WORKSHOP ON QUANTITATIVE METHODS FOR RESEARCH ON ANTIVIRAL RESISTANCE May 11-12, 2006 Boston, MA

Sponsored by the Forum for Collaborative HIV Research With special support from Vircolab Inc, GlaxoSmithKline, and Bayer Health Care Diagnostics

Workshop Chairs: Dominique Costagliola & Victor DeGruttola

Organizing committee members: Lee Bacheler, Francoise Brun-Vezinet, Ben Cheng, David Hall, Richard Haubrich, Veronica Miller, Mark van der Laan

PROGRAM OVERVIEW

SESSION 1 Setting the Stage	May 11	8:00 - 9:30
SESSION 2 Definitions, Cut-offs and Metrics	May 11	9:45 - 1:00
SESSION 3 Predictions and Validations	May 11	2:00 - 4:30
Poster Session	May 11	4:30 - 5:30
SESSION 4 Quantitative Analysis in Drug Development	May 12	8:30 - 10:00
SESSION 5 Data Management and Integration	May 12	10:15 - 11:20
FINAL DISCUSSION	May 12	11:20 - 12:30

Session 1: Setting the Stage Moderators: V DeGruttola, F Brun-Vezinet

8:00	Welcome	V DeGruttola
8:05	Introduction to the Forum's program on HIV drug resistance	V Miller
8:15	What are the scientific and clinical questions for which sophisticated quantitative methods are needed?	F Brun-Vezinet R Haubrich
8:45	Methodological Challenges in Modeling the Development and Consequences of HIV Drug Resistance	D Costagliola V DeGruttola
9:15	Discussion	

Coffee Break 9:30-9:45

Session 2: Definitions, Cut-Offs & Metrics Moderators: D Costagliola & R Haubrich

9:45	Genotype analyses: issues in metrics and data reduction	P Flandre
10:00	<u>A1</u> Testing for quantitative interaction between subtype and amino acid mutations induced by selective drug pressure	DT Dunn
10:15	<u>A2</u> Explorative analysis for the development of a score-based interpretation system to predict abacavir susceptibility using the FCHR database	A Cozzi-Lepri
10:30	<u>A3</u> The evolutionary potential of HIV predicts response to antiretroviral therapy	N Beerenwinkel
10:45	Discussion	
11:15	Phenotype analysis: issues from a virology perspective	L Bacheler
11:30	Phenotype analysis: issues from a statistician's perspective	C Chappey
11:45	<u>A4</u> Prediction of HIV-1 drug susceptibility phenotype from the viral genotype by linear regression modeling	H Vermeiren
12:00	<u>A5</u> Effect of selection bias due to lack of resistance in the study population on Virco®TYPE clinical cutoff estimates for new drugs	B Winters
12:15	Inhibitory Quotient: issues in analysis	D Kempf
12:30	Discussion	
	Lunch 1:00 – 2:00	

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Session 3: Predictions & Validation Moderators: D Hall, V DeGruttola

2:00	Approaches to validations	M Van der Laan
2:30	<u>A6</u> Variable importance measures to rank the effects of viral mutations on clinical virologic response	ML Petersen
2:45	<u>A7</u> Resampling-based multiple testing methods with covariate adjustment: application to investigation of antiretroviral drug susceptibility	Y Yang
3:00	<u>A8</u> Comparing HIV-1 genotype-phenotype models using the minimum description length principle	RJ Murray
3:15	<u>A9</u> Predicting in vivo evolution of HIV under treatment based on mutation, fitness and epistasis as first principles	K Deforche
3:30	<u>A10</u> Developing methodologies which combine in-vitro and in-vivo data: a Bayesian approach to predicting resistance to combination therapy	F Lewis
3:45	Discussion	
Refreshments & Poster Presentations		
	All workshop abstract presentations	

All workshop abstract presentations <u>P1</u> Emergence of drug resistance is associated VD Lima with an increased risk of death among patients first starting HAART <u>P2</u> Use of HIV-1 genotype interpretation system (Retrogram) enables prediction of the viral response in HIV-1 infected patients AMJ Wensing

Session 4: QUANTITATIVE ANALYSES IN DRUG DEVELOPMENT MODERATORS: V MILLER, R HAUBRICH

8:30	The pharmaceutical perspective on quantitative analysis in drug development	R Demasi D Hall
9:00	FDA perspective: challenges of incorporating HIV resistance data into package inserts	L Naeger
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9:30 Discussion

Coffee Break 10:00 – 10:15

Session 5: Data Management & Integration Moderators: L Bacheler, D Costagliola

10:15	Data management & integration issues	B Lober
10:45	A11 HIV resistance analysis using HyPhy	SL Kosakovsky Pond
10:55	<u>A12</u> Resolving the problem of multiple reference sequences in the UK HIV drug resistance database	EL Fearnhill
11:05	Discussion	

Final Discussion Session Moderators: V DeGruttola, V Miller

- 11:20Recap and ConsensusAll
- 12:30 Workshop Adjourned