



Patterns of resistance mutations in B versus (vs) non-B patients (p) with previous PI failure

S. De Wit¹, R. Boulmé², B. Poll¹, D. Konopnick¹, JC. Schmit², N. Clumeck¹

1 Saint-Pierre University Hospital, Belgium, 2 ABL Advanced Biological Laboratories and CRP-Santé, Luxembourg

BACKGROUND : Patterns of resistance mutations differ between B and non-B HIV-1 subtypes but few studies have compare these patterns in p. with previous treatment (T) failure including failure on PI containing regimen. The objective of this study is to evaluate the prevalence of mutations in the Reverse Transcriptase (RT) and the Protease genes in B vs non-B p. who have previously failed at least twice on treatment from which at least once on a PI containing regimen.

METHODS : 139 p. fulfilling the inclusion criteria who underwent sequencing were retrieved from the database. RT and PR sequencing was done by TruGene (VGI) and ViroSeq (ABI) sequencing kits and viral subtype characterisation by i-Subtyping (ABL), HIV-SEQ (Stanford) University and NCBI. Chi-square, Fisher's exact and Wilcoxon tests were used for comparison.

RESULTS : 79 p. were infected with B versus 60 with non-B subtypes. Most B p. were Caucasian (81%) homosexual (83%) males (78%) whereas most non-B p. were African (84%) heterosexual (78%) females (78%). T. history of both groups was similar in terms of mean duration of T.(7.65 vs 7.03 years), number (n) of previous failures, n. of failures on PI and exposure to each individual NRTI or PI. Duration of exposure to NRTI's was similar (6.6 vs 5.9y; p=ns) as well as exposure to Thymidine analogues (6.2 vs 5.3y; p=ns) TAM's were found in 80 vs 60 % (p=0.01) of the RT sequences (<= 2: 46 vs 58 %, 3-4: 48 vs 40 %, >=5: 6 vs 2 %). UPAM's were found in 72 vs 58 % (p=ns) of the PR sequences(<=2: 89 vs 95 %, >3: 11 vs 5 %).

CONCLUSIONS : Despite similar treatment history, and in particular, comparable exposure to NRTI's, patients infected with non-b subtypes seem to be less prone to develop TAM's. The clinical implication of this finding should be further explored

Abstracts