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Editorial

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Genomics and Bioinformatics in Entomology

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The number of genomic studies has increased exponentially in the field of Entomology over the last ten years. This has been a direct effect of the increase in genome sequencing as a result of diminishing costs, with the advent of new technologies.

The first insect genome to be sequenced was that of *Drosophila melanogaster* (Fruit fly) in the year 2000 [1]. The genomes of *Anopheles gambiae* (Mosquito- the vector for malaria), *Bombyx mori* (Domestic silk worm), and *Apis mellifera* (Honey bee) were sequenced in 2002, 2004 and 2006 respectively [2-4]. Since then there has been a surge in the sequencing of insect genomes, most of which are that of Dipteran and Hymenopteran insects. However, genomes of insects that belong to the orders Lepidoptera (Butterflies; [5], Diamondback moth; [6], Coleoptera (Beetles; [7,8]), Hemiptera (Pea Aphid; [9]) and Phthiraptera (Head louse; [10]) have also been sequenced.

With the deluge of sequence information, researchers have become increasingly interested in mining these data in order to find the answers to complex biological questions. Advancements in the field of bioinformatics to handle huge amount of data has also played a key role in this process. The availability of multiple insect genomes has created an outstanding potential for comparative genomics among insects that can lead to a wealth of information on organismal biology [11]. Research in the field of Phylogenomics, where genomic data is used for inferring phylogenies of, and investigating phylogenetic relationships among, different species has also been growing over the last few years [11].

Although, much of the recent focus has been on genome sequencing and annotation, this has lead to functional genomics studies that includes analyses of the genetic basis of complex traits, quantification of global gene expression and systematic gene disruption projects [12]. Microarrays have long been the preferred method for studying tissue and time specific differential gene regulation; more recently, techniques like RNA-seq are becoming increasingly popular. Expressed Sequence Tag (EST) based studies are also being used to decipher relevant information related to the regulation of genes. RNA interference, that depletes specific transcripts and eventually leads to loss-of-function phenotypes, has also been extremely useful in the field of functional genomics. All of these techniques are reliant upon bioinformatics analyses of the sequence information.

This trend of increasing genomics and bioinformatics studies in the field of Entomology, likely to continue for sometime, even though researchers have started to look at the proteomes (proteomics) and the metabolomes (metabolomics) of insects, as logical extensions of the genomic studies. Therefore, we are going to have significantly more information within the next few years, and one must be careful about how best to analyze and decipher the age of "OMICS".

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