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ButterflyBase: a platform for lepidopteran genomics

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ABSTRACT

With over 100,000 species and a large community of evolutionary biologists, population ecologists, pest biologists and genome researchers, the Lepidoptera are an important insect group. Genomic resources [expressed sequence tags (ESTs), genome sequence, genetic and physical maps, proteomic and microarray datasets] are growing, but there has up to now been no single access and analysis portal for this group. Here we present ButterflyBase (http://www.butterflybase.org), a unified resource for lepidopteran genomics. A total of 273,077 ESTs from more than 30 different species have been clustered to generate stable unigene sets, and robust protein translations derived from each unigene cluster. Clusters and their protein translations are annotated with BLAST-based similarity, gene ontology (GO), enzyme classification (EC) and Kyoto encyclopedia of genes and genomes (KEGG) terms, and are also searchable using similarity tools such as BLAST and MS-BLAST. The database supports many needs of the lepidopteran research community, including molecular marker development, orthologue prediction for deep phylogenetics, and detection of rapidly evolving proteins likely involved in host–pathogen or other evolutionary processes. ButterflyBase is expanding to include additional genomic sequence, ecological and mapping data for key species.

INTRODUCTION AND MOTIVATION

The Lepidoptera (butterflies and moths) are remarkably diverse containing more than 100,000 described species. There is a long tradition of research and a number of disciplines use lepidopteran models to investigate fundamental biological phenomena including development and gene regulation, population genetic processes (gene flow, colonization and extinction), adaptation and morphological innovation, speciation and co-evolutionary processes such as host–plant and insect–parasite interactions. As a result, there is a wealth of ecological and genetic knowledge for Lepidoptera.

The silkworm Bombyx mori is a model for insect physiology and molecular biology, as well as being an important crop animal. Currently, two whole genome shotgun sequence assemblies are publicly available (1,2) and a joint genome assembly by the Chinese and Japanese teams is expected within 2007. The genomic sequence data are anchored by a number of bacterial artificial chromosome (BAC) libraries, high-density linkage maps of sequence tag sites (STS), cDNA and microsatellite (simple sequence repeats, SSR) markers (3–6) as well as cytogenetic studies (7) which provide a chromosomal framework for genome assembly. Thus the chromosomal framework for genome assembly is in place and as the annotation of the B. mori genome progresses, it will facilitate comparative analysis of other species with less complete genomic information (8).

In addition to genomic resources in Bombyx, there is increasing amount of EST data for a growing number of Lepidoptera species. Large to moderate-sized EST datasets are becoming easier and less expensive to produce and can be powerful source of markers for comparative mapping, population genetic analysis and studies of adaptive evolution (9). For example, there are large public genomic datasets for the moth pest Spodoptera frugiperda, and the butterflies Bicyclus anynana, Heliconius melpomene and Heliconius erato. The generation of sequences for these and other species has led to the discovery that around half of the sequenced genes in Lepidoptera have little or no sequence similarity to proteins from other taxa (8). Species-specific public databases are available for these taxa, but vary widely in accessibility and format (10–13). What is lacking is a central platform for accessing lepidopteran data and more importantly for conducting comparative between species analyses.

To allow the community to benefit from the comparative genomic data available in Lepidoptera, we developed

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METHODOLOGY

Datasets

ESTs and full-length cDNA sequences were obtained from public depositions in the EMBL/GenBank/DDBJ database, and clustered using a modified version of the PartiGene suite (14). When the original sequencer chromatograms were available (H. erato and H. melpomene) we processed them with trace2dbest (14). All other data were pre-processed to remove vector contamination, poly(A) tails and sequences smaller than 150 bp. For some cDNA libraries (where sequence quality was poor), further trimming was performed using a customized version of est_trimmer.pl [provided by Thomas Thiel through the MISA program (15)]. SSR prediction was performed using MISA (15), single nucleotide polymorphisms (SNPs) were predicted using SEAN (16) and databased using custom Perl scripts. A SEAN Java viewer is available as a modified applet, provided by the SEAN author. The methodology of SEAN does not rely on quality information and therefore can be used with our datasets. Instead, it only marks putative SNPs if a single nucleotide change is present in at least two members of the EST cluster and there are no other nucleotide inconsistencies 15 bp up- and downstream of the putative SNP.

