

previously shown to influence the rate of fibrosis progression. Hepatic fibrosis change was determined using the serum-derived Enhanced Liver Fibrosis (ELF) Index. Four putative genes with polymorphisms that have been previously associated with the development or progression of hepatic fibrosis were evaluated using Taqman SNP genotyping assays. Cytokine assays were performed using Luminex chipsets. Samples were analyzed using Statistix 10.0 using ANOVA and least square regression models.

**Results.** 58 unique subjects were evaluated. The mean age was 38 years, and all were male. 74% were HIV infected and 97% were HCV infected (76.8% coinfection). Controlling for the effect of CCR5, only the TLR7 A -> G polymorphism was predictive of change in the ELF Index. There was no statistically significant predictive difference between genotypes in the other three polymorphisms. Subjects with the TLR7 A allele ( $n = 47$ ) had an average increase in ELF of 0.79 units, while the G allele ( $n = 11$ ) had an increase in ELF of 2.1 units ( $P = 0.008$ ). A regression model identified TLR7 as a key factor in ELF change, as well as HCV/HIV coinfection. Interferon alfa-2 levels were highly associated (increased,  $P = 0.0007$ ) with the TLR7 A -> G polymorphism, while RANTES levels were inversely associated (decreased,  $P = 0.0443$ ) with it.

**Conclusion.** Of the gene polymorphisms investigated, only TLR7 (rs179009) is an independent predictor of development of hepatic fibrosis in HCV/HIV coinfecting subjects. The mechanism may involve modulation of inflammatory response pathways.

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### 360. Advanced Liver Disease in HIV/Hepatitis B Coinfected Patients: Associated with Race, Age, and Comorbidities

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**Session:** 45. HIV Complications: Hepatitis Co-Infections  
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**Background.** Hepatitis B virus (HBV) coinfection is common in people with HIV. Compared with HBV mono-infected individuals, those that are HIV/HBV coinfecting show evidence of more rapid progression to advanced liver disease (ALD) and increased mortality rate. In this study, we identified characteristics in an HIV/HBV cohort associated with ALD.

**Methods.** We retrospectively examined an HIV/HBV coinfecting cohort to determine the prevalence of ALD and its correlation with selected variables. Data were drawn from HIV and HBsAg+ patients at three HIV clinics in Houston, Dallas, and San Antonio, Texas. Those without chronic HBV were excluded. ALD was defined as cirrhosis, decompensation, and/or hepatocellular carcinoma, as determined by imaging. Variables included demographics, HIV risk factors, comorbidities, HBsAg loss, HepBeAg, CD4+ count, HBV DNA, and HIV RNA viral load. Bivariate analysis was performed using chi-square and student t-test as appropriate; a logistic regression model was used to identify independent associations among significant variables (STATA).

**Results.** Within those with HIV/HBV coinfection ( $n = 501$ ), 89 (18%) met the criteria for ALD (92% male, 47% Black, 33% White, 16% Hispanic, 73% >40 years old). Amongst these ( $n = 89$ ), significant differences were observed with race ( $P = 0.039$ ), age ( $P = 0.001$ ), patients identified as MSM/Bisexuals ( $P = 0.047$ ), diabetes mellitus (DM) ( $P = 0.01$ ) and hepatitis C virus (HCV) coinfection ( $P \leq 0.001$ ). Compared with Whites, Blacks are less likely to have ALD (95% CI 0.27, 0.79,  $P = 0.004$ ), and those age 40-49 (95% CI 1.28, 10.92,  $P = 0.016$ ) and >50 (95% CI 1.63, 15.54,  $P = 0.005$ ) were more likely. The multivariate logistic regression analysis showed patients that are White race, age >50, have DM, and those with HCV coinfection had increased risk for ALD (Table 1). No differences were seen with gender, insurance, alcohol use, HBsAg loss, HepBeAg status or baseline CD4+ count, HBV DNA, HIV RNA, and AIDS.

**Conclusion.** Increased monitoring for the presence of ADL should be conducted in HIV/HBV coinfection. Particular attention and surveillance should be paid to those with the following risk factors: Whites, elder age (>50), and comorbidities of DM and HCV. These should be taken into consideration when approaching the development and treatment of ADL in HIV/HBV patients.

