

DISPERSAL PROCESSES DRIVING PLANT MOVEMENT: RANGE SHIFTS IN A CHANGING WORLD

What is long-distance dispersal? And a taxonomy of dispersal events

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Summary

1. Dispersal is a key individual-based process influencing many life-history attributes and scaling up to population-level properties (e.g. metapopulation connectivity). A persistent challenge in dispersal ecology has been the robust characterization of dispersal functions (kernels), a fundamental tool to predict how dispersal processes respond under global change scenarios. Particularly, the rightmost tail of these functions, that is the long-distance dispersal (LDD) events, are difficult to characterize empirically and to model in realistic ways.

2. But, when is it a LDD event? In the specific case of plants, dispersal has three basic components: (i) a distinct (sessile) source, the maternal plant producing the fruits or the paternal tree acting as a source of pollen; (ii) a distance component between source and target locations; and (iii) a vector actually performing the movement entailing the dispersal event. Here, I discuss operative definitions of LDD based on their intrinsic properties: (i) events crossing geographic boundaries among stands; and (ii) events contributing to effective gene flow and propagule migration.

3. Strict-sense long-distance dispersal involves movement both outside the stand geographic limits and outside the genetic neighbourhood area of individuals. Combinations of propagule movements within/outside these two spatial reference frames result in four distinct modes of LDD.

4. *Synthesis.* I expect truncation of seed dispersal kernels to have multiple consequences on demography and genetics, following to the loss of key dispersal services in natural populations. Irrespective of neighbourhood sizes, loss of LDD events may result in more structured and less cohesive genetic pools, with increased isolation by distance extending over broader areas. Proper characterization of the LDD events helps to assess, for example, how the ongoing defaunation of large-bodied frugivores pervasively entails the loss of crucial LDD functions.

Key-words: dispersal, frugivory, plant–animal interactions, pollination, seed dispersal

Introduction

Dispersal is a key individual-based process influencing many life-history attributes and scaling up to population-level properties (e.g. metapopulation connectivity; Cousens, Dytham & Law 2008). In the specific case of plants, largely sessile organisms, dispersal has three basic components: (i) a distinct (sessile) source, the maternal plant producing the fruits or the paternal tree acting as a source of pollen; (ii) a distance component between source and target locations; and (iii) a vector actually performing the movement entailing the dispersal event. While realized dispersal also depends upon stages subsequent to dissemination (e.g. successful germination and

seedling establishment; Schupp 1995), the three previous components fully characterize the dispersal process per se. Therefore, plant movement differs in important natural history details from animal dispersal, yet both can be assessed within a common conceptual framework (e.g. Nathan 2006). Characteristically, animal-assisted plant dispersal has three distinct, highly integrated components missing in the process of animal dispersal: the properties of the source (parental) plant, that mediate in the foraging of the animal vector (pollinator or frugivore), the intrinsic properties of the propagule and the functional characteristics of the animal vector who performs the movement (Nathan *et al.* 2008a).

The movement of pollen and seeds by animals and its consequences have intrigued population geneticists and field ecologists since the infancy of both research disciplines. Each has

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generated an impressive body of theoretical and empirical research through the past decades, yet advances have long been coexisting in parallel worlds and the great synergistic potential of population genetics and demography for the study of plant dispersal by animals remains little explored. Knowledge gaps still having the imprint of this conceptual disconnection include the idea of long-distance dispersal, and the paradoxes of forest fragmentation effects on genetic diversity (Kramer *et al.* 2008), survival and persistence of relict tree species (Hampe & Jump 2011), and rapid post-Pleistocene recolonization of vast continental areas in response to climate modification (Clark 1998; Clark *et al.* 1998), among other persisting issues. This conceptual isolation has been exacerbated by technical difficulties for the robust characterization of dispersal events, especially those involving movement over long distances (long-distance dispersal, LDD). Some progress has recently been made through the fast-paced implementation of molecular tools in ecological research laboratories and the availability of cutting-edge technology for biotelemetry applications. But much of the population geneticist and ecologist communities remains unaware of the state of the art in each other and likely underappreciates their potential to validate and enrich dispersal studies (Jones & Muller-Landau 2008). In particular, LDD events remain difficult to assess, both technically – with serious methodological problems for its reliable estimation – and conceptually. My aim is to review the LDD concept with a specific emphasis on dispersal of plant propagules (seeds and pollen), providing an extended definition that might be helpful in the robust quantification of LD events.

An added difficulty to bridge ecological processes of dispersal with their genetic consequences is the fact that dispersal per se does not necessarily imply realized gene flow (Mallet 2001). Yet in the genetics literature, the inescapable difficulty to robustly estimate the standard deviation of parent–offspring distances, σ_x , as a proxy for realized gene flow distance, is analogous to the ecological scenario. Strongly leptokurtic distributions of dispersal distances would lead to severe underestimation of σ_x , for example in mark–recapture studies limited to local sites where the long tail of LDD events escapes detection beyond the edges of the study area (Mallet 2001). Thus, fat-tailed distributions of dispersal distances tend to homogenize distant populations, leading to stronger reductions in F_{ST} than expected from local records of dispersal events (Rousset 1997). Despite such difficulties, comparative approaches (e.g. Bohonak 1999) demonstrate that dispersal makes a measurable contribution to population genetic differentiation in most animal species in nature and that gene flow estimates are rarely so overwhelmed by population history, departures from equilibrium or other microevolutionary forces as to be uninformative. The relationship between dispersal and realized gene flow is key to understand how migration interacts with drift in driving the dynamics of genetic pools and population differentiation (Garant, Forde & Hendry 2007).

While my main focus is on population-level scenarios and the role of animal vectors, recent research has shown how relevant is habitat and landscape context in determining the occurrence and directionality of LDD (Schurr, Steinitz &

Nathan 2008; Carlo *et al.* 2013). On the other hand, dealing with habitat effects seems obligated if aimed to discuss global change drivers (i.e. habitat loss and fragmentation). Two main conceptual approaches have been used to assess dispersal (Fig. 1). The forward (Lagrangian) approach attempts to track the dispersal events away from the known sources, for example by tracking the movement patterns of frugivores as they leave fruiting plants after feeding (Fig. 1a). This is the main approach used in the movement ecology framework (Nathan *et al.* 2008a), with extensive application to animal movement based on the use of advanced biotelemetry. The backward (Eulerian) approach attempts to reconstruct the most likely source of a dispersed propagule by inferring the sources given the propagule delivery pattern, the fecundity of potential sources and the dispersal function (Fig. 1b), that is using an inverse-modelling approach. The main technical challenge in Fig. 1a is to sample enough dispersal events away from the source to be able to fully characterize the tail (LDD events) of the dispersal function. In Fig. 1b, the main challenge is to have a robust sampling scheme with propagule collectors (e.g. seed traps) and a good characterization of the potential sources to derive robust estimates of the actual sources. Both approaches are limited logistically by the difficulties to sample the vast areas required to assess LDD events from the focal source population.

