

Identifying the genes regulated by the *wntA* signaling pathway in the black pattern expression in the wings of *Heliconius* butterflies.

This experiment aims to identify the genes involved in the black pattern expression in the *Heliconius* butterfly wings that are regulated by the *wntA* signaling pathway. The *wntA* signaling gene has been linked to the expression of the black pattern in *Heliconius* butterfly's wings by in-situ hybridization and linkage-mapping). Recent gene-editing techniques allow the specific knock-out (KO) of genes to study their functionality. The KO of the *wntA* signaling molecule by CRISPR technology in *Heliconius erato demophoon* results in loss of the black pattern in the proximal region and an extension of the red, mid-band, into the proximal region. By comparing the expression profile of the wild type and *wntA* KO wing tissue (proximal, medium and distal) will allow me to identify the genes which expression has changed. Those genes which expression changed after the *wntA* KO between the wild type and mutant are expected to be involved in the black melanin expression. The extraction has been done on the larvae 5th instar (when they are about to become crawlers) and 24 hours after pupation. The RNA will be extracted by chloroform and sequence in the illumina sequencing machine. The library reads will be analyzed using R statistics.