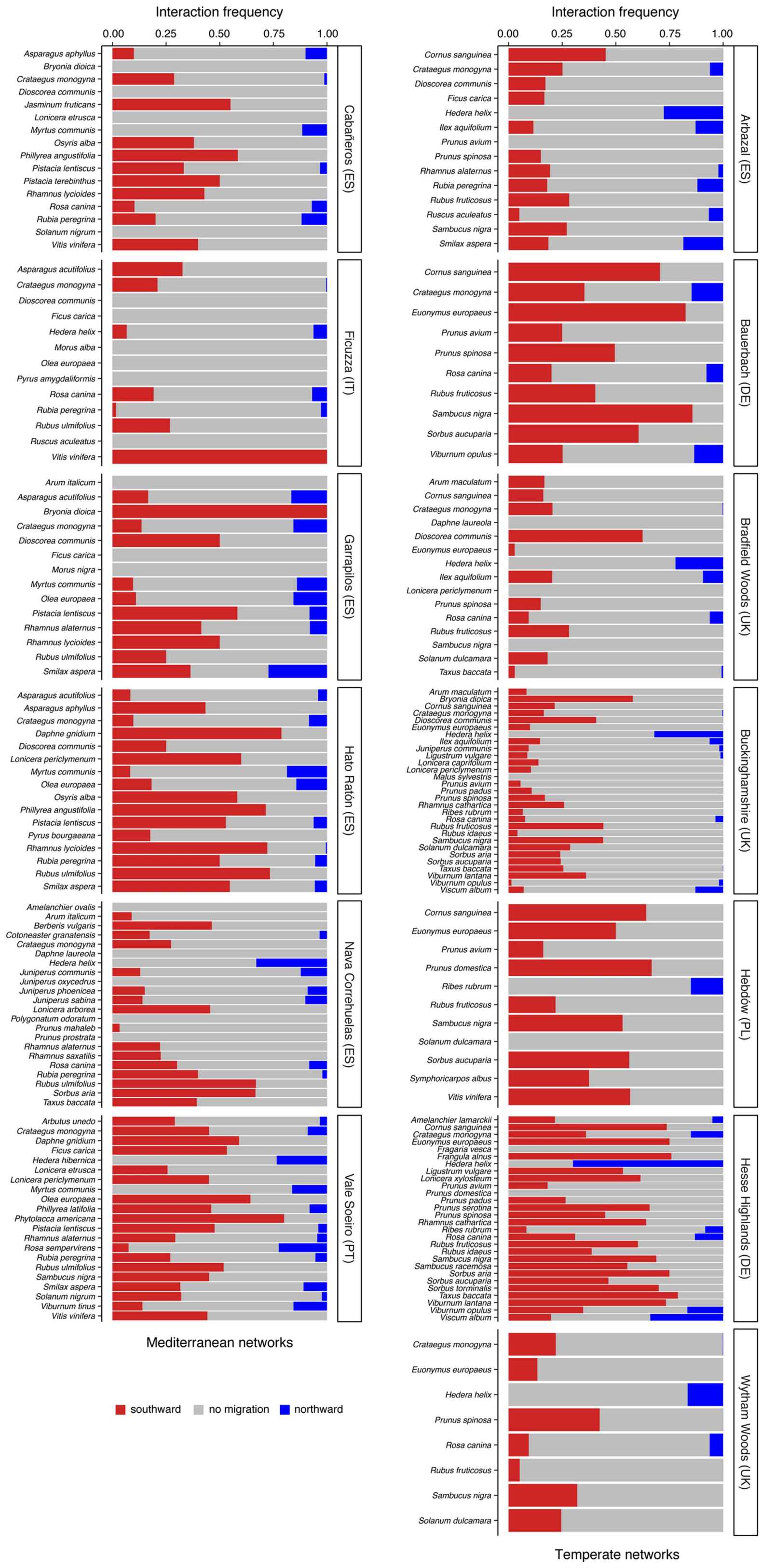
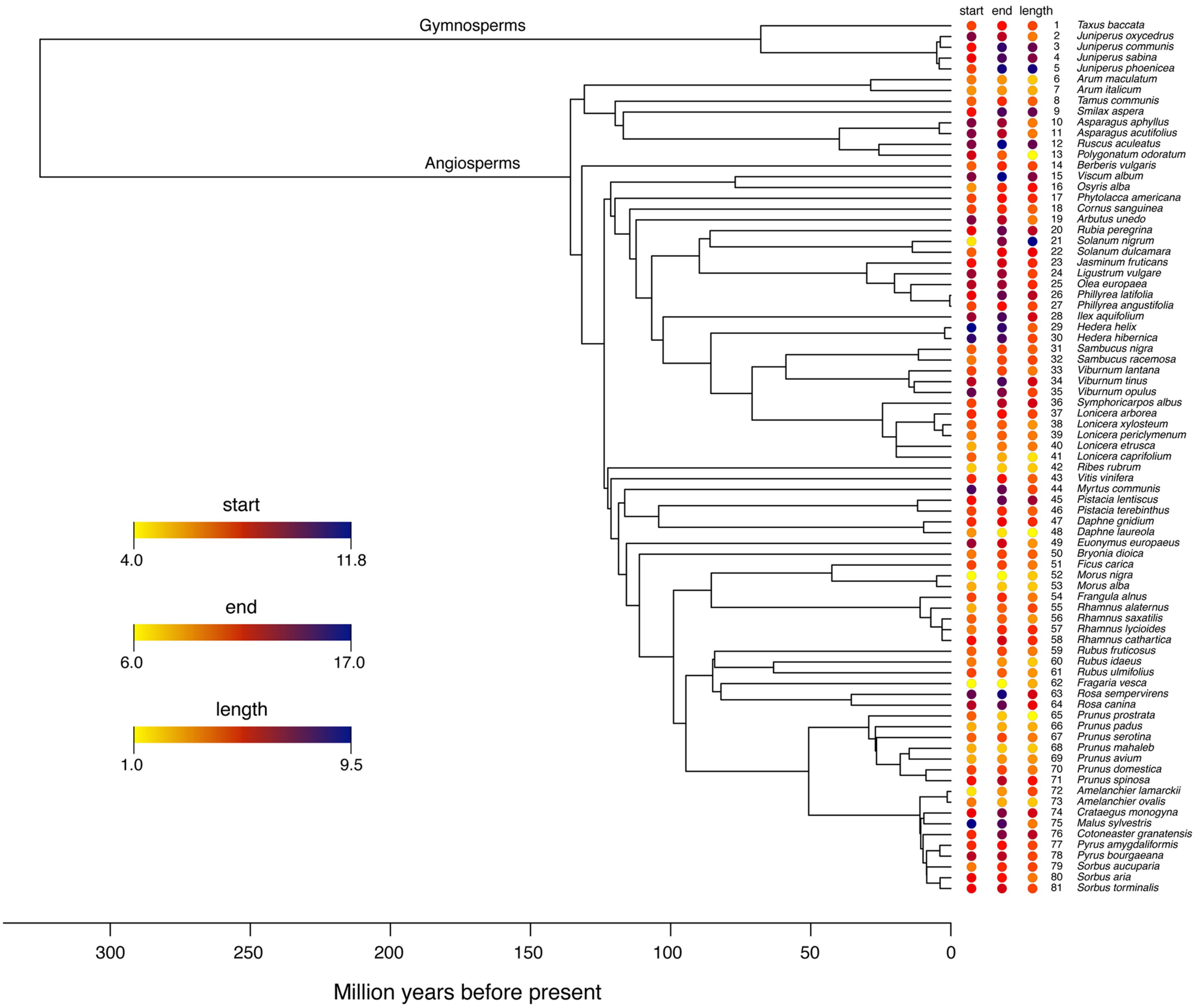


