2018 NATIONAL RYAN WHITE CONFERENCE ON HIV CARE & TREATMENT

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Using Standardization and Analysis of HIV Quality Measures Data to Identify Treatment Gaps and Disparities

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Learning Objectives

- Root cause analysis for improving patient care
- Best practices for improving clinical care using data standardization and analytic methods with HIV quality measures data
- Identification and evaluation of treatment gaps and health disparities in patient populations

Why Evaluate Community Viral Load?

- Viral load suppression is the ultimate measure of health for individuals living with HIV [1]
- Comparing viral load results over time or between groups requires evaluation of community viral load (CVL) – an average of all viral load results taken from among those in the populations compared
- CVL analysis is important in identifying disparities in HIV care outcomes

[1] White House Office of National AIDS Policy. (2015). National HIV/AIDS strategy for the United States: Updated to 2020. https://files.hiv.gov/s3fs-public/nhas-update.pdf

Barriers to Analysis

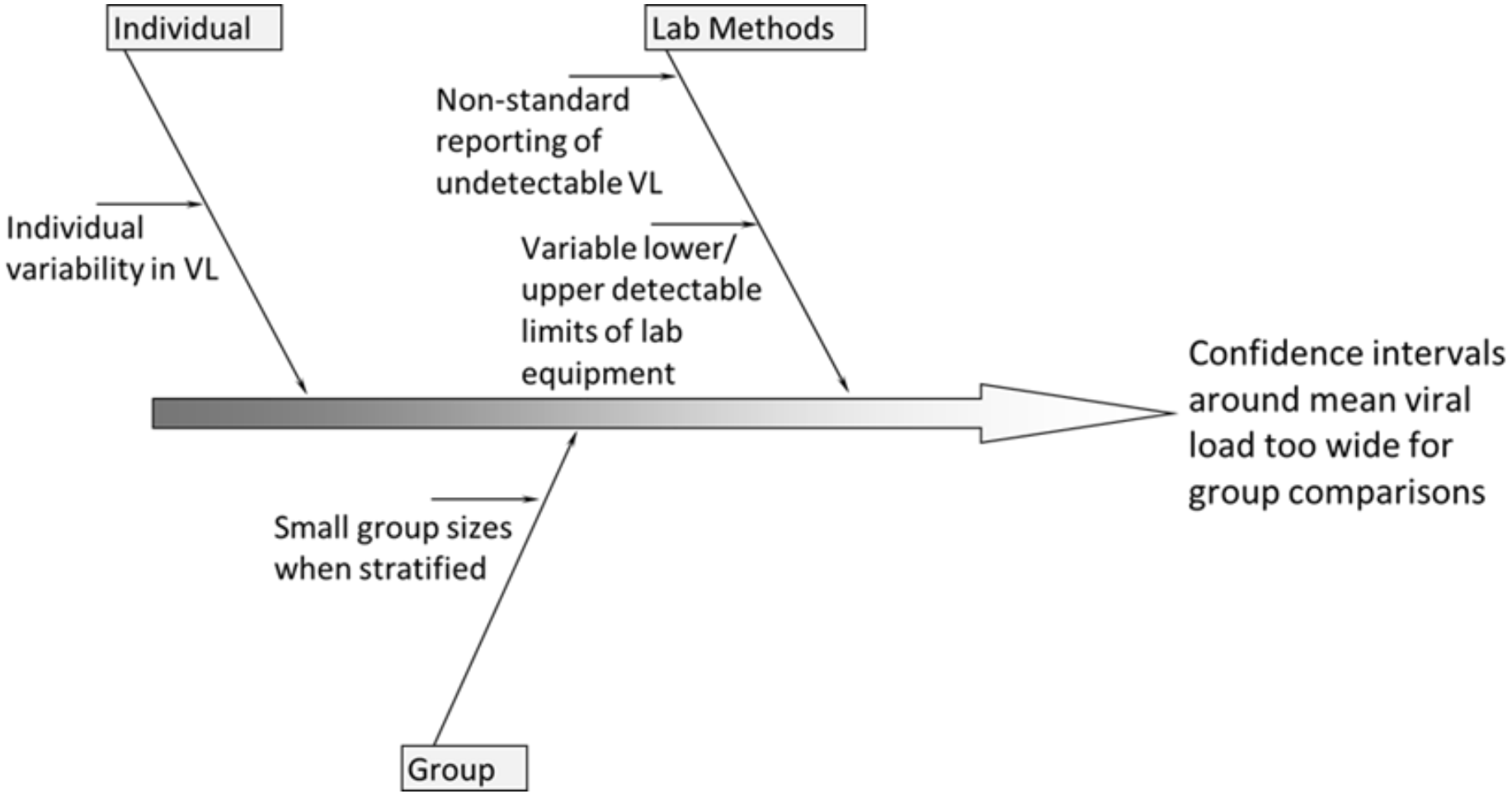
- The Ryan White/HIV Services Program in the Indianapolis transitional grant area (TGA) has historically evaluated viral load among residents, but confidence intervals were too wide for group comparisons

