Adhesion of human and animal Escherichia coli strains in association with their virulence-associated genes and phylogenetic origins - DTU Orbit (23/12/2018)

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Intestinal colonization is influenced by the ability of the bacterium to inhabit a niche, which is based on the expression of colonization factors. Escherichia coli carries a broad range of virulence-associated genes (VAGs) which contribute to intestinal (inVAGs) and extraintestinal (exVAGs) infection. Moreover, initial evidence indicates that inVAGs and exVAGs support intestinal colonization. We developed new screening tools to genotypically and phenotypically characterize E. coli isolates originating in humans, domestic pigs, and 17 wild mammal and avian species. We analyzed 317 isolates for the occurrence of 44 VAGs using a novel multiplex PCR microbead assay (MPMA) and for adhesion to four epithelial cell lines using a new adhesion assay. We correlated data for the definition of new adhesion genes. inVAGs were identified only sporadically, particularly in roe deer (Capreolus capreolus) and the European hedgehog (Erinaceus europaeus). The prevalence of exVAGs depended on isolation from a specific host. Human uropathogenic E. coli isolates carried exVAGs with the highest prevalence, followed by badger (Meles meles) and roe deer isolates. Adhesion was found to be very diverse. Adhesion was specific to cells, host, and tissue, though it was also unspecific. Occurrence of the following VAGs was associated with a higher rate of adhesion to one or more cell lines: afa-dra, daaD, tsh, vat, ubeA, fyuA, mat, sfa-foc, malX, pic, irp2, and papC. In summary, we established new screening methods which enabled us to characterize large numbers of E. coli isolates. We defined reservoirs for potential pathogenic E. coli. We also identified a very broad range of colonization strategies and defined potential new adhesion genes.

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