

Epidemiología molecular del VIH-1 en Uruguay: una retrospectiva de 15 años

(Añasco, Agustina)

Bibliografía:

1. Barré-Sinoussi, F., Chermann, J. C., Rey, F., Nugeyre, M. T., Chamaret, S., Gruest, J., Dautet, C., Axler-Blin, C., Vézinet-Brun, F., Rouzioux, C., Rozenbaum, W., & Montagnier, L. (1983). Isolation of a T-Lymphotropic Retrovirus from a Patient at Risk for Acquired Immune Deficiency Syndrome (AIDS). *Science*. (220); 868-871.
2. ONUSIDA, 2022. <http://aidsinfo.unaids.org/>
3. Informe Epidemiológico VIH/SIDA-MSP, 2022.
4. Abecasis, A., & Vandamme, A.-M. (2015). Origin and Distribution of HIV-1 Subtypes. *Encyclopedia of AIDS*. 1–16.
5. Informe Epidemiológico VIH/SIDA-MSP, 2011.
6. Y. Alemán et al., —Performance of an in-house human immunodeficiency virus type 1 genotyping system for assessment of drug resistance in Cuba, *PLoS One*, vol. 10, no. 2, 2015.
7. Siepel A, Halpern A, Macken C, & Korber B. (1995). A Computer Program Designed to Screen Rapidly for HIV Type 1 Intersubtype Recombinant Sequences. *AIDS Research and Human Retroviruses*. 11(11).
8. Pineda-Peña, A. C., Faria, N. R., Imbrechts, S., Libin, P., Abecasis, A. B., Deforche, K., Gómez-López, A., Camacho, R. J., de Oliveira, T., & Vandamme, A. M. (2013). Automated subtyping of HIV-1 genetic sequences for clinical and surveillance purposes: Performance evaluation of the new REGA version 3 and seven other tools. *Infection, Genetics and Evolution*. 19; 337–348.
9. Struck, D., Lawyer, G., Ternes, A. M., Schmit, J. C., & Bercoff, D. P. (2014). COMET: Adaptive context-based modeling for ultrafast HIV-1 subtype identification. *Nucleic Acids Research*. 42(18).
10. Katoh, K., Misawa, K., Kuma, K.-I., & Miyata, T. (2002). MAFFT: a novel method
11. for rapid multiple sequence alignment based on fast Fourier transform. *Nucleic Acids Research*. 30(14); 3059-3066.
12. Larsson, A. (2014). AliView: A fast and lightweight alignment viewer and editor for large datasets. *Bioinformatics*. 30(22); 3276–3278.
13. Nguyen, L. T., Schmidt, H. A., von Haeseler, A., & Minh, B. Q. (2015). IQ-TREE: A fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Molecular Biology and Evolution*. 32(1); 268–274.

14. Zhang, M., Zhang, A., Schultz, A. K., Calef, C., Kuiken, C., Leitner, T., Korber, B., Morgenstern, B., & Stanke, M. (2006). jpHMM at GOBICS: A web server to detect genomic recombinations in HIV-1. *Nucleic Acids Research*. 34, 463–465.
15. Lole, K. S., Bollinger, R. C., Paranjape, R. S., Gadkari, D., Kulkarni, S. S., Novak, N. G., Ingersoll, R., Sheppard, H. W., & Ray, S. C. (1999). Full-Length Human Immunodeficiency Virus Type 1 Genomes from Subtype C-Infected Seroconverters in India, with Evidence of Intersubtype Recombination. *Journal of Virology*. 73(1).
16. Ruchansky, D., Casado, C., Russi, J. C., Arbiza, J. R., & Lopez-Galindez, C. (2009). Identification of a new HIV Type 1 Circulating Recombinant Form (CRF38_BF1) in Uruguay. *AIDS Research and Human Retroviruses*. 25(3).
17. Gräf, T., Bello, G., Andrade, P. *et al.* HIV-1 molecular diversity in Brazil unveiled by 10 years of sampling by the national genotyping network. *Sci Rep* 11, 15842 (2021).