

INVITED REVIEW

Genetic quality and sexual selection: an integrated framework for good genes and compatible genes

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Abstract

Why are females so choosy when it comes to mating? This question has puzzled and marveled evolutionary and behavioral ecologists for decades. In mating systems in which males provide direct benefits to the female or her offspring, such as food or shelter, the answer seems straightforward — females should prefer to mate with males that are able to provide more resources. The answer is less clear in other mating systems in which males provide no resources (other than sperm) to females. Theoretical models that account for the evolution of mate choice in such nonresource-based mating systems require that females obtain a genetic benefit through increased offspring fitness from their choice. Empirical studies of nonresource-based mating systems that are characterized by strong female choice for males with elaborate sexual traits (like the large tail of peacocks) suggest that additive genetic benefits can explain only a small percentage of the variation in fitness. Other research on genetic benefits has examined nonadditive effects as another source of genetic variation in fitness and a potential benefit to female mate choice. In this paper, we review the sexual selection literature on genetic quality to address five objectives. First, we attempt to provide an integrated framework for discussing genetic quality. We propose that the term ‘good gene’ be used exclusively to refer to additive genetic variation in fitness, ‘compatible gene’ be used to refer to nonadditive genetic variation in fitness, and ‘genetic quality’ be defined as the sum of the two effects. Second, we review empirical approaches used to calculate the effect size of genetic quality and discuss these approaches in the context of measuring benefits from good genes, compatible genes and both types of genes. Third, we discuss biological mechanisms for acquiring and promoting offspring genetic quality and categorize these into three stages during breeding: (i) precopulatory (mate choice); (ii) postcopulatory, prefertilization (sperm utilization); and (iii) postcopulatory, postfertilization (differential investment). Fourth, we present a verbal model of the effect of good genes sexual selection and compatible genes sexual selection on population genetic variation in fitness, and discuss the potential trade-offs that might exist between mate choice for good genes and mate choice for compatible genes. Fifth, we discuss some future directions for research on genetic quality and sexual selection.

Keywords: direct benefit, Fisherian, genetic benefits, genetic compatibility, indirect benefit, mate choice, multiple mating

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Introduction

Evolutionary and behavioral ecologists have long been interested in, and puzzled by mate choice. In many species,

females are highly selective when it comes to mating (Darwin 1871; Bateson 1983; Andersson 1994; Kokko *et al.* 2003). In some of these species, females are congruent in their mate preference for a particular male, while in other species, females are incongruent in their preference, with each preferring a different male. The least controversial models of female mate choice emerged from resource-based mating systems. In such systems, males provide resources

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directly to females or offspring such as food, shelter, parental care and protection from predators. These resources obviously could have a profound impact on female fitness. Therefore, it was straightforward to posit that natural selection could lead to the evolution of the preference through direct selection. Furthermore, researchers realized that natural selection could lead to the evolution of male indicator traits that facilitated mate choice by advertising the quality or quantity of a male's resources (reviewed in Møller & Jennions 2001).

However, there are many other mating systems (and perhaps most mating systems) in which females receive no resources from males (called nonresource-based mating systems), yet females still express a preference among males. For example, in some taxa, males display at fixed courtship, territories known as leks and these males provide only genes (i.e. sperm) to their mates. Females visiting leks typically show congruence in their mating preference for males with the most elaborate trait (Höglund & Alatalo 1995). This congruence appears paradoxical given that a female only receives genes from the male she selects (termed the 'paradox of the lek'; reviewed in Kirkpatrick & Ryan 1991; Tomkins *et al.* 2004). Attempts to resolve the paradox have postulated that females receive an indirect benefit in the form of increased genetic quality of their offspring. Specifically, models have shown that the preferred male must provide genes that increase the survivorship or mating success of the offspring as compared to the genes provided by less desirable males (reviewed in Kokko *et al.* 2003; Mead & Arnold 2004). Empirical research on lek mating systems, as well as other nonresource-based mating systems have confirmed the association between mate preference and increased offspring viability, although the fitness effects appear small at only a few percent (Møller & Alatalo 1999; Jennions *et al.* 2001; also see Kirkpatrick & Barton 1997). However, few studies have examined the association between mate preference and the subsequent mating success of offspring, which might be a particularly important component of fitness in systems where females choose mates on the basis of elaborate secondary sexual ornaments (Hunt *et al.* 2004).

What about mating systems in which females each prefer a different male and yet receive no resources from any of them? Researchers have postulated that these females also must be selecting males that increase the genetic quality of their offspring. However, unlike good gene mating systems, in these mating systems genetic quality reflects interactions between paternal and maternal genomes. Based on these gene–gene interactions, the genetic compatibility hypothesis was proposed (Trivers 1972; Zeh & Zeh 1996; Zeh & Zeh 1997). This hypothesis suggests that favorable interactions between genes within an individual can lead to increased survivorship through, for example, heterozygote advantage (overdominance).

The purpose of this review is to provide a synthesis of the literature on genetic quality from the perspective of sexual selection. We build on previous reviews, which have focused on either additive genetic effects (e.g. Møller & Alatalo 1999; Hunt *et al.* 2004) or nonadditive genetic effects (e.g. Zeh & Zeh 1996, 1997; Tregenza & Wedell 2000), and provide a framework to integrate both types of genetic quality. We begin by (re)defining genetic quality in terms of both 'good genes' and 'compatible genes', providing examples of each from biological systems, and distinguishing between genetic quality and genetic benefits.

Defining genetic quality based on good genes and compatible genes

We define genetic quality based on the contribution a gene variant (allele) or genotype (alleles) makes to an individual's fitness; an individual is of higher genetic quality when it possesses an allele or genotype that increases its fitness relative to that of an individual with a different allele or genotype. Fitness, in turn, can be defined by the individual's lifetime reproductive success (LRS), which is composed of both survivorship and breeding success: $LRS = \sum l_x \times m_x$; where l_x is the survivorship to age x , m_x is the breeding success (number of offspring produced) at age x , and the summation is over an individual's lifetime (Stearns 1992). Thus, genetic quality can be defined without explicitly differentiating between benefits of increased survivorship or increased breeding success. Conversely, it is not just one of these components but both l_x and m_x are important for determining genetic quality (Kokko *et al.* 2002; Hunt *et al.* 2004). Because genetic quality is defined based on an individual's fitness, it must have two components — additive genetic effects, which we refer to as 'good genes', and nonadditive genetic effects, which we refer to as 'compatible genes' (Box 1–3).

Consider the following examples. Studies of the major histocompatibility complex (MHC) have provided some of the best examples of compatible genes (reviewed by Potts & Wakeland 1990; Apanius *et al.* 1997; Edwards & Hedrick 1998; Tregenza & Wedell 2000; Bernatchez & Landry 2003). MHC is found in all vertebrates and is a cluster of linked genes broadly classified into either class I or class II (in humans, MHC is referred to as the HLA, human leukocyte antigen). The protein products of these genes are involved in immune response regulation. In many populations, the MHC is highly polymorphic and most individuals are heterozygous at the coding loci possibly because heterozygous individuals are able to present a wider range of foreign peptides to T-cells (Klein & Figueroa 1986). In such populations, any nonidentical homologues at either the class I or II genes can be considered compatible.

For example, Arkush *et al.* (2002) used *in vitro* fertilization techniques with chinook salmon (*Oncorhynchus tshawytscha*)

Box 1 Defining genetic quality

Genetic quality has two components, good genes and compatible genes:

A *good gene* is defined as an allele that increases fitness independent of the architecture of the remaining genome, which, in diploid organisms, includes the homologue to the particular 'good allele'. Across the genome, good genes will show additive genetic variation. Thus, when variation in fitness exists as a result of good genes, the population will respond to directional selection.

A *compatible gene* is defined as an allele that increases fitness when in a specific genotype; i.e. when paired with

a specific homologue (overdominance) or allele at another gene locus (epistasis). Across the genome, compatible genes will show nonadditive genetic variation. Thus, when variation in fitness exists because of compatible genes, the population will not respond to directional selection, but the mechanisms of acquiring compatible genes (e.g. preference alleles) will respond to directional selection. NB. We use the term 'gene' broadly in the sense of a region of DNA that can be inherited independent of another region of DNA. Thus, a gene may include several different coding regions when these regions are in close proximity on a chromosome such that recombination is infrequent.

to produce individuals that varied in their diversity at the MHC. Specifically, they were able to generate full-siblings that were either homozygous or heterozygous at the MHC class II set of genes. The researchers then exposed the families to infectious hematopoietic necrosis virus (IHVN). IHVN causes epizootics among salmonid fish and is considered to be one of the most important viral pathogens affecting these fish in North America (see Arkush *et al.* 2002). They found that for seven of 10 families, survival was higher in the heterozygous siblings than the homozygous siblings, and they calculated the selection disadvantage of homozygotes to be 8.5%. Their experimental approach was particularly powerful because by comparing full siblings carrying different MHC genotypes, effects as a result of other segregating genes were minimized. Analogous results have been found in MHC-congenic mouse strains (McClelland *et al.* 2003).

The MHC also provides an excellent example of good genes and serves to illustrate the distinction between good genes and compatible genes. Lohm *et al.* (2002) investigated interactions between specific MHC alleles and resistance to bacterial infection by *Aeromonas salmonicida* in Atlantic salmon (*Salmo salar*). Full-sibling broods were generated that contained individuals with different combinations of alleles. The researchers focused on two alleles, referred to as *e* and *j*. In the first experiment, they generated siblings that were *e/+*, *j/+* and *e/j*; where + represents an allele other than *e* or *j*. Over an 18-d period post infection, they found that *j/+* individuals had the lowest survivorship, while *e/+* and *e/j* individuals had similar levels of survivorship. In a similar second experiment, they generated siblings that were *e/e*, *j/j* and *e/j*, and found that *j/j* individuals had the lowest survivorship, while *e/e* and *e/j* individuals had similar levels of survivorship. In this paper, MHC heterozygosity was not important for increasing fitness, but possessing the *e* allele was important for increasing fitness. Indeed, Lohm *et al.* (2002) calculated the

fitness advantage of possessing the *e* allele to be as high as 49%. Thus, in a population challenged predominately by *A. salmonicida*, the *e* allele would clearly confer a fitness advantage and thereby represent a good gene. A similar result also has been demonstrated in whitefish, *Coregonus* sp. (Wedekind *et al.* 2004).

Measuring genetic quality and genetic benefits

To measure genetic quality and genetic benefits (see box 2), variation in both genes and fitness must be assessed. An individual's fitness includes both survivorship and breeding success (LRS) and, ideally, the LRS of the individual's sons and daughters (Hunt *et al.* 2004). Researchers have employed a variety of approaches to assess genetic benefits. These approaches can be grouped into three categories: (1) measuring genetic benefits from good genes; (2) measuring genetic benefits from compatible genes; and (3) measuring genetic benefits from both good genes and compatible genes.

Measuring genetic benefits from good genes

Many studies of good genes have used a correlational approach, whereby a phenotypic attribute of a set of parents, usually of males, is related to a surrogate of fitness in their offspring. The square of the correlation coefficient represents the proportion of variation in fitness attributable to good genes. These studies make two important assumptions. First, they assume that the measured phenotypic trait captures genetic variation among individuals. This assumption should be well supported when condition-dependent indicator traits (e.g. sexual ornaments) are measured because such traits should capture additive genetic variation (Rowe & Houle 1996; Tomkins *et al.* 2004; also see Cotton *et al.* 2004). Second, they assume that nongenetic effects are uniform or random (with respect to the trait)

Box 2 Distinguishing between genetic quality and genetic benefits

We have defined genetic quality based on both good gene effects and compatible gene effects on fitness (Box 1). Previous work instead has defined genetic quality more narrowly as the 'breeding value for total fitness', where the breeding value is the 'sum of the additive effects of the genes of an individual on a given trait' (Hunt *et al.* 2004). We emphasize our broader definition, which includes both additive and nonadditive genetic effects, because both effects clearly can contribute to an individual's fitness and thus both components will be subject to natural and sexual selection.

Based on our definition of genetic quality, females do not necessarily obtain a genetic benefit—increased genetic quality of their offspring—by mating with a male that is himself of high genetic quality (Table 1). Only the good gene portion of the genome is heritable and provides a genetic benefit. For example, all else being equal, the offspring of a male with good genes will, on average, have higher fitness than the offspring of a male without the good genes. Thus, all females will benefit from mating with the male with the good gene through increased offspring fitness. Conversely, the offspring of a male with compatible genes will not have higher (or lower) fitness than the offspring of a male without compatible genes, all else being equal, and each female will benefit from mating with a different male that may or may not be of high genetic quality himself.

