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1 The causes and consequences of inbreeding avoidance and

tolerance in cooperatively breeding vertebrates

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- 7 **Short title:** Inbreeding in cooperative breeders

Abstract

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Cooperative breeders provide a particularly interesting scenario for studying inbreeding. Such populations are viscous due to delayed dispersal and short dispersal distances, resulting in the build-up of relatives in the local population. This leads to a high risk of inbreeding, and consequently of inbreeding depression. This has driven the evolution of an array of inbreeding avoidance mechanisms resulting in a relatively low level of close inbreeding in the majority of cooperative breeders. However, there are a number of species where inbreeding occurs relatively frequently. The presence of regular inbreeding (in cases where inbreeding is not a result of recent population declines), suggests that inbreeding tolerance and even preference can evolve under some circumstances. Both inbreeding and inbreeding avoidance mechanisms have enormous downstream fitness consequences for cooperative breeding species. For example, they can influence reproductive dynamics leading to a monopolisation of breeding opportunities by dominant individuals. Inbreeding and its avoidance are also likely to impact on the evolution of cooperative breeding itself through influencing levels of relatedness between potential cooperators. Finally, in some cooperative breeders, a high degree of inbreeding avoidance can be detrimental to population viability, and hence is of particular concern to conservationists. In this review, I discuss these issues in detail and also briefly consider recent advances in the methods available for the study of inbreeding in natural populations.

Key words: cooperation, inbreeding, incest, heterozygosity, kin-recognition, relatedness, dispersal, extra-pair paternity

Introduction

Breeding between close relatives (Box 1) generally entails a fitness cost, known as inbreeding depression (Darwin 1900), and mainly results from the increased homozygosity of recessive deleterious alleles. The detrimental effects of inbreeding are well documented empirically

under laboratory and captive conditions as well as in the wild (Keller & Waller 2002), and can lead to a substantial reduction in offspring fitness (Charlesworth & Charlesworth 1987, Ralls, Ballou & Templeton 1988). It is consequently not surprising that inbreeding avoidance is widespread in the animal kingdom (Keller & Waller 2002). However, inbreeding avoidance is also associated with costs. Dispersal to find an unrelated mate is commonly associated with increased mortality (Clutton-Brock & Lukas 2012) whereas 'too much' outbreeding can reduce offspring fitness by breaking up adaptive gene clusters (known as outbreeding depression (Bateson 1983, Helgason *et al.* 2008)). Furthermore, theoretical work predicts that inbreeding can have a substantial positive effect on inclusive fitness through increasing the reproductive success of relatives (Dawkins 1979, Lehmann & Perrin 2003, Kokko & Ots 2006) and increasing the benefits of cooperation (Hamilton 1964), implying that even close inbreeding should be tolerated under some circumstances (Kokko & Ots 2006, Thunken *et al.* 2007).

dilemma (reviewed in Szulkin *et al.* (2013)), but the natural history of inbreeding has proved particularly difficult to study. Empirical work on wild populations has often been hampered by the difficulty of obtaining accurate coefficients of inbreeding (Pemberton 2004), and many short-term studies may fail to detect environment-dependent inbreeding depression. Furthermore, studies on populations that have suffered recent declines or habitat fragmentation may lack relevance due to artificially high levels of inbreeding (Jamieson *et al.* 2009). On the other hand, laboratory investigations can fail to replicate natural social or environmental conditions (Pemberton 2008), while theoretical predictions often appear to mismatch empirical evidence (Lehmann & Perrin 2003, Kokko & Ots 2006). Moreover, few attempts have been made to study the interplay between inbreeding and cooperative behaviour. At its most basic level, inbreeding and inbreeding avoidance both affect patterns of relatedness, which can in turn affect the evolution of cooperation (Koenig & Haydock 2004). In addition, the 'quality' of individuals can influence reproductive competition and cooperative behaviours (Heinsohn & Legge 1999, Meagher, Penn & Potts 2000), and this may also be

influenced by inbreeding (Meagher et al. 2000). Consequently, studies of inbreeding in highly cooperative species are well-placed to provide insights into its effects on the dynamics and evolution of animal social systems.

Despite the logistical challenges, substantial advances have been made in the field of inbreeding in cooperative breeders since the last major review of Koenig and Haydock (2004). First, although data on many species is still lacking, the growing number of long-term studies of wild populations of cooperative breeders incorporating genetic, behavioural, life-history and environmental data have allowed us to quantify the occurrence and distribution of inbreeding in many more species than previously possible (Koenig & Dickinson 2016). Such studies have also allowed us to investigate the diversity of ways by which inbreeding is avoided, and also to uncover some of the impacts of inbreeding avoidance on individual fitness, dispersal patterns, group structure and relatedness dynamics. Furthermore, methods for studying inbreeding have improved substantially over recent years (Pemberton 2008, Hoffman et al. 2014, Bérénos et al. 2016, Huisman et al. 2016). In particular there have been consistent advances in the genetic methods available to identify inbreeding, and also in our understanding of the caveats of these methods (Pemberton 2008, Szulkin et al. 2010). Such methods therefore provide much promise for expanding our knowledge of the natural history of inbreeding in the wild.

In this review, I first highlight why inbreeding and inbreeding avoidance are of particular interest in cooperatively breeding species. I then go on to evaluate the prevalence and distribution of inbreeding among cooperative species, before exploring ways through which inbreeding is avoided, and why some species may tolerate frequent inbreeding. Following this, I discuss the consequences of inbreeding avoidance and tolerance for cooperative breeders. Finally, I outline developments in the methods used to study inbreeding and briefly discuss their relative merits.

Box 1: Definitions

Inbreeding: mating between individuals with one or more common ancestors.

Close inbreeding: mating between first order relatives such as full-siblings or parent and offspring, often referred to as incest. Offspring resulting from close inbreeding have an inbreeding coefficient (*f*) of 0.25.