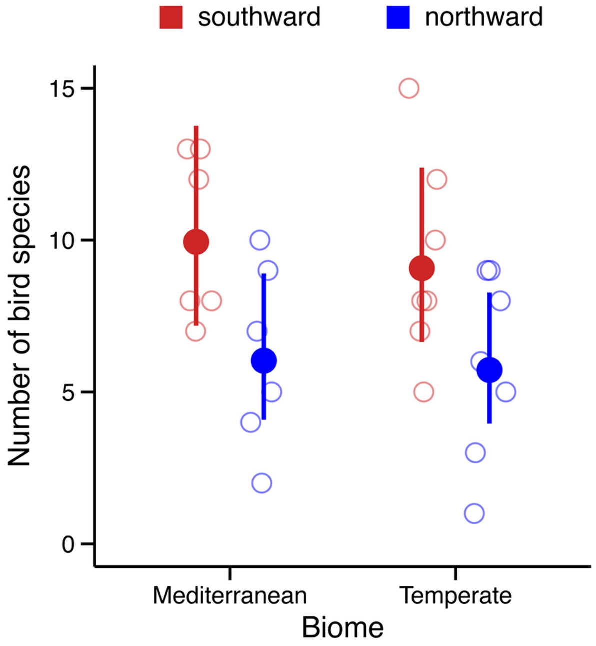
Extended Data Fig. 1 | Conceptual diagrams showing directional patterns of long-distance seed dispersal by migratory birds and phenological overlaps between seed-dispersal periods and bird migrations. a, Yellow and black arrows denote long-distance seed dispersal within and beyond the current range of a plant species, respectively. Seed dispersal mediated by birds migrating south (left), non-migrating birds (centre) and birds migrating north (right). The colour gradient from red to blue represents a climatic gradient from warmer to cooler latitudes (from south to north in the Northern Hemisphere), respectively. In the diagram on the right, seed dispersal within the range is necessary for warm-adapted populations to colonize cooler areas that are warming owing to climate change, whereas seed dispersal beyond the range is necessary for range shifts. **b**, Three hypothetical examples of phenological overlap between the seed-dispersal period of plant species *i* and bird species *j* while the bird migrates northwards (top), southwards (middle) or during both migrations (bottom). The examples include a wintering migrant with a winter–spring fruiting plant (top); a summer migrant with a summer–autumn fruiting plant (middle); and a transient migrant with an autumn–winter fruiting plant (bottom). In some cases, there is also phenological overlap during non-migration periods. More details on phenological overlaps in relation to the migratory strategy of birds are provided in Supplementary Fig. 3.