Long-distance dispersal events have two key characteristics that make them extremely important for population dynamics, yet being very difficult to characterize: LDD events are infrequent, but with a disproportionately high influence on contemporary gene flow and structure of the genetic pools (e.g. Schurr *et al.* 2009; Clobert *et al.* 2012; Travis *et al.* 2013). Long-distance dispersals can connect disparate populations, allowing for genetic connectivity, colonization of vacant habitat and range expansion across changing landscapes, and maintain global persistence in the face of local extinctions (Trakhtenbrot *et al.* 2005; Baguette & Schtickzelle 2006; Ronce 2007; Schloss, Nunez & Lawler 2012). With their influence on the structure of genetic pools, LDD events can also drive population differentiation and speciation (Garant, Forde & Hendry 2007; Ronce 2007).

No explicit definition of what constitutes an LDD event exists. Long-distance dispersal is a characteristically extreme event of propagule movement in any plant or animal population, typically occurring with an extremely low probability but potentially reaching an extremely long distance. Previous approaches (e.g. Nathan 2006; Schurr *et al.* 2009) include both absolute and proportional definitions to characterize LDD events. This means providing information about the absolute distances moved by a given percentile of the events and/or providing data on the proportion of events exceeding a given distance threshold, that is an operational definition (Nathan *et al.* 2008b). The exact proportional or absolute thresholds selected remain somehow arbitrary, as no reference spatial frame is provided within the definition of LDD. This leaves the consideration of LDD as an extreme form of context-dependent phenomenon, strongly dependent upon the scale of the biological process studied (Kinlan, Gaines &

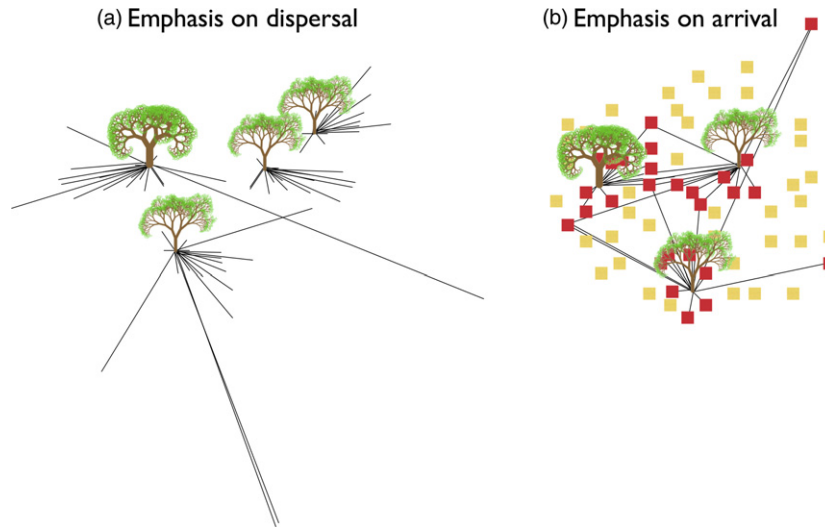


Fig. 1. The two approaches used in analyses of dispersal processes in plants. (a) The forward approach attempts to track the dispersal events away from the known sources, for example by tracking the movement patterns of frugivores as they leave fruiting plants after feeding (i.e. the Lagrangian approach; Nathan *et al.* 2003). (b) The backward approach attempts to reconstruct the most likely source of a dispersed propagule by inferring the sources given the propagule delivery pattern, the fecundity of potential sources and the dispersal function (i.e. the Eulerian approach). The main technical challenge in 'a' is to sample enough dispersal events away from the source to be able to fully characterize the tail (long-distance dispersal (LDD) events) of the dispersal function. In 'b', the main challenge is to have a robust sampling scheme with propagule collectors (e.g. seed traps) and a good characterization of the potential sources to derive robust estimates of the actual sources with inverse-modeling techniques. [Colour figure can be viewed at wileyonlinelibrary.com]

Lester 2005) and of the specific organism considered. For example, Kinlan, Gaines & Lester (2005) used a spatial reference frame to characterize LDD events of marine organisms, where sedentary adults and larvae differ enormously in the spatial scales of their dispersal (D'Aloia *et al.* 2013). Therefore, any measure of extent and reach of LDD events requires reference to an explicit spatial frame or 'local' scale (Kinlan, Gaines & Lester 2005; Byrne *et al.* 2014).

I aim at providing a general framework for the quantitative analysis of LDD events so that estimates of their frequency and extent could be comparable across different study systems. I argue that both demographic and genetic elements are needed for this framework, most likely requiring a combination of field-based movement data and genetic analyses. These elements can be overlaid on previous definitions based on absolute and proportional characterizations of LDD. I start with a definition of LDD events within a spatially explicit mechanistic framework allowing an unambiguous meaning for setting long-distance thresholds. I then use a case study to assess differential contributions of animal frugivores performing LDD.

Long-distance dispersal is currently one of the most debated topics in dispersal ecology; it defines the connectedness within the network of local populations and the possibilities for range expansion and successful colonization events. I propose a first demogenetically based, operational definition of what a LDD event actually is, and review existing empirical literature on distance thresholds from population and genetic perspectives. I also show how molecular tools have been used to identify the respective contributions of different animal species to the LDD portion of dispersal kernels of pollen and seeds by setting empirically derived distance

thresholds. Finally, I highlight potential applications of molecular markers beyond the quantification of just the dispersal distances that prevails in current studies, for example experimental approaches to assess dispersal limitation and Janzen–Connell effects.

LDD within a demogenetic perspective: a taxonomy of dispersal events

Here, I propose an explicit definition of LDD and what constitutes a LDD event. Previous definitions of dispersal patterns emphasized only their distance components and characterized LDD events basically in terms of geographic distance between a dispersed propagule (or an established early seedling) and its most likely maternal or paternal (in case of pollen) source. Absolute and proportional definitions for the LDD events have been proposed depending on arbitrary thresholds of either the distance beyond which a dispersal event is LDD or the proportion of events occurring beyond a specific distance (Nathan 2005; Nathan *et al.* 2008b). Thus, two key biological aspects of LDD events involve the transport of propagules outside a reference area: moving away from the source stand or population, and moving away from the area where relatives stand (Kinlan, Gaines & Lester 2005). These two movements do not necessarily concur: a propagule may move over a very long distance yet still be disseminated within the reach of the neighbourhood where parental individuals mate. Within a demogenetic framework, it is easy to envision a combination of situations concerning the spatial scale of the dispersal processes (Table 1) and unambiguously define different types of LDD events. The

Table 1. Types of dispersal as a function of population area limits and genetic neighbourhood limits

| Genetic neighbourhood limit | Population geographic limit | |
|-----------------------------|--|--|
| | Within | Outside |
| Within | Local, short-distance dispersal, SDD_{loc} | Within-neighbourhood, long-distance dispersal, LDD_{neigh} |
| Outside | Local, long-distance dispersal, LDD_{loc} | Strict-sense long-distance dispersal, LDD_{ss} |

See Fig. 2 for a graphical representation of the four scenarios.

idea that dispersal occurs in reference to these two spatial reference frames, that is the population or stand and the genetic neighbourhood area, is motivated by the fact that dispersal entails the movement of both an individual propagule (i.e. a pollen grain or a seed) and a distinct set of genes (i.e. the male genotype in case of pollen, or a seed genotype). Thus, dispersal entails simultaneous demographic and genetic effects through recruitment of new individuals in the population and through contributions to gene flow (Harper 1977). When considered its combined influence on demography and population genetics, the concept of LDD nicely bridges these two paradigms embedded in the biological definition of population (Waples & Gaggiotti 2006).