(*A confidence interval is a statistical measure of how sure we are about the results*)

Root Cause Analysis

- Root cause analysis was conducted during the 2016-2017 Part A grant year in order to identify the root causes of wide confidence intervals

Root Cause Analysis



Root Cause Analysis

- Findings:
  - Labs are not consistent in their instrumentation and reporting
  - HIV viral load varies widely from person to person and group to group

- Resolution:
  - Viral load results were standardized and evaluated in a manner that helped ensure that statistically significant comparisons could be made

New Analysis Procedures

- Standardization (CDC recommended [2]):
  - Lower and upper detectable limits (LDL and UDL) are collected from labs
  - Results lower than the LDL are standardized to a number equal to half the reported LDL
    - Exp. **Report of 0 from a lab with a LDL = 20 would be standardized to 10 c/mL**
  - Results higher than the UDL are standardized to a number of UDL + 1
    - Exp. **Report of >1,000,000 from a lab with a UDL = 750,000 would be standardized to 750,001 c/mL**
  - Where LDL and/or UDL are missing, results are standardized to the most commonly reported LDL and UDL values for the time period examined

[2] CDC. (2011). Guidance on community viral load: A family of measures, definitions, and method for calculation. https://stacks.cdc.gov/view/cdc/28147/cdc_28147_DS1.pdf

New Analysis Procedures

- Use of Geometric Mean (GM) versus Arithmetic Mean:
  - GM is a logarithmic transformation calculated by averaging the log transformed values of a set of viral load results
  - This calculated average is then transformed back to the original (linear) scale as it is a more intuitive value
    - *The base used for the log transformation has no effect on the final GM estimate; however, using log base 10 has an advantage by its relationship to the value on the original scale.*
    - Exp. **A value of 2 on the log10 scale = 100 on the original scale; 3 corresponds to 1,000; 4 to 10,000; and so forth.**
  - *It is important to note that GM is not a true viral load result and should not be construed as anything but a way to compare the viral load of different populations. Arithmetic mean should be provided to reduce confusion.*

Why These New Procedures?

- Normalizes data by reducing the influence of outlying values such as the extremely high viral loads seen in those newly infected
- Enables evaluation of data covering several orders of magnitude
- Tightens confidence intervals allowing statistically significant comparisons to be made

Our Analysis & Findings

SAS Program & R Program

- Originally developed using SAS Enterprise Guide 7.1 to compare geometric mean viral loads using Indianapolis TGA viral load data from eHARS
- Replicated in R 3.4.1 to provide open source option for partners to freely conduct their own analysis
- R program will be made available for use upon request

More Information on SAS and R

- SAS is a commercial software developed by SAS Institute with a strong variety of statistical evaluation methods, but can be cost-prohibitive for many organizations
- R is the open source alternative to SAS and is free for use with over 15,000 packages available for use in the Comprehensive R Archive Network (CRAN) commonly used with the RStudio integrated development environment (IDE)
- R and RStudio are available for download here: https://www.rstudio.com/products/rstudio/download/
- The list of all available R packages in CRAN is available here: https://cran.r-project.org/web/packages/available_packages_by_name.html
- Packages can be easily installed and loaded with two commands via the R shell. Example:
    - > install.packages("ggplot2")
      > library(ggplot2)

