resistance-associated substitutions (RAS) is an important contributor to this decision-making process. In the present study in an Irish cohort, we performed a retrospective analysis on all HCV samples received for drug resistance testing at the Irish National Virus Reference Laboratory between September 2014 and May 2016. Particular attention was paid to patients who experienced virological failure in an attempt to identify predictors of failure. Sanger sequence data covering the HCV NS3 protease coding region were obtained for 682 samples received during the study period. These were analysed using PAUP phylogenetic software. Sequence data for the NSSA and NSSB regions in some samples were also obtained. The rs12989860 single nucleotide polymorphism site was examined by allelic discrimination real-time PCR. Analysis of the NS3 viral sequences demonstrated that 85.5% (583/682) were HCV subtype 1a, 14.2% (97/682) subtype 1b and 0.3% (2/682) subtype 1c infections, subtype 1a was further differentiated into 76% clade 1 (443/583) and 24% clade 2 (140/583). RAS proven to reduce susceptibility to NS3 inhibitor treatment were detected in 45.9% of cases (313/682). Although the vast majority of all RAS detected were found in subtype 1a viruses, 7.2% (7/97) subtype 1b samples also contained one or more RAS. The Q80K polymorphism was found in 313/583 (57.3%) of HCV subtype 1a, and almost exclusively in clade 1 (242/443; 54.6%) versus clade 2 viruses (2/140; 1.4%). This distribution is reflected in the neighbour joining tree. Among the cohort of patients who experienced virological failure whilst on treatment, RAS could be detected in 11/17 (64.7%) patients for whom sequence could be generated. These included Y366M/L (6/11; 54.5%), Q80K (5/11; 45.5%), R155K/T (3/11; 27.3%) and T54S (1/11; 9.1%). The majority of these patients were found to possess the deleterious “T” single nucleotide polymorphism (SNP) at the rs12989860 site within the Interferon lambda 4 (IFN4) gene locus. Nine of eleven patients with detected RAS were found to be either CT or TT at rs12989860, one patient was CC at this SNP. Preliminary data from patients experiencing treatment failure on NS5A/B inhibitors also indicate the presence of RAS in 4 of 7 individuals. The high incidence of RAS within HCV NS3 protease sequences, the detection of RAS in NS5A sequences, and the apparent risk of treatment failure, albeit in a small number of patients, when the RAS are present, highlights the importance of sequencing these viruses prior to commencing treatment with protease inhibitors, and the need to identify additional predictors of failure.

HIV drug resistance over a decade of antiretroviral therapy scale-up for HIV/AIDS patients in Vietnam

