Methods. We analyzed data for those referred to the PrEP program from 3/2018 to 2/2020. We determined the proportion of TGW who were linked to the program, provided a PrEP prescription, started PrEP, and persisted in PrEP care, defined as having at least one follow-up visit within 6 months. Using a multivariate regression model, including age, race, ethnicity, mental health co-morbidities, and substance use, we determined factors associated with persistence in PrEP care. We calculated rates of sexually transmitted infections (STIs) and HIV incidence.

Results. Of the 321 total referrals for PrEP, 42 (13%) were TGW. 81% of TGW were referred from a co-located gender clinic. Median age was 28.5 years (IQR 23-34), 62% were Black, 21% had mental health co-morbidities, 45% used substances, and 35% engaged in transactional sex. Of all TGW who were referred, 37 (88%) were eligible for PrEP and linked to care, 36 (85.7%) were prescribed and initiated PrEP, and 22 (52.4%) persisted in care at the end of the study period. There were no factors associated with persistence in PrEP care. The most common STIs during the first visit were pharyngeal gonorrhea (22.7%) and syphilis (16.7%). STI incidence was highest for rectal chlamydia (12.5%) and pharyngeal gonorrhea (6.5%). There was one HIV seroconversion during the study period.

Conclusion. In a public hospital-based PrEP clinic in Atlanta with a co-located gender clinic, TGW had high rates of linkage to care and PrEP prescription and initiation, despite high rates of mental health diagnoses and substance use. However, there was a significant drop-off in persistence. STI prevalence and incidence were high, but there was only one HIV seroconversion, highlighting the potential benefits of PrEP. Future studies are needed to assess interventions to optimize persistence in PrEP care among TGW.

Disclosures. Bradley L. Smith, PharMD, AAHIVP, Gilead Sciences, Inc (Advisor or Review Panel member)

974. The Effects of Changes in State-Level Policies Affecting Eligibility for the Supplemental Nutrition Assistance Program (SNAP) on Annual HIV Diagnoses in the United States

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Session: P-46. HIV: Prevention

Background. The connection between food insecurity and HIV outcomes is well-established. The Supplementary Nutrition Assistance Program (SNAP), the primary program in the United States that addresses food insecurity, may have collateral impacts on HIV incidence, but the extent to which it does is unknown. "Broad-based categorical eligibility" for SNAP is a federal policy that provides a mechanism for states to increase the income or asset limits for SNAP eligibility. The Department of Agriculture under the Trump Administration has proposed eliminating this policy.

Methods. We estimated the association between the number of new HIV diagnoses from 2010 to 2014 for each state and (1) state income limits for SNAP eligibility as a percentage of the federal poverty level and (2) state asset limits for SNAP eligibility (increased/eliminated vs. unchanged). We fitted multivariable negative binomial regression models with annual incidence of HIV diagnoses specified as the outcome; SNAP policies as the primary explanatory variable of interest; state and year fixed effects; and time-varying covariates related to the costs of food, health care, housing, employment, SNAP outreach, and total spending on Temporary Assistance for Needy Families (TANF) programs.

Results. From 2010 to 2014, 204,034 new HIV diagnoses occurred in the United States. HIV diagnoses within states had a statistically significant inverse association with state income limits for SNAP eligibility (IRR 0.94 per increase in the income limit by 35% of federal poverty level, 95% CI 0.91-0.98), but no statistically significant association with state asset limits (increased asset limit vs. no change, IRR 1.02, 95% CI 0.94-1.10; eliminated asset limit vs. no change, IRR 1.04, 95% CI 0.99-1.10) (Table).

Table

Table – The relationship between state-level policies affecting Supplementary Nutrition Assistance Program (SNAP) eligibility – income limit as a percentage of the federal poverty level (FPL) and asset limit, either increased or eliminated compared to unchanged – and the annual number of new HIV diagnoses from 2010 to 2014 using negative binomial regression models.

		Unadjusted		State/year fixed effects		Both policies, fixed effects, and time-varying covariates	
		IRR	95% CI	IRR	95% CI	IRR	95% CI
Income limit (per increase of 35% FPL)		1.11	1.01-1.23	0.95	0.92-0.98	0.94	0.91-0.98
Asset limit	No change	Ref		Ref		Ref	
	Increased	0.92	0.61-1.39	0.96	0.89-1.04	1.02	0.94-1.10
	Eliminated	1.23	0.99-1.53	0.98	0.94-1.03	1.04	0.99-1.10

Abbreviations: CI, confidence interval; FPL, federal poverty level; IRR, incidence rate ratio; SNAP, Supplementary Nutrition Assistance Program

Notes: Time-varying covariates include average meal cost in a food secure household, health expenditure per capita, house price index, high school graduation rate, unemployment rate, uninsured rate, state spending on SNAP outreach, and total Temporary Assistance for Needy Families (TANF) spending.

