



Review

Virulence Factors of Enteric Pathogenic *Escherichia coli*: A Review

Babak Pakbin ^{1,2,3} , Wolfram M. Brück ^{1,*} and John W. A. Rossen ²

¹ Institute for Life Technologies, University of Applied Sciences Western Switzerland Valais-Wallis, 1950 Sion 2, Switzerland; b.pakbin@ut.ac.ir

² Department of Medical Microbiology and Infection Prevention, University Medical Center Groningen, University of Groningen, 9713 GZ Groningen, The Netherlands; john.rossen@gmail.com

³ Medical Microbiology Research Center, Qazvin University of Medical Sciences, Qazvin 15315-3419, Iran

* Correspondence: wolfram.bruck@hevs.ch

Abstract: *Escherichia coli* are remarkably versatile microorganisms and important members of the normal intestinal microbiota of humans and animals. This harmless commensal organism can acquire a mixture of comprehensive mobile genetic elements that contain genes encoding virulence factors, becoming an emerging human pathogen capable of causing a broad spectrum of intestinal and extraintestinal diseases. Nine definite enteric *E. coli* pathotypes have been well characterized, causing diseases ranging from various gastrointestinal disorders to urinary tract infections. These pathotypes employ many virulence factors and effectors subverting the functions of host cells to mediate their virulence and pathogenesis. This review summarizes new developments in our understanding of diverse virulence factors associated with encoding genes used by different pathotypes of enteric pathogenic *E. coli* to cause intestinal and extraintestinal diseases in humans.

Keywords: enteric pathogenic *Escherichia coli*; *E. coli* pathotypes; virulence factor genes



Citation: Pakbin, B.; Brück, W.M.; Rossen, J.W.A. Virulence Factors of Enteric Pathogenic *Escherichia coli*: A Review. *Int. J. Mol. Sci.* **2021**, *22*, 9922. <https://doi.org/10.3390/ijms22189922>

Academic Editor: Tanneke Den Blaauwen

Received: 15 August 2021

Accepted: 12 September 2021

Published: 14 September 2021

Publisher's Note: MDPI stays neutral with regard to jurisdictional claims in published maps and institutional affiliations.



Copyright: © 2021 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

1. Introduction

Escherichia coli, rod-shaped and gram-negative bacteria belonging to the Enterobacteriaceae family, were first isolated from infant stool and characterized by Theodor Escherich in 1885 [1]. A few hours after birth, *E. coli* colonize and inhabit the gastrointestinal tract of infants. Regarding several mutual benefits, humans and commensal *E. coli* strains coexist without any adverse effects. However, commensal *E. coli* may cause disease in patients with breached gastrointestinal barriers or immunocompromised hosts [2]. Notably, certain *E. coli* mediate various diseases, including intestinal and extraintestinal disorders in humans and animals worldwide. Nine pathovars have been described for *E. coli* strains isolated from humans causing diarrheagenic and extraintestinal diseases [3]. Of these, seven pathotypes have been described as enteric pathogenic *E. coli*, including Enteropathogenic *E. coli* (EPEC), Enterohaemorrhagic *E. coli* (EHEC), Enterotoxigenic *E. coli* (ETEC), Enteroinvasive *E. coli* (EIEC), Enterocaggregative *E. coli* (EAEC), Diffusely adherent *E. coli* (DAEC), and, a new pathotype, Adherent-Invasive *E. coli* (AIEC), causing mostly diarrhea and intestinal disorders. However, the EHEC pathotype has been implicated in extraintestinal diseases such as Hemolytic Uremic Syndrome (HUS) [4]. Many of these pathotypes constitute public health concerns as foodborne pathogens and caused several fatal outbreaks in developing and developed countries [5,6]. Enteric *E. coli* pathotypes are implicated in many diseases through distinctly different pathogenesis. Pathogenesis is the process by which pathogens cause disease or disorder, often by expressing virulence-factor-encoding genes [7,8].

Virulence factors are specific molecules, primarily proteins produced and released by bacteria, fungi, protozoa, and viruses. These factors are encoded by specific genes located on the chromosome or mobile genetic elements (e.g., plasmids or transposons) in bacterial pathogens [9,10]. Each *E. coli* pathotype has its characteristic pathogenicity mechanisms and