INVITED REVIEW

Advances in our understanding of mammalian sex-biased dispersal

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Abstract

Sex-biased dispersal is an almost ubiquitous feature of mammalian life history, but the evolutionary causes behind these patterns still require much clarification. A quarter of a century since the publication of seminal papers describing general patterns of sex-biased dispersal in both mammals and birds, we review the advances in our theoretical understanding of the evolutionary causes of sex-biased dispersal, and those in statistical genetics that enable us to test hypotheses and measure dispersal in natural populations. We use mammalian examples to illustrate patterns and proximate causes of sex-biased dispersal, because by far the most data are available and because they exhibit an enormous diversity in terms of dispersal strategy, mating and social systems. Recent studies using molecular markers have helped to confirm that sex-biased dispersal is widespread among mammals and varies widely in direction and intensity, but there is a great need to bridge the gap between genetic information, observational data and theory. A review of mammalian data indicates that the relationship between direction of sex-bias and mating system is not a simple one. The role of social systems emerges as a key factor in determining intensity and direction of dispersal bias, but there is still need for a theoretical framework that can account for the complex interactions between inbreeding avoidance, kin competition and cooperation to explain the impressive diversity of patterns.

Keywords: competition, cooperation, gene flow, inbreeding avoidance, kin selection, mating systems, sex-biased dispersal

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Introduction

Dispersal of individuals from the natal group in order to breed is one of the most important aspects of an organism's life history. Among animals, there are normally large differences between the sexes in terms of distances travelled during dispersal and/or dispersal rates. Sex-biased dispersal (SBD) therefore has important consequences for the genetic makeup of populations (Clobert *et al.* 2001).

In the early 1980s, analyses of general patterns of sex-biased dispersal in both mammals and birds set the framework for subsequent research on the predictions and theory of SBD (Greenwood 1980; Dobson 1982). Greenwood (1980) reviewed mating systems and dispersal strategies and

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found that male-biased dispersal (MBD), and female philopatry were the norm in mammals, whereas birds tended to exhibit female-biased dispersal (FBD) and male philopatry. This observation led Greenwood to hypothesize that direction of dispersal bias was tightly linked to the mating system, with female-defence polygyny, a common breeding system of mammals, leading to male-biased dispersal, and resourcedefence monogamy, more typical of birds, favouring dispersal by females. Since then, this important topic has been the focus of extensive theoretical and empirical work, and many papers have attempted to explain the patterns of SBD. The main evolutionary models invoke inbreeding avoidance (Bengtsson 1978; Packer 1979; Dobson 1982; Waser et al. 1986; Pusey 1987; Clutton-Brock 1989; Wolff 1994; Perrin & Mazalov 2000), or kin selection arguments including local resource competition (LRC, Greenwood 1980; Clarke 1978), local mate competition (LMC, Hamilton 1967; Dobson 1982; Moore & Ali 1984), and more recently, cooperative behaviour among kin including local resource enhancement (LRE, e.g. Perrin & Lehmann 2001; Le Galliard *et al.* 2006). Many variations on these models and proximate explanations for SBD have also been invoked, all of which can be quite bewildering to newcomers to the field.

The study of sex-biased dispersal is inherently multidisciplinary, combining complex evolutionary theory with population dynamics modelling and long-term field studies of animal behaviour. More recently, the field has been augmented by advances in molecular genetic techniques that allow investigation of how individual movements are translated into effective dispersal and gene flow. Our aims in this review are to synthesize the major theoretical models that address the evolutionary causes of dispersal for those working in population genetics, to encourage direct testing of evolutionary hypotheses for SBD, and to provide guidelines for measuring sex-biased dispersal using molecular data. We begin with an appraisal of our theoretical understanding of the evolutionary causes of SBD. We then turn to a review of empirical data of SBD in mammals and comment on proximate explanations and modes of SBD. Finally, we discuss recent advances in statistical genetics that allow us to measure both direction and rate of sex-biased dispersal and gene flow.

Evolutionary explanations for sex-biased dispersal: advances in our theoretical understanding

Dispersal strategies can evolve under a large variety of selective pressures, being opposed by some of them, and favoured by others. Selective pressures that do not favour dispersal are threefold. First, dispersers may incur significant mortality costs when crossing unfavourable habitats to reach suitable patches. In small mammals for example, survival rate can be almost 50% lower for dispersers than for philopatric individuals (Johnson & Gaines 1990). Second, familiarity with natal area becomes important when resource acquisition involves complex interactions with the environment. Immigrants reaching a suitable patch are likely to be at a disadvantage when competing with residents for a limiting resource. Third, the benefits of kin cooperation may provide further competitive advantages to residents, and thereby promote philopatry. Cooperation should help to acquire or defend mates or resources, but also prevent unrelated competitors joining the group (e.g. Le Galliard et al. 2006). This pressure, which is likely to play a role in all social species, might become crucial in societies that use good kin-recognition abilities (as evidenced in several species groups, such as mammals, e.g. house mice, Kareem & Barnard 1986; chimpanzees, Parr & de Waal 1999; birds, Nakagawa & Waas 2004; fish, e.g. migratory charr, Fraser et al. 2004) to build cooperative interactions (Perrin & Lehmann 2001; Lehmann & Perrin 2002).

Selective pressures that *do* favour dispersal are also threefold. The first is set by spatio-temporal variability in *resource availability*. Provided resources available in the new patch are not correlated to those in the natal patch (i.e. when autocorrelation is weak), it pays to leave natal patches when resources are locally depleted, or when there is a risk of extinction (Comins *et al.* 1980). Second, by dispersing, individuals avoid *kin competition* for mates (LMC) or resources (LRC), since leaving natal patches frees these resources for relatives (Hamilton & May 1977; Clarke 1978). The third pressure is set by *inbreeding avoidance*. Dispersal lowers the risk of mating with relatives, and hence the cost of inbreeding depression (Cockburn *et al.* 1985; Motro 1991; Gandon 1999; Perrin & Mazalov 1999).

The evolutionary stable patterns of dispersal result from a balance between the above forces. As these forces are often sex-specific, equilibrium values are likely to differ between males and females. Mating systems are thus a priori expected to affect dispersal patterns. Among the forces opposing dispersal, familiarity with natal area is crucial for the sex responsible for territory acquisition and defence (Greenwood 1980), namely males in resourcedefence systems (many birds and some mammals), but females in female-defence systems (many mammals). In social species, resource acquisition relies on kin cooperation. The building of social bonds among members of one sex is expected to reinforce the pressure against dispersal in this sex, and hence contribute to sex-biased dispersal. Cooperation among related males may help access to territory and mates in resource defence systems (e.g. red grouse, Watson et al. 1994). In female-defence systems, cooperation may occur among related females, for example to rear offspring (e.g. lions, Packer & Pusey 1987; Townsend's voles, Lambin 1994; grey mouse lemur, Radespiel et al. 2001, 2003) but also among related males, for example to acquire and defend females (e.g. lions, Packer & Pusey 1987). Mating systems also play a role in favouring SBD since limiting resources are often sex-specific (Perrin & Mazalov 2000). In female-defence systems for instance, local mate competition in males is likely to exceed local resource competition in females, so that kin competition avoidance is expected to induce male-biased dispersal (Perrin & Mazalov 2000).

