GENOMICS, ONE HEALTH, AND THE FUTURE OF INFECTIOUS DISEASE PREPAREDNESS

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In recent years, the landscape of infectious disease surveillance and diagnostics has undergone a profound transformation, driven by rapid advances in molecular biology, sequencing technologies, and bioinformatics. Emerging and re-emerging pathogens, increasing global mobility, climate-driven ecological changes, and intensified human-animal-environment interactions continue to challenge public health systems worldwide. In this context, the ability to detect, characterize, and monitor pathogens with high resolution and speed has become a cornerstone of effective preparedness and response.

Metagenomic and targeted genomic approaches now offer unprecedented opportunities to move beyond pathogen detection alone toward a deeper understanding of transmission dynamics, pathogen evolution, and population-level risk. These technologies enable unbiased discoveries of known and novel agents, support real-time outbreak investigations, and provide critical insights into genomic diversity that inform diagnostics, therapeutics, and public health decision-making. Importantly, they also bridge traditionally separated domains-human health, veterinary medicine, wildlife surveillance, and environmental monitoring embodying the principles of the One Health approach.

At the same time, translating these powerful tools into routine public health practice remains a complex task. Challenges related to sensitivity, standardization, cost-effectiveness, data interpretation, and integration into existing surveillance frameworks must be addressed thoughtfully and collaboratively. Capacity building, interdisciplinary cooperation, and the sharing of methodological experience across regions and institutions are therefore essential to ensure that genomic technologies deliver their full societal benefit.

This volume brings together expert perspectives that reflect both the promise and the practical realities of modern pathogen genomics. By highlighting methodological advances, applied case studies, and future directions, it contributes to a more informed and resilient public health infrastructure. I hope that the contributions presented here will stimulate dialogue, foster collaboration, and support the continued integration of genomic approaches into evidence-based public health action.

Sincerely,

Dániel Cadar