



Escherichia coli: Chapter 7. Shigella and enteroinvasive Escherichia coli: Paradigms for pathogen evolution and host-parasite interactions

Anthony T. Maurelli

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Shigella spp. and enteroinvasive Escherichia coli are agents of bacillary dysentery, a disease that remains a scourge of impoverished communities with little access to clean water. Because of the low infectious dose needed to cause disease, refugees and displaced peoples are also at risk of dysentery outbreaks. The characteristics of dysentery (diarrhea, fever, blood in stools) are direct results of the bacteria's ability to invade epithelial cells of the large intestine and induce a robust inflammatory response. Genes encoding invasion and a type III secretion system and its secreted effectors are all found on a large plasmid. Other virulence genes are encoded in pathogenicity islands on the chromosome. The four species of Shigella are genetically closely related to E. coli and evidence suggests that Shigella evolved independently from at least seven ancestral lineages of E. coli. The evolution of Shigella by gene acquisition (virulence plasmid) and gene loss (black holes and antivirulence genes) provides a paradigm for the evolution of bacterial pathogens from commensal ancestors.

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