PartiGene (14) uses megablast and the CLOBB approach to cluster EST sequences into groups putatively derived from the same mRNA molecule (17). These clusters are subsequently aligned using Phrap (with the forcelevel option set to maximum) (18, Green.P., unpublished software). Sequenced organisms in Lepidoptera are often outbred and may, therefore, exhibit substantial allelic variation. Essentially, the presence of low quality, multiple SNPs, sequencing errors, alternative splicing or short indels may allow megablast to generate a cluster of highly similar sequences which is not subsequently aligned by Phrap, thus leading to some clusters containing more than one contig.

ButterflyBase uses a two-letter code to signify the species ID and a third letter to signify molecule type (P for protein, C for nucleotide cluster (or unigene) and in the future B for BAC clone). Each cluster of ESTs and cDNAs has a unique numerical ID, which is stable when additional sequences are added to the dataset. When there is more than one contig per cluster these are indicated by a trailing number. Thus HEC00123_1 is the first contig of a nucleotide cluster from H. erato and its protein translation is HEP00123_1. Cluster identifiers are conserved as more sequences are added.

Protein prediction

The protein predictions are ButterflyBase’s strongest asset. We use, prot4EST, a protein prediction tool developed specifically for EST data (19). Briefly, this program utilizes a four-tier methodology: first, similarity to known proteins is used in order to detect the open reading frame (ORF) and correct for any potential sequencing errors [using the high-scoring segment pair (HSP) tiling approach], if that fails (e.g. for novel or Lepidoptera-specific genes) ESTSCAN is utilized (20) and if that fails too then DECODER (21) and finally the longest ORF from the six-frame translation. As prior training data (codon usage tables and base composition estimates) for probabilistic prediction of ORFs were not available for many lepidopteran species, we utilized data derived from high-scoring BLAST matches to populate species-specific parameter sets.

Database schema and dataset annotation

The database is driven by PostgreSQL with a customized version of the PartiGene schema. The central entity is a mRNA sequence cluster. Each cluster is annotated with a number of facilities. The most frequently accessed are pre-computed BLAST similarity searches versus a variety of databases: Uniref100; a collection of possible contaminants (e.g. fungi, viruses, bacteria, molecular biology vectors) and phylogenetically selected, nested databases. We chose a number of such databases including B. mori nucleotides and proteins; Lepidoptera nucleotides without B. mori; proteins from released Arthropoda genomes; Arthropoda sequences without those genomes or Lepidoptera. All BLAST searches have an E-value cutoff of $1E^{-4}$. Furthermore, predictions enhance the utility of the consensus: a robust protein translation as well as SSR and SNP predictions are currently offered. The protein predictions in turn are annotated with enzyme classification (EC), gene ontology (GO) and Kyoto encyclopaedia of genes and genomes (KEGG) terms. These latter annotations are derived from BLAST searches of annotated protein databases using the annot8r tool (Schmid,R. and Blaxter,M., unpublished software), and a cut-off E-value of $1E^{-5}$. Furthermore, ButterflyBase provides domain annotations from InterProScan (22) and basic protein statistics to facilitate downstream proteomic and biochemical investigations. Annotations are updated on a 4-month cycle and new sequence data are imported ~2 months after the release of at least 1000 sequences from any lepidopteran species. Communication with the database curators regarding an imminent release will shorten this time. Metadata linked to each mRNA or EST sequence (life cycle stage, tissue, sex, etc.) have also been databased. Original sequence accession numbers are also listed on each cluster page and linked to EMBL, and can
be searched for with the ‘Jump to’ search box on the left hand side of every page.