Consider the following example of a nonresource-based mating system and a simple single-locus model with two alleles denoted A and B. If the A allele is a good gene, for example the A allele provides resistance to a common pathogen, then the AA male has the highest genetic quality, and all females will maximize the genetic quality of their offspring by mating with the AA male because this ensures that their offspring obtain at least one copy of the good gene (Fig. 1a). Conversely, if the A and B alleles instead are compatible genes, for example when there is overdominance, then the AB male has the highest genetic quality, but each female will maximize the genetic quality of her offspring by mating with a different male (Fig. 1b). The AA female should mate with the BB male to ensure that all of her offspring are heterozygous. The BB female should mate with the AA male for the equivalent reason. The AB female could mate with any male because in any case half of her offspring will be heterozygous and half will be homozygous. Only when eggs can differentiate among sperm based on haplotype (reviewed by Zeh & Zeh 1997; Birkhead & Pizzari 2002), will the AB female maximize the fitness of her offspring by mating

exclusively with the AB male because in this case all of her offspring potentially can be heterozygous—i.e. an A egg can select a B sperm, the B egg can select an A sperm.

In resource based mating systems, genetic benefits from compatible genes will trade-off with nongenetic (direct) benefits when direct benefits are positively correlated with male genetic quality. Consider the example in which the A and B alleles are compatible genes. From the AA female's perspective, mating with the BB male will produce offspring with the highest genetic quality, but the BB male is himself of low genetic quality (because he is homozygous) and may have less of direct benefits, such as food or shelter, to provide the female or her offspring (Table 1). Such a trade-off does not occur with good genes because the male that will produce offspring of high genetic quality from the perspective of any female is himself also of high genetic quality (e.g. the AA male in the good genes example above).

Box 2, Table 1 In resource based mating systems, genetic and nongenetic benefits can tradeoff

Male genetic quality	Direct benefit to female or offspring (nongenetic)*	Indirect benefit to offspring (genetic)
Good genes (AA)	+	+
Compatible genes (AB)	+	-

*Assumes that males of high genetic quality provide more direct benefits to females.

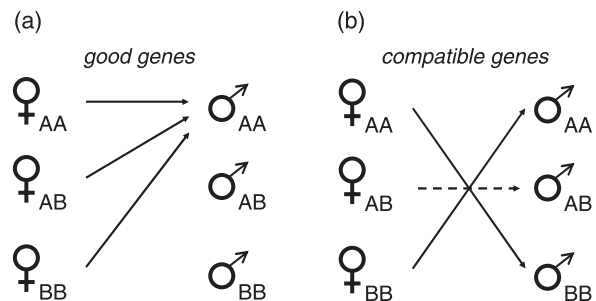


Fig. 1 Genetic quality can be classified as either good genes (additive effects on fitness) or compatible genes (non-additive effects on fitness). (a) When the A allele is a good gene, all females will maximize the fitness of their offspring by mating with the AA male, all else being equal. (b) When the A and B alleles instead represent compatible genes, each female will maximize the fitness of their offspring by mating with a different male, all else being equal. In the absence of haplotype-specific sperm selection by the egg (see text), the AB female could mate with any male because regardless of male genotype, half of her offspring will be heterozygous (dashed line).

Box 3 Mate choice for genetic compatibility vs. avoidance of genetic incompatibility

Mate choice for compatible genes also has been discussed in the context of 'genetic incompatibility avoidance' (Zeh & Zeh 1996, 2003). While fundamentally mate choice for compatible genes is equivalent to avoidance of incompatible genes, this latter context may more effectively capture the essence of genetic quality under some situations. For example, certain strains of *Drosophila melanogaster* carry the P transposon. When females that lack the transposon (called 'M females') mate with males that carry the transposon (called 'P males'), their offspring exhibit high rates of mutation, chromosomal rearrangements and sterility (Rio 1991). All other combinations of matings appear to produce normal offspring. Thus, M females and P males are

incompatible (Zeh & Zeh 1996). Equivalently, we could indicate that M females are compatible with M males, and P females are compatible with both M males and P males.

Inbreeding avoidance may be a second example where genetic incompatibility avoidance better reflects the dynamics of genetic quality than mate choice for compatible genes. When inbreeding depression results from the expression of a deleterious recessive allele, it can be said that the recessive allele is incompatible with an equivalent copy of the allele. Similarly, we could indicate that all other (nondeleterious) alleles at the locus are compatible with the deleterious recessive allele. In this review we elected always to use the compatible gene terminology partly because it mirrors the benefit aspect of mate choice for genetic quality that is implied by the term good gene.

across families. This assumption should be well supported in nonresource-based mating systems (Barber & Arnott 2000; Jennions & Petrie 2000; but see Reyer *et al.* 1999), but may not be well supported in resource-based mating systems (Burley 1988; Sheldon 2000b; Kotiaho *et al.* 2003).

For example, in one of the first studies of mate choice for good genes, Reynolds & Gross (1992) mated female guppies to males that varied in body length at maturation. Guppies are live-bearing, promiscuous tropical fish with a nonresource-based mating system. Reynolds and Gross show that male body length is a trait preferred by females in their population. The authors then estimated the fecundity of daughters when they sexually matured based on offspring weight of their first two broods, and correlated fecundity to their father's body length. The correlation coefficient was $r = 0.65$, and therefore good gene effects explained 42% ($= 0.65^2$) of the variation in daughter fecundity, which is one component of fitness (there was no apparent effect of male body length on daughter survivorship). There is no evidence that female guppies can adjust investment in offspring postfertilization, so this paper demonstrated a strong effect of good genes quality, at least in the laboratory environment in which it was conducted.

In a study on peacocks (*Pavo cristatus*), Petrie (1994) assigned groups of four females to each of eight males in a random breeding design. Peacocks are a lekking species where males provide no resources to their mates or offspring. Males have elaborate tail feathers (called a train) that they display to females during mate choice. The average area of the 'eyes' — brilliant green and blue spots on the tail feathers — is a good measure of the elaboration of the train and of a male's attractiveness to females (Petrie & Halliday 1994). Petrie therefore calculated the average eye area for the eight males and correlated this with the growth

rate and survival of each male's offspring. She found that offspring sired by males with greater eye area had higher survivorship when released into a seminatural environment (correlation between father eye area and offspring survivorship: $r = 0.79$, $r^2 = 0.62$). Petrie concluded that females gain good genes for their offspring by mating with males that have large eyes on their train. However, in other birds, it has been suggested that females put more resources into eggs (by laying larger eggs or by adding more testosterone) that are sired by attractive males (Gil *et al.* 1999; Cunningham & Russell 2000). If peahens are also capable of such differential investment then the effect size resulting from good genes from Petrie's study may be inflated (but see Petrie *et al.* 2001).

Møller & Alatalo (1999) performed a meta-analysis on 22 studies that examined the correlation between a phenotypic trait of sires and the survivorship of their offspring. They estimated the overall effect of good genes to be $r = 0.22$ ($r^2 = 0.048$; range $r = -0.30$ – 0.79). When the studies were weighted by sample sizes, this estimate dropped to $r = 0.12$ ($r^2 = 0.014$), which is consistent with estimates of heritability of fitness as a result of additive genetic variation (Gustafsson 1986; Charlesworth 1987; Burt 1995; Morjan & Rieseberg 2004; but see Houle 1992). A second meta-analysis performed on 47 studies (40 species total) was consistent with the original study (Jennions *et al.* 2001). However, many of the studies included in the meta-analyses may have been confounded by environmental effects across families because the mating systems analyzed were resource-based, therefore the survivorship estimates may have included direct effects such as parental care. If males with a larger or otherwise better trait provided more food or other direct benefits to their offspring than males with a smaller trait (e.g. Keyser & Hill 2000), then the estimated

effect size would be an overestimate of good gene effects. Conversely, if males with a larger trait provided less food to their offspring than males with a smaller trait (e.g. Duckworth *et al.* 2003), then the estimated effect size would be an underestimate of good gene effects. Additionally, if the good genes underlying the expression of the male trait also increase the breeding success (m_x), then the estimated good gene effect size would further be underestimated. Thus, the mean fitness effect of good genes is unclear (Hunt *et al.* 2004; Tomkins *et al.* 2004).

To avoid confounding effects of direct benefits and differential maternal investment, other studies have utilized split-clutch *in vitro* fertilization (e.g. Welch *et al.* 1998; Barber *et al.* 2001; Sheldon *et al.* 2003; Neff 2004). For example, Welch *et al.* (1998) split clutches of eggs from female gray tree frogs (*Hyla versicolor*) and fertilized one half with sperm from a male that called for a long duration and the other half with sperm from a male that called for a short duration. Long calling males are preferred over short calling males by most females. The authors then compared the performance (e.g. growth rate, survivorship) of the maternal half-siblings and found that those sired by long calling males generally outperformed those sired by short calling males. For instance, in 1 year of their high food treatment, they found that survivorship during the larval period was 10% higher (0.702 vs. 0.637) for offspring sired by long calling males than offspring sired by short calling males.

In bluegill sunfish (*Lepomis macrochirus*), Neff (2004) split clutches from females and fertilized one half with sperm from a male adopting the parental life history, and the other half with sperm from a male adopting the cuckold life history. Females may prefer to mate in the presence of cuckolders as they appear to release three times as many eggs when mating simultaneously with a cuckold male and parental male than when mating only with a parental male (Fu *et al.* 2001). Neff found that offspring sired by cuckold males were 5% larger at the end of the endogenous feeding period than the half-sibling counterparts sired by parental males. Based on size-dependent predation by *Hydra canadensis*, a major predator of bluegill larvae (Elliott *et al.* 1997), Neff predicted that the increased size of the cuckold offspring conferred upwards of 3.5-fold higher survivorship than the parental offspring.

Measuring genetic benefits from compatible genes

A male with good genes should produce offspring with higher fitness regardless of the maternal genetic contribution, while a male with compatible genes will produce offspring with higher fitness only when matched with a specific maternal haplotype. Based on this premise, Johnsen *et al.* (2000) examined genetic quality in bluethroat (*Luscinia svecica*) offspring and provided the first evidence for compatible gene mate choice in an extra-pair mating

system. Bluethroats are a socially monogamous passerine bird with biparental care. Females frequently copulate with extra-pair males (i.e. males that are not their social mate). The extra-pair males provide no direct benefits and, as in other birds, there is no evidence that male parents differentiate between their own offspring and extra-pair young (see Kempenaers & Sheldon 1996). To examine offspring genetic quality, Johnsen and colleagues measured cell-mediated immunity for each chick in their study by a subcutaneous injection of phytohemagglutinin (PHA) in one of the wings. PHA causes a local swelling response that reflects T-cell reactivity, and the response is heritable and correlated with survival and longevity in other passerines (e.g. Saino *et al.* 1997; Birkhead *et al.* 1999). The authors compared the immune response of a male's offspring from his social mate (within-pair young, WPY) and his offspring with a second extra-pair female (extra-pair young, EPY). Johnsen and colleagues (2000) postulated that if females seek extra-pair matings for good genes, then there should be no difference in the immune response of the WPY and EPY for a given male (i.e. paternal half-siblings). Conversely, if females seek extra-pair matings for compatible genes then the immune response of EPY should be better than that of the WPY for a given male. Across 14 paternal half-sibling comparisons, the authors found that for 12 comparisons, the EPY had better immunocompetence than that of the WPY. Furthermore, offspring type (EPY or WPY) captured 13% of the variation in immune response, while paternal identification captured only 4%. These data are best explained by mate choice for compatible genes through extra-pair matings (also see Blomqvist *et al.* 2002; Foerster *et al.* 2003; Freeman-Gallant *et al.* 2003).

A second approach to quantify the potential genetic benefits from compatible genes is to analyze the effect of specific genes known to contribute to nonadditive genetic variation. For example, Penn *et al.* (2002) exposed mixed populations of MHC homozygous and heterozygous mice (*Mus domesticus*) to various strains of avirulent and virulent *Salmonella enterica serovar*, *Salmonella typhimurium* and *Listeria monocytogenes*. Over a 30-week trial, they found that heterozygous individuals had an approximately 2% survivorship advantage to the avirulent strains than homozygous individuals, but no advantage to the virulent strains. In a second mixed population that was not experimentally exposed to specific pathogens (but was exposed to uncontrolled, 'natural' pathogens), they found that heterozygous individuals had approximately 19% higher survivorship than homozygous individuals over the 30-week trial.

