



Resistance Testing in HIV-1 Infected Patients Treated with Indinavir/Ritonavir 800mg/100mg BID After at Least One Protease Inhibitor-Based Therapy Failure

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BACKGROUND: To investigate the predictive value of resistance testing in patients (p.) who previously failed protease inhibitor (PI) therapy and were treated with a new regimen including indinavir (IDV) 800mg + ritonavir (RTV) 100mg BID.

METHODS: We identified p. who had had genotyping (TruGene), viral load (VL) measurement and from whom information on antiretroviral therapy (ART) was available. Resistance data were interpreted using the ViroScorer™ system (www.ablnetworks.com). Uni- and multivariate analyses were performed according to the Resistance Collaborative Group (RCG) data analysis plan (DAP). Number of PI failures were entered as a covariate and estimated odds-ratios (OR) and 95% confidence intervals (CI) were reported.

RESULTS : From 11/98 to 11/2000, 96 p. were enrolled. 70% were male, 60% Caucasian, 53% heterosexual and 51% had at least experienced 2 or more lines of PI therapy. VL (4.4 log cp/ml) and DAP genotypic sensitivity score (GSS=2) were comparable in both groups in p. with one PI failure (group1,(g1)) or more (group2, (g2)), whereas the median number of drugs previously received (g1 n=5, g2 n=9, p<.0001) and the median number of mutations (g1 n=5, g2 n=9, p<.006) were different. The number of new drugs, PI mutations and previous PI failures (dropouts considered as censored) were significant predictors of outcome (defined as VL<400copies/ml at month 6) in the univariate (OR=.59, CI=.39-.92, p<.02; OR=1.33, CI=1.08-1.63, p<.006; OR=2.84, CI=1.20-6.76, p<.02 respectively) and in the multivariate (OR=.51, CI=.29-.89, p<.02; OR=1.47, CI=1.16-1.86, p<.001; OR=2.64, CI=1.09-6.43, p<.03 respectively) model. In contrast, the GSS was not a significant predictor of response.

CONCLUSIONS : In this study, the number of PI mutations, new drugs and lines of PI failures were significant independent predictors of outcome but not the interpreted genotype. The data support the use of viral genotype information but in conjunction with ART history.

Abstracts