Two important components of plant dispersal ecology concern the movement of propagules away from the source population, a type of dispersal relevant to colonization ability and range expansion (Howe & Miriti 2004), and the movement away from the location of close relatives, that is a movement away from the genetic neighbourhood (Hardesty, Hubbell & Bermingham 2006; Jones & Muller-Landau 2008). If we classify dispersal events according to these two spatial frameworks (Table 1), we end up with four distinct types of events depending on whether or not dispersed propagules are disseminated within these reference areas. Setting the limits of a

population can be problematic (Waples & Gaggiotti 2006), yet we can identify with relative ease the geographic limits of plant stands, patches, habitat spots or other types of habitat or microhabitat discontinuities that determine landmark boundaries of biological significance (see Kinlan, Gaines & Lester 2005, for further discussion of boundaries for dispersal). These ‘frontiers’ set biological limits to what a LDD event is in relation to the geographic limits of the source population. Most plants are distributed as clumped patches, discrete stands or relatively isolated populations, so we may distinguish between short-distance and LDD events that end up with dissemination within or beyond, respectively, the stand or population geographic boundaries (Table 1; SDD_{loc} or LDD_{loc}) (Fig. 2).

A second consideration in terms of spatial boundaries, with effects on dispersal patterns, is the genetic neighbourhood area N_e^b , that is the spatial extent including a subset of panmictic individuals within a population (Wright 1943, 1946). Thus, the N_e^b area can be equal to the whole extent of the population whenever the population is unstructured and there is evidence for random mating events among all the individuals. However, most populations and stands of long-lived trees show highly aggregated and clumped distributions (Seidler & Plotkin 2006), where relatively long distances may separate groups of individuals within the same population. In these cases, we might expect N_e^b area to be substantially smaller than the total population area. Therefore, at least four possible scenarios exist with distinct implications in terms of consequences for dispersal (Table 1). In the case of dispersal events not extending beyond the geographic limits of the population or reference area, actual LDD events may involve dissemination beyond a reduced neighbourhood area that is smaller than the geographic extent of the population, originating local LDD (LDD_{loc}) events (Table 1; Fig. 2a). Actual short-distance dispersal would then involve those situations where the propagule is disseminated within *both* the population limits and the genetic neighbourhood boundary (SDD_{loc}). Along a

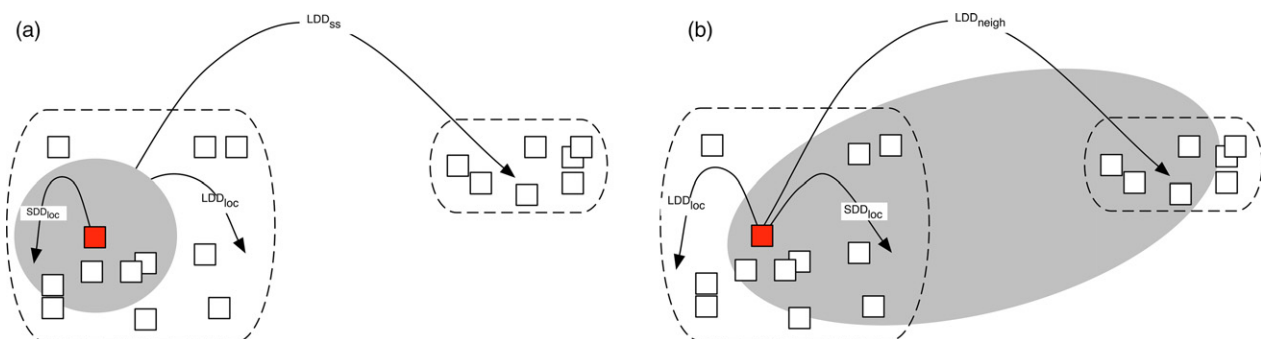


Fig. 2. Schematic representation of different types of long-distance dispersal events in relation to the geographic limits of local populations (dashed lines) and the genetic neighbourhood area N_e^b (grey area) of specific individual plants (squares). Dispersal events (arrows) can be classified depending on their actual incidence on propagule movement outside these spatially explicit reference areas (Table 1). Strict-sense long-distance dispersal events (LDD_{ss}) just include the LDD events that disseminate propagules out of *both* the population and genetic neighbourhood boundaries. (a) The neighbourhood area is included within the geographic limits of the population, with some dispersal events potentially contributing local LDD; (b) the neighbourhood area is much larger than the geographic limits of the population. Both LDD_{ss} and LDD_{loc} may contribute genetic novelty by moving propagules outside the N_e^b area or the population limit, area or both. [Colour figure can be viewed at wileyonlinelibrary.com]

similar reasoning, dispersal events outside the population limits will not necessarily convey LDD (Table 1; Fig. 2b): this is expected in cases where the genetic neighbourhoods are extensive, going beyond the geographic limits of local populations, as in fig trees (Nason, Herre & Hamrick 1998) with long-distance pollination, generating LDD events within the genetic neighbourhood (LDD_{neigh}). Note that pollen and seeds may have contrasting movement patterns in reference to the distinct spatial scales of the population limits and of the genetic neighbourhood. For example, wind-dispersed species with reduced seed mobility (in terms of distance), such as oaks, can have large genetic neighbourhoods with extensive pollen dispersal (Streiff *et al.* 1999) (but see, e.g., Smouse *et al.* 2001; Dutech *et al.* 2005; for fragmented stands) so that LDD_{neigh} dispersal events might frequently move beyond the physical limits of the population, patch, or stand but remain within the genetic neighbourhood. Finally, strict-sense LDD events would involve dissemination outside *both* the population limits and the genetic neighbourhood boundary (LDD_{ss}) (Table 1; Fig. 2a).

While both SDD_{loc} and LDD_{loc} can be crucial for assuring the local persistence of populations, LDD_{neigh} and LDD_{ss} would be extremely important contributors to the structuring of genetic pools, realized gene flow and maintaining connectivity in metapopulation scenarios. I argue that both the demographic and the genetic references are relevant for a proper definition of LDD. Accounting for these references may have different implications in relation to the dispersal biology of species. For example, frugivorous vertebrates, particularly the large-sized ones, tend to disperse a high number of half-sibs propagules, from the same mother tree to the same deposition site (Jordano *et al.* 2007; Karubian *et al.* 2010; Scofield *et al.* 2012), potentially increasing the frequency of LDD_{neigh} events if dispersal distances are relatively short (Fig. 3).