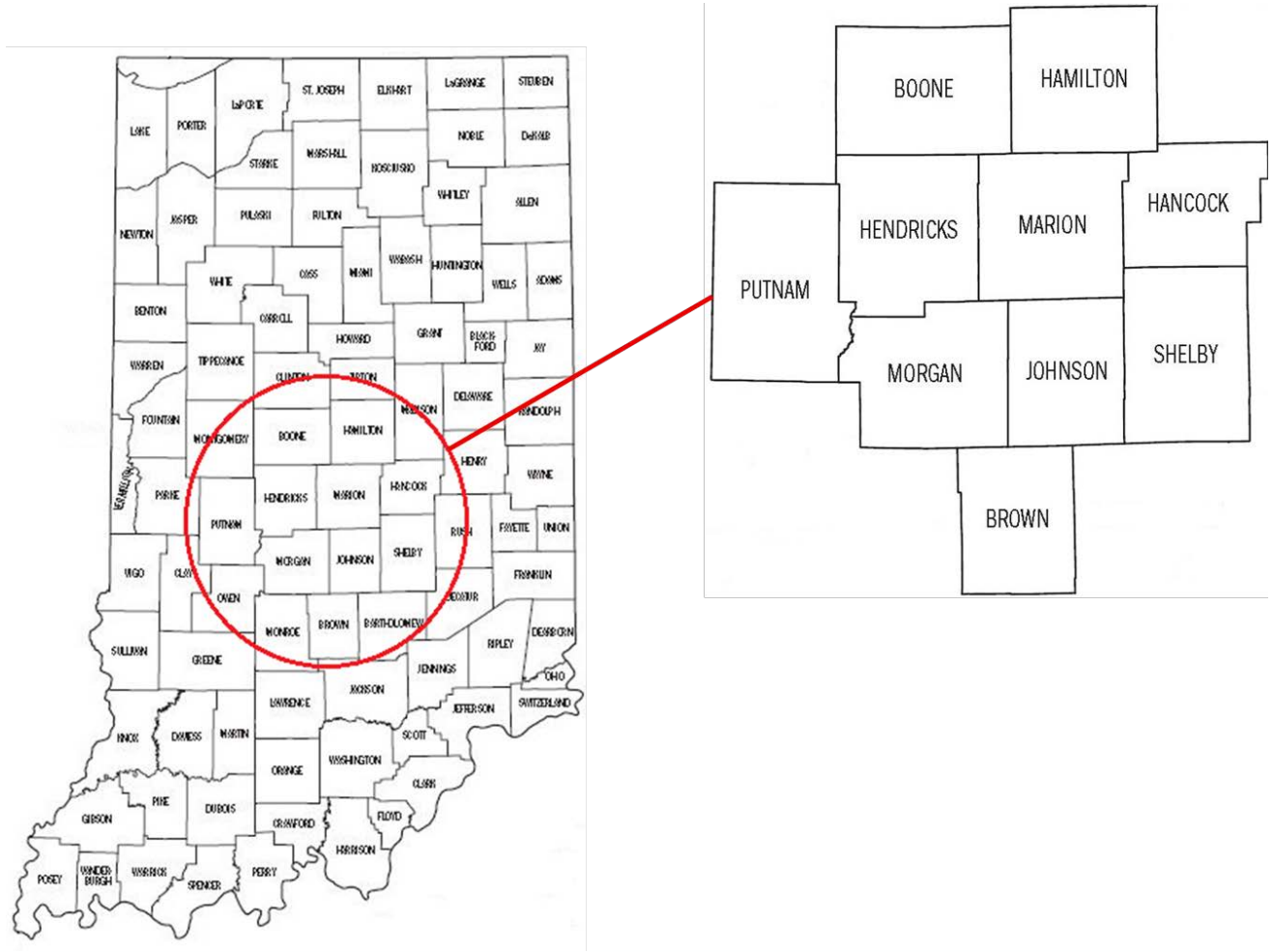
Input

- Standardized HIV data with year, viral load, and additional variables of interest for comparison such as county, retention status, birth sex, and race
    - We have utilized eHARS Person and Labs data for Indy TGA

Output

- Community arithmetic and geometric mean viral loads with 95% CI for variables known among all PLWH/A in the TGA and by following categories:
    - Race, Age, Gender, County, Risk, Retention in Care status, Ryan White status, and Facility

