

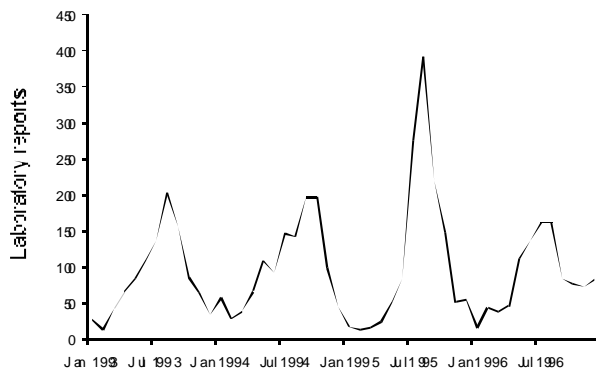
Rotavirus diversity: what surveillance will tell us

Paul J Masendycz, Enzo A Palombo, Graeme L Barnes, Ruth F Bishop,
National Rotavirus Reference Centre, Department of Gastroenterology and Clinical Nutrition,
Royal Children's Hospital, Flemington Road, Parkville Victoria 3052,
email: masenyp@cryptic.rch.unimelb.edu.au

Rotaviruses are the major cause of severe acute diarrhoea in infants and young children throughout the world.^{1,2} In Australia, the pathogen is believed to be responsible for the annual admission of up to 12,000 children to hospitals nationwide.³ Rotavirus infection is the cause of approximately 50% of the admissions to hospital with acute gastroenteritis of children under 5 years of age.³ The rates of hospitalisation between the States can vary markedly, with New South Wales, Queensland and South Australia having almost twice the rate of hospitalisation as Victoria.³

Rotavirus incidence generally follows a typical seasonal pattern in temperate regions of the country, with peaks in mid to late winter² (Figure 1) (personal communication, Professor Ruth Bishop, Department of Gastroenterology, Royal Children's Hospital, Parkville Victoria).

Figure 1. Laboratory reports of rotavirus, Australia 1993-1996, by month of specimen collection



Source of data: Four year Australia-wide rotavirus surveillance study, 1993-1996 (personal communication, Professor Ruth Bishop, Department of Gastroenterology, Royal Children's Hospital, Parkville Victoria).

Previous studies in the laboratories at the Royal Children's Hospital have shown the prevalence of the four major serotypes G1, G2, G3 and G4 differs from centre to centre and from year to year, with serotype G1 strains the most prevalent.⁴ Larger population centres generally experience greater serotype diversity within any one year. Analysis of the strains by gel electrophoresis has shown up to 10 different electropherotypes can exist within a serotype within one year and are often replaced by new electropherotypes every season. The coexistence of similar electrophoretic strains between adjacent centres such as Melbourne and Hobart is not uncommon.

New rotavirus strains are emerging continually. We have identified novel human strains that have been assigned serotype G6 and G8.^{5,6} These serotypes are rare in humans and are normally associated with disease in cattle. The strains are believed to be derived from reassortment between human and bovine viruses. These reassortant strains are new to Australia and their novel genetic make-up gives us an indication of how rotaviruses evolve and diversify. Our genetic analysis of the strains generated from rotavirus surveillance provides information about the existence of distinct genetic lineages of rotaviruses within serotypes and the temporal changes occurring in these.

Rotavirus strains with unusual genetic and antigenic properties were discovered in children in Alice Springs and Darwin between December 1993 and August 1994.⁷ The strains were responsible for outbreaks resulting in the hospitalisation of approximately 140 children. DNA analysis of the strains causing the outbreak found them to be reassortants between the two major defined genogroups of human rotaviruses. Information about the diversity of rotaviruses enables us to assess the efficacy of rotavirus vaccines.

A candidate rhesus tetravalent rotavirus vaccine should be available in Australia soon. It uses a genetically modified rhesus rotavirus strain carrying genes expressing the major human G serotype specificities. Prior to the vaccine's release, accurate baseline data of rotavirus infections and the degree of antigenic and genetic variation in strains causing disease in humans, needs to be established. A comprehensive rotavirus surveillance study should address some of these issues. Such a study is currently being undertaken by the newly formed National Rotavirus Reference Centre (NRRC). The NRRC was established with the aims of conducting rotavirus surveillance, determining rotavirus prevalence, monitoring epidemics and characterising representative specimens by rotavirus serotype.

Established sentinel centres around Australia already collect rotavirus positive specimens for the centre. The NRRC is seeking rotavirus notifications from Australian laboratories that screen for rotavirus and would like to be informed about rotavirus outbreaks or epidemics. It is planned that representative numbers of positive specimens will be serotyped by enzyme immune assay and polymerase chain reaction (PCR). Findings for the first year of operation will be provided to the National Centre for Disease Control. Data will be collated and findings reported in *Communicable Diseases Intelligence* on a regular basis (approximately every 2 months). Assistance with this Australia-wide rotavirus surveillance will enable

the creation of a more comprehensive epidemiological profile of rotavirus infection in Australia.

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