

Random mating in a hybrid zone between two putative climate-adapted bird lineages with predicted mitonuclear incompatibilities

Lana Austin¹, J. Nevil Amos¹, Diana Robledo-Ruiz¹, Jessica Zhou¹, Rohan Clarke¹, Alexandra Pavlova¹, and Paul Sunnucks¹

¹Monash University

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Abstract

Mitonuclear interactions have been proposed as evolutionary drivers of sexual reproduction, sexual selection, adaptation, and speciation. We investigated the role of pre-mating isolation in maintaining functional mitonuclear interactions in a wild population with divergent sets of proposed co-adapted mitonuclear genotypes. Two lineages have been identified in the eastern yellow robin *Eopsaltria australis* - putatively climate-adapted to 'inland' and 'coastal' climates. The lineages differ by ~7% of mitochondrial DNA positions, whereas nuclear genome differences are concentrated into a sex-linked region enriched with mitochondrial genes. This pattern can be explained by female-linked selection accompanied by male-mediated gene flow across the narrow hybrid zone in which the two lineages coexist. It remains unknown whether lineage divergence is driven by intrinsic incompatibilities (particularly in females, under Haldane's rule), extrinsic incompatibilities, or both. We tested whether non-random mating with respect to partners' mitolinesages or Z-linked variation could facilitate lineage divergence. We used field data, Z-linked and mitolineage genetic markers from two locations where the lineages hybridize, to test whether females choose to mate with (1) males of their own mitolineage and/or bearing similar Z-linked variation, as might be expected if hybrids experience intrinsic incompatibilities, or (2) putatively locally-adapted males, as expected under environmental selection. Comparisons of field observations and simulations present no evidence of non-random mating: the observed reduced female gene flow likely operates via post-mating isolation. Future studies testing for female-biased mortality at different life stages and female habitat selection should clarify the mechanisms of selection.

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