# Analysis of a uropathogenic *Escherichia coli* clinical isolate from a patient with recurrent urinary tract infections

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Worldwide, over 400 million people suffer from urinary tract infections (UTIs) each year, and with widespread antibiotic resistance, recurrent UTIs (RUTI) have become a health and economic burden. The primary etiologic agent of UTIs is uropathogenic *Escherichia coli* (UPEC). This study focuses on a patient with RUTIs that has sought medical care at Emplify Health in La Crosse, Wisconsin. The UPEC isolate named GLMC BS-1 underwent antimicrobial susceptibility testing, phylogroup typing, and whole genome sequencing (WGS). E-test analysis using fosfomycin and azithromycin showed GLMC BS-1 had minimum inhibitory concentrations of 0.38 μg/ml and 2.0 μg/ml, respectively. WGS performed using Illumina and subsequent bioinformatic analysis revealed GLMC BS-1 typed as a D phylogroup, O86:H2 serotype, and subtypes as an ST349 clonal complex. Further bioinformatic analysis suggested GLMC BS-1 is multidrug-resistant and contains several intriguing virulence factors. Two of these unique genes were *eilA*, a *Salmonella* HilA homolog for activation of a type III secretion system, and *tia*, an invasion locus for enterotoxigenic *E. coli*. These results reinforce the idea that coupling WGS with traditional susceptibility testing is a powerful framework for monitoring resistance trends and optimizing treatment outcomes in RUTIs.