

models propose that perpetual antagonistic coevolution between males and females drives divergence in postmating characters that eventually will confer reproductive isolation among allopatric populations. Besides representing a significant departure from conventional views over the catalysts of speciation, the general importance of sexual conflict to species diversification arises from the proposed ubiquity of antagonistic coevolution between the sexes. A new study by Arnqvist *et al.* tests these contentions by assessing whether rates of speciation in insects covary with the intensity of postmating sexual conflict.

Arnqvist *et al.* use a series of phylogenetic contrasts to compare extant species richness in pairs of related insect clades that differ in the opportunity for postmating sexual conflict. These comparisons are made between polyandrous and monandrous insect groups. Under polyandry, there should be ample opportunity for postmating sexual conflict, and therefore also for antagonistic coevolution between the sexes, because the ejaculates of several males compete over fertilization within the female. Even if male

traits convey costs to females, they will be favored if they enhance his reproductive success. In contrast, the opportunity for postmating sexual conflict will be absent or minimal in monandrous species. They find that species diversity, as predicted, is significantly higher in insects groups in which females mate with many males compared with groups where females mate only once. Because the two clades in a given contrast share a common ancestor, this difference in species richness reflects a higher rate of speciation in the polyandrous clade relative to the monandrous clade. By examining the potential confounding effects of differences in the trophic ecology, range of geographic distribution and latitude between poly- and monandrous clades, they show that this conclusion is not only robust to but was actually strengthened when such effects were controlled for. Their study doesn't examine whether differences in the 'opportunity' for sexual conflict between polyandrous and monandrous insects actually correspond to differing amounts of postmating reproductive divergence. However, to the extent that this

association holds, their results do suggest that increased rates of speciation are an evolutionary corollary of divergence in postmating characters.

Further study is needed to decipher what processes actually drive the rapid divergence of postmating characters. Nevertheless, whether this divergence can be ascribed to the opportunity for postmating sexual conflict, or some other postmating sexual selection, the effect on rates of speciation is indeed intriguing. Arnqvist *et al.*'s study suggests that by studying the evolutionary dynamics of these postmating characters we can gain insight into the processes generating patterns of diversity.

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Reference

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Finding Mr Right: good genes and multiple mating by females

Understanding why males and females multiply mate is at the heart of behavioural ecology. Generally, theory suggests that while a male's reproductive success is limited by the number of mates he has, a female's success is limited by the number of viable eggs she produces. Since sperm is relatively cheap and plentiful, a female should be able to maximize her reproductive success by mating with only a single male. However, females of most animal species mate with more than one male (sometimes referred to as polyandry). This apparent contradiction with the theory has motivated extensive research over the past decade. A large number of empirical studies, particularly in insects, have now shown that males provide material resources to their mates. These resources can include such things as nutrients that the female consumes, care for her offspring, or protection from predators, and are referred to as direct benefits. Females that mate with multiple males can therefore acquire more resources and increase their reproductive success. Direct benefits provide a satisfying resolution to the apparent paradox of polyandry. However, in some mating systems, males provide only sperm (genes) and no direct benefits, yet females still multiply mate. In these systems, females might benefit indirectly by obtaining good genes or genes that better complement their own. When it is difficult to assess male quality prior to copulation, these females may mate with multiple males and rely on post-copulatory cues, such as sperm competitiveness, to select the ideal father. A recent study on guppies provides some much needed empirical evidence showing that females do in fact mate with multiple males in search of good genes.

Jon Evans and Anne Magurran¹ examine the predator avoidance abilities of juvenile guppies that were produced by females that had either mated with four different males or a single male four times. They show that multiply mated females produce offspring that have better developed schooling and predator escape behaviours. Because male guppies provide no direct benefits, they attribute these results to good genes. Evans and Magurran¹ also show that multiply mated females produce larger broods with a shorter gestation time. However, this latter result might also be explained by potential sperm limitation in the females mated to only a single male. Nevertheless, this study provides compelling evidence that females mate with multiple males in search of good genes.

Although the importance of polyandry and postcopulatory paternity biasing or 'cryptic female choice' is becoming clear, little is still known about the proximate mechanisms involved. For example, females might play a passive role, only facilitating sperm competition, or they might play an active role by removing undesired sperm. The fact that females may be in search of not only good genes, but genes that better complement their own, might help to explain apparent disparities in mate choice, and warrants consideration in mate choice studies. Evidently, promiscuity is not only rewarding for males, but also females.

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How does recombination affect phylogeny estimation?

Phylogenetic methodology is being increasingly used in diverse areas of biological sciences. Although there are many examples of the utility of a phylogenetic approach, all these studies rely on accurate estimates of phylogenetic relationships. Traditional methods of phylogeny estimation, such as maximum parsimony, minimum evolution or maximum likelihood, assume that a single evolutionary history underlies the sequences in question. However, the development of automatic PCR-based sequencing has led to the accumulation of a considerable amount of

population sequence data in which the presence of recombination – that allows for different parts of the sequences to have different phylogenetic histories – violates this fundamental assumption. Despite this fact, recombination has been traditionally ignored and its possible consequences neglected.

Schierup and Hein^{1,2} are the first to characterize thoroughly the effect of ignoring recombination in phylogenetic analysis. They use the coalescent with recombination to simulate recombining sequences, from which phylogenetic trees are inferred under the