Table 1. Logistic Regression Analysis

Variables	Adjusted Odds Ratio	95% CI	P value
<b>Race/Ethnicity</b>			
White	Reference		
Black	0.51	0.29, 0.90	0.02
Hispanic	0.73	0.34, 1.55	0.41
Other	1.15	0.33, 3.98	0.82
<b>Age group</b>			
< 30 years	Reference		
30-39 years	1.46	0.46, 4.60	0.52
40-49 years	2.87	0.96, 8.63	0.06
>50 years	3.79	1.16, 12.38	0.03
<b>Diabetes</b>	1.98	1.02, 3.83	0.04
<b>Hepatitis C</b>	3.2	1.72, 5.94	<.001

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### 361. Residual Lamivudine-Resistant Hepatitis B Virus Detected on Next-Generation Sequencing of Treatment-Experienced HIV Patients Failing Antiretrovirals

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**Background.** Hepatitis B is highly prevalent in the Philippines, with 17% of the population infected. With the fastest-growing HIV epidemic in the Asia-Pacific, 12% of HIV patients are HBsAg reactive. With the use of lamivudine and tenofovir-based antiretrovirals (ARVs), hepatitis B virus (HBV) treatment in co-infected HIV patients is not usually an issue. However, there is a potential to develop HBV resistance when patients are switched off tenofovir when antiretroviral resistance develops. With high rates of acquired K65R tenofovir resistance, the potential for inadvertently causing re-emergence of lamivudine-resistant HBV is present. We report two HIV patients with residual whole-genome HBV with lamivudine and telbivudine resistance mutations.

**Methods.** As part of a surveillance study on acquired drug resistance in the Philippines, samples with an HIV viral load >1,000 copies underwent Sanger sequencing of RT and PR for genotyping and HIV drug-resistance testing. Near-whole-genome next-generation sequencing (NGS) for HIV using Illumina HiSeq was also performed on these samples.

**Results.** Two patients had coincidental whole-genome amplification of HBV on NGS (Table 1). HBV serology for both showed reactive anti-HBsAg and non-reactive HBsAg and Anti-HBc. The two HBV samples were genotype A and were resistant to lamivudine and telbivudine, with intermediate resistance to entecavir.

**Conclusion.** Residual HBV may be present in patients on ARVs. Antibody responses for HBV serology may not be very reliable in highly immunosuppressed patients. The potential of lamivudine-resistant HBV to emerge when HIV patients are shifted off tenofovir due to resistance in patients should be considered when deciding on second-line ARVs.

Table 1. Patient characteristics and viral mutations.

	Case 1: 22/M	Case 2: 42/M
Baseline CD4 count (cells/mm <sup>3</sup> )	269	45
Nadir CD4 count (cells/mm <sup>3</sup> )	7	45
Baseline HIV viral load (copies/mL)	101,000	97,000
HIV genotype	PR: CRF01_AE RT: CRF01_AE	PR: CRF01_AE RT: CRF01_AE
HIV mutations	NRTIs: K65R  NNRTIs: G190A, Y181C, Y188L  PIs: none	NRTIs: K65R, D67N, M184I  NNRTIs: G190Q  PIs: none
Initial ART Regimen	tenofovir/lamivudine/efavirenz	tenofovir/lamivudine/efavirenz
Revised ART Regimen	zidovudine/lamivudine/lopinavir-ritonavir	zidovudine/lamivudine/lopinavir-ritonavir
HBV viral load (copies/mL, limit of detection is 179)	undetectable	undetectable
HBV Genotype	A	A
HBV mutations	L180M, M204, L223M, M247V	L180M, M204, L223M, M247V

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### 362. Hepatitis C Virus (HCV) Co-Infection in Women Living with Human Immunodeficiency Virus (HIV) in Northwest Louisiana

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**Background.** HIV and HCV infection are emerging global public health problems. People living with untreated HIV infection have higher HCV viral loads and more rapid HCV disease progression with twice the rates of perinatal HCV transmission. Data are lacking in HCV coinfecting women living with HIV. Our study reviewed underrepresented minority group of women living with HIV/HCV in Northwestern Louisiana to better understand epidemiology, risk factors and access to care among this cohort.

**Methods.** Women with HIV/HCV coinfection aged 18-70 years who presented to an academic medical center between November 2011 and November 2018 were included for analysis. A retrospective chart review was conducted. Data were collected and analyzed on demographics (age, race), risk factors (sexual history, drug use), HIV