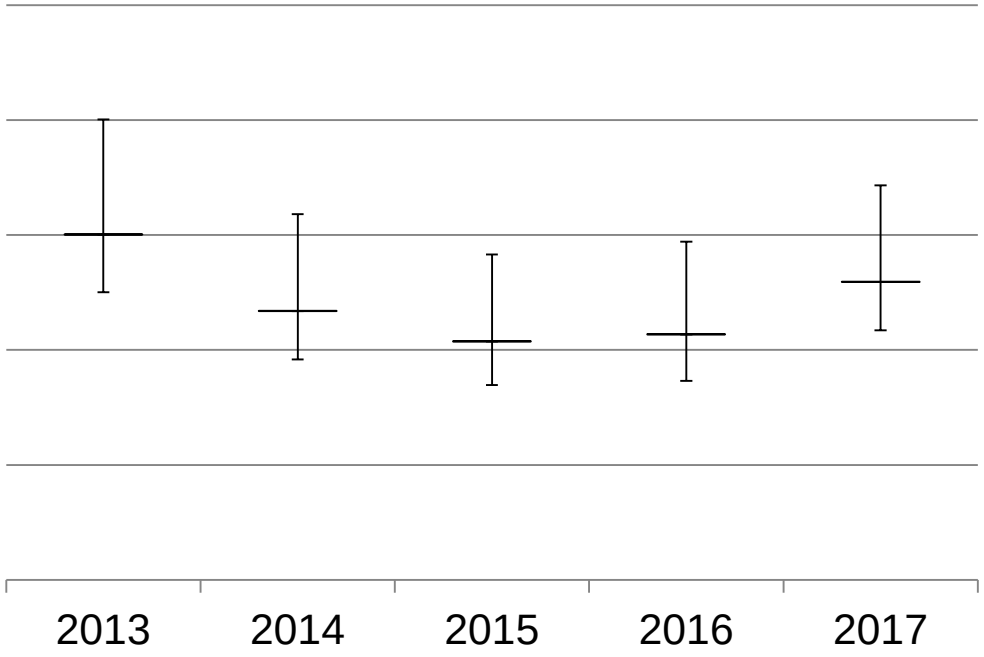
Geographic Area Included

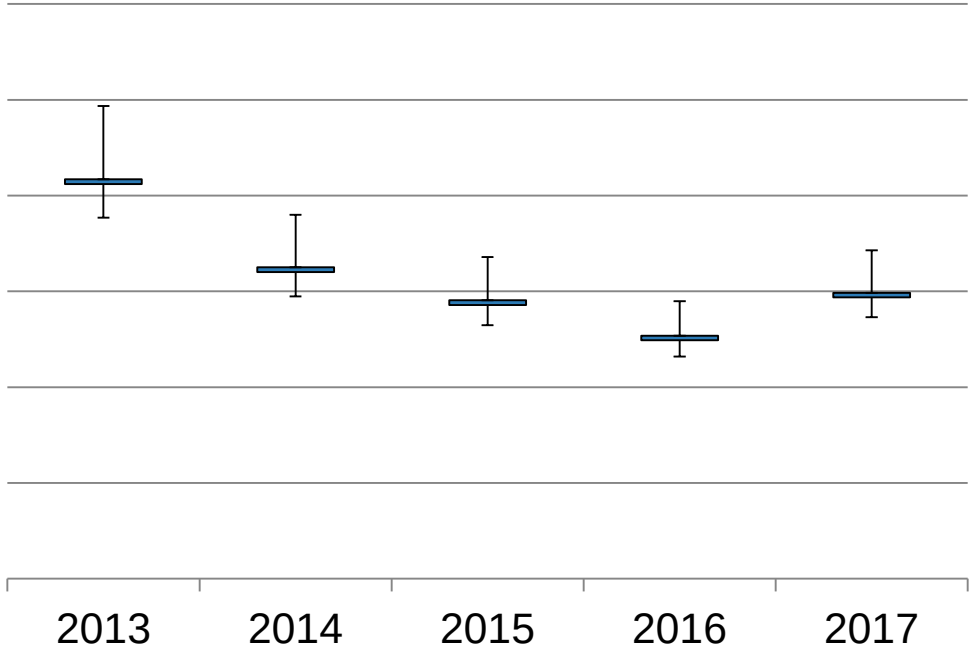


4,513 HIV-positive TGA residents who received HIV-related medical care at least once were included in the analysis

Arithmetic vs. Geometric Mean Results

- We can see that viral loads were *statistically* lower in 2017 than in 2013 using geometric mean (right). This difference would not have been identified using only arithmetic mean

