York, [7]Medicine, University of South Carolina School of Medicine, Greenville, SC, [8]Department of Medicine, Montefiore Medical Center, Bronx, New York

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Background. HIV and HCV are both treatable viruses for which routine screening among specific age cohorts is recommended. New York State requires patient consent prior to screening for HIV but not HCV. To estimate the impact of the consent requirement, we compared rates of HIV and HCV screening.

Methods. We performed a retrospective study of all adult patients admitted to a tertiary-care hospital in the Bronx, NY, between April 2015 and June 2016. During the study period, automated prompts in the electronic medical record facilitated screening for HIV among patients ages 21–64, and for HCV among patients born between1945-1965. We compared the proportions of patients qualifying for screening for HIV, HCV, or both who were appropriately screened prior to discharge to calculate an adjusted risk difference between performance of HIV and HCV screening. Using the local prevalence of undiagnosed HIV, we estimated the number of missed HIV diagnoses attributable to the difference in screening rates.

Results. A total of 21,413 unique hospitalized patients ages 21–64 and/or born between 1945–1965 were analyzed. Among those qualifying for screening for HIV alone or HCV alone, 39.7% and 58.6% were screened prior to discharge, respectively. Among those qualifying for both HIV and HCV screening, 6.7% were screened for HIV alone, 29.3% were screened for HCV alone, and 30.3% were screened for both. The risk difference between HCV and HIV screening adjusted for patient and admission characteristics was 22.0% (95% CI 20.6%-23.4%). Using an estimated prevalence of undiagnosed HIV of 0.2%, this risk difference corresponds to approximately four (95% CI 3.6–4.1) missed cases of HIV during the study period.

Conclusion. There was a large difference in the number of patients appropriately screened for HIV compared with HCV. While the requirement for consent was the only operational difference in performing routine screening for HIV compared with HCV, differences in how the two viruses are perceived may also have contributed to the observed difference in screening rates. Nevertheless, our findings suggest that removing the requirement for consent prior to HIV screening may increase the number of cases of previously undiagnosed HIV identified by routine screening.

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1279. Prevalence of HIV Among the Youth Aged 15–24 in Nigeria: A Need to Increase Access for Young Adolescents to HIV Counseling and Testing

Ezinne Ezenekwe, Medical student[1]; Nevis Essien Uduak, MBBS[2] and Catherine Nnamani, PhD[3]; [1]Windsor University School of Medicine, Cayon, Saint Kitts, [2]National Agency for Control of AIDS(NACA), Abuja, Nigeria, [3]Ebonyi State University, Abakaliki, Nigeria

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Background. Nigeria with a population of over 173 million people, HIV/AIDS remains a growing public health issue. The people living with the virus are about 3.2 million and it is observed that there is an increase of new infection among the adolescents and young people. We decided to study the prevalence of HIV among young people aged 15–24 in the country. The country was divided into six regions for the purpose of this study.

Methods. We adapted the secondary data that were collected from the report of the National HIV/AIDS and reproductive survey (NARSH 2012) on Prevalence of HIV/AIDS on adolescents and young people in Nigeria in 2012. Data collection on the survey were from the primary source documents in health facilities that offer HIV/AIDS services

Results. Among the six geopolitical zones, South–South zone has the highest (4.9%) prevalence rate of HIV infection among the adolescents and young people, more than the National median prevalence of 3.6%, while south -East has the lowest prevalence of (1.1%). Results showed that adolescent and young people, aged 20–24 had higher prevalence of 3.2% while ages 15–19 had prevalence of 2.9%. Results from the segregated data by sex showed that between the ages (15–24), the prevalence is higher (3.3%) with female gender than the male (2.4%) counterpart. HIV/AIDS in Africa and Nigeria in particular has a feminine face due to culture of silence, early child marriage and religious barriers that forbids female gender to discuss issues around sexuality or seek reproductive health services at age 15.

Conclusion. The age limit for access to HIV counseling and testing (HCT) should be adjusted to include young people who are sexually active as early as age 15. Findings revealed that the legal framework on access to HCT (HIV Counselling and Testing), of WHO at 18 years and above have created a barrier to young people who are below 18 and are active sexually to access HCT as the Health personnel would ask for the parental consent.

