

late-PET experiment, viral mRNA was present in the CNS of challenged animals from day 2 pi. Untreated and PEP animals all succumbed at day 5 pi. Late-treated animals survived over 340 days (100% in d2 pi and 58.33% in d3 pi), showing clinical signs from d4 pi and recovering by d24 pi. Significant differences were observed in viral loads between untreated and late-treated groups.

**Conclusion:** Despite the mAb-driven clearance of rabies virus from the CNS has long been investigated in the past, scarce data are available in literature to support its efficacy. Our data provides evidence for the potential efficacy of mAbs, alone or in combination with other antiviral drugs, to treat rabies infection. Further studies are needed to explore alternative routes of administration possibly extending the therapeutic window.

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### Host-symbionts interactions between bats and coronaviruses



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**Purpose:** Alpha and beta Coronaviruses (CoVs) show highest diversity and geographical range in bats, suggesting a long-standing host-symbiont association and a key-role of these animals as reservoir. This study investigates the evolutionary dynamics shaping CoVs evolution in their bat hosts, which influences their potential to cross the species barrier.

**Methods & Materials:** We investigated the phylogeny of alpha and beta-CoVs through the Bayesian approach implemented in MrBayes v3.2.4 using two separate datasets, including RdRp sequences either from bats only (461) or from all mammals (561). We tested CoVs compartmentalization using BaTS.beta.build2 and evaluated the phylogenetic congruence between hosts and symbionts using the Parafit.Test implemented in R v3.2.5. Spills-over between different bat genera and sustained transmissions within the recipient host were defined as previously described.

**Results:** Our data supported CoV's speciation upon the bat host genus, while species-specific clusters were not consistent with distinctive CoV species. However, CoVs also showed compartmentalization upon the bat species, particularly in genera highly diversified in alimentation, reproduction and roosting ecology (i.e. *Myotis*). Similarly, we detected intra-specific geographical structuring of bat CoVs, especially in non-migrant species. These findings suggest CoV's adaptation in bats rather than the concomitant speciation of hosts and symbionts. Highest CoV diversity was detected in the genera *Rhinolophus*, *Pipistrellus* and *Hipposideros*, associated with both alpha and beta CoVs. Genetic analyses supported 24 spills-over between bat genera, also disproving co-speciation as the major evolutionary mechanism of CoVs. Of note, spills-over were particularly frequent in Rhinolophids, bats that usually co-roost with species from different genera. Spillover between related genera was more likely to lead to sustained within-species transmission in the recipient host. This data, coupled with the phylogenetic congruence between bats and CoVs as derived by distance-based analyses, suggest a preferential host shift towards phylogenetically related hosts.

**Conclusion:** Our study suggests host shift rather than co-divergence as being the major evolutionary force shaping CoV diversity in bats. This would suggest high potential for bat CoVs

to emerge in new hosts through host jumps. We suggest that the risk might be enhanced in bats showing alpha and beta CoV co-infections, which might lead to a higher chance for recombination.

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### Nipah virus ecology and infection dynamics in its bat reservoir, *Pteropus medius*, in Bangladesh



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**Purpose:** Nipah virus (NiV) is an emerging zoonotic virus that causes seasonal outbreaks of encephalitis in Bangladesh with >75% mortality. Little is known about NiV dynamics in *Pteropus medius*, the putative bat reservoir in Bangladesh. Date palm sap consumption is the primary route of transmission to humans. The aim of this study was to determine whether seasonal dynamics or distribution of NiV in bats accounts for human outbreak patterns.

**Methods & Materials:** Between 2006 and 2012, urine, blood, feces and saliva was collected from 100 *P. medius* from each of eight districts across Bangladesh. Additionally, 100 bats from Faridpur were sampled quarterly for 6 years. Samples were screened for NiV RNA by PCR. Sera were screened for anti-NiV IgG antibodies by ELISA and Luminex. Serological data was modelled to identify seasonal trends.

**Results:** 2,790 bats were sampled. NiV RNA was detected in 0 – 3.8% of bats per sample ( $n \sim 100$ ) and was detected outside the Nipah Belt and outside the human NiV season. Bats were sero-positive throughout Bangladesh (seroprevalence: 20% – 56%). Models showed recurring outbreaks within the study