Measuring genetic benefits from both good genes and compatible genes

In many mating systems, females mate with more than one male during a single reproductive event (Andersson 1994;

Table 1 Multiple mating and genetic quality. The data are from 12 species and 14 studies that experimentally manipulated the degree of multiple mating (low or high) by females and measured a component of fitness

Species	Measure of fitness	Degree of multiple mating*		Effect size (%)†	Controlled direct benefits‡	Reference
		low	high			
Australian field cricket (<i>Teleogryllus oceanicus</i>)	hatching success	0.48	0.55	15	yes	Simmons 2001
Bulb mite (<i>Rhizoglyphus robini</i>)	offspring number produced by daughters (standardized)	0.93	1.2	29	yes	Konior <i>et al.</i> 2001; also see Kozielska <i>et al.</i> 2004
Bumble-bee (<i>Bombus terrestris</i>)	offspring number (males [top] or queens [bottom])§,¶	19 2	37 5	95 ns	yes	Baer & Schmid-Hempel (1999)
Cuis (<i>Galea musteloides</i>)	offspring survivorship	0.54	0.92	70	no	Keil & Sachser (1998)
Decorated cricket (<i>Grylloides sigillatus</i>)	offspring survivorship (<i>ad libitum</i> treatment)¶	0.65	0.69	ns	no	Sakaluk <i>et al.</i> (2002)
Field cricket (<i>Gryllus bimaculatus</i>)	hatching success	0.41	0.53	29	yes	Tregenza & Wedell (1998)
Grain beetle (<i>Tenebrio molitor</i>)	hatching success	0.82	0.84	ns	yes	Worden & Parker (2001)
Ground cricket (<i>Allonemobius socius</i>)	hatching success	0.19	0.55	189	yes	Fedorka & Mousseau (2002)
Guppy (<i>Poecilia reticulata</i>)	offspring number§	5.1	8.8	73	no	Evans & Magurran (2000)
Pseudo scorpion (<i>Cordylochernes scorpioides</i>)	offspring number§	38	49	29	no	Zeh (1997)
	offspring number§	137	181	32	yes	Newcomer <i>et al.</i> (1999)
Red flour beetle (<i>Tribolium castaneum</i>)	offspring number sired by sons (average of 3 trials)	1.4	2.0	43	no	Pai & Yan (2002)
Sierra dome spider (<i>Neriene litigiosa</i>)	hatching success	0.65	0.78	ns	no	Watson (1998)

*For all studies 'low' refers to females mated to a single male except for the bees, in which case the singly mated females were mated to four males which were brothers. When more than two multiple mating groups were examined, 'high' represents the group with the largest number of mates; †Calculated from high value/low value - 1; 'ns' denotes a nonsignificant difference between the two mating treatments at $\alpha = 0.05$; ‡Controlled for potential direct benefits passed to female via ejaculates; for example, by controlling the number of matings or the number of spermatophores; §Offspring number is a measure of offspring survivorship (see text); ¶Values were approximated from results reported in a figure in the cited reference.

Birkhead & Møller 1998). In the absence of direct benefits from males, such as food or shelter, it has been hypothesized that female multiple mating evolved as a mechanism to increase overall genetic quality of the offspring (reviewed by Jennions & Petrie 2000). Presumably, a female could obtain sperm from multiple males and fertilize her egg with the sperm that would produce an offspring of the highest possible genetic quality. Thus, to calculate the fitness effects of overall genetic quality (both good genes and compatible genes), researchers have taken advantage of mating systems in which females multiply mate and employed experiments that randomly allocate females to

either a single mating group, in which females are given one male with which to mate, or a multiple mating group, in which females are given multiple males with which to mate (Table 1). Females in the multiple mating group should produce offspring of higher fitness than females in the single mating group, and the magnitude of the genetic benefits can be calculated from the difference in the fitness of offspring from the two groups. These studies typically cannot distinguish between good gene and compatible gene effects on fitness. They assume that there are mechanisms that enable the selective utilization of sperm based on genotype (e.g. Eberhard 1996; also see biological

mechanisms in succeeding section), and sperm is not limited in the single mating group. Furthermore, several of these studies did not control for the number of matings between the single and multiple mating groups and therefore assumed that there are no direct benefits passed to the female via, for example, nutrients in the ejaculate.

As an example, Zeh (1997) studied pseudoscorpions (*Cordylochernes scorpioides*) and mated one group of females to a single male and a second group of females to two or three males. Females were then left largely undisturbed until the offspring hatched from the female's brood sac, at which time the offsprings were counted. The number of offspring each female produced was adjusted for her size (using cephalothorax length as a covariate in the analysis) in an attempt to remove maternal environmental effects such as variation in fecundity because of body size. Thus, Zeh's measure of offspring number represents the viability (early survivorship) of the offspring through to emergence from the brood sac. She found that females from the multiple mating group produced 29% more offspring than females from the single mating group. However, Zeh did not control for the number of matings between her two groups and thus the number of spermatophores accepted by females in each group. Nevertheless, a follow-up study by her group, which controlled for the number of spermatophores, found nearly identical results (Newcomer *et al.* 1999). In an attempt to tease apart good gene and compatible gene effects, Zeh (1997) also mated a set of males each to a different pair of females and compared offspring viability. She found no correlation between the number of offsprings hatched by the pairs of females and therefore suggested that the increased viability of offspring from females in the multiple mating group was attributable to compatible gene effects. However, in this latter experiment, any paternal good gene effect might be masked by differences in genetic and environmental effects between the two females.

In a similar study on field crickets (*Gryllus bimaculatus*), Tregenza & Wedell (1998) created three experimental groups. In the first group, females each were mated to a single male four times, in the second group, females were mated to two different males twice each, and in the third group, females were mated to four different males once each. Their design therefore controlled for mating number and potential direct benefits that males may pass to females along with their ejaculate. Tregenza and Wedell (1998) found no significant difference in the number of eggs laid by females in the three treatments (consistent with an assumption of no difference in maternal environmental effects across the three treatments), but they did find a significant difference in the number of eggs that hatched. On average, 41% of the eggs hatched from females mated to a single male, 47% hatched from females mated to two males, and 53% hatched from females mated to four

males. Thus, offspring from females that mated with four males had 29% higher (= 53/41) hatching success than offspring from females that mated with only one male.

In total, across 14 experimental studies on 12 different species, researchers have found anywhere from no significant difference in offspring fitness between single mated and multiple mated females to 189% increase in fitness for offspring from multiple mated females (Table 1).

Other studies have taken advantage of natural variation in the degree of multiple mating among females to investigate genetic quality (e.g. Madsen *et al.* 1992; Olsson *et al.* 1994, 1996; Kempenaers *et al.* 1999). For example, Madsen *et al.* (1992) examined multiple mating and offspring genetic quality in adders (*Vipera berus*), a small venomous snake. Using detailed behavioral observations during the breeding season, they were able to determine the number of males the females mated with. Females were then collected and maintained in the laboratory until they gave birth. The authors found that females that mated with more males had a smaller proportion of their brood still born ($r = -0.40$, $n = 34$, $P < 0.02$). They propose that by multiply mating, females increase intrauterine sperm competition, which would increase the genetic quality of the offspring if sperm competitiveness was correlated with the quality of its genes (also see Olsson & Madsen 2001). Correlative studies arguably are not as strong as experimental manipulation studies because the correlative studies cannot easily rule out confounding effects, such as maternal environmental effects, that might be associated with the degree of multiple mating.

A third type of study has attempted to measure offspring genetic quality in nonresource-based mating systems by mating some males or females to a preferred mate and other males or females to a nonpreferred mate. These studies attribute differences in the fitness of offspring from preferred and nonpreferred matings to offspring genetic quality. For example, in house mice (*Mus musculus*), Drickamer *et al.* (2000) found that offspring from preferred matings had higher survivorship than offspring from nonpreferred matings. Specifically, offspring from preferred matings had a 76% survivorship 60 days after being introduced into seminatural enclosures while offspring from nonpreferred matings only had a 44% survivorship (also see Drickamer *et al.* 2003; Gowaty *et al.* 2003). The authors, however, could not rule out direct benefits (differential investment) because females may pass more resources to their embryos via the placenta when mated to a preferred male. In deep-snouted pipefish (*Syngnathus typhle*), Sandvik *et al.* (2000) found that offspring of preferred matings had higher survivorship than the offspring of nonpreferred matings, both when females were allowed to select a mate (proportion surviving predation: *c.* 68% vs. 48%) and when males were allowed to select a mate (*c.* 58% vs. 39%). In guppies (*Poecilia reticulata*), however, Nicoletto (1995) found no evidence for a difference in offspring fitness from the two types of matings.

A more comprehensive approach for measuring genetic benefits from both good genes and compatible genes is the use a breeding design that examines all crosses between two sets of individuals (sometimes referred to as the 'North Carolina Design II'; see Lynch & Walsh 1998; p. 598). A set of N_s sires are mated in all combinations with a set of N_d dams and $N_s \times N_d$ families are generated. Some measure of fitness, such as hatching success or survivorship, is obtained for each family, and a two-way ANOVA can be used to partition the variation in fitness among additive genetic effects (good genes), nonadditive genetic effects (compatible genes), environmental maternal effects and other (unmeasured) environmental effects.

The North Carolina Design II was utilized by Wedekind *et al.* (2001) to examine genetic quality of alpine whitefish (*Coregonus* sp.). The authors performed all 100 crosses of 10 males and 10 females (i.e. a statistically balanced design). Whitefish are external fertilizers and therefore eggs can be easily stripped from females and fertilized with milt from a male. Each family was then split into four to provide a replicated design. The eggs were reared in the same environment and mortality for each family replicate was documented during two phases of development: (1) early mortality – the proportion of eggs that were dead at day 30; and (2) late mortality – the proportion of eggs that died during the period from day 30 to hatching. Mortality within each family was not correlated during the two phases; thus, early and late mortality provided two different measures of offspring quality (Wedekind *et al.* 2001).

The authors entered sire and dam identification as random factors because the 10 sires and 10 dams were representative of a larger population. If the sires and dams had represented the entire population or the individuals that were of specific interest, then their identifications instead

would be entered as fixed factors. Overall, dam, sire and dam \times sire effects explained 87% ($= [1.35 \times 10^{-2} + 1.48 \times 10^{-4} + 7.75 \times 10^{-4}] / 1.65 \times 10^{-2}$) of the phenotypic variation in mortality (Table 2). Although all three effects were statistically significant, most of the explained variation was attributed to dam effects, which include both maternal genetic effects and environmental effects such as egg nutrients. Because males in this species provide only genes to the offspring, the sire effect provides an estimate of additive genetic effects (good genes). Specifically, assuming that epistatic genetic variance is of negligible importance, the additive genetic effects can be calculated from four times the Sire component of variance (Lynch & Walsh 1998; p. 601) and for the whitefish this value is 5.92×10^{-4} ($= 4 \times 1.48 \times 10^{-4}$), which represents about 3.5% ($= 5.92 \times 10^{-4} / 1.65 \times 10^{-2}$) of the phenotypic variance in mortality. The dam \times sire effect provides an estimate of nonadditive genetic effects (compatible genes), and again assuming that epistatic genetic variance is of negligible importance, the dominance genetic variance is calculated as four times the dam \times sire component of variance. For the whitefish, this value is 3.10×10^{-3} ($= 4 \times 7.75 \times 10^{-4}$), which represents about 19% of the phenotypic variance in mortality. Finally, the difference between the dam and sire components of variance provides an estimate of maternal environmental effects, and for the whitefish, this value is 1.34×10^{-2} ($= 1.35 \times 10^{-2} - 1.48 \times 10^{-4}$), which represents about 81% of the phenotypic variance in mortality. The statistical significance of the maternal environmental effects can be determined from the F -statistic calculated from the ratio of the mean squares for the dam and sire effects. For the whitefish, the maternal environmental effects were highly significant ($F_{9,9} = 49.2, P < 0.001$). Thus, effects of good genes, compatible genes and maternal environmental effects, respectively,

Table 2 Summary of the two-way ANOVA results in whitefish from Wedekind *et al.* (2001). The results include source of variation, sum of squares (SS), degrees of freedom (DF), mean square (MS), F statistic, P -value, and variance (σ^2)

Source of variation	SS	DF	MS	F	P	σ^2 *
Early egg mortality						
Dam	4.91	9	0.5456	104.39	< 0.0001	1.35×10^{-2}
Sire	0.10	9	0.0111	2.14	0.035	1.48×10^{-4}
Dam \times Sire	0.42	81	0.0052	2.52	< 0.0001	7.75×10^{-4}
Error	0.62	300	0.0021			2.07×10^{-3}
Total						1.65×10^{-2}
Late egg mortality						
Dam	1.21	9	0.1344	4.69	< 0.0001	2.64×10^{-3}
Sire	0.85	9	0.0944	3.28	0.002	1.64×10^{-3}
Dam \times Sire	2.32	81	0.0286	0.85	0.81	-1.32×10^{-3}
Error	10.17	300	0.0339			3.39×10^{-2}
Total						3.82×10^{-2}

*Variance estimates were calculated from formulas presented in Lynch & Walsh (1998; p. 600) and Table 1 of Graham & Edwards (2001; p. 507); the negative variance component was treated as zero, for discussion on negative variance components see Graham & Edwards (2001; p. 509).

account for 3.5%, 19% and 81% of the variance in early mortality in the Alpine whitefish population studied by Wedekind *et al.* (2001). When there is epistatic genetic variance, the estimate of good gene effects and maternal environmental effects will be overestimated. This may explain why the percentages in the whitefish example add up to more than 100%.

