Development of lepidopteran insect ortholog database

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Japan has many researchers with long history of insect studies, and plenty of insect specimens. However, there have not been many cooperative studies with genome biology. It is essential to provide a wide variety of insect genomic information to the knowledge revealed by long-term insect research in order to enhance the insect research and gain a big social benefit. This study aims at developing a cross-search database for vast amount of insect genes containing public complete genomes, draft genomes, cDNA library, RNA-seq, and cloned genes, with novel sequencing using next generation sequencers.

Bioinformatics Center, Institute for Chemical Research, Kyoto University, has been collecting various genome sequences read by researchers worldwide, developing KEGG database http://www.genome.jp/kegg/. However, taking all insect taxonomy into consideration, the insect species with complete genomes are limited to a small number of specific groups, and the sequence information of other species are spread across the Internet. It is not yet possible to cross-search the insect genes. In order to better understand the biodiversity of insects, it is beneficial to enable cross-search of vast amount of insect genes even if they are not complete genome sequences. We also intend to add other related information such as taxonomic classification of insects, their feeding habits and their symbionts, hoping for the development of a valuable tool to convert the knowledge of entomology into the genomic-level understanding.