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Since 2005, Vietnam has remarkably scaled-up Antiretroviral therapy (ART) for HIV-infected people. The number of people receiving ART has increased from 2,670 in 2005 to 78,438 adults and 4,204 children at the end of 2013. ART coverage increased to 67% (60.0% in adults and 78.1% in children), against current eligibility criteria per National Guideline (CD4 cells <350 cells/ml). Standardized ART was delivered at 364 outpatient clinics at the end of 2013. Since 2010, the Ministry of Health has recommended the first-line prioritized ART regimens with two NRTIs (d4T + 3TC or ZDV + 3TC) plus one NNRTI (nevirapine [NVP]). In the context of rapid ART scale-up, the extent of HIV drug resistance (HIVDR) in Vietnam has been concerned, studies on transmission and emergence of HIV drug resistance were carried out in 2013-4. HIVDR study protocols were adapted from WHO guidelines for transmitted drug resistance (TDR) (2012) and acquired drug resistance (ADR) (2014). In brief, the TDR survey was implemented in a total of 15 voluntary counseling and testing (VCT) sites located in the old Hanoi. A total of 74 eligible VCT clients, aged 18-24, detected HIV positive, had no history of ART exposure, had no previous pregnancy if female, and were sequentially sampled. HIV genotyping was done in order of enrollment date until DR prevalence could be classified. For the ADR survey, 8 ART outpatient clinics were sampled from a total of 114 clinics that had ART available for more than 3 years up to the end of 2010, in the North, using probability proportional to proxy size (PPPS) sampling method. From each selected VCT, 23 patients who had received ART for more than 36 months were consecutively recruited into the study. All patients were taken blood for evaluating viral suppression and HIV drug resistance if viral load above 1,000 copies/ml. The prevalence of transmitted HIV drug resistance was classified as moderate between 5 and 15%, mainly to NRTIs/NNRTIs, no protease inhibitor (PI) resistance. In 181 patients on ART for more than 36 months, 93.9% (95% CI: 90.4–97.4%) had viral load suppression and 5.5% (95% CI: 2.2–8.9%) had drug resistance. Notably, 100% of individuals with viral suppression failure are resistant to all drugs in both their initial and current ART regimens receiving. Against 7 NRTIs and 4 NNRTIs recommended for the first-line ART as per the national guideline, resistance rates ranged between 75 and 100%. No resistance to PIs was found. The most common mutations are M184V (90%), D67G (60%), K70RES (60%), K103N (50%), Y184C (50%), T215FYN (50%), and K219QE (50%). The scaled-up ART program in Vietnam was proven to be effective with high rate of viral suppression at 36 months on the first-line prioritized ART regimens. Transmitted HIV DR to NRTIs/NNRTIs was increased, requiring the national program on HIV DR surveillance and prevention be strengthened to maximize long-term effectiveness of first-line ART regimens.

Comprehensive characterisation and evolutionary analysis of endogenous retroviruses in the mouse genome

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It is well established that the genome of the mouse (Mus musculus) contains large numbers of transposable elements, including many endogenous retroviruses (ERVs). Murine ERV lineages have been characterized piecemeal, but a comprehensive analysis has yet to be implemented. In this study, we address this by combining high-throughput in silico screening of the mouse genome with in-depth phylogenetic analysis of murine ERVs. Based on phylogenetic analysis of ERV polymerases, we establish the presence of at least 22 major ERV lineages in the murine genome, of which only 14 have been previously described. The majority of the previously unreported lineages are relatively low copy number (<100). Using a combination of automated and manual approaches we were able to recover representative internal regions and long terminal repeats (LTRs) for four of the eight novel lineages. LTR sequences were used to infer calibrated timelines of ERV invasion and intragenomic expansion within the mouse genome. These data were transposed against a timeline of murine evolution and phylogeography, providing new insights into the coevolutionary
relationships between mice and retroviruses. In particular, we establish the presence of a more ancient ERV component in the murine genome, comprised of isolated, highly degraded insertions. These sequences evidence a transition in murine evolutionary history, beginning about one million years ago, wherein the ancient ERV families that have counterparts in humans and other large mammals were overthrown by a wave of newly acquired and/or transpositionally active ERVs.

**A15** Rapid radiation of treponema pallidum pertenue in wild non-human primates

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Bacteria of the species Treponema pallidum are causative agents of venereal syphilis (Treponema pallidum pallidum), Bejel (T. p. endemicum), and yaws (T. p. pertenue) in humans. We documented Treponema pallidum infections associated with disease in wild sooty mangabeys (Cercocebus atys) in Tai National Park, Côte d’Ivoire, and green monkeys (Chlorocebus sабaeus) from Bijilo Forest Park, Gambia and Niokolo-Koba National Park, Senegal. To examine the evolutionary relatedness of these treponemes to those responsible for diseases in humans and for previously documented infections in baboons (Papio papio), we conducted a hybridization capture experiment to enrich Treponema pallidum DNA from samples collected from symptomatic individuals. This approach allowed us to sequence the full genomes of Treponema pallidum strains infecting sooty mangabeys (n = 2) and green monkeys (n = 4). Phylogenomic analyses revealed that all Treponema pallidum strains infecting non-human primates are most closely related to the sub-species T. p. pertenue. Strains infecting humans and non-human primates do not appear to be reciprocally monophyletic. The star-like phylogenetic branching pattern of the T. p. pertenue clade, with short basal branches receiving low statistical support, suggests a rapid initial radiation across humans and non-human primates. These results greatly broaden the known host range of T.p. pertenue and suggest the existence of a vast zoonotic reservoir that could possibly contribute to the failure of global eradication efforts.

