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Australian Rotavirus Surveillance Program: Annual Report, 2017

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Table 2: Rotavirus G- and P- genotype distribution in infants, children and adults, 1 January to 31 December 2017

Centre	Type total	G1P[8]		G2P[4]		G3P[8]		G3P[8] ^a		G8P[8]		G9P[8]		G12P[8]		Other ^b		Non-type ^c	
		%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n
ACT	19	-	0	-	0	11	2	84	16	5	1	-	0	-	0	-	0	-	0
New South Wales	363	1	4	9	32	7	25	51	185	25	91	3	12	<1	1	2	9	1	4
Northern Territory ^d	100	-	0	99	99	-	0	-	0	-	0	-	0	-	0	1	1	-	0
Queensland	56	2	1	9	5	20	11	-	0	13	7	32	18	-	0	5	3	20	11
South Australia	112	2	2	68	76	13	15	5	6	4	4	1	1	-	0	4	4	4	4
Tasmania	65	2	1	40	26	3	2	48	31	2	1	-	0	-	0	5	3	2	1
Victoria	70	4	3	9	6	4	3	10	7	43	30	6	4	14	10	9	6	1	1
Western Australia	229	1	3	66	151	12	27	4	10	14	32	1	2	<1	1	1	2	<1	1
TOTAL	1,014	1	14	39	395	8	85	25	255	16	166	4	37	1	12	3	28	2	22

a Equine-like G3P[8]

b See Table 3

c A specimen where G- and/or P- genotype was not determined

d Specimens collected in NT were received from interstate laboratories in SA (SA Pathology; n=25) and WA (PathWest Laboratory Medicine/Western Diagnostics Pathology; n=75)

Table 3: Mixed and unusual G- and P- genotypes identified in infants, children and adults, 1 January to 31 December 2017

Genotype	RotaTeq						Rotarix ^a				Total
	Qld	SA	Vic	WA	NSW	NT	Tas				
EqG3P[6]	-	-	1	-	-	-	-	-	-	1	
G2P[8]	-	1	-	1	1	-	-	-	-	3	
G3P[3] feline/canine	-	-	-	-	-	1	-	-	-	1	
G3P[4]	-	-	1	-	-	-	-	-	-	1	
G3P[6]	-	-	1	-	-	-	-	-	-	1	
G3P[9] feline/canine	-	-	2	-	-	-	-	-	-	2	
G4P[8]	-	-	-	-	3	-	-	2	-	5	
G6P[8]	-	-	1	-	-	-	-	-	-	1	
G8P[1]	-	-	-	-	1	-	-	-	-	1	
G9P[4]	1	3	-	1	4	-	-	1	-	10	
G9P[9]	1	-	-	-	-	-	-	-	-	1	
MIXED G1/G3P[8]	1	-	-	-	-	-	-	-	-	1	
Total	3	4	6	2	9	1	-	3	-	28	

a ACT values are not shown since no ACT detections of these genotypes were made.

the remaining 22 samples represented 10 uncommon rotavirus genotypes. Seven of these strains included unusual combinations, such as G2P[8], G3P[4], G3P[6], Equine-like G3P[6], G6P[8], G9P[4], and G9P[9]. The remaining were represented by strains that contained an animal VP7 and/or VP4 component. Feline/canine-like G3P[3] was identified in one sample from the NT, feline/canine-like G3P[9] were identified in two samples in Vic, while bovine-like G8P[1] (n=1) was identified in NSW.

Genotypes identified in samples from children ≤5 years of age

449 wildtype rotavirus samples in total were collected from children ≤5 years of age (Table 4). Within this subset, G2P[4] was the most common genotype identified, found in 32% of all samples. Equine-like G3P[8] was the second most common genotype (29%), and G8P[8] strains were the third most common genotype (16%). G1P[8], G3P[8], G9P[8], and G12P[8], represented minor genotypes, identified in 1–10% of all genotypes. (Table 4).

Genotypes identified in samples from individuals >5 years of age

A total of 565 rotavirus samples were collected from children >5 years, adults, and patients with an unknown age (n=76) (Table 5). As with the ≤5 years of age group, G2P[4] was the main genotype identified (44%), followed by equine-like G3P[8] (22%) and G8P[8] (17%).

