1281. Emergence of a B/F1 HIV Recombinant in the Philippines: A Potentially New Circulating Recombinant Form

Brian Schwem, PhD; Nina Dungca, MS; Geraldine Arevalo, BS; Christian Francisco, MD, FPCP; Christine Penalosa, MD; Katerina Leyritana, MD; Raul Destura, MD, FPCP, FIPMID; Rosario Tacutacan-Abrenica, MD; Elizabeth T. Rongene Solante, MD; and Edsel Maurice Salvana, MD, DTM&H, FIDSA 1,2,3; 1Institute of Molecular Biology and Biotechnology, National Institutes of Health, University of the Philippines (UP-NIH), Manila, Philippines, 2Department of Medicine, Section of Infectious Diseases, University of the Philippines - Philippine General Hospital, Manila, Philippines, 3Sustained Health Initiatives of the Philippines (SHIP), Mandaluyong City, Philippines, 4Philippine Genome Center, Quezon City, Philippines, 5Section of Infectious Diseases, University of the Philippines-Philippine General Hospital, Manila, Philippines, 6San Lazaro Hospital, Department of Health, Manila, Philippines, 7STD and AIDS Cooperative Center Laboratory (SACCLI), San Lazaro Hospital, Department of Health, Manila, Philippines

Session: 141. HIV: Molecular Epidemiology
Friday, October 5, 2018: 12:30 PM

Background. The Philippines has one of the fastest growing HIV epidemics globally. This was accompanied by a switch from subtype B to CRF01_AE. With a large population of returning overseas workers, new subtypes are being introduced regularly. Because diagnosis of HIV in the Philippines is usually late, superinfections can occur and may give rise to new circulating recombinant forms (CRFs). We propose a new CRF from the Philippines.

Methods. Following institutional board approval, treatment-naive patients from two HIV treatment hubs (San Lazaro Hospital and the Philippine General Hospital) were recruited. Blood samples underwent Sanger sequencing of the PR and RT regions and next-generation sequencing (NGS) of near-full length genomes. Sequences were analyzed for recombination using the online tool jumping profile Hidden Markov Model (http://jphmm.gobics.de/).

Results. 247 samples underwent Sanger sequencing of the PR and RT regions of the pol gene. Phylogenetic analysis indicated a fraction of four of the samples. Further analysis showed all four samples had the same breakpoints at nucleotides 2875, 2996, and 3001 (HXB2 numbering). All four patients were male, MSM, with a mean age of 28 years old (24–32), and >10 sexual partners. Mean CD4 count was 464 cells/µL and median viral load was 2.6 × 10^5 copies/mL. Two patients had sex with foreigners. To get a better overall view of subtype composition, we performed NGS using Illumina HiSeq. NGS showed the majority of the genome to be subtype F1 with segments of subtype B inserted in the pol, vpu, and env genes. A blast analysis of the consensus new CRF genome showing subtype components.

Conclusion. Mutation and recombination contribute to the extensive genetic diversity of HIV. Understanding this is important in choosing treatment regimens, developing future vaccines, and pursuing epidemiological investigations. The emergence of a new CRF in the Philippines underscores the importance of conducting routine surveillance for new HIV recombinant forms.

1282. Detection of HIV Transmitted Drug Resistance by Next-Generation Sequencing in a CRF01_AE Predominant Epidemic

Edel Maurice Salvana, MD, DTM&H, FIDSA 1,2,3; Nina Dungca, MS; Teresilas Angat, BS; Katrina Leyritana, MD; Christian Francisco, MD, FPCP; Christine Penalosa, MD; Raul Destura, MD, FPCP, FIPMID; and Brian Schwem, PhD; 1Institute of Molecular Biology and Biotechnology, National Institutes of Health, University of the Philippines (UP-NIH), Manila, Philippines, 2Deparment of Medicine, Section of Infectious Diseases, University of the Philippines - Philippine General Hospital, Manila, Philippines, 3Philippine Genome Center, Quezon City, Philippines, 4Section of Infectious Diseases, University of the Philippines-Philippine General Hospital, Manila, Philippines

Disclosures. All authors: No reported disclosures.

