

vaccination of insectivorous bats, although this strategy may be feasible for these important RABV reservoirs.

Molecular Evolution of European Bat Lyssavirus Type 2

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In Europe, bat rabies accounts for a relatively small proportion of the total rabies cases reported to Rabies Bulletin Europe (0.1%). Of the 857 bat rabies cases reported in Europe between 1977 and 2007, the vast majority were associated with European Bat Lyssavirus Type 1. European Bat Lyssavirus Type 2 (EBLV-2) infections are much rarer, with reported bat cases limited to The Netherlands, Switzerland, United Kingdom and Germany. Human rabies cases in Finland in 1985 and Scotland in 2002 were also attributed to EBLV-2. Passive surveillance of bats has been undertaken in the UK since 1986, with in excess of 8,000 dead bats sampled. In England, EBLV-2 has been confirmed in 7 of 164 *Myotis Daubentonii* (Daubenton's bats) tested. In addition, Germany have recently reported their first isolation of EBLV-2 in this species. In contrast, no evidence of EBLV-2 was detected in 111 Daubenton's bats sampled in the Netherlands between 1983 and 2003. To further understand the role that viral evolution has played in the limited epidemiology of EBLV-2, we have partially sequenced a panel of virus isolates, collected between 1985 and 2008 (N and G gene). Using phylogenetic and molecular clock analysis software (Phylip, BEAST) we have estimated the evolutionary rate for EBLV-2 and compared it to other lyssaviruses.

Rabies in Florida Bats

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Background: Bats currently represent 10% of animals testing positive for rabies in Florida, and the majority of endemic human rabies cases in the US are caused by bat variants. However in 2006, less than half (35%) of rabid bats reported nationally were identified by species, and we have limited knowledge of bat rabies epizootiology. Improved knowledge of current bat rabies epizootiology may help identify risk factors leading to exposures in people and domestic pets, and improved disease control.

Methods: Data from 248 rabid bats collected by Florida Department of Health from 1953-1973 were compared to data from 195 rabid bats of 1,742 total bats submitted from 1994-2006. A subsample of recent submissions from representative species was typed by the Poxvirus and Rabies Branch of Centers for Disease Control and Prevention (CDC) using RT-PCR amplicons from the rabies virus N gene and compared with archival Florida bat samples from the 1980's. Alignment of the sequences was performed using Bioedit 7.0. A phylogenetic tree was produced using the Mega 4.0 software and the neighbor-joining algorithm and bootstrap analysis of 100 replicates. Results: In the twenty year period between 1953-1973, *L. intermedius* (Li) represented 75.8% of bats identified as rabid in Florida, compared with 11.9% of speciated cases from 1994-2006. Brazilian free-tailed bats (*Tadarida brasiliensis*) represented 5.2 % of historical cases, and 51.3% of current speciated cases. The number of positive bats peaked during August for both time periods. The lowest proportion of positive bats for 1994-2006 was in June. Four distinct clades containing *L. borealis* (Lb) rabies virus variant were identified which included most samples from *L. seminolus* (Ls), Li and Lb bats. Virus variants from Lb and Ls bats appear more related to *L. cinereus* (Lc) bats than variants from other Lc bats. Two clades of Tb rabies virus variants primarily included Tb samples and clustered tightly together. Only archival Tb samples were found in Tb clade 2.