Distribution of genotypes according to vaccine tendered in children ≤5 years of age

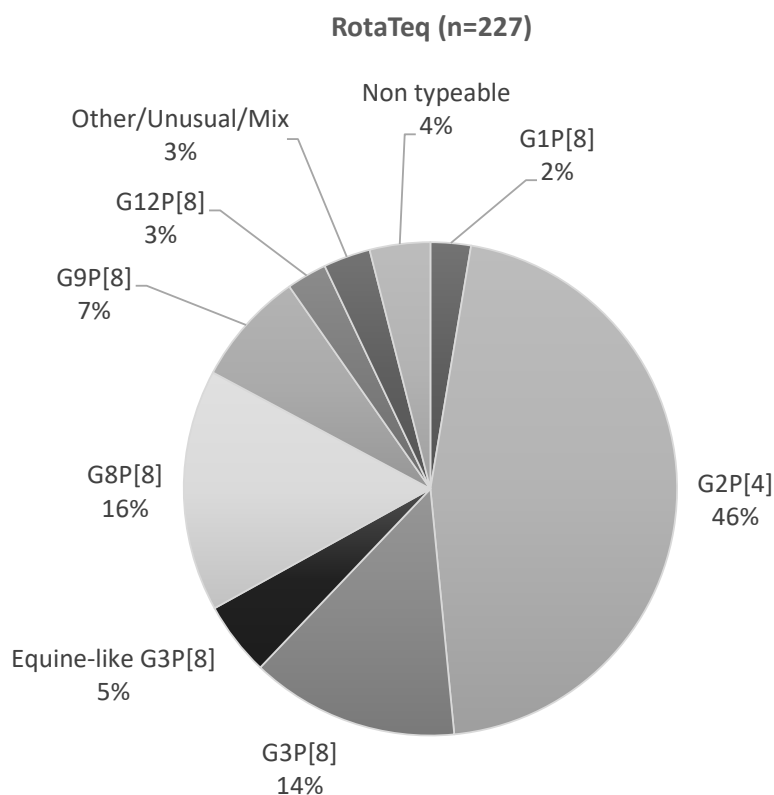
G- and P- genotypes of the 449 wildtype rotavirus samples were divided according to vaccine use (Figure 3). In states where RotaTeq was in use, G2P[4] was the dominant strain overall, representing 46%, compared to 18% in Rotarix states/territories. G8P[8] was the second most common genotype identified, representing 16% of all genotypes identified in RotaTeq states. However, in states and territories that used

Rotarix, Equine-like G3P[8] was the dominant strain, representing 54%, compared to 5% in RotaTeq states (Figure 3).

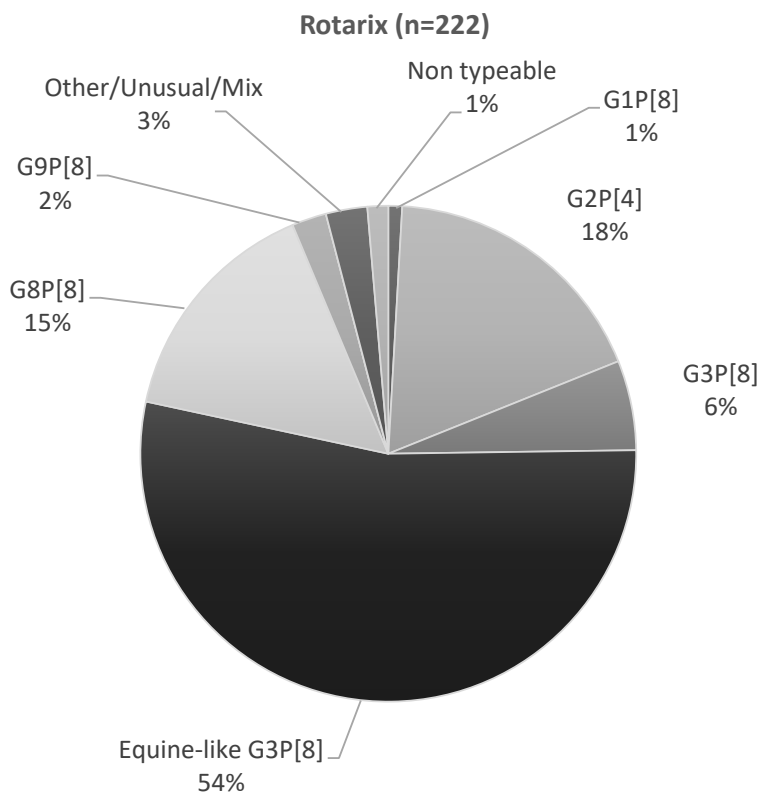
On 1 July 2017, Rotarix replaced RotaTeq in WA, Vic, SA, and Qld. After 1 July 2017, all states and territories of Australia exclusively used Rotarix vaccine against rotavirus under the NIP. To identify if the change in vaccination schedule could have had an impact on genotype distribution, further analysis based on date of collection was performed (Figure 4). Although samples were not able to be analysed for the full 6 months after the change from RotaTeq to Rotarix in all four states affected (Queensland, SA, Victoria, and WA) there was a good representation of data from Victoria and WA. In addition, no samples were received from NT for the period of 1 Jun – 31 Dec, therefore data presented in this report for this period is limited to ACT, NSW, and Tasmania for the states and territories that administered Rotarix in the NIP for the full 12 months in 2017. In states where RotaTeq was in use from Jan to Jun, 2017, G2P[4] strains were the dominant genotype in children ≤5 years, identified in 63% of samples, however after the change to Rotarix in July, G2P[4] reduced to 16% (Jul–Dec 2017). However, a similar decrease in G2P[4] strains was observed in jurisdictions that used Rotarix for the whole year, from 56% for the period of Jan–Jun, to 7% in Jul–Dec. In the states that used Rotarix for the full 12 months in 2017, the decrease in G2P[8] strains coincided with an increase of equine-like G3P[8], from 23% (Jan–Jun) to 62% (Jul–Dec). In contrast, equine-like G3P[8] maintained low levels of circulation (≤6%) between Jan–Jun and Jul–Dec in states that changed vaccines in July. An increase in G8P[8] strains was observed in all states and territories irrespective of vaccine used, from ≤4% in Jan–Jun, to 39% and 18% in Jul–Dec respectively (Figure 4).

