

P16 - Regulatory variation in pigmentation loci underlies polymorphism in *Podarcis muralis*

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Many lizard species exhibit alternative colour morphs co-existing in sympatry in variable frequencies across their distribution. These morphs are often connected to differences in life-history, behaviour and physiology, providing an excellent opportunity to investigate the evolution and maintenance of complex polymorphisms. In particular, the genetic basis underlying colour morphs in lizards remains unsolved: are multi-trait differences explained by a large number of genes (a 'supergene' architecture), or by a small number of large-effect loci? To tackle this question, we investigated the molecular basis of colour polymorphism in the common wall-lizard (*Podarcis muralis*), a species that exhibits three pure morphs differing in throat and belly coloration (orange, yellow and white) and two intermediate morphs (orange-white and orange-yellow). We carried out phenotypic (biochemical and histological) analysis and used a *de novo* reference genome assembly as a backbone to conduct genomic and gene expression analysis. We demonstrate that the genomes of the different colour morphs show residual differentiation, with the exception of very localized regions. Fine-scale analyses show that these difference map to small noncoding regions immediately upstream of pterin and carotenoid metabolism genes, explaining variation in orange and yellow colouration driven by pterin and carotenoid pigments, respectively. Gene expression analysis shows that down-regulation of these genes is responsible for both the orange and yellow phenotypes. Haplotype analysis indicates a deep divergence in the orange locus, with divergent haplotypes being shared by other species in the genus. This pattern is explained either by recent introgression or by long-term balancing selection. With this work we demonstrate that the covariance between coloration and other phenotypic traits is not explained by a supergene organization but is most likely driven by pleiotropic effects of pigmentation genes on other physiological aspects.