

Thesis abstract

Introgression, sperm and mitonuclear interactions in the long-tailed finch (*Poephila acuticauda*)

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Modern genomic sequencing has revealed that hybridisation and the resulting gene flow between biological lineages is widespread across taxonomic groups. This gene flow, known as introgression, varies across the genome, with some genomic regions introgressing readily between lineages and others not. Naturally hybridising organisms offer an opportunity to observe introgression, but to test the mechanisms underpinning the observed heterogeneity ultimately requires experimental approaches, which has rarely been possible with naturally hybridising organisms. In this thesis I investigate the processes underpinning introgression and reproductive isolation by exploiting the well-established and tractable system of the naturally hybridising long-tailed finch subspecies, *Poephila acuticauda acuticauda* and *P. a. hecki*. This system exhibits various degrees of introgression: bill colour has introgressed 350 km east of the genomic hybrid zone; the mitochondrial DNA hybrid cline centre has introgressed 55 km west across the nuclear hybrid cline centre; and an inversion on the Z-chromosome appears resistant to introgression between the subspecies. In this thesis I use behaviour trials to reveal that the bill colour introgression is not driven by a universal female preference for yellow bills; instead, females display an assortative mating prefer-

ence that, combined with dominance patterns in the genes underlying bill colour, may be driving this bill colour introgression. I reveal that, when the mitochondrial and nuclear genomes of the two subspecies are mixed in hybrids, they interact and compromise cellular aerobic respiration. This is the first evidence of a mitonuclear interaction in a bird and it may be driving the westward introgression of mitochondrial genome across the nuclear hybrid zone. Next, I confirm that sperm morphology is divergent between the long-tailed finch subspecies, but find no evidence that the sperm of admixed individuals, or those with mitonuclear mismatch, is different from that of the parental subspecies, and so find no new evidence that sperm morphology is contributing to reproductive isolation in this system. Finally, I opportunistically investigate the genetic basis of sperm morphology in the long-tailed finch, and identify a rare sex-linked inversion that acts as an allele of large effect on sperm morphology, where carrier males have significantly shorter sperm midpiece, flagellum and total sperm lengths. Together, this research provides new insights into the mechanisms underlying introgression and reproductive isolation in a recently diverged, naturally hybridising avian system.

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