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Molecular characterization of Novel Serotype 1c strains of *Shigella flexneri*

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Slatyer Seminar Room, R N Robertson Building (#46)



The enterobacterium *Shigella* causes endemic bacillary dysentery in humans which is often fatal in children in developing countries. To date, there is yet to be a successful vaccine strategy in the prevention of *Shigella* infections partly due to broad serodiversity in various species and emergence of new uniquely immunoreactive strains (serotypes). Despite the fact that *S. flexneri* serotype 1c first emerged in the late 1980s, it is only in recent times that we have begun to understand the molecular aspects of this little known serotype.

In this study, the *gtrIC* gene cluster of serotype 1c strains from several geographic areas are compared at nucleotide level. The function of this gene cluster was analysed. Besides, this project also investigates the genetic arrangement and evolutionary origins of O-antigen modification genes in the genome of serotype 1c by examining the DNA sequences flanking the *gtr1c* gene cluster. The thesis also determined the effect of the modification caused by this gene cluster on the virulence of *Shigella flexneri*.

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