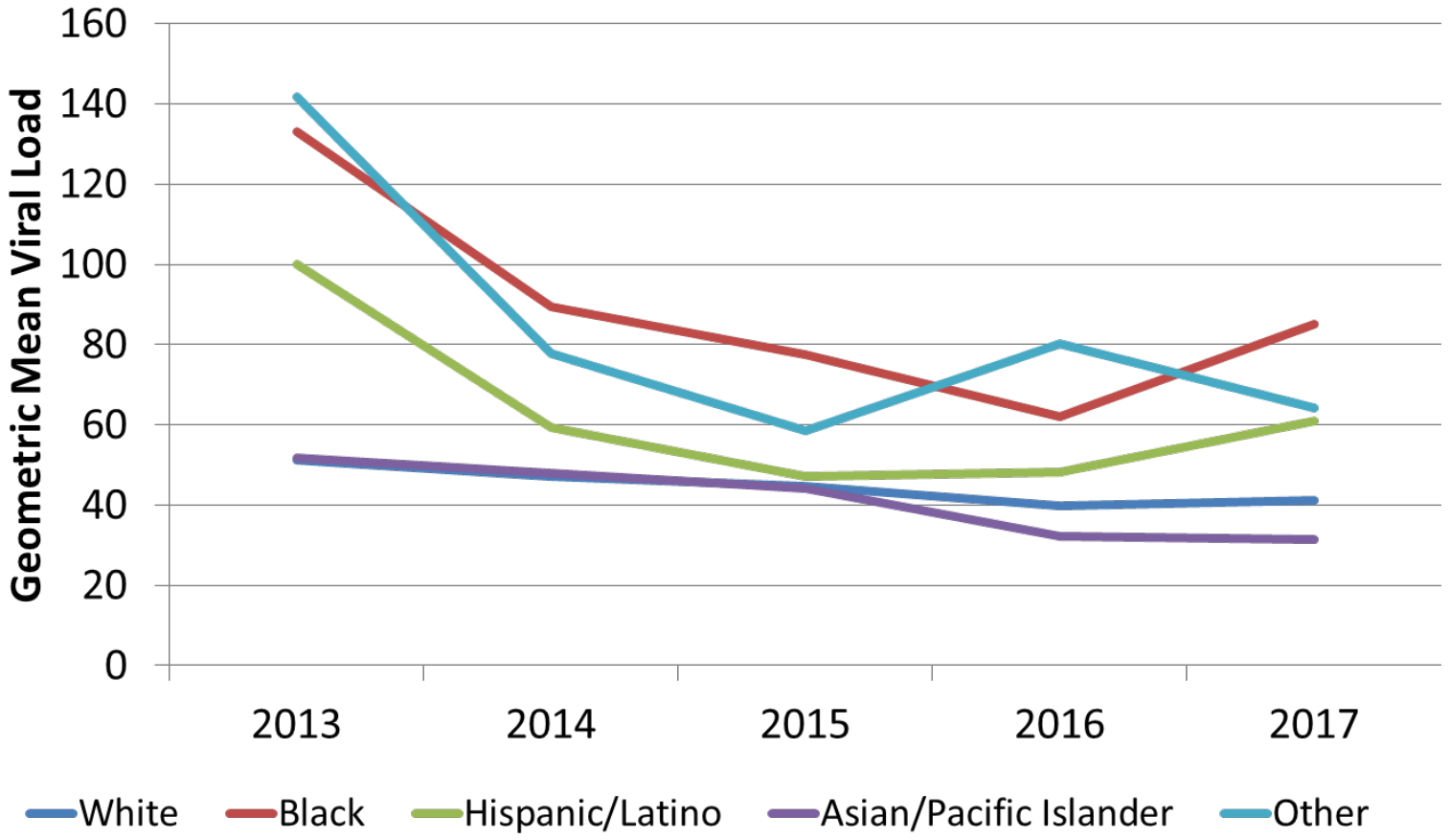




Results

- Geometric mean viral load of African Americans was **twice** that of their white peers
- Hispanic/Latino viral load was about **50% higher** than that of white PLWH

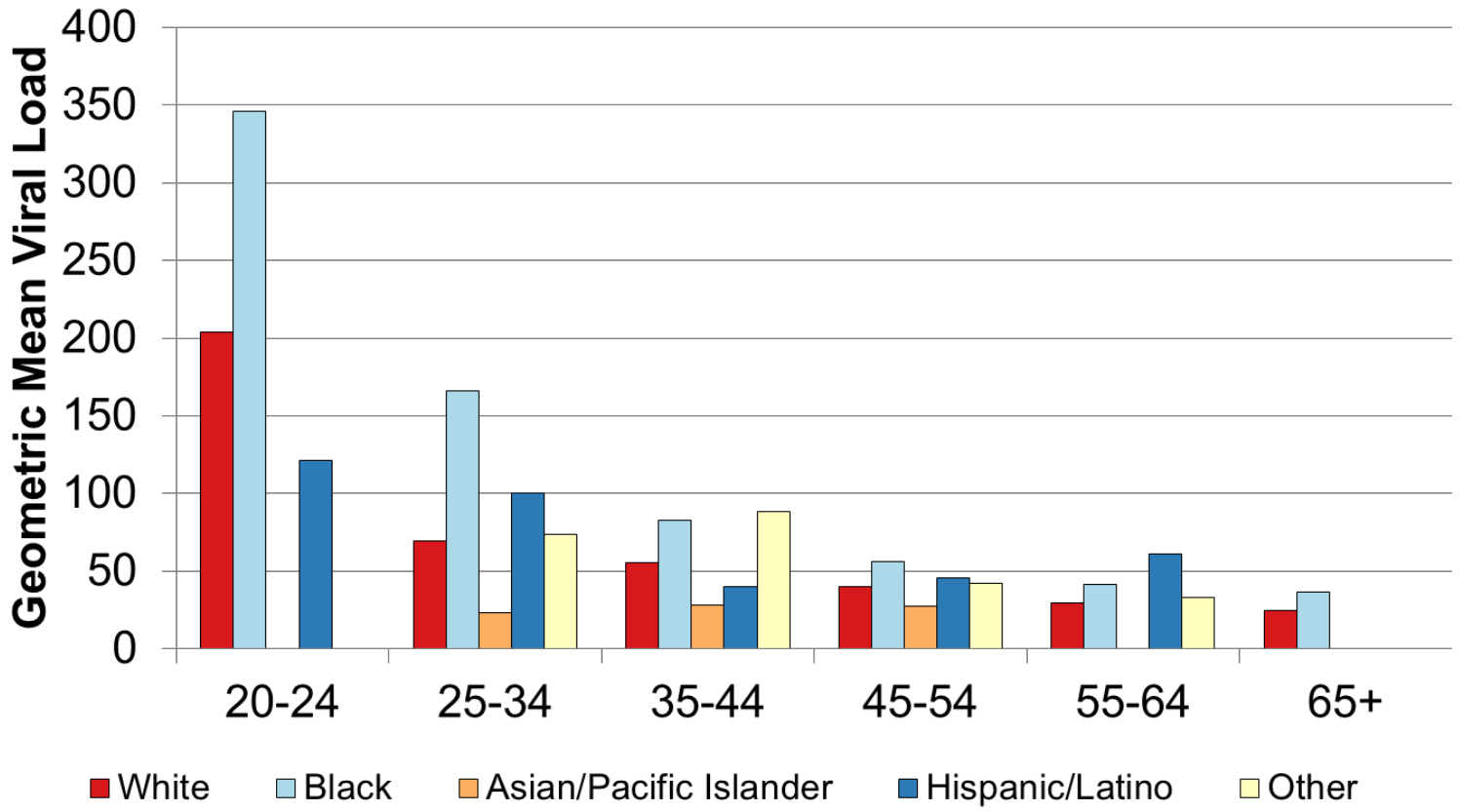
Geometric Mean Viral Load (c/mL) among TGA Residents with at Least One Viral Load Test, by Race/Ethnicity: 2013-2017



