CORECEPTOR PREDICTION BASED ON *ENV* V3 SEQUENCE IN PAIRED PBMC AND PLASMA SAMPLES.

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Background: HIV V3 has determinants of viral tropism. The '11/25' basic residue rule may predict tropism and bioinformatic tools have been developed, but specificity and sensibility limit its application. The analysis of other compartments may provide additional information useful to improve these methodologies.

Objective: To evaluate paired PBMC and plasma tropism HIV prediction using 11/25 rule and bioinformatics methods.

Material and Methods: DNA and RNA from HIV-1 partial *env* region from paired PBMC and plasma samples (n=34) were sequenced using BigDye^{TM} at ABI3100, manually edited at Sequencher software.Tropism was predicted based in positive amino acids at either 11 or 25 positions and submited to bioinformatics sites Geno2Pheno(http://coreceptor.bioinf.mpi-inf.mpg.de/)and WEBPSSM(http://indra.mullins.microbiol.washington.edu/pssm/)

Results: Mean age 40 yo, 71% males, 91% ARV treated with mean TCD4^{+} 307cell/mm^{3} and VL 4,90log .Assuming 11/25 rule as standard, 88% (30/34) showed concordant PBMC/plasma phenotype **(**27% X4 8/30 and 73% R5 22/30). Geno2Pheno2,5% and 20% were concordant to 11/25 rule in 87%(26/30) and 63%(19/30) respectively. PSSM 94%(15/16) concordance, 14 not analyzed due excess mixture. Among 4 discordant samples (all PBMC X4, plasma R5), 3/4 were predicted as X4 in plasma and PBMC and 1/4 with X4 only from PBMC by at least one other methods. GWGR motif at V3 was observed in 9/34(26%), all R5 at 11/25.

Conclusion: The evaluation of different tools may provide better genotype based tropism algorithms. Phenotype evaluation and clinical response to CCR5 antagonists drugs are needed to make the necessary adjustments and validate these methodologies.