6

young women (not in school/at work). The first author interviewed 4 local service providers. Thematic analysis relied on Nvivo.

Findings: The most vulnerable young women experience serious difficulties accessing government support programs. Lack of selfconfidence and ambiguous navigating procedures block institutional assistance. Long delays in processing applications and lack of feedback on application status are discouraging. Successful candidates experienced community-level barriers like third parties unwilling to collaborate. Although motivated to help young women, service providers complained about youth attitudes and behaviour negatively affecting support program success-rates. Agricultural support programs may be incompatible with ambitions of youth unwilling to stay in rural areas. Lack of financial, material, and human resources hamper effective assistance and follow-up of applicants. Lack of available program placements and funding contribute to delays in support. Despite their ideas for improvement, service providers believe that effective change depends on political will, and national-level coordination and direction.

Interpretation: The available programs involved at least five line ministries; lack of coordination results in service gaps, overlap and competition, contributing to confusion among clients. Local service providers could improve vulnerable young women's access to programs by providing targeted and accessible assistance in application procedures, followed by timely and transparent feedback on application status. Stakeholder-constructed solutions are needed to overcome identified structural barriers.

Source of Funding: Canadian IDRC grant nr: 107531-001.

Abstract #: LAN.007

Crowdsourcing to Promote HIV Testing among MSM in China: A Pragmatic Stepped Wedge Randomized Controlled Trial of a Crowdsourced Intervention

T. Zhang¹, W. Tang², T. SESH study group², J. Tucker³; ¹Loyola University Chicago Stritch School of Medicine, Forest Park, IL, USA, ²UNC Project-China, Guangzhou, China, ³University of North Carolina at Chapel Hill, Chapel Hill, NC, USA

Program/Project Purpose: Improving HIV testing for marginalized populations is critical to controlling the HIV epidemic. However, the HIV testing rate among men who have sex with men (MSM) in China remains consistently low. Crowdsourcing, the process of shifting individual tasks to a group, has been increasingly adopted to enhance public health programs and may be a useful tool for spurring innovation in HIV testing campaigns. We designed a multi-site study to develop a crowdsourced HIV test promotion campaign and evaluate its effectiveness against conventional campaigns among MSM in China.

Structure/Method/Design: The intervention was developed using crowdsourcing at multiple stages and is being evaluated with a stepped wedge randomized controlled trial (RCT). Intervention development consisted of a nationwide crowdsourcing contest followed by a designathon. The crowdsourcing contest solicited campaign content through an open call, judging, and recognition of finalist entries, which became materials for the designathon. The designathon adopted the concept of a hackathon and allowed individuals

to collaborate on designing a comprehensive HIV test promotion campaign. The design elements of the winning entry were included in a HIV test promotion campaign to be evaluated through a stepped wedge RCT. Eight major metropolitan cities in China will be randomized to sequentially initiate intervention in groups of two at 3-month intervals.

Outcome & Evaluation: 1347 MSM who are 16 years of age or over, live in the intervention city, did not have HIV testing in the past 3 months, and are not living with HIV were recruited. Recruitment took place through banner advertisements on a large gay dating app along with other social media platforms. The intervention is ongoing. Participants will complete one follow-up survey every 3 months for 12 months to evaluate their HIV testing uptake in the past 3 months as the primary outcome.

Going Forward: Our large-scale RCT can improve understanding of crowdsourcing's long-term effectiveness in public health campaigns, expand HIV testing coverage among a key population, and inform intervention design in related public health fields. This study has been registered on ClinicalTrials.gov (NCT02796963) and obtained IRB approvals from the Guangdong Provincial Center for Skin Diseases and STI Control, University of North Carolina at Chapel Hill, and University of California San Francisco.

Source of Funding: NIH (#1R01AI114310-01).

Abstract #: LAN.008

HIV Therapy without HBV Co-management in Ethiopia Fosters Emergence of Unintended HBV Drug Resistance and Vaccine Evasive Variants

Y.B. Akal¹, M. Maier², U.G. Liebert²; ¹University of Gondar, Gondar, Amhara Regional state, Ethiopia, ²Institute of Virology, Medical Faculty, Leipzig University, Germany, Leipzig, Germany

Background: Hepatitis B virus (HBV) drug resistance and vaccine escape gene mutants were determined in patients with human immunodeficiency virus (HIV) co-infection and antiretroviral therapy (ART) exposure of with unknown HBV status. Moreover, the reciprocal HIV drug resistance profiles were examined in HBV-HIV co-infected patients who developed HBV drug resistance.

Methods: A total of 161 hepatitis B surface antigen (HBsAg) positive sera from HIV co-infected with and without ART exposure and drug naïve HBV mono-infected individuals were characterized using direct sequencing.

Findings: In 35 out of 161 study subjects (21.7%) HBV drug resistance mutations (DRMs) were detected with a frequency of 1.2% rtT184S, 6.2% rtV173L, 10.6% rtL180M, 10.6% rtM204V/I and 8.1% rtI233V which confer resistance mainly for entecavir, lamivudine and adefovir. The prevalence of the major DRMs in HBV-HIV co-infected individuals (with no significance difference among ART status) was higher than mono-infected individuals (41.4% vs. 10.7%). In contrast, none of HIV-1 patients showed no nucleos(t) ide reverse transcriptase inhibitors (NTRIs) drug resistance. However, 62.5% of them developed non NRTIs resistance mutations which confer resistance to nevirapine, efavirenz, etravirine