Inbreeding avoidance should also contribute to sex-biased dispersal (Bengtsson 1978; Packer 1979; Dobson 1982; Waser et al. 1986; Pusey 1987; Clutton-Brock 1989; Wolff 1994; Perrin & Mazalov 2000). If members of one sex disperse only to avoid inbreeding, there is no risk to the other sex and therefore theory predicts that one sex remains strictly philopatric, while the other sex (arbitrarily male or female) disperses (Gandon 1999; Perrin & Mazalov 1999). Though such a bistable equilibrium is prevented when kin competition interacts with inbreeding (unless inbreeding load is very high; Gandon 1999; Perrin & Mazalov 2000), inbreeding still makes the equilibrium more sensitive to sex

asymmetries in local competition and thereby contributes significantly to SBD (Perrin & Goudet 2001). Furthermore, inbreeding may also induce intrinsic directional biases. In polygynous species, females pay a higher cost by inbreeding since they have higher reproductive investment than males, and hence are expected to disperse more than males (Waser et al. 1986). This prediction is reversed if mate choice is allowed. For inbreeding load exceeding a threshold value (set by relatedness), females should prefer immigrant males, and hence boost male dispersal (Lehmann & Perrin 2003). At low inbreeding load by contrast, kin selection should induce females to prefer male relatives, and hence boost male philopatry (Lehmann & Perrin 2003). The level of inbreeding load thus appears an important issue in this context. Analytical models usually assume constant and fixed inbreeding load; however, individual-based simulations by Guillaume & Perrin (2006) show that if it is allowed to evolve, the contribution of inbreeding in driving SBD is small. Owing to strong purge and low genomic mutation rate (U≈0.03 per generation, assumed by Guillaume & Perrin 2006), large-effect deleterious mutations do not contribute significantly to dispersal pressure. Mildly deleterious mutations have higher mutation rates ($\approx 0.1 < U < 1$) but only contribute dispersal pressure if strongly recessive. Altogether, simulations show that under biologically plausible parameter values, evolutionary stable dispersal rate is increased by only one-third over the value expected from kin competition avoidance, and that inbreeding depression cannot build up at levels high enough to induce bistable sex-asymmetries in dispersal.

These conclusions might still be conservative, for example in species that have evolved alternative ways to avoid inbreeding, such as kin recognition (Lehmann & Perrin 2002; as demonstrated for example in house mice, Manning *et al.* 1992). On the one hand, kin recognition increases the potential for altruism and cooperation, promoting philopatry (with possible bias for the sex in which resource acquisition crucially depends on social bonds). On the other hand, it avoids the potential for close inbreeding, and indirectly selects for dispersal in partners of the sex that less crucially depends on social bonds (Lehmann & Perrin 2003). Such conflicting pressures are likely to induce a strong sex-bias in dispersal (Perrin & Goudet 2001).

The effects of complex social structure on dispersal deserve further formalization. Assumptions underlying analytical models typically lack a great deal of realism (Travis & French 2000). In particular, condition-dependence in dispersal strategies, documented in many empirical studies (e.g. Dieckmann *et al.* 1999; De Fraipont *et al.* 2000; Bowler & Benton 2005), is rarely incorporated. Efforts should be invested in this area, since proximate conditions determining the timing and mode of dispersal (e.g. density dependence, patterns of local kinship, aggressiveness and eviction, etc.) have the potential to shed light on its ultimate causes.

Patterns of sex-biased dispersal

While sex-biased dispersal is an almost ubiquitous feature of mammalian life history, there is enormous diversity in terms of the mode of dispersal and in the proximate causes that have been invoked to explain it (Tables 1 and 2). Even in species that are traditionally labelled philopatric (e.g. the banner-tailed kangaroo rat, Winters & Waser 2003), or those in which both sexes disperse (e.g. guanacos, Sarno et al. 2003), there appear to be differences between the sexes in terms of dispersal distance and rate. Dispersal rate is male-biased in the great majority of mammal species (Greenwood 1980; see Table 1 for examples) and males also appear to disperse greater distances than females (Waser 1985). It is important to note that a complete bias, where one sex remains completely philopatric while all individuals of the other sex disperse, is quite rare (e.g. white sifaka, Richard et al. 1993; Bechstein's bat, Kerth et al. 2002; ringtailed lemur, Sussman 1992; Barbary macaque, Pusey & Packer 1987). In most species, some dispersal also occurs in the typically philopatric sex, even though the magnitude of the bias may be strong. This distinction is important for understanding the evolutionary and proximate causes of sex-biased dispersal, since as mentioned above, theory predicts that if inbreeding avoidance is the only evolutionary cause of SBD, one sex should remain completely philopatric.

Although a few empirical studies have demonstrated a difference in *dispersal distance* between the sexes (e.g. opposums, Ji *et al.* 2001; otters, Blundell *et al.* 2002; shrews, Fontanillas *et al.* 2004), information is currently quite limited. The distribution of dispersal distances should be very informative for understanding evolutionary causes of dispersal (Murrell *et al.* 2002; Rousset & Gandon 2002) because the reasons for long-distance and short-distance dispersal are likely to be very different (Ronce *et al.* 2001). Short distance dispersal is probably sufficient for avoiding inbreeding or kin competition, whereas long distance dispersal might function to colonize a new territory or escape crowding (Perrin & Goudet 2001). Dispersal distance is therefore an important avenue for future research.

The *timing* of dispersal might also provide interesting clues to ultimate causes. Although it is often assumed that individuals undergo natal dispersal as juveniles (Dobson 1982), the timing of dispersal can be quite variable, which highlights the importance of understanding the species' life history for genetic analyses (see 'Measuring sex-biased dispersal'). Belding's ground squirrel males, for example, disperse up to 2 years before reaching sexual maturity (Smale et al. 1997), whereas male forked-marked lemurs wait 3 years after puberty before dispersing (Schülke 2003). Many species undergo secondary dispersal later in life, which is important to distinguish from natal dispersal,

Table 1 Examples of mammal species with male-biased dispersal

Taxonomy	Species	Common name	Mating system†	Social unit‡	Evolutionary causes§	Proximate causes¶	Hypothesis invoked for SBD**	Ref.
Primates								
Lemuridae	Propethicus verreauxi	White sifaka	Prom	Sm-MMU	LMC, IA	PD, EV, IhR-F	Both LMC and IA drive natal and secondary MBD. Relative importance of each determined by Mage, mating history and local demography	1,2
	Lemur catta	Ring-tailed lemur	Prom	Lg-MMU	LMC, IA, COOP-M	PD, IhR-F, FC	LMC, FC and IA drive MBD. M cooperate during dispersal. IhR-F promotes F philopatry	3,4
	Microcebus berthae	Pygmy mouse lemur	Prom	Sol	LMC		High LMC drives MBD	5
	Microcebus murinus	Gray mouse lemur	Prom	Sol	LMC, IA COOP-F, LRE, IA?		Competition (M) and cooperation (F) potentially important. IA needs further investigation	6,7
	Eulemur fulvus rufus	Red-fronted lemur	Prom	Sm-MMU	LMC, COOP- F, LRD-F		Cooperation among related F to defend resources important determinant of F philopatry	8
	Mirza coquereli	Coquerel's dwarf lemur	Polyg	Sol	LMC		Benefits to F from familiarity with safe sleeping sites promotes philopatry. M able to encounter more potential mates by dispersal	9
	Phaner furcifer	Fork- marked lemur	Monog	M-F		EV, IhR-F	IhR-F important factor in F philopatry. M tolerated in group until adult then evicted. Very high cost to dispersal in terms of acceptance into new group	10
Cebidae	Cebus apella	Brown or tufted capuchin	Prom	Sm-MMU		EV	Typically MBD during aggressive takeovers but F disperse (in parallel) when LRC is high	11,12
	Cebus capucinus	White-faced capuchin	Prom	Lg-MMU	LMC	EV, EGA, PD	Attraction to dispersing group mates and other groups important in natal dispersal. Dispersal coalitions important for successful group takeover. Eviction of adult M after takeovers related to secondary transfer	13,14,1
	Cebus olivaceus	Wedge- capped capuchin	Polyg	Lg-MMU or OMU	LMC	EV	High LMC drives MBD. M evicted after group takeover	11
	Saimiri sciureus	Common squirrel monkey	Prom	Lg-MMU	LMC	EV	High LMC drives MBD. M evicted after group takeover	11
Cercopithecidae	Macaca fuscata	Japanese macaque	Polyg	Lg-MMU	IA	PD, EV, EGA	Voluntary dispersal of resident M may be in response to maturing daughters, but also attributed to overall decline in mating success after several years in group	16
	Macaca sylvanus	Barbary macaque	Prom	Lg-MMU	IA		IA invoked	16
	Lophocebus albigena	Gray- cheeked mangabey	Polyg	Lg-MMU		EGA	M attracted to other social units with oestrus F	17
	Papio anubis	Olive baboon	Polyg	Lg-MMU	IA, LMC	EV	IA invoked to explain natal dispersal. Secondary transfer more likely to relate to reproductive enhancement. LMC high. M evicted	18,19