Disclosures. **All authors:** No reported disclosures.

1280. Geospatial Spread of HIV in the Cologne-Bonn Region, Germany: From 2001 to 2016

Melanie Stecher, MSc. Public Health[1,2]; Martin Hoenigl, MD[3]; Anna-Maria Eis-Huebinger, Prof.[4]; Clara Lehmann, PD Dr. Med.[1,2]; Gerd Fätkenheuer, Univ.-Prof. Dr. Med.[1,2]; Jan-Christian Wasmuth, MD[4]; Elena Knops, PhD[2]; Sanjay Metha, Prof.[3]; Janne Vehreschild, Prof. Dr. Med.[5] and Antoine Chaillon, MD, PhD[3]; [1]German Center for Infection Research, Cologne-Bonn, Cologne, Germany, [2]University Hospital of Cologne, Cologne, Germany, [3]University of California San Diego, San Diego, California, [4]University Hopital of Bonn, Bonn, Germany, [5]Department I of Internal Medicine, University Hospital of Cologne, Cologne, Germany

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Background. Geographical targeting of interventions of hotspots of HIV transmission increases the impact of HIV intervention. We combined molecular epidemiology and geospatial analyses to provide insights into the drivers of HIV transmission and the contribution of geographical hot spots to the rapidly evolving local HIV epidemic of Cologne-Bonn.

Methods. We included 714 HIV-1-infected ART naïve individuals, followed at the University Hospitals Cologne and Bonn between 2001 and 2016. Phylogenetic and network analyses were performed to infer putative relationships. Assortativity index (AI, i.e., shared attributes) and characteristics of genetically linked individuals were analyzed. The geospatial diffusion of the local epidemic (i.e., viral gene flow) was evaluated using a Slatkin-Maddison approach. Geospatial dispersal of local HIV transmission was determined by calculating the average distance between genetically linked individuals (centroids of 3-digit zip code of residency, ArcGIS®).

Results. Of 714 sequences, 217 (30.4%) had a putative linkage with at least one other sequence, forming 77 clusters (size range: 2–8). Genetically linked individuals were significantly more likely to live in suburban areas ($P = 0.035$), <30 years of age ($P = 0.013$), infected with HIV-1 subtype B ($P = 0.002$). AI for concurrent area of residency showed that individuals were nonassortative in the network (−0.0026, $P = 0.046$), indicating that clustering individuals tended to cluster with individuals living in a different zip code. Geospatial analyses revealed that the median distance between genetically linked individuals was 23.4 km, significantly lower than expected (median 39.68 km; $P < 0.001$) (Figure 1A). Slatkin Maddison analyses revealed increased gene flow originating from Central Cologne toward the surrounding areas ($P < 0.001$, Figure 1B).

Conclusion. Phylogeographic analysis suggests that central Cologne may be a significant driver of the regional epidemic. While clustering individuals lived closer than unlinked individuals, they were less likely to be linked to others from their same zip code. This may reflect individuals reaching out of their neighborhoods and social circles to meet new partners.

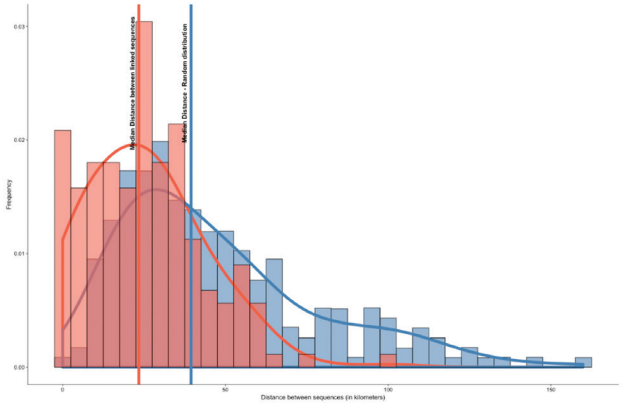

Figure 1. Median distance between linked sequences and a random distribution. The distance between linked sequences (median 23.4 kilometers (IQR 11.3-34.6) was significantly lower than the random distribution (median 39.68 kilometers, IQR 23.79-62.59, p<0.001).

