domestic rabbits in China. The recombination signal is only observed in Nigeria camel-HKU23, suggesting a regional varied evolutionary history of camel-HKU23. Our findings extended the knowledge of the evolutionary relationship among Group 2a CoVs. Further surveillance in other African camels will be important to elucidate the evolution of camel-HKU23.

A55 Molecular systematics of sturgeon nucleocytoplasmic large DNA viruses

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Namao virus (NV) is a sturgeon nucleocytoplasmic large DNA virus (sNCLDV) that can cause a lethal disease of the integumentary system in lake sturgeon *Acipenser fulvescens*. As a group, the sNCLDV have not been assigned to any currently recognized taxonomic family of viruses. In this study, a dataset of NV DNA sequences was generated and assembled as two non-overlapping contigs of 306 and 448 base pairs (bp) and then used to conduct a comprehensive systematics analysis using Bayesian phylogenetic inference for NV, other sNCLDV, and representative members of six families of the NCLDV superfamily. The phylogeny of NV was reconstructed using protein homologues encoded by nine nucleocytoplasmic virus orthologous genes (NCVOGs): NCVOG0022—mcp, NCVOG0038—DNA polymerase B elongation subunit, NCVOG0076—VV A18-type helicase, NCVOG0249—VV A32-type ATPase, NCVOG0262—AL2 VLTF3-like transcription factor, NCVOG0271—RNA polymerase II subunit II, NCVOG0274—RNA polymerase II subunit I, NCVOG0276—ribonucleotide reductase small subunit, and NCVOG1117—mRNA capping enzyme. The accuracy of our phylogenetic method was evaluated using a combination of Bayesian statistical analysis and congruence analysis. Stable tree topologies were obtained with datasets differing in target molecule(s), sequence length, and taxa. Congruent topologies were obtained in phylogenies constructed using individual protein datasets and when four proteins were used in a concatenated approach. The major capsid protein phylogeny indicated that ten representative sNCLDV form a monophyletic group comprised of four lineages within a polyphyletic Mimi-Phycodnaviridae group of taxa. Overall, the analyses revealed that Namao virus is a member of the Mimiviridae family with strong and consistent support for a clade containing NV and CroV as sister taxa.

A56 Visualization of recombination in deformed wing virus infecting bees

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Honey bees suffer increasing colony mortality worldwide, partially caused by the spread of viral pathogens. Among these pathogens, deformed wing virus (DWV) is one of the major, widespread viruses of honey bees resulting in wing deformities and weakening colonies. DWV can be found in honey bees, bumble bees, and other wild bees as three major genotypes named DWV-A, -B (also named Varroa destructor virus 1), and -C. Various recombinants of DWV-A and -B have been previously found in honey bees, some of which have been suggested to have higher virulence over non-recombinant, parental virus. In most of these cases, recombinants were only shown as consensus sequences from previous assemblies and alignments and may not reflect the biological reality of all variants present within a host bee. It is therefore important to build a method of recombinant detection and quantification within mixed infections in single-host individuals, including both parental and various recombinant genomes, so as to evaluate the relevance of recombinants for viral genome evolution and the impact on hosts. Here, we propose to visualize and quantify these recombinants using next-generation sequencing data to better understand how these genomes evolve within bees. Our method will be performed directly from raw sequence reads from various datasets (including field and lab experiments as well as screening of public databases) in order to obtain an overview of DWV recombination in various *in vivo* and *in vitro* conditions. Recombination of viral genomes is a key point for virus evolution. The detection and quantification of recombination will facilitate analysis of the determinants of recombination and help in understanding the routes by which new viral variants emerge. The emergence of new (more virulent) recombinant viruses can result from acquisition of new capabilities, such as escape from host immunity or increased transmission rates. Recombination can also lead to adaptation to new environments and new hosts by a change in cell tropism, allowing cross-species transmission, which may be particularly relevant for bumble bees and wild bees infected by honey bee-derived DWV.

A57 An evolutionary framework to guide the hunt for human dsDNA viruses

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It is becoming increasingly obvious that we only know a fraction of the human virome. The development of next-generation sequencing (NGS) technologies has dramatically increased our ability to hunt viruses. Yet, the small genomes and low copy numbers characteristic of most viruses make undirected (shotgun) hunts a relatively inefficient strategy. Here, we propose to speed-up the rate of double-stranded DNA (dsDNA) virus discovery by combining NGS with evolutionary thinking. dsDNA viruses are thought to have co-diverged with their hosts. As this applies to the hominine lineages (gorillas, humans, chimpanzees, and bonobos), it is theoretically possible to estimate the phylogenetic position of cryptic human viruses by identifying co-divergent viral lineages infecting non-human hominines. Where these lineages do not comprise a human-infecting counterpart, a yet-unknown human virus may be hiding. The first phase of this project will consist in the high-throughput characterization of dsDNA viruses (herpesviruses, papillomaviruses, and polyomaviruses) infecting wild gorillas, chimpanzees, and bonobos. For this, we will use an exhaustive collection of fecal samples (in terms of hominine species/sub-species diversity) and apply a discovery strategy combining in-solution capture and NGS. This strategy has been developed in the ancient DNA field but has a very broad applicability; it will constitute a nice addendum to the institute technical portfolio. Thanks to the massive amount of information collected, we will be able to reconstruct the evolutionary history of many dsDNA virus lineages and to identify those where a human virus would be expected but is still unknown. This will pave the way to the second phase of the project which will consist in a pre-oriented dsDNA human virus hunt based on the use of specific PCR systems implemented in multiplex. We expect that this project will generate an unprecedented amount of data on the processes at play along dsDNA virus evolution (co-divergence versus cross-species transmission), help determine the directionality, frequency, and timing of cross-species transmission events between hominines and unveil the existence of yet-to-be-discovered human viruses.

A58 Epidemic dynamics of ancient disease outbreaks

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Bayesian phylogenetic analysis allows for the estimation of the time to the most recent common ancestor (tMRCA) of sequences sampled at different times, as long as they prove to be 'measurably evolving', which means that the time between sampling dates was long enough to allow the appearance of a measurable amount of genetic changes. This 'temporal signal' can be tested with the software TempEst (Rambaut et al. 2016), which generates a regression of the root-to-tip genetic distance on sampling times and finds the best-fitting root that produces the lowest residual sum of squares. For the case of pathogen single nucleotide