Table 1 Continued

Taxonomy	Species	Common name	Mating system†	Social unit‡	Evolutionary causes§	Proximate causes¶	Hypothesis invoked for SBD**	Ref.
	Papio cynocephalus	Yellow baboon	Polyg	Lg-MMU	IA, LMC	EV, EGA	IA important. High reproductive costs for M to remaining in natal group. M evicted after losing fights with other males in group	16,20
	Presbytis entellus	Gray langur	Prom	Lg-MMU or OMU		EV	Eviction of maturing M drives dispersal	19,21,22
Hylobatidae	Hylobates lar	Common gibbon	Monog	M-F	LMC, COOP, IA		Highly cooperative species. No cost to dispersal in terms of acceptance into new group. IA, obtaining a mate and obtaining resources potentially important	23
Carnivora								
Hyaenidae	Crocuta crocuta	Spotted hyena	Polyg/ prom	Sm-MMU		EGA, IhR-F, FC	M dispersal related to attraction of unrelated F in neighbouring groups and F mate choice. F occasionally disperse to avoid LRC	24,25
Felidae	Panthera leo	Lion	Polyg	Sm-MMU	IA, COOP, LRE	PD, EV	IA potentially important. M-M competition and eviction during takeovers likely proximate cause. Dispersal coalitions important for successful takeover	19
Chiroptera							1	
Vespertilionidae	Myotis bechsteinii	Bechstein's bat	Prom		IA, LMC, COOP-F, LRE		IA invoked to explain MBD because F completely philopatric and unlikely to cope with inbreeding depression	26
	Nyctalus noctula	Noctule bat	Polyg	Lg-OMU	LMC, LRD		Territory defence by males leads to strong LMC and variance in M reproductive success which drives MBD	27
Rodentia							1	
Sciuridae	Spermophilus sp.	Ground squirrels	Polyg/ prom	Lg-MMU	COOP-F, LRE?	PD, EGA	Cooperation and LRE promotes F philopatry. M disperse in coalitions and attracted by strange extra group F	28,29,30
Cricetidae	Microtus townsendii	Townsend's vole	Monog /polyg*	Sm-MMU or OMU	LRE, COOP-F		Combination of cooperation between related F and LRE promotes F philopatry	31
Cetacea								
Delphinidae	Tursiops aduncus	Bottlenose dolphins	Prom	Lg-MMU	LMC, COOP- M,F	EV	LMC and aggression between M probably drive male dispersal	32

[†]Polyg, polygynous (males mate with more than one female); Monog, monogamous (males and females have only one mate at a time); Prom, promiscuous (both males and females mate successfully with different partners).

[‡]Sm, small; Lg, large; MMŪ, multimale unit; OMU, one-male unit; Sol, solitary or nongregarious; M-F, male-female pair.

[§]LMC, local mate competition; LRC, local resource competition; IA, inbreeding avoidance; COOP, cooperation; LRD, local resource defence, LRE, local resource enhancement. ¶PD, parallel dispersals (coalitions); EV, eviction; Ihr, inheritance of rank; FC, female mate choice; EGA, extra-group attraction.

^{**}M, males; F, females.

Ref, references: (1) Richard et al. 1993, (2) Lawler et al. 2003, (3) Pereira & Weiss 1991, (4) Sussman 1992, (5) Dammhahn & Kappeler 2005, (6) Radespiel et al. 2001, (7) Radespiel et al. 2003, (8) Wimmer & Kappeler 2002, (9) Kappeler et al. 2002, (10) Schülke 2003, (11) Robinson & Janson 1987, (12) Izar 2004, (13) Fedigan & Jack 2004, (14) Jack & Fedigan 2004a, (15) Jack & Fedigan 2004b, (16) Melnick & Pearl 1987, (17) Olupot & Waser 2001, (18) Packer 1979, (19) Pusey & Packer 1987, (20) Alberts & Altmann 1995, (21) Hrdy 1977, (22) Struhsaker & Leland 1987, (23) Brockelman et al. 1998, (24) Holekamp & Smale 1995, (25) Smale et al. 1997, (26) Kerth et al. 2002, (27) Petit et al. 2001, (28) Nunes et al. 1997, (29) Smale et al. 1997, (30) Devillard et al. 2004, (31) Lambin 1994, (32) Möller & Beheregaray 2004.

^{*}depending on season.

Table 2 Mammal species with female-biased dispersal

Taxonomy	Species	Common name	Mating system†	Social unit	Evolutionary causes	Proximate causes‡	Hypothesis for SBD	Ref.
Eutheria Primates								
Lemuridae	Hapalemur griseus alaotrensis	Alaotran gentle lemur	Polyg (RDP)	Sm-MMU	LRD-M	EV	Benefits to M from philopatry in acquiring and defending territory. F evicted by other F	33
Atelidae	Lagothrix lagotricha	Woolly monkey	Prom?	Lg-MMU		EGA, FC	Home ranges overlapping. Interactions between groups common, hence familiarity with other groups important. F face low aggression if copulate early on arrival in new group	34
	Ateles sp*	Spider monkey	Polyg/prom	Lg-MMU	LRC	EGA, SR-F	Strong LRC promotes FBD. Sex-ratio allocation in favour of females varies with habitat. F accepted into new group easily	35
	Brachyteles arachnoides	Muriqui	Prom	Lg-MMU		FC, EGA	F transfer directly without aggression to new group during intergroup encounters	11,36
	Alouatta seniculus	Red howler monkey	Polyg	Sm-MMU or OMU	LRC, COOP	PD, EV	LRC most important factor. F reproduction in natal group limited by other F. IA unlikely since M also transfer and some F stay in natal group, also M tenure < F age at maturity. F reproductive success increased by cooperation	37,38
	Alouatta palliata	Mantled howler monkey	Polyg	Lg-MMU	LRC		LRC most important factor. F reproduction in natal group NOT limited by other F. M only disperse when evicted. IA unlikely as for <i>A. seniculus</i>	37
Cercopithecidae	Papio hamadryas	Hamadryas baboon	Polyg	Sm-OMU	COOP, IA?	EV, ABD	Philopatric M benefit from cooperation with male kin in defending F. Abduction of F by other groups also important	19,39,40,4
	Colobus badius rufomitratus	Red colobus	Polyand	Lg-MMU		AGG	Avoidance of aggression/infanticide from extra- group M when resident M unable to protect	19,22,42
	Presbytis thomasi	Thomas langurs	Polyg	Sm-OMU	IA?		IA possible as M tenure < F age at maturity. LRC low	43
Hominidae	Gorilla gorilla beringei	Mountain gorilla	Polyg	Sm-MMU or OMU	IA	TO, AGG	IA potentially important. Avoidance of aggression/ infanticide important for timing of dispersal	19,44,45
	Gorilla gorilla gorilla	Western lowland gorilla	Polyg	Sm-OMU	LRC, IA	AGG, PD-F	IA potentially important. Indirect evidence for aggression avoidance. F transfer to groups with fewer F, consistent with LRC	45,46,47
	Pan troglodytes	Chimpanzee	Prom	Lg-MMU	LRC, IA	EGA	IA often invoked but unlikely to be sole cause. Potentially combination of LRC and IA important. F attracted to high-ranking M from other groups	18,19,48
	Pan paniscus Homo sapiens**	Bonobo Human	Prom Monog/ (polyg/ prom)	Lg-MMU M-F (Sm- OMU)	LRE?	EGA	F attracted to high-ranking M from other groups LRE potential factor in patrilocal societies where men inherit land and/or herds for example	48 49