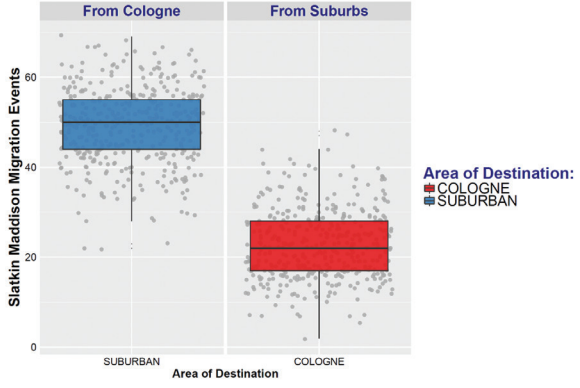

Figure 2. Viral gene flow between Central Cologne and the suburban areas. We used a Slatkin-Maddison approach on 1,000 of random subsets of equal number of sequences per location (Cologne vs. Suburban areas) to identify the diffusion of the epidemic. The HIV gene flow was significantly higher from central Cologne (p<0.001), illustrating the potential role of central Cologne as geographical hotspot in the spread of the local epidemic.

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

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

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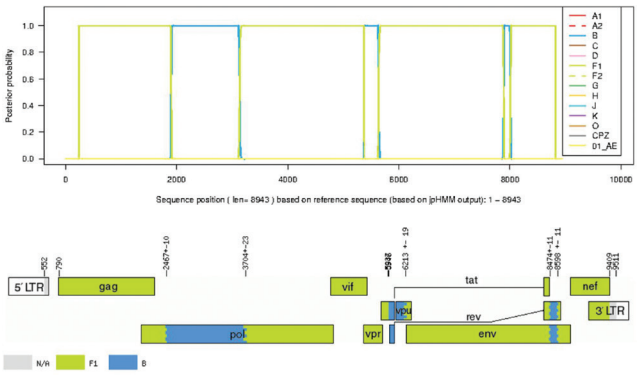
Background. The Philippines has one of the fastest growing HIV epidemics globally. This was accompanied by a switch from subtype B to CRF01_AE. With a large population of returning overseas workers, new subtypes are being introduced regularly. Because diagnosis of HIV in the Philippines is usually late, 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 clustering 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 2.67×10^4 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 sequence showed 8,932 out of 8,943 nucleotides (99%) matched a 1999 sample from Argentina. Phylogenetic analysis of these samples show clustering of the four B/F1 recombinants with some South American sequences. No drug resistance mutations were identified.

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 underlies the importance of conducting routine surveillance for new HIV recombinant forms.

Figure 1. New CRF genome showing subtype components.



Disclosures. **All authors:** No reported disclosures.

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

Edsel Maurice Salvana, MD, DTM&H, FIDSA[1,2,3]; Nina Dungca, MS[1]; Geraldine Arevalo, BS[1]; Katerina Leyritana, MD[4]; Christian Francisco, MD, FPCP[2]; Christine Penalosa, MD[2]; Raul Destura, MD[1,2,3]; Jodor Lim, MD, FPCP, FPSMID[5] and Brian Schwem, PhD[1]; [1]Institute of Molecular Biology and Biotechnology, National Institutes of Health, University of the Philippines (UP-NIH), Manila, Philippines, [2]Department of Medicine, Section of Infectious Diseases, University of the Philippines - Philippine General Hospital, Manila, Philippines, [3]Philippine Genome Center, Quezon City, Philippines, [4]Sustained Health Initiatives of the Philippines (SHIP), Mandaluyong City, Philippines, [5]Section of Infectious Diseases, University of the Philippines-Philippine General Hospital, Manila, Philippines

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Background. The Philippines has the fastest growing HIV epidemic in the Asia-Pacific. Concurrent with this is a subtype shift from B to CRF01_AE. We have previously documented transmitted drug resistance (TDR) locally. However, the lack of drug pressure and the insensitivity of Sanger-based sequencing (SBS) may leave archived drug-resistance mutations (DRMs) undetected. To better detect TDR, we performed next-generation sequencing (NGS) on treatment-naïve patients and compared this with SBS.

