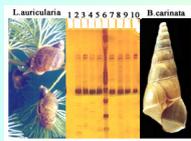
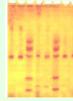


Canine distemper virus (CDV) is a member of the morbillivirus genus, Paramyxoviridae family. CDV caused the epizootic in the populations of Baikal seals (*Phoca sibirica*) in 1987-1988 practically simultaneously with PDV (Phocine distemper virus) morbilliviruses outbreak at seals in Northern Europe (Grachev, 1989; Osterhaus, 1988). Our CDV studies in the Baikal seal population revealed distinct differences of the development of epizooties on Lake Baikal and in Northern Europe. After the 1988 epizooty, PDV (Phocine distemper virus) in European seals was not registered, but in 2002 it caused another destructive epizooty, the virus of which was almost unchanged (Jensen, 2002). CDV is constantly present in 40% of the Baikal seal population without causing a visible increase of mortality (Belikov, 1999). Heterogeneity of virus in the population is high (Butina, 2003). It means that there is a high probability of frequent change of the host.

Electrophoresis of RT PCR analysis of CDV isolated from Baikal mollusks and the mollusks' outward appearance.



Mustela putorius



PAAG electrophoresis of the amplification products of CDV gene P isolated from ferrets infected with CDV and the mollusk homogenate.



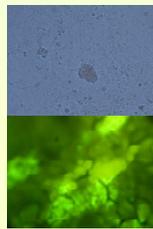
Immunoenzyme analysis of the organs of ferrets infected with either the virulent CDV strain (Snider Hill) or with a mollusk homogenate.

In 2002, we showed for the first time that canine distemper virus was able to accumulate in organisms of poikilothermal animals (Gastropods of the families *Baicaliidae* and *Limnaeidae*) without losing infectiousness. The virus accumulated in mollusks was tested for biological activity by infecting of virus-sensitive animals, namely, ferrets (*Mustela putorius*) (Kondratov, 2003).

The virus was isolated from *Limnea* in MDCK cell.

The following primers complementary to the conserved regions of the phosphoprotein gene (P gene) of the virus (Barrett, 1993) were used in polymerase chain reaction:
5' GAAGAGGTTAAGGGAATCGAA and 5' CGATCCAGCAACTATCCCCA.
The amplicon length was 389 bp.

Cell culture MDCK (native and FITC antibodies labelled)



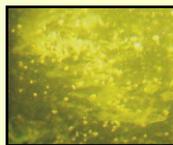
Induction of fusion in MDCK cells infected by CDV from mollusk homogenate
Magnification, x 220
FITC antibodies labelled MDCK cells infected by CDV from mollusk homogenate
Magnification, x 1000



Limnea auricularia



Ova of the mollusks



Young mollusks

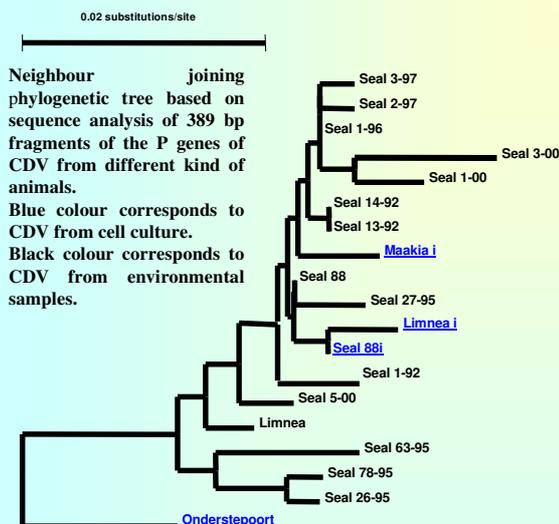


389 bp. amplicon

PAAG electrophoresis of the CDV fragments products after parents mollusks, ova of the mollusks and young mollusks cDNA amplification. Silver staining.

Limnea population is able to transfer CDV transovarially. Besides, we confirmed the ability of the virus to replicate in organisms of gastropods. Thus, there has been found one of natural reservoirs of morbilliviruses.

Heterogeneity of CDV in lake Baikal ecosystem

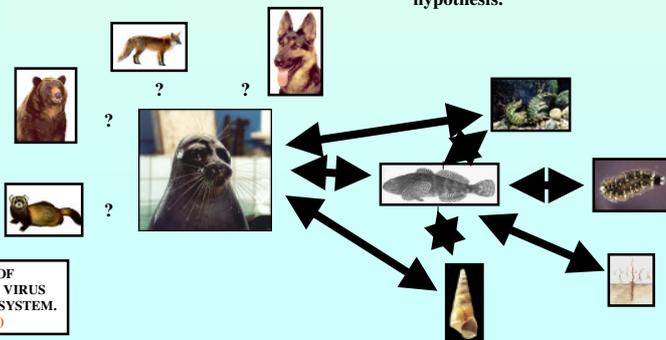


Neighbour joining phylogenetic tree based on sequence analysis of 389 bp fragments of the P genes of CDV from different kind of animals.
Blue colour corresponds to CDV from cell culture.
Black colour corresponds to CDV from environmental samples.

Nucleotide sequence of a gene fragment of phosphoprotein was determined. We examined other poikilothermal animals from Lake Baikal. Virus can present in organisms of different species of amphipods and fish. The number of infected specimens varies depending on species, site and time of sampling. The data obtained prove the possibility of the virus to be transferred along the food web and to circulate in the ecosystem without participation of homoithems. However, it is necessary to carry out further research to test this hypothesis.

CDV in poikilothermal animals from Lake Baikal

Pisces	<i>Coregonus autumnalis migratorius, Comephorus baicalensis, Comephorus dybowski, Cottocomephorus inermis, Cottocomephorus grewingkii, Paracottus knerii, Batrachocottus baicalensis, Batrachocottus talievi, Leocottus kesslerii, Limnocottus griseus, Procottus major, Asprocottus intermedius, Lota vulgaris, Brachymystax lenok</i>
Crustacea	<i>Macrohectopus branickii, Acanthogammarus grewingkii, Ommatogammarus albinus, Eulimnogammarus maaki</i>
Mollusca	<i>Limnea auricularia, Limnea stagnalis, Limnea fragilis, Baicalia carinata, Baicalia herderiana</i>
Annelida	<i>Lumbricus sp., Sergentia sp.</i>
Plathelminthes	<i>Baicalobia sp.</i>



The map of probes collection.