Table 2 Continued

Taxonomy	Species	Common name	Mating system†	Social unit	Evolutionary causes	Proximate causes‡	Hypothesis for SBD	Ref.
Carnivora								
Procyonidae	Potos flavus	Kinkajou	Polyg/prom	Sol	LRD, COOP	IhR-M	Cooperation between M within group, inheritance of rank and LRD potential reasons for M philopatry	50
Canidae	Lycaon pictus	African wild dog	Monog (soc)	Sm-MMU	LRC, LRE, IA, COOP	PD, EV	Often considered an FBD species but male dispersal important in some populations. Both sexes may disperse to avoid LRC. Avoidance of inbreeding even when given opportunity supports IA	51,52,53
Chiroptera Emballonuridae Insectivora	Saccopteryx bilineata	White-lined bat	Polyg (RDP)	Lg-OMU	LRD		Philopatric males defend territories for breeding (LRD)	54
Soricidae	Crocidura russula	Greater white- toothed shrew	Monog (soc)	M-F	LRC, LRD		LRC most likely explanation for FBD. Intensity of FBD dependant on spatial scale	55
Rodentia								
Cricetidae	Peromyscus californicus	California mouse	Monog	M-F	IA		IA invoked	56
Erthizontidae	Erethizon dorsatum	North American porcupine	Polyg (RDP)	Sm-OMU	IA, LRD		IA invoked because F age at first conception < M tenure. Dominant males defend breeding territories, hence benefit from philopatry	57
Perissodactyla		1 1					1 1 3	
Equidae	Equus caballus	Horse	Polyg	Lg-OMU	IA	EGA	Evidence that IA main function of FBD. F dispersal is nonrandom. F prefer to move to groups with familiar F (otherwise suffer aggression from native mares) but strange M	58
Methatheria								
Diprotodontia								
Vombatidae	Vombatus ursinus	Common wombat	Polyg***	Sol	LRD, COOP	ТВ	LRD and cooperative behaviour by related M in close burrows potentially explains male philopatry	59,60

Legend as for Table 4 except:

[†]RDP, resource defence polygyny; Polyand, polyandrous (females mate with more than one male).

[‡]ABD abduction, SR sex-ratio allocation (a female-biased sex ratio is predicted to favour FBD), TB territory bequeathal to offspring by breeding females.

Ref, references: (33) Mutschler et al. 2000, (34) Nishimura 2003, (35) McFarland Symington 1987, (36) Strier & Ziegler 2000, (37) Crockett & Eisenberg 1987, (38) Pope 2000, (39) Kummer 1968, (40) Stammbach 1987, (41) Hammond et al. 2006, (42) Marsh 1979, (43) Sterck 1997, 1998, (44) Harcourt et al. 1976, (45) Stokes et al. 2003, (46) Stewart & Harcourt 1987, (47) Bradley et al. 2004, (48) Nishida & Hasegawa 1987, (49) Wilkins & Marlowe 2006 (review, see text for examples), (50) Kays et al. 2000, (51) Frame & Frame 1976, (52) Malcolm & Marten 1982, (53) McNutt 1996, (54) Bradbury & Vehrencamp 1976, 1977, (55) Favre et al. 1997, (56) Ribble 1992, (57) Sweitzer & Berger 1998, (58) Monard & Duncan 1996, (59) Banks et al. 2002, (60) Skerratt et al. 2004. *Ateles sp. A. belzebuth, A. fusciceps, A. geoffroyi, A. paniscus. Note these species are 'potentially polygynous' but females are also promiscuous.

^{**}Intraspecific variation is found in humans in terms of sex-biased dispersal, mating and social system. See main text for more details.

^{***}In this case both males and females mate successfully with different partners, but males have higher variance in reproductive success (Ref. 59).

since it is likely to be motivated by very different reasons. For example, there is good evidence that close inbreeding avoidance is an important driving force behind natal male dispersal in olive baboons, but secondary dispersal (by about a quarter of all males) is more likely to result from aggressive eviction, which seems to be a more important determinant of secondary transfer than natal dispersal (Packer 1979).

Proximate causes of sex-biased dispersal

Eviction, attraction to members of other groups, and benefits of group dispersal are among the most important proximate explanations for sex-biased dispersal (Tables 1 and 2). Whereas emigration seems voluntary in most species, forceful eviction has been documented in some cases, and as mentioned above, is a potentially important reason for secondary transfer. Eviction is often the result of aggression from adult males in response to increasing maturity of male adolescents (e.g. howler monkey, grey langur, gibbon, Table 1) but is also a consequence of group takeover (e.g. white-faced capuchin, Jack & Fedigan 2004; Table 1). While aggressiveness leading to eviction is more common among males, it has also been documented among females, particularly if low-ranking (e.g. chimpanzees, Pusey & Packer 1987; Table 2, spotted hyenas, Holekamp & Smale 1995; Smale *et al.* 1997; Table 1). While intrasex eviction points to competition for mates (in males) or resources (in females), intersex eviction (e.g. in white-footed mice, Wolff 1992; several macaque species, Packer & Pusey 1987) invokes inbreeding avoidance as the most likely ultimate cause.

Attraction to sexual partners outside the natal group is a potentially important trigger of dispersal, which is independent of social structure. Extra-group attraction has been shown to drive emigration in several group-living primate species such as chimpanzees, macaques, mangabeys, vervets and guenons (Pusey & Packer 1987; Olupot & Waser 2001; Jack & Fedigan 2004a; Tables 1 and 2). In this case, the timing of dispersal generally coincides with the mating season. Emigration occurs at sexual maturity and clusters around the peak breeding season, suggesting male sexual attraction to extra-group females (Jack & Fedigan 2004a). Olive baboon males, for example, are attracted to oestrus females in neighbouring groups and females may solicit the attention of potential dispersers (Packer 1979). In grey-cheeked mangabeys, spatio-temporal availability of oestrus females is a major proximate factor influencing transfer, and males show a greater tendency to move into new groups that contain higher numbers of oestrus females than their previous group (Olupot & Waser 2001). Generally though, males are not necessarily attracted to groups with many females but rather to groups containing unfamiliar females (Pusey & Packer 1987).

If there is cooperation between relatives (for example in acquisition of resources or in raising young), there are clear benefits to individuals by remaining philopatric. Under these circumstances, cooperation is likely to oppose dispersal. However, this cost can be circumvented if individuals disperse as a group. Parallel dispersal maintains coalitions and familiar relationships for dispersing individuals. Although most mammals tend to disperse individually, parallel dispersal is known in some species (Tables 1 and 2). Dispersing in a coalition may be of particular benefit to immature males in aiding initial entry into a foreign group. In lions for example, coalitions of related males from the same cohort leave the natal group together (Pusey & Packer 1987). Coalitions are more successful at taking over new prides and there are clearly inclusive fitness benefits to subordinate males by dispersing with dominant kin (Pusey & Packer 1987). In white-faced capuchins, 82% of male transfers take place in the company of older maternal siblings or members of the same age cohort, which are likely to be close relatives (Jack & Fedigan 2004a). However, group dispersal might sometimes occur simply because the limited duration of female oestrus influences the period when transfer occurs (e.g. macaques, Melnick & Pearl 1987).

Is sex-biased dispersal linked to social complexity?

An increase in the magnitude of sex-biased dispersal with increased social complexity (i.e. the degree of sociality and communicative complexity) is expected on theoretical grounds, from the interaction between the benefits of kin cooperation and the costs of inbreeding (Perrin & Goudet 2001). Greenwood (1980) noticed that the degree of sociality influences the magnitude of the sex bias in dispersal, and sex differences are indeed particularly striking among long-lived, highly social, polygynous mammals (Pusey 1987; Smale et al. 1997). Moreover, there is also a close link between sex-biased dispersal and social organization in birds (especially communal breeders, e.g. Florida scrub jay, Greenwood & Harvey 1982). In line with prediction, Devillard et al. (2004) found an increase in the magnitude of male-biased dispersal with increasing social complexity in polygynous ground dwelling sciurids (ground squirrels, marmots and prairie dogs). The increased bias, however, was determined solely by an increased male dispersal, and not, as also expected, by a concomitant decreased female dispersal (Perrin & Goudet 2001). Unfortunately, levels of polygyny and sociality are linked, so the correlation between male dispersal rate and social complexity is probably confounded by a mating system effect (Devillard et al. 2004). This important question therefore warrants investigation in other species groups to address the effect of mating system and to establish whether this is a phylogenetically independent pattern.

