Assessing patterns of genetic and antigenic diversity in Calliphoridae (blowflies)

Submitted by

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Signature Date
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The blowflies (Diptera: Calliphoridae) include some of the world’s most economically significant parasites of livestock. The defining characteristic of blowflies is the need for their larval stages to feed on a proteinaceous substrate, often including the tissues of a living vertebrate host, a process known as myiasis. While the evolution of myiasis has been linked to the development of key adaptations in behaviour and physiology (Stevens et al., 2006), patterns of blowfly evolution suggest that parasitism evolved independently in different blowfly groups after periods of geographic isolation (Stevens et al., 2006).

However, understanding the origin and evolution of myiasis in Calliphoridae is restricted by a lack of agreed theories of evolutionary relationships and taxonomic classification (Stevens, 2003). Mitochondrial genes are some of the most widely used molecular markers in insect systematics, yet most studies have utilised only single genes, with few having systematically assessed which if any are best suited for studying particular insect orders. Accordingly, this thesis presents a comprehensive analysis of 62 hexapod mitochondrial genomes, including 55 from Insecta, and assesses the ability of mitochondrial genes to recover currently recognised insect orders as monophyletic groupings. The greatest amount of phylogenetic signal was recovered when all mitochondrial genes were analysed together, regardless of optimality criterion used (PhyML, RaxML, MrBayes). Of the single-gene analyses, COX1 out-performed all other genes, even performing as well as a combined-gene analysis under Bayesian inference. In view of this finding, nucleotide sequence data from COX1 (mitochondrial protein-coding), EF-1α (nuclear protein-coding gene), and 28S (nuclear rRNA) were combined to present one of the most comprehensive multi-gene phylogenetic studies of Calliphoridae to date, resolving many ambiguous relationships, and also including several taxa that have not previously been analysed in molecular phylogenetic studies.

Within Calliphoridae, Cochliomyia hominivorax (New World screwworm fly), is widely considered one of the most destructive insect parasites of livestock in the Western hemisphere. While successful eradication programmes using sterile insect technique (SIT) have been completed in North and Central America, and on some Caribbean islands, in some areas SIT has failed. It has been hypothesized that failure of SIT may be related to genetic differentiation between populations of C. hominivorax. Consequently, intra-specific variation using nucleotide sequence data from both mitochondrial (COX1 and 12S) and nuclear (EF-1α) markers, was explored. Phylogenetic analysis of these data confirmed some population sub-structuring and suggested a South American origin to all Caribbean island populations, with the exception of Cuba. In agreement with previous studies, Cuban populations appeared distinct from all other Caribbean populations; however, our findings do not support a North American origin for Cuba, as has previously been suggested.

Finally, this thesis attempted to explore the relationship between antigenic proteins expressed in larvae from species displaying different forms of parasitism, and in doing so assessed the utility of such target proteins as potential candidates for species-specific vaccines and diagnostic tools. However, while this work discovered distinct antigenic profiles for different blowfly species, the ability to characterize specific antigens was fundamentally limited by an apparent lack of homologous proteins in current databases.
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