

Comparative genomics of the sheep blow fly *Lucilia cuprina*

Christine J. Picard & Anne A. Andere
Department of Biology
Indiana University Purdue University Indianapolis

Insects employ different adaptive strategies in response to selective pressures, such as competition for limited resources. Carrion insects provide the ideal case to study these fundamental processes of adaptive evolution due to the intense selective pressures placed on developing larvae with limited food resources, their widespread and abundant distributions, and the presence of geographically distinct populations with specialized adaptations. One adaptation is facultative ectoparasitism, where the insect strikes a healthy animal and feeds on the living flesh, providing a developmental advantage over competitor fly species, but causing significant harm to the host. *Lucilia* species, which hybridize in the wild and form geographically distinct subpopulations in other regions, are diverging, meaning that we can observe and quantify early biological adaptive processes that govern speciation as they are occurring over hundreds, instead of millions, of years. The draft genome of a North American male *Lucilia cuprina* fly (carrion breeder) was assembled using a combination of short and long read sequences. This genome is compared to an existing Australian draft genome (ectoparasite) by elucidating genomic structure in key adaptive processes (i.e. immune system evasion) via high-throughput re-sequencing of parasitic specimens, gene prediction and annotation. The carcass colonized by or animal parasitized by both species, with some geographic overlap, provides a semi-controlled environment within the larger context of the ecosystem to sample a large number of individuals with similar life history strategies, allowing for direct comparative studies to elucidate the correlation between structure and function in the genomes of carrion flies – allowing us to understand biological adaptation and speciation.