Genomic studies suggest that rapid evolution is often underpinned by standing genetic variation or hybridization, rather than novel mutations. However, insights into the prevalence of each of these trajectories to phenotypic evolution are still limited. In the present talk, I introduce a study system – wheatears (genus Oenanthe) – that promises diverse insights into the roles of ancestral variation, hybridization, and novel mutations in phenotypic evolution. I show how we combine evidence from phylogenomic and population genetic perspectives to infer the molecular architecture of plumage coloration and trace the evolutionary history of color variation in wheatear and ultimately gain insights into the complex histories of phenotypic evolution.