During the second phase of development, dam, sire and dam \times sire effects explained only 11.2% of the phenotypic variance in mortality (Table 2). Additive genetic effects (good genes) accounted for 17% of the phenotypic variance in late mortality, maternal environmental effects accounted for less than 3%, and the interaction effect was not significant, indicating no nonadditive genetic effects. Interestingly, only the late phase of mortality was correlated with the size of the sires' breeding tubercles, a sexually selected character (Wedekind *et al.* 2001), and good gene effects were about 11-fold higher for late mortality than early mortality.

Two difficulties with using an ANOVA in the North Carolina Design II are the possibility of negative variance components and its sensitivity to an unbalanced design (e.g.

when there is variance in the number of offspring analyzed from each family). Modifications to the model design and sum of squares have been proposed to account for such effects (Searle *et al.* 1992), although the sampling properties of the modified sum of squares are not yet well understood. Alternatively, maximum likelihood (ML) and restricted maximum likelihood (REML) estimators that are analogous to the ANOVA have been developed, and these estimators do not yield negative variance components and are not particularly sensitive to unbalanced designs (see Lynch & Walsh 1998; p. 779).

Biological mechanisms for acquiring genetic benefits

We propose that there are three fundamental stages during breeding which are important for differentiating among mechanisms of increasing offspring genetic quality: (1) precopulatory [mate choice]; (2) postcopulatory, prefertilization [sperm utilization]; and (3) postcopulatory, postfertilization [differential investment] (Fig. 1).

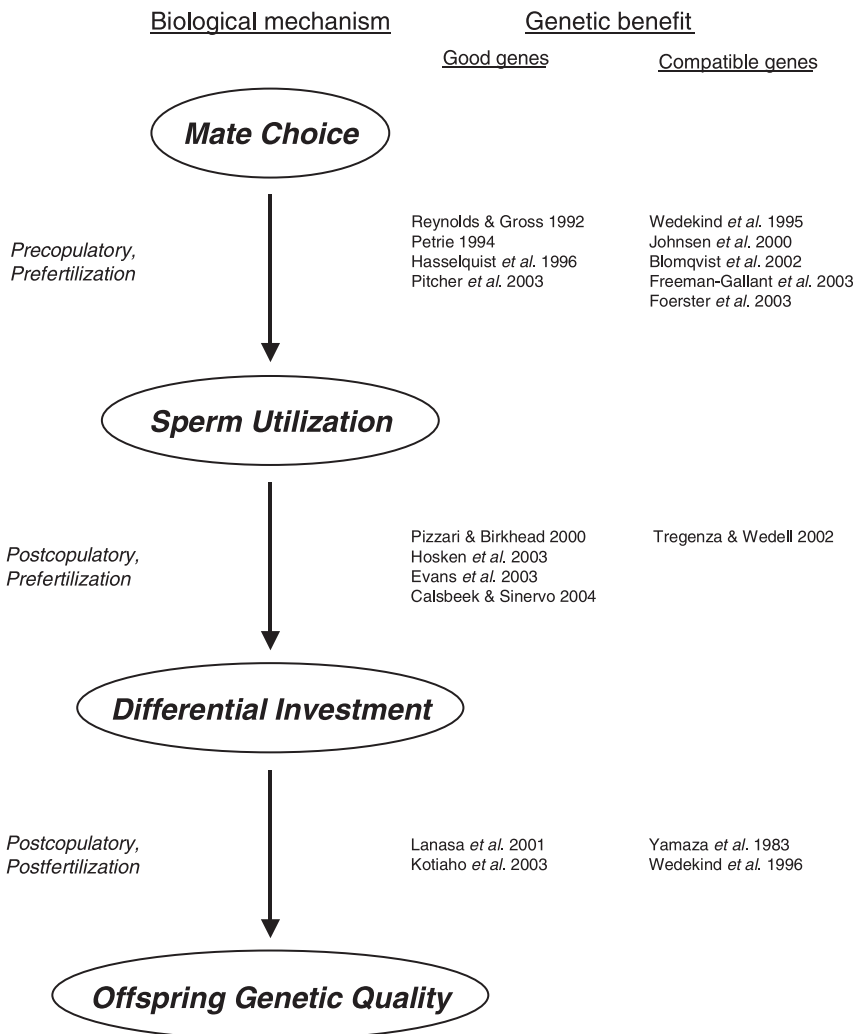


Fig. 1 The three fundamental biological mechanisms for increasing offspring genetic quality. Listed are examples of studies that demonstrate each mechanism for acquiring benefits resulting from either good genes or compatible genes.

Mate choice (precopulatory)

Choosy females can increase the genetic quality of their offspring by mating only with males that will contribute good genes or compatible genes to their offspring. Good genes can be conveyed by condition-dependent traits (Rowe & Houle 1996). For example, we have discussed that female guppies prefer to mate with longer males and peahens prefer to mate with males with larger eye-spots because these males pass on to the offspring good genes that increase their fitness (Reynolds & Gross 1992; Petrie 1994). Mate choice also can be used to select males with compatible genes. For example, Wedekind *et al.* (1995) examined mate preference in humans for HLA dissimilarity. In humans, heterozygosity of HLA loci can increase survivorship (e.g. Thursz *et al.* 1997). The authors asked females to rank the pleasantness of the odor of t-shirts that were worn for two days by various males. Specifically, each female was asked to rank six t-shirts, three of which were worn by males that were dissimilar to the female (dissimilar males) at the HLA loci (based on the HLA-A, -B and -DR regions) and the other three were worn by males that were similar to the female at the HLA loci (similar males). Females not taking oral contraceptives ranked the pleasantness of dissimilar males higher than that of similar males, and also indicated that the dissimilar males reminded them of their mate or ex-mate more so than did the similar males. Thus, these data suggest that human females use odor during mate choice to increase diversity at the MHC of their offspring (or perhaps increase genome-wide diversity; see Wedekind & Furi 1997). Interestingly, females taking oral contraceptives ranked the pleasantness of similar males higher than that of dissimilar males, possibly because the contraceptives hormonally mimic pregnancy.

Mate choice for genetic quality also may involve multiple mating (e.g. Yasui 1997). Females of several species have been shown to 'trade-up' to a second mate with good genes relative to their first mate (e.g. Gabor & Halliday 1997; Bateman *et al.* 2001). For example, in great reed warblers (*Acrocephalus arundinaceus*), Hasselquist *et al.* (1996) found that male song repertoire size was positively correlated with the survival of their offspring and that females selected extra-pair mates (which provide no direct benefits) that had greater repertoire size than their social mate. In fish, Pitcher *et al.* (2003) presented two male guppies, which differed in the amount of orange area they had on their bodies, sequentially to females. In the population studied by the authors, females prefer to mate with males that have greater orange area, presumably because these males have good genes (e.g. Evans *et al.* 2004). Based on detailed behavioral data, they showed that females were more receptive to mating with the second male when he had more orange area than the first male that she mated with. The authors also showed that the difference in orange

area between the second and first male was correlated with the difference in their paternities; the more orange area the second male had relative to the first male, the more paternity he garnered.

Females also may trade-up for compatible genes, for example, as discussed in bluethroats (Johnsen *et al.* 2000). In addition, Freeman-Gallant *et al.* (2003) found that female yearling Savannah sparrows (*Passerculus sandwichensis*) avoided pairing with MHC-similar males and females paired to MHC-similar males were more likely to seek extra-pair matings than females paired to MHC-dissimilar males. Presumably, MHC-similarity of parents is negatively correlated with their offspring's fitness (also see Blomqvist *et al.* 2002; Foerster *et al.* 2003).

Sperm utilization (postcopulatory, prefertilization)

Females may increase the genetic quality of their offspring by differentiating among sperm and utilizing only sperm with good or compatible genes. There are two basic mechanisms by which this can be accomplished, sperm competition and cryptic female choice (Eberhard 1996; Birkhead & Møller 1998). First, by facilitating sperm competition, females can increase the genetic quality of their offspring when the sperm from the male that will generate the fittest offspring with her is most successful at fertilizing her eggs. There is some support emerging from the literature that the competitiveness of a male's sperm (ejaculate) is an indicator of good genes. For example, in a laboratory experiment with yellow dung flies (*Scathophaga stercoraria*), Hosken *et al.* (2003) randomly paired males and mated each male with a different female. They then compared the development time of the offspring of each paired male as a measure of fitness. Development time is an indicator of offspring survivorship because of the ephemeral nature of dung in the wild. Next, the authors allowed the pairs of males to compete with each other and copulate with a third female. Across the pairs, they found that males that sired fitter offspring also had more competitive sperm (i.e. sperm that was more likely to fertilize the eggs when in competition with another male's sperm).

In another study, Evans *et al.* (2003) used artificial insemination to investigate male genetic quality and sperm competitiveness in guppies. They introduced equal numbers of sperm into females from two males that differed in the amount of orange area on their bodies (orange area may be an indicator of offspring viability; Evans *et al.* 2004). Using genetic markers, they were able to show that the difference in orange area between the two males was correlated with the difference in their paternities; males with more orange area sired more offspring than males with less orange area.

When sperm competitiveness is heritable and most females multiply mate, the genes that underlie sperm competitiveness are themselves good genes (Curtsinger 1991;

Keller & Reeve 1995; Yasui 1997; but see Pizzari & Birkhead 2002). There are two lines of evidence that provide support for the heritability of sperm competitiveness: (i) direct measures of heritability of sperm competitiveness or sperm traits correlated with sperm competitiveness such as length or speed (Woolley & Beatty 1967; Radwan 1998; Ward 1998, 2000; Morrow & Gage 2001); and (ii) indirect measures which compare the competitiveness of sperm from sons of polyandrous vs. monandrous females (Holland & Rice 1999; Bernasconi & Keller 2001; Pitnick *et al.* 2001; Pai & Yan 2002). Thus, in addition to potential viability benefits, females that facilitate sperm competition also may ensure that their offspring obtain the sperm competitive genes.

Second, females may exercise 'cryptic choice' where they directly manipulate sperm usage and bias fertilization to the male that will produce offspring of higher genetic quality. Several mechanisms by which females manipulate sperm have been reported in the literature (reviewed by Eberhard 1996). Pizzari & Birkhead (2000) studied sperm ejection in a free-living population of feral fowl (*Gallus gallus domesticus*). In feral fowl, male social rank is presumed to be an indicator of good genes. The authors found that males of low social rank were more likely to have their sperm ejected by females — through cloacal contractions immediately after insemination — than males of high social rank. Next, the authors removed some males from their population to experimentally manipulate the social status of the males that remained. Once a new social hierarchy was established, the authors again quantified the probability of sperm ejection for each male, and found results analogous to those of the first experiment; males that increased in social status after the manipulation experienced a decrease in the probability that their sperm was ejected. This latter result suggests that females reassess the relative genetic quality of males and select the sperm from the best available male.

