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HIV molecular epidemiology: How much have we missed?

A rapid growth of identified HIV strains has imposed a great challenge on genotyping quality control that lays the basis for HIV research and global surveillance. Inspired by our previous study that has shown inadequate genotyping in epidemiologically important areas, we performed the first systematic examination of global HIV-1 genotyping information. Our results showed uneven distribution of genotyping quality in different geo-regions, across the viral genome, and among the risk groups, indicating robust and standardized genotyping tools are urgently needed. Our results also suggested a close monitoring of HIV-1 genotyping quality is needed for the heterosexual group in West Central Africa, IDU group in South America, and IDU and mother-to-child groups in China.

Biography

Ming Zhang received her PhD (Summa Cum Laude) from University of Gottingen, Germany. She has over a decade of experience in infectious diseases, in particular in HIV molecular epidemiology and molecular evolution. She is an Assistant Professor of Epidemiology at University of Georgia, USA, and affiliated with Faculty of Infectious Diseases, Institute of Bioinformatics, and Biomedical and Health Sciences Institute at University of Georgia. She leads an interdisciplinary research group towards understanding pathogen diversity under various epidemiology settings. She enjoys teaching and educating next generation of critical thinkers and innovators in epidemiology.

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