

Pediatric Pathology & Laboratory Medicine

Jyotsna Agarwal, Richa Srivastava and Sugandha Srivastava
King George's Medical University, India

Temporal and spatial expression of genes in induced bladder epithelium may be associated with difference in the pathogenesis of urinary tract infection (UTI) and fecal *E. coli* carriage. In order to better understand the pathogenesis of UTI, genetic and functional expression profiles of fecal *E. coli* carriage were analyzed in the present study. Functional expression and dominant fecal *E. coli* form were analyzed by sequencing their mRNA and identifying the virulence genes (VG) i.e. *mH*, *papG* alleles, *hlyA*, *iutA* and *traT* along with the genetic typing. Prevalence of *hlyA* gene was 48% and 40% (respectively) and higher prevalence of VG *mH* (82% and 78%), followed by *traT* (66% and 46%), and *iutA* (44% and 40%) was observed.