

Section «Bioengineering and Bioinformatics»

Frequent recombination in Hepatitis A Virus and reproductive isolation of genotypes

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Isolation of distinct recombinant Hepatitis A virus (HAV) strains has been reported previously [1,3], however prevalence of natural recombination and its role in HAV genetics remained obscure.

Analysis of full genome sequences revealed evidence of common intratypic recombination among the most prevalent subtypes IA and IIIA. Most of available complete sequences of these genotypes carried phylogenetic signs of recombination in all genome regions without obvious hotspots. We also analyzed a dataset of 106 published HAV sequences for VP1-2A and 3CD genome regions [2]. Multiple instances of phylogenetic incompatibility were found among subtypes IA and IIIA, indicating common intratypic recombination in HAV. There were no signs of recombination between different HAV genotypes, despite the fact that co-circulation of genotypes IA and IIIA was commonly reported in different parts of the world and many sequences in our sampling originated from the same geographic region.

Our results indicate that there is reproductive isolation between genotypes of HAV, just as between enterovirus species [4]. We suggest that common intratypic recombination constrains the diversity within a genotype and maintains HAV genotypes as global gene pools.

References

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