National Health and Nutrition Examination Survey

2015-2016 Data Documentation, Codebook, and Frequencies

Trichomonas - Urine (TRICH_I)

Data File: TRICH_I.xpt

First Published: September 2017

Last Revised: NA

Component Description

Trichomonas vaginalis infection is the most common curable sexually transmitted infection among women in the United States; it can cause inflammation that has been associated with an increased risk of HIV transmission and acquisition, and low birth weight.

Prevalence in adult men has never been measured in a nationally representative sample. Trichomonas vaginalis infection is not reportable and so few other sources exist for obtaining national data.

Eligible Sample

Examined participants aged 14-59 years were eligible. This public data file only includes examined participants aged 18-59 years. See *Analytic Notes* for information on participants aged 14-17 years.

Description of Laboratory Methodology

The GEN-PROBE APTIMA trichomonas vaginalis assay combines the technologies of target capture, Transcription-Mediated Amplification (TMA), and Dual Kinetic Assay (DKA).

Specimens are collected and transferred into their respective specimen transport tubes. The transport solutions in these tubes release the rRNA targets and protect them from degradation during storage. When the APTIMA trichomonas vaginalis assay is performed in the laboratory, the target rRNA molecules are isolated from specimens by the use of capture oligomers in a method called target capture; magnetic microparticles are another key feature of target capture. The capture oligomers contain sequences complementary to specific regions of the target molecules as well as a string of deoxyadenosine residues. A separate capture oligomer is used for each target. During the hybridization step, the sequence specific regions of the capture oligomers bind to specific regions of the target molecules. The capture oligomer: target complex is then captured out of solution by decreasing the temperature of the reaction to room temperature. This temperature reduction allows hybridization to occur between the deoxyadenosine region on the capture oligomer and the poly-deoxythymidine molecules that are covalently attached to the magnetic particles. The microparticles, including the captured target molecules bound to them, are pulled to the side of the reaction vessel using magnets and the supernatant is aspirated. The particles are washed to remove residual specimen matrix that may contain amplification reaction inhibitors. After the target capture steps are completed, the specimens are ready for amplification.

Target amplification assays are based on the ability of complementary oligonucleotide primers to specifically anneal and allow enzymatic amplification of the target nucleic acid strands. The GEN-PROBE TMA reaction replicates a specific region of the small ribosomal subunit from T. vaginalis via DNA and RNA intermediates and generates RNA amplicon molecules. Detection of

the rRNA amplification product sequences is achieved using nucleic acid hybridization (HPA). A single-stranded chemiluminescent DNA probe, which is complementary to a region of the target amplicon, is labeled with different acridinium ester molecule. The labeled DNA probe combines with amplicon to form stable RNA: DNA hybrids. The Selection Reagent differentiates hybridized from unhybridized probe, eliminating the generation of signal from unhybridized probe. During the detection step, light emitted from the labeled RNA: DNA hybrids is measured as photon signals in a luminometer, and are reported as Relative Light Units (RLU).

Refer to the Laboratory Method Files section for a detailed description of the laboratory methods used.

There were no changes to the lab method, lab equipment, or lab site for this component in the NHANES 2015-2016 cycle.

Laboratory Method Files

Trichomonas vaginalis (December 2017)

Laboratory Quality Assurance and Monitoring

Urine samples are processed, stored, and shipped to the Division of STD Prevention, National Center for HIV/AIDS, Viral Hepatitis, STD and TB Prevention, Centers for Disease Control and Prevention, Atlanta GA for analysis.

Detailed instructions on specimen collection and processing are discussed in the NHANES Laboratory Procedures Manual (LPM). Vials are stored under appropriate frozen (–30°C) conditions until they are shipped to Division of STD Prevention Laboratory for testing.

The NHANES quality assurance and quality control (QA/QC) protocols meet the 1988 Clinical Laboratory Improvement Act mandates. Detailed QA/QC instructions are discussed in the NHANES LPM.

Mobile Examination Centers (MECs)
Laboratory team performance is monitored using several techniques. NCHS and contract consultants use a structured competency assessment evaluation during visits to evaluate both the quality of the laboratory work and the quality-control procedures. Each laboratory staff person is observed for equipment operation, specimen collection and preparation; testing procedures and constructive feedback are given to each staff member. Formal retraining sessions are conducted annually to ensure that required skill levels were maintained.

Analytical Laboratories
NHANES uses several methods to monitor the quality of the analyses performed by the contract laboratories. In the MEC, these methods include performing blind split samples collected on “dry run” sessions. In addition, contract laboratories randomly perform repeat testing on 2% of all specimens.

NCHS developed and distributed a quality control protocol for all CDC and contract laboratories, which outlined the use of Westgard rules (Westgard, et al. 1981) when running NHANES specimens. Progress reports containing any problems encountered during shipping or receipt of specimens, summary statistics for each control pool, QC graphs, instrument calibration, reagents, and any special considerations are submitted to NCHS quarterly. The reports are reviewed for trends or shifts in the data. The laboratories are required to explain any identified areas of concern.

Data Processing and Editing

The data were reviewed. Incomplete data or improbable values were sent to the performing laboratory for confirmation.

Analytic Notes

Refer to the 2015 - 2016 Laboratory Data Overview for general information on NHANES laboratory data.

Please refer to the NHANES Analytic Guidelines and the on-line NHANES Tutorial for further details on the use of sample weights and other analytic issues.

Demographic and Other Related Variables
The analysis of NHANES laboratory data must be conducted using the appropriate survey design and demographic variables. The NHANES 2015-2016 Demographics File contains demographic data, health indicators, and other related information collected during household interviews as well as the sample weight variables. The recommended procedure for variance estimation requires use of stratum and PSU variables (SDMVSTRA and SDMVPSU, respectively) in the demographic data file.

The laboratory data file can be linked to other NHANES data files using the unique survey participant identifier (i.e., SEQN).

The public release data file includes Trichomonas - urine data for participants aged 18-59. Trichomonas - urine data for youth aged 14-17 years are available through the NCHS Research Data Center (RDC).

Detection Limits
Since this data is reported as qualitative data the use of lower LLODs isn't applicable.
Please refer to the NHANES Analytic Guidelines and the on-line NHANES Tutorial for further details on the use of sample weights and other analytic issues.

References

- NA

Codebook and Frequencies

SEQN - Respondent sequence number

Variable Name:	SEQN
SAS Label:	Respondent sequence number
English Text:	Respondent sequence number.
Target:	Both males and females 18 YEARS - 59 YEARS

URXUTRI - Trichomonas, Urine

binary

Variable Name: URXUTRI

SAS Label: Trichomonas, Urine

English Text: Trichomonas, Urine

Target: Both males and females 18 YEARS - 59 YEARS

Code or Value	Value Description	Count	Cumulative	Skip to Item
1	Positive	92	92	
2	Negative	3742	3834	
3	Indeterminate	0	3834	
.	Missing	92	3926	