

Molecular Characterization of a Virulent Uropathogenic *Escherichia coli* from a Patient with Recurrent Urinary Tract Infections

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Introduction

Escherichia coli is the leading causative organism of urinary tract infection (UTI). Predominant clonal lineages of extraintestinal pathogenic *E. coli* (ExPEC) were reported to disseminate worldwide [1]. Here we recovered a virulent uropathogenic *E. coli* (UPEC) strain from a patient with recurrent urinary tract infections, which belongs to one of the major clonal groups of ExPEC in humans and food and companion animals.

Materials and Methods

Bacterial strains

- *E. coli* GU140823 was isolated from urine of a female outpatient with recurrent lower urinary tract infections. She had frequent urination, bloody urine and severe pain and burning sensation when urinating. She had clinical and microbiological response to amoxicillin therapy, resulting in clearance of the organisms in the urine.

Methods

- The genome of *E. coli* GU140823 was sequenced on a PacBio RSII single-molecule real-time (SMRT) sequencing instrument (Pacific Biosciences) and assembled using SMRT Analysis 2.1.
- Serotype, MLST, virulence and resistance genes were identified by CGE services (<https://cge.cbs.dtu.dk>) or described as previously [2].
- The major *E. coli* phylogenetic group (A, B1, B2, or D) was determined by the Clermont phylo-typing method [3].

Results

- Assembly of the PacBio sequencing reads yielded 12 contigs.
- *E. coli* GU140823 derived from phylogroup B2 and belonged to ST73 of the ST73 Clpx (clonal complex) with predicted serotype O6:H1.
- GU140823 contained *papC*, *papEF*, *papG*, *fimH*, and *sfa/foc* gene clusters, encoding various types of fimbriae.
- GU140823 also encoded hemolysin (*hlyCABD*), cytotoxic necrotizing factor 1 (*cnf1*), *sat*, *pic*, *vat*, *iha*, *gad*, *iss* virulence genes and siderophore receptors (*ireA*, *fyuA*, *iutA*) which helped GU140823 survive and invade in the host.
- However, GU140823 was susceptible to many classes of antibiotics such as ampicillin, gentamicin, ciprofloxacin, trimethoprim/sulfamethoxazole, and fosfomycin which was consistent with the absence of resistance genes in the genome.

Conclusions

E. coli GU140823 was a highly virulent uropathogenic *E. coli* strain encoding multiple virulence-associated factors, but highly susceptible to the antibiotics used to treat a urinary tract infection. ST73 *E. coli* O6:H1 clone has globally spread in healthcare facilities and communities [1].

References

1. Riley LW. 2014. Clin Microbiol Infect 20:380-390.
2. Johnson JR, Murray AC, Gajewski A, et al. Antimicrob Agents Chemother 2003; 47:2161-8.
3. Clermont, O., Bonacorsi S., and Bingen E.. 2000. Appl. Environ. Microbiol. 66:4555-4558.