Moderate inbreeding: Mating between second order relatives such as half-siblings, uncle and niece, aunt and nephew, grandparent and grandchild or double first cousins. Here, f of offspring is 0.125.

Distant or weak inbreeding: Any inbreeding below the second-order relative level. Here, f is below 0.125, but above 0.

Cooperative breeder: here defined in its broadest sense as species where individuals other than parents care for offspring.

Why are cooperative breeders particularly interesting for the study of inbreeding?

Cooperative breeders present a particularly interesting scenario for studying inbreeding (for definitions see Box 1). Here, dispersal is usually delayed until after sexual maturity, and offspring remain with their parents and help to rear subsequent broods or litters, often consisting of full or half-siblings (Koenig & Dickinson 2004, Russell 2004, Lukas & Clutton-Brock 2012). This leads to a situation where groups often, although not always, consist of close opposite-sex relatives with the potential to inbreed (Koenig & Haydock 2004). Early studies predicted that inbreeding would enhance cooperation through increasing relatedness between group members (Hamilton 1964, Marshall et al. 2002). This premise appeared to be confirmed by findings of a high level of bandsharing in DNA fingerprints within eusocial naked mole-rat *Heterocephalus glaber* colonies, demonstrating close inbreeding in one of the most cooperative vertebrate societies known (Reeve *et*

al. 1990). However, the level of inbreeding in naked mole-rats has since been re-evaluated. Subsequent studies showed higher dispersal levels than previously thought (Braude 2000, Pemberton 2008), evidence of inbreeding avoidance (Ciszek 2000) and inbreeding depression (Ross-Gillespie, O'Riain & Keller 2007), and biases in the original sampling towards a severely bottlenecked population (Ingram et al. 2015). In addition, studies of other cooperative breeders, including another eusocial mole-rat *Fukomys damarensis*, have demonstrated that regular inbreeding is not required for the evolution of extreme social complexity, cooperation and reproductive skew (Burland et al. 2002, Pemberton 2004).

Despite opportunities for regular inbreeding in cooperative breeders, close and moderate levels of inbreeding have been shown to be rare within most cooperative species (Koenig & Haydock 2004). As a typical example, in the Florida scrub jay, a socially and genetically monogamous cooperative breeder, only 0.6% of nestlings are the product of close inbreeding (Fitzpatrick & Bowman 2016). A low level of inbreeding across cooperative breeders likely results from a lack of breeding from subordinate helpers, in part due to individual restraint when there are no unrelated group-members to breed with, and partly due to suppression by dominant breeders (O'Riain *et al.* 2000, Koenig & Dickinson 2004, Huisman et al. 2016).

Within-group inbreeding may be more likely to occur in species where mate-choice is particularly constrained. For example, in the banded mongoose *Mungos mungo* (Figure 1), which lives in large mixed-sex groups with relatively low reproductive skew, the majority of breeding occurs within groups despite the presence of close relatives as potential mates (Nichols et al. 2014). This is likely due to the high cost of seeking mates from outside the social group (Nichols, Cant & Sanderson 2015) and leads to 9% of pups being the product of close inbreeding and 17% of pups being the product of moderate inbreeding (Nichols et al. 2014) (see Box 1 for definitions)). Several other cooperatively breeding vertebrates have been proposed to inbreed regularly, including both birds (pukekos *Porphyrio melanotus* (Craig & Jamieson 1988), green wood hoopoes *Phoeniculus*

purpureus (Du Plessis 1992), common moorhens *Gallinula chloropus* (McRae 1996) and Seychelles warblers *Acrocephalus sechellensis* (Richardson, Komdeur & Burke 2004)) and mammals (such as dwarf mongooses *Helogale parvula* (Keane, Creel & Waser 1996) and red wolves *Canis rufus* (Sparkman *et al.* 2012)). However, genetic data is often either unavailable or is not of sufficient quality to accurately quantify inbreeding rate (reviewed in Koenig & Haydock, 2004). Exceptions are the Seychelles warbler and the red wolf, which have microsatellite genotypes available (see Box 2). In the Seychelles warbler, 5% of pairings were likely to be between first order relatives, while in the red wolf, 8% of pairs were close relatives. However, both of these species are endangered and have experienced severe bottlenecks which may have both eroded genetic diversity and constrained mate choice (Richardson et al. 2004, Sparkman et al. 2012), so neither may be representative of wild animal populations.

The examples of the red wolf and Seychelles warbler highlight the need to interpret the observed inbreeding strategy in the context of historical and current population ecology. In some populations, the encounter rate with opposite sex relatives is a product of the species breeding system and patterns of dispersal. However in others the encounter rate may have been largely skewed by recent changes to population size and connectivity, which results in a higher frequency of inbreeding (Szulkin et al. 2013). Indeed, it is only under stable, long-term environmental selective pressures that behavioural mechanisms of inbreeding tolerance and/or avoidance could have evolved.

The broadest trend in terms of the distribution of inbreeding within cooperative breeders is that inbreeding appears more common at the population (between-group) level than at the withingroup level. For example, inbreeding may occur when an individual immigrates into a group already containing kin with which the disperser is unfamiliar. In meerkats *Suricata suricatta* (Figure 1), which live in large groups of close kin with the occasional unrelated immigrant, almost all inbreeding occurs at the between-group level (Nielsen *et al.* 2012). Similarly, in two species of canids, within-group

inbreeding is avoided, but outside of the natal group, mates were selected independent of relatedness (Geffen *et al.* 2011). Such patterns may occur because the costs of avoiding inbreeding at the population level generally exceed the benefits; avoiding kin would require a sophisticated method of inbreeding avoidance and could result in lost breeding opportunities (Brouwer *et al.* 2011). Also, in a large outbred population, there is unlikely to be strong selection to avoid inbreeding at a population level; in Geffen et al.'s (2011) study, the probability of encountering full siblings as potential mates outside of the natal group was as low as 1%, depending on the population.

Why is inbreeding avoided?

