

**HOW TO SIMULTANEOUSLY ACHIEVE THE THIN AND WHITE WING OF A BUTTERFLY**

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Clouds in the sky and snow flakes have very high reflectance as expected from their whiteness. This high reflectance is realized by their large thickness which causes multiple scattering of light. On the other hand, the butterfly wing is very thin. A single scale is several  $\mu\text{m}$  in thickness, and the total thickness of the whole wing, which consists of the scales on both side and the wing substrate, reaches only  $10\ \mu\text{m}$  at most. Nevertheless, the wing of a butterfly, e.g., *Pieris rapae*, can be rather white. The wing should weight light, because the butterfly wing serves a tool for locomotion. Under this constraint, how butterflies produce the clear whiteness? We will compare the white part of the wing of several species of butterfly.

**DEVELOPMENT OF EXPERIMENTAL DATA MANAGEMENT SYSTEM FOR NEUROBIOLOGY**○Hidetoshi Ikono<sup>1</sup>, Takuto Nishioka<sup>1</sup>, Yoichi Seki<sup>2</sup>, Ryohei Kanzaki<sup>2</sup><sup>1</sup>School of Human Science and Environment, University of Hyogo, Himeji, Hyogo 670-0092, Japan, <sup>2</sup>Department of Mechano-Informatics, Graduate School of Information Science and Technology, Bunkyo-ku, Tokyo 113-8656, Japan

Physiological experimental data on the neuron is important resources for understanding neuronal mechanisms of neural network. Enormous quantity of data is accumulated with progress of studies in many laboratory. In this study, we are developing a database system for accumulating, utilizing and sharing neurobiological experimental data. The system is developed by innovation of cutting edge of Web technology, Contents Management System (CMS). Our system was used PHP-based CMS, XOOPS, for the base system and realized as a XOOPS module. Confocal image and electrophysiological recording data files in predefined folders can be registered with keywords and notes through the web browser. Registered data can be accessed by the browser through the local area network. Useful functions, such as attachment of comments, contents search and link to local application, are provided based on demands on experimenter. More than 700 of morphological and physiological experimental data on silkworm moth have been registered and managed by the system in Kanzaki Lab. The system can be used in many laboratories for laboratory groupware tool by addition of extra modules.

**DIGESTIVE SYSTEMS OF HOLOCELLULOSE IN TERMITES**○Gaku Tokuda<sup>1</sup>, Gaku Arakawa<sup>1</sup>, Hirofumi Watanabe<sup>2</sup><sup>1</sup>Center of Molecular Biosciences (COMB), University of the Ryukyus, 1 Senbaru, Nishihara-cho, Okinawa 903-0213, Japan, <sup>2</sup>National Institute of Agrobiological Science, Tsukuba, Ibaraki 305-8634, Japan

Holocellulose is termed for a complex of cellulose and hemicellulose, which are the main constituents of plant cell walls. Digestive mechanisms of holocellulose in termites have been primarily studied in terms of cellulolytic actions of endoglucanases. In the present study, we analyzed holocellulolytic mechanisms by measuring carbohydrolase activities against cellulosic and hemicellulosic substrates and by detecting changes in expression for such enzymes in the salivary glands and the guts of diverse, wood-feeding termites. Cellulolytic and hemicellulolytic activities markedly differed among species. Our results suggest that the holocellulolytic systems were changed in course of evolution in termites and we show preliminary evidence that some microbial carbohydrolases such as cellobiohydrolases or xylanase are also involved in holocellulose digestion in termites. Electron microscopy also indicated that wood particles are degraded by bacteria in the hindgut of the wood-feeding termite *Nasutitermes takasagoensis*. In the light of these results, we discuss how digestive mechanisms of termites altered during their evolutionary history.

**QUALITATIVE AND QUANTITATIVE DIFFERENCES OF CUTICULAR LIPIDS IN SUMMER-, WINTER- AND NON-DIAPAUSE PUPAE OF MAMESTRA BRASSICAE**○Chihiro Katagiri<sup>1</sup>, Osamu Uda<sup>1</sup>, Junichi Kaneko<sup>2</sup>, Yuuji Kimura<sup>3</sup>, Kazuhiro Tanaka<sup>4</sup><sup>1</sup>Biochemistry Laboratory, Institute of Low Temperature Science, Hokkaido University, Kita-ku, Sapporo 060-0819, Japan, <sup>2</sup>National Agricultural Research Center for Hokkaido Region, Hitsujigaoka 1, Sapporo 062-8555, Japan, <sup>3</sup>Prefectural Agriculture and Forestry Research Center, Kuroishi 036-0389, Japan, <sup>4</sup>Miyagi Gakuin Women's University, Sendai 981-8557, Japan

The cabbage armyworm *Mamestra brassicae* exhibits winter and summer pupal diapause. Diapause is one of the strategies for animals to survive the severe seasons. During this stage, they must avoid dehydration. The cuticle serves as a protective barrier between the internal tissues and the external environment. It is covered with cuticular lipids, mainly hydrocarbon and wax. We investigated their qualitative and quantitative differences among winter-, summer- and non-diapause pupae. The compositions of cuticular lipids demonstrate no difference among them. The amount of cuticular lipids of the non-diapause pupae is smaller than those of diapausers. Moreover, winter diapauser is covered with thicker cuticular lipids than non-diapauser.