Individual and population neighbourhoods as reference

Continuous populations can be modelled with the concepts of isolation by distance and neighbourhood size (Wright 1943, 1946). The former refers to the case that limited gene dispersal in continuous populations produces demes that are panmictic internally, but are isolated to some extent from adjacent demes. Each group of reproducing individuals is the neighbourhood, defined as the population of a region in a continuum, from which the parents of individuals born near the centre may be treated as if drawn at random (Wright 1969). The importance and influence of the dispersal process in determining the size of the neighbourhood is given by this equation, which shows how the spatial dispersion (pattern of spatial distribution) of the population influences the effective population size. This influence on the effective size is given by:

$$N_e^{nb} = 4\pi\sigma\delta \quad \text{eqn 1}$$

where δ is the density of adults per unit area and σ is the standard deviation of the distance between birth and breeding sites. This formulation is often called the neighbourhood size and assumes a normal distribution of distances between parents and offspring (out in a perfect circular shape from the source). Thus, changes in the variance of dispersal distance can affect N_e^{nb} (highly clumped populations will have reduced N_e^{nb}). This is the basic model of 'isolation by distance' proposed by Wright (1943, 1946). Under this type of model, migration (gene flow) is given by the variance in dispersal, and not by the proportion of the population that is composed of migrants (denoted m), as is the case with island models (Slatkin 1985). With enough distance separating them, two plant individuals have a low probability of mating and can be considered members of distinct genetic

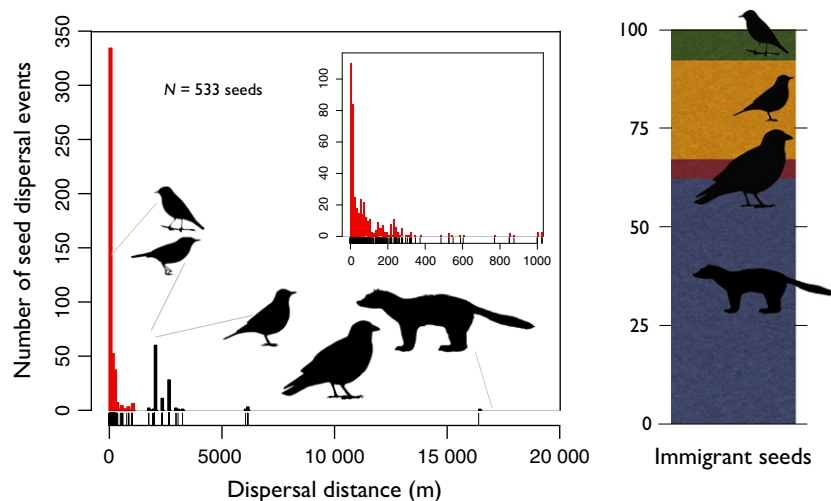


Fig. 3. Empirical frequency distributions of seed dispersal events as a function of dispersal distance by animal frugivores consuming *Prunus mahaleb* fruits. In red, left (inset), frequencies of within-population dispersal events inferred from direct assignment based on seed endocarp genotypes and maternal trees genotypes. Larger frame, left, contributions of four functional frugivore groups (small birds, medium- and large-sized birds, and mammals) to seed dissemination and proportional contributions (right bar) to dispersal of the inferred immigrant seeds (i.e. those not matching any maternal tree in the study population) (Jordano *et al.* 2007). [Colour figure can be viewed at wileyonlinelibrary.com]

Table 2. Relative frequencies of *Prunus mahaleb* seed dispersal events for different frugivore groups according to population area limits and genetic neighbourhood limits

| Frugivore group | Within-population, within-neighbourhood SDD_{loc} | Within-population, long-distance LDD_{loc} | Outside-population, within-neighbourhood LDD_{neigh} | Strict-sense long-distance LDD_{ss} | N seeds |
|-----------------|---|--|--|---------------------------------------|-----------|
| Small birds | 0.7842 | 0.0171 | 0.00 | 0.1986 | 292 |
| <i>Turdus</i> | 0.2370 | 0.5549 | 0.00 | 0.2081 | 173 |
| Large birds | 0.0435 | 0.3913 | 0.00 | 0.5652 | 23 |
| Mammals | 0.0120 | 0.2455 | 0.00 | 0.7425 | 167 |

See Fig. 2 for a graphical representation of the four scenarios. $N = 655$ seeds (see Table 1 in Jordano *et al.* 2007). Given that the estimated neighbourhood size is smaller than population area, LDD_{neigh} would be zero.

populations even if they are not located in geographically distinct populations.

For plants, gene flow may be accomplished by both seeds and pollen, so the variance may be decomposed to account for different patterns of seed and pollen dispersal, and to take into account the mating system (outcrossing rate, t). Thus, neighbourhood size can be defined with the following equation (Crawford 1984):

$$N_e^b = 4\pi \left(\sigma_s + \frac{t\sigma_p^2}{2} \right) \delta(1+t) \quad \text{eqn 2}$$

where σ_s is the standard deviation of seed dispersal distance, σ_p is the standard deviation of pollen dispersal distance and δ is the density of potential parents.

Neighbourhood size in plants can be estimated by marking pollen and seeds with fluorescent dyes, tags or stable isotope enrichment (Carlo, Tewksbury & Martínez 2009). However, these methods do not measure effective pollen or seed movement, but they may be combined with genetic analysis to assess genetic identity and relatedness with hypervariable DNA markers (Levin 1988; Nason, Herre & Hamrick 1998; Godoy & Jordano 2001) to achieve reliable estimates of both effective population size and neighbourhood area.

The extent of neighbourhood area in plants can be extremely variable, depending on life-history attributes such as life span, spacing patterns and mating system. Even a limited sample of available information (Table S1, Supporting Information) highlights the fact that the size of neighbourhood areas can in some cases exceed the geographic limits of local populations (Nason, Herre & Hamrick 1998). The size of neighbourhood areas may encompass at least four orders of magnitude, 10^{-2} – 10^2 km in radius, and include many individuals. Therefore, reference to this ‘genetic/evolutionary’ paradigm and reference to the geographic boundaries (sensu Waples & Gaggiotti 2006) may be instrumental to understand the actual role of LDD events in shaping the structuring of genetic pools and contributing to gene dispersal.

Whenever there is a large discrepancy between population area extent and N_e^b , we might expect the frequency of LDD_{loc} and LDD_{neigh} to differ enormously. For example, relatively small N_e^b may raise the importance of LDD_{loc} in preserving scenarios of panmixia within a local population, as most distant dispersal events will disseminate seeds outside the neighbourhood of maternal plants.

Empirical analysis of contributions to LDD

Empirical evaluation of differential contributions to the different forms of LDD events outlined in Table 1 requires identification of source trees as well as assignment of the dispersed propagules to specific vectors or functional groups of vectors (Jordano *et al.* 2007). Recently, DNA-barcoding techniques have been developed and successfully applied to the identification of frugivore species contributing to specific seed dispersal events whose source can be identified with genetic, direct assignment techniques (González-Varo, Arroyo & Jordano 2014). Otherwise, visual identification can reliably assign the genotyped seeds to frugivore species groups based on specific characteristics of scats and regurgitations (Jordano *et al.* 2007).

We inferred the frugivore groups contributing dispersal events by visually identifying scats and regurgitations in seed traps and line transects (see Jordano *et al.* 2007; and Appendix S1). These frugivore functional groups include up to 38 bird and four mammal species feeding on *Prunus mahaleb* fruits (Jordano & Schupp 2000). Here, we differentiate four major frugivore groups: large carnivorous mammals (such as foxes, badgers and stone martens); two species of medium-sized frugivorous birds, mistle thrushes (*Turdus viscivorus*) and carrion crows (*Corvus corone*); and a pool of small-sized frugivorous birds, including warblers, redstarts and robins (Jordano *et al.* 2007; Fig. 3).

