Silkworm nucleotide databases - Current trends and future prospects

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Abstract:
The domesticated silkworm, Bombyx mori serves as an ideal representative of lepidopteran species for a variety of scientific studies. As a result, databases have been created to organize information pertaining to the silkworm genome that is subject to constant updating. Of these, four main databases are important for store nucleotide information in the form of genomic data, ESTs and microsatellites. These databases also store data related to other lepidoptera and important insects, which help in insect biological studies elucidating evolutionary relationships, mapping and population genetics and forensic studies. Thus silkworm databases are essential for insect biology studies.

In light of these needs, a few databases have been created to store the data generated from genomic and cDNA sequencing operations carried out on the B. mori. To date, there are four major databases, that store nucleotide data, that are available in the public domain. Of these, two are genomic databases: the Silkworm KnowledgeBase (http://silkworm.genomics.org.cn) hosted by the Beijing Genomics Institute (BGI) in China and the Silkworm Genome Database (http://papilio.ab.a.u-tokyo.ac.jp/genome/index.html) hosted by the Insect Genetics and Bioscience (IGB) lab at the University of Tokyo in Japan [4]. The IGB lab also hosts the EST database for the silkworm namely, the Silk Base. This database contains all the EST sequences expressed in B. mori at various stages of growth and development, in various tissues. Another database, namely the Silk moth Microsatellite Database (SilkSatDb - http://www.cdf1.org.in/silksatdb) hosted by the Centre for DNA Fingerprinting and Diagnostics at Hyderabad, India is a relational database of microsatellites extracted from available EST and Whole Genome Shotgun (WGS) Sequences of B. mori. The database stores three kinds of data: the microsatellite repeats found in the B. mori EST, WGS sequences and details pertaining to each sequence and information on the primers developed for each of these microsatellites [5].

Silkworm knowledgebase
The Silkworm KnowledgeBase (Silk Db) is a web-based repository for the curation, integration and study of silkworm genetic and genomic data maintained by many key institutes in China, mainly the Beijing Genomics Institute (BGI). After the
This database contains 16,425 EST clusters based on the sequencing of 80,470 ESTs from B. mori tissues, 554 lepidopteran genes, 521 B. mori homologs of other lepidopteran genes and SNPs identified from the ESTs [7]. Using the B. mori genome sequence as a reference, comparative analysis can be done between B. mori and B. mandarina, other lepidopterans and the sequenced dipterans (Fruit fly and Mosquito). The silkworm genome has been assembled in the form of contigs onto a scaffold using mapped genetic markers and BAC-based physical maps, complete with packages for sequence assembly, gene annotation and identification of transposable elements. This in turn serves as a framework to organize information for other lepidopterans and, along with the database’s search-engine and MapView program, provides an information resource and a comparative genomics platform for genome related research of both, silkworm and other insects. The genomic data are organized into 3 modules for effective management namely; scaffold, gene and transposable elements. The scaffold module contains 23,156 scaffolds for the 28 chromosomes organized from whole genome shotgun contigs that span 428.7 Mb of the B. mori genome covering 90.9% of all known silkworm genes. The gene module contains the sequences of 18,510 annotated genes from GenBank. The transposable elements (TE) module catalogues the 6,01,225 TEs that have been identified in silkworm genes from GenBank. The transposable elements (TE) module catalogues the 6,01,225 TEs that have been identified in silkworm genes from GenBank.

Important genes of silkworm, B. mori

Though the silkworm databases contain information on all genes discovered in the silkworm, there are some genes that are of greater importance as they play a major role in the biology of the silkworm and other lepidoptera [9]. Presently there are about 3000 silkworm genotypes being maintained in Europe and Asia. The genetic stocks consist of about 500 mutants that vary in different physical, physiological and biochemical traits. As a result the genes responsible for determination of these characteristics have been extensively studied.

Among the genes of interest, the silk gland and the chorion genes are most important. The silk-gland- because it is the best source of DNA for genomic studies as each cell accumulates between 400,000 to 800,000 copies of the haploid genome, whereas the chorion is a very effective indicator of mutation in genotype. The homeobox genes have also been studied extensively as they are responsible for embryonic tissue differentiation and normal development of all organisms. In addition, the immune genes that code for anti-bacterial and antiviral proteins have also been extensively studied as lepidopterans constitute the most important class of biological pests [10].

Current applications:

From the above discussion, the importance of databases cataloguing biological information related to lepidopterans can be understood. Different databases store various types of information that have found many applications in lepidopteran research. The silkworm genomic databases store information in various forms. Contig information allows viewing of the
complete genome with necessary information at all relevant locations, so that the structural organization of genes and other genetic elements such as transposable elements can be analyzed inside the genome as a whole. Clustering of genes involved in common processes can also be studied. Gene-wise BLAST searches help to identify similar orthologous sequences in other organisms. This helps find genes in other organisms that show homology in function, which helps to identify conserved regions in the sequence, in homology modeling of putative proteins and elucidating the phylogenetic relationship between orthologous and paralogous sequences [11, 12, 13]. Information on transposable elements (TE) has helped to explain the difference in genome size of *Drosophila* and *B. mori*. They also help in studies of gene activation-deactivation and in recombination studies. The EST databases help in the construction of molecular linkage maps that show where the different ESTs are located in the genome and how the genes are organized and located in relation to each other. Using the same ESTs, Bacterial Artificial Chromosome (BAC) contigs have also been created, with each contig being assigned an average of 3-4 EST markers. EST data is also useful for serial analysis of gene expression (SAGE), microarray analysis in expression profile and genome studies where large amount of data are analyzed at once [14, 15, 16, 17]. Microsatellite data helps measure genetic distance, to carry out genetic fingerprinting of silkmoths, construct molecular linkage and single nucleotide polymorphism maps and carry out phylogenetic analysis between silkmoths and other lepidopteran species [18, 19, 20]. A combination of all these data has also been used in the prediction of microRNAs [21].

**Future prospects:**
At present extensive databases are available that contain nucleotide information at different levels. In the future, protein databanks could be created that store structural information about various silkworm proteins, their structure and sequence information, family classification and several others. With a more detailed knowledge about the *B. mori* genome, greater number of ESTs could be generated that could aid in a more precise construction of BAC contigs for the silkworm genome. Currently work is being done to improve the quality of genomic data available. This in turn would be useful for generating accurate maps and representations of EST clusters which would aid in comparative genomic studies of *B. mori* with other silkmoths, lepidopterans and insects.

Efforts are also being made to complete the microsatellite database, so that linkage maps for microsatellite loci can be generated. Phylogenetic comparison of microsatellites between heterologous species can then be carried out, to elucidate a clearer evolutionary relationship. Thus, in the future, it is hoped that generation of a more complete draft of the silkworm genome will help in better understanding of lepidopteran species. Protein databases for silkworms would be useful in modeling projects looking for methods to help control lepidopteran pests and help in the study of their immune system. Hence, a lot is yet to be done to make data related to insect genomes and proteomes readily available to researchers.

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