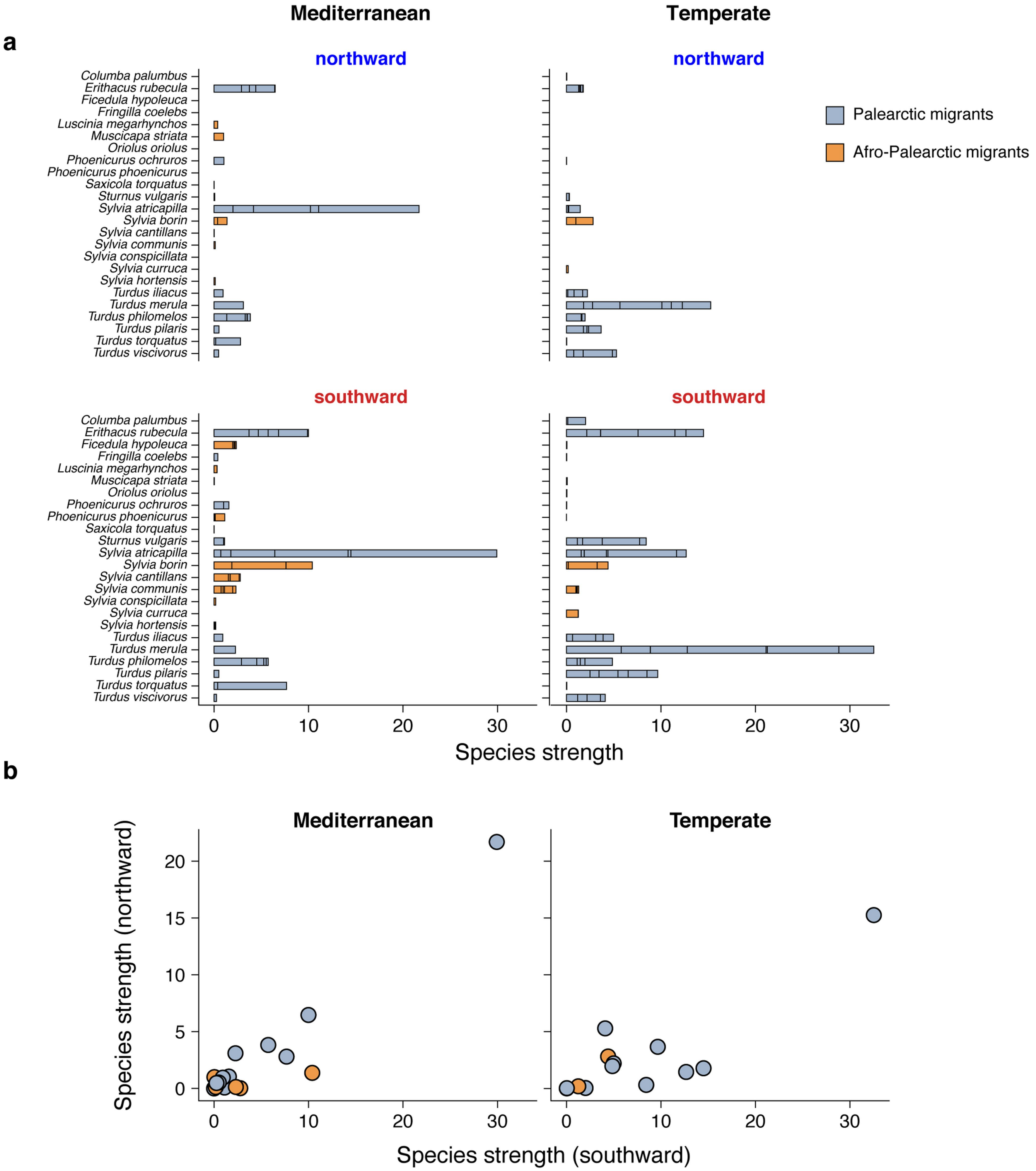
Extended Data Fig. 2 | Estimated interaction frequencies of plant species within each study network with birds migrating northwards, southwards or not migrating. Blue, interactions during northward migration; red, interactions during southward migration; grey, non-migration interactions. Each panel represents a seed-dispersal network. The left column of panels includes Mediterranean networks, whereas the right column includes temperate networks. DE, Germany; ES, Spain; IT, Italy; PL, Poland; PT, Portugal; UK, United Kingdom.



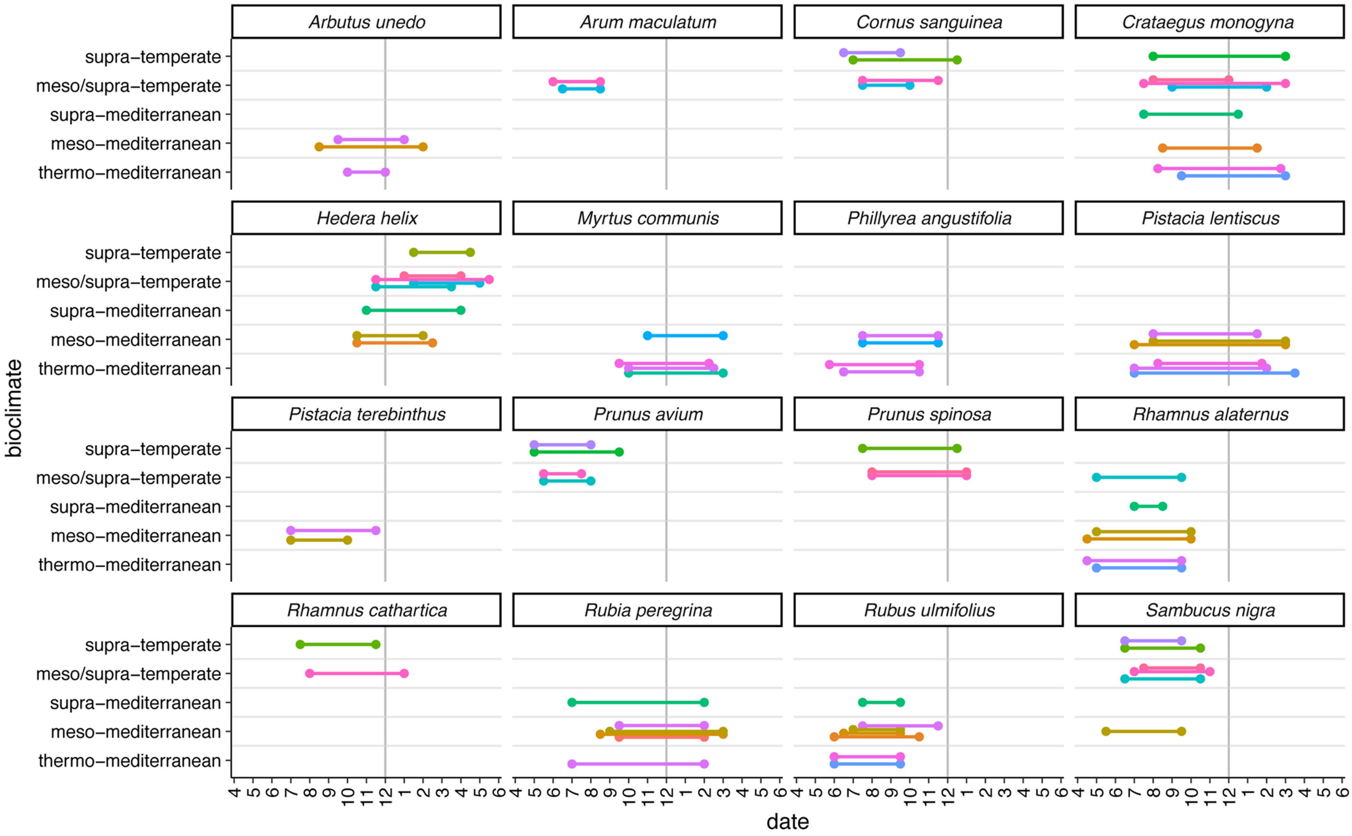
Extended Data Fig. 3 | Variables of the seed-dispersal phenology across the phylogenetic tree of plants. Phylogenetic signal was tested in plant-species means across networks in start and end dates (D_{start} and D_{end}), as well as in length ($D_{\text{length}} = D_{\text{end}} - D_{\text{start}}$) of the seed-dispersal period ($n = 81$ plant species) by means of Pagels' λ, as described in 'Phylogenetic signal in plants' in 'Statistical analyses' (Methods). The three phenological variables showed significant phylogenetic signal (D_{start}, $\lambda = 0.800$, $P = 0.0103$; D_{end}, $\lambda = 0.781$, $P = 0.0015$; and D_{length}, $\lambda = 0.419$, $P = 0.0343$). To test for phylogenetic signal, we previously calculated the species-level means for D_{start}, D_{end} and D_{length} across bioclimates (Extended Data Fig. 6). For this reason, we assessed the amount of variance in these phenological variables that is accounted for by bioclimate, as compared to that accounted for by species through linear-mixed models (LMMs) that included 'bioclimate' as fixed factor and 'plant species' as random factor to account for the repeated measures per species. Bioclimate accounted for only a minor fraction of variance (1–3%) in D_{start}, D_{end} and D_{length}, as shown by the marginal R^2 values (variance explained by fixed effects; $R^2_{\text{LMM}(m)} = 0.028$, 0.01 and 0.023, respectively). By contrast, the high conditional R^2 values (variance explained by both fixed and random effects; $R^2_{\text{LMM}(c)} = 0.780$, 0.845 and 0.643, respectively) indicated that plant species accounted for most variance in the three phenological variables. LMMs were fitted with the R package package lme4 (v.1.1-19)[105].



