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From Field to Genome: Genomic characterization of pneumococcal strains circulating at the human-wildlife interface in Sub-Saharan Africa

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Lower respiratory tract infections are among the leading causes of death for children under five in Sub-Saharan Africa, with *Streptococcus pneumoniae* being the most common causative agent. Beyond its public health impact, *S. pneumoniae* has been shown to have implications for the conservation of endangered species, as humans have inadvertently transmitted the bacteria to wild great apes resulting in lethal outbreaks. Understanding serotype diversity and antimicrobial resistances at a local scale can guide tailored public health interventions, such as the selection of appropriate vaccines and antibiotic treatment, which can reduce disease burden and the risk of transmission to wildlife.

We conducted genomic characterization of pneumococcal strains carried asymptotically by humans living and working in proximity to great apes in Taï National Park, Côte d'Ivoire, and Dzanga-Sangha Protected Areas, Central African Republic. A total of 473 nasopharyngeal swabs were collected; from these, 43 *S. pneumoniae* strains were isolated directly in the field using a solar-powered incubator. Molecular and genomic analyses were performed at the Institut Pasteur de Bangui, Centre Hospitalier Universitaire de Bouaké and the Helmholtz Institute for One Health in Greifswald. We revealed the circulation of multiple serotypes, including both vaccine-covered and non-covered types, and the presence of distinct antimicrobial resistance patterns. This study highlights how genomic surveillance can provide relevant data to inform prevention and treatment policies within a One Health framework.

Keywords

Whole Genome Sequencing, human-wildlife interface, genomic surveillance, conservation, public health

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Professional Status of the Speaker

PhD Student

Junior Scientist Status

Yes, I am a Junior Scientist.

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