# Multielement profiling analyses of seawater in coral reef area and the biogeocemical processes of trace metals in bivalve with symbiotic zooxanthellae

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In coral reef area, a characteristic ecosystem is formed by many kinds of marine animals and plants in spite of uneutrophic conditions. This may be attributed to the fact that various chemical species are effectively taken and available by lower animals and plants. A symbiotic relationship often found among different animals and plants is considered to be working as one of such processes. In a present study, firstly, multielement determination of major-to-ultratrace elements in seawater and each organ of bivalve with symbiotic zooxanthellae (*Tridacna crocea*) were carried out by ICP-AES, ICP-MS and CHN coder. Secondly, the biogeochemical processes of trace metals in *Tridacna crocea* were investigated by the laboratory experiments using stable enriched isotopes of $^{111}$Cd and $^{68}$Zn.

The analytical results for seawater showed that the concentrations of the bioactive elements such as Co, Ni, Cu, Zn, Cd, and Pb were in the range from 0.5-5 fold, compared to the literature values [1, 2] for open surface seawater. From the multielement profiles for nutrient type elements, it was suggested that the concentrations of Zn and Cd in seawater normalized to open surface seawater were higher than those of Ni and Cu. In the laboratory experiment about *Tridacna crocea*, the ratios of $^{68}$Zn to other Zn isotopes increased with time for the mantle, in which symbiotic zooxanthellae exist, but they showed almost same with natural abundances for the kidney, while the ratios of $^{111}$Cd to other isotopes showed the highest for the kidney among all organs. These results suggested there are the difference of bioavailability between Cd and Zn.

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# Zygote isotopy and the epigenetic code

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Self-sufficiency and self isolation of the zygote cleavage process is a unique peculiarity specific for a whole diversity of multicellular life forms. That means, the complete circle of primary embryogenesis stage does not require a special biological environment. An appropriate physic-chemical conditions are the only requirements need to promote this process. Once these conditions maintained, a normal embryogenesis is to processed. This makes. possilible to study this process in vitro which itself is a unique possibility for further epigenesist research since this particular embryogenesis step leads to the beginningof the genetically unified embryonic cell differential determination. Epigenetic directions for selective reading of DNA information in differently specializing cells derives from their individual development programs which fits perfectly their functional patterns. There are up to some hundred programs of that sort in one single organism. Thus, a zygote possesses a high potential of directing programs that caused by the top-regularity mechanism for its reproduction throughout a long chain of generations of the wide majority of organisms. It is known that the selective methylation of several DNA loci regulates genome expression, i.e. performs the gene expression epigenetic control. However, an exact mechanism of this regular methylation selectivity still remains obscure.

The biological isotope fractionation research revealed a non-random character of both intermolecular and itramolecular isotopes distribution in biological processes [1].This was taken as a basis for study on distribution of ectopically different nucleotide forms in blastomer DNA during the zygote cleavage [2,3]. The data obtained reveals a non-random and a high-order character of distribution of isotopically different nucleotide forms between complementary chains in DNA double helixes. Noteworthy, the high order comes due to the zygote cleavage circle self-isolation and therefore such an algorithm would be relevant for all multi-cell life forms as well. Owing to the work of different kind of effects, a differential distribution of isotopically different nucleotide forms in blastomer DNA should lead to a selective DNA methylation. The latter could be a background of the very nature of epigenetic code.

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