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Your abstract entitled [**Antiretroviral Phenotypic Susceptibility Score as a Predictor of Treatment Response in Persons with Multidrug-Resistant HIV-1**] has been submitted. Please keep this confirmation until you receive your disposition via email on or around November 20th.

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Contact Information

Dr. Jody Lawrence, M.D.
Assistant Clinical Professor of Medicine
Univ. of California, San Francisco
3180 - 18th St.
Suite 305
San Francisco, CA, 94110 US

Phone: (415) 514-0550, ext. 402

Fax: (415) 476-6736

E-mail: jlawrence@php.ucsf.edu

Category, Keywords and Other Information

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Presented or Published Before?	No
Conflict of Interest	Yes
Conflict(s)	Several of the named co-authors are employed by Monogram Biosciences, the producer of the phenotyping susceptibility test (PhenoSense) mentioned in this abstract.
Young Investigator	No
International	No

Abstract Information

Title	Antiretroviral Phenotypic Susceptibility Score as a Predictor of Treatment Response in Persons with Multidrug-Resistant HIV-1
Authors and Affiliations	<p>Jody Lawrence*¹, Katherine Huppler Hullsiek², Eoin Coakley³, Michael Bates³, Jodi Weidler³, Yolanda Lie³, Rick Pesano³, Lisa Thackeray², John Baxter⁴, and the 064 Study Team of the Terry Beinr Community Programs for Clinical Research on AIDS</p> <p>Univ. of California, San Francisco, CA, USA¹~ Univ. of Minnesota, Minneapolis, MN, USA²~ Monogram Biosciences, South San Francisco, CA, USA³~ and Cooper Hospital/RWJ Medical School, Camden, NJ, USA⁴</p>
Body	<p>Background: Methods for optimizing treatment and improving virologic suppression in HIV-1 infected patients with multidrug-resistant (MDR) virus are greatly needed.</p> <p>Methods: CPCRA 064 studied HIV+ antiretroviral (ARV) treatment experienced patients with virologic failure and MDR virus who switched to a new (optimized) salvage regimen (enrollment 8/2000-6/2002). Here we characterize the baseline susceptibility to the new regimen chosen at entry in the control (no-STI) arm. Using original genotypic data (CPCRA interpretive algorithm) and phenotypic data (PhenoSense) obtained retrospectively, a value was assigned for each drug in the new regimen (1 if sensitive, 0.5 if intermediate, and 0 if resistant). An incremental phenotypic susceptibility score (iPSS) was defined as the sum of these values according to phenotype; iGSS was defined similarly according to genotype. A dichotomous phenotypic susceptibility score (dPSS) was defined by summing only those drugs to which the virus was fully sensitive by phenotype. To estimate the changes in HIV RNA at months 2 and 4, univariate and multivariate linear regression models were created with dPSS, iPSS and iGSS as predictors. All models were adjusted for baseline HIV RNA.</p> <p>Results: N=110 patients. At baseline, mean CD4=182 cells/mm³, nadir CD4=79, log₁₀ HIV RNA=5.0, # of previous ARVs used=10.5 and # of ARV mutations=9. Mean # of drugs in the new regimen=3.9. Mean dPSS, iPSS and iGSS for the new regimen were 1.28, 1.85 and 1.78, respectively. At months 2 and 4, mean changes in log₁₀HIV RNA were a decrease of 0.95 and 0.90, respectively. For change in HIV RNA at both time points, dPSS, iPSS and iGSS were all significant predictors in univariate models. The model with iPSS had the highest R² value. The univariate model with iPSS as a predictor was not significantly improved by adding either iGSS or dPSS to the model. However, the univariate model with iGSS as a predictor was significantly improved by adding iPSS to the model.</p> <p>Conclusions: The iPSS of the new salvage regimen was the strongest single predictor of virologic response among the resistance measures analyzed. Adding iPSS to the iGSS model improved the predictive response compared to iGSS alone. These data suggest that for patients with MDR HIV-1 treatment failure and limited effective treatment options the use of phenotypic susceptibility scoring may provide added benefit in the selection of new drugs which may result in improved treatment responses.</p>