

Modular regulation and convergent evolution of ASIP underpins color variation in wheatears

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Adaptation to novel environments is likely faster if selection can act on segregating variation, present either from pre-existing standing genetic variation or introduced through introgression, as opposed to variation that needs to arise by mutation. Determining the circumstances under which each of these evolutionary routes fast-tracks evolution is best addressed in systems with abundant phenotypic convergence. Here, we made use of two powerful natural laboratories – phenotypic convergence and hybrid zones – to investigate the molecular basis and evolutionary history of coloration in wheatears (genus *Oenanthe*). First, by leveraging a color polymorphism and hybrid color phenotypes within the *hispanica*-complex we inferred strong associations of two plumage traits with coding and non-coding SNPs, all located within or upstream of the ASIP gene. We then show that across the genus, the very same phenotypes are not associated with SNPs uncovered in the *hispanica*-complex. Taken together, our results show that i. within- and between-species variation in plumage coloration is determined by modular regulation of ASIP expression in the *hispanica*-complex, and ii. convergent genetic bases underpin plumage color convergence at the phylogenetic scale in wheatears. By combining a population genomic with a comparative approach, our study provides insights into how regulatory variation at a master locus, likely derived from shared ancestral variation within the *hispanica*-complex, but not across the genus controls wheatear coloration.