1023

Sexually Transmitted Enteric Infections in Southern Taiwan, 2019-2024

Chin-Shiang Tsai[1,2], Jiun-Ling Wang[1], Nan-Yao Lee[1,2], Po-Lin Chen[1,2], Huey-Pin Tsai[3], Sung-Hsi Huang[4], Szu-Ying Chen[2,3], Yu-Wen Tang[2], Ying-Jun Lin[3], Pei-Fang Tsai[3], Lin-Wen Mao[1], Wen-Chien Ko[1,2]

1. Department of Internal Medicine, National Cheng Kung University Hospital, College of Medicine, National Cheng Kung University, Tainan, Taiwan. 2. Center for Infection Control, National Cheng Kung University Hospital, College of Medicine, National Cheng Kung University, Tainan, Taiwan.
3. Department of Pathology, National Cheng Kung University Hospital, College of Medicine, National Cheng Kung University, Tainan, Taiwan. 4. Department of Internal Medicine, National Taiwan University Hospital Hsinchu Branch, Hsinchu, Taiwan

BACKGROUND

Sexually transmitted enteric infections (STEIs) have been rarely investigated in Asia as a whole. In Taiwan, there is ongoing transmission of STEIs among men who have sex with men (MSM) and people with HIV (PWH), and the association of asymptomatic STEIs with proton pump inhibitors has also been reported. This study aimed to comprehensively assess the prevalence, risk factors, and pathogen associations of STEIs among MSM and PWH in southern Taiwan.

METHODS

A cross-sectional surveillance study was conducted from March 2019 to March 2024 at National Cheng Kung University Hospital, a 1300-bed tertiary medical center in southern Taiwan. MSM underwent systematic screening using BDMax panels (BD Diagnostics, USA) for seven enteric pathogens (**GI panel**: *Entamoeba histolytica*, *Giardia*, *Cryptosporidium*, *Shigella*, *Salmonella*, *Campylobacter*, shiga-toxin *E. coli* [STEC]) and rectal sexually transmitted infections (**STI panel**: gonorrhea and chlamydia, including rectal lymphogranuloma venereum [LGV] detected by clinical symptoms and *ompA* sequencing). Clinical characteristics and behavioral data were collected by electronic medical records and questionnaires. Multivariable logistic regression has identified independent association factors.

Figure 1. The flowchart of the present study.

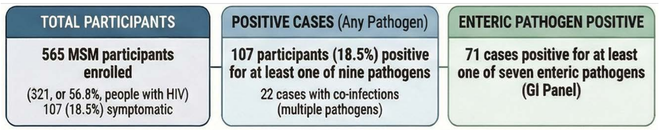
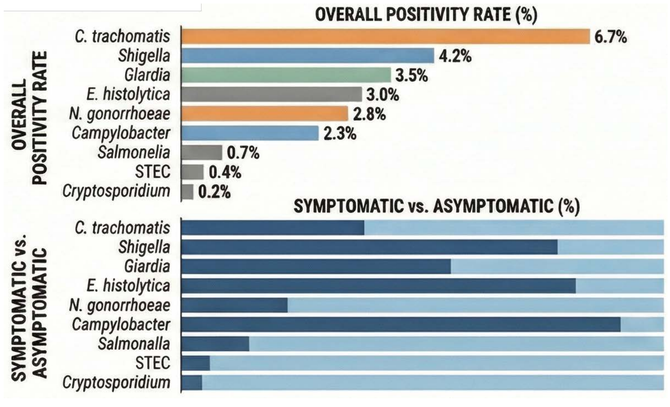


Figure 2. Pathogen prevalence and symptomology.



A surveillance during 2019-2024 in southern Taiwan showed
18.5% of MSM or PWH with a significant STEIs burden;
20.6% of infected individuals had multiple pathogens.

Independent association factors for enteric pathogens infections (GI panel)

10.8x increased odds
Associated with rectal LGV (*C. trachomatis* genovariant L2b)

7.3x increased odds
Associated with proton pump inhibitors (PPIs) use

6.8x increased odds
Associated with rectal gonorrhea

3.2x increased odds
Associated with insertive anal sex

Shigellosis-specific association factors

12.1x increased odds
Associated with syphilis history, suggesting dense sex networks