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The primary cost of inbreeding is inbreeding depression, resulting mainly from an increase in homozygosity which allows for the expression of harmful but recessive alleles (reviewed by Charlesworth and Willis (2009)). Inbreeding depression has been found in the vast majority of species where it has been investigated (reviewed by Pusey and Wolf (1996)) and can manifest in many forms such as reduced growth (Brzeski et al. 2014), survival and reproductive success (Liberg et al. 2005), and increased susceptibility to disease (Townsend et al. 2009). Although inbreeding depression is most severe in pairings between first order relatives, it also occurs to some degree between moderate and distant relatives. In cooperatively breeding meerkats, inbreeding depression was found in a range of early life traits even though close inbreeding was successfully avoided in the population (Nielsen et al. 2012). Furthermore, although inbreeding depression is usually most severe in juveniles, the development of more powerful techniques for detecting inbreeding (Box 2) are also resulting in inbreeding depression being found in adults. For example, in (non-cooperative) red deer Cervus elaphus, matings between half-siblings resulted in a decline in lifetime breeding success in females by 72% and males by 95% (Huisman et al. 2016). In addition, inbreeding depression can have cross-generational effects, with inbred mothers producing smaller lambs in (non-cooperative) Soay sheep Ovis aries (Bérénos et al. 2016) and fawns with lower survival to recruitment in red deer (Huisman et al. 2016).

How is inbreeding avoided?

Despite living and breeding while surrounded by kin, cooperative breeders often avoid close inbreeding. This is accomplished through a wide variety of methods, outlined below. These methods are not mutually exclusive and there is often evidence for a single species avoiding kin as mates in a variety of ways, depending upon the context.

Dispersal

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Although cooperative breeders typically show delayed dispersal, this does not mean that dispersal is absent; helping is usually a temporary role, and can last for less than one breeding season in some species (Sharp et al. 2005). When dispersal does occur, there is often evidence that it is related to inbreeding avoidance. First, dispersal and/or greater dispersal distances are often biased towards one sex, which reduces the encounter rate between opposite sex relatives. It is therefore not surprising that inbreeding avoidance has been proposed as one of the main drivers of dispersal behaviour (Clutton-Brock 1989, Szulkin & Sheldon 2008, Clutton-Brock & Lukas 2012). Second, even when sex-biased dispersal doesn't occur, typical dispersal distances can put dispersers out of the range within which close relatives are found (Cockburn et al. 2003, Nelson-Flower et al. 2012). Third, inbreeding avoidance may sometimes trigger dominant breeders to give up their breeding position and disperse. For example, if a dominant breeder dies, the remaining dominant may abandon their position if the highest-ranking opposite-sex subordinate is a close relative (Cockburn et al. 2003). However, while inbreeding avoidance may play a part in determining patterns of dispersal, cooperative breeders of either sex generally disperse only short distances (Zack 1990, Riehl & Stern 2015), and in many species, inbreeding avoidance is not the primary determinant of dispersal decisions. For example, in two species of cooperative mongoose, aggressive eviction events occurring almost exclusively whilst dominant females are pregnant indicate that reproductive competition, rather than inbreeding avoidance is the main driver of dispersal, at least among females (Cant et al. 2010, Clutton-Brock et al. 2010).

One particular type of dispersal that has received limited attention is divorce. Divorce in social monogamous species has been traditionally associated with low breeding success, or movement to a breeding vacancy on a better quality territory (Ens, Safriel & Harris 1993). However, in cooperative breeders, incest avoidance has also been implicated. Aranzamendi *et al.* (2016) found that incest avoidance was the key predictor of divorce in the purple-crowned fairy-wren *Malurus coronatus*, with 64% of incestuous partnerships divorcing shortly after formation, and none lasting over 1 year. Similar patterns have been found in other cooperatively breeding birds, with females that become socially paired with their sons after their partner dies often divorcing their sons but accepting unrelated helpers as mates (Daniels & Walters 2000, Cockburn et al. 2003).

Kin recognition

Among cooperative breeders, where populations are viscous and dispersal delayed, selection pressure to evolve mechanisms of inbreeding avoidance other than dispersal is likely to be particularly high (reviewed across birds by Riehl and Stern (2015)). Supporting this idea, a literature search of mating patterns in birds found that almost all cooperative species with pedigree or genetic data showed evidence of inbreeding avoidance via kin discrimination whilst very few singular-pair species did (Jamieson et al. 2009). There are various ways by which kin-recognition may occur, including learning to identify familiar relatives, using simple rules to identify likely kin, and assessing genetic relatedness directly via phenotype matching (Komdeur & Hatchwell 1999). Note that although these mechanisms are often treated as being mutually exclusive, many species may use a combination of mechanisms that are context dependent.

The degree of association between individuals among group-living species usually co-varies with kinship as social groups usually contain family members. It is therefore often possible for individuals to assess the likely level of relatedness between themselves and other individuals by associative learning through social familiarity (Moore & Ali 1984), a mechanism which appears to be both effective and widespread (Pusey & Wolf 1996). Often there is a critical period in which the

learning of relatives takes place, usually during infancy (Kuester, Paul & Arnemann 1994), although continued association with relatives through phenotypic changes is important for kin recognition in some species (Ihle & Forstmeier 2013).

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Among cooperative species, recognising relatives is also likely to be important in directing kin-selected helping behaviour, hence many studies demonstrating evidence of kin recognition come from investigations of helping decisions. Particularly revealing are experiments that have involved manipulating the degree of relatedness between individuals, whilst keeping familiarity constant (and vice versa). In Seychelles warblers and western bluebirds Sialia mexicana, cross-fostered offspring from extra-pair matings help at their adoptive parents nest at similar rates to true offspring (Komdeur, Richardson & Burke 2004, Dickinson et al. 2016). Here, individuals appear to use familiarity to adults that tended to them prior to fledging as a proxy for relatedness despite relatively high rates of extra pair paternity (Komdeur et al. 2004, Dickinson et al. 2016). Similarly, in the long-tailed tit Aegithalos caudatus, Russell and Hatchwell (2001) conducted an experiment where they provided potential helpers with a choice of nests to help at that either contained relatives or non-relatives. In 94% of cases, helpers chose to help at the nests of relatives, demonstrating kin recognition. Further experiments on the same study system showed that learned vocal cues are used as a mechanism for kin-recognition in this species, with nestlings learning and emulating the calls of their close family (Sharp et al. 2005). Indeed, learned vocal cues may provide a reliable indication of relatedness across many bird species (reviewed by Riehl and Stern (2015), McDonald and Wright (2011), Hatchwell (2016)).