**EXTENSIVE SEARCH FOR PEPTIDE TOXINS FROM THE VENOM GLAND OF THE TARANTULA**

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Venom from poisonous animals contains various bioactive substances, and enormous efforts have been directed toward isolation and characterization of the molecules. It is suggested that 1000 or more peptide toxins are in the venom of the tarantula, however, only about 20 peptide toxins are well characterized. In this research, we focused on the spider toxins and by applying improved molecular biological techniques we achieved extensive screening from a cDNA library prepared from the venom gland. To date, 35 novel toxin-like peptides, 19 peptides with ICK motif and 16 peptides of other family, have been identified.

**CLONING AND SEQUENCING OF VITELLOGENIN IN THE MUD SHRIMP UPOGEBIA MAJOR**○Bong Jung Kang<sup>1</sup>, Jae Min Lee<sup>2</sup>, Masatsugu Hatakeyama<sup>2</sup>, Oleg Gusev<sup>1</sup>, Chang-Hee Han<sup>3</sup>, Masayuki Saigusa<sup>1</sup><sup>1</sup>Graduate School of Natural Science and Technology, Okayama University, 3-1-1, Tsushima, Okayama 700-8530, Japan, <sup>2</sup>Developmental Mechanisms Laboratory, Developmental Biology Department, National Institute of Agrobiological Sciences, 1-2 Ohwashi, Tsukuba, Ibaraki 305-8634, Japan, <sup>3</sup>Laboratory of Marine Molecular Biology, Department of Molecular Biology, Dong-eui University, Korea

Vitellogenin (vtg) is a major yolk protein which are first synthesized as a precursor, and then secreted into hemolymph and sequestered in maturing eggs. A large increase of vtg concentrations in the hemolymph occurs during vitellogenesis in a number of decapod crustaceans. Two types of vtg genes were cloned in several decapods. One gene was expressed only in hepatopancreas, and another was expressed in both hepatopancreas and ovary. Although there are several reports describing the characterization of vtg in shrimps, little is known about the gene organization. This study reports the cloning of cDNA encoding vitellogenin from the mud shrimp *Upogebia major*. We constructed cDNA libraries using the hepatopancreas of the female, and cloned a partial cDNA of vtg. The deduced amino acid sequence showed 30-35% similarity to vtgs of other crustaceans. An approximately 8.7 kb long transcript of vtg gene was detected in the hepatopancreas of female by Northern blot analysis, but was not observed in the male hepatopancreas and female ovary. These results indicate that the hepatopancreas is one of the major organ of vtg synthesis in *U. major*.

**STUDY ON PRO-PHENOLOXIDASE CASCADE OF THE FRUITFLY, DROSOPHILA MELANOGASTER**

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Pro-phenoloxidase (proPO) is an inactive precursor of phenoloxidase (PO). ProPO is activated into PO through the limited proteolysis by the reaction of proPO cascade. PO catalyzes the oxidation of phenolic substances such as tyrosine and dopa, which is the key reaction of melanin synthesis. Recognition proteins against peptidoglycan or  $\beta$ -1,3-glucan are implicated in proPO activation, and PO mediated melanin synthesis is thought to be an important defense reaction of insects. In the *Drosophila* genome, there are three proPO genes (*Black cell*, *CG2952* and *CG8193*). Among them, *Black cell* corresponds to proPO A1, one of two proPO isoforms (proPO A1 and proPO A3) which are distinguishable by their mobility in native-PAGE and substrate specificity. However it had not been known which of the *CG2952* and *CG8193* is the gene of proPO A3. In this study, by using antibodies specific to CG2952 protein and CG8193 protein, we showed which of the two genes is the gene encoding proPO A3. Furthermore, the proteolytic processing of proPO A3 was demonstrated by western analysis of adult flies homogenate. The suppression of proPO A3 processing by recombinant serpin27A was also demonstrated.

**A NOVEL MEMBER OF THE PEPTIDOGLYCAN RECOGNITION PROTEIN FAMILY IN THE SILKWORM, BOMBYX MORI**

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Peptidoglycan recognition proteins (PGRPs) are considered to play some important roles in innate immunity of insects and mammals. *Drosophila* has 13 PGRP genes that are transcribed into at least 17 PGRP proteins. Some of these proteins act as pattern recognition molecules for bacterial peptidoglycan, and others are thought to possess *N*-acetylmuramoyl-L-alanine amidase activity as documented for PGRP-SC1b and PGRP-LB. However, PGRP having the amidase activity has not been found in the silkworm. In this study, we isolated a cDNA clone of *Drosophila* PGRP-SC1b homolog from a silkworm fat body and expressed the translated product in *E. coli*. The amino acid sequence