Figures and figure supplements

Unravelling the history of hepatitis B virus genotypes A and D infection using a full-genome phylogenetic and phylogeographic approach

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Figure 1. Midpoint rooted phylogeographic tree estimated by RAxML v8.0.20. HBV genotype D sequences (N = 916) categorized according to the geographic region of sampling were used in the analysis. Monophyletic clusters are indicated as triangles. Major clusters are indicated in Roman numerals.

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Figure 1—figure supplement 1. Midpoint rooted phylogeographic tree on 916 HBV genotype D sequences categorized according to the country/geographic region of sampling.

DOI: https://doi.org/10.7554/eLife.36709.005
Figure 1—figure supplement 2. Midpoint rooted phylogeographic tree on HBV genotype D sequences after the inclusion of RS-D5. DOI: https://doi.org/10.7554/eLife.36709.006
Figure 1—figure supplement 3. Phylogenetic analysis of genotype D including the RS-D5 in two non-overlapping subgenomic areas (1–2000 nts) and (2001–3078 nts). RS-D5 sequences are shown in red.
DOI: https://doi.org/10.7554/eLife.36709.007
Figure 2. Putative major dispersal pathways of genotype D as estimated by phylogeographic analysis. The origin is depicted with dotted line. Subgenotypes and their corresponding dispersal routes are shown with different colors. Colored circles depict the geographic areas where subgenotypes are the most prevalent.

DOI: https://doi.org/10.7554/eLife.36709.010
Figure 2—figure supplement 1. Putative major dispersal pathways of genotype D as estimated by phylogeographic analysis after the inclusion of RS-D5. DOI: https://doi.org/10.7554/eLife.36709.011
Figure 3. Midpoint rooted phylogeographic tree estimated by RAxML v8.0.20. HBV genotype A sequences (N = 493) categorized according to the geographic region of sampling were used in the analysis. Monophyletic clusters are indicated as triangles. Major clusters are indicated in Roman numerals.

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Figure 3—figure supplement 1. Midpoint rooted phylogeographic tree on 493 HBV genotype A sequences categorized according to the country/geographic region of sampling.
DOI: https://doi.org/10.7554/eLife.36709.015
Figure 4. Putative major dispersal pathways for genotype A as revealed by the phylogeographic analysis. The putative geographic origin of genotype A is in the Middle East/Central Asia. Subgenotypes and their corresponding dispersal routes are shown with different colors. Colored circles depict the geographic areas where subgenotypes are the most prevalent. Dotted lines represent the source and sinks for distant dispersal pathways.

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