Whilst familiarity is often a good indicator of relatedness, in some societies the use of familiarity alone to identify potential relatives may not be sufficient to avoid inbreeding, for example in species with a high level of extra-group paternity (EGP) or where multiple females contribute to a communal litter or brood. Here, individuals may follow behavioural rules, some of which rely on familiarity and some of which do not. One simple cue to relatedness in relatively viscous populations

is likely to be distance. In red-winged fairywrens *Malurus elegans*, females that have inherited a territory are more likely to seek EGP, or seek EGP from further away than females that have dispersed before breeding (Brouwer et al. 2011). Similarly, superb fairy-wren *Malurus cyaneus*, and pied babbler *Turdoides bicolor* females disperse further from their natal groups than non-natal groups (Cockburn et al. 2003, Nelson-Flower et al. 2012). Other potential rules may include discriminating against particular age groups likely to contain relatives, or based on previous mating experience, for example to avoid daughters of females that males previously mated with (Archie *et al.* 2007). Simple behavioural rules may also explain why individuals of many species refrain from breeding in their natal groups, sometimes regardless of whether or not this group contains unrelated immigrants (Harrison *et al.* 2013a).

When Koenig and Haydock (2004) reviewed inbreeding in cooperative breeders, there were no convincing cases of kin recognition more sophisticated than rejecting familiar natal groupmembers as mates. However, since then, evidence has emerged that direct cues to genetic relatedness exist in many species including cooperative breeders and other group-living species (e.g. cooperatively breeding meerkats (Leclaire et al. 2013); Neolamprologus pulcher cichlids (Le Vin, Mable & Arnold 2010) and bell miners Manorina melanophrys (McDonald & Wright 2011); and group-living Belding's ground squirrels Urocitellus beldingi (Mateo 2010) and zebrafish Danio rerio, (Gerlach & Lysiak 2006)). Such mechanisms are likely to be involved in inbreeding avoidance and can be effective even without environmental and social cues to relatedness. Direct cues may therefore be particularly important in promiscuous species where social cues are of limited use (Hain & Neff 2006), but may also occur in monogamous species where there are benefits. For example, in the nepotistic (but not cooperatively breeding) Siberian jay Perisoreus infaustus, dominant breeders vary in their level of aggression towards unfamiliar immigrants depending on their level of genetic relatedness, implying that genetic kin recognition is involved (Griesser et al. 2015).

Direct cues to relatedness are thought to occur primarily via phenotype matching, which can be either self-referent or referent to their mother or siblings and learned during infancy. In self-referent phenotype matching, individuals recognise their own phenotype and assess other individuals on degree of similarity to themselves. This appears to occur in house mice *Mus musculus domesticus* (Sherborne *et al.* 2007) and bluegill sunfish *Lepomis macrochirus* (Hain & Neff 2006), neither of which are regular cooperative breeders, but both species sometimes rear broods of mixed parentage. It is also possible that 'recognition alleles' exist, as proposed by Hamilton (1964) and extended into the 'green beard effect' by Dawkins (1979), but the existence of such alleles in vertebrates has been very difficult to test and currently lacks direct evidence (Tang-Martinez 2001, Leclaire et al. 2013), but see (Gardner & West 2010).

In many vertebrates, direct kin-recognition involves the use of chemical cues. For example, in cooperatively breeding meerkats (Leclaire et al. 2013), individuals are able to discriminate between anal gland odours of unfamiliar relatives and non-relatives, while in cooperatively breeding cichlids, individuals associate with others based on chemical cues to relatedness (Le Vin et al. 2010). In humans Homo sapiens, body-odour based mate choice has been shown to be associated with both kinship (Weisfeld et al. 2003) and genetic diversity (Havlicek & Roberts 2009, Lie, Simmons & Rhodes 2010), particularly at Major Histocompatibility Complex (MHC) loci: genes that are involved in the immune response. The MHC, but not diversity or relatedness at other loci, has also been implicated in mate choice in cooperatively breeding Seychelles warblers. Here, females seek EGP if their social partner has low MHC diversity, which in turn is linked to offspring survival (Brouwer et al. 2010). Probably one of the best understood species in terms of chemical cues to relatedness is the house mouse. Here, although the MHC may play a part, the primary cue to relatedness appears to come from Major Urinary Proteins (MUPs) which have been shown to strongly influence mating decisions with regards to relatedness (Sherborne et al. 2007). It is possible that MUPs are important in identifying relatives in other cooperative species, however the presence of such proteins across a wide range of vertebrates remains to be tested and other phylogenetic groups may use alternative

methods to discriminate between kin. For example, studies have failed to find evidence of MUPs in two cooperatively breeding mole-rat species (Hagemeyer *et al.* 2011).

There is also evidence that inbreeding avoidance can occur postmating. Although such mechanisms appear relatively common in invertebrates (Tregenza & Wedell 2002), there is currently little evidence from vertebrates (Brekke *et al.* 2011). However, there are some relatively convincing cases. For example, in wild-derived house mice that were experimentally mated to both siblings and unrelated males, unrelated males sired more offspring (Firman & Simmons 2008). Post-copulatory mechanisms could be important in many cooperative breeding species and is likely to provide a fruitful area of future research. In particular, cooperative species where females mate multiply often show patterns consistent with post-copulatory mechanisms of inbreeding avoidance (see section below on extra-group mating). However in field-based studies, it is difficult to exclude the possibility that copulation frequency between males may vary, or that inbreeding depression may cause some offspring to die prior to birth. Although difficult to investigate, laboratory experiments provide a better opportunity to assess the degree to which such patterns are a result of pre or post copulatory mechanisms.