Exceptions to the rule: female-biased dispersal in mammals

Although female-biased dispersal is rare in mammals (Greenwood 1980), it is found in phylogenetically diverse taxonomic groups, with varying social structures and mating systems, suggesting a wide range of evolutionary and proximate explanations. As is often the case in evolutionary biology, studying the exceptions to a rule can provide unique insights into more general explanations, and we therefore address the patterns and causes of female-biased dispersal in some detail. In Table 2 we provide a summary of all mammal species with FBD for which there is good data available. Inspection of Tables 1 and 2 together reveals four general points.

First, in some cases, several closely related species all exhibit FBD (e.g. Atelidae, Hominidae, Table 2). More often though, both FBD and MBD can be found in groups of closely related species with apparently similar life histories, and in some cases there is phylogenetic evidence that FBD has evolved independently from the ancestral state of MBD (e.g. hamadryas baboons, Hammond et al. 2006). Second, although mating system is often considered to be a good predictor of direction of SBD, dispersal is male-biased in several monogamous species (Table 1), and several polygynous species have predominantly female dispersal (Table 2), suggesting that the hypothesis of Greenwood (1980) is too simplistic. Third, several species that live in one male units (OMUs), which are known to have high local mate competition, exhibit FBD (e.g. hamadryas baboons, gorillas, horses). These first three points illustrate the enormous diversity in terms of taxonomy, mating system, social unit and the direction of sex-biased dispersal. Finally, there appears to be an overrepresentation of primates with FBD compared to other mammal groups, but it is unclear whether this reflects the disproportionate investment in field studies of these species (highlighted by the high representation of primate species in both Tables 1 and 2), and good quality data is needed from other taxonomic groups to investigate this.

In terms of evolutionary explanations for female-biased dispersal, FBD makes intuitive sense in species with resource defence systems, where males take the leading role in acquisition and defence of resources and there are considerable benefits to males by remaining philopatric. This strategy is quite common in pair-breeding birds (Greenwood 1980), and the same logic could account for FBD in pair-breeding mammals, such as the greater white-toothed shrew, in which males take a major role in territory acquisition and defence (Favre *et al.* 1997; Bouteiller-Reuter & Perrin 2005). However, resource defence may also account for FBD in some polygynous mammals (in which case the mating system is termed 'resource defence polygyny'), such as the white-lined bat, Alaotran gentle

lemur and North American porcupine (Table 2). In FBD species with high local mate competition, both inbreeding avoidance and cooperation certainly play a role. First, when dominant males have long tenure in their social groups (be they OMUs or multimale units, MMUs, Tables 1 and 2), their daughters disperse on approaching sexual maturity to avoid mating with their potential father (e.g. gorillas, hamadryas baboons, chimpanzees, howler monkeys, African wild dogs, Clutton-Brock 1989). Second (and not exclusively), males may benefit from kin cooperation and form coalitions to prevent extra-group males gaining access to females. In both OMU and MMU species, the advantages to an individual male from kin-cooperation may sometimes outweigh those of dispersal and promote male philopatry. Cooperation among male kin for territory acquisition and mate attraction might be important in mammal species that form 'dispersed male networks' to defend females (e.g. western gorillas, Bradley et al. 2004; possibly hamadryas baboons, Hammond et al. 2006). Finally, local resource competition has been invoked to explain several cases of FBD, even in polygynous species where LMC is expected to be greater than LRC (Table 2). This is highlighted by spider monkeys, in which female dispersal is driven by a combination of sex-ratio bias in favour of females and LRC between females, which are directly related to habitat pressures (McFarland Symington 1987).

Several proximate causes are also important to consider when attempting to explain female-biased dispersal. Extragroup attraction, aggression avoidance, eviction and benefits of parallel dispersal are important determinants of FBD as well as MBD (Tables 1 and 2). Another important consideration is that the cost of immigration might be less for females than for males, since they are more readily accepted into a new group (e.g. spider monkeys, muriquis, hamadryas baboons, Table 2), particularly if they copulate early on arrival into their new group (e.g. woolly monkey, Table 2). An extra explanation that is probably specific to females is that of abduction by males from outside the group during aggressive encounters (e.g. hamadryas baboons, Table 2). Post-weaning territory bequeathal to offspring has been invoked to explain female dispersal in species where juveniles need to acquire a key resource such as a burrow to survive. Bequeathal involves active, strategic dispersal by breeding females and appears to be condition-dependent (Price & Boutin 1993). Since adult females may be able to obtain this resource more easily than juveniles, territory bequeathal may increase the female's fitness. However, most of the species in which bequeathal has been observed have male-biased dispersal (e.g. red squirrels, Price & Boutin 1993; Berteaux & Boutin 2000, hairy-nosed wombat, Johnson & Crossman 1991; Columbian ground squirrels, Harris & Murie 1984, except common wombat, Banks et al. 2002; which has FBD, Table 2), so this cannot be taken as a general explanation for FBD.

Finally, it has also been argued that females transfer to avoid infanticidal males (Marsh 1979; Stokes *et al.* 2003), but there appears to be very little direct evidence supporting prevalence of infanticide in FBD species (except for red colobus monkeys, mountain gorillas, and Thomas's langurs, Table 2). We would argue that it seems even more risky a strategy to attempt to immigrate into a new group with an infant who has not been sired by a resident male, or to emigrate following the death of an infant as a direct result of a male takeover (e.g. Stokes *et al.* 2003), and therefore this explanation seems an unlikely general explanation for FBD.

What about humans?

Far too often, there is a gap between studies of dispersal patterns in humans and those of other mammals, while in fact humans provide an important example for the occurrence of intraspecific variation in sex-biased dispersal (e.g. Hamilton *et al.* 2005a), and highlight the importance of geographical scale on dispersal patterns. We therefore believe a discussion of human patterns of sex-biased dispersal is justified here.

The conflicting results from the many papers describing sex-biased dispersal patterns in humans can be rather bewildering. The first global comparison of mitochondrial DNA (mtDNA) and Y chromosome patterns indicated a much higher migration rate for females than for males (Seielstad et al. 1998). By contrast, a more recent study, also on a global scale, found no evidence for sex-biased dispersal (Wilder et al. 2004), although reasons for this discrepancy could be methodological differences such as sampling strategy (the samples used in the Wilder study came from sparsely distributed populations). At a regional level, patterns can usually be explained by cultural differences or known historical events. Consistent with Seilestad et al. (1998), the majority of regional-scale studies have reported female-biased dispersal, which is typically associated with patrilocality (Perez-Lazaun et al. 1999; Oota et al. 2001; Bolnick et al. 2006). Patrilocality and female-biased dispersal is much more common in pastoral communities, where males who inherit their father's land and herds tend to be more successful in attracting a wife (Wilkins & Marlowe 2006), than in hunter-gatherer societies, where resource accumulation is less important (Destro-Bisol et al. 2004; Wood et al. 2005). One interesting related point is that a shift to patrilocal societies and female-biased dispersal may have occurred since the agricultural revolution, which started approximately 10 000 years ago, since modern huntergatherers (which are often seen as models for pre-agricultural societies) are characterized by similar patterns of male and female dispersal or occasionally male-biased dispersal (Wilkins & Marlowe 2006). The relationship between patrilocality and female-biased dispersal is however, not apparent in highly endogamous patrilocal populations from the Indian subcontinent, which questions the universality of this hypothesis (Kumar *et al.* 2006). Male-biased dispersal has been documented in connection to matrilocality (Bolnick *et al.* 2006), which is rare in human societies compared to patrilocality, and immigration seems to be much less regulated in matrilocal compared to patrilocal populations (Hamilton *et al.* 2005a). MBD tends to be more associated with historical events than with cultural practices, for example the introgression of European Y chromosomes, but not mtDNA, in the Americas post 1492 (Mesa *et al.* 2000; Seielstad 2000; Bolnick *et al.* 2006; see Bosch *et al.* 2003; Al-Zahery *et al.* 2003 for examples from other regions).

