study for detecting and assembling complete HPV genomes in cervical samples from a cohort of young women attending cervical screening with access to HPV vaccination in Luxembourg. DNA extracts of eighty-one cervical swabs from women (mean age 23 years) positive for HPV by AnyplexIIHPV28® (Seegene) were enriched by rolling circle amplification and sequenced on Illumina Miseq. Reads were mapped to 182 PaVE reference sequences of known HPV types using BBMap and assembled using VELVET. Complete HPV genomes obtained were aligned with genomes published in Genbank using MEGA6. Overall, an average of 1 per cent of reads mapped to HPV. Among the eighty-one positive samples, NGS-RCA detected 186 different HPV types spanning thirty-six of the fifty-one known mucosal types. HPV types 42, 53, 51, 56, 90, and 31 were most frequently detected in twenty-two, fifteen, ten, ten, nine, and seven samples, respectively. Detection of HPV types by NGS-RCA was highly correlated with viral load of Anyplex. About sixty-seven consensus sequences of complete HPV genomes were assembled including two novel lineages of HPV66 and HPV90 and two novel sublineage of HPV67 and HPV73, respectively. NGS-RCA is a powerful method for obtaining complete HPV genomes from cervical samples with a high viral load ($Ct < 30$). After eight years of the vaccination programme in Luxembourg, vaccine-related types 6, 11, 16, and 18 were infrequently detected in the targeted age group.

A45 Merkel-cell polyomavirus and human polyomavirus 6 in Argentina, Uruguay, and Spain: Deep characterization of the South American types

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New human polyomaviruses have been discovered in the last years, including the Merkel-cell (MCPyV) and the human polyomavirus 6 (HPyV6). Although their infection is usually asymptomatic, in immunocompromised hosts they can cause life-threatening pathologies. In particular, MCPyV has been associated with Merkel cell carcinoma, an aggressive skin cancer arising in the elderly and in chronically immunosuppressed individuals. Despite being prevalent viruses, epidemiological data from South America are scarce, as too are the viral types circulating and their origin. The aims of this work were to characterize MCPyV and HPyV6 from environmental samples with different geographical origins and to analyze the phylogenetic and phylogeographic profiles to study their spatio-temporal dispersion patterns, particularly for MCPyV. Partial and complete genome sequences were obtained from sewage samples from Argentina, Uruguay, and Spain. Phylogenetic analysis showed that MCPyV sequences distributed according to their geographic origin in Europe/North America, Africa, Asia, South America, and Oceania groups, suggesting that viral diversification might have followed human migrations across the globe. In fact, the analysis of the viruses reported here emphasized this behavior, given that they reflected the origin of the current population in each country. The South American group presented a high level of clustering, showing subgroups exclusively formed by sequences from southern South America, possibly associated with local diversification events related to early migratory movements in the region. Regarding HPyV6, sequences from South America grouped with high support and were separated from all other sequences available, from USA, France, Australia, and China. The analysis of viruses from the environment allowed us to characterize prevalent infections in different geographic regions, revealing that viruses circulating in each population reflected its origin and that there are specific lineages associated with South America.

A46 Partial genetic characterization of a Brazilian strain of yellow fever virus from an epizootic outbreak in 2009

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Yellow fever is the prototype virus of the *Flavivirus* genus in the Flaviviridae family. Its genome consists of a single-stranded positive-sense RNA molecule of ~10 kb presenting a single open reading frame. It is translated into a polyprotein which is processed by viral and host proteases into three structural (C, prM, and E) and seven non-structural proteins (NS1, NS2A, NS2B, NS3, NS4A, NS4B e NS5). As an arbovirus it is maintained in nature through a cycle in which the virus alternates between vertebrate (human/non-human primates) and invertebrate hosts (*Haemagogus* sp., *Sabethes* sp., and *Aedes* sp.). The species involved in the sylvatic and urban transmission cycles differ and since 1942 no cases related to urban transmission have been reported in Brazil. During a series of epizootics caused by Yellow fever virus in Brazil between 2007 and 2009, a monkey (*Alouatta* sp.) was found dead (May 2009) in a sylvatic area in the State of Paraná (southern Brazil). Brain samples from this animal were used for virus isolation. RNA was extracted from the cell culture supernatant and used to amplify an 861-bp segment, comprising the coding sequence of the C and prM proteins (nucleotides 119–979, according to GenBank accession number U17066). Sequence analyses demonstrated that it is closely related with two isolates from Venezuela (99.5 per cent identity), one isolated in 2005 from a human case and the other isolated in 2007 from *Alouatta seniculus*. Phylogenetic analysis groups them all within South American genotype I. This sequence was also compared to other sequences available in GenBank that presented only partial coverage but 100 per cent nucleotide identity (nucleotides 641 to 981, according to GenBank accession number U17066) and were not included in the phylogenetic analysis. This data indicates that this new Brazilian isolate may be part of the same epizootic that affected monkeys in the state of São Paulo (2008) and the Missiones province (2008 and 2009) and stresses the importance of yellow fever surveillance through sentinel monkeys.

A47 Whole-genome analysis of rotaviruses isolated from humans and domestic animals in Uganda, 2012–2014 reveals possible anthroponosis and multiple rotavirus reasortment events between species

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