MOLECULAR CHARACTERIZATION OF VIRULENCE FACTORS IN DIARRHEAGENIC E*SCHERICHIA COLI* ISOLATES FROM CHILDREN AT THE MBAGATHI DISTRICT HOSPITAL, NAIROBI, KENYA.

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ABSTRACT

Diarrheal diseases constitute a major public health problem, particularly in the developing world, where the rate of mortality and morbidity is still very high. Among the bacterial causes, diarrheagenic *Escherichia coli* (DEC) is the most important etiologic agent of childhood diarrhea and represents a major public health problem in developing countries. Growing evidence suggests that major differences in virulence between groups of DEC pathotypes may be related to the presence of specific pathogenicity islands (PAIs). The objective of this study was to identify the different DEC pathotypes and pathogenicity islands associated with pathogenesis and clinical presentation of diarrhea and outcome. A total of two hundred and seven *E. coli* isolates from Walter Reed Project (WRP)-ENTERICS laboratory situated in Kenya Medical Research Institute (KEMRI), Nairobi were used in the study. Multiplex and conventional PCR assays were used to identify the DEC pathotypes and PAIs respectively. The predominant DEC pathotype isolated was Enteropathogenic *E.coli* (EPEC) 40/207(19.3%), followed by Enterotoxigenic *E. coli* (ETEC) 15/207 (7.25%), Entereoaggreggative *E. coli* (EAggEC) 8/207 (3.86%), Shiga toxin producing *E. coli* (STEC) 2/207 (0.97%) and Enteroinvasive *E. coli* (EIEC) 1/207 (0.48%). The PAIs detected were Enteropathogenic secreted protein C (EspC) 8/66 (12.2%), Locus of enterocyte effacement (LEE) 41/66 (62.1%), High Pathogenicity island (HPI) 38/66 (57.6%), 4/66 (6%) expressed only *fyuA* gene, 8/66 (12.2%) *irp2* only and 26/66 (39.4%) expressed both fyuA and *irp2* genes, SHI-2 26/66 (39.4%), *she* 4/66 (6%) and O island 22/66 (33.3%), 13/66 (19.8%) expressed only *efa/lifA* gene, 5/66 (7.6%) *pag C*

gene only and 4/66 (6.1%) expressed both *efa/lifA* and *pag C* genes. TIA PAI was not detected in any of the DEC pathotypes. This study revealed that in addition to *eaeA, stx, eagg, einv, st* and *lt* virulence genes exhibited in the different DEC pathotypes there were also present numerous PAIs in the DEC pathotypes. The PAIs increase gene mobility within various mobile elements such as plasmids, and from chromosomal location to mobile elements, which has implications for spread of virulence factors from DEC to commensal *E. coli.* The PAIs play a significant role in pathogenesis of DEC and increased virulence in disease presentation particularly in children below 5 years of age. There is need for continued research on DEC pathotypes to establish the extent of mobility of virulence genes in the intestinal *E. coli* strains to estimate potential risk for DEC strains, and to institute appropriate management for such infections**.**