Extra-group mating

Studies of cooperative breeders, and also of socially monogamous but non-cooperative species, have found that extra-pair or extra-group mates are often less related to females than their within-pair mates (Blomqvist *et al.* 2002, Foerster *et al.* 2003, Bishop, O'Ryan & Jarvis 2007, Brouwer et al. 2011), suggesting that extra group paternity (EGP) could be used to avoid inbreeding. In some species, females appear more likely to mate extra-group if their social partner is a relative (meerkats (Leclaire et al. 2013) grey crowned babblers *Pomatostomus temporalis* (Blackmore & Heinsohn 2008), red-backed fairy-wrens *Malurus melanocephalus* (Varian-Ramos & Webster 2012), red-winged fairy-wrens *Malurus elegans* (Brouwer et al. 2011) and purple-crowned fairy-wrens *Malurus coronatus* (Kingma, Hall & Peters 2013)), suggesting that seeking EGP may be an adaptive strategy to

avoid inbreeding when there are constraints on social mate choice. This possibility is supported by a recent meta-analysis across birds (Arct, Drobniak & Cichoń 2015), but inbreeding avoidance may be a particularly important factor driving EGP in cooperative breeders, where populations are particularly viscous and so individuals may be restricted in their choice of social partners (Brouwer et al. 2011).

Note that, whilst there is convincing evidence that EGP is used to avoid inbreeding in some species, the generality of EGP as an inbreeding avoidance strategy has been questioned for several reasons. First, in some species, direct fitness benefits may drive the evolution of EGP, for example the paternity confusion caused by multiple mating may reduce infanticide (reviewed by Lukas and Huchard (2014)). Females may also seek 'good genes' for their offspring and so favour males with particular traits (reviewed by Jennions and Petrie (2000)) and EGP may also occur for non-adaptive reasons such as genetic constraints whereby the alleles associated with extra-pair mating are selected for their positive impact on other traits (Forstmeier et al. 2014). Second, in some cooperative breeders, population viscosity may reduce the effectiveness of EGP as a way to avoid inbreeding. In the white-browed sparrow weaver Plocepasser mahali, extra-group mates were more closely related to females than their social mates (Harrison et al. 2013b). The authors suggest that the presence of relatives in the local population may restrict opportunities for inbreeding avoidance, and instead male-male competition may be driving patterns in EGP in this species. Future metaanalyses, focused on cooperative breeders, will be necessary to properly evaluate the evidence for EGP as a method of inbreeding avoidance and to investigate the factors driving variance in the use of EGP across cooperative breeders.

Why is inbreeding not always avoided?

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Given the mechanisms of inbreeding avoidance that animals appear to have at their disposal, it is perhaps surprising that inbreeding occurs at all. However, it is important to recognise that both inbreeding and inbreeding avoidance are likely to have costs, and how these balance against each

other appears to result in substantial variation in inbreeding rates between individuals, populations and species. Furthermore, in some situations constraints against inbreeding avoidance may apply, whilst in others there may be active benefits of inbreeding, although this possibility remains controversial.

One reason why inbreeding may not be avoided in some populations is that the costs of inbreeding may be particularly low. Inbreeding depression appears to have a strong environmental component, with greater effects under more adverse conditions (Armbruster & Reed 2005). For example, in the Seychelles warbler, females with low genetic heterozygosity (hence are likely to display inbreeding depression) produce offspring with lower survival chances, but only in years where survivorship is poor in the population generally (Brouwer, Komdeur & Richardson 2007). Cross-fostering showed that this is not the result of poor maternal care as survival was unrelated to the foster mother's genetic heterozygosity (Brouwer et al. 2007). Among cooperative breeders, the social environment is likely to have a large impact on offspring fitness. It is therefore feasible that helper contributions to care could to some extent offset the negative impacts of inbreeding depression. Such a relationship has been shown in non-cooperative burying beetles *Nicrophorus vespilloides*, where maternal care increases the survival of inbred offspring to a greater extent than outbred offspring (Pilakouta *et al.* 2015). However, the possibility that helpers buffer the effects of inbreeding depression has rarely been tested in cooperative vertebrates (but see Nielsen et al. (2012)) and is likely to provide a fruitful area of future research.

In species or populations that have undergone frequent inbreeding in the past, the impact of inbreeding depression may be reduced through so-called 'genetic purging', whereby the increased homozygosity resulting from inbreeding exposes recessive deleterious alleles to natural selection, thereby purging them from the genome (Keller & Waller 2002). Further inbreeding would then cause little or no reduction in fitness. While this possibility has received some support in laboratory experiments (Crnokrak & Barrett 2002), its effect in most wild populations is likely to be relatively

minor due to a variety of factors including genetic overdominance, immigration and large population sizes (Keller & Waller 2002, Edmands 2007). So far, there is little evidence of purging in wild cooperatively breeding vertebrates, even in those where inbreeding occurs frequently. For example, there is evidence of inbreeding depression in banded mongooses, which regularly inbreed (Sanderson *et al.* 2015).