Methods. Following ethics approval, newly-diagnosed adult Filipino HIV patients were recruited from the Philippine General Hospital HIV treatment hub. Demographic data were collected, and blood samples underwent SBS with a WHO-approved protocol. Whole-genome NGS was performed using Illumina HiSeq through a commercial provider (Macrogen, Korea). Genotype and DRMs were analyzed and scored using the Stanford HIV Drug Resistance Database.

Results. 113 patients were analyzed. Median age was 29 years (range 19–68), mean CD4 count was 147 cells/μL (range 0–556) and median viral load was 2.8×10^6 copies/mL. Genotype distribution was: CRF01_AE (93), B (13), possible CRF01_AE/B recombinants (5), CRF02_AG (1), possible URF (1). TDR prevalence by SBS and NGS at different minority variant cutoffs are shown in Table 1. All DRMs on SBS were found on NGS. Some samples had multiple DRMs. No factors were significantly associated with TDR, genotype, viral load or baseline CD4 count.

Conclusion. NGS is a more sensitive tool for detecting TDR compared with SBS. Nearly double the DRMs were found at an NGS cutoff of ≥5%, including INSTI DRMs. With increasing HIV drug resistance worldwide, switching to NGS may help decrease rates of initial treatment failure, especially in settings with limited repertoires of ARVs.

Table 1. TDR Prevalence by SBS and NGS ($N = 113$).

Method		All (%)	NRTI (%)	NNRTI (%)	PI (%)	INSTI (%)
SBS		11 (9.7)	2 (1.8)	7 (6.2)	3 (2.7)	0 (0)*
NGS	≥1%	59 (52.2)	15 (13.3)	29 (25.7)	19 (16.8)	17 (15.0)
	≥2%	39 (34.5)	7 (6.2)	19 (16.8)	9 (8.0)	10 (8.8)
	≥5%	22 (19.5)	3 (2.7)	15 (13.3)	5 (4.4)	2 (1.8)
	≥10%	19 (16.8)	1 (0.9)	14 (12.4)	4 (3.5)	2 (1.8)
	≥15%	15 (13.3)	1 (0.9)	12 (10.6)	3 (2.7)	1 (0.9)
	≥20%	13 (11.5)	1 (0.9)	10(8.8)	2 (1.8)	1 (0.9)

*SBS for INSTI only done for those with INSTI DRM on NGS ≥ 1% minority variant

Disclosures. **All authors:** No reported disclosures.

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

Melanie Stecher, MSc. Public Health[1,2]; Martin Hoenigl, MD[3]; Anna-Maria Eis-Huebinger, Prof.[4]; Clara Lehmann, PD Dr. Med.[1,2]; Gerd Fätkenheuer, Univ.-Prof. Dr. Med.[1,2]; Jan-Christian Wasmuth, MD[4]; Elena Knops, PhD[2]; Sanjay Metha, Prof.[3]; Janne Vehreschild, Prof. Dr. Med.[1,2] and Antoine Chaillon, MD, PhD[3]; [1]German Center for Infection Research, Cologne-Bonn, Cologne, Germany, [2]University Hospital of Cologne, Cologne, Germany, [3]University of California San Diego, San Diego, California, [4]University Hopital of Bonn, Bonn, Germany

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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/NNNRTI) resistance mutations were detected in 49 (7%) and 97 (13.6%) individuals, with the E138A in 29 (4.1%) and K103N in 11 (1.5%) being the most frequent. Frequency of DRM was comparable in clustering and not clustering individuals (17.1% vs. 17.5%). Transmission network analysis indicated that the frequency of DRM in clustering individuals was the highest in PWID (3/7, 42.9%) (Figure 1A). Genetically linked individuals harboring shared DRMs were more likely to live in suburban areas 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.