To a large extent, short-distance dispersal events (strict-sense, SDD_{loc} events) are contributed by small- and medium-sized (*Turdus*) frugivorous birds (Table 2). Given the relatively reduced N_e^b area of *P. mahaleb* (Table S1), <1 km², well below the extent of the local study population (García *et al.* 2005; García, Jordano & Godoy 2007), we cannot estimate LDD_{neigh} events (Table 2), as all LDD events outside the reference population occur, by definition, outside the N_e^b area. Larger frugivores such as corvids and the pigeon *Columba palumbus* contribute most LDD events, and most immigrant seeds potentially dispersed from other populations (Fig. 3; Fig. S2). Notably, strict-sense LDD (LDD_{ss}) appears consistently associated with large-bodied frugivores (Table 2), most likely associated with a greater frequency of movements outside the local population (Fig. 4).

Empirically mapping of dispersal events for either pollen or seed disseminated by animals may result in a complex pattern

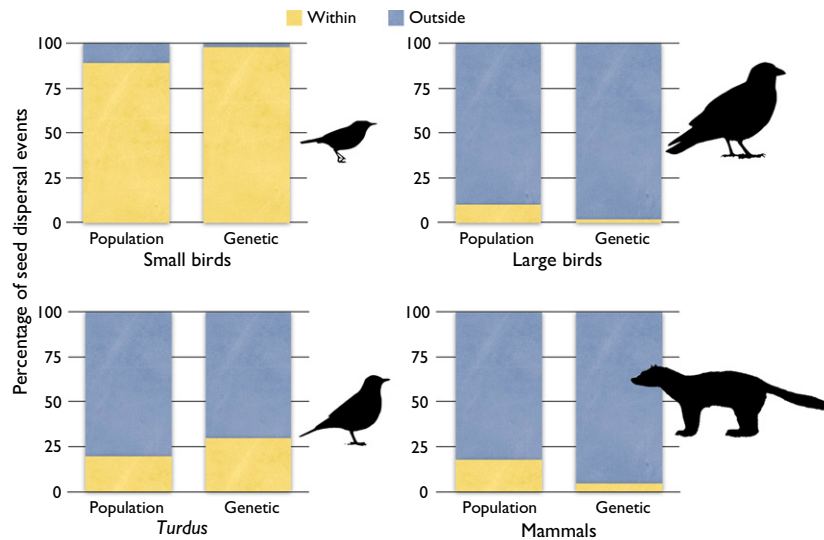


Fig. 4. Differential contributions of functional groups of frugivores to the four combinations of *Prunus mahaleb* seed dispersal events outlined in Table 1. These result from dissemination within (yellow) or outside (blue) the population geographic limits; within-population dispersal events can either be short-distance (SDD_{loc}) or local LDD (LDD_{loc}) depending on the size of the genetic neighbourhood. Dispersal outside the local population can entail short-distance dispersal, if within the genetic neighbourhood area limits (SDD_{neigh}) (yellow) or represent strict-sense LDD (LDD_{ss}) (blue). [Colour figure can be viewed at wileyonlinelibrary.com]

of different combinations of dispersal events (Fig. S1), as animal movements are overlaid onto plant populations occupying complex landscapes, resulting in different types of SDD and LDD events.

Long-distance dispersal: the ecology of extreme events

Long-distance dispersal is a major component of the population dynamics, genetic structure and biogeographic history of plant species. It determines the colonization ability of new habitats and the possibilities for fragmented populations to sustain a cohesive metapopulation by immigration–emigration dynamics that rely on LDD events (Nathan *et al.* 2008b; Schurr *et al.* 2009). Yet our current understanding of the extent, frequency and consequences of LDD is very limited. On the one hand, theoretical models fail to predict accurately the behaviour of the tail of the dispersal functions, and thus fail to predict very basic properties of LDD. On the other hand, we have very limited documentation of actual LDD events in natural populations and we still see LDD as a sporadic, rarely far-reaching process still marked with the stamp of natural history curiosity.

Combining spatially explicit references to the geographic population limits and the genetic neighbourhood area extent (N_e^b) helps avoiding some imprecision in setting distance thresholds to characterize LDD events (Jones & Muller-Landau 2008). In addition, the framework outlined in Table 1 bridges the combined demographic and genetic effects of LDD events. When methods available to assign frugivore taxa to the analysed dispersal events, as in the study case with *P. mahaleb*, a classification in the four categories of events is possible.

The frugivore assemblage of *P. mahaleb* is composed by a diversified set of animal species spanning a wide size range,

c. 12–14 000 g in body mass. We might expect that this extreme variation translates in an ample pattern of foraging modes, movement distances and fruit/seed processing (Jordano & Schupp 2000). If the results for *P. mahaleb* are generalizable to other disperser assemblages, it seems that the functional roles of frugivore species in terms of contributions to LDD events are structured in two distinct groups: small-bodied frugivores, with substantial contributions to SDD events, and large-bodied species, with a disproportionate contribution to LDD events. Both components of this sort of diplochorous (vander Wall & Longland 2004) dispersal system are very frequent in fleshy-fruited plants with diversified frugivore assemblages (Galetti *et al.* 2013). In such cases, small-bodied frugivores largely contribute the short-distance dispersal key to support in situ recruitment and population persistence. Yet the large-bodied frugivores distinctly contribute LDD events that sustain the connectivity of metapopulation scenarios (Urban & Keitt 2001). As shown in Table 1, SDD and LDD events can be more complex when we consider the contributions to gene flow via seed and the consequences in terms of structure and spatial distributions of the genetic pools. For example, local, within-population dispersal events may vary enormously in terms of genetic effects and local structuring of the genetic pools depending on whether they specifically contribute SDD_{loc} or, instead, LDD_{loc} . Note that only the latter actually contribute erasing any form of local genetic structure by contributing to increased genetic neighbourhoods.

A number of classic studies have demonstrated that the activity of large frugivores may also significantly contribute to SDD events and inefficient dispersal because of, that is, territorial defence, short gut retention times relative to on-tree foraging, frequent revisitation of same trees and perches, etc., resulting in substantial SDD events (Pratt & Stiles 1983; Pratt

1984; Snow & Snow 1984, 1988; Wheelwright 1991). Yet these large-bodied frugivores are crucial for both LDD_{loc} and LDD_{ss} , given that extensive movement patterns and extremely large foraging ranges may frequently contribute dissemination beyond distance thresholds defined with either spatial landscape or genetic references. Recent analyses of the movement ecology of large frugivores, coupled with results of their seed dispersal services emphasize that LDD are by no means exceptional, either in terms of frequency and extent (e.g. Westcott *et al.* 2005; Bueno *et al.* 2013; Carlo *et al.* 2013; Morales *et al.* 2013). In addition, medium-sized birds such as thrushes (*Turdus* spp.) can contribute substantial LDD_{loc} events, that is local LDD events contributing to erase local population genetic structuring, effectively increasing the size of genetic neighbourhoods. In the case of *P. mahaleb* up to 55–49% of their dispersal events are LDD_{loc} events. These birds are efficient seed dispersers of *P. mahaleb* and other fleshy-fruited species (Snow & Snow 1988; Jordano & Schupp 2000; Carlo *et al.* 2013), also showing significant contributions of LDD_{ss} events.

