recombination may lead to better ways to inhibit infections and develop new antiviral treatments.

A31 A large-scale screening for hepaciviruses in African rodents

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Hepatitis C virus (HCV) is considered to be a major public health problem, infecting >3% of the human population and causing acute and chronic liver disease. To date, the zoonotic origins of HCV remain elusive, since no animal population has been identified with closely related hepaciviruses. Inspired by recent findings of divergent hepaciviruses in rodents, we have screened a comprehensive set of African rodent samples that have been collected through various collaborations. Screening was performed by employing a highly sensitive nested PCR assay directed against the NS3 protease-helicase gene. From the 2,361 samples that were screened, 74 were found positive for the presence of hepaciviruses. At this stage, we focus on generating longer stretches of genomic information based on previously described protocols that make use of host rRNA depletion and a simple viral enrichment methodology followed by NGS approaches. By generating and analyzing sequence data from these samples we aim to perform in-depth phylogenetic and phylogeographic analyses gaining valuable insight into the evolutionary origins and epidemic emergence of HCV. Emphasis will be put on the identification of novel hepacivirus lineages more closely related to HCV, as well as the examination of host-specific adaptation and geographic structuring of these viruses.

A32 Search for viral integration insertion sites into the human genome—strategy matters

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During one of our previous works we investigated the integration of a low-risk human papillomavirus' (HPV) genetic material into the human genome, we aimed to elucidate whether the integration event(s) had helped facilitate the manifestation of cancer in an individual with a HPV11-positive sinonasal squamous cell carcinoma. To elucidate viral integration sites, whole-genome sequencing (WGS) was applied to the tissue sample of sinonasal carcinoma. We employed three different analysis strategies – data pipelines with different topologies that should intuitively all yield qualitatively the same result with minor variations. One of the pipeline topologies was adopted after Li et al. (2013) with slight modifications, whereas the other two were simple meta-algorithms that should generally answer the same question. Although the bulk of the breakpoints yielded through the three different topologies did overlap to some degree, a great deal of breakpoints varied greatly between the approaches.

A33 The cervico-vaginale microbiota in chlamydia trachomtais notified women: a case–control study at the sexually transmitted infection outpatient clinic in Amsterdam

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Increasing evidence suggests that the cervico-vaginal microbiome (CVM) plays an important role in acquiring sexually transmitted infections (STIs). Here we studied the CVM in women exposed to *Chlamydia trachomatis* (Ct). We included 98 women who were notified by Ct-positive sex partners via contact-tracing at the STI outpatient clinic in Amsterdam, the Netherlands. Cervico-vaginal samples and clinical data were collected for all women. CVM compositions were characterized by sequencing of the V3/V4 region of the 16srRNA gene using the Illumina MiSeq platform. High quality reads were assigned to operational taxonomic units and classified using a vaginal reference package. Hierarchical clustering delineated CVM clusters based on microbial relative abundances. Possible determinants for acquiring Ct were analyzed using multivariable logistic regression. The CVM was characterized for 93 women, of whom 52 were Ct positive and 41 Ct negative. We identified three major CVM clusters. Clustered CVM predominantly comprised either diverse anaerobic bacteria ($n = 39$; 42%), Lactobacillus iners ($n = 32$; 34%) or Lactobacillus crispatus ($n = 22$; 24%). In multivariable analysis, we found that the CVM was significantly associated with C. trachomatis infection (OR = 4.2 (95% confidence interval, CI: 1.2–15.4) for women with diverse anaerobic CVM and OR = 4.4 (CI: 1.3–15.6), for women with L. iners-dominated CVM, compared to women with L. crispatus-dominated CVM), as was younger age (OR = 3.1, CI: 1.1–8.7, for those ≤21 years old) and reporting a steady sex partner (OR = 3.6, CI: 1.4–9.4). Women who tested positive for Chlamydia trachomatis infection after having been contact-traced by a chlamydia positive partner were more likely to have CVM dominated by *L. iners* or by diverse anaerobic bacteria, than by *L. crispatus*.

A34 Automated profiling of the human virome from raw metagenomic data

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Viruses influence human health as conventional pathogens, as modulators of gene expression and through their involvement in complex host-microbiome interactions. Next generation sequencing (NGS) has enabled us to explore the role of the microbiome in human health and disease. Metagenomic sequencing should allow us to profile all biological elements in a clinical sample in an unbiased, hypothesis-free way. However viruses display much greater variation than all other elements, and the existing tools and methods for virus identification and