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In some species, inbreeding may occur relatively frequently due to constraints on mate choice and dispersal. In the naked mole-rat, dispersal is particularly constrained due to its subterranean desert habitat, where dispersal above ground is extremely hazardous (Bennett & Faulkes 2000). Although outbreeding is preferred and new colonies are formed by large 'disperser' morphs, which breed away from their natal group (Ciszek 2000), close inbreeding may be tolerated in colonies where one or both of the founding breeders have died (Ingram et al. 2015). Here, the costs of abandoning large, successful colonies and dispersing upon breeder death may outweigh the costs of inbreeding. Similarly, in the banded mongoose, the costs of dispersal are high as members of newly founded groups suffer an annual adult mortality rate (0.33) almost three times that of resident groups (0.12) (Cant, Vitikainen & Nichols 2013), whilst the costs of seeking extra-group paternity are high due to aggressive encounters with rival groups which account for the deaths of 20% of pups and 12% of adults (Nichols et al. 2015). Here, individuals often remain and breed in their natal groups for their entire lives which results in an increase in inbreeding levels as groups age (Nichols et al. 2014). This occurs despite the presence of inbreeding depression in pups, suggesting that the costs of inbreeding avoidance sometimes outweigh the benefits in this species (Sanderson et al. 2015).

One further suggestion for why some species may tolerate inbreeding is that it may confer benefits under some circumstances. First, inbreeding could act to preserve beneficial clusters of coadapted genes, which could be broken up by breeding with unrelated mates, thereby leading to selection for an optimal level of inbreeding (Bateson 1983). In support of this idea, Helgason et al.

(2008) found that the fertility of human couples was highest when they were related at the level of 3rd and 4th cousins, although they were not able to explicitly test the mechanism behind this. Second, there may be kin-selected benefits of inbreeding as the offspring of inbred matings are more closely related to their parents due to their inheritance of alleles identical by descent from both parents (Puurtinen 2011, Szulkin et al. 2013). Theoretical work predicts that the net kin-selected benefits of inbreeding will be high when inbreeding depression is low and that such benefits are likely to vary between the sexes and depending on the mating system (Waser, Austad & Keane 1986), potentially creating sexual conflict (Szulkin et al. 2013). Recent extensions to this theoretical work consider simultaneous versus sequential mate choice and relative investment in parental care, and suggest that inbreeding should be tolerated under a wider range of inbreeding depression values than previously thought (Kokko & Ots 2006). Among cooperative breeders, there could be additional benefits of increased relatedness among groups as it may also promote kin-selected helping behaviour, but despite this, the evidence that inbreeding is favoured in either cooperative or noncooperative vertebrates is scarce (Kokko & Ots 2006). The best evidence comes from a cichlid with biparental care, Pelvicachromis taeniatus, where laboratory experiments showed that both sexes prefer mating with unfamiliar close kin over non-kin, and inbred pairs were more cooperative and invested more in their offspring than unrelated parents (Thunken et al. 2007). The source population for the cichlids used in the experiment was relatively small, isolated and had low genetic diversity, presenting the possibility that this population has undergone the purging of deleterious alleles and therefore a reduction of the costs of inbreeding (Langen et al. 2011), although this remains to be tested explicitly. A small number of studies have also reported higher relatedness in extra-group mates than within-group mates, which could result from inbreeding preference (Wang & Lu 2011, Harrison et al. 2013b). For example, in cooperative breeding ground tits Parus humilis, although social pairs were unrelated, extra-pair mates were relatives (mean r = 0.137) (Wang & Lu 2011). As no evidence of inbreeding depression via reduced offspring weight was found, the authors suggest that inbreeding occurs as a result of the kin-selected benefits of providing relatives with mating

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opportunities. The authors were able to exclude the possibility that inbreeding occurs due to increased relatedness of local mates, which may explain high relatedness in extra-pair mates of white-browed sparrow weavers (Harrison et al. 2013b).

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It is possible that the general mismatch between theoretical work, which predicts that inbreeding tolerance will occur relatively commonly (Kokko & Ots 2006, Puurtinen 2011) and empirical work, which rarely finds evidence of inbreeding preference, is due to an underestimation by theorists of the effects of inbreeding depression in the wild. The majority of studies on inbreeding depression measure a selection of early-life traits and few consider lifetime breeding success. Future studies using long-term life-history data combined with powerful techniques to detect inbreeding, such as the large panel of single nucleotide polymorphisms (SNPs) used in Huisman et al. (2016), may reveal higher levels of inbreeding depression than previously thought. Alternatively, conditions favouring low levels of inbreeding tolerance may be common in nature. For example, in cases where the costs of choosing an unrelated mate are high. Also, species in which both sexes invest in offspring approximately equally and fairly substantially, and where mate encounter rate is high, are predicted to have some degree of inbreeding tolerance (Kokko & Ots 2006), and these conditions may occur in some cooperatively breeding species. Another possibility is that mating patterns resulting in regular inbreeding may be relatively common but researchers are reluctant to interpret this as evidence for inbreeding tolerance or preference, perhaps due to a lack of awareness of theoretical predictions (Kokko & Ots 2006). Instead, such mating patters are generally interpreted as occurring due to constraints against inbreeding avoidance (Kokko & Ots 2006, Szulkin et al. 2013). Those conducting studies on inbreeding should therefore consider the possibility that inbreeding may be preferred under some circumstances. Further work is necessary to shed light on the mismatch between theoretical and empirical studies of inbreeding tolerance, and should include both of these types of approach.

The consequences of inbreeding tolerance and avoidance

Many behavioural strategies have evolved to avoid the negative consequences of inbreeding, including dispersal (Koenig, Haydock & Stanback 1998, Griffin *et al.* 2003), reproductive restraint (Cooney & Bennett 2000, Clutton-Brock *et al.* 2001b), the immigration of non-relatives (Koenig et al. 1998) and extra-group copulations (Brouwer et al. 2011). All of these behaviours in turn feed back into group and population structure, influencing the dynamics of the population as a whole (Nichols et al. 2012).

