Winter presence of *Prochlorococcus* in the East China Sea

As early as in 1983, Gieskes and Kraay isolated a highly concentrated unknown pigment which had a red-shifted r-soret peak of 8—10 nm compared to chlorophyll a with normal-phase high-performance liquid chromatography (HPLC). This pigment was ultimately identified as divinyl chlorophyll a (DV-Chl a), and was shown to be associated with a small oxygenic prokaryote called *Prochlorocoocus*. The latter connection was made possible through the simultaneous use of HPLC and shipboard flow cytometry, which revealed the presence of very small red-fluorescing cells which appeared to have chlorophyll b as an accessory pigment. Since the discovery of *Prochlorococcus*, DV-Chl a has been recognized as an index of its presence and the ratio of DV-Chl a to Chl a has been used to estimate the significance of *Prochlococcus* in marine ecosystems. In addition, flow cytometry has been proven to be a powerful tool for the efficient identification and enumeration of *Prochlorococcus* throughout the world's oceans.

Prochlorococcus is widely distributed in the euphotic zone of the tropical and subtropical oceans, and almost always co-occurs with *Synechococcus* ——another very important picoplankton in marine ecosystems. With a cell size of about 0.7 microns in diameter, *Prochlorococcus* is the smallest known oxyphototrophic organism. Except for a mutant of corn, it is the only species with divinyl DV-Chl a as a major photosynthetic pigment, instead of normal chlorophyll a. It also contains DV-Chl b, Chl b and alpha-carotene. *Prochlorococcus* was initially found in the deep euphotic zone in a well stratified open ocean environment. The fact that it was abundant in the entire euphotic zone was discovered when high-sensitivity flow cytometry became available. It has been proven that *Prochlorococcus* is a major primary producer and an important contributor to the deep maximum chlorophyll layer in the low latitude open ocean.

Although many investigations of *Prochlorococcus* have been made in the past decade, data from marginal seas are limited and there has been no report on the East China Sea. In the East China Sea in 1994, we detected DV-Chl a and b using HPLC, which indicated that *Prochlorococcus* might be present. In February and March, 1997 we conducted a large-scale survey of the East China Sea, and analyzed samples using flow cytometry. The results confirmed that the pigments measured were indeed indicative of the presence of *Prochlorococcus* in the East China Sea.

Prochlorococcus was present at stations 115(32°N, 127°E), 412(28.5°N, 126°E) and eastward in the study period in the East China Sea. No *Prochlorococcus* was found at the coastal stations 105 (32°N, 124°E) and 408(27.5°N, 124°E). Cell concentrations ranged from 1×10^3 to 5×10^4 cell/mL, and increased from coast to offshore and from north to south with the maximum of 5.6×10^4 cell/mL appearing at 30 m depth at station 418(27.5°N, 127.3°E). At stations 204(30°N, 129°E) and 418, *Prochlorococcus* surpassed *Synechococcus* and picoeukaryotes in abundance and numerically dominated the entire water column.

(*Continued from page* 876)

studying one-parameter Markov process, such as the concepts of contract semigroup, infinite small operator, first reach time and so on. In order to have a further study on these basic two-parameter Markov processes, the book advances some new concepts and new methods with some unexpected results, for example, Poisson sheet has no general three-point transitional function family.

But it should be pointed out that the research on Markov processes has lasted for almost a century. Many famous mathematicians advance many profound problems and suppositions. Some of them have been solved and some are still in research. Furthermore, the found and development of all the new branches such as potential theory, infinite partical system, the theory of percolation, etc., have close connection with the thorough research on Markov processes. Compared with the valuable achievements in one-parameter Markov processes, the study on two-parameter Markov processes is still at the beginning. I think the theoretical frame established in the book should be further improved and the research on the basic processes involved should be deepened, and more profound problemes and relative research directions should be advanced. Certainly, this may also be what the writers of the book expects.

DAI Yonglong
Department of Mathematics, Zhongshan University, Guangzhou 510275, China

Prochlorococcus not only dominates in the outer region of the sea where the Kuroshio currents pass along, it is also present far away at stations 115 and 412. This is in contrast to the situation in the western Atlantic, where *Prochlorococcus* is mainly confined to the Gulf Stream and further south.