An important outcome from recent studies of human dispersal is that patterns seen at the local scale may not reflect those at a larger geographical scale (Kumar *et al.* 2006), and that large geographical scale patterns are likely to be representative of long-term demographic processes, whereas local-scale patterns detect events in the recent history of that region (Wilkins & Marlowe 2006). This could have important implications for studies of natural populations that wish to determine if the relative rates of male and female migration have changed over time, for example in response to climatic events, habitat fragmentation or anthropomorphic factors.

Measuring sex-biased dispersal

Our ability to detect, quantify and interpret sex-biased dispersal will depend on the choice of appropriate methods to study its occurrence in natural populations. Ideally, a combination of both field observations and genetic methods is required to obtain a comprehensive picture of dispersal patterns and to make inferences about the proximate and ultimate causes for SBD. Field data provide valuable insights into the species' social and reproductive behaviour, which are essential to better understand the potential reasons for SBD, but they do not always allow quantification of how dispersal translates into gene flow, since effective dispersal can be low even when there is high mobility (Gandon 1999). Moreover, for species that are particularly vagile, difficult to individually identify or to mark and recapture, estimating sex-biased dispersal by direct observation is not always feasible. Genetic methods can be used to complement and reduce the invasiveness, effort and expense of markrecapture studies and give insights into how dispersal translates into effective dispersal and gene flow. An appreciation of the species' life history is essential, at the very least to establish when dispersal is likely to occur. As a guideline, many species undergo natal dispersal before maturity (but see 'Patterns of sex-biased dispersal'). Sampling juveniles therefore provides access to predispersal individuals, while sampling adults provides a mixture of residents and immigrants. It is important to emphasize that these different

Assumptions and application of the island model:

To understand how dispersal can be measured, it is important to consider dispersal in a population genetics framework. The simplest approach is to imagine an island model of populations (Wright 1931). Each deme has N individuals, and a proportion, m, of the individuals are immigrants. Under migration-drift equilibrium, $F_{\rm ST}$ provides an indirect measure of migration in the form, $N_e m$ (where N_e is the effective size of the deme, subpopulation or population, and m is the number of immigrants) from Wright's (1943) formula for a diploid locus:

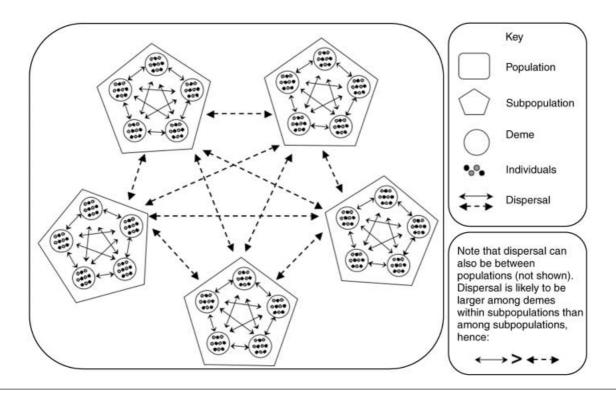
$$\hat{F}_{\rm ST} \approx \frac{1}{4N_e m + 1} \tag{1}$$

Access to sex-specific markers enables us to expand this approach to investigate sex-specific gene flow. Different functions of male and female dispersal rate and effective population sizes are substituted in equation 1, depending on the marker considered (Table 3).

Unfortunately there are several assumptions to the island model that are rarely met in practice, so any estimation of $N_e m$ by this method should be interpreted with great care (see Whitlock & McCauley 1999 for a detailed argument of this, and Balloux & Lugon-Moulin 2002 for a discussion on the limitations of $F_{\rm ST}$ for estimating $N_e m$). The assumptions are:

- 1 All populations are stable in size
- 2 All populations have $N_e m$ individuals arriving as migrants per generation
- 3 Migration is random with respect to distance (in other words there is no isolation by distance)

However, if we assume that the assumptions apply equally to both sexes (which is probably fair, except perhaps for assumption 3), relative estimates of $F_{\rm ST}$ can be useful to compare the number of migrant males and females, and hence to measure the direction of sex-biased dispersal.



cohorts should be analysed separately. Doing otherwise would not only reduce the ability of tests to detect SBD (Prugnolle & de Meeûs 2002), but also lose the opportunity to gain insightful information from the contrast between pre- and post-dispersal samples (see below).

Conventional genetic methods for measuring direction of SBD have been previously classified into those that measure sex-biased gene flow, or instantaneous dispersal (Prugnolle & de Meeûs 2002). Both of these approaches assume a classical island model of populations (Box 1),

Table 3 Effective population size (N_e) and dispersal rate (m) to be used for different genomic regions in equation 1 (Box 1) as functions of male and female effective sizes and dispersal rates

	N_e	m
Autosomal markers	$\frac{4N_mN_f}{N_m+N_f}$	$\frac{m_m + m_f}{2}$
X chromosome	$\frac{9N_mN_f}{4N_m+2N_f}$	$\frac{m_m + 2m_f}{3}$
Y chromosome	$\frac{N_m}{2}$	m_m
mtDNA	$\frac{N_f}{2}$	m_f

and a simple population genetics framework. The simplest approach builds on Wright's (1943) formula for genetic differentiation between subpopulations (equation 1, Box 1), which provides us with an indirect measure of the effective dispersal rate. Although $F_{\rm ST}$ offers only an approximate solution (since it relies on simplistic assumptions, Whitlock & McCauley 1999; Box 1), even though underlying assumptions of the island model (and hence summary statistics that assume it, such as $F_{\rm ST}$ and relatedness) are unrealistic in many situations, this does not affect the *relative* estimates of male and female migration rates.

Sex-biased gene flow

Direction of sex-biased gene flow can be measured using sex-specific markers, i.e. maternally inherited mtDNA or the paternally inherited nonrecombining region of the Y chromosome (NRY). Since these markers are nonrecombining, information on historical patterns of gene flow is maintained in successive generations. Sex-biased gene flow can be inferred most simply through patterns of haplotype distribution (e.g. Eriksson et al. 2006), or from the relative estimate of gene flow in males compared to females obtained by calculating $F_{\rm STY}$ and $F_{\rm STmtDNA}$ (e.g. Hammond et~al.2006). This can be estimated assuming an effective population size (N_o) of Y-chromosomes and mtDNA one-quarter that of the autosomes (due to copy number differences alone, Box 1 and Table 3). In addition, the parameter $N_{\rm e}v = (1/F_{\rm ST})$ -1, where v incorporates mutation (μ) and migration (m) $(v = m + \mu - m\mu)$ has been used several times to estimate the relative effective population size and/or rate of gene flow from sex-specific markers (Seilestad et al. 1998; Destro-Bisol et al. 2004; Eriksson et al. 2006). A high ratio of $N_e v_{\rm mt}$ $N_e v_y$, such as that recently found in bonobos ($N_e v_{\rm mt}/N_e v_{\rm Y} =$ 282, Eriksson et al. 2006) indicates a much higher effective size for females and/or rate of gene flow, and a ratio greater than one has been described in several human populations (e.g. Seilestad et al. 1998; Destro-Bisol et al. 2004).

It is important to stress that difference in F_{ST} between Y and mtDNA may stem from differences in male and female effective population size as well as dispersal rate. In hamadryas baboons for instance, female-biased dispersal combines with a highly polygynous mating system and a female-biased adult sex ratio to generate a particularly small male N_e and a strong contrast in F_{ST} between Y and mtDNA ($F_{STY} \ll F_{STmtDNA'}$ Hammond *et al.* 2006). Fortunately, Chesser & Baker (1996) and Laporte & Charlesworth (2002) provide joint analyses of the combined effects of dispersal patterns and mating systems on the effective population size and population structures for sex-specific markers, which provide informative guidelines for interpreting patterns. Other caveats also apply though when analysing gene flow using sex-specific markers. First, a large sampling variance is associated with Y and mtDNA markers owing to their lack of recombination, so differences may be simply stochastic. Second, there can be a large difference in the mutation rate between these loci, depending on the type of marker selected, and this needs to be considered. Finally, this method obviously relies on characterizing informative sex-specific markers, and relative lack of variability on the Y chromosome may be a limiting factor here (Hellborg & Ellegren 2004; Hammond et al. 2006; Lawson Handley et al. 2006a,b). However, the increasing availability of Y-linked markers (Hellborg & Ellegren 2003), particularly microsatellites (Erler et al. 2004; Lawson Handley & Perrin 2006) will hopefully facilitate its future use in this type of study.

