

Molecular Evolutionary Relationships Between O-Antigens of Enteric Bacteria

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Abstract : Enteric bacteria *Escherichia coli* is the predominant facultative anaerobe of the colonic flora, and some specific serotypes are associated with enteritis, hemorrhagic colitis, and hemolytic uremic syndrome. *Shigella* spp. are human pathogens that cause diarrhea and bacillary dysentery (shigellosis). They are in effect *E. coli* with a specific mode of pathogenicity. Strains of *Salmonella enterica* are responsible for a food-borne infection (salmonellosis), and specific serotypes cause typhoid fever and paratyphoid fever. All these bacteria are closely related in respect to structure and genetics of the lipopolysaccharide, including the O-polysaccharide part (O-antigen). Being exposed to the bacterial cell surface, the O antigen is subject to intense selection by the host immune system and bacteriophages giving rise to diverse O-antigen forms and providing the basis for typing of bacteria. The O-antigen forms of many bacteria are unique, but some are structurally and genetically related to others. The sequenced O-antigen gene clusters between conserved *galF* and *gnd* genes were analyzed taking into account the O-antigen structures established by us and others for all *S. enterica* and *Shigella* and most *E. coli* O-serogroups. Multiple genetic mechanisms of diversification of the O-antigen forms, such as lateral gene transfer and mutations, were elucidated and are summarized in the present paper. They include acquisition or inactivation of genes for sugar synthesis or transfer or recombination of O-antigen gene clusters or their parts. The data obtained contribute to our understanding of the origins of the O-antigen diversity, shed light on molecular evolutionary relationships between the O-antigens of enteric bacteria, and open a way for studies of the role of gene polymorphism in pathogenicity.

Keywords : enteric bacteria, O-antigen gene cluster, polysaccharide biosynthesis, polysaccharide structure

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