

## Large-Scale Integration of Bioinformatics is Necessary for Strengthening HIV Prevention Efforts in Jamaica

ANEISHA COLLINS-FAIRCLOUGH, PHD  
University of Technology, Jamaica

### Abstract

*The Human Immunodeficiency Virus (HIV) is a debilitating virus that infects 35 million people worldwide. To date Jamaica's HIV response has heavily utilized behavioral, clinical and social observations in creative ways to inform and guide prevention and treatment efforts. With the emergence of new threats to successful HIV management in the island, treatment and prevention would benefit from increased insights from HIV genetic sequences. To validate this assessment, a meta-analysis was conducted on studies that have reported bioinformatics analyses of HIV genetic sequences from Jamaica. This meta-analysis revealed that nucleotide sequence is available for no more than 1% of the approximately 32,000 persons living with HIV in Jamaica. This situation exists despite the generation of crucial insights from the few HIV genetic studies conducted in the island; further it emerged that only 52% of nucleotide sequence data is shared by scientists who report HIV nucleotide sequences in Jamaica, even after publication of their study. Together, the data suggest that increasing utilization of HIV sequencing and bioinformatics will be highly beneficial to supporting HIV prevention and treatment in Jamaica, as well as protecting prior successes gained in Jamaica's HIV response.*

**Keywords:** Bioinformatics, Genotyping, Human Immunodeficiency Virus

Corresponding author: \*Aneisha Collins-Fairclough: acollinsy@utech.edu.jm

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