The reproductive tract, ovarian fluids or even the eggs themselves may also play an important role in facilitating the use of sperm with good genes or compatible genes (reviewed by Birkhead *et al.* 1993; Eberhard 1996; Zeh & Zeh 1997; Birkhead 1998; Vacquier 1998; Birkhead & Pizzari 2002; also see Riffell *et al.* 2004). For example, Tregenza & Wedell (2002) used families of field crickets to assign one of four sisters to each of the following treatments: (1) one mating to each of two of the female's brothers (sibling-sibling, SS) (2) one mating to each of two males that were brothers but unrelated to the female (nonsibling-nonsibling, NN) (3) one mating to the female's brother and then one mating to an unrelated male (SN), and (4) one mating to an unrelated male then one mating to the female's brother (NS). Eggs were collected shortly after laying and reared until hatching when the hatching success was calculated. There was no significant difference in the number

of eggs each of the four sisters laid, so hatching success provided a measure of offspring survivorship. The authors found that mean hatching success was about 34% for the SS treatment, 53% for the NN treatment, 58% for the SN treatment and 51% for the NS treatment. A randomized block analysis (with sisters representing the blocks) revealed that the hatching success in the SS treatment was significantly lower than that in the other three treatments, which were not significantly different from each other. Furthermore, the hatching success in the SN and NS treatments were greater than the mean of the hatching success for the SS and NN treatments combined (which represents the null hypothesis under the assumption that sperm fertilization was random). The authors ruled out several alternative hypotheses such as differential allocation to the eggs, differential sperm allocation by males, and differences in precopulatory behavior of females. Therefore, these results imply that compatible sperm — i.e. sperm from an unrelated male — are differentially selected for fertilization. Indeed, a follow-up study confirmed that unrelated males were in fact more successful at garnering paternity than were siblings of the females in the SN and NS trials (Bretman *et al.* 2004).

In another study, Calsbeek & Sinervo (2004) presented data that suggest physiological mechanisms exist in side-blotched lizards (*Uta stansburiana*) to differentiate between sperm carrying an X chromosome and sperm carrying a Y chromosome. Apparently, sons of large males have higher fitness than daughters of large males because of negative genetic effects of growth genes on the female reproductive functions. The opposite is true for the offspring of small males — daughters have higher fitness than sons. Thus, it might be adaptive if there was a physiological mechanism by which Y sperms were preferentially used from large males and X sperms were preferentially used from small males to fertilize the offspring (assuming that daughters from small males have higher fitness than daughters from large males). The authors test this hypothesis by examining the paternity and sex of progeny from polyandrous females collected from the wild. They found statistical support that within multiply mated clutches, the larger male sired a greater proportion of sons and the smaller male sired a greater proportion of daughters. Interestingly, across 2 years of data, it appears that small and large males sire similar numbers of offspring. The authors ruled out some male mechanisms of sperm selection based on a laboratory breeding experiment which showed that large and small males both appear to produce similar numbers of X and Y sperm. The possibility that the female reproductive physiology can differentiate between X and Y sperm is fascinating and suggests that mechanisms may exist to differentiate between other aspects of the genes carried by a sperm such as their genetic compatibility with the egg (also see Birkhead & Pizzari 2002).

Differential investment (postcopulatory, postfertilization)

After fertilization, parents may be able to promote the overall genetic quality of their brood through differential investment among the offspring. Specifically, females that invest proportionately more resources into offspring of high genetic quality than offspring of low genetic quality may ensure that their surviving young are of the highest possible genetic quality. This is the so-called 'differential allocation hypothesis' first proposed by Burley (1988) in the context of good genes (reviewed by Sheldon 2000). For example, Kotiaho *et al.* (2003) reported results from an experiment on the horned dung beetle (*Onthophagus taurus*) and showed that females differentially allocate parental resources (dung) to their offspring based on the offspring's genetic quality. Male horned dung beetles exhibit dimorphic horn morphology in which some males have virtually no horns (minor males) while other males have large, well-developed horns (major males). Major males may have good genes because they typically are competitively superior and have higher fitness than minor males (Hunt & Simmons 1997, 2000), although heritability of life history appears to be low (Emlen 1994; but see Hunt & Simmons 2002; Kotiaho *et al.* 2003). The authors housed 106 males from the field, including both minor and major males, each with four laboratory-reared virgin females. After all of the females mated with their assigned male, they were placed in breeding chambers (without their mate to exclude paternal care effects). After 7 d, each female's brood mass, which consists mostly of dung that the developing young use for nutrients, was weighed as a measure of maternal investment. They found that females mated to males with large horns had brood masses that were about 10% heavier than females mated to males with small horns. Because the authors showed that females invest more in offspring sired by males with good genes (males with larger horns), any observed effect on fitness is not only attributable to paternal good genes effects, but also maternal environmental effects. Indeed, the authors showed that the additive genetic variation attributable to paternal good genes would have been overestimated by 10%–20% had they not accounted for the maternal environmental effects.

Another extreme example of differential investment occurs when females abort offspring with low genetic quality. This type of mechanism likely is to be more common in viviparous species — i.e. those where females nourish developing embryos via a placenta or other means (Zeh 1997). For example, in humans, spontaneous abortion has been linked to genetic defects in the embryo such as X-linked recessive disorders (Lanasa *et al.* 2001; also see Campana *et al.* 1986). In laboratory mice, Yamazaki *et al.* (1983) demonstrated that females are more likely to prevent embryo implantation (called the Bruce effect) when a new suitor is MHC-dissimilar to their previous mate. In

humans, Ober *et al.* (1998) showed that couples that share antigens for one or more HLA loci have a greater chance of spontaneous abortion. In pseudoscorpions, Newcomer *et al.* (1999) found that females that mated with two different males gave birth to 32% more offspring than did females that mated with the same male twice. The difference in offspring production was because of an elevated rate of spontaneous abortion by females that mated with only a single male. Spontaneous abortion could be adaptive if these females were able to re-mate sooner and produce offspring of higher genetic quality than singly mated females that did not terminate pregnancy.

Selective second meiotic division after the sperm has entered the egg may represent another mechanism of differential investment. In a laboratory population of mice, Wedekind *et al.* (1996) have argued that eggs that are fertilized prior to the second meiotic division may selectively discard genetic material via the polar body to ensure the offspring contain compatible genes. They used *in vitro* fertilization to cross two inbred mouse strains congenic for their MHC. Specifically, they were able to cross eggs from MHC heterozygous females (containing the *b* and *k* alleles at the H-2 locus) with males homozygous for either the *b* or *k* allele. If eggs selectively discard genetic material, then they predicted that there should be a significant deviation from a 1:1 ratio of homozygous to heterozygous offspring. Although they found no deviation, they found a negative relationship between that proportion and the date the experiment was conducted. They suggest that the negative relationship is consistent with their proposed mechanism because they found no relationship between mortality rate and experimental date — i.e. no evidence of MHC genotype dependent mortality postfertilization. However, they did not actually know the genotype of the fertilized eggs that died, and it is unclear what advantage females gain by adjusting the proportion of MHC-heterozygous offspring based on mating date.

Mate choice and population genetic variation in fitness

We propose that there are two types of mating systems with respect to genetic quality that define a continuum. First, there are mating systems in which fitness variation from genetic quality predominately is the result of additive genetic variation and female mate choice (or male mate choice in sex-role reversed species or species in which mating costs limit polygyny) primarily is for good genes. Second, there are mating systems in which fitness variation from genetic quality predominately is resulting from nonadditive genetic variation and female mate choice primarily is for compatible genes. In a population that is dominated by good gene effects, females should have congruent mate preference for the male with the good genes. Such mate preference will lead to a large skew in male reproductive

success and strong directional selection on the good genes. Assuming the environment is stable (i.e. the directional selection is consistent through evolutionary time), additive genetic variation in fitness should decrease. This process of directional selection typifies polyandrous, nonresource based mating systems, such as leks (Höglund & Alatalo 1995), where at least some additive genetic variation may be maintained in the population through mutation (assuming that many genes underlie good gene quality; Pomiankowski & Møller 1995; Rowe & Houle 1996).

Conversely, compatible genes are dependent on the interaction of female and male genotypes and thus different pairings are required to increase offspring fitness. In a population dominated by compatible gene effects, females will be incongruent in their mate preference and no directional selection will occur (albeit there likely will be directional selection on the genes underlying the mechanism used to obtain compatible genes, but not on the compatible genes themselves). In compatible gene mating systems, female choice should maintain nonadditive genetic variation in fitness, while enabling mutation to increase additive genetic variation.

Recently, Colegrave *et al.* (2002) used a modeling approach to address the potential trade-off between mate choice for good genes and mate choice for compatible genes. Although they did not specifically model population genetic variation, their model included parameters representing the benefits from good genes (Q) and benefits from compatible genes (I). Basically, the model showed that females will mate for good genes when $Q/I > \beta$, but will mate for compatible genes when $Q/I < \beta$ (where β depends on the relative cost for females to acquire good genes vs. compatible genes). If we assume that mate choice for good genes reduces Q relative to I and mate choice for compatible genes has the opposite effect, then it is plausible that a mating system will oscillate across the equilibrium condition $Q/I = \beta$; i.e. between a good genes mating system and a compatible genes mating system (Fig. 2a).

We envision two scenarios that might emerge from the mate choice trade-off between good genes and compatible genes (Fig. 2b). First, additive and nonadditive genetic variation may settle at an intermediate level with only small fluctuations in variation through evolutionary time. This may occur when females evolve mate choice for both good genes and compatible genes. Such simultaneous choice might be mediated through an evolutionarily stable strategy (ESS; Maynard Smith 1982) where all females simultaneously optimize their choice for good genes and compatible genes. Roberts & Gosling (2003) provide supporting evidence for such an ESS from a laboratory population of mice. They show that females consider indicators of both good genes (scent-marking rate) and compatible genes (cues regarding MHC dissimilarity mediated by urinary odor) when selecting mates; although compatible genes influenced female

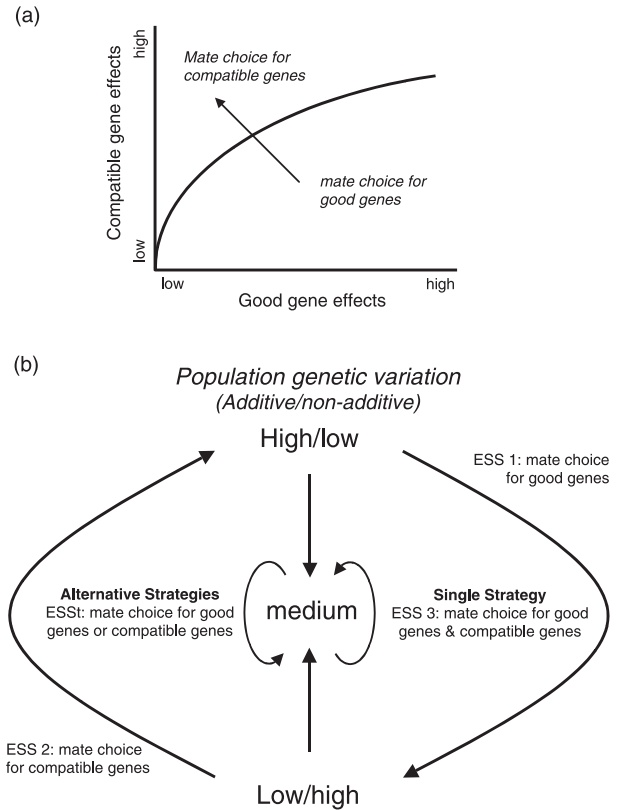


Fig. 2 Consequences of variation in good genes and compatible genes on the evolution of female mate choice. (a) When fitness effects of compatible genes are greater than those of good genes, females should evolve mate choice predominately for compatible genes (upper left portion of graph). Conversely, when fitness effects of good genes are greater than those of compatible genes, females should evolve mate choice predominately for good genes (lower right portion of graph). The line represents an equilibrium between good gene and compatible gene fitness effects. Figure adopted from Colegrave *et al.* (2002). (b) Schematic of potential cycling of female mate choice strategies for good genes and compatible genes. When additive genetic variation is high and nonadditive variation is low, natural selection leads to a female evolutionarily stable strategy of mate choice for good genes (ESS 1), which erodes additive genetic variation. When additive genetic variation is low and nonadditive variation is high, natural selection leads to a female evolutionarily stable strategy of mate choice for compatible genes (ESS 2), which leads to an increase in additive genetic variation. When both additive and nonadditive genetic variation are intermediate, natural selection may lead to a female evolutionarily stable strategy of mate choice that optimally trades off fitness benefits from good genes and compatible genes (ESS 3) or to two alternative strategies in an evolutionarily stable state (ESSst) in which some females exclusively choose mates for good genes and other females exclusively choose mates for compatible genes. For both the ESSst and ESS 3, their should be only small fluctuations in additive and nonadditive genetic variation.

choice only when there was relatively little variation in good genes quality among potential mates. Alternatively, simultaneous choice might be mediated through an evolutionarily stable state (ESSst) where some females choose

only for good genes and other females choose only for compatible genes. The ESS would be stable when there is negative frequency dependent selection on the two female types.