Instantaneous dispersal

Recombining biparental markers (such as autosomal microsatellites) measure sex-biased dispersal in one generation since parental alleles are independently assorted in the offspring. Relative estimates of $F_{\rm ST}$ for post-dispersal males and females can therefore be used to measure the direction of sex-biased instantaneous dispersal (e.g. Goudet *et al.* 2002; Prugnolle & de Meeûs 2002; Hammond *et al.* 2006), whereas dispersal *rates* can be quantified by contrasting adults and predispersal juveniles (Vitalis 2002; Fontanillas *et al.* 2004).

Standard statistical tests for measuring the direction of instantaneous SBD are based on population-level genetic structure of males and females ($F_{\rm IS}$, $F_{\rm ST}$ or relatedness r, Weir & Cockerham 1984; Whitlock & McCauley 1999; Goudet et~al. 2002) or the probability of an individual's assignment to a population (mean and variance of the corrected assignment index, mAIc and vAIc, respectively, Paetkau et~al. 1995; Favre et~al. 1997; Waser & Strobeck 1998; Goudet et~al. 2002). The logic and predictions of these standard tests are detailed in Table 4. The power to detect sex-biased dispersal by these methods depends on the intensity of the bias and on the rate of dispersal (Goudet et~al. 2002). If only one sex disperses, then the bias is normally detectable by

 Table 4
 Logic and predictions of statistical tests for sex-biased dispersal

	Pre-dispersal MBD FBD References	F < M F > M 1,2,11	F > M $F < M$ 1,2,3,4,11	F > M $F < M$ 2,7,8,9, 10,11	F > M $F < M$ 2,3,5,6,11	F < M F > M 2,3,5,6,11
) FBD	A F > 1	I F < I	A F < 1	A F < 1	A F > 1
	MBD	F < N	F > N	F > N	F > N	F < N
Prediction	Pre-dispersal	F = M	F = M	F = M	F = M	F = M
	Logic	Expect higher $F_{\rm IS}$ and heterozygote deficit in the dispersing sex due to $F=M$ Wahlund effect, since individuals sampled from a single patch will be a mixture of residents and immigrants	Expect philopatric sex to exhibit higher $F_{\rm ST}$ than dispersing sex	Expect individuals living in close proximity to be more related on average than individuals taken from the whole population. Individuals of the philopatric sex will have higher r than those of the dispersing sex	A positive <i>Alc</i> value indicates that the genotype is more likely to come from the sampled population. An individual with a negative <i>Alc</i> value is more likely to be an immigrant. <i>mAlc</i> will be lower in the dispersing sex.	As above, but $vAIc$ will be larger in the dispersing sex because they are $F=M$ expected to be a mixture of residents and immigrants.
	Definition	Measure of inbreeding within subpopulations relative to the total	Genetic differentiation among subpopulations	Degree of relatedness among individuals within subpopulations	The mean probability of assignment of an individual to a population	The variance in the probability of assignment of an individual to a population
	Statistic	$F_{ m IS}$	$F_{ m ST}$	Relatedness (r)	Mean corrected assignment index (mAIc)	Variance of corrected assignment index $(vAlc)$
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(1) Weir & Cockerham 1984, (2) Goudet et al. 2002, (3) Prugnolle & de Meeus 2002, (4) Mossman & Waser 1999, (5) Paetkau et al. 1995, (6) Favre et al. 1997, (7) Ishibashi et al. 1997, (8) Piertney et al. 1998, (9) Knight et al. 1999, (10) Surridge et al. 1999, (11) Hammond et al. 2006. Predictions of test statistics based on a predispersal sample of males and females (representing a null control), and populations of postdispersal male and female adults, under a hypothesis of male-biased dispersal (MBD) or female-biased dispersal (FBD) any of the methods described here, so long as sampling is intensive (i.e. many individuals from many populations), but only F_{ST} and mAIc retain enough power when the bias intensity drops to 80:20. When dispersal rate is high, a population will consist of a large proportion of immigrants, and populations are less differentiated as a result. When dispersal rate is very low, immigrants constitute only a small proportion of the individuals sampled and may not be detected at all. Not surprising perhaps then that the maximal power for all tests is achieved when dispersal rate is at an intermediate value (approximately 10% per generation), but some tests perform better than others under different rates of dispersal. vAIc is particularly sensitive to rare alleles, whereas $F_{\rm ST}$ is more sensitive if dispersers constitute a larger proportion of the sample, and mAIc is somewhere in between these two. When dispersal is lower than 10% per generation, vAIc outperforms the other statistics, whereas F_{ST} is more robust in terms of bias intensity and sampling regime (Goudet et al. 2002).

It is essential to keep in mind the relative power (or lack of power) of these tests when designing experiments, since sampling design and choice of number and variability of loci can influence the possibility to detect SBD. Simulation experiments have shown that it is better to increase the number of individuals per population rather than the number of populations sampled (Goudet et al. 2002). This makes intuitive sense because with more individuals per population, there is more opportunity for sampling immigrant genotypes and allele frequencies are better estimated, and therefore, immigrant and resident genotypes can be more readily distinguished. The power of certain statistics $(F_{ST}, r, mAlc \text{ and } vAlc)$ to detect SBD can be improved by increasing the number of polymorphic loci, but no significant gain is expected above 20 polymorphic microsatellites, and Goudet et al. (2002) caution that it is better to invest in the number of individuals rather than the number of loci. It may seem that the lack of power to detect SBD using these statistics is restrictive, but the growing number of case studies that have employed these methods and successfully detected SBD would suggest that bias intensity is often sufficiently high in practice.

Although the summary statistics described above can be informative for estimating the direction of SBD, they cannot be relied upon to provide quantitative estimates of dispersal rates (unless estimates are compared before and after dispersal, see below) since any summary statistic represents a population 'average' as far as genotypes are concerned.

Towards more quantitative estimates of sex-biased dispersal

While the direction of mammalian sex-biased dispersal, which is comparatively easy to establish, appears to strongly

favour males, the magnitude and intensity of the bias are more difficult to measure and vary greatly between species and even within the same species. Recent advances in statistical approaches mean that quantitative estimates of sex-biased dispersal rate can be more readily obtained. Vitalis (2002) showed that, assuming an island model of dispersal (Box 1), the ratio of sex-specific $F_{\rm ST}$ estimated after dispersal over $F_{\rm ST}$ estimated before dispersal is a simple function of the sex-specific dispersal rate. This function estimates the proportion of immigrant individuals in a subpopulation per generation, a parameter that includes differential dispersal costs to the sexes (Vitalis 2002).

The selective pressures on dispersal are likely to depend on the spatial scale considered (Ronce *et al.* 2001), and so far, few studies have considered that dispersal bias might vary with geographical scale. In one example, fine-scale variation in SBD was detected in the Australian bush rat using spatial autocorrelation analyses, illustrating the potential for this type of analysis to measure variation in dispersal with spatial scale (Peakall et al. 2003). Fontanillas et al. (2004) extended the Vitalis (2002) approach to account for the hierarchical structure of populations. An application to the greater white-toothed shrew showed that dispersal was significantly female-biased at the breeding group level, but not at the among population level. Moreover, the total dispersal rate of females was almost four times higher than that of males, but when broken down into local and larger geographical scales the authors noted that the male dispersers were travelling further than the females, so that among villages, dispersal was no longer female biased. Individual-based simulations showed that, to compare spatial scales, sampling should include the highest hierarchical level at which dispersal is thought to occur, the number of groups per population should approximate the number of populations in the sample, and sampling should be as exhaustive as possible within groups

Box 2 Glossary and Abbreviations

Dispersal: movement of individuals from one group, deme, subpopulation or population to another in which they successfully breed (thus resulting in potential changes in allele frequencies). Also referred to as 'effective dispersal' (as opposed to ecological dispersal which is simply the movement of an individual from one place to another). Unless stated otherwise (e.g. under secondary transfer), we consider dispersal as emigration from the natal group.