**A16** A distributed pan-viral typing framework

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With the increasing amount of DNA sequence information obtained from new sequencing methods, opening up the possibility for a complete viral screen of a host, there is an increasing need for the rapid and accurate identification of the virus types as well as their epidemiological background. While in the past, typing tools have been developed and made available (such as the Rega HIV-1 subtyping tool) and hosted at multiple sites, these tools require maintenance to track the ongoing evolution of the virus. The setup and the maintenance of typing tools, which are often deployed at multiple sites, has been a challenge. Within the EU-funded VIROGENESIS project (Horizon 2020), the Rega typing tool framework is being redesigned to separate clearly the framework from the specifics for an individual tool. This will (1) enable an expert to independently and easily setup, create and maintain a typing tool for a new pathogen; (2) establish an online repository of typing tools/versions to which participants can push updates and from which up-to-date versions can be fetched to a distributed network of servers hosting the typing tools; and (3) create a pan-viral typing tool to identify the correct pathogen and which will allow further analysis of the sequences using the specialized typing tool for that pathogen. The transformation of the framework is expected to be completed by September 2016, at the same time co-evolving existing typing tools already available (including HIV, HCV, HTLV, Enterovirus, Norovirus), and new typing tools (including Chikungunya, Coronavirus, Dengue virus, Zika virus) that are being designed by partners within the VIROGENESIS project. Within the VIROGENESIS project, the existing typing tools based upon the Rega typing tool framework will evolve into a distributed pan-viral typing tool.

**A17** Molecular characteristics of hepatitis B virus (HBV) isolated from chronic hepatitis B patients in South Vietnam

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Chronic infection with hepatitis B virus (HBV) is a major health problem due to its worldwide distribution and its long-term effects. Vietnam is a country with a high HBV burden and the prevalence of chronic HBV infection in general population is 8.8–12.3%. In East Asia, the most common HBV genotypes are B and C. Despite high prevalence of HBV, data on HBV (genotype and subgenotype, virulence markers, drug resistance mutations and prevalence of recombinant strains) is limited in Vietnam. There are only few reports on HBV genotypes in Vietnam, mostly based on pre-S/S gene sequences. We have analyzed whole genome sequence of 98 HBV isolates from chronic HBV patients attending at Hospital for Tropical Disease, Ho Chi Minh City, Vietnam, who were under treatment for 1–6 years. HBV genome was amplified in 4 overlapping fragments (777–1,136bp) and the amplicons were subjected to deep sequencing by using Illumina MiSeq system. Sequence assembly, genome analysis and phylogenetic analysis were performed within Geneious package. A sequence was assigned to a certain genotype and subgenotype if it was contained within a well-supported phylogenetic cluster (bootstrap value >75%) and the intra-genotypic nucleotide divergence was <7.5 and >4.5%, respectively. Mutations in Basal core promoter (BCP), pre-CORE, and CORE gene regions were determined by comparing with reference sequences. Finally, screening of minor (sub-consensus) variants was performed using the SNP detection tool available in Geneious. 1% frequency and 500-fold coverage were chosen as cut-off values. Among the isolates, 71.43% were genotype B, 27.55% were genotype C and one isolate was a recombinant (between B and C). Among genotype B isolates, 65 were subgenotype B4 (92.86%) and 5 were B2 (7.14%). 92.6% of subgenotype C belong to C1, 3.7% is subgenotype C2 and the remaining 3.7% to C3. Mutations G1752A, T1753C, G1757A, A1762G/T, G1764A and C1766G on BCP and CORE were found in 76 of 98