Figure 3: Overall distribution of wildtype rotavirus G- and P- genotypes identified in Australian children ≤5 years of age, based on vaccine use^a, Australia, 1 January to 31 December 2017

RotaTeq^a states



Rotarix states and territories



^a Australian NIP changed to Rotarix exclusively on 1 July, 2017

Table 4: Rotavirus G- and P- genotype distribution in infants and children ≤5 years of age, 1 January to 31 December 2017

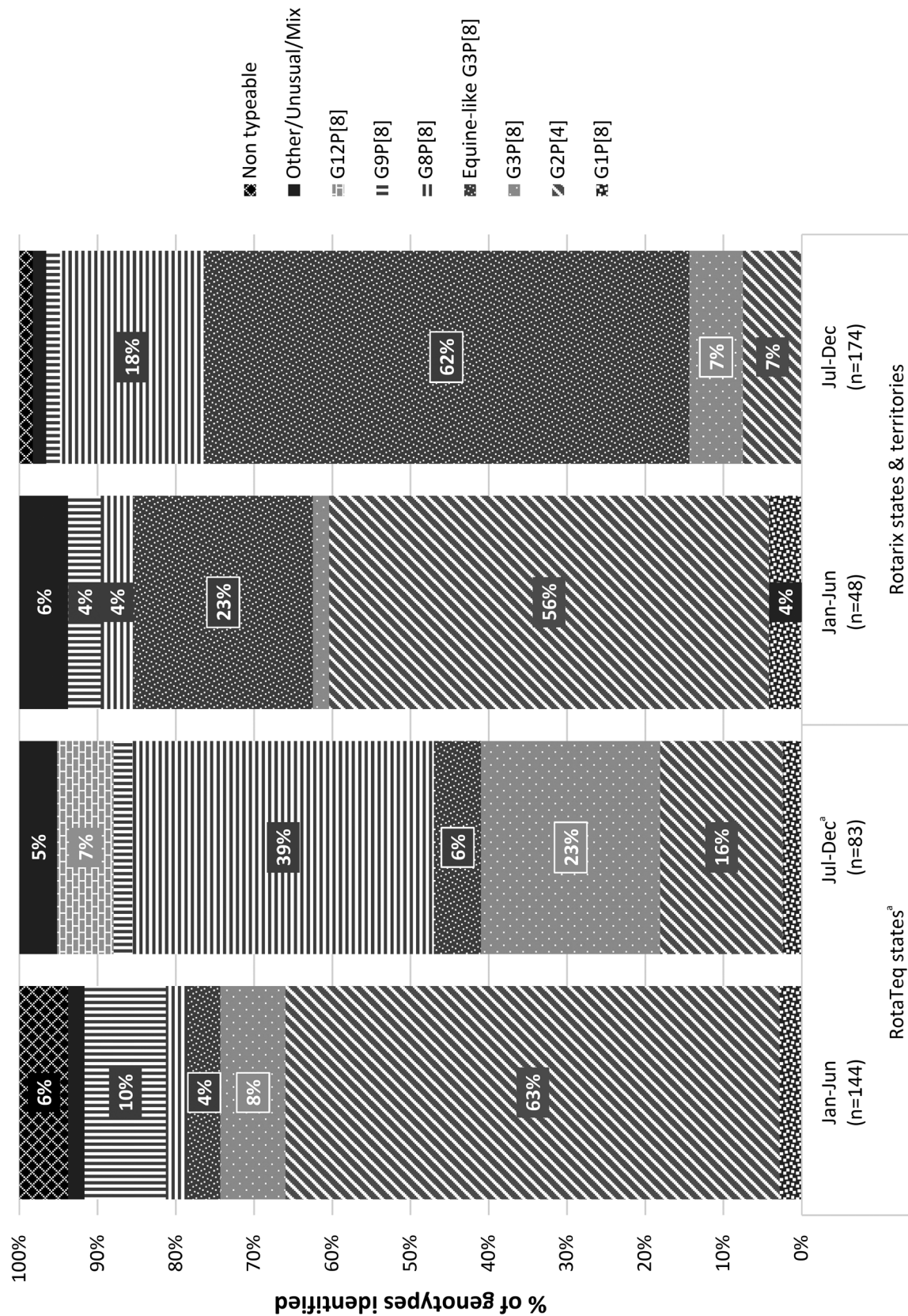
Centre	Type total	G1P[8]		G2P[4]		G3P[8]		G3P[8] ^a		G8P[8]		G9P[8]		G12P[8]		Other ^b		Non-type ^c	
		%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n
ACT	16	-	0	-	0	13	2	88	14	-	0	-	0	-	0	-	0	-	0
New South Wales	165	1	2	10	16	6	10	56	93	20	33	3	5	-	0	2	4	1	2
Northern Territory	19	-	0	95	18	-	0	-	0	-	0	-	0	-	0	5	1	-	0
Queensland	32	-	0	-	0	22	7	-	0	13	4	41	13	-	0	6	2	19	6
South Australia	30	3	1	63	19	17	5	10	3	-	0	-	0	-	0	-	0	7	2
Tasmania	22	0	0	27	6	5	1	55	12	5	1	-	0	-	0	5	1	5	1
Victoria	42	5	2	10	4	5	2	7	3	45	19	7	3	14	6	7	3	-	0
Western Australia	123	2	3	66	81	14	17	4	5	11	13	1	1	-	0	2	2	1	1
Total	449	2	8	32	144	10	44	29	130	16	70	5	22	1	6	3	13	3	12

