# The phylodynamics of the rabies virus in the Russian Federation

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**Abstract**
Near complete rabies virus N gene sequences (1,110 nt) were determined for 82 isolates obtained from different regions of Russia between 2008 and 2016. These sequences were analyzed together with 108 representative GenBank sequences from 1977-2016 using the Bayesian coalescent approach. The timing of the major evolutionary events was estimated. Most of the isolates represented the steppe rabies virus group C, which was found over a vast geographic region from Central Russia to Mongolia and split into three groups (C0-C2) with discrete geographic prevalence. A single strain of the steppe rabies virus lineage was isolated in the far eastern part of Russia (Primorsky Krai), likely as a result of a recent anthropogenic introduction. For the first time the polar rabies virus group A2, previously reported in Alaska, was described in the northern part of European Russia and at the Franz Josef Land. Phylogenetic analysis suggested that all currently circulating rabies virus groups in the Russian Federation were introduced within the few last centuries, with most of the groups spreading in the 20th century. The dating of evolutionary events was highly concordant with the historical epidemiological data.

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