Extended Data Fig. 4 | Number of migratory bird species interacting with plants during migration per network in relation to migration direction and biome. Large dots and bars denote means ± 95% confidence intervals estimated by a GLMM, whereas circles denote values for each seed-dispersal network (*n* = 26 observations, 13 networks × 2 directions). Only migration direction had significant effects on the number of migratory bird species interacting with plants during migration in the GLMM (Poisson family and log-link function) testing the effects of migration direction (Wald $\chi^2 = 11.08$, $P = 0.0009$), biome (Wald $\chi^2 = 0.17$, $P = 0.6789$) and their interaction (Wald $\chi^2 = 0.02$, $P = 0.8921$). Model estimates ± s.e.: intercept = 2.297 ± 0.156; direction (northward) = −0.500 ± 0.208; biome (temperate) = −0.091 ± 0.215; direction (northward) × biome (temperate) = 0.039 ± 0.288; southward and Mediterranean were used as the reference categories (intercepts) for the factors direction and biome, respectively. A mean of 9.5 bird species per community dispersed plants during their southward migration, but only 5.9 species did so during the northward migration.



Extended Data Fig. 5 | Individual and cumulative bird species strengths accumulated across seed-dispersal subnetworks. a, Bird species strength accumulated across seed-dispersal subnetworks between plants and birds migrating southwards or northwards, and in Mediterranean and temperate biomes; species strength quantifies the relevance of a bird species across the entire fleshy-fruited plant community[104] ($n = 24$ species). Some bird species have stacked values from several subnetworks, whereas other species participated only in a single subnetwork. **b**, The cumulative species strength across the southward and northward subnetworks were significantly correlated in the Mediterranean (Kendall's $\tau = 0.396$, $P = 0.0129$) and the temperate biome ($\tau = 0.588$, $P = 0.0006$), indicating that bird species generally display a proportional role in both migrations. However, the cumulative species strength in the Mediterranean and temperate biome were not correlated, neither across the northward ($\tau = 0.276$, $P = 0.1089$) nor across the southward subnetworks ($\tau = 0.263$, $P = 0.0764$) (correlation between left and right panels in **a**). These results indicate discordance between biomes in the identity of bird species contributions to community-wide seed dispersal during each migration. Pearson's *r* yielded qualitatively similar results, with higher coefficient values in the significant correlations ($r = 0.946$ and 0.847).



Extended Data Fig. 6 | Bioclimate-level plant phenology from several sources. Subset of 16 out of the 81 plant species present in the study networks illustrating how, in many cases, we obtained data on seed-dispersal phenology from several sources for the same plant species–bioclimate combination. Colour codes denote different data sources. A vertical grey line divides the calendar year.