a Equine-like G3P[8]

b See Table 3

c A specimen where G- and/or P- genotype was not determined

Figure 4: Overall distribution of wildtype rotavirus G- and P- genotypes identified in Australian children ≤5 years of age, based on vaccine usage, Australia, 1 January to June, and 1 July to 31 December, 2017



^a NIP across Australia changed to Rotarix exclusively from 1st July, 2017.

Note: No samples have been processed after August in Rotarix states Old and SA. The majority of Rotarix samples are represented by WA and Victoria, for which complete year analysis has been performed. Northern Territory represents data from Jan–May, as no samples after May 2017 were received for this reporting period.

Table 5: Rotavirus G- and P- genotype distribution in children >5 years of age and adults, 1 January to 31 December 2017

Centre	Type total	G1P[8]		G2P[4]		G3P[8]		G3P[8] ^a		G8P[8]		G9P[8]		G12P[8]		Other ^b		Non-type ^c	
		%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n	%	n
ACT	3	-	0	-	0	-	0	67	2	33	1	-	0	-	0	-	0	-	0
New South Wales	198	1	2	8	16	8	15	46	92	29	58	4	7	1	1	3	5	1	2
Northern Territory	81	-	0	100	81	-	0	-	0	-	0	-	0	-	0	-	0	-	0
Queensland	24	4	1	21	5	17	4	-	0	13	3	21	5	-	0	4	1	21	5
South Australia	82	1	1	70	57	12	10	4	3	5	4	1	1	-	0	5	4	2	2
Tasmania	43	2	1	47	20	2	1	44	19	-	0	-	0	-	0	5	2	-	0
Victoria	28	4	1	7	2	4	1	14	4	39	11	4	1	14	4	11	3	4	1
Western Australia	106	-	0	66	70	9	10	5	5	18	19	1	1	1	1	-	0	-	0
Total	565	1	6	44	251	7	41	22	125	17	96	3	15	1	6	3	15	2	10

a Equine-like G3P[8]

b See Table 3

c A specimen where G- and/or P- genotype was not determined