Results

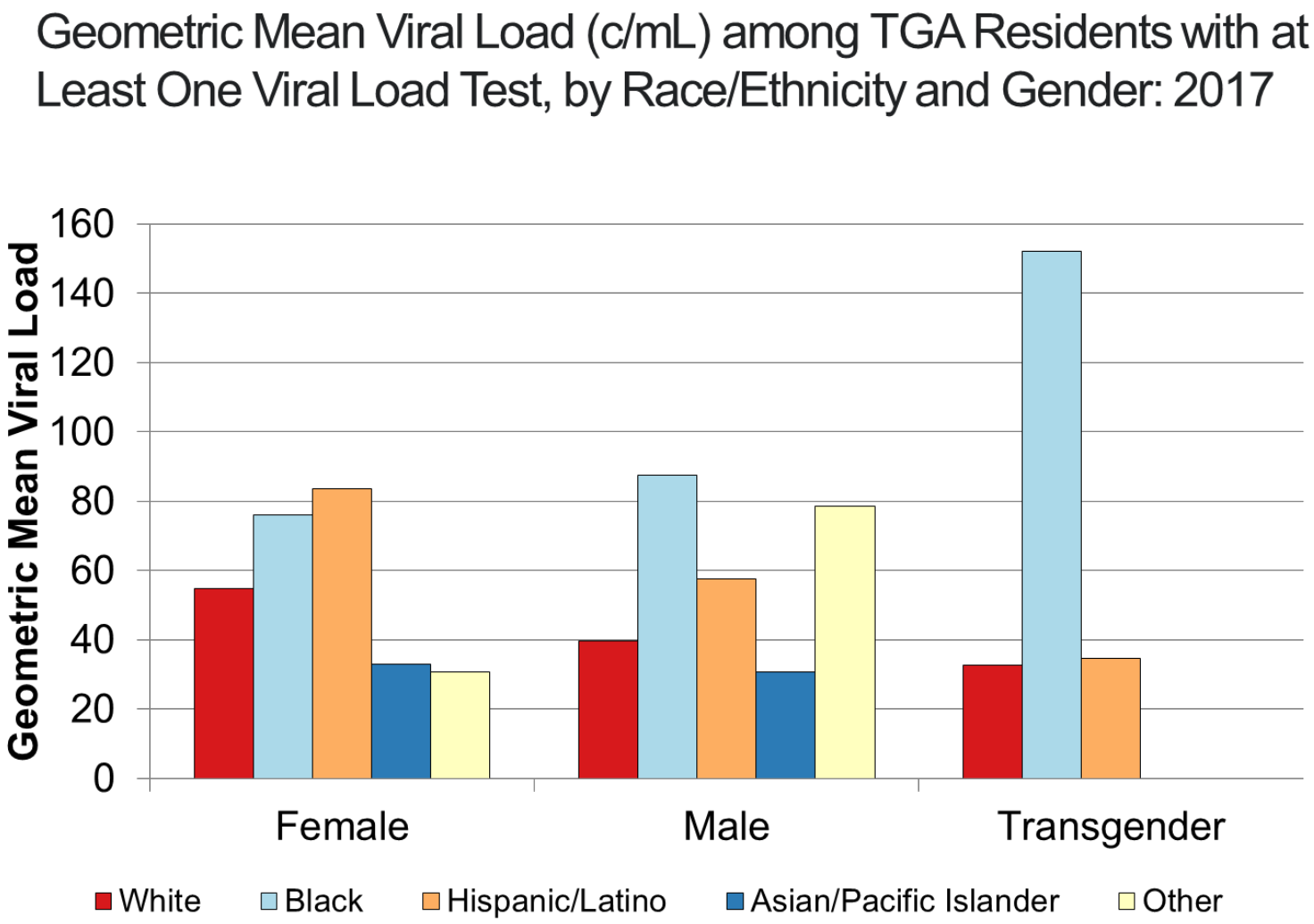
- African Americans do not differ significantly from other racial groups in middle to late adulthood
- 20-34 year old African Americans differs significantly from that of their peers