Extended Data Table 1 | Characteristics of the European seed-dispersal networks that we studied

N	Country	Network name	Source	Sampling type	Biome	Bioclimate	Latitude	Longitude	Years (*n*)	N_{plant}	N_{bird}	N_{int}
1	Spain	Hato Ratón	A	Mist-netting	Mediterranean	thermo-	37.1804	–6.3240	1981–1983 (2)	16	17	120
2	Spain	Nava Correhuelas	A	Observations	Mediterranean	supra-	37.9409	–2.7927	1997–1999 (2)	22	21	111
3	Spain	Garrapilos	B	DNA-barcoding	Mediterranean	thermo-	36.6589	–5.9493	2013–2015 (2)	14	21	56
4	Spain	Cabañeros	B	DNA-barcoding	Mediterranean	meso-	39.3213	–4.2896	2016–2017 (1)	16	14	44
5	Spain	Arbazal	B	DNA-barcoding	temperate	thermo/meso-	43.4313	–5.4971	2016–2017 (1)	14	14	52
6	Portugal	Vale Soeiro	C	Mist-netting	Mediterranean	meso-	40.3127	–8.4035	2012–2018 (6)	21	13	76
7	Italy	Ficuzza	B	DNA-barcoding	Mediterranean	meso-	37.8923	13.3749	2016–2017 (1)	13	12	30
8	UK	Buckinghamshire	D	Observations	temperate	meso/supra-	51.8910	–0.9120	1980–1985 (5)	29	19	204
9	UK	Wytham Woods	E	Observations	temperate	meso/supra-	51.7667	–1.3333	1979–1980 (1)	8	8	24
10	UK	Bradfield Woods	B	DNA-barcoding	temperate	meso/supra-	52.1808	0.8239	2016–2017 (1)	15	11	36
11	Germany	Hesse Highlands	F	Observations	temperate	supra-	51.3957	8.9427	1997–1999 (2)	28	18	128
12	Germany	Bauerbach	B	DNA-barcoding	temperate	supra-	50.7950	8.8230	2016–2017 (1)	10	9	30
13	Poland	Hebdów	B	DNA-barcoding	temperate	supra-	50.1429	20.4274	2016–2017 (1)	11	16	38

N_{plant}, N_{bird} and N_{int} denote the number of plant species, bird species and plant–bird interactions in each network, respectively. Network biomes were obtained from refs. [47,48]; network bioclimates were obtained from ref. [48]. Source A is ref. [49]; source B is this study (EU project MobileLinks); source C is this study (unpublished data provided by L.P.d.S. and R.H.H.); source D is ref. [50]; source E is ref. [27]; and source F is ref. [51].

Extended Data Table 2 | List of bird and plant species of the 13 study networks

Bird species list		Plant species list			
Bird species	Bird family	Plant species	Plant family	Plant species	Plant family
Alectoris rufa	Phasianidae	*Amelanchier lamarckii*	Rosaceae	*Prunus avium*	Rosaceae
Columba palumbus	Columbidae	*Amelanchier ovalis*	Rosaceae	*Prunus domestica*	Rosaceae
Corvus corax	Corvidae	*Arbutus unedo*	Ericaceae	*Prunus mahaleb*	Rosaceae
Corvus corone	Corvidae	*Arum italicum†*	Araceae	*Prunus padus*	Rosaceae
Corvus monedula	Corvidae	*Arum maculatum†*	Araceae	*Prunus prostrata*	Rosaceae
Cyanistes caeruleus	Paridae	*Asparagus acutifolius*	Asparagaceae	*Prunus serotina*	Rosaceae
Cyanopica cooki	Corvidae	*Asparagus aphyllus*	Asparagaceae	*Prunus spinosa*	Rosaceae
Dendrocopos major	Picidae	*Berberis vulgaris*	Berberidaceae	*Pyrus amygdaliformis*	Rosaceae
Emberiza calandra	Emberizidae	*Bryonia dioica†*	Cucurbitaceae	*Pyrus bourgaeana**	Rosaceae
Erithacus rubecula	Muscicapidae	*Cornus sanguinea*	Cornaceae	*Rhamnus alaternus*	Rhamnaceae
Falco tinnunculus	Falconidae	*Cotoneaster granatensis*	Rosaceae	*Rhamnus cathartica*	Rhamnaceae
Ficedula hypoleuca	Muscicapidae	*Crataegus monogyna*	Rosaceae	*Rhamnus lycioides*	Rhamnaceae
Fringilla coelebs	Fringillidae	*Daphne gnidium*	Thymelaeaceae	*Rhamnus saxatilis*	Rhamnaceae
Gallinula chloropus	Rallidae	*Daphne laureola*	Thymelaeaceae	*Ribes rubrum*	Grossulariaceae
Garrulus glandarius	Corvidae	*Euonymus europaeus*	Celastraceae	*Rosa canina*	Rosaceae
Lanius excubitor	Laniidae	*Ficus carica*	Moraceae	*Rosa sempervirens*	Rosaceae
Luscinia megarhynchos	Muscicapidae	*Fragaria vesca†*	Rosaceae	*Rubia peregrina‡*	Rubiaceae
Muscicapa striata	Muscicapidae	*Frangula alnus*	Rhamnaceae	*Rubus fruticosus*	Rosaceae
Oriolus oriolus	Oriolidae	*Hedera helix‡*	Araliaceae	*Rubus idaeus*	Rosaceae
Parus major	Paridae	*Hedera hibernica‡*	Araliaceae	*Rubus ulmifolius*	Rosaceae
Phasianus colchicus	Phasianidae	*Ilex aquifolium*	Aquifoliaceae	*Ruscus aculeatus*	Asparagaceae
Phoenicurus ochruros	Muscicapidae	*Jasminum fruticans*	Oleaceae	*Sambucus nigra*	Adoxaceae
Phoenicurus phoenicurus	Muscicapidae	*Juniperus communis*	Cupressaceae	*Sambucus racemosa*	Adoxaceae
Pica pica	Corvidae	*Juniperus oxycedrus*	Cupressaceae	*Smilax aspera‡*	Smilacaceae
Picus sharpei	Picidae	*Juniperus phoenicea*	Cupressaceae	*Solanum dulcamara†*	Solanaceae
Picus viridis	Picidae	*Juniperus sabina*	Cupressaceae	*Solanum nigrum†*	Solanaceae
Saxicola torquatus	Muscicapidae	*Ligustrum vulgare*	Oleaceae	*Sorbus aria*	Rosaceae
Sitta europaea	Sittidae	*Lonicera arborea*	Caprifoliaceae	*Sorbus aucuparia*	Rosaceae
Streptopelia decaocto	Columbidae	*Lonicera caprifolium‡*	Caprifoliaceae	*Sorbus torminalis*	Rosaceae
Sturnus unicolor	Sturnidae	*Lonicera etrusca‡*	Caprifoliaceae	*Symphoricarpos albus*	Caprifoliaceae
Sturnus vulgaris	Sturnidae	*Lonicera periclymenum‡*	Caprifoliaceae	*Dioscorea communis†*	Dioscoreaceae
Sylvia atricapilla	Sylviidae	*Lonicera xylosteum*	Caprifoliaceae	*Taxus baccata*	Taxaceae
Sylvia borin	Sylviidae	*Malus sylvestris*	Rosaceae	*Viburnum lantana*	Adoxaceae
Sylvia cantillans	Sylviidae	*Morus alba*	Moraceae	*Viburnum opulus*	Adoxaceae
Sylvia communis	Sylviidae	*Morus nigra*	Moraceae	*Viburnum tinus*	Adoxaceae
Sylvia conspicillata	Sylviidae	*Myrtus communis*	Myrtaceae	*Viscum album*	Santalaceae
Sylvia curruca	Sylviidae	*Olea europaea*	Oleaceae	*Vitis vinifera‡*	Vitaceae
Sylvia hortensis	Sylviidae	*Osyris alba*	Santalaceae		
Sylvia melanocephala	Sylviidae	*Phillyrea angustifolia*	Oleaceae		
Sylvia undata	Sylviidae	*Phillyrea latifolia*	Oleaceae		
Turdus iliacus	Turdidae	*Phytolacca americana†*	Phytolaccaceae		
Turdus merula	Turdidae	*Pistacia lentiscus*	Anacardiaceae		
Turdus philomelos	Turdidae	*Pistacia terebinthus*	Anacardiaceae		
Turdus pilaris	Turdidae	*Polygonatum odoratum†*	Asparagaceae		
Turdus torquatus	Turdidae				
Turdus viscivorus	Turdidae				