Two-dimensional patterns in the *P. mahaleb* seed rain and the individual seed shadows, accurately tracked with DNA-based genotyping methods, thus reflect the complex effects of frugivore foraging, habitat preferences and heterogeneous landscapes. This situation is probably generalizable to other plant–frugivore interactions where the combined spatial dynamics of habitat use and digestion processes determine complex seed shadows (Jordano *et al.* 2007; Nathan *et al.* 2008b). Much of this complexity can be adequately handled by mechanistic models (Nathan *et al.* 2002) incorporating very simple rules (Guttal *et al.* 2011). For example, earlier results (Jordano 2007) showed that the dispersal distances contributed by *P. mahaleb* frugivores closely map the spacing patterns of fruiting trees, but only up to a certain distance (≤ 100 m) (Fig. 10.3a in Jordano 2007). Beyond this, frugivores were probably responding to other major landscape elements (e.g. rock outcrops, forest edges, large patches of open grassland) that cause the fat tail of the seed dispersal distribution, adding more frequent LDD events than expected from a Brownian random walk pattern generated by a tracking of the crops of the fruiting trees. For instance, the long flights performed by *T. viscivorus* (Jordano & Schupp 2000) frequently faced the pine forest edge, at distances ≥ 100 m of most *P. mahaleb* fruiting trees. If these medium-sized birds are selecting habitat with tall woody vegetation (e.g. pines ≥ 6 m height), then they should be perceiving a much more patchy landscape, and thus requiring longer flights than, for example, small warblers seeking vegetation cover < 0.5 m (Fig. 10.3b in Jordano 2007).

As defined in our framework (Table 1), LDD and, in particular, LDD_{ss} events are a specific case of extreme events (García & Borda-de-Água 2017), consistently associated with large-sized frugivores, yet including also medium-sized and highly efficient frugivorous bird species. Robustly characterizing the expected frequencies and extent of those extreme events would be crucial to properly assess the functional role

of frugivores and the full range of influences (demographic, genetic) in plant populations.

Challenges and future avenues for research

Pollen and seed dispersal in plants are essentially spatially structured processes for which the outcomes of interactions with dispersal vectors is intimately linked to landscape features. Given this mechanistic link between the features of the vector and the environments where its displacement occurs (Nathan *et al.* 2008a), consideration of landscape is key to understand the consequences of LDD events. Yet these consequences hit two central aspects of plant life histories: the demographic recruitment process (Harper 1977), and the genetic signatures of pollen- and seed-mediated gene flow in complex landscapes (Sork *et al.* 1999). Recent evidences point out that the selective extinction of large-bodied frugivores may significantly impact plant populations dependent on frugivores both in terms of recruitment (Traveset, González-Varo & Valido 2012; Pérez-Méndez, Jordano & Valido 2015) and genetic connectivity (Pérez-Méndez, Jordano & Valido 2016). Frugivore downsizing represents a lasting challenge for the collapse of seed dispersal processes where LDD_{ss} events are crucial for population persistence and the cohesion of fragmented populations within metapopulation scenarios.

I advocate (also see Jordano & Godoy 2002; Nathan *et al.* 2003; Jones & Muller-Landau 2008; Hardesty, Metcalfe & Westcott 2011) a combination of approaches including large-scale biotelemetry to characterize animal movement, coupled with large-scale genetic sampling of dispersed propagules, and demogenetic approaches that combine both demographic and genetic research. A crucial aspect would be to effectively associate the role of individual frugivore species to specific dispersal outcomes, by identifying the actual disperser contributing a dissemination event (González-Varo, Arroyo & Jordano 2014) and simultaneously characterizing the source maternal plant (Jordano & Godoy 2002).

Long-distance dispersal, and its variation across coexisting plant species, could also have far-reaching consequences for community assembly and forest physiognomy. Yet very few previous analyses address this point. Comparative information on LDD across species sharing a common environment have found strong differences in LDD potential among plants with different (e.g., Clark *et al.* 1999; Martínez & González-Taboada 2008) or even with the same dispersal syndrome (García, Carlo & Martínez 2016).

The actual challenges to properly characterize the typologies of LDD events outlined in Table 1 will probably persist. We need more efficient quantitative approaches to assess these infrequent events that occur over enormous spatial scales and that need to be documented with sample sizes sufficient to facilitate modelling efforts and robust statistical inferences. These are not trivial difficulties given the urgency to assess how forest loss, defaunation, genetic purging due to logging, etc. alter plant populations.

Acknowledgements

I am indebted to Cristina Garca, Jos A. Godoy, Manolo Carrión, Juan Luis García-Castaño, Jesús Rodríguez and, especially, Juan Miguel Arroyo for generous help with field and laboratory work and making possible this study. I appreciate the help and advice of Cristina García and Etienne Klein during the final stages of the manuscript. The study was supported by a Junta de Andalucía Excellence grant (RNM-5731), as well as a Severo Ochoa Excellence Award from the Ministerio de Economía y Competitividad (SEV-2012-0262) and CGL2013-47429P grant. The Consejería de Medio Ambiente, Junta de Andalucía, provided generous facilities that made possible this study in the Andalusian natural parks (Sierra de Cazorla, Alcornocales) and authorized my work there.

Data accessibility

This review does not use new raw data, but includes some re-analyses of previously published material. All the original data supporting the paper, R code, supplementary figures and summaries of analytical protocols are available at the author's GitHub repository (<https://github.com/pedroj>) and also deposited in the Dryad Digital Repository (Jordano 2017): <http://datadryad.org/resource/doi:10.5061/dryad.k0v67>.

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Received 28 June 2016; accepted 13 October 2016

Handling Editor: Mark Rees

Supporting Information

Additional Supporting Information may be found in the online version of this article:

Appendix S1. Methods.

Fig. S1. Dispersal events for pollen (left) and seeds (right) traced for *Prunus mahaleb* trees (white dots).

Fig. S2. Differential contributions of functional groups of frugivores to the short (SDD_{loc}) and long-distance (LDD_{loc}) local seed dispersal events for *Prunus mahaleb*.

Table S1. Summary of neighbourhood area sizes and estimated neighbourhood radius for tree species with different combination of dispersal modes.

Supplementary Material

What is long-distance dispersal? And a taxonomy
of dispersal events

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Sevilla, October 10, 2016

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Key words: ***

Manuscript information: ** Words; ** Chars; ** Pages, * Figures; * Tables.

1 Methods

2 **Species and Study Site.** The tree species we use as a case study to illustrate
3 different types of dispersal events, *Prunus mahaleb* (L.) (Rosaceae), is a shrub or
4 small tree that produces fleshy fruits that are consumed by frugivores, who disperse
5 seeds after regurgitating or defecating them. This species is frequently visited
6 during July to mid-August by small- and medium-sized birds and carnivorous
7 mammals that include fruits in their diets during late summer to winter (Jordano
8 & Schupp, 2000). *P. mahaleb* occurs in a patchy distribution at the regional scale,
9 with relatively isolated populations consisting of dozens to hundreds of trees. Our
10 study population included a total of 196 adult reproductive trees distributed over
11 an area of 26 ha in patches of variable density. Other populations within 20 km
12 exist as scattered patches of 10–150 trees, with some containing $\geq 1,000$ trees. The
13 nearest population is 1.5 km away. Additional information on the study population
14 and description of methodological approaches is reported by Jordano *et al.* (2007)
15 and Garcia *et al.* (2009) and references therein.

