# Article information:

Highly diversified shrew hepatitis B viruses corroborate ancient origins and divergent infection patterns of mammalian hepadnaviruses | PNAS  
<https://www.pnas.org/doi/full/10.1073/pnas.1908072116>

# Article summary:

1. Shrews, ancient insectivorous mammals, carry hepatitis B virus (HBV) homologs at low prevalence across a broad geographic and host range.

2. The shrew HBVs comprise separate species with distinct genotypes and corroborate the ancient origins of mammalian HBVs dating back about 80 million years.

3. Shrew HBVs show important similarities with human HBV infection patterns but cannot infect human cells or use the canonical HBV receptor molecule for cellular entry.

# Article rating:

May be slightly imbalanced: The article presents the information in a generally reliable way, but there are minor points of consideration that could be explored further or claims that are not fully backed by appropriate evidence. Some perspectives may also be omitted, and you are encouraged to use the research topics section to explore the topic further.

# Article analysis:

The article "Highly diversified shrew hepatitis B viruses corroborate ancient origins and divergent infection patterns of mammalian hepadnaviruses" published in PNAS describes the discovery of hepatitis B virus (HBV) homologs in shrews, an ancient order of insectivorous mammals. The study found that shrews host HBVs at low prevalence across a broad geographic and host range, with phylogenetically divergent shrew HBVs comprising separate species termed crowned shrew HBV (CSHBV) and musk shrew HBV (MSHBV), each containing distinct genotypes.

The article provides important insights into the genealogy of HBV and suggests that coevolution with hosts may play a role in the evolution of hepadnaviruses. However, there are some potential biases and limitations to consider. For example, the study only sampled a limited number of shrew species from Europe and Western Africa, which may not be representative of all shrew populations worldwide. Additionally, the study did not investigate the potential risks associated with shrew HBVs infecting humans or other animals.

Furthermore, while the article notes that shrew HBVs universally showed mutations in their genomic preCore domains impeding hepatitis B e antigen (HBeAg) production and resembling those observed in HBeAg-negative human HBV, it does not explore why this might be the case or what implications it could have for understanding HBV pathogenesis. Similarly, while the article notes that deep sequencing and in situ hybridization suggest that HBeAg-negative shrew HBVs cause intense hepatotropic monoinfections and low within-host genomic heterogeneity, it does not explore what factors might contribute to these infection patterns or how they compare to human infections.

Overall, while the article provides valuable insights into the diversity and evolution of hepadnaviruses in non-human hosts, there are some limitations to consider when interpreting the findings. Further research is needed to fully understand the implications of these discoveries for human health and disease.

# Topics for further research:

* Shrew HBV transmission to humans
* HBeAg-negative HBV pathogenesis
* Host-virus coevolution in hepadnaviruses
* Geographic distribution of shrew HBVs
* Within-host genomic heterogeneity in HBV infections
* Risks associated with zoonotic transmission of HBVs

# Report location:

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