

Methods: Plasma was collected from HIV-1 seropositive subjects in Yaounde and Douala, Cameroon. Total nucleic acid was extracted and subjected to RT-PCR for amplification of a fragment of the env gp120 (360 bp). The PCR fragments were sequenced directly using automated sequencer. Sequence wild-type polio eradication. It also suggests that surveillance for phenotypically wild polioviruses should continue far beyond the disappearance of polio-associated clinical paralytic cases, and environmental sampling can serve as the surveillance method.

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Analysis of molecular-genetic diversity of Hantavirus strains circulating in the southern and northern regions of the Russian far east

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Hantaviruses (HV) are widely distributed among various species of rodent population in the world. As a rule, genetic and antigenic relationships among different HV strains correlate with their geographic distribution, though, there are exceptions. Earlier, we showed circulation of four HV serotypes, Hantaan (HTN), Seoul (SEO), Puumala (PUU), and Khabarovsk (KHAB) in the south of the Russian Far East, and demonstrated the presence of seropositive rodents (*O.hyperborea*, *Cl.rufocanus*, *M.fortis*, *A.peninsulae* and *C.sikotanensis*, *M.oeconomus*, *R.norvegicus*) inhabiting the northern regions of the Russian Far East (Magadan region, Kamchatka peninsula, Sakhalin island and Kuril islands). To study the genetic relationships among HV strains, RT-PCR of total RNA extracted from infected cell cultures, lung tissues of rodents and blood of HFRS patients was used to amplify regions of M and S genome segments followed by sequencing of cDNA.

The results of these molecular-genetic analysis allowed us to separate HV strains into four groups. Strains of the first group, isolated from the samples from *A.agrarius*, *Cl.rufocanus*, *Cl.sikotanensis*, *O.hyperborea* and HFRS patients, revealed similarity with HTN. The second group united strains from *A.peninsulae*, *M.oeconomus* and HFRS patients and showed similarity with PUU. Strains of the third group were similar to SEO and were isolated from *R.norvegicus* and HFRS patients. Strains of the fourth group, isolated from *M.fortis*, revealed similarity with KHAB.

In particular, it was shown that strains isolated from seropositive *M.fortis* were closely related to KHAB in showing 80% nucleotide identity in the S segment. For a HV strain isolated from the blood of HFRS patient the region of 2740–2870 bases of the M segment showed 98.1% identity on the nucleotide level with HTN, and less similarity with SEO (78.4%) and PUU (60.7%). A HV strain from another HFRS patient showed high similarity (94-96%) with SEO virus M RNA (2560–2700 bp) and less similarity with HTN (79.8%), PUU (62%) and Sin Nombre (59%), which illustrates the epidemiological importance of SEO-like strains from rats, together with HTN-like strains from mice and voles for the Russian Far East.

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Genetic variability of HIV-1 from Cameroonian isolates

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