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Unravelling problems in food safety

Public awareness on Attaching-effacing Escherichia coli (AEEC) has been caused due to their implication in outbreaks of lethal haemolytic uremic syndrome (HUS), resulting from consumption of contaminated food products. This has led the scientific community to seek the molecular, immunological and epidemiological basis of AEEC, in order to design effective strategies for the control of its resultant infections in humans and animals alike.

Attaching-effacing Escherichia coli (AEEC) constitutes a group of pathogenic E. coli common to humans and animals. E. coli belongs to the normal intestinal flora as all mammals are generally colonised by E. coli at birth. However not all strains of E coli are harmless. Enterohaemorrhagic E. coli (EHEC), for example is a causative agent of human haemorrhagic colitis and haemolytic uremic syndrome (HUS), and enteropathogenic E. coli (EPEC), an agent of diarrhoea in infants and newborn animals.

The E. coli that causes these diseases has specific characteristics (called virulence attributes) that enable them to cause disease. Therefore, the presence of gene encoding for virulence attributes can be used to distinguish these pathogens from the nonpathogenic E. coli normally carried in the intestine.

Twelve European, Canadian and Israeli research laboratories from the medical and veterinary sectors worked together to unravel the molecular, immunological and epidemiological basis for controlling zoonotic AEEC infections. The study of AEEC pathogenesis is of primary importance in order to determine the virulence factors allowing the eradication strategy to focus on the defined pathotypes.

The virulence factors of pathogenic bacteria may be encoded by particular regions of the prokaryotic genome termed pathogenicity islands. Pathogenicity islands belong to the class of genomic islands which are common genetic elements sharing a set of unifying features. They are present in the genome of pathogenic strains of a given species but absent or only rarely present in those of non-pathogenic variants of the same or related species.

Genomic islands have been acquired by horizontal gene transfer and as they promote genetic variability, they play an important role in microbial evolution. Enteropathogenic Escherichia coli (EPEC) and enterohemorragic E. coli (EHEC) possess a pathogenicity island (PAI), termed the locus of enterocyte effacement (LEE), which confers the ability to cause the characteristic attaching and effacing lesions of the brush border. In contrast to other E. coli pathogenicity islands, the LEE was supposed to be stable. However, in an effort to quantify and analyse the stability of the LEE in AEEC strains in vivo and in vitro, research results have proved that the LEE was also unstable.

Since AEEC infections can have a severe impact on public health both as a human and as an animal disease, achievements in the understanding of the molecular, immunological and epidemiological basis of AEEC infections are of high importance to public health. Subsequent adverse consequences on human food safety could be avoided with the successful understanding of this pathogen.

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