Geometric Mean Viral Load (c/mL) among TGA Residents with at Least One Viral Load Test, by Race/Ethnicity and Age: 2017



Results

- Geometric mean viral load of African American men was more than **twice** that of white men during 2017
- Viral load among females was not significantly different from males

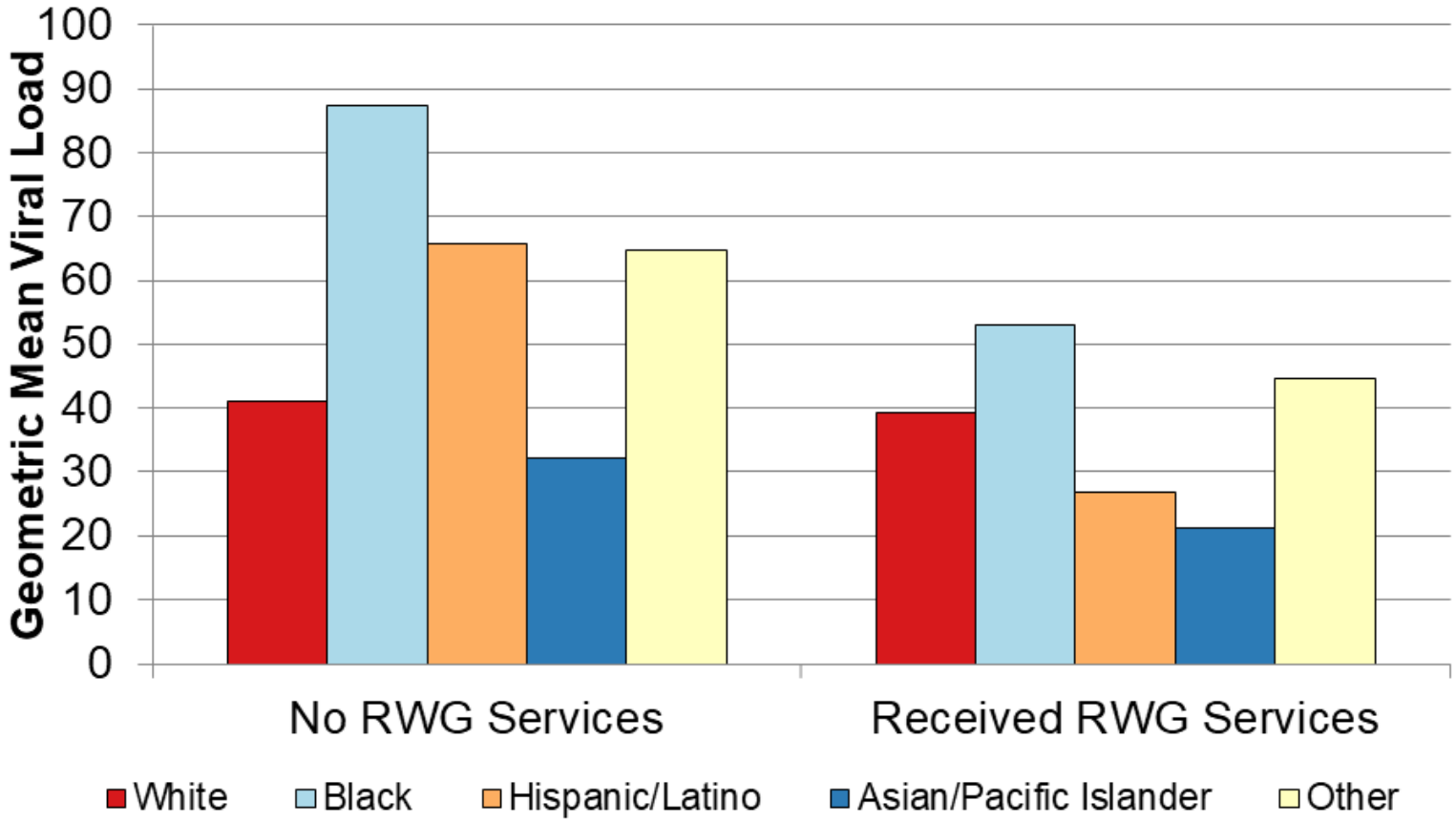


Results

- Geometric mean viral load among all racial/ethnic minorities not utilizing Ryan White services in the Indy TGA was higher than among Ryan White clients