16 **Sampling dispersed seeds.** To estimate the relative contribution of each dis-
17 persal vector to the different categories of dispersal events defined in Table 1,
18 we first collected dispersed seeds, following different sampling schemes according
19 to the functional group of dispersal vector. We used this grouping of frugivores
20 giving the difficulties of resolving the identification of scats, pellets and regurgi-
21 tated seeds down to species level just based on visual cues. We differentiated four
22 major frugivore types: large carnivorous mammals (such as foxes, badgers, and
23 stone martens); two species of medium- and large-sized frugivorous birds, mistle
24 thrushes (*T. viscivorus*), and carrion crows (*C. corone*); and a pool of small-sized
25 frugivorous birds, including warblers, redstarts, and robins (Jordano *et al.*, 2007).
26 Seeds were collected in 1997–1999 and 2003–2005. The sampling schemes are
27 described in detail elsewhere (Jordano *et al.*, 2007; Garcia *et al.*, 2009) and include
28 a combination of seed traps and direct sampling of mammal feces along fixed
29 transects. We haphazardly collected 130 samples of mammal feces during the
30 *P. mahaleb* fruit ripening period and recorded their location relative to potential

31 source trees. Overall, we genotyped 167 seeds from 20 fecal samples. Most samples
32 were from red fox (*Vulpes vulpes*) and stone marten (*Martes foina*); some (10
33 samples) were from badger (*Meles meles*) (Jordano *et al.*, 2007).

34 In addition we sampled directly the pellets of large corvids (*Corvus corone*) and
35 from *Turdus viscivorus*, the latter by direct sampling beneath pine trees and scats
36 from seed traps (see Jordano *et al.*, 2007, for details). Finally, a seed sample di-
37 rectly from seed traps included seeds dispersed by small- and medium-sized passer-
38 ines, such as *Phoenicurus ochruros*, *Turdus merula*, *Erithacus rubecula*, *Sylvia com-*
39 *munis*, *Sylvia atricapilla*, etc. (Jordano *et al.*, 2007). The total seed sample thus
40 consisted of seed endocarps collected from the seed traps (mostly small passerines)
41 ($n=465$), mammal scats ($n=167$), and *C. corone* pellets ($n=23$) (see Table 1 in
42 Jordano *et al.*, 2007).

43 **Seed genotyping.** We used material described in Jordano *et al.* (2007), and
44 genotyping methods described in detail in previous work (Godoy & Jordano, 2001;
45 Garcia *et al.*, 2007, 2009). Briefly, we used a set of 10 polymorphic microsatellite
46 markers (simple DNA sequence repeats) (Godoy & Jordano, 2001) to obtain the
47 multilocus genotypes of both of the adult trees (candidate source trees from the
48 study population) and the sample of seed endocarps. Given that all adult trees
49 in the population had a distinct multilocus genotype, an unambiguous assignment
50 of each seed to its source tree could be made. When a full match between the
51 endocarp genotype and any of the adult-tree genotypes in the population was not
52 possible, we assumed that the seed came from another population. To assess the
53 effect of genotyping errors, we reexamined the exclusion of genotypes due to a single
54 locus mismatch, two loci mismatches, etc. At the analysis level, any exclusion of
55 identity between a seed and a potential mother tree based on mismatches of only
56 one or two loci was rechecked. We used GIMLET software (Valière, 2002) to find
57 the matching adult multilocus genotype for each endocarp with eight or more
58 loci successfully typed. Because each seed belonged to one of the four groups of
59 dispersers, we could thus derive the relative contribution of each frugivore group
60 to different classes of seed dispersal events and to seed immigration.

61 **Contribution of dispersal vectors to types of dispersal events.** We con-
62 sidered each dispersed seed as an independent replicate, because each represented
63 a dispersal event from the perspective of plant population genetics, i.e., an in-
64 dependent "arrival" event resulting from the dispersal process mediated by the
65 frugivore.

66 Once the maternal source tree of each individual seed was identified (or its prove-
67 nance from outside the study population determined) we assessed the dispersal
68 distance and grouped the seeds separately as coming from trees located within
69 or outside the population. In addition, for seeds originating from local trees we
70 determined whether dispersal distances were ≥ 45 m to sort out LDD_{loc} dispersal
71 events from SDD_{loc} events. All the events involving immigrant seeds were con-
72 sidered LDD_{ss} by definition, given that the neighborhood size was very reduced
73 (radius= 0.045 km) relative to the geographic limits of the study population (max-
74 imum length for a within-population dispersal event: 1220 m)(Garcia *et al.*, 2009).
75 Along this reasoning, LDD_{neigh} events were considered non-existent in this partic-
76 ular case study given that neighborhood size area was smaller than the population
77 area.

Table S1. Summary of neighborhood area sizes and estimated neighborhood radius for tree species with different combinations of dispersal modes. Data from Nason *et al.* (1998); Smouse *et al.* (2001); Garcia *et al.* (2005, 2007); Dutech *et al.* (2005); Ottewell *et al.* (2012) and present study.

| Species | Pollinator | Seed disperser | Density (ha^{-1}) | Breeding unit (km^2) | Radius (km) |
|--------------------------------|-------------|----------------|-----------------------|--------------------------|-------------|
| <i>Ficus dugandii</i> | Fig wasp | Vertebrates | 0.004 | 631.7 | 14.2 |
| <i>Ficus obtusifolia</i> | Fig wasp | Vertebrates | 0.072 | 105.9 | 5.8 |
| <i>Prunus mahaleb</i> | Bees, flies | Vertebrates | 0.003 | 0.87 | 0.042 |
| <i>Frangula alnus</i> | Bees, flies | Vertebrates | 0.0004 | 0.45 | 0.013 |
| <i>Astrocaryum mexicanum</i> | Beetle | Vertebrates | 1364.0 | 0.011 | 0.06 |
| <i>Calophyllum longifolium</i> | Bees | Vertebrates | 0.28 | 1.241 | 0.629 |
| <i>Platypodium elegans</i> | Bees | Wind | 0.78 | 0.866 | 0.525 |
| <i>Oenocarpus bataua</i> | Wind | Vertebrates | 1.45 | 0.185 | 0.303 |
| <i>Quercus lobata</i> | Wind | Vertebrates | 3.0 | 0.072 | 0.719 |
| <i>Quercus alba</i> | Wind | Vertebrates | 92.8 | 0.0009 | 0.017 |
| <i>Cedrus atlantica</i> | Wind | Wind | 61.7 | 0.151 | 0.22 |
| <i>Fraxinus americana</i> | Wind | Wind | 24.7 | 0.008 | 0.05 |
| <i>Pseudotsuga menziesii</i> | Wind | Wind | 25.0 | 0.078 | 0.158 |