Session: 141. HIV: Molecular Epidemiology
Friday, October 5, 2018: 12:30 PM

Background. We detected 123 DRMs in our study population (17.2% of all sequences). Prevalence of any DRM was comparable among risk groups and was highest among people from an endemic area (i.e., country with HIV prevalence ≥1%) (11/51, 21.6%). Nucleoside and non-nucleoside reverse transcriptase inhibitor (NRTI/NNRTI) resistance mutations were detected in 49 (7%) and 97 (13.6%) individuals, with the EF13 mutation being the most frequent. Frequency of DRM was comparable in clustering and non-clustering individuals (17.1% vs. 17.5%). Transmission network analysis indicated that the frequency of DRM in clustering individuals was the highest in PWID (57/3, 42.9%) (Figure 1A). Genetically linked individuals sharing DRMs were more likely to live in the same area than in Central Cologne (18.8% vs. 8% of clustering sequences with DRM; Figure 1B).

Conclusion. The rate of DRMs was exceptionally high in the Cologne/Bonn area. Network analysis elucidated frequent cases of shared DRMs among genetically linked individuals, revealing the potential spread of DRMs and the need to prevent onward transmission of DRM in the Cologne/Bonn area.

1283. Pretreatment HIV-1 Drug Resistance in Transmission Clusters of the Cologne-Bonn Region, Germany

Melanie Stecher, MSc. Public Health; 2Martin Hoengl, MD; 3Anna-Maria Eis-Hubinger, Prof; 1Clara Lehmann, PD Dr. Med; 1,2Gerd Fatkenheuer, Univ.-Prof. Dr. Med.; 1,2Christian Wacker, Prof; 1Sanjay Math, Prof; 1,2Jörg Tschäpe, PD; 2German Center for Infection Research, Cologne-Bonn, Cologne, Germany, 3University Hospital of Cologne, Cologne, Germany, 4University of California San Diego, San Diego, California, 5University Hospital of Bonn, Bonn, Germany

Disclosures. All authors: No reported disclosures.

Session: 141. HIV: Molecular Epidemiology
Friday, October 5, 2018: 12:30 PM

Background. In Germany, previous reports have demonstrated transmitted HIV-1 drug resistance mutations (DRM) in 10% of newly diagnosed individuals, affecting treatment failure and the choice of antiretroviral therapy (ART). Here, we sought to understand the molecular epidemiology of HIV DRM transmission throughout the Cologne-Bonn region, an area with one of the highest rate of new HIV infections in Europe (13.7 per 100,000 habitants).

Methods. We analyzed 714 HIV-1 ART naïve infected individuals diagnosed at the University Hospitals Cologne and Bonn between 2001 and 2016. Screening for DRM was performed according to the Stanford University Genotypic Resistance Interpretation. Shared DRM were defined as any DRM present in genetically linked individuals (<1.5% genetic distance). Phylogenetic and network analyses were performed to infer putative relationships and shared DRMs.

Results. We detected 123 DRMs in our study population (17.2% of all sequences). Prevalence of any DRM was comparable among risk groups and was highest among people from an endemic area (i.e., country with HIV prevalence ≥1%) (11/51, 21.6%). Nucleoside and non-nucleoside reverse transcriptase inhibitor (NRTI/NNRTI) resistance mutations were detected in 49 (7%) and 97 (13.6%) individuals, with the EF13A mutation in 29 (4.1%) and 103N in 11 (1.5%) being the most frequent. Frequency of DRM was comparable in clustering and non-clustering individuals (17.1% vs. 17.5%). Transmission network analysis indicated that the frequency of DRM in clustering individuals was the highest in PWID (57/3, 42.9%) (Figure 1A). Genetically linked individuals sharing DRMs were more likely to live in the same area than in Central Cologne (18.8% vs. 8% of clustering sequences with DRM; Figure 1B).

Conclusion. The rate of DRMs was exceptionally high in the Cologne/Bonn area.
Disclosures. M. Hoenigl: Gilead, Basilea, Merck: Speaker’s Bureau, Research grant and Speaker honorarium.

1284. Study of Single Nucleotide Polymorphisms Associated with HIV-1 Set-Point Viral Load in Antiretroviral Therapy-Naïve HIV-Positive Participants of the START Study

