

Molecular-phylogenetic studies on Baikalian invertebrates in Limnological Institute

D.Yu. Sherbakov

Limnological Institute SB RAS, Irkutsk,

Irkutsk State University

Molecular phylogenetic studies of Baikalian invertebrates had been initiated at Limnological Institute in two laboratories approximately simultaneously. They exploited the possibilities offered by PCR newly advented by the time. Following methodological progress in the field, the scope of studies changed at LIN.

The first molecular phylogenetic studies used SSU rRNA in order to resolve evolutionary relationships in Turbellarians (Kuznedelov et al), Amphipods and molluscs belonging to Baicaliidae. Since in many groups the amount of variation accumulated in ribosomal DNA of Baikalian species flocks happened to be insufficient for good resolution of many taxa, later mitochondrial markers (COIII and COI for invertebrates, cyt b and D-loop for vertebrates) became more widely used. More species flocks have been examined later at LIN and other groups: Lumbriculidae, Ostracoda, Chironomidae (*Sergentia*), Sponges etc. Animal groups which did not give rise to spectacular species flocks in the lake were studied as well. Among them there were Polychaets and Isopods. Recently thorough molecular phylogenetic study have revealed high diversity of Microsporidian parasites in Baikalian amphipods and most recently these parasites were found in other invertebrates of the lake. Interestingly in case of the Microsporidians parasiting the Amphipods the degree of endemism was found to be exceptionally high with only few cosmopolitan lineages represented in the lake. Still there are major groups of potential interest remain unstudied. One example is the Nematods.

Most recently the main scope of molecular studies shifted more towards population studies. Few papers had been published during last couple of years describing micro-evolutionary processes in Baicaliids and Amphipods. In these studies mitochondrial and nuclear DNA markers have been employed along with microsatellites. Lack of published primers and genomic information in general impede the use of microsatellites for population studies.

The main conclusions resulting molecular phylogenetic work at the lake so far are:

1. There are only two types of evolutionary histories found in Baikalian species flocks: ancient and highly diverse, most likely polyphyletic groups (for example, Amphipods, Chironomids), their age may be compared to the age of giant lake in confines of Baikal; the other type is very young (3-4 MYA) flocks with star-like species radiation(s) in basal part of a tree (Baicaliidae, Ostracods, Lumbriculidae, Sponges etc).
2. Molecular evolutionary studies did not reveal a single case of coevolution between predator and prey or between hosts and parasites even in the cases where this assumption was very likely;
3. Micro-evolutionary studies show that in the few cases examined very fast speciation took place in relatively restricted stretches of the shore, sometimes in a parallel fashion in different parts of Lake Baikal.

Further studies will turn more towards genetic systems directly involved in adaptive evolution rather than towards more extensive use of neutral molecular markers of evolution on one hand, and towards more detailed and intense involvement of ecological information in population genetic and evolutionary studies. Both directions seem to be critically important for the elucidation of mechanisms generating Baikalian huge diversity of life.