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Detection of Human papillomavirus and Co-infection With Other Sexually Transmitted Pathogens in Northern Peru

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Purpose: The epidemiology of human papillomavirus (HPV) and co-infections with other sexually transmitted infections (STIs) remains poorly characterized in Peru. The aim of this study was to identify HPV infections and the presence of co-infections by other important STIs (*Chlamydia trachomatis*, *Trichomonas vaginalis*, and *Herpes simplex virus*) in women attending the public health system in northern Peru.

Methods & Materials: We conducted a prospective cross-sectional study in asymptomatic women attending the cervical cancer screening program in a public hospital of Cajamarca, Peru. Exclusion criteria were: pregnancy, recent gynecological bleeding, previous hysterectomy, previous history of HPV-related disease including cervical intraepithelial lesions, cancer, warts and cutaneous manifestations. A cervical swab was collected from each patient using a disposable cytobrush. Detection of sexually transmitted pathogens was performed by polymerase chain reaction (PCR). The pathogens evaluated were: HPV, *Chlamydia trachomatis*, *Trichomonas vaginalis*, and *Herpes simplex virus* 1 (HSV-1) and 2 (HSV-2).

Results: A total of 300 asymptomatic women were enrolled in the current study. The pooled prevalence of HPV detected in our study was 19.33% (16.33% as single infection and 3.00% in co-infections) from the total samples. Co-infections between the different pathogens were also observed in 15 cases, being HPV and *T. vaginalis* the most frequent with 10 cases (66.67%). The most frequent type identified in HPV mono-infections were HPV-16 (16.33%), HPV-52 (14.29%) and HPV-31 (8.16%). Co-infection by multiple HPV types were also identified with up to 4 genotypes at the same time in a single patient. The majority of patients with high-risk HPV were between 18 - 39 years old (60.87%) and had a sexual partner in the last 6 months (93.48%). Also, the majority of the patients with high-risk types did not report frequent condom use (89.13%).

Conclusion: We found an important prevalence of HPV in asymptomatic women from northern Peru. The most common genotypes were HPV-16, HPV-52 and HPV-31. Among the STIs studied, *T. vaginalis* was the most common pathogen detected in co-infections with HPV. Education on condom use and timely screening should be encouraged in the Peruvian population to prevent the expansion of HPV and other sexually transmitted pathogens.

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Metagenomic Discovery of a Novel Sarbecovirus in the United Kingdom at the Western Extreme of the Range of Rhinolophidae

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Purpose: The origin of the current COVID-19 pandemic is unknown but horseshoe bats, of the family *Rhinolophidae*, are natural hosts to a suite of sarbecoviruses. Global surveillance is key to monitoring potentially pathogenic viral strains and improving the capacity for surveillance across Europe will bolster our understanding of viral populations within zoonotic reservoirs.

Methods & Materials: Faecal samples were collected from Lesser horseshoe bats (*Rhinolophus hipposideros*) in the UK during annual population monitoring surveys, stored in RNAlater and frozen prior to genomic analysis. For metagenomic analysis, the Sequence-independent Single-Primer Amplification (SISPA) method was employed and sequencing completed using Illumina Nextera and the Oxford Nanopore GridION platforms.

Results: A *De novo* hybrid assembly utilising shorter Illumina reads with longer Nanopore reads acting as a scaffold, generated a 29kb contig named RhGB01. Mapping raw reads against RhGB01 demonstrated a combined depth of 50x across the genome. Sequence alignment exhibits genomic organisation comparable to other sarbecoviruses isolated from animal and human hosts. Within the receptor binding domain, but excluding the receptor binding motif, RhGB01 has 77% and 81% amino acid homology compared to SARS-CoV-2 and SARS respectively. Maximum likelihood phylogenies inferred from the nucleotide sequence of RNA dependent RNA polymerase, spike glycoprotein and entire coding sequence exhibit clustering with the only other fully sequenced zoonotic Sarbecovirus from Europe which was isolated from *Rhinolophus blasii*. The structure of the receptor binding domain of RhGB01 was predicted by homology modelling using a crystal structure of the receptor binding domain of SARS-CoV as a template. This model was selected with a Global Model Quality Estimate (GMQE) > 0.7 and Quaternary Structure Quality Estimate (QMEAN) of -2.18. Structural comparisons between the predicted receptor binding domain of RhGB01 and SARS-CoV-2 highlight structurally different regions which house hACE2 contact residues.

Conclusion: Phylogenetic inference and structural modelling suggest an absence of pathogenic potential for RhGB01. However, the discovery of a novel Sarbecovirus at the western limit of Lesser horseshoe bats demonstrates their presence throughout the entire horseshoe bat distribution and indicates the need for viral surveillance systems in Western Europe.

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Immunized Goat with a Conjunctival Vaccine Prevent the Abortus Despite Revaccination with the Same Strain

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