

EVOLUTIONARY GENETICS

Supergene yields super sperm

The remarkable diversity in sperm morphology and performance in zebra finches is generated by a supergene on a sex chromosome and maintained by a heterozygous advantage.

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The function of sperm — to find and fertilize ova — is universal throughout nature, yet the form of these utilitarian cells is remarkably diverse. If all sperm share a common goal, what generates this diversity? Variation among species is shaped by sexual selection, sexual conflict, fertilization mode and evolutionary history, but even within a species, a surprising amount of variation can also exist¹. Understanding how this variation is maintained within a species where the selective regime is shared among individuals, remains largely unresolved. Two contributions in this issue of *Nature Ecology & Evolution* by Kim et al.² and Knief et al.³ reveal how a genetic inversion, acting as a ‘supergene’ may be responsible for linking beneficial mutations that control suites of sperm traits in zebra finches. Moreover, because heterozygous males carrying one allele with an inversion and one without, produce the most successful (‘super’) sperm, both alleles are maintained in the population, which gives rise to a range of sperm phenotypes.

Sperm are streamlined cells with a flagellum used for propulsion and a head containing genomic DNA. The midpiece of the flagellum houses the cell’s mitochondria, and its length is positively correlated with flagellum length in most birds⁴, but in the zebra finch, this relationship is more complex and distinctly non-linear. Moreover, the amount of inter-male variation in midpiece and flagellum length is unusually high and highly heritable in these finches⁵; these features suggest a simple genetic basis, such as one or two loci of large effect. Yet sperm morphology is a complex trait, and complex traits are generally controlled by numerous interacting genes⁶. Kim et al. and Knief et al. independently discovered that an inversion on the Z chromosome^{7,8} — a structural rearrangement of a large portion of the chromosome that is excised, flipped and reinserted in the reverse direction — is responsible for most of the variation in sperm morphology in this species. Importantly, inversions disrupt the process of

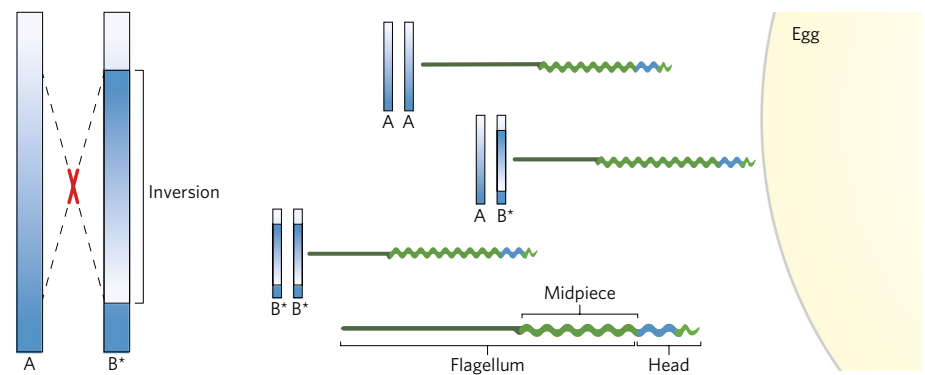


Figure 1 | A large inverted region on the Z chromosome in zebra finch restricts genetic recombination and allows suites of mutations on different genes within the region to accumulate together. Males homozygous for the inversion (bottom) produce sperm with shorter flagella but longer midpiece than those homozygous for the ancestral allele (top). Heterozygous males (middle), carrying only one copy of the inversion, produce the most successful sperm with both long flagella and midpiece, enabling them to swim with greater velocity.

recombination during meiosis, meaning that sets of mutations are inherited together and beneficial mutations have the opportunity to accumulate on one region of the chromosome. The result is a complex polygenic trait with an inheritance pattern more typically seen in monogenic traits.

Both teams found that male finches with two copies of the ancestral Z chromosome (genotype AA) produce sperm with long flagella but very short midpiece regions (Fig. 1). Conversely, sperm from males with two copies of the Z with an inversion (B^*B^* , following the notation in Knief et al. for simplicity) have long midpiece, but overall short flagella. Knief et al. showed that this combination of traits in B^*B^* males results in sperm with reduced motility and fertility. How, then, is this derived allele maintained in the population if it produces less fertile sperm? The answer is a heterozygote advantage. Both groups of researchers found that males heterozygous for the inversion polymorphism (AB^*) produce sperm with long flagella (although not as long as AA males) and extremely long midpieces. Knief et al. showed that the sperm

of these heterozygous males do indeed swim faster and fertilize a higher proportion of ova than both homozygous groups. Both teams used captive populations to identify the effect of the inversion on sperm morphology, but also showed that the polymorphism segregates in the wild and is not an artefact of captivity. Taken together, these studies clearly demonstrate how a heterozygous advantage maintains genetic and phenotypic variation in wild Australian zebra finches.

An important and equally interesting layer of these studies is the location of the inversion on the Z chromosome. Birds have a ZW sex-determination system, meaning that males are the homogametic sex (ZZ) and females are heterogametic (ZW). Thus, all sperm are Z, and ova are either Z or W. Evolutionary theory predicts that genes controlling sexually dimorphic traits that benefit the homogametic sex (in this case, male zebra finches) will accumulate on the avian Z⁹, but until now this theory has been difficult to prove. The Z chromosome represents only 7% of the zebra finch genome, yet Kim et al. showed that 67–90% of the additive

genetic variance in sperm morphology is derived from this very small portion of the genome. Gametes are potentially the most dimorphic of all sexually dimorphic traits, and traits that improve sperm competitive ability will undoubtedly benefit males. These studies, therefore, provide empirical evidence to support an important theoretical prediction.

The full story is more complicated than detailed here. There is not just one inversion, but at least two, as well as a putative double crossover creating some rare intermediate genotypes. Analysing each of these inversions, and particularly the rare intermediate genotypes, may provide a foothold in working to identify some of the causal genes associated with particular phenotypes. This next step is essential to understanding the functional and

evolutionary mechanisms that have shaped sperm diversity, but distinguishing these targets in the zebra finch will be an uphill battle. The same chromosomal inversion that produced this supergene and allowed genes to co-evolve together results in extreme linkage disequilibrium between the genes¹⁰, making traditional mapping approaches challenging to say the least. Although Kim et al. name a handful of interesting candidate genes, at this stage of research, the most interesting findings from these two complementary studies explain how variation can be maintained in nature, even under the intense selective pressures of sexual selection. □

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Competing interests

The author declares no competing financial interests.