A SHORT TOUR
For security and efficiency reasons, the user-interface pages allow the user to explore the data with certain predefined queries (but see access statement below). ButterflyBase permits simple text searches against the sequence annotation. The definition lines of similar sequences are searched, with the option to define a cut-off value for the precomputed BLAST similarity searches. KEGG (23), GO (24) and EC codes and definitions can also be searched. All searches can be limited to a specific organism or cDNA library.

Once a cluster of interest is found, the cluster page shows a range descriptive data, including the raw data (such as sequence traces if available), the number of ESTs in the cluster, the cDNA libraries they belong to, similarity information from BLAST searches against three databases (Uniref, Drosophila melanogaster proteins from FlyBase (25) and B. mori predicted proteins from ButterflyBase), and links to the output of all the other BLAST similarity searches. The alignment of the constituent sequences to the consensus can be viewed using an interactive image, a Java applet driven by SEAN or a non-Java text view. These alignment views allow the user to pinpoint database SNPs. The linked protein page contains basic descriptive data, the predicted sequence, the results of BLAST similarity searches and KEGG, EC, GO and InterPro domain annotation.

EST sequences are a key resource for the development of sequence-specific markers for genetic mapping (26). ButterflyBase facilitates marker development by providing sequence information and a tool for designing degenerate or conserved primers. A protein-driven nucleotide alignment of two orthologous lepidopteran clusters is generated and then used for design of primers using Primer3 (27). EST sequences are also of great utility for the design of microsatellite markers (28). Although transcribed microsatellites are often less polymorphic than non-coding ones (15), they are less likely to be multi-copy or mobile (29). In addition, primers are designed on exon sequences, thus reducing the possibility of null alleles.

We provide a simple tool to output any microsatellite present in a specific sequence and also a table of all the microsatellite detected in each species’ dataset.

ButterflyBase offers also a BLAST server. Three BLAST search modes are available (NCBI-BLASTALL, PSI-BLAST and WU-BLAST-driven MS-BLAST). MS-BLAST (30) allows a user to query protein databases with multiple short peptide sequences derived from high-throughput mass spectrometry data. PSI-BLAST is particularly effective in the detection of distant similarity and will become an important method for detecting lepidopteran homologues of target genes as the database grows. For more complex queries, a database dump file can be downloaded for local replication of the database, as can species-specific FASTA files of the nucleotide cluster consensus and protein predictions, and custom-built annotation databases used in ButterflyBase.

All datasets, including a SQL flatfile of the database are provided for download with their checksum codes. We also provide FASTA files of some of the custom sequence databases used to carry out similarity searches. One drawback of public EST data, however, is the lack of a raw sequence trace repository. PartiGene can utilize these traces to assist the Phrap alignments, but we are also using them to check manually for the quality of specific libraries or clusters of interest. For this reason, all sequence traces we process are publicly available for download from their respective cluster pages along with a short text file on how the sequence was processed by trace2dbest. This is, unfortunately, only available for sequence trace data we have access to, namely Heliconius sp. and B. anynana. We are, however, encouraging the community to submit to us their raw sequence data.

SUMMARY OF CONTENT AND UTILITY
Website usage is outlined in the online User’s Manual but a summary of the content follows. The main webpage provides an up-to-date overview of the content of the database. At the time of print, ButterflyBase has processed 273 077 mRNA sequences from 32 lepidopteran species belonging to a total of 12 families giving circa 71 000 gene and almost as many protein objects. Although most of the sequences are from B. mori, there are nonetheless now 17 species with more than 500 sequences, and 12 species with more than 1000, representing a valuable comparative dataset (Table 1). Nearly half of the ButterflyBase clusters have similarity to known proteins outside the Lepidoptera clade. Although identity of sequence does not necessarily translate into identity of function, sequence similarity is a first step towards gene finding in this taxon. Also, ~58% of the genes in ButterflyBase are significantly similar to at least one more ButterflyBase species, thus facilitating annotation and the design of degenerate or conserved markers. What is also apparent is the relatively high proportion of Lepidoptera-specific genes, about one-third of the clusters have hits only in sequences derived from Lepidoptera but in B. mori (which is the most complete dataset) the proportion is about half of the gene objects (Table 1). The number of gene objects is an overestimate of the exact number of actual genes due to the nature of EST datasets and the lack of a genome backbone. Thus, two sets of ESTs from the same gene will appear as two unigenes if they do not overlap, however, accuracy will increase as sequence information from more Lepidoptera is provided. Furthermore, the whole of the B. anynana dataset and ca. 16% of the B. mori dataset contains 3’ sequences. Therefore, these gene objects may contain long untranslated regions (UTRs) which are not conserved. In any case, these observations warrant an in-depth investigation and any putative Lepidoptera-specific genes need to be examined in a phylogenetic context in order to determine if they have evolved novel functions specific to Lepidoptera or if they have retained ancestral functions despite gross sequence divergence on the protein level.
Phylogenetics

