individuals (21.5%). Additional clustering was done by parsing the two datasets by subtype 1a ($n = 714$) and 1b ($n = 151$). The genotype 1a network demonstrates a majority, 65.8 per cent, of participants in clusters. Moreover, two large clusters can be observed with baseline participants towards the center and recent participants on the outskirts indicative of high linkage at baseline. The genotype 1b network produced a single large cluster but subclusters were observed. The sequences between the two time points co-mingled but subclusters were also observed. Interestingly, the two large clusters from 1988 to 1989 were still evident in the 2005–16 viral sequences. We observed greater cluster diversity in more recently diagnosed individuals, indicative of a less connected network of individuals sharing transmission risk, though major viral strains did persist over time in this cohort.

A24 Phylogeographic analysis of hepatitis A virus in Russia

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Hepatitis A virus (HAV) is a positive-stranded RNA virus, a member of Picornaviridae, and a representative of genus Hepatovirus. It is unique among picornaviruses with regards to its hepatotropism, structure, and life cycle. HAV is spread via the fecal-oral route as a non-enveloped particle, while, in the blood the virus circulates in an envelope formed from the host cell membrane. HAV causes acute hepatitis in adults and is usually asymptomatic in children <6 years of age. The clinical features include fever, malaise, anorexia, nausea, abdominal discomfort, dark urine, and jaundice, all of which usually last >2 months. There is no evidence of chronic liver disease or persistent infection following acute infection. Due to its mode of transmission, HAV prevails in areas with low hygiene standards but does not give rise to epidemics because most people are infected at an early age and derive a life-long immunity. Thus, HAV infection has more impact on countries with higher socio-economical level where it is mostly registered as an outbreak in adults, which is the case in Russia. One feature distinguishing HAV from other picornaviruses is its remarkably slow mutation rate. HAV genotyping is typically carried out using highly variable regions VP1/2A and 2C/3A. Recently, it was shown that resolution provided by short fragments is not enough for reliable results. Unfortunately, previous research in HAV phylogeography was carried out only on these short sequences and did not include Russia or CIS territories. HAV comprises six genotypes, of which I and III are most frequent in humans and are both divided into A and B subgenotypes. Preliminary phylodynamic analysis of 80 highly variable region sequences (carried out by A. Neverov) has shown a particular pattern of geographical distribution of HAV genotypes in Russia. There are only two subgenotypes widely spread: IA predominates in the European part of Russia, and IIIA is found mainly in the Asian part. However, the history of HAV spread in Russia remains unclear. We hypothesized that IIIA subgenotype originated from India, while IA subgenotype came later from Europe and is still expanding. The Central Research Institute of Epidemiology kindly provided us with the unique collection of HAV isolates obtained from more than 30 subjects of the Russian Federation, as well as a number of isolates obtained from CIS countries. Samples (>500 isolates) were collected from 1999 to 2015 and characterized by one or both of the two most variable fragments of HAV genome (VP1/2A and 2C regions). The dataset includes 145 unique sequences of 2C/3A region, length ~650 bp, and 243 sequences of VP1/2A region, length ~400 bp. For each sample, date and location of collection are indicated. Whole-genome sequences of HAV from GenBank database were also used. They were aligned with MUSCLE, and the target 2C/3A and VP1/2A fragments were extracted. Partial HAV sequences from GenBank were not added to the analysis due to too little overlap with our sequences. Initial phylogeographic analysis was carried out in BEAST. Results were checked with the Tracer program, and the Spread3 package was used to visualize the results of the phylogeographic analysis in continuous space [16]. The BEAST output supports the hypothesis that IIIA subgenotype originated from India, whereas the situation with the IA subgenotype remains unclear. The reason for this might be either poor sampling of the Mediterranean area and Middle East in our analysis or low precision provided with variable fragments. The next step is to obtain full-genome sequences of approximately 100 of our samples to increase resolution and make use of hundreds of partial sequences of HAV genomes available in GenBank.

A25 Impact of polymorphism in the hepatitis B surface gene on human leukocyte antigen (HLA) class II

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There is still no cure for chronic hepatitis B virus infection (CHBV), a major cause of liver cancers and related malignancies. Elucidating the role of CD4+ T-helper cells in activating immunological responses that clear antigenic peptides during primary HBV infection holds a potential strategy for developing potent vaccines. Since the strength of CD4+ T cell responses is dictated by binding of viral epitopes to class-II human leukocyte antigens (HLAs), we hypothesize that the quality of immunological responses in CHBV patients is influenced by host genetics and HBV genotypes. Here, ninety-two non-recombinant complete HBV surface-gene proteins (PreS1/S) from Botswana were sequenced (genotype A 44(47.8%); D 48(52.2%)) and 15-mer binding epitopes restricted to nine HLA-class II molecules (DRB5/1) were mapped *in silico*. The HLAs used have high population coverage in Botswana. The total predicted epitopes per HLA were 94-(genotype A) and 105-(genotype D) for PreS1, 42 (A and D) for PreS2, and 105 (A and D) for S. Epitope densities (binding peptides to total epitopes) were 3 per cent and 6 per cent (PreS1A&D), 4 per cent and 2 per cent (PreS2A&D), and 23 per cent and 22 per cent (S1A&D). SA&D proteins had most polytopes: CPGYRWMCLRRFII66-81, PGYRWMCLRRFIIF67-82, GYRWMCLRRFIIFL68-83, and YRWMCLRRFIIFLF69-84 binding to 5 (55.6%) HLAs (DRB1*0101/0701/1101/1501 and DRB5*0101) used. HLA-DRB*0101 bound the most epitopes, and the least were bound by HLA-DRB*0302/0701/0401 for both genotypes. PreS1D polytope: PAFRANTANPDWDFN32-46 binds to DRB1*0101/0401/1302 and PreS2 polytopes: TAFHQALQDPRVRG6-19 and AFHQALQDPRVRGL7-20 bind to DRB1*010/1501 alleles. Non-synonymous mutations impair peptide-HLA binding when assessed as combinations of >2. The least active HLAs may be associated with CHBV and vice-versa for HBV clearance, thus the algorithm may be used to predict HBV prognosis for different haplotypes. The results favor the use of epitopes from S protein as broad genotype vaccine. This study highlights the need to explore further the mechanisms of PreS1 and its effect on the immune system.

A26 Molecular epidemiology of hepatitis E virus in Ireland 2016

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Foodborne viruses such as hepatitis E virus (HEV) pose an increasing risk to public health and to confidence in Irish food. Hepatitis E has been acknowledged as a significant pathogen of likely zoonotic transmission, with pork products and shellfish being implicated as potential sources. The European Food Safety Authority has recommended that systematic strain typing of viruses in humans, animals, and food commodities is needed to improve understanding of etiological agents and foodborne transmission pathways, in particular for HEV. The dominant autochthonous genotype of HEV in Europe is genotype 3, thought to be associated with consumption of contaminated food, specifically pork products. However, little is known about the epidemiology of HEV in Ireland. In 2016, HEV became a notifiable disease in Ireland. Following this, as part of the Department of Agriculture, Food and the Marine-funded FoVIRA study, the molecular epidemiology of HEV in Irish clinical samples has been characterized for the first time. HEV RNA-positive clinical