Second, additive and nonadditive genetic variation may continually cycle between low and high levels (Fig. 2b). When the population is in a state of high additive genetic variation, but low nonadditive genetic variation, natural selection should favor the evolution of an ESS, in which all females choose good genes. High mating skew should deplete additive genetic variation, yet increase nonadditive genetic variation through, for example, an increase in genetic load. Subsequently, when the population is in a state of low additive genetic variation but high nonadditive genetic variation, natural selection should favor the evolution of an ESS in which all females choose for compatible genes. Low mating skew should deplete nonadditive genetic variation (e.g. reduce genetic load), yet increase additive genetic variation through mutational buildup and thereby return the population to good genes mating system.

Conclusion and future directions

There now is substantial evidence that mate choice for genetic benefits is an important component of many breeding systems. Indeed, many sophisticated biological mechanisms that have been described increase offspring genetic quality. The magnitude of the fitness effect of genetic quality, however, remains to be established. An initial meta-analysis suggests that good gene effects are variable among mating systems (effect size range for Pearson's correlation $r = -0.30-0.79$) and on average explained only about 1.5% of the variation in survivorship (Møller & Alatalo 1999; also see Jennions *et al.* 2001). This initial estimate may be conservative because the studies did not examine variation in breeding success (m_x), which might be a particularly important component of fitness in the underlying studies which focused on indicator traits — i.e. traits expressed in males that females use in mate choice decision-making (Kokko *et al.* 2002; Hunt *et al.* 2004). Our analysis of 14 studies that experimentally manipulated the degree of multiple mating by females and examined effects of overall genetic quality averaged 44% higher fitness, but ranged from no effect to 189% higher fitness; the latter result representing hatching success in a ground cricket (Fedorka & Mousseau 2002). If good gene effects are actually in the order of a few percent, then much of this 44% increase in fitness would be the result of compatible gene effects. The three studies that we discussed which were able to directly estimate the effects resulting from compatible genes found that these effects explained between 2% and 19% of the variation in fitness (Johnsen *et al.* 2000; Wedekind *et al.* 2001; Penn *et al.* 2002). The data from those

three studies suggest that compatible gene effects are more important than good gene effects.

In nonresource-based mating systems, fitness effects as a result of compatible genes will likely show up only in the survivorship component (l_x) of fitness because compatible genes are not themselves heritable and therefore not likely to increase a male's mating success (the same is not true for resource-based mating systems; see Box 2). Furthermore, mate choice for compatible genes does not impose directional selection on the underlying genes and therefore such choice can maintain genetic diversity in fitness within a population. We have suggested that compatible gene mate choice and good gene mate choice may cycle in populations (over evolutionary timescales) along with the variance in the two types of genetic quality (see Fig. 2). However, only a few models have examined the interaction of good gene and compatible gene mate choice (e.g. Colegrave *et al.* 2002).

One difficulty with many of the studies of genetic benefits is confounding environmental effects. For example, several of the studies that compared singly mated females to multiply mated females were unable to control for potential differences in direct benefits such as the number of spermatophores which females receive. Direct benefits could increase the fitness of the offspring independent of its genetic quality and could result in an overestimation of genetic benefits. Conversely, when mating has direct costs to the female, such as sexually transmitted diseases, it is plausible that these costs could lead to reduced offspring fitness and an underestimate of genetic benefits. Females may also invest disproportionately in offspring based on their genetic quality by providing more resources to offspring of high genetic quality. For example, Kotiaho *et al.* (2003) showed in the horned dung beetle that the additive genetic variation attributable to paternal good genes would have been overestimated by 10%–20% had they not accounted for the maternal environmental effects.

Mating systems with external fertilization and no parental care may provide the ideal systems to assess the potential genetic benefits from good genes and compatible genes. Breeding experiments based on the North Carolina Design II approach can effectively partition fitness variation among good genes, compatible genes, and maternal environmental effects. For mating systems with internal fertilization, researchers must carefully control for maternal environmental effects (differential investment). Artificial fertilization techniques may provide one method of accomplishing this goal (e.g. Evans *et al.* 2003), but this approach will be effective only when there are postcopulatory mechanisms (sperm utilization) of acquiring genetic quality. Regardless of the experimental approach, it is imperative that measures of fitness incorporate multiple components including both survivorship and reproductive success (Hunt *et al.* 2004). For example, Dawson (1965)

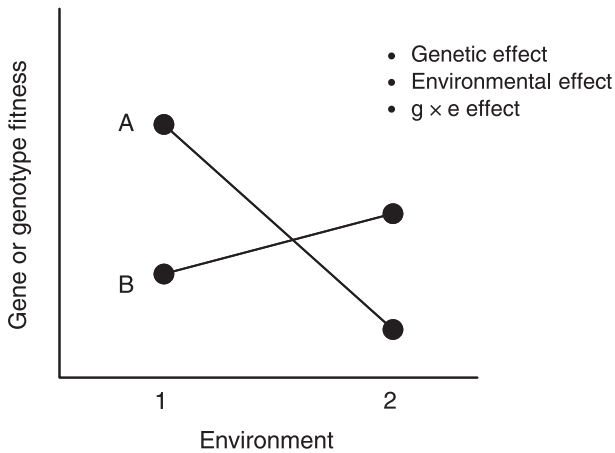


Fig. 3 Variation in the fitness of a gene or genotype can be attributed to genetic effects, environmental effects and genetic \times environmental interaction ($g \times e$) effects. The A allele (or genotype) has higher fitness than the B allele (or genotype) only in environment 1. Because the lines are not parallel, there is a $g \times e$ effect and there is a change in the fitness rank of the alleles (or genotypes). A $g \times e$ effect may confound many studies of genetic quality that are conducted in unnatural environments such as those conducted in laboratories.

found that 59% of variation in developmental rate (presumably a correlate of survivorship) in larval flour beetles was attributable to nonadditive genetic variation, yet another study that estimated fitness based on mating success of sons found no significant genetic effects (Pai & Yan 2002).

A second difficulty with many of the studies of genetic benefits is they ignore genetic \times environmental interaction effects on fitness (Fig. 3). The interaction effect occurs when the quality of a gene or genotype varies across environmental contexts. For example, the MHC *e* allele identified by Lohm *et al.* (2002) confers resistance to infection by *Aeromonas salmonicida* and may be a good gene in any environment where there is intense exposure to this species of bacterium (allele A in environment 1, Fig. 3). Alternatively, in an environment where *A. salmonicida* is absent, the *e* allele may have little fitness benefit (allele A in environment 2, Fig. 3). Although most genes or genotypes likely will vary in quality across environments to some extent, few studies calculate fitness of individuals in multiple environments and therefore ignore genetic \times environmental interaction effects (for exceptions see Welch *et al.* 1998; Sakaluk *et al.* 2002; Welch 2003). An interaction effect will be particularly important when the environment used to assess genetic quality does not accurately reflect the organism's natural environment as may be true for many laboratory environments. Ideally, experiments should be conducted in an organism's natural environment, or artificial environments should be designed to present a realistic environmental challenge such as exposure to a natural pathogen or predator.

What about the kinds of genes that underlie genetic quality? To date, the best examples of nonadditive genetic effects have come from studies on the MHC (Bernatchez & Landry 2003). However, there likely are other important loci involved in compatible gene effects, which deserve attention (reviewed by Zeh & Zeh 1996, 1997). For example, the gene complex underlying the P450 enzyme system may provide evidence of compatible gene effects (Gonzalez & Nebert 1990; Grahn *et al.* 1998). P450 enzymes are involved in the metabolism of organochlorine pollutants into water-soluble products that can be excreted from the body. Variants of the P450 enzymes differ in their efficiency of metabolizing various organochlorine pollutants. Thus, individuals that are heterozygous for P450 genes may be better able to excrete a broader range of the pollutants than individuals that are homozygous for P450 genes.

Loci underlying foraging polymorphisms also might provide excellent candidates for compatible gene effects through the action of coadapted gene complexes. Foraging polymorphisms have been described in many populations and typically involve two morphs that are morphologically and behavioral specialized to feeding in one type of habitat or another (Robinson & Wilson 1994; Smith & Skúlason 1996). For example, in pumpkinseed sunfish (*Lepomis gibbosus*) some individuals develop into a pelagic morph, which inhabits open waters, while other individuals develop into a benthic morph, which inhabits shoreline waters (Robinson *et al.* 1993). Each morph appears to be 'adapted' to swimming and feeding in their respective environments (Robinson *et al.* 1996). If the variation between morphs has a genetic component, the complexes might display compatible gene effects.

Nearly all of the examples of good gene effects have come from studies of condition-dependent traits (Møller & Alatalo 1999). Perhaps surprisingly there are few examples of individual genes that contribute to good gene effects. Lohm *et al.* (2002) provided an example from Atlantic salmon where the *e* allele at the MHC conferred upwards of a 49% fitness advantage. It is possible that most good genes each only have a tiny effect on fitness and thus studying a specific good gene would be difficult and largely uninformative.

The importance of genetic quality to conservation biology recently has been recognized (Grahn *et al.* 1998; Wedekind 2002; Rowe & Hutchings 2003). However, few programs have been developed that capitalize on natural biological mechanisms, such as sexual selection, to ensure the maintenance and propagation of genetic quality. For example, many enhancement programs use fertilization techniques designed to maximize genetic diversity as measured by indices such as heterozygosity (reviewed by Grahn *et al.* 1998; Keller & Waller 2002; Wedekind 2002). These programs may be effective when populations are inbred (low effective population size) and have high genetic load (e.g. Saccheri *et al.* 1998; Madsen *et al.* 1999).

They might also be effective when the goal is to maintain or maximize the 'evolvability' of the population (i.e. preserve future genetic quality). For example, if the environment that a species occupies is likely to change unpredictably then the goal of the program might be to maintain as much genetic diversity as possible in hopes of retaining genes that can persist in the new environment. However, if the goal is to enhance or rehabilitate current populations then simply maximizing genetic diversity fails to recognize the importance of good genes (which can depend on specific environmental context) and compatible genes outside of those associated with inbreeding depression. It is conceivable that in some situations — for example hatchery programs designed to enhance wild fish populations — approaches that incorporate natural breeding mechanisms will produce offspring of higher genetic quality than would approaches that simply maximize genome-wide diversity. Surprisingly, there has been limited attempt to incorporate sexual selection into enhancement breeding protocols and insufficient evaluation of its potential impact for species conservation (but see Roberts & Gosling 2004; Rowe & Hutchings 2003; Wedekind *et al.* 2004).

