

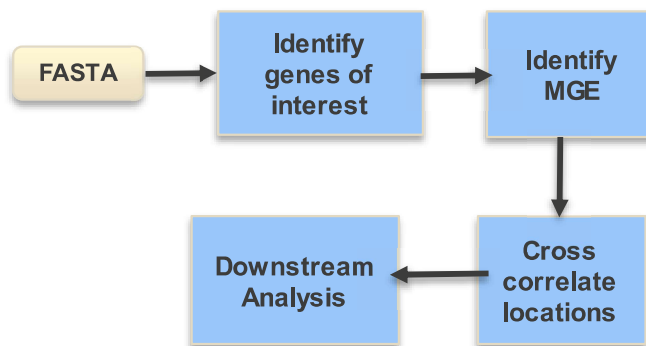
# INSIGHTS TO PATHOGENIC POTENTIAL: CHARACTERIZING HOW MOBILE GENETIC ELEMENTS CONTRIBUTE TO VIRULENCE IN UROPATHOGENIC *E. COLI*

GRACE MORALES<sup>1,2</sup>, BENJAMIN ABELSON<sup>3</sup>, SETH REASONER<sup>1,2</sup>, JORDAN MILLER<sup>1</sup>, MARIA HADJIFRANGISKOU<sup>1,2,3</sup>, JONATHAN SCHMITZ<sup>1,3</sup>  
DEPARTMENTS OF: <sup>1</sup>PATHOLOGY, MICROBIOLOGY & IMMUNOLOGY; <sup>2</sup>VANDERBILT INSTITUTE FOR INFECTION, INFLAMMATION, AND IMMUNOLOGY, <sup>3</sup>UROLOGY  
VANDERBILT UNIVERSITY MEDICAL CENTER  
NASHVILLE, TN, USA.

## Abstract

- Uropathogenic *E. coli* is the most common cause of urinary tract infections.
- There is no correlation of virulence factors in UPEC with disease severity.
- Mobile genetic elements (MGE) contribute to the pathogenic potential of a bacteria by carrying virulence factors and antimicrobial resistance genes.
- This study aims to address MGE carriage in UPEC, and how they contribute to the pathogenic potential of the strain.

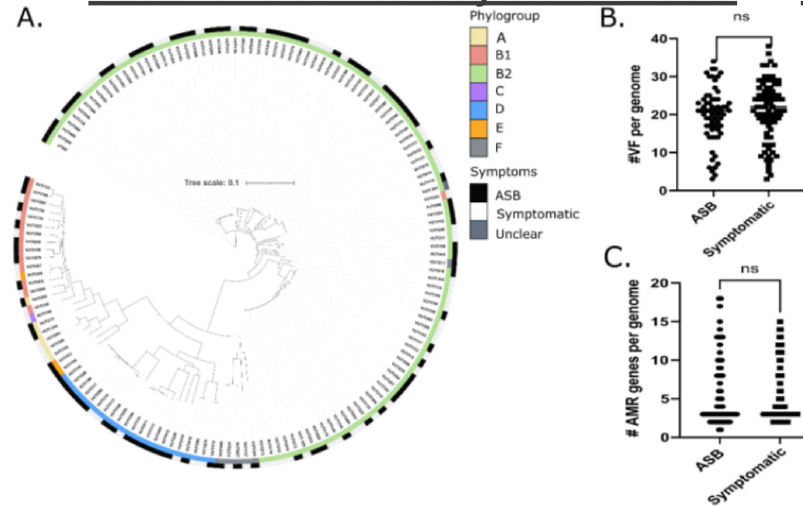
## Methods



**Methods:** Mobile elements were identified using PHASTER<sup>1</sup>, plasmidSPADES<sup>2</sup>, and MobileElementFinder<sup>3</sup>. MGE were cross correlated with fitness factors. We analyzed how many MGE carried these factors in each strain.

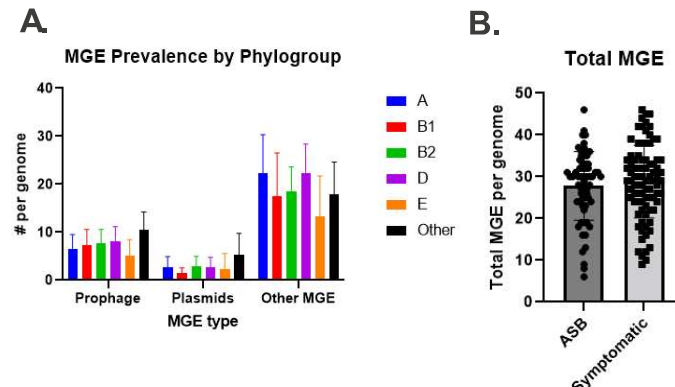
1. Arndt et al. 2016. Nucleic Acids Res. 2. Antipov et al. 2016. Bioinformatics. 3. Johansson et al. 2021. J Antimicrob Chemother.

## Bacteriuria is caused by diverse *E. coli*



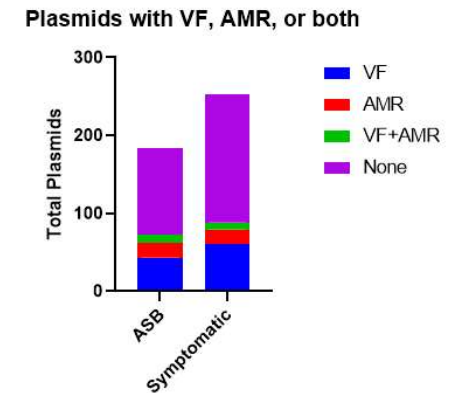
*E. coli* isolated from urinary sources are diverse. They are found in all phylogroups, with no association with symptom presence (A). Virulence factors and antimicrobial genes are equally distributed by clinical presentation (B and C).

## MGE are equally distributed in UPEC



Mobile genetic elements are equally distributed by both phylogroup (A) and by clinical presentation of the source patient (B).

## Plasmids carried the most fitness factors of all MGE identified



Plasmids most frequently carried virulence factors, AMR genes, or both out of all MGE identified. Plasmids carried about 20% of AMR genes and 6% of virulence factors.

## Conclusions

- MGE are not a significant contributor to the carriage of VF or AMR genes.
- AMR genes and VF were more most frequently carried by plasmids than any other mechanism.
- MGE do not constitute a defining feature of UPEC.

## Funding:

NIH Training Grant 5T32AI112541  
1P20DK123967-01  
Vanderbilt Trans-Institutional Program (TIPS)