

## *De Novo* Genome Assembly of *Phormia regina* (Diptera: Calliphoridae)

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

*Phormia regina* (Meigen), commonly known as the black blow fly, is a dipteran that belongs to the family Calliphoridae (blow flies). Calliphorids play an important role in various research fields like ecology, medical studies, veterinary and forensic sciences. *P. regina* is one of the common forensically relevant insects in North America and is typically used to assist in estimating post-mortem intervals (PMI).

To better understand the roles it plays in the numerous research fields, we aim to re-construct its genome using next generation sequencing technologies. We are specifically focusing on generating a reference genome by *de novo* assembly then use the genomic data to identify genetic markers (microsatellites, single nucleotide polymorphisms) that contribute to intra- and inter-population variation with regards to geographic location.

DNA was extracted from five adult male and female flies and was sequenced using the Illumina HiSeq2000 sequencing platform. More than 250 million high quality reads were produced from each sex. These reads were used in the *de novo* genome assembly of the female, male and combined sexes. The assembled draft genomes produced approximately 251,115 contigs, 306,273 contigs, and 325,664 contigs respectively. The assembled genome sizes totaled to ~524 Mbp and ~508 Mbp for the female and male flies, respectively. Compared to the estimated genome sizes from a previous study of 529 Mbp for females and 517 Mbp for males, we can conclude that a majority of the genome sequence (~99%) is included in the assembly. Gene prediction and annotation of the draft genomes are currently in progress.

The draft reference genomes assembled from this study will provide an important resource for analyzing genetic basis of variations between and among blow fly species, which will ultimately facilitate ongoing studies in various areas of research that utilize blow flies as study models. It will also be a source where reliable genomic data can be readily available and used in downstream analysis to increase the understanding of the genetic, molecular and cellular processes of blow flies.

**Key words:** *Phormia regina*, *de novo* genome assembly, Illumina, next generation sequencing