Deciphering Adaptive Evolution using Multi-Omics

The advent of large-scale genomics data has been transformative for understanding evolution at the molecular scale, yet most work has focused on how changes in coding regions give rise to novel protein functions. Changes in non-coding regions, however, can be equally consequential, altering downstream processes including transcription, translation and post-translational modification. Such changes are increasingly recognised as key drivers of adaptive and morphological evolution. Because these variants often reside in regulatory regions, their functional consequences are inherently difficult to define, particularly when changes at one locus influence distant genomic targets through trans-acting mechanisms. Our aim is to integrate multi-omics data to understand how regulatory variation translates into changes in protein expression and, ultimately, adaptive phenotypes.

We are addressing this question using the house sparrow (*Passer domesticus*), a globally successful invasive species that has colonised some of Australia's most challenging environments despite arriving on the continent only ~160 years ago. Specifically, we are investigating how sparrow populations in lead (Pb) mining towns such as Broken Hill and Mount Isa have adapted to chronic heavy metal exposure over remarkably short evolutionary timescales. By combining genomics, transcriptomics, proteomics and metabolomics, we aim to trace the path from regulatory variation in the genome through to altered gene expression and protein abundance, providing a mechanistic account of rapid local adaptation in wild populations.

Expected Outcome: Our multi-omics integration framework (Figure 1) will provide a mechanistic account of how wild vertebrate populations adapt to severe anthropogenic stress, and establish a transferable pipeline for linking genomic variant-informed expression changes to adaptive phenotypes across diverse population-level studies.

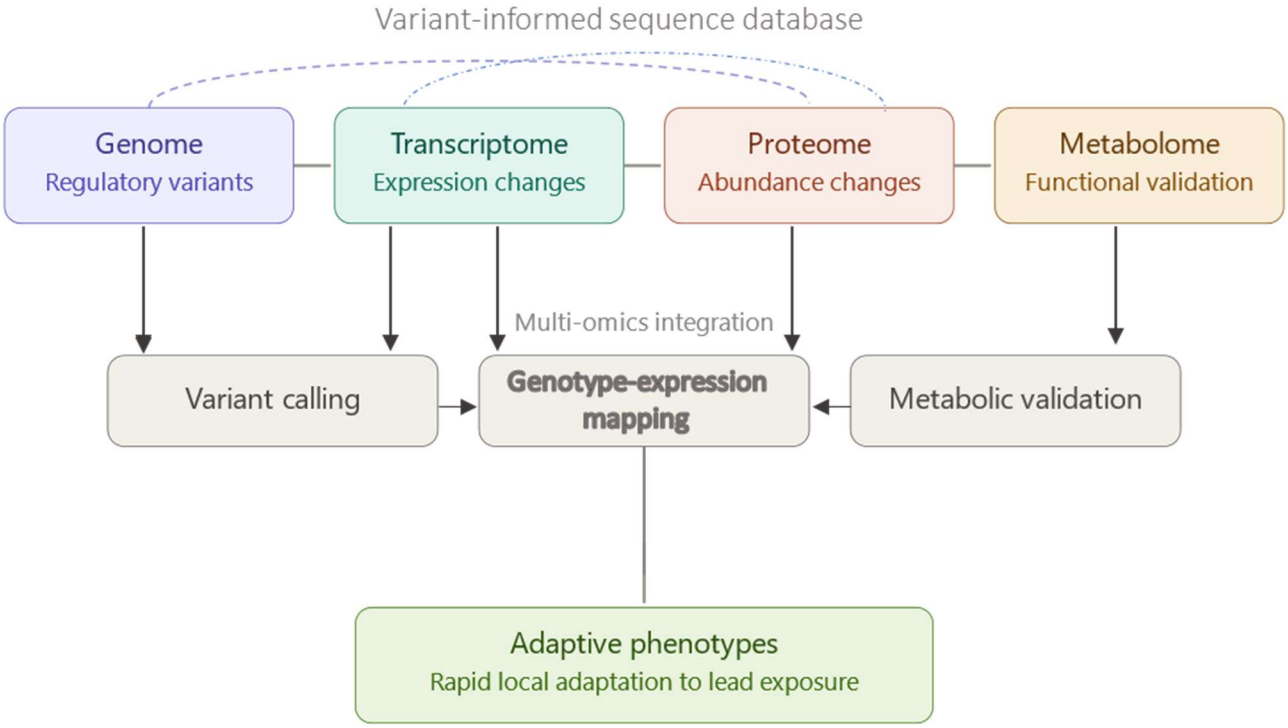

Figure 1. Multi-omics integration framework for deciphering adaptive evolution in lead-exposed house sparrow populations. Genomic variants, including SNPs and haplotypes from non-coding regulatory regions, are combined with a static reference genome and transcriptomic variant calls to construct a variant-aware protein database. This database enables large-scale DIA proteomics to detect protein abundance changes attributable to genomic variation, while targeted metabolomics provides independent functional validation of proteomic findings. Together, these four omics layers trace the molecular path from regulatory variation to adaptive phenotypes in Passer domesticus populations inhabiting Australian lead mining towns.