We followed taxonomy from 'Birds of the World' (www.birdsoftheworld.org)[78] for birds and a previously published[96] phylogenetic tree (ALLMB) for plants. Plants are defined as herbs (†), woody vines (‡) or trees and shrubs (all other species).

**Pyrus bourgaeana* (Iberian wild pear) was not present in ref. [96] but 'World Flora Online' (www.worldfloraonline.org) considers this species as a synonym of *Pyrus communis* auct. iber. We thus matched *P. bourgaeana* to *P. communis* in the phylogenetic tree to test for phylogenetic signal.

Extended Data Table 3 | Significance of the fixed factors migration direction and biome, and their interaction, in GLMMs testing effects on seed-dispersal interactions of plants with migrating birds

Fixed-effects	(*i*) Proportion of plant species (Binomial, logit link)		(*ii*) Frequency of seed-dispersal interactions (Beta, logit link)		(*iii*) Number of bird species per plant (Poisson, log link)	
Hypothesis testing	χ^2	*P*	χ^2	*P*	χ^2	*P*
Direction (D)	51.02	**2.0×10^{-16}**	159.60	**2.0×10^{-16}**	5.75	**0.0165**
Biome (B)	0.09	0.7612	0.21	0.6452	0.67	0.4142
D × B	7.03	**0.0080**	6.51	**0.0107**	1.26	0.2623
Conditional model	Estimate ± se		Estimate ± se		Estimate ± se	
Intercept	**1.414 ± 0.310**		**–0.418 ± 0.207**		**1.004 ± 0.125**	
D (northward)	**–1.734 ± 0.368**		**–1.842 ± 0.164**		**–0.307 ± 0.124**	
B (temperate)	0.714 ± 0.426		–0.322 ± 0.274		0.085 ± 0.168	
D × B	**–1.310 ± 0.494**		**0.642 ± 0.251**		0.194 ± 0.173	
Dispersion model	Estimate ± se		Estimate ± se		Estimate ± se	
Intercept	–		**1.028 ± 0.140**		–	
D (northward)	–		**1.874 ± 0.266**		–	
B (temperate)	–		**0.754 ± 0.198**		–	
D × B	–		**–1.575 ± 0.389**		–	
Random effects	Variance		Variance		Variance	
Plant species: Network	0.368		3.4×10^{-9}		0.157	
Network	0.077		0.174		0.052	

Proportion of plant species interacting with birds during migration (*n* = 434 observations) (i) (Fig. 2a), frequency of seed-dispersal interactions with birds during migration whenever these interactions occurred (non-zero frequencies; *n* = 260 observations) out of the total interaction weight (ii) (Fig. 2b) and number of bird species dispersing each plant species during migration whenever these interactions occurred (*n* = 260 observations) (iii) (Fig. 2c). Family and link functions are shown in parentheses. All models included network identity and plant species nested within network as random factors to account for the repeated measures at these levels. Model (ii) also includes a dispersion model because the dispersion parameter Φ of the beta distribution was allowed to vary in response to the interactive effects of direction and biome[95]. *P* values (two-sided) < 0.05 and significant model estimates (*P* < 0.05) are shown in bold.
In all models, southward and Mediterranean were used as the reference categories (intercepts) for the factors direction (*D*) and biome (*B*), respectively.

