

Open Access

O122. Calibration and accuracy of the geno2pheno co-receptor algorithm for predicting HIV tropism for single and triplicate measurements of V3 genotype

Table 1

LC Swenson, D Knapp, PR Harrigan*

From Tenth International Congress on Drug Therapy in HIV Infection Glasgow, UK. 7-11 November 2010

Background

The geno2pheno algorithm (g2p) can give dichotomous tropism based on a selectable "false positive rate" (FPR), reflecting the proportion of individuals inappropriately called "non-R5" and falsely excluded from taking CCR5 antagonists. The effect of replicate genotype measures and different FPR values remains controversial. Here we characterize different FPR "cut-points" in predicting tropism for single vs multiple replicates for interpreting V3 genotype based on data from the clinical trials of Maraviroc (MVC) in experienced patients.

Methods

The first study population comprised all patients screened for MOTIVATE 1 (N=1399; 44% non-R5 by original Trofile) for whom both triplicate and single V3 genotypes were available. We also examined virological response (defined as a week 8 decrease ≥ 2 logs and/or to <50 copies/ml) in an outcome dataset of 547 patients who received MVC+optimized background therapy in the MOTIVATE-1, 2 or A4001029 studies with very limited background antiviral activity from other agents (wSS <1).

Results

Triplicate sequence analyses typically identified 10-25% more individuals with non-R5 virus compared to single replicates. A comparison of the predicted FPR by g2p to the virologically defined FPR at different g2p cut-points showed an excellent correlation (r2 =0.99; see Table 1),

BC Centre for Excellence in HIV/AIDS, Vancouver, Canada

Full list of author information is available at the end of the article

MOTIVATE-1 Screening Virological Outcome Set (N=1399) (N=547) G2p Number non-Rf Number Non-Rf Actual FPR FPR (single) (triplicate) (single) (triplicate) (single) (triplicate) 1 100 114 6 9 06 06 2 241 288 25 36 1.3 1.3 2.3 3 303 368 39 47 26 4 427 48 3.6 4.2 362 57 5 396 459 52 64 45 52 5.75 57 423 486 71 6.1 7.4 6 433 496 62 77 68 84 7 476 533 71 89 84 100 8 507 563 78 98 97 117 9 548 605 88 114 12.0 139 10 562 620 89 116 12.3 13.9 15 715 646 132 161 21.4 23.6 20 742 805 174 205 28.5 32.4

but appeared to be calibrated conservatively (slope =1.5 for single assays or 1.7 for triplicate assays). Some of this miscalibration likely reflects a contribution from background therapies. For comparison, the FPR of Tro-file in this population was 3.9% (N=49 DM patients).

Conclusions

The g2P algorithm shows the expected association with observed virological response, but this testing procedure may be more conservative than expected from the nominal FPR values, particularly for triplicate sequence analysis. A g2p FPR value above 10 likely



© 2010 Harrigan et al; licensee BioMed Central Ltd. This is an open access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/2.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited. excludes too many individuals who could respond to therapy if this cut-off is employed to screen individuals for maraviroc.

Published: 8 November 2010

doi:10.1186/1758-2652-13-S4-O8

Cite this article as: Swenson *et al.*: **O122. Calibration and accuracy of** the geno2pheno co-receptor algorithm for predicting HIV tropism for single and triplicate measurements of V3 genotype. *Journal of the International AIDS Society* 2010 **13**(Suppl 4):O8.

Submit your next manuscript to BioMed Central and take full advantage of:

- Convenient online submission
- Thorough peer review
- No space constraints or color figure charges
- Immediate publication on acceptance
- Inclusion in PubMed, CAS, Scopus and Google Scholar
- Research which is freely available for redistribution

BioMed Central

Submit your manuscript at www.biomedcentral.com/submit