- This difference was not found among white PLWH in the TGA

Geometric Mean Viral Load (c/mL) among TGA Residents with at Least One Viral Load Test, by Race/Ethnicity and Ryan White Part A/MAI Client Status: 2017

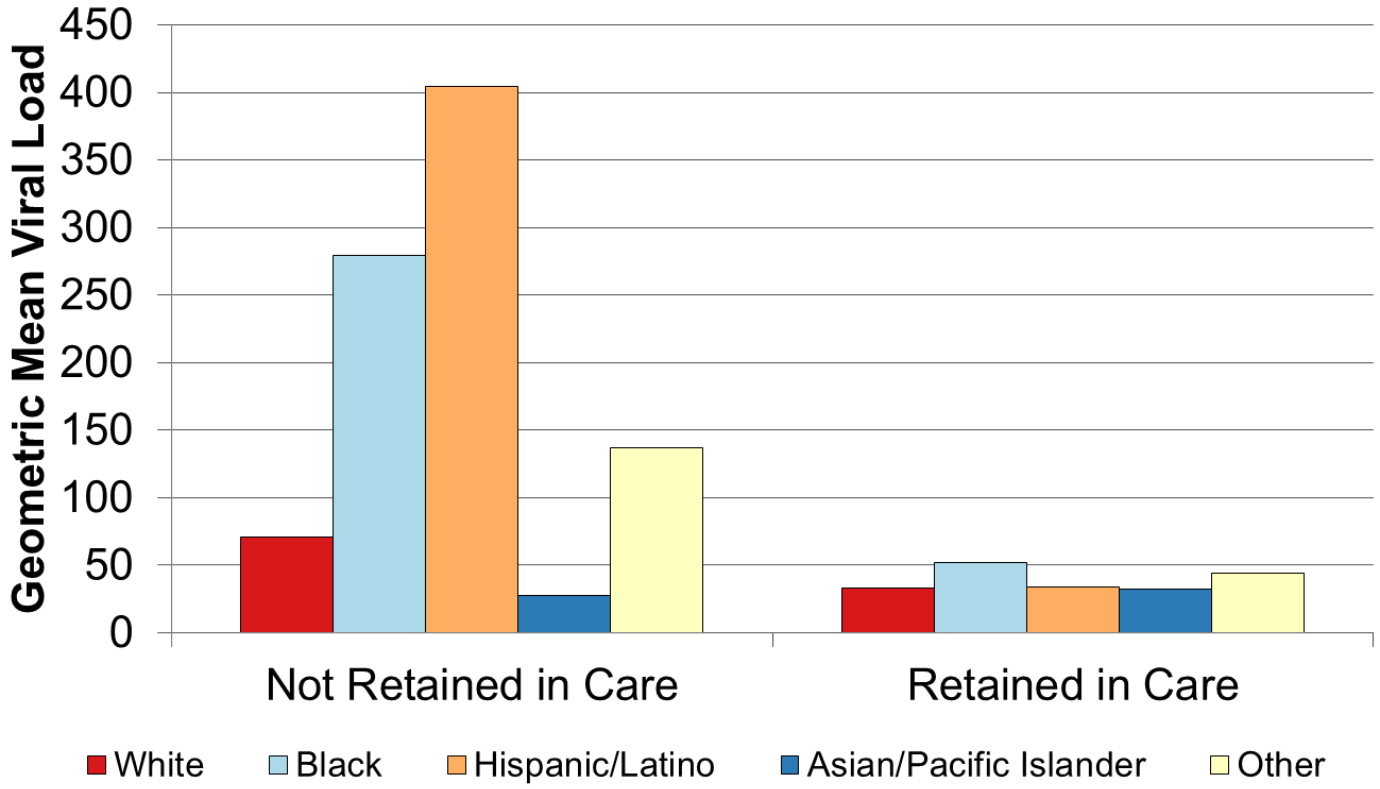


Results

- Among individuals not retained in care, Hispanic/Latinos and African Americans experienced the highest viral loads

- ***Even when retained in care***, African Americans experienced poorer outcomes, with viral loads **50% higher** than their white peers

Geometric Mean Viral Load (c/mL) among TGA Residents with at Least One Viral Load Test, by Race/Ethnicity and Retention in Care Status: 2017



Conclusions

- Using data standardization and geometric mean analysis has allowed us to **make better comparisons between groups**
- Allows for **better allocation of resources to target interventions** to those most likely to have increased viral loads

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