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One of the defining characteristics of cooperative breeding systems is the presence of subordinate helpers that rarely (if ever) breed but instead help to rear the offspring of others. Originally, it was thought that the primary reason for the lack of breeding among subordinates is due to reproductive suppression from dominant breeders (Emlen 1982), and many theoretical models of reproductive skew are based on this assumption (reviewed in Hager and Jones (2009)). However, reproductive skew can also be increased via inbreeding avoidance. For example, in Damaraland mole-rats Fukomys damarensis, colonies contain only one female breeder and subordinate females are usually her daughters. Subordinates usually show little or no signs of reproductive behaviour, however when unrelated males are experimentally introduced to a colony, subordinate females show physiological and behavioural signs of sexual activity and often breed with the introduced male (Cooney & Bennett 2000). Subordinate restraint based on inbreeding avoidance may be particularly likely to be found in species where extra-group mating is difficult (Koenig & Haydock 2004), as is likely to be the case in mole-rats, which live in subterranean burrows and rarely venture above ground (Bennett & Faulkes 2000). Similar patterns have been shown in other species, and a large body of evidence now exists to demonstrate the importance of inbreeding avoidance in determining reproductive skew (reviewed in Koenig and Haydock (2004)). Nevertheless, inbreeding avoidance is still rarely considered in theoretical models of reproductive skew (reviewed in Hager and Jones (2009)).

Inbreeding avoidance via female promiscuity is likely to impact on helping behaviour. Unless the extra-pair or extra-group male is related to the within-group male breeder, EGP will likely reduce relatedness between group-members and hence may have a negative impact on helping effort. Although this possibility has not been tested directly, it has been shown that even fine-scale differences in relatedness to the brood can impact on helping rates (e.g. bell miners *Manorina melanophrys* (Wright *et al.* 2009)). In Seychelles warblers, helping behaviour has been linked to EGP as female helpers use the presence of their mother but not their social fathers (i.e. the dominant male present on the territory where they hatched) as a cue to help, as the high level of EGP means that the social father may well not be a relative (Komdeur et al. 2004). This may result in a reduction or absence of helping behaviour if the female breeder on a territory dies, regardless of whether or not the genetic father is still present.

Although relatedness to young does not always impact on individual decisions of whether to provide help (Clutton-Brock *et al.* 2001a), comparative studies across birds and mammals find that relatedness between group members is important in the evolution of cooperative breeding (Griffin & West 2003). It is therefore likely that the method of inbreeding avoidance that a species uses directly influences whether or not that species evolves cooperative breeding, via its influence on relatedness. In species where subordinates avoid inbreeding by restraint, reproductive skew is likely to be high and monogamy may be the most likely mating system. Phylogenetic analyses have indeed shown that monogamy promotes the evolution of cooperative breeding through increasing withingroup relatedness (Cornwallis *et al.* 2010, Lukas & Clutton-Brock 2012). Conversely, inbreeding avoidance via promiscuity reduces within-group relatedness and is therefore likely to lead to the loss of cooperative breeding over evolutionary time (Cornwallis et al. 2010, Lukas & Clutton-Brock 2012).

Inbreeding may have additional impacts on helping behaviour besides influencing relatedness within groups. Those studying helping behaviour have often remarked on the high level of individual differences in contributions to cooperative activities (Bergmüller, Schürch & Hamilton

2010, English, Nakagawa & Clutton-Brock 2010). Some of these differences can be explained by differences in the relative costs and benefits of helping which co-varies with factors including (but not limited to) age, sex and condition as well as relatedness (reviewed in (Heinsohn & Legge 1999, Russell 2004). However, much variation in helping effort remains unexplained. It is possible that inbreeding may play a part; if inbred individuals are of lower quality than outbred individuals, inbreeding may lead to a reduction in propensity to help. Alternatively, inbred individuals may be poor competitors over reproductive opportunities, and may therefore increase their input into help thus gaining indirect fitness benefits. Although these possibilities have not been tested explicitly (but see tentative evidence from Nielsen (2013)), studies have shown that inbreeding depression impacts on body condition (Keller & Waller 2002), and condition in turn influences cooperation (Clutton-Brock *et al.* 2002, van de Crommenacker, Komdeur & Richardson 2011), therefore providing a plausible mechanism for inbreeding effects.

Finally, both inbreeding and inbreeding avoidance in cooperatively breeding species are likely to have implications for population growth and viability, and therefore may be of particular interest in species of conservation concern. Anthropogenic habitat fragmentation often constrains dispersal and hence can lead to increased levels of inbreeding and inbreeding depression (Edmands 2007). In this situation, conservationists may attempt 'genetic rescue' whereby unrelated individuals are introduced from another population, an approach that has proved to be successful for several species (Edmands 2007). Such translocations also risk inducing outbreeding depression if the population exhibits some degree of local adaptation, however the costs of inbreeding are likely to outweigh the risk of outbreeding depression in the majority of cases.

The effects of inbreeding and outbreeding are likely to be important in the conservation management of all species, but cooperative breeders require additional consideration. For example, when making predictions about population viability, conservationists often make the assumption of

random mating, however the assumption is unlikely to be valid in species with additional kin recognition mechanisms, such as occurs in many cooperative breeders (Jamieson et al. 2009). Here, inbreeding avoidance can reduce opportunities for breeding and so can lead to substantial population declines by lowering the effective population size. For example, in a reintroduced population of ~220 African wild dogs *Lycaon pictus*, inbreeding avoidance mechanisms have been projected to massively increase population extinction risk from just 1.6 % over 100 years to certain extinction within 19 - 63 years (Becker *et al.* 2012). In the acorn woodpecker *Melanerpes formicivorus*, inbreeding avoidance means that breeding vacancies that arise after the death of a dominant often remain unfilled, leading to a reduction in the reproductive potential by 9-12%, representing a ~2% annual decline in population growth (Koenig, Stanback & Haydock 1999). In such species, it may be worth considering employing additional measures to increase encounter rate with unrelated individuals such as increasing habitat connectivity or, where this is not possible, moving dispersers between populations.

Conclusion

Although the issue of inbreeding has been a subject of great historical interest, we have achieved a much better understanding of its extent, consequences, and the mechanisms by which it acts in the last 13 years. In particular, cooperative breeding systems evolve and are shaped by many factors linked to inbreeding such as relatedness and population dynamics. Consequently, not only are cooperative breeders particularly tractable systems for many remaining questions in the study of inbreeding more generally, but they also present many unique questions and challenges that will lead to a much better understanding of the link between genetic and social attributes of a population. Finally, the information gained from such studies will be important not only from an academic perspective, but also promises to inform conservation programmes for cooperative species.

