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Background: Inflammatory bowel disease (IBD) is used to describe a state of idiopathic, chronic inflammation of the gastrointestinal tract. The two main phenotypes of IBD are Crohn's disease (CD) and ulcerative colitis (UC). The major cause of IBD-associated mortality is colorectal cancer. Although both host-genetic and exogenous factors have been found to be involved, the aetiology of IBD is still not well understood. In this study we characterized thirteen Escherichia coli strains from patients with IBD by comparative genomic hybridization employing a microarray based on 31 sequenced E. coli genomes from a wide range of commensal and pathogenic isolates. Results: The IBD isolates, obtained from patients with UC and CD, displayed remarkably heterogeneous genomic profiles with little or no evidence of group-specific determinants. No IBD-specific genes were evident when compared with the prototypic CD isolate, LF82, suggesting that the IBD-inducing effect of the strains is multifactorial. Several of the IBD isolates carried a number of extraintestinal pathogenic E. coli (ExPEC)-related virulence determinants such as the pap, sfa, cdt and hly genes. The isolates were also found to carry genes of ExPEC-associated genomic islands. Conclusions: Combined, these data suggest that E. coli isolates obtained from UC and CD patients represents a heterogeneous population of strains, with genomic profiles that are indistinguishable to those of ExPEC isolates. Our findings indicate that IBD-induction from E. coli strains is multifactorial and that a range of gene products may be involved in triggering the disease.

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