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References

- Andersson M (1994) *Sexual Selection*. Princeton University Press, Princeton.
- Apanius V, Penn D, Slev PR, Ruff LR, Potts WK (1997) The nature of selection on the major histocompatibility complex. *Critical Reviews in Immunology*, **17**, 179–224.
- Arkush KD, Giese AR, Mendonca HL, McBride AM, Marty GD, Hedrick PW (2002) Resistance to three pathogens in the endangered winter-run chinook salmon (*Oncorhynchus tshawytscha*): effects of inbreeding and major histocompatibility complex genotypes. *Canadian Journal of Fisheries and Aquatic Sciences*, **59**, 966–975.
- Baer B, Schmid-Hempel P (1999) Experimental variation in polyandry affects parasite loads and fitness in a bumble-bee. *Nature*, **397**, 151–154.
- Barber I, Arnott SA (2000) Spit-clutch IVF: a technique to examine indirect fitness consequences of mate preferences in sticklebacks. *Behaviour*, **137**, 1129–1140.
- Barber I, Arnott SA, Braithwaite VA, Andrew J, Huntingford FA (2001) Indirect fitness consequences of mate choice in sticklebacks: offspring of brighter males grow slowly but resist parasitic infections. *Proceedings of the Royal Society of London Series B*, **268**, 71–76.
- Bateman PW, Gilson LN, Ferguson JWH (2001) Male size and sequential mate preference in the cricket *Gryllus bimaculatus*. *Animal Behaviour*, **61**, 631–637.
- Bateson PPG (1983) *Mate Choice*. Cambridge University Press, Cambridge, UK.
- Bernasconi G, Keller L (2001) Female polyandry affects their sons' reproductive success in the red flour beetle *Tribolium castaneum*. *Journal of Evolutionary Biology*, **14**, 186–193.
- Bernatchez L, Landry C (2003) MHC studies in nonmodel vertebrates: what have we learned about natural selection in 15 years? *Journal of Evolutionary Biology*, **16**, 363–377.
- Birkhead TR (1998) Cryptic female choice: criteria for establishing female sperm choice. *Evolution*, **52**, 1212–1218.
- Birkhead TR, Fletcher F, Pellatt EJ (1999) Nestling diet, secondary sexual traits and fitness in the zebra finch. *Proceedings of the Royal Society of London Series B*, **266**, 385–390.
- Birkhead TR, Møller AP (1998) *Sperm Competition and Sexual Selection*. Academic Press, London.
- Birkhead TR, Møller AP, Sutherland WJ (1993) Why do females make it so difficult for males to fertilize their eggs? *Journal of Theoretical Biology*, **161**, 51–60.
- Birkhead TR, Pizzari T (2002) Postcopulatory sexual selection. *Nature Review Genetics*, **3**, 262–273.
- Blomqvist D, Andersson M, Kupper C, *et al.* (2002) Genetic similarity between mates and extra-pair parentage in three species of shorebirds. *Nature*, **419**, 613–615.
- Bretman A, Wedell N, Tregenza T (2004) Molecular evidence of postcopulatory inbreeding avoidance in the field cricket *Gryllus bimaculatus*. *Proceedings of the Royal Society of London Series B*, **271**, 159–134.
- Burley N (1988) The differential allocation hypothesis — an experimental test. *American Naturalist*, **132**, 611–628.
- Burt A (1995) Perspective — the evolution of fitness. *Evolution*, **49**, 1–8.
- Calsbeek R, Sinervo B (2004) Within-clutch variation in offspring sex determined by differences in sire body size: cryptic mate choice in the wild. *Journal of Evolutionary Biology*, **17**, 464–470.
- Campana M, Serra A, Neri G (1986) Role of chromosome-aberrations in recurrent abortion — a study of 269 balanced translocations. *American Journal of Medical Genetics*, **24**, 341–356.
- Charlesworth B (1987) The heritability of fitness. In: *Sexual Selection: Testing the Alternatives*. (eds Bradbury JW, Andersson MB), pp. 21–40. Wiley, Chichester, UK.
- Colegrave N, Kotiaho JS, Tomkins JL (2002) Mate choice or polyandry: reconciling genetic compatibility and good genes sexual selection. *Evolutionary Ecology Research*, **4**, 911–917.
- Cotton S, Fowler K, Pomiankowski A (2004) Do sexual ornaments demonstrate heightened condition-dependent expression as predicted by the handicap hypothesis? *Proceedings of the Royal Society of London Series B*, **271**, 771–784.
- Cunningham EJA, Russell AF (2000) Egg investment is influenced by male attractiveness in the mallard. *Nature*, **404**, 74–75.
- Curtsinger JW (1991) Sperm competition and the evolution of multiple mating. *American Naturalist*, **138**, 93–102.
- Darwin C (1871) *The Descent of Man, and Selection in Relation to Sex*. John Murray, London.
- Dawson PS (1965) Estimation of components of phenotypic variance for development rate in *Tribolium*. *Heredity*, **20**, 403–417.
- Drickamer LC, Gowaty PA, Holmes CM (2000) Free female mate choice in house mice affects reproductive success and offspring viability and performance. *Animal Behaviour*, **59**, 371–378.
- Drickamer LC, Gowaty PA, Wagner DM (2003) Free mutual mate preferences in house mice affect reproductive success and offspring performance. *Animal Behaviour*, **65**, 105–114.

- Duckworth RA, Badyaev AV, Parlow AF (2003) Elaborately ornamented males avoid costly parental care in the house finch (*Carpodacus mexicanus*): a proximate perspective. *Behavioral Ecology Sociobiology*, **55**, 176–183.
- Eberhard WG (1996) *Female Control: Sexual Selection by Cryptic Female Choice*. Princeton University Press, Princeton.
- Edwards SV, Hedrick PW (1998) Evolution and ecology of MHC molecules: from genomics to sexual selection. *Trends in Ecology and Evolution*, **13**, 305–311.
- Elliott JK, Elliott JM, Leggett WC (1997) Predation by Hydra on larval fish: Field and laboratory experiments with bluegill (*Lepomis macrochirus*). *Limnology and Oceanography*, **42**, 1416–1423.
- Emlen DJ (1994) Environmental control of horn length dimorphism in the beetle *Onthophagus acuminatus* (Coleoptera, Scarabaeidae). *Proceedings of the Royal Society of London Series B*, **256**, 131–136.
- Evans JP, Kelley JL, Bisazza A, Finazzo E, Pilastro A (2004) Sire attractiveness influences offspring performance in guppies. *Proceedings of the Royal Society of London Series B*, **271**, 2035–2042.
- Evans JP, Magurran AE (2000) Multiple benefits of multiple mating in guppies. *Proceedings of the National Academy of Sciences (USA)*, **97**, 10074–10076.
- Evans JP, Zane L, Francescato S, Pilastro A (2003) Directional postcopulatory sexual selection revealed by artificial insemination. *Nature*, **421**, 360–363.
- Fedorka KM, Mousseau TA (2002) Material and genetic benefits of female multiple mating and polyandry. *Animal Behaviour*, **64**, 361–367.
- Foerster K, Delhey K, Johnsen A, Lifjeld JT, Kempenaers B (2003) Females increase offspring heterozygosity and fitness through extra-pair matings. *Nature*, **425**, 714–717.
- Freeman-Gallant CR, Meguerdichian M, Wheelwright NT, Sollecito SV (2003) Social pairing and female mating fidelity predicted by restriction fragment length polymorphism similarity at the major histocompatibility complex in a songbird. *Molecular Ecology*, **12**, 3077–3083.
- Fu P, Neff BD, Gross MR (2001) Tactic-specific success in sperm competition. *Proceedings of the Royal Society of London Series B*, **268**, 1105–1112.
- Gabor CR, Halliday TR (1997) Sequential mate choice by multiply mating smooth newts: females become more choosy. *Behavioral Ecology*, **8**, 162–166.
- Gil D, Graves J, Hazon N, Wells A (1999) Male attractiveness and differential testosterone investment in zebra finch eggs. *Science*, **286**, 126–128.
- Gonzalez FJ, Nebert DW (1990) Evolution of the P450-gene superfamily – animal plant warfare, molecular drive and human genetic differences in drug oxidation. *Trends in Genetics*, **6**, 182–186.
- Gowaty PA, Drickamer LC, Schmid-Holmes S (2003) Male house mice produce fewer offspring with lower viability and poorer performance when mated with females they do not prefer. *Animal Behaviour*, **65**, 95–103.
- Graham MH, Edwards MS (2001) Statistical significance versus fit: estimating the importance of individual factors in ecological analysis of variance. *Oikos*, **93**, 505–513.
- Grahn M, Langefors A, von Schantz T (1998) The importance of mate choice in improving viability in captive populations. In: *Behavioral Ecology and Conservation Biology* (ed. Caro T), pp. 341–368. Oxford University Press, Oxford.
- Gustafsson L (1986) Lifetime reproductive success and heritability – empirical support for Fisher fundamental theorem. *American Naturalist*, **128**, 761–764.
- Hasselquist D, Bensch S, vonSchantz T (1996) Correlation between male song repertoire, extra-pair paternity and offspring survival in the great reed warbler. *Nature*, **381**, 229–232.
- Höglund J, Alatalo RV (1995) *Leks*. Princeton University Press, Princeton, NJ.
- Holland B, Rice WR (1999) Experimental removal of sexual selection reverses intersexual antagonistic coevolution and removes a reproductive load. *Proceedings of the National Academy of Sciences (USA)*, **96**, 5083–5088.
- Hosken DJ, Garner TWJ, Tregenza T, Wedell N, Ward PI (2003) Superior sperm competitors sire higher-quality young. *Proceedings of the Royal Society of London Series B*, **270**, 1933–1938.
- Houle D (1992) Comparing evolvability and variability of quantitative traits. *Genetics*, **130**, 195–204.
- Hunt J, Bussière LF, Jennions MD, Brooks R (2004) What is genetic quality. *Trends in Ecology and Evolution*, **19**, 329–333.
- Hunt J, Simmons LW (1997) Patterns of fluctuating asymmetry in beetle horns: an experimental examination of the honest signalling hypothesis. *Behavioral Ecology Sociobiology*, **41**, 109–114.
- Hunt J, Simmons LW (2000) Maternal and paternal effects on offspring phenotype in the dung beetle *Onthophagus taurus*. *Evolution*, **54**, 936–941.
- Hunt J, Simmons LW (2002) The genetics of maternal care: direct and indirect genetic effects on phenotype in the dung beetle *Onthophagus taurus*. *Proceedings of the National Academy of Sciences (USA)*, **99**, 6828–6832.
- Jennions MD, Møller AP, Petrie M (2001) Sexually selected traits and adult survival: a meta-analysis. *Quarterly Review of Biology*, **76**, 3–36.
- Jennions MD, Petrie M (2000) Why do females mate multiply? A review of the genetic benefits. *Biology Reviews*, **75**, 21–64.
- Johnsen A, Andersen V, Sunding C, Lifjeld JT (2000) Female bluethroats enhance offspring immunocompetence through extra-pair copulations. *Nature*, **406**, 296–299.
- Keil A, Sachser N (1998) Reproductive benefits from female promiscuous mating in a small mammal. *Ethology*, **104**, 897–903.
- Keller L, Reeve HK (1995) Why do females mate with multiple males – the sexually selected sperm hypothesis. *Advances in the Study of Behaviour*, **24**, 291–315.
- Keller LF, Waller DM (2002) Inbreeding effects in wild populations. *Trends in Ecology and Evolution*, **17**, 230–241.
- Kempenaers B, Congdon B, Boag P, Robertson RJ (1999) Extra pair paternity and egg hatchability in tree swallows: evidence for the genetic compatibility hypothesis? *Behavioral Ecology*, **10**, 304–311.
- Kempenaers B, Sheldon BC (1996) Why do male birds not discriminate between their own and extra-pair offspring? *Animal Behaviour*, **51**, 1165–1173.
- Keyser AJ, Hill GE (2000) Structurally-based plumage coloration is an honest signal of quality in male blue grosbeaks. *Behavioral Ecology*, **11**, 202–209.
- Kirkpatrick M, Barton NH (1997) The strength of indirect selection on female mating preferences. *Proceedings of the National Academy of Sciences (USA)*, **94**, 1282–1286.
- Kirkpatrick M, Ryan MJ (1991) The evolution of mating preferences and the paradox of the lek. *Nature*, **350**, 33–38.
- Klein J, Figueroa F (1986) The evolution of class I MHC genes. *Immunology Today*, **7**, 41–44.
- Kokko H, Brooks R, Jennions MD, Morley J (2003) The evolution of mate choice and mating biases. *Proceedings of the Royal Society of London Series B*, **270**, 653–664.