Conclusion. State income limits for SNAP eligibility were inversely associated with the number of new HIV diagnoses for states between 2010-2014. Proposals to eliminate the use of broad-based categorical eligibility to increase the income limit for SNAP may undercut efforts to end the HIV epidemic in the United States.

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

975. Why Sex Make a Difference in HIV Clinical Course? Bioinformatics Analysis of Differential Expressed Gene in Females and Males with HIV Disease

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Session: P-46. HIV: Prevention

Background. Human immunodeficiency virus (HIV) disease progression are different among genders, in which women usually progress to acquired immunodeficiency syndrome (AIDS) faster than men. The mechanisms resulting in the gender biases of HIV progression are unclear. We conducted a bioinformatics analysis of differentially expressed genes (DEGs) in women and men with HIV disease to understand the sex-based differences in HIV pathogenesis.

Methods. We obtained microarray data from the Gene Expression Omnibus (GEO) database using our pre-defined search strategy and analyzed data using the GEO2R platform. The t-test was done to compare DEGs between females and males with HIV diseases. The Database for Annotation, Visualization, and Integrated Discovery (DAVID) was implemented to systematically extract biological features and processes of retrieving DEGs via gene ontology (GO) analysis. A Systemic search was performed to evaluate each DEG function and its possible association with HIV.

Results. One gene expression profiling data were retrieved: GSE 140713, composed of 40 males and 10 females with HIV1 infected samples. A GEO2R analysis yielded 19 DEGs (Table 1). The GO analysis result was demonstrated in Tables 2 and 3. Following a systemic search, we found two DEGs, which have previous studies reported an association with HIV: DDX3X (20 studies) and PDS5 (1 study). We proposed DDX3X (t 5.3, p 0.0037) is responsible for gender inequalities of HIV progression because of: 1. DDX3X is needed in the HIV1 life cycle. 2. Several studies confirmed a positive correlation between DDX3X expression and HIV1 replication. 3. Our study found an up-regulated DDX3X expression in women corresponded to the fact that women progress to AIDS faster than men. 4. Our GO analysis showed female up-regulated genes were enriched in positive regulation of the gene expression pathway, which can be explained by DDX3X and its underlying mechanism.

Table 1: DEGs in women and men with HIV1 disease

Down-regulated genes in female compare to male with HIV1 disease				
Genes	Adjusted P value	t	B	logFC
RPS4Y2	1.74e-47	-69.61	58.56	-9.96
RPS4Y1	1.26e-44	-60.22	57.58	-9.21
UTY	7.62e-39	-45.75	54.97	-5.27
TXLNGY	2.84e-31	-31.75	49.4858	-5.073
DDX3Y	2.08e-25	-31.75	49.4858	-5.073
EIF1AY	5.47e-25	-23.75	43.24326	-7.96
KDM5D	5.04e-21	-23.19	42.66616	-6.036
ZFY	1.90e-20	-18.85	37.21756	-4.085
TTTY10	7.00e-08	-8.43	14.21921	-2.185
TTTY15	6.75e-07	-7.78	12.24742	-2.613
PRKY	4.29e-05	-6.6	8.54374	-1.449
TTTY14	8.23e-04	-5.73	5.82023	-1.038
Up-regulated genes in female compare to male with HIV1 disease				
XIST	1.06e-31	32.55	49.9428	11.789
EPB41L4B	6.71e-04	5.8	6.03312	1.507
DDX3X	3.73e-03	5.3	4.46087	0.798
PDS5B	5.62e-03	5.17	4.06903	1.663
HEPH	7.98e-03	5.06	3.72446	1.55
LANCL2	7.98e-03	5.05	3.70198	1.553
EIF1AX	1.48e-02	4.86	3.12847	0.562

Table 2: GO functional enrichment pathway analyses of overall retrieving DEGs

GO enrichment analyses of the DEGs
GO pathway: Biological process (BP)
- Translational initiation and Regulation of gene expression
- RNA secondary structure unwinding
- Chromosome segregation
- Oxidation-reduction
GO pathway: Cellular component (CC)
- Cytosolic small ribosomal subunit and Nucleus
GO pathway: Molecular function (MF)
- Histone demethylase activity
- ATP and rRNA binding
- Translation initiation factor activity
- ATP-dependent RNA helicase activity