6.4x increased odds
Associated with *Campylobacter*

RESULTS

Among 565 MSM, 321 (56.8%) were PWH and 107 (18.5%) were symptomatic. Overall, 107 participants (18.5%) tested positive for at least one of nine tested pathogen, with 71 (12.6%) positive for GI panel **(Figure 1)**. The most prevalent pathogens were *Shigella*, *C. trachomatis*, *Giardia, E. histolytica*, *N. gonorrhoeae*, and *Campylobacter*. High proportions of asymptomatic infections were observed **(Figure 2)**. Co-infections occurred in 22 cases, revealing complex interconnected transmission patterns **(Figure 3)**. We compared GI-panel positive vs. negative cases **(Table 1)**, and likewise *Shigella* positive vs. negative cases. In multivariable analysis, rectal LGV (aOR 10.78, *P*=0.005), rectal gonorrhea (aOR 6.79, *P*=0.015), proton pump inhibitor use (aOR 7.28, *P*<0.001), and insertive anal sex (aOR 3.18, *P*=0.007) were independently associated with positive enteric pathogen results. Syphilis was the strongest predictor for shigellosis (aOR 12.10, *P*=0.001) **(Table 2)**.

Table 1. Logistic regression analysis of association factors with positive GI panel.

	Univariable analysis			Multivariable analysis		
	OR	95%CI	*P*	aOR	95%CI	*P*
Age	0.99	0.96-1.03	0.704	1.002	0.95-1.05	0.930
HIV	1.37	0.82-2.29	0.234			
Syphilis	**2.14**	**1.23-3.67**	**0.006**			
Gastrointestinal symptoms	**7.06**	**4.15-12.01**	**<0.001**			
Rectal gonorrhea	**5.89**	**2.12-16.37**	**0.001**	**6.79**	**1.46-31.67**	**0.015**
Rectal chlamydia	**2.73**	**1.26-5.89**	**0.011**			
Rectal LGV (*C. trachomatis* genovariant L2b)	**9.02**	**2.68-30.42**	**<0.001**	**10.78**	**2.08-55.90**	**0.005**
Oroanal sex	**2.02**	**1.15-3.54**	**0.014**			
Persistent diarrhea (≥14 days)	1.87	0.98-3.57	0.060			
Sexual activity in the past year	1.80	0.83-3.90	0.137			
Insertive anal sex	**2.83**	**1.40-5.71**	**0.004**	**3.18**	**1.38-7.33**	**0.007**
Condomless sex	**2.34**	**1.16-4.72**	**0.018**			
Chemsex	**2.29**	**1.16-4.52**	**0.016**			
Proton pump inhibitors	**4.56**	**1.93-10.73**	**0.001**	**7.28**	**2.56-20.66**	**<0.001**

Figure 3. Distribution of co-infections (n=22) with UpSet Plot.

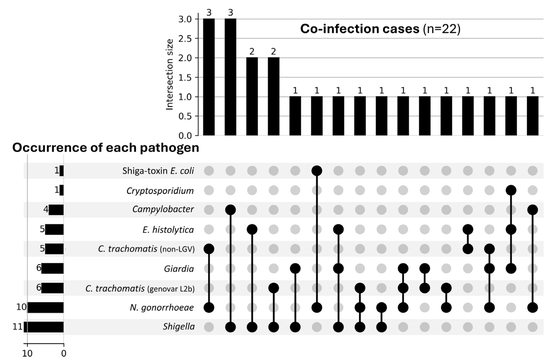


Table 2. Analysis of association factors with *Shigella*

	Multivariable analysis		
	aOR	95%CI	*P*
Syphilis	**12.10**	**2.73-53.57**	**0.001**
Positive for *Entamoeba histolytica*	4.95	0.93-26.39	0.061
Positive for *Campylobacter*	**6.38**	**0.92-26.39**	**0.036**
Rectal LGV	3.56	0.68-18.56	0.132

CONCLUSIONS

The prevalence of STEIs, even among asymptomatic individuals, suggests routine screening may be warranted for MSM, PWH, and at-risk populations. Rectal LGV, rectal gonorrhea, proton pump inhibitors (PPIs), and insertive anal sex were associated with positive enteric pathogen results. PPIs use emerged as a significant risk factor for STEIs, with clinical implications and further PPI stewardship. These findings can inform targeted prevention strategies and management guidelines in Taiwan.

ADDITIONAL KEY INFORMATION

Author Contact Information

Chin-Shiang Tsai, MD, PhD. Email: jasonmammal@gmail.com

Acknowledgements

Special thanks to the Diagnostic Microbiology & Antimicrobial Resistance Laboratory and the Biostatistics Consulting Center, National Cheng Kung University Hospital, Tainan, Taiwan, for the technical and statistical support, respectively. This research was supported by National Cheng Kung University Hospital (NCKUH-11402063) and National Science & Technology Council, Taiwan (NSTC 114-2629-B-006-001).

References

Emerg Microbes Infect. 2022;11(1):498-506.
J Microbiol Immunol Infect. 2024; 57(3):346-353.
J Microbiol Immunol Infect. 2023;56(2):408-415.
Int J Infect Dis. 2024:149:107273