Box 2. Measuring inbreeding

Pedigrees: A common way to investigate the frequency, distribution and consequences of inbreeding is to use a pedigree. This approach requires accurate parentage assignments, which generally requires genetic parentage analysis, at least to determine paternity. Parentage is usually assigned using a panel of 5-30 microsatellites; short repetitive sequences of DNA that occur throughout the genome. Microsatellites provide an ideal genetic marker for parentage assignment because the laboratory work involved is relatively cost-effective, they provide single locus information, are codominant, are highly variable, and can be amplified from relatively poor-quality DNA allowing non-invasive sampling techniques (Pemberton 2008). Parentage analysis can then be conducted using a variety of computer programmes including Cervus (Marshall et al. 1998), Colony (Wang & Santure 2009), and MasterBayes (Hadfield 2009) which is implemented in statistical programme R. Pemberton (2008) and Walling et al. (2010) provide further details on these programmes and their respective advantages and disadvantages. Once a pedigree has been constructed, the inbreeding coefficient (f) of each individual can be estimated. An f of 0.25 indicates close inbreeding while an f of 0.125 indicates moderate inbreeding (see Box 1). f values can be estimated from pedigrees, even when the pedigree is incomplete (very few pedigrees derived from wild populations have parentage assigned to all individuals (Marshall et al. 2002)), but pedigree depth, accuracy and structure must be taken into account when performing downstream analyses (Pemberton 2008).

Genetic markers: When it is not possible to generate a pedigree, for example when long-term life-history data is not available, a panel of microsatellites can be used to directly estimate inbreeding. Inbred individuals are expected to be less genetically diverse (heterozygous) than

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outbred individuals so inbreeding depression can be assessed through investigating associations between heterozygosity and fitness-related traits (known as heterozygosity-fitness correlations (HFCs)). The relative ease of this approach has resulted in a large number of studies investigating HFCs, many of which find positive associations (reviewed by Lehmann and Perrin (2003), Pemberton (2008), Chapman et al. (2009), Szulkin, Bierne and David (2010)). However, the effectiveness of this approach has been called into question as the correlation between inbreeding coefficient and microsatellite heterozygosity is often low (Balloux, Amos & Coulson 2004, Pemberton 2008, Szulkin et al. 2010). Nevertheless, where inbreeding is relatively common (for example due to disassortative mating between relatives, small population sizes, bottlenecks, admixture or immigration), HFCs may be detectable using microsatellites (Szulkin et al. 2010), especially where a large panel of markers is used (Stoffel et al. 2016). Furthermore, where HFCs have been found, there has also been debate about their cause. Although they may be a result of an effect of genome-wide heterozygosity on fitness (known as general effects), they can also result from linkage between a single locus and a fitness trait (known as local effects) (however, small microsatellite datasets are rarely suitable for the detection of local effects, reviewed in Pemberton (2004), Szulkin et al. (2010)).

As the ability of genetic markers to detect inbreeding increases with the number of markers used (Hoffman 2014), more recent studies have used genomic data such as large panels of **single nucleotide polymorphisms (SNPs)** to investigate inbreeding (e.g. over 10 000 individual SNPs) (reviewed in (Kardos *et al.* 2016)). With such a large number of markers, heterozygosity correlates well with pedigree inbreeding and the problem of local effects driving HFCs disappears (Heinsohn & Legge 1999, Hoffman *et al.* 2014). Although currently limited by expense, genomic methods have been shown to reveal inbreeding depression in cases where pedigrees have failed to do so, such as in (non-cooperative) deer and sheep (Bérénos *et al.* 2016, Huisman *et al.* 2016). Similar genomic studies in cooperative breeders will provide much greater power in quantifying inbreeding and its effects.

Box 2. Cont.

Measuring population-level inbreeding: Some studies estimate the level of inbreeding in a population by calculating Wright's F-statistics using a panel of genetic markers (usually microsatellites). Three F-statistics are commonly calculated (1) F_{ST}: the degree of reduction in heterozygosity of subpopulations due to population subdivision, (2) Fis: the reduction in heterozygosity of individuals relative to their subpopulation, caused by non-random mating within subpopulations, and (3) Fit: the reduction in heterozygosity of individuals relative to the entire population. Note that such statistics do not measure individual-level inbreeding and hence caution should be applied when interpreting them and statements such as 'F_{IS} was zero, hence there was no evidence for inbreeding in the population' are misleading (Keller & Waller 2002). Instead, an F_{IS} of zero simply suggests random mating within the subpopulation, and is not equivalent to finding a lack of mating between relatives using a pedigree. Interpreting F-statistics may be particularly challenging for species with complex social and/or mating systems (as many cooperative breeders do). As an example, banded mongoose social groups have significantly negative F_{IS} values and F_{IT} values close to zero (Nichols et al. 2012), which could be interpreted as outbreeding within groups and low levels of inbreeding in the population. However, a pedigree of the same population reveals high levels of inbreeding, with 8% of pups being the product of close inbreeding and 27% of pups being the product of moderate inbreeding (Nichols et al. 2014).

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Figures

Figure 1. Two closely related species (family Herpestidae) with contrasting patterns of inbreeding. The banded mongoose (a) shows low reproductive skew within groups and high levels of natal philopatry with both sexes frequently breeding within natal groups. This results in relatively high levels of close and moderate inbreeding (8% and 27% pups respectively) (Nichols et al. 2014). The meerkat (b) shows high reproductive skew within groups, with natal subordinate females breeding occasionally with immigrant males. Here, close inbreeding is absent and moderate inbreeding occurs in 6.6% of the population, almost always occurring between unfamiliar relatives from different natal groups (Nielsen et al. 2012).