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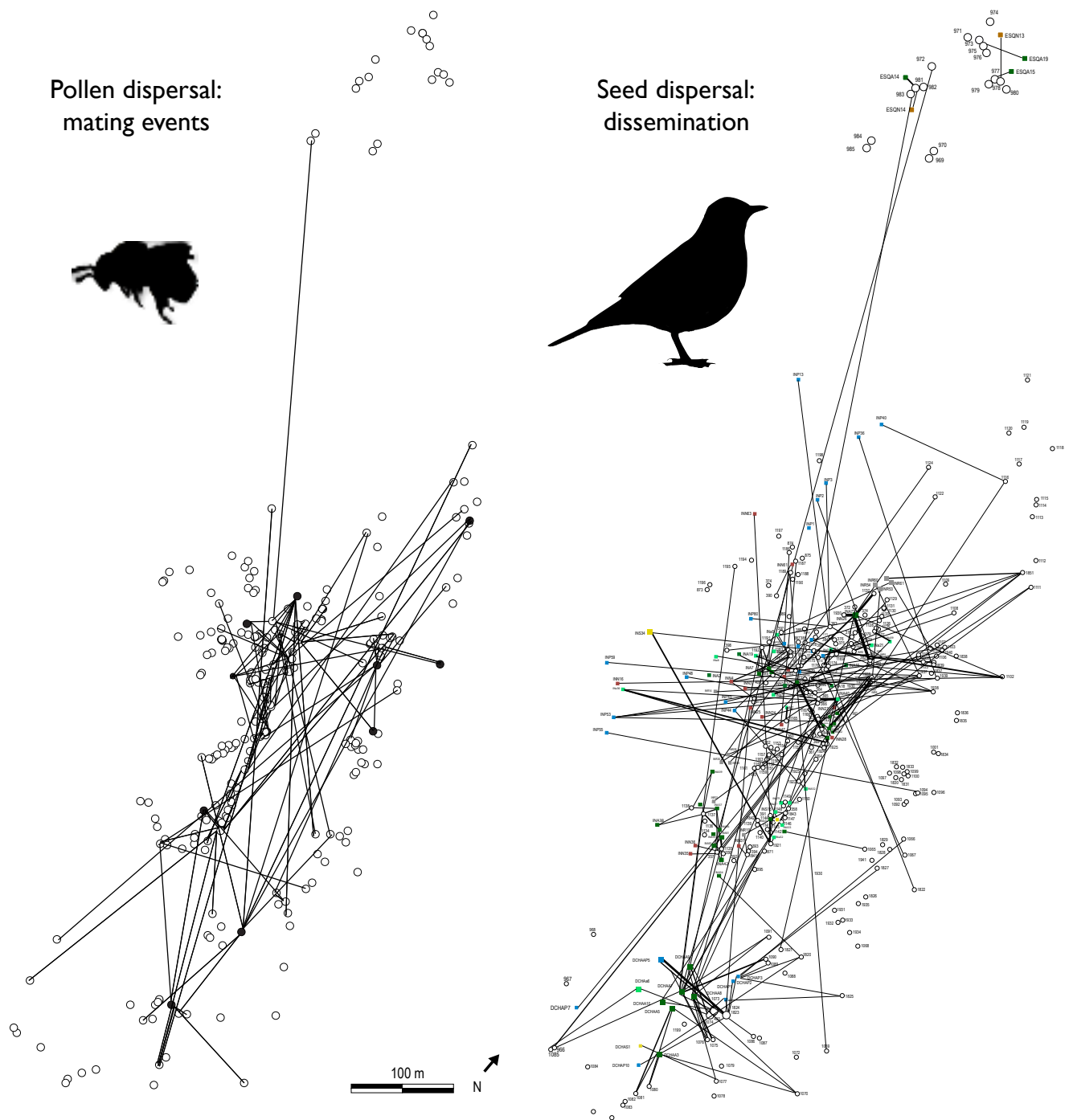


Figure S1. Dispersal events for pollen (left) and seeds (right) traced for *Prunus mahaleb* trees (white dots). All the adult, reproductive, trees in the population are mapped. Lines indicate mating events of pollen dispersal among trees (left) or seed dissemination events from source fruiting trees to seed traps (squares; right). Line thickness is proportional to the number of events recorded.

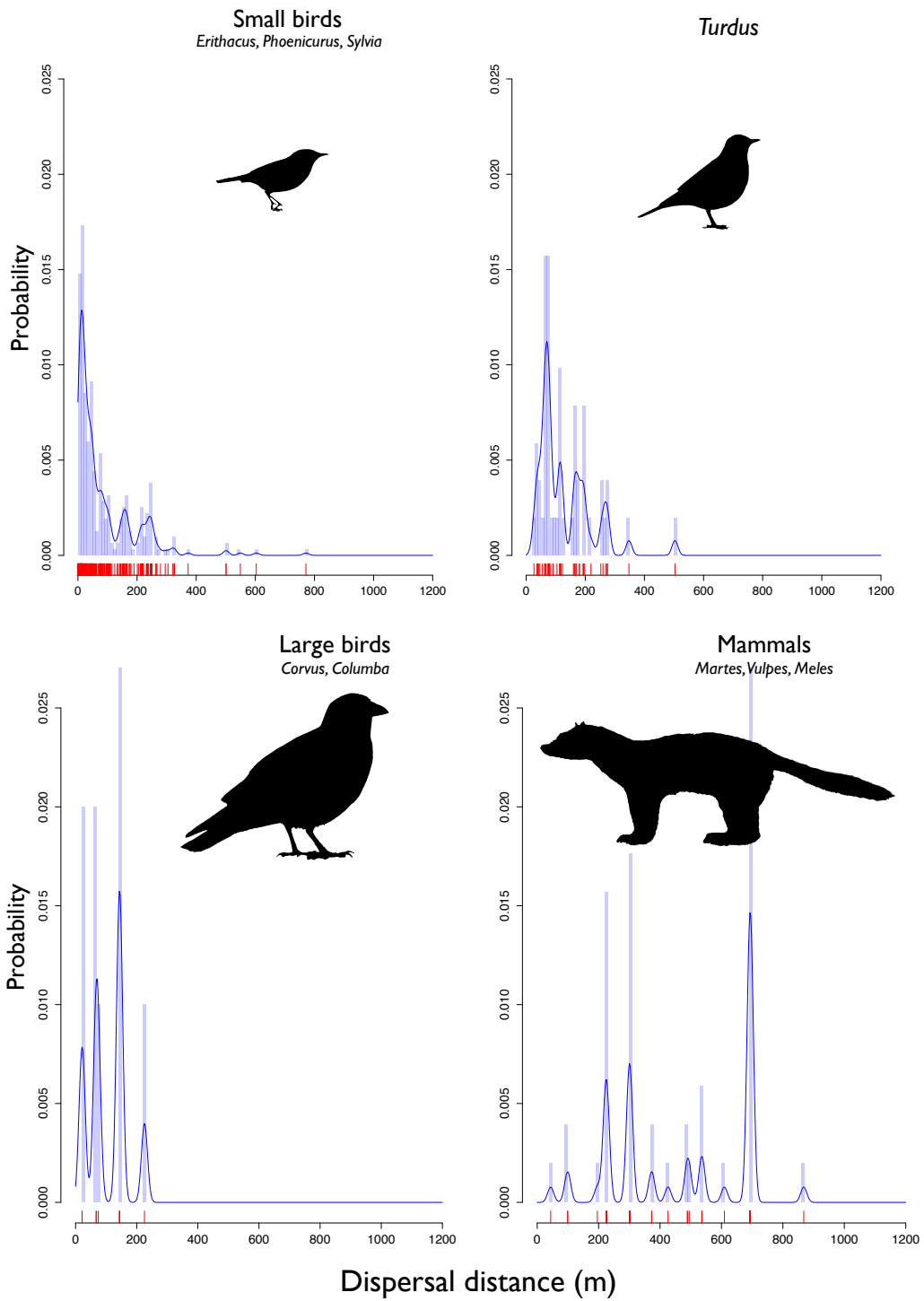


Figure S2. Differential contributions of functional groups of frugivores to the short- (SDD_{loc}) and long-distance (LDD_{loc}) local seed dispersal events for *Prunus mahaleb*.