Female-defence polygyny: mating system in which a dominant male defends mating access to a harem of several females (common in mammals).

Gene flow: dispersal followed by successful reproduction. In this review we use the term 'gene flow' to refer to historical patterns maintained in successive generations (as opposed to 'instantaneous dispersal').

Inclusive fitness benefits: an expansion of the concept of 'fitness' to include benefits accrued to relatives. Since relatives share their genetic material an apparently altruistic act toward a relative may in fact enhance the inclusive fitness of the individual performing the act.

Inbreeding avoidance (IA): avoidance of mating with closely related individuals.

Inbreeding depression: decline in fitness due to breeding with close relatives.

Inbreeding load: a function of the number of deleterious alleles in a population (i.e. the genetic load) governed by the deleterious mutation rate (U) as well as selection and dominance coefficients.

Instantaneous dispersal: dispersal in one generation. Measured using biparentally inherited, recombining markers since parental alleles are independently assorted in the offspring.

Kin selection: the concept that an individual gains inclusive fitness benefits by enhancing the reproduction of relatives (Hamilton 1964).

Local mate competition (LMC): competition for mates among related, same-sex individuals. Typical among males in polygynous mammals.

Local resource competition (LRC): competition for resources among related individuals. Typical among males in species with resource-defence monogamy.

Local resource enhancement (LRE): the benefits gained from local interactions with relatives.

Patrilocality: the tendency in human populations for a wife to move into her husband's natal household (opposite: matrilocality).

Philopatric: an individual that remains in its natal group to breed (i.e. does not undergo dispersal).

Resource-defence monogamy: monogamous mating system in which males take the leading role in acquisition and defence of resources (common in pair-breeding birds).

Secondary transfer: dispersal after initial departure from natal group, for reasons potentially very different to natal dispersal (e.g. eviction after group takeover).

Other abbreviations used:

SBD, sex-biased dispersal

MBD, male-biased dispersal

FBD, female-biased dispersal

OMU, one-male unit

MMU, multimale unit

(Fontanillas *et al.* 2004). One should also consider that if the scale over which dispersal is measured is smaller than the scale over which organisms actually move, then average dispersal distances can be grossly underestimated (the so called 'right censoring problem', Dieckmann *et al.* 1999).

Individual-based assignment tests based on likelihood (e.g. Waser & Strobeck 1998) or Bayesian principles (e.g. Pritchard et al. 2000) offer several advantages over summary statistics and should be more powerful because they do not average over the population, allow immigrant individuals to be readily identified, are more geographically explicit, and in the latter do not require populations to be predefined (see Manel et al. 2005 for a review). Although individual assignment techniques based on Bayesian principles applied to multilocus genotypes are becoming standard tools in molecular ecology (Manel et al. 2005), their potential for studying dispersal has perhaps yet to be realized (but see Fraser et al. 2004; Natoli et al. 2005; for exceptions). They do, however, provide a particularly interesting and powerful alternative to the moment-based methods that underlie the statistical inferences mentioned above (Beaumont & Rannala 2004). The accuracy of partial Bayesian (Rannala & Mountain 1997; Cornuet et al. 1999; implemented in the software geneclass) and fully Bayesian (Pritchard et al. 2000 implemented in STRUCTURE) methods of individual-based assignment to measure dispersal was recently assessed by comparing microsatellite data to longterm mark-recapture records in the grand skink (Berry et al. 2004). Encouragingly, similar estimates of the proportion of dispersing individuals were obtained and assignment tests correctly identified the natal population of 65-100% of individuals even when dispersal was quite common (5-20% of the population consisted of dispersers). Moreover, assignment tests provided a qualitative idea of the scale of dispersal and quantitative estimates of the number of dispersers, which in both cases was comparable to estimates obtained from mark-recapture studies (Berry et al. 2004). These methods could be extended to studies of SBD by simply comparing males and females separately.

Developments in Bayesian (or partial Bayesian) methods also have relevance for studying sex-biased dispersal *rates*. The principle of this approach is to compare summary statistics (in this case, e.g. nucleotide diversity for sequence data or heterozygosity for microsatellite data) from observed data with those simulated under a model for which the parameters are known (Beaumont *et al.* 2002). Since models of any complexity can in theory be simulated, those that more closely reflect biological reality can be estimated. Recently, approximate Bayesian methods were used to compare differences in male and female dispersal levels in natural populations of the common vole (Hamilton *et al.* 2005b). An extreme sex bias in dispersal was found, with males dispersing at ~20 times the rate of females. The authors caution though that this method could overestimate the

effective number of migrants if there is a large discrepancy in dispersal distance between sexes (Hamilton *et al.* 2005b). Interestingly, this approach could be used to compare autosomal microsatellites and mtDNA data to obtain estimates of male dispersal, bypassing the need for male-specific markers (Hamilton *et al.* 2005b).

Conclusions and prospects

The recent rise of molecular tools has helped to document empirical patterns of dispersal, confirming that SBD is widespread among mammals, and varies widely in direction and intensity. The evolutionary causes behind these patterns though still require much clarification. The main emerging insight relates to the crucial role of social systems, but the complex interactions between inbreeding avoidance, kin competition and cooperation makes the building of a theoretical framework able to account for the impressive diversity of patterns difficult.

From this review, a few directions can be identified from which new insights would be particularly welcome. First, concerning evolutionary modelling, efforts are needed to incorporate the subtleties of social interactions, since social life turns out to play a crucial role in promoting sex-bias in dispersal. More emphasis should also be put on the incorporation of condition dependence of sex-specific dispersal, which might gain crucial importance when interpreting observed patterns in terms of evolutionary causes. On the empirical front, progress is expected from the development of male-specific markers (Y chromosome), from investigations on sex differences in dispersal distances, and from the delineation of condition dependence in dispersal (modes and proximate causes). There is a real need to properly integrate genetic information and careful observational data, since the two approaches provide complementary information (e.g. on proximate causes and effectiveness of gene flow) required for any interpretation in evolutionary terms. For instance, only observational data will be able to disentangle emigration from immigration and evaluate dispersal costs. It is also worth considering that sex-biased dispersal may result from differences in emigration rate or in dispersal mortality (e.g. Waser et al. 1994), and hence stem from very different evolutionary causes. The separation of dispersal into its component stages (emigration, interpatch movement and immigration), which involve very different decisions, is still rarely taken into account in empirical studies (Bowler & Benton 2005). Intraspecific variation in sex-biased dispersal is clearly important in humans (see above), has been demonstrated in other mammals (e.g. shrews, Fontanillas et al. 2004), and is an essential avenue for further research, to explore the effects of varying ecology and demography on dispersal. Data analysis and statistical treatments will gain from the spread and implementation of Bayesian approaches, which allow

more realism in the scenarios to be tested. Bayesian methods of individual assignment, for instance, may allow some freedom from the constraints of predefining populations (see general review in Manel *et al.* 2005).

Sex-biased dispersal has been confirmed in other taxonomic groups including birds (Cooke et al. 1975; Greenwood 1980; Clarke et al. 1997; Scribner et al. 2001; Hansson et al. 2003; Wright et al. 2005), fish (Knight et al. 1999; Pardini et al. 2001; Hutchings & Gerber 2002; Taylor et al. 2003; Bekkevold et al. 2004), and amphibians (Austin et al. 2003; Palo et al. 2004). However, as reflected in this review, there has been a disproportionate investment in studies of SBD in mammal compared to nonmammal species. It will be important to overcome this trend for three main reasons: (i) to obtain deeper insights into the generality of evolutionary models for SBD; (ii) to allow a priori testing of SBD predictions; and (iii) to avoid the confounding effects of phylogeny and social structure. Invertebrates and lower vertebrates should prove excellent models for experimental testing of evolutionary models without prior assumptions, particularly because social systems are highly diverse in such groups. However, mammals are highly diverse in terms of their social systems and patterns of SBD, and there is still much to be learned. Focus on exceptional model species (i.e. species displaying strong contrasts with related species and/or general trends) should prove particularly insightful. Studying the evolution of mammalian FBD in a comparative phylogenetic framework, for example, should provide a powerful means to explore the link between SBD and life history traits.

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