Christina Elenberg, MD; Man-Hung Eric Tang, PhD; Daniel D Murray, PhD; Cameron MacPherson, PhD; Brad T Sherman, MSc; Marcelo Losso, MD; Robin Wood, MD; Roger Paredes, MD; Jean-Michel Molina, MD; Marie Helleberg, MD; Nureen Jina, MD; Casy M Kityo, MD; Eric Florence, MD; Mark N Polizotto, MD; James D Neaton, PhD; H. Clifford Lane, MD; and Jens D Lundgren, MD; 1Centre of Excellence for Health, Immunity and Infections (CHIP), Department of Infectious Diseases, Rigshospitalet, University of Copenhagen, Copenhagen, Denmark, 2Laboratory of Human Retrovirology and Immunoinformatics, Leidos Biomedical Research, Inc., Frederick National Laboratory for Cancer Research, Frederick, Maryland, 3Hospital General de Agudos JM Ramos, Buenos Aires, Argentina, 4Desmond Tutu HIV Foundation Clinical Trials Unit, Cape Town, South Africa, 5Infectious Diseases Service and mriCaixa AIDS Research Institute, Hospital Universitari Germans Trias i Pujol, Badalona, Spain, 6Department of Infectious Diseases, University of Paris Diderot, Sorbonne Paris Cité; Hôpital Saint-Louis, Assistance Publique-Hôpitaux de Paris, Paris, France, 7Clinical HIV Research Unit, Wits Health Consortium, Department of Medicine, University of the Witwatersrand, Helen Joseph Hospital, Thembu Lethu Clinical, Johannesburg, South Africa, 8Joint Clinical Research Center, Kampala, Uganda, 9Institute of Tropical Medicine, Antwerp, Belgium, 10Kirby Institute, University of New South Wales, Sydney, Australia, 11Division of Biostatistics, School of Public Health, University of Minnesota, Minneapolis, Minnesota, 12National Institute of Allergy and Infectious Diseases, Division of Clinical Research, Bethesda, Maryland

Session: 141. HIV: Molecular Epidemiology

Friday, October 5, 2018: 12:30 PM

Background. HIV-1 set-point viral load (SPVL) is predictive of disease progression and shows variability across HIV-1-positive (HIV+) persons. Various factors may influence SPVL including viral features, environmental exposure and host genetics. To identify single nucleotide polymorphisms (SNPs) associated with SPVL, we performed a genome-wide association study (GWAS) on a subset of participants from the Strategic Timing of AntiRetroviral Treatment (START) study covering a demographically diverse population.

Methods. Consenting participants were antiretroviral therapy (ART)-naïve and SPVL was taken as log₁₀ (HIV RNA) at study entry. Genotypic data were generated on a custom content Affymetrix Axiom SNP array covering 770,558 probes. The Ensembl Gene database, assembly GRCh37.p13, was used for annotation. Principal component analysis (PCA) was used to identify population structures, and analysis of variance (ANOVA) was performed independently on both subsets. Two SNPs were associated with SPVL. Additional SNPs were associated with SPVL.

Results. Among the 2,544 participants, PCA showed distinct population structures with strong separation between black (n = 578) and nonblack (n = 1,966) participants. Figure 1. ANOVA was performed independently on both subsets. Two SNPs associated with SPVL under the null hypothesis (P < 0.05) in non-black population: rs4418214 (P = 1.74 × 10⁻¹⁰) and rs57989216 (P = 3.96 × 10⁻⁶), Figure 2. Two additional SNPs, rs9264942 (P = 5.99 × 10⁻¹⁰) and rs7356880 (P = 9.69 × 10⁻¹⁵), in the same region approached significance. The minor alleles of all four SNPs were associated with lower SPVL, Figure 3. While no SNPs reached genome-wide significance in the black group, we observed similar trends toward lower SPVL for both rs4418214 and rs57989216.

Conclusion. In this study we confirm the association of a previously reported SNP, rs4418214, and identify a novel candidate SNP, rs57989216, associated with lower SPVL in a population of nonblack, ART-naïve HIV+ persons. Current findings suggest that the effects of these SNPs are consistent across race groups, but further studies are required to confirm this. Our results suggest future studies that variation in the MHC class I region is a major host determinant of HIV-1 control.

Disclosures. D. D. Murray, Centre of Excellence for Health, Immunity and Infectious diseases (CHIP), Department of Infectious Diseases, Rigshospitalet, University of Copenhagen, Copenhagen, Denmark: Employee, Salary. I. M. Molina, Gilead: Scientific Advisor, Consulting fee. Merck: Scientific Advisor, Consulting fee. ViiV: Scientific Advisor, Consulting fee. Teva: Scientific Advisor, Consulting fee.

1285. Impact of an Educational Program on Knowledge, Attitude and Practice to Prevent HIV Infection Among HIV-Negative Heterosexual Partners of HIV-Infected Patients

Thana Khawcharoenporn, MD, MSc; Chanika Sirrach, RN2 and Krongtip Chunloy, RN, MPH; 1Department of Medicine, Faculty of Medicine, Thammasat University, Pathumthani, Thailand, 2Thammasat University Hospital, Pathumthani, Thailand

Session: 142. HIV: Prevention

Friday, October 5, 2018: 12:30 PM