The phylogenetic context of Lepidoptera is one of the taxon’s strongest advantages for the study of ecology and evolution. Although the amount of public genomic data in Lepidoptera is increasing rapidly, the phylogenetic coverage is limited to the Ditrysia and non-existent for basal clades. A broader phylogenetic sampling, of at least a handful of chosen genes will help improve much of the clades. A broader phylogenetic sampling, of at least a handful of chosen genes will help improve much of the clades. A broader phylogenetic sampling, of at least a handful of chosen genes will help improve much of the clades. A broader phylogenetic sampling, of at least a handful of chosen genes will help improve much of the clades. A broader phylogenetic sampling, of at least a handful of chosen genes will help improve much of the clades. A broader phylogenetic sampling, of at least a handful of chosen genes will help improve much of the clades.

Annotation

ButterflyBase is primarily an annotation platform. Currently, the only information provided is similarity
to known sequences, including to other lepidopteran sequences. The aim of the annotation platform is to host enough information to allow researchers to judge if their sequence of interest has a specific annotation identity. This annotation will be essential for annotating novel sequences especially short reads generated in some projects such as cDNA–AFLPs. Currently, we do not provide curated annotation information but in the near future we will publish analysis on orthologue groupings. We plan to allow the community itself to contribute annotations for each ButterflyBase object perhaps by using a Wiki-based annotation platform (31) or the Generic Model Organism Database toolkit (GMOD). In addition, we hope to expand the annotation platform to include both non-EST sequence data and genetic/pheno-
ing peptides by mass spectrometric (MS) data are more error-prone and can be misleading. The MS-BLAST server facilitates identification using the ButterflyBase predicted (and often partial) proteins.

Support small-scale sequencing
During the construction of ButterflyBase we used all available Lepidoptera ESTs hosted in the public domain. A fraction of them was unfortunately lacking information, or contained vector contamination and/or low-quality sequence. ButterflyBase provides the facility to host trace information and currently holds raw trace data from H. erato, H. melpomene and B. anynana. In the future, ButterflyBase’s pipeline will judge the quality of a cDNA library based on the number of errors as detected from ESTs from other libraries or published full-length mRNAs. This is only possible, however, for species where multiple libraries of sufficient depth exist. In addition, ButterflyBase can offer the service of processing raw traces and generate dbest submission reports to researchers who request so and thus allow for a more standardized collection of Lepidoptera sequence information. In the near future, a new international Advisory Board will guide ButterflyBase and will post a set of recommendations for submissions of data to GenBank.

DATA SUBMISSION AND ACCESS STATEMENT
All ButterflyBase data are freely and publicly accessible. To be included in ButterflyBase, EST and mRNA data should be submitted to EMBL/GenBank/DDBJ (a step which we can handle upon request). We strongly encourage submission of raw trace files (in SCF format) to ButterflyBase. Although the user is limited to predefined queries and can download a copy of the database, we can also run custom queries upon request (email query at butterflybase.org). Our goal for the future is to develop the project guided by the community. Therefore, we welcome requests and contributions.

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Conflict of interest statement. None declared.

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