Shimada has reported the appearance of *Prochlorococcus* in Suruga Bay, Japan. He attributed this fact to a branch of the warm tropical Kuroshio Current flowing into the bay. *Prochlorococcus* has also been found close to shore in the Gulf of Aquba. As a matter of fact, these areas have narrow and steep shelves and are affected significantly by the open sea. Presence of *Prochlorococcus* in those waters can be easily understood. However, *Prochlorococcus* has also been found in the areas that are clearly not oceanic in character as the case in the East China Sea, where *Prochlorococcus* not only dominates in the outer region of the sea, but is also distributed far away from the Kuroshio Current in stations 115 and 412. A larger distribution range in summer is expected based on the ecology of *Prochlorococcus*. Further studies on the relationship between environmental factors and the distribution of *Prochlorococcus* are in progress.

Acknowledgement This work was supported by the National Natural Science Foundation of China (Grant Nos. 39625008, 39570143).

JIAO Nianzhi[1], YANG Yanhui[1], Elizabeth Mann[2], Sallie W. Chisholm[2] and CHEN Nianhong[1]

1. Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, China; 2. Massachusetts Institute of Technology, Cambridge, MA 02139 USA

Cloning of HumCyr61 gene expressing down-regulatedly in Rhabdomyosarcoma

RHABDOMYOSARCOMA (RMS) is a kind of malignant tumor of skeletal muscle the phenotype of which is poor differentiation towards skeletal muscle. RMS can be divided into 3 major histological categories: embryonic RMS (eRMS), alveolar RMS (aRMS) and multiform RMS. The eRMS is often detected in orbit, peritonealor or limb, and the patients are mainly children. One characteristic of eRMS is a consistent loss of hetrozygosity on chromosome.

Homologous amplification by PCR (HA-PCR) has been proved to be a powerful method for isolating the new members of a known gene family. Based on this strategy, we developed a new method to clone eRMS related genes. A cDNA fragment (BA-1) was obtained from an embryonic skeletal muscle cDNA library. Comparing with GenBank/EMBL/DDBJ and PDB nucleic acid sequence database, it indicates that: (i) partial sequence of BA-1 fragment is identical to a 304 bp cDNA fragment (GenBank accession number: Z50168) which is down-regulated expressing in human eRMS cell line RD cells[1]; (ii) the BA-1 sequence shares 86.2% homology with mouse Cry61 gene (a cysteine rich gene originally identified by its cDNA 3CH61) which promotes proliferation, migration and adhesion[2] of embryonic cells; (iii) the BA-1 sequence also shares 68% homology with connective tissue growth factor (CTGF) gene. An embryonic skeletal muscle cDNA library was screened by using the BA-1 cDNA fragment as a probe, and five positive clones were selected from 5×10^5 plaques. A cDNA with 1887 bp in length encoding for 381 amino acids (see fig. 1) was obtained after 4 of the 5 cDNA fragments to be sequenced respectively.

1	MSSRIARALALVVTLLHLTRLALSTCPAAC	31	HCPLEAPKCAPGVGLVRDGCGCCKVCAKQL
61	NEDCSKTQPCDHTKGLECNFGASSTALKGI	91	CRAQSEGRPCEYNSRIYQNGESFQPNCKHQ
121	CTCIDGAVGCIPLCPQELSLPNLGCPNPRL	151	VKVTGQCCEEWVCDEDSIKDPMEDQDGLLG
181	KELGFDASEVELTRNNELIAVGKGSSLKRI	211	PVFGMEPRIRYNPLQGQKCIVQTTSWSQCS
241	KTCGTGISTRVTNDNPECRLVKETRICEVR	271	PCGQPVYSSLKKGKKCSKTKKSPEPVRFTY
301	AGCLSVKKYRPKYCGSCVDGRCCTPQLTRT	331	VKMRFRCEDGETFSKNVMMIQSCKCNYNCP
361	HANEAAFPFYRLFNDIHKFRD		

Fig. 1. Amino acid sequence deduced from an open reading frame of HumCyr61 cDNA.

As mentioned above, the gene cloned shows very high homology to mouse Cry61 gene; that is, they have 81% homology in nucleotide sequence and 92% identity in related amino acid sequence. So it was named HumCry61 (Human Cyr61) gene, of which the GenBank accession number is AF031385. Besides, it also shares homology with human CTGF, chicken Cef-10 (chicken embryonic fibroblasts ex-