Extended Data Table 4 | Significance of the fixed factors migration direction and biome, and their interaction, in GLMMs testing effects on the proportion of migratory bird species that were Palaearctic migrants, and in the network-level frequency of seed-dispersal interactions with Palaearctic migrants

Fixed-effects	(*i*) Proportion of migratory bird species that were Palearctic migrants (Binomial, logit link)		(*ii*) Interaction frequency during migrations with Palearctic migrants (Beta, logit link)	
Hypothesis testing	χ^2	*P*	χ^2	*P*
Direction (D)	7.98	**0.0047**	32.47	**2.0×10^{-16}**
Biome (B)	9.14	**0.0025**	12.98	**0.0003**
D × B	0.11	0.7458	7.12	**0.0076**
Conditional model	Estimate ± se		Estimate ± se	
Intercept	0.034 ± 0.363		**1.188 ± 0.449**	
D (northward)	**1.004 ± 0.466**		**2.508 ± 0.503**	
B (temperate)	**1.429 ± 0.534**		**2.219 ± 0.531**	
D × B	0.268 ± 0.825		**–1.516 ± 0.568**	
Dispersion model	Estimate ± se		Estimate ± se	
Intercept	–		**1.318 ± 0.560**	
D (northward)	–		**3.404 ± 0.994**	
B (temperate)	–		**2.936 ± 0.742**	
Random effects	Variance		Variance	
Network	0.336		0.088	

Family and link functions are shown in parentheses. Models included network identity as random factor to account for the repeated measures within networks (*n* = 26 observations, 13 networks × 2 directions). We used data only from Palaearctic migrants because the frequencies from both migrant types are fully interdependent (Fig. 3a, b). Model (ii) also includes a dispersion model because the dispersion parameter Φ of the beta distribution was allowed to vary in response to the additive effects of direction and biome[95]. *P* values (two-sided) < 0.05 and significant model estimates ($P < 0.05$) are shown in bold. Results for the species richness of all migrant species pooled are provided in Extended Data Fig. 4.

In all models, southward and Mediterranean were used as the reference categories (intercepts) for the factors direction (*D*) and biome (*B*), respectively.

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Last updated by author(s):	May 10, 2021

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☐	☒	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☐	☒	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

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Software and code

Policy information about availability of computer code

Data collection	Our study includes both data collection (field sampling and molecular analyses) and data compilation from previous studies. We used SEQUENCHER v. 4.9, BioEdit v. 7.0.9 and Chromas v. 2.5.1 for sequence alignment and editing. We used the online platforms BOLD (www.boldsystems.org) and BLAST (https://blast.ncbi.nlm.nih.gov/Blast.cgi) for species identification from amplified DNA sequences (i.e. DNA barcoding).
Data analysis	We conducted all analyses in R version 3.5.2. We used the R packages glmmTMB (v. 0.2.3), car (v. 2.1-6), ape (v. 5.3), phytools (v. 0.6-99), lme4 (v. 1.1-19) and bipartite (v. 2.13). We made the figures using the R packages 'ggplot2' (v. 3.3.0) and cowplot (v. 0.9.4). The R scripts used to generate all results and figures are available through the Dryad Digital Repository (https://doi.org/10.5061/dryad.15dv41nx3).

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All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

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- A list of figures that have associated raw data
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All data used in the analyses are available through the Dryad Digital Repository (https://doi.org/10.5061/dryad.15dv41nx3). The dated phylogeny of seed plants (Spermatophyta) used to obtain our phylogenetic tree is available through GitHub (https://github.com/FePhyFoFum/big_seed_plant_trees/releases). Data on bird body weight used for size classification (Supplementary Figure 2) were obtained from EltonTraits 1.0 available through Figshare (https://dx.doi.org/10.6084/m9.figshare.c.3306933).

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Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	We combined phenological and migration information with data on 949 seed-dispersal interactions between 46 bird and 81 plant species from 13 woodland communities across Europe. The study design is factorial, as we tested the interactive effect between migration direction and community biome (direction x biome) on different response variables. The data structure is hierachical because we have species-level data for plants at birds nested within sites. The data structure also has repeated (paired) measures, with a data points per migration direction (southward and northward).
Research sample	Research sample includes seed-dispersal networks, that is, interacting communities of 46 frugivorous bird species that disperse the seeds of 81 fruiting plant species from 13 woodland communities across Europe (see Extended Data Table 2). Seed dispersal networks are expressed as interaction matrices where each row i represents a plant species and each column j represents a bird species. Elements in the matrices (wij) denote whether pairwise plant-bird interactions were observed (wij > 0) or not (wij = 0) and, if so, their value account for interaction weight. In this case, the quantity of seeds of each plant species dispersed by each bird species. The total sample size for plants, the main subject of the study, includes 434 observations (i.e. "plant-species / site / migration" combinations). Sex and age of the individuals is not relevant for the purposes of this study.
Sampling strategy	All the study networks (n = 13) were sampled all year-round, a prerequisite to cover the entire fruiting periods of all local fleshy-fruited species, as well as the prenuptial and postnuptial migration periods of all migratory birds. Our study includes a combination of networks from previous studies (n = 5) and newly sampled networks (n = 8). The number of networks was evenly distributed between the Mediterranean (n = 6) and the temperate biomes (n = 7) of Europe, which allowed a sufficient sample size to test for biome effects.
Data collection	Seven of the eight new networks were sampled through field sampling of bird-dispersed seeds and subsequent disperser identification by means of DNA-barcoding analysis. Individual seeds or droppings with seeds were sampled for DNA-barcoding analysis into 1.5- or 2.0-ml sterile tubes that were labelled and stored in a freezer at −20°C until DNA extraction. The molecular analyses for species identification was conducted by J.M.A. and J.C.I. The other new network was sampled through dietary analysis of birds captured in mist nets. Captured birds were individually placed in ringing bags for up to 30 min until they ejected droppings. The networks compiled from previous studies were obtained either through focal plant observations of birds feeding on fruits or through dietary analysis of birds captured in mist nets. Bird samples were collected in the field by J.P.G.-V., J.A., J.M.A., R.S.B., T.B., G.E.-A., N.F., D.G., J.C.I., P.J., P.K., W.J.S., E.V., L.P.d.S. and R.H. The networks from previous studies were compiled by B.I.S. Data on fruiting phenology and bird migrations was gathered by B.R., J.P.G.-V. and A.T.
Timing and spatial scale	New data in this study was collected between 2012 and 2018. Data available from previous studies were collected between 1981 and 1999. Sampling consisted on periodical surveys during 1–6 years, generally every 2 weeks, in which seed traps were revised, birds were mist-netted or focal plants were observed. Such frequency of sampling during all-year-round allows recording interactions between all bird adn plant species of each community, regardless the season. See details in Table S1. The data was collected in 13 sites across Europe and each site spans several square kilometers.
Data exclusions	No data were excluded.
Reproducibility	The analyses conducted in this study can be reproduced using the R code, which we will made publicly available once the article is accepted for publication. Moreover, we will make available in the DRYAD repository the complete dataset with the detailed information for each sample and its corresponding sequence obtained through DNA barcoding. The sequences include the sample code and all information associated: sampling date, site, seed species and number of seeds of the sample, bird species identified through DNA barcoding, percentage of similarity with best matched sequence and GenBank accession number of best matching sequence. In addition, we keep the DNA aliquots of all DNA extractions from each sample (voucher numbers correspond with 'sample_code') in our labs at University of Oviedo and EBD-CSIC (Spain). These aliquots are available under request. All seed samples are stored by J.P.G.-V at the laboratory of Botany in the University of Cádiz (Spain).
Randomization	Randomization does not apply as we did not conduct experiments. However, we did assess potential biases regarding the sampling methods of study networks and the approach used to obtain seed-dispersal periods (see Supplementary Discussion 2; Supplementary Figures 5-7).

