

PHYLOGENETIC RELATIONSHIPS OF ECHINODERMS DEDUCED FROM KINETIC SIMILARITY OF GLUCOSE-6-PHOSPHATE DEHYDROGENASE

N. Matsuoka.

Dept. of Biol., Fac. of Sci., Hirosaki Univ., Hirosaki.

The phylogenetic relationships among four classes of the phylum Echinodermata (Asterozoa, Echinozoa, Holothurozoa and Ophiurozoa) have been much disputed among many zoologists. As a first step to elucidate the phylogenetic relationships at the molecular level, the author purified glucose-6-phosphate dehydrogenases (G6PDs), which are the first step enzyme of the pentose phosphate shunt, from gonads of four echinoderm classes and compared the enzymatic (kinetic) properties with each other. The kinetic parameters examined in this study were K_m values for three substrates (G6P, Gal6P and dG6P) and one coenzyme (NADP) and the effects of pH and three chemical substances (PCMB, DEA and $MgCl_2$) on G6PD activity. The phylogenetic relationships of four echinoderms were estimated from the kinetic similarities between their G6PDs and the molecular dendrogram was constructed by using the UPGMA clustering method. The molecular results demonstrated the followings: (1) Asterozoa and holothurians are the most closely related to each other. (2) Ophiurozoa are more closely related to the cluster consisted of asterozoa and holothurians than echinoids. (3) Echinoids are the most distant group of four echinoderms. The molecular dendrogram also suggested that echinoids are more primitive group than other three echinoderms, and that asterozoa and holothurians are more recent groups. The evolutionary process of echinoderms was speculated from the molecular phylogenetic tree and non-molecular evidence.

AMINO ACID SEQUENCE OF DOMAIN 1 OF A HEMOCYANIN SUBUNIT, HR6, FROM A HORSESHOE CRAB, *CARCINOSCORPIUS ROTUNDICAUDA*.

H. Sugita¹ and F. Shishikura². ¹Inst. of Biol. Sci., Univ. of Tsukuba, Ibaraki and ²Dept. of Biol., Nihon Univ. Sch. of Med., Tokyo.

Arthropod hemocyanins are built from individual subunits of about 75,000 daltons. These subunits consist of 3 domains and domain 1 containing N-terminal sequence was the most variable of these 3 domains.

HR6, an immunologically identical subunit of *C. rotundicauda* hemocyanin to subunit HT4 of *Tachyleus tridentatus* hemocyanin, has been partially sequenced and its domain 1 was compared with that of HT4. Domain 1 of HR6 appeared to consist of 150 amino acid residues in comparison with complete sequence of domain 1 composed of 149 residues of HT4. Amino acid residues of 142 positions in domain 1 of HR6 were determined in which only 2 residues (1.4%) were substituted between HR6 and HT4. Residues of 75 positions (51%) in domain 1 of HR6 were different from *Limulus polyphemus* hemocyanin subunit II (LPII). This difference (51%) was similar to differences (46-61%) obtained from the comparison among HT4, LPII, and 3 hemocyanin subunits from a spider. Thus, we can estimate more accurately the divergence pattern and time by comparing amino acid sequences of the immunologically related subunits among horseshoe crabs.

OVARIAN STRUCTURE AND OOGENESIS IN SOME BRANCHIOPOD CRUSTACEANS

H. Ando and T. Makioka. Inst. of Biol. Sci., Univ. of Tsukuba, Ibaraki.

Two types of the ovarian structure and oogenetic modes were distinguished in the Branchiopoda. In *Triops longicaudatus*, *T. granarius* (Notostraca) and *Leptodermis kawachiensis* (Conchostraca), the tubular ovary had many branches, at each terminal of which the germarium produced egg-follicles. Each egg-follicle containing an oocyte and three nurse cells migrated outward and protruded into the haemocoel, where the oocyte grew and became mature. Mature eggs were ovulated into the ovarian lumen. In *Branchinella kugenumaensis* (Anostraca) and some species of the Cladocera, however, the tubular ovary was not branched. Four-celled units, each of which consisted of an oocyte and three nurse cells, were produced in the germarium running longitudinally in the ovarian wall. The four-celled units migrated not toward the haemocoel, but toward the ovarian lumen, where the oocytes grew and then became mature.

These two types of the ovarian structure and oogenetic modes suggest close relationships between the Notostraca and the Conchostraca, and between the Anostraca and the Cladocera, respectively, but do not support the relationship between the Conchostraca and the Cladocera which is mostly believed at present.

TOWARDS A DIAGNOSIS OF THE FACETOTECTA (CRUSTACEA: MAXILLOPODA: THECOSTRACA).

M.J. Grygier. Seto Mar. Biol. Lab., Fac. of Sci., Kyoto Univ., Shirahama, Wakayama.

The diagnosis of *Hansenocaris* Itô serves for cypris y, but none has been proposed for nauplius y. To avoid assigning unrelated nauplii to the Facetotecta and to justify that group's independent taxonomic status, such a diagnosis is needed. Published descriptions, an SEM study of Okinawan nauplius y, and some of T. Itô's naupliar molt series were surveyed for possible diagnostic characters, and a plate-based nomenclature for dorsal setae and pores was devised. Distinctive features of y-nauplii include: 1) cephalic shield continuous with free trunk dorsum; 2) no frontolateral horns; 3) common plan of cephalic shield ridges; 4) common positions of window and certain dorsal setae and pores; 5) ventral side of cephalic region flat, round with wide rim; 6) no frontal filaments; 7) A_1 2-3-segmented with ≤ 8 setae on distal one; 8) A_2 and M_d unchanged through 5 instars, with reduced, narrowly definable segmentation and setation; 9) no paragnaths or ventral setation; 10) Mx_1 as pair of setae or absent; 11) no furcal setae, but pair of furcal spines and medial spine. Most of these may be apomorphic (not 2 and 6) and the pedomorphic limbs are perhaps convergently similar to those of early thoracican nauplii and of lecithotrophic and brooded nauplii elsewhere in the Thecostraca.