From genome to action: pathobase transforms zoonotic pathogen tracking

FAYETTEVILLE, GA, UNITED STATES, September 16, 2025 /EINPresswire.com/ -- The rapid identification and genomic analysis of zoonotic pathogens are critical for safeguarding public health and controlling outbreaks. PathoBase, an advanced computational platform, provides a comprehensive, efficient, and freely accessible tool for genomic data analysis based on core-genome multilocus sequence typing (cgMLST).

Zoonotic pathogens, capable of crossing between animals and humans, pose escalating threats due to antimicrobial resistance, genetic diversification, and complex transmission patterns. While genomic technologies have advanced rapidly, the global distribution of pathogen genome databases remains uneven, with many platforms serving primarily Western research needs. Such disparities create data-processing delays and limit access for researchers in other regions. Moreover, existing databases often lack integrated tools for functional genomic analysis, hindering real-time outbreak tracing and intervention. Based on these challenges, there is a pressing need to develop a regionally responsive, methodologically rigorous platform for comprehensive zoonotic pathogen genomic analysis.

Suzhou Medical College and Iotabiome Biotechnology Inc. have launched PathoBase, a cutting-edge genomic analysis platform for zoonotic pathogens, announced (DOI: https://doi.org/10.1186/s44280-025-00087-x) in early 2025 in One Health Advances Built on the proven EnteroBase framework, PathoBase offers enhanced speed, accessibility, and analytical depth for researchers worldwide. It integrates genome assembly, cgMLST typing, hierarchical clustering, and SNP-based genotyping into a single interface, enabling real-time tracking of pathogen evolution and transmission. The platform currently includes Acinetobacter and Staphylococcus datasets, with additional bacterial genera and functional modules under active development.

PathoBase addresses critical gaps in pathogen surveillance by combining high-performance genomic assembly, advanced typing methods, and intuitive visualization tools. The platform leverages the EToKi assemble module, offering both de novo assembly (SPAdes, MEGAHIT) and reference-guided approaches (minimap2, Pilon). Its cgMLST system translates genetic variations in core bacterial genes into standardized digital fingerprints, enabling scalable comparisons of thousands of genomes. The integrated HierCC framework supports multi-level clustering, facilitating high-resolution outbreak tracing. Currently, PathoBase hosts curated datasets of 112 Acinetobacter and 20 Staphylococcus strains, along with SNP-based typing for direct

metagenomic samples. Future expansions include typing schemes for Klebsiella pneumoniae, plasmid tracing in antimicrobial-resistant isolates, and modules for virulence factor detection, antimicrobial resistance gene profiling, and mobile genetic element identification. Interactive visualization interfaces and expanded pathogen repositories will enhance user experience and analytical capability. By integrating these features, PathoBase supports cross-disciplinary research, bridging clinical microbiology, epidemiology, and bioinformatics within the One Health framework to strengthen outbreak prevention and response.

"PathoBase represents a significant step forward in genomic epidemiology," said Dr. Zhemin Zhou, co-developer of the platform. "Our goal was to design a resource that not only matches the analytical rigor of existing global databases but also addresses the latency and accessibility issues faced by researchers outside Western infrastructure hubs. By providing an integrated, user-friendly system for pathogen typing and source tracing, we hope to empower more scientists and public health agencies to respond rapidly and effectively to emerging infectious threats."

PathoBase's integrated tools have the potential to revolutionize zoonotic pathogen surveillance, enabling real-time source tracking, rapid risk assessment, and targeted outbreak interventions. By providing a regionally optimized, globally accessible platform, it can bridge gaps in genomic data sharing and analysis, particularly for underrepresented regions. The addition of antimicrobial resistance profiling and virulence factor analysis will further support the development of predictive models for pathogen spread and evolution. Ultimately, PathoBase strengthens global One Health initiatives, fostering collaboration across human, animal, and environmental health sectors to mitigate the impact of bacterial infections and enhance preparedness for future pandemics.

References
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