Blinding	Blinding does not apply as we did not conduct experiments.

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions	We conducted fieldwork on several sites all year round during, for 1-6 years. The field conditions varied seasonally and between sites. The exact field conditions are not relevant because they do not impact the results. In the case of mit-netting, field work was only conducted when it was not raining .
Location	The latitude and longitude of the study sites is provided in Extended Data Table 1.
Access & import/export	Permits to access to the study sites of the new data collected in this study (see Extended Data Table 1): - Garrapilos (Spain): military site; permission given by “Servicio de Cría Caballar de las Fuerzas Armadas” to J.P.G.-V. (CC-42B00100-S-13-5090; 16 October 2013). - Cabañeros (Spain): national park; permission given by the director of the “Cabañeros National Park” to E.V. (June 2016). - Arbazal (Spain): private site; permission given by local authority and owners to D.G. (February 2016). - Vale Soeiro (Portugal): permission for mist-netting and bird ringing given by ICNF ("Instituto da Conservação da Natureza e das Florestas") to L.P.d.S. (117/2012, 126/2013, 130/2014, 137/2015, 140/2016, 146/2017 and 123/2018). - Ficuzza (Italy): private site; permission given by owners to R.S.B. (May 2016). - Bradfield Woods (UK): natural reserve; permission given by “Suffolk Wildlife Trust” to J.P.G.-V. and W.J.S (30 March 2016). - Bauerbach (Germany): public site; permission by local authority to N.F. (6 April 2016). - Hebdów (Poland): public and private sites; permission by local authority and owners to P.K. (May 2016).
Disturbance	Our study did not entail disturbance at the study sites. We placed seed traps in the field sites or used mist-nets, which are placed temporarily and do not cause impacts.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☐	☒ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	No laboratory animals were used in the study.
Wild animals	For sampling the seed-dispersal network from Portugal (Vale Soeiro), birds were caught in the field using mist-nets and immediately released in the same location after they ejected droppings in the cloth bag. No bird was injured, killed or kept captive. Overall, 45 species were captured in a total of 4462 bird captures including 3123 individuals. In 1330 captures (846 individuals) of such captures, the bird produced droppings with seeds (13 bird species). Full list of bird species captured (n = 45 species): Accipiter nisus, Acrocephalus scirpaceus, Aegithalos caudatus, Alcedo atthis, Anthus trivialis, Caprimulgus europaeus, Caprimulgus ruficollis, Carduelis chloris, Carduelis spinus, Certhia brachydactyla, Cyanistes caeruleus, Dendrocopos major, Erithacus rubecula, Ficedula hypoleuca, Fringilla coelebs, Fringilla montifringilla, Garrulus glandarius, Hippolais polyglotta, Lophophanes cristatus, Luscinia megarhynchos, Muscicapa striata, Parus major, Passer domesticus, Periparus ater, Phoenicurus ochruros, Phoenicurus phoenicurus, Phylloscopus collybita, Phylloscopus ibericus, Phylloscopus trochilus, Picus sharpei, Prunella modularis, Pyrrhula pyrrhula, Regulus ignicapillus, Serinus serinus, Streptopelia turtur, Sylvia atricapilla, Sylvia borin, Sylvia cantillans, Sylvia communis, Sylvia melanocephala, Sylvia undata, Troglodytes troglodytes, Turdus iliacus, Turdus merula and Turdus philomelos. List of bird species that produced droppings with seeds (n = 13 species): Cyanistes caeruleus, Erithacus rubecula, Ficedula hypoleuca, Parus major, Phoenicurus phoenicurus, Sylvia atricapilla, Sylvia borin, Sylvia cantillans, Sylvia communis, Sylvia melanocephala, Sylvia undata, Turdus merula and Turdus philomelos.

	Sex and age of the individuals is unknown (and not relevant for this study).
Field-collected samples	Seed samples collected in the field were stored in the freezer at –20ºC until DNA-barcoding analyses.
Ethics oversight	No ethical approval was required as no bird was killed, injured or kept captive and we used normal procedures for mist-netting.

Note that full information on the approval of the study protocol must also be provided in the manuscript.