P2129

Abstract (poster session)

Bioinformatic application to facilitate the genotypic determination of HIV-1 tropism

M. Parra Sánchez*, I. Zakariya-Yousef Breval, J. Córdoba García, I. Ferrero, E. Martín Mazuelos, J.C Palomares Folía (Seville, ES)

Objectives: We have developed a bioinformatic tool in order to simplify the computer analysis of the genotypic study of HIV tropism by means of the V3 loop of the gp120 protein. To get this, we have to analyze the FASTA sequence obtained after sequencing the V3 region by Geno2pheno (G2p) and/or WebPSSM (WP) algorithms individually. With this tool, we can obtain simultaneously the interpretation of both algorithms. Furthermore, with G2p analysis you can obtain results with two false positive ratios (% FPR). The first one is the analysis from MOTIVATE clinical data: (2 and 5.75% FPR). The second one is the Recommendations from the European Consensus Group (10%FPR). Methods: We have analyzed with G2p and WP a total of 653 protein sequences of V3 regions of HIV-1 obtained from Los Alamos database and sequences analyzed in the laboratory of Molecular Microbiology of the Valme University Hospital. These sequences correspond to 443 sequences with CCR5 (R5) genotype and 123 sequences with CXCR4 (X4) genotype (X4 or R5X4). 87 sequences with discordant results (9 sequences R5 by G2p but X4 by WP, and 78 sequences X4 by G2p but R5 by WP) were also included. These sequences belong to subtypes A (80 sequences, including A1 and A2 subtypes), B (501 sequences) and C (72 sequences) of HIV-1. (The next update will include approximately 1600 sequences with different subtypes of HIV-1 and HIV-2 and several CRFs) Results: At running a new sequence, the result will show a % of similarity to any of the sequences of our database that will be used as reference sequence, and three tropism predictions of the model sequence: 1. the result obtained by analyzing the sequence of G2p with a FPR = 10%. 2. the result obtained by analyzing the sequence by G2P with a FPR = 2.5 and 5.75% and 3. the result obtained by analyzing the sequence with PSSM matrix using the "subtype B: X4/R5" (for C subtype we used the subtype C SI/NSI matrix). Besides, this application gets an automatically full expansion of your sequence. To test this application ten sequences randomly selected were used obtaining the same tropism interpretation in 9 cases. Conclusion: 1.We oversimplified the methods for tropism analysis unifying the bioinformatics tools used for determining it. 2. We had obtained excellent results using this application, but it is necessary to increase the number of sequences in our database to optimize results and minimize discordant results that are generated after entering the sequence of study.