- Kokko H, Brooks R, McNamara JM, Houston AI (2002) The sexual selection continuum. *Proceedings of the Royal Society of London Series B*, **269**, 1331–1340.
- Konior M, Radwan J, Kolodziejczyk M (2001) Polyandry increases offspring fecundity in the bulb mite. *Evolution*, **55**, 1893–1896.
- Kotiaho JS, Simmons LW, Hunt J, Tomkins JL (2003) Males influence maternal effects that promote sexual selection: a quantitative genetic experiment with dung beetles *Onthophagus taurus*. *American Naturalist*, **161**, 852–859.
- Kozielska M, Krzeminska A, Radwan J (2004) Good genes and the maternal effects of polyandry on offspring reproductive success in the bulb mite. *Proceedings of the Royal Society of London Series B*, **271**, 165–170.
- Lanasa MC, Hogge WA, Kubik CJ, *et al.* (2001) A novel X chromosome-linked genetic cause of recurrent spontaneous abortion. *American Journal of Obstetrics and Gynecology*, **185**, 563–568.
- Lohm J, Grahn M, Langefors A, Andersen O, Storset A, von Schantz T (2002) Experimental evidence for major histocompatibility complex-allele-specific resistance to a bacterial infection. *Proceedings of the Royal Society of London Series B*, **269**, 2029–2033.
- Lynch M, Walsh B (1998) *Genetics and Analysis of Quantitative Traits*. Sinauer Associates Inc, Sunderland, Massachusetts.
- Madsen T, Shine R, Loman J, Hakansson T (1992) Why do female adders copulate so frequently. *Nature*, **355**, 440–441.
- Madsen T, Shine R, Olsson M, Wittzell H (1999) Conservation biology – restoration of an inbred adder population. *Nature*, **402**, 34–35.
- Maynard Smith J (1982) *Evolution and the Theory of Games*. Cambridge University Press, Cambridge.
- McClelland EE, PenNDJ, Potts WK (2003) Major histocompatibility complex heterozygote superiority during coinfection. *Infection and Immunity*, **71**, 2079–2086.
- Mead LS, Arnold SJ (2004) Quantitative genetic models of sexual selection. *Trends in Ecology and Evolution*, **19**, 264–271.
- Møller AP, Alatalo RV (1999) Good-genes effects in sexual selection. *Proceedings of the Royal Society of London Series B*, **266**, 85–91.
- Møller AP, Jennions MD (2001) How important are direct fitness benefits of sexual selection? *Naturwissenschaften*, **88**, 401–415.
- Morjan CL, Rieseberg LH (2004) How species evolve collectively: implication of gene flow and selection for the spread of advantageous alleles. *Molecular Ecology*, **13**, 1341–1356.
- Morrow EH, Gage MJG (2001) Artificial selection and heritability of sperm length in *Gryllus bimaculatus*. *Heredity*, **87**, 356–362.
- Neff BD (2004) Increased performance of offspring sired by parasitic males in bluegill sunfish. *Behavioral Ecology*, **15**, 327–331.
- Newcomer SD, Zeh JA, Zeh DW (1999) Genetic benefits enhance the reproductive success of polyandrous females. *Proceedings of the National Academy of Sciences (USA)*, **96**, 10236–10241.
- Nicoletto PF (1995) Offspring quality and female choice in the guppy, *Poecilia reticulata*. *Animal Behaviour*, **49**, 377–387.
- Ober C, Hyslop T, Elias S, Weitkamp LR, Hauck WW (1998) Human leukocyte antigen matching and fetal loss: results of a 10-year prospective study. *Human Reproduction*, **13**, 33–38.
- Olsson M, Gullberg A, Tegelstrom H, Madsen T, Shine R (1994) Can female adders multiply? *Nature*, **369**, 528–528.
- Olsson M, Madsen T (2001) Promiscuity in sand lizards (*Lacerta agilis*) and adder snakes (*Vipera berus*): causes and consequences. *Journal of Heredity*, **92**, 190–197.
- Olsson M, Shine R, Madsen T, Gullberg A, Tegelstrom H (1996) Sperm selection by females. *Nature*, **383**, 585–585.
- Pai AT, Yan GY (2002) Polyandry produces sexy sons at the cost of daughters in red flour beetles. *Proceedings of the Royal Society of London Series B*, **269**, 361–368.
- Penn DJ, Damjanovich K, Potts WK (2002) MHC heterozygosity confers a selective advantage against multiple-strain infections. *Proceedings of the National Academy of Sciences (USA)*, **99**, 11260–11264.
- Petrie M (1994) Improved growth and survival of offspring of peacocks with more elaborate trains. *Nature*, **371**, 598–599.
- Petrie M, Halliday T (1994) Experimental and natural changes in the peacocks (*Pavo cristatus*) train can affect mating success. *Behavioral Ecology Sociobiology*, **35**, 213–217.
- Petrie M, Schwabl H, Brande-Lavridsen N, Burke T (2001) Maternal investment – sex differences in avian yolk hormone levels. *Nature*, **412**, 498.
- Pitcher TE, Neff BD, Rodd FH, Rowe L (2003) Multiple mating and sequential mate choice in guppies: females trade up. *Proceedings of the Royal Society of London Series B*, **270**, 1623–1629.
- Pitnick S, Miller GT, Reagan J, Holland B (2001) Males' evolutionary responses to experimental removal of sexual selection. *Proceedings of the Royal Society of London Series B*, **268**, 1071–1080.
- Pizzari T, Birkhead TR (2000) Female feral fowl eject sperm of subordinate males. *Nature*, **405**, 787–789.
- Pizzari T, Birkhead TR (2002) The sexually-selected sperm hypothesis: sex-biased inheritance and sexual antagonism. *Biology Reviews*, **77**, 183–209.
- Pomiankowski A, Møller AP (1995) A resolution to the lek paradox. *Proceedings of the Royal Society of London Series B*, **260**, 21–29.
- Potts WK, Wakeland EK (1990) Evolution of diversity at the major histocompatibility complex. *Trends in Ecology and Evolution*, **5**, 181–187.
- Radwan J (1998) Heritability of sperm competition success in the bulb mite, *Rhizoglyphus robini*. *Journal of Evolutionary Biology*, **11**, 321–327.
- Reyer HU, Frei G, Som C (1999) Cryptic female choice: frogs reduce clutch size when amplexed by undesired males. *Proceedings of the Royal Society of London Series B*, **266**, 2101–2107.
- Reynolds JD, Gross MR (1992) Female mate preference enhances offspring growth and reproduction in a fish, *Poecilia reticulata*. *Proceedings of the Royal Society of London Series B*, **250**, 57–62.
- Riffell JA, Krug PJ, Zimmer RK (2004) The ecological and evolutionary consequences of sperm chemo-attraction. *Proceedings of the National Academy of Sciences (USA)*, **101**, 4501–4506.
- Rio DC (1991) Regulation of *Drosophila* – P element transposition. *Trends in Genetics*, **7**, 282–287.
- Roberts SC, Gosling LM (2003) Genetic similarity and quality interact in mate choice decisions by female mice. *Nature Genetics*, **35**, 103–106.
- Roberts SC, Gosling LM (2004) Manipulation of olfactory signaling and mate choice for conservation breeding: a case study of harvest mice. *Conservation Biology*, **18**, 548–556.
- Robinson BW, Wilson DS (1994) Character release and displacement in fishes – a neglected literature. *American Naturalist*, **144**, 596–627.
- Robinson BW, Wilson DS, Margosian AS, Lotito PS (1993) Ecological and morphological differentiation of pumpkinseed sunfish in lakes without bluegill sunfish. *Evolutionary Ecology*, **7**, 451–464.
- Robinson BW, Wilson DS, Shea GO (1996) Trade-offs of ecological specialization: an intraspecific comparison of pumpkinseed sunfish phenotypes. *Ecology*, **77**, 170–178.
- Rowe L, Houle D (1996) The lek paradox and the capture of genetic variance by condition dependent traits. *Proceedings of the Royal Society of London Series B*, **263**, 1415–1421.

- Rowe S, Hutchings JA (2003) Mating systems and the conservation of commercially exploited marine fish. *Trends in Ecology and Evolution*, **18**, 567–572.
- Saccheri I, Kuussaari M, Kankare M, Vikman P, Fortelius W, Hanski I (1998) Inbreeding and extinction in a butterfly metapopulation. *Nature*, **392**, 491–494.
- Saino N, Calza S, Møller AP (1997) Immunocompetence of nestling barn swallows in relation to brood size and parental effort. *Journal of Animal Ecology*, **66**, 827–836.
- Sakaluk SK, Schaus JM, Eggert AK, Snedden WA, Brady PL (2002) Polyandry and fitness of offspring reared under varying nutritional stress in decorated crickets. *Evolution*, **56**, 1999–2007.
- Sandvik M, Rosenqvist G, Berglund A (2000) Male and female mate choice affects offspring quality in a sex-role-reversed pipefish. *Proceedings of the Royal Society of London Series B*, **267**, 2151–2155.
- Searle SR, Casella G, McCulloch CE (1992) *Variance Components*. John Wiley and Sons, New York.
- Sheldon BC (2000a) Environmental dependence of genetic indicator mechanisms. In: *Animal Signals: Signaling and Signal Design in Animal Communication* (ed. Espmark Y, Amundsen T, Rosenqvist G), pp. 195–207. Tapir Academic Press, Trondheim.
- Sheldon BC (2000b) Differential allocation: tests, mechanisms and implications. *Trends in Ecology and Evolution*, **15**, 397–402.
- Sheldon BC, Arponen H, Laurila A, Crochet PA, Merila J (2003) Sire coloration influences offspring survival under predation risk in the moor frog. *Journal of Evolutionary Biology*, **16**, 1288–1295.
- Simmons LW (2001) The evolution of polyandry: an examination of the genetic incompatibility and good-sperm hypotheses. *Journal of Evolutionary Biology*, **14**, 585–594.
- Smith TB, Skúlason S (1996) Evolutionary significance of resource polymorphisms in fishes, amphibians, and birds. *Annual Review of Ecology and Systematics*, **27**, 111–133.
- Stearns SC (1992) *The Evolution of Life Histories*. Oxford University Press, Oxford, U.K.
- Thursz MR, Thomas HC, Greenwood BM, Hill AVS (1997) Heterozygote advantage for HLA class-II type in hepatitis B virus infection. *Nature Genetics*, **17**, 11–12.
- Tomkins JL, Radwan J, Kotiaho JS, Tregenza T (2004) Genic capture and resolving the lek paradox. *Trends in Ecology and Evolution*, **19**, 323–328.
- Tregenza T, Wedell N (1998) Benefits of multiple mates in the cricket *Gryllus bimaculatus*. *Evolution*, **52**, 1726–1730.
- Tregenza T, Wedell N (2000) Genetic compatibility, mate choice and patterns of parentage: invited review. *Molecular Ecology*, **9**, 1013–1027.
- Tregenza T, Wedell N (2002) Polyandrous females avoid costs of inbreeding. *Nature*, **415**, 71–73.
- Trivers RL (1972) Parental investment and sexual selection. In: *Sexual Selection and the Descent of Man* (ed. Campbell B), pp. 136–179. Aldine Press, Chicago.
- Vacquier VD (1998) Evolution of gamete recognition proteins. *Science*, **281**, 1995–1998.
- Ward PI (1998) Intraspecific variation in sperm size characters. *Heredity*, **80**, 655–659.
- Ward PI (2000) Sperm length is heritable and sex-linked in the yellow dung fly (*Scathophaga stercoraria*). *Journal of Zoology*, **251**, 349–353.
- Watson PJ (1998) Multi-male mating and female choice increase offspring growth in the spider *Neriene litigiosa* (Linyphiidae). *Animal Behaviour*, **55**, 387–403.
- Wedekind C (2002) Sexual selection and life-history decisions: implications for supportive breeding and the management of captive populations. *Conservation Biology*, **16**, 1204–1211.
- Wedekind C, Furi S (1997) Body odour preferences in men and women: do they aim for specific MHC combinations or simply heterozygosity? *Proceedings of the Royal Society of London Series B*, **264**, 1471–1479.
- Wedekind C, Chapuisat M, Macas E, Rüllicke T (1996) Nonrandom fertilization in mice correlates with the MHC and something else. *Heredity*, **77**, 400–409.
- Wedekind C, Muller R, Spicher H (2001) Potential genetic benefits of mate selection in whitefish. *Journal of Evolutionary Biology*, **14**, 980–986.
- Wedekind C, Seebeck T, Bettens F, Paepke AJ (1995) MHC-dependent mate preferences in humans. *Proceedings of the Royal Society of London Series B*, **260**, 245–249.
- Wedekind C, Walker M, Portmann J, Cenni B, Müller R, Binz T (2004) MHC-linked susceptibility to a bacterial infection, but no MHC-linked cryptic female choice in whitefish. *Journal of Evolutionary Biology*, **17**, 11–18.
- Welch AM (2003) Genetic benefits of a female mating preference in gray tree frogs are context-dependent. *Evolution*, **57**, 883–893.
- Welch AM, Semlitsch RD, Gerhardt HC (1998) Call duration as an indicator of genetic quality in male gray tree frogs. *Science*, **280**, 1928–1930.
- Woolley DM, Beatty RA (1967) Inheritance of midpiece length in mouse spermatazoa. *Nature*, **215**, 94.
- Worden BD, Parker PG (2001) Polyandry in grain beetles, *Tenebrio molitor*, leads to greater reproductive success: material or genetic benefits? *Behavioral Ecology*, **12**, 761–767.
- Yamazaki K, Beauchamp GK, Wysocki CJ (1983) Recognition of H-2 types in relation to the blocking of pregnancy in mice. *Science*, **221**, 186–188.
- Yasui Y (1997) A 'good-sperm' model can explain the evolution of costly multiple mating by females. *American Naturalist*, **149**, 573–584.
- Zeh JA (1997) Polyandry and enhanced reproductive success in the harlequin-beetle-riding pseudoscorpion. *Behavioral Ecology Sociobiology*, **40**, 111–118.
- Zeh JA, Zeh DW (1996) The evolution of polyandry I: intra-genomic conflict and genetic incompatibility. *Proceedings of the Royal Society of London Series B*, **263**, 1711–1717.
- Zeh JA, Zeh DW (1997) The evolution of polyandry II: post-copulatory defences against genetic incompatibility. *Proceedings of the Royal Society of London Series B*, **264**, 69–75.
- Zeh JA, Zeh DW (2003) Toward a new sexual selection paradigm: polyandry, conflict and incompatibility (invited article). *Ethology*, **109**, 929–950.

The authors are interested in mating system evolution.
