

Protecting and improving the nation's health

Laboratory reports of hepatitis A infections in England and Wales, 2019

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Introduction

There were a total of 503 laboratory reports of new patients who tested positive for acute hepatitis A infection in England and Wales in 2019, excluding the known false positive reports, and including additional patients reported by the Virus Reference Department (Table 1, Figure 1).

Laboratory reports were received via the Second Generation Surveillance System (SGSS) which is a voluntary electronic reporting system. False positives were defined as 'patients' with:

- a) samples that were received by the Virus Reference Department (VRD) where recent hepatitis A virus (HAV) infection was not confirmed by serology or where HAV RNA was not detected
- b) samples for which the reporting laboratory notified the VRD of false positive results or reporting issues, for example through returning the letters received as part of the HAV enhanced surveillance system, or
- c) samples which the VRD identified as laboratory quality controls.

A total of 291 false positive reports were identified, which included 206 where the samples were sent to the VRD and recent infection was not confirmed.

The VRD confirmed HAV infection in specimens belonging to an additional 107 patients that were not reported through SGSS. A total of 396 cases were reported through SGSS, after excluding the known false positive reports.

The greatest number of reports were among those in the 15 to 24 year age group (85, 16.9%) closely followed by those in the 25 to 34 year age group (83, 16.5%) and those aged 65 years and over (66, 13.1%). One report of HAV in the under 1 year age group was received. More reports were received for females than males in the first and third quarters of 2019, with more reports among males during the remaining quarters (Table 1).

Table 1. Laboratory reports of hepatitis A by age, sex, and quarter, England and Wales, 2019*

Age group (years)	Q1 January to March			Q2 April to June			Q3 July to September			Q4 October to December			Total
	<1	0	0	0	0	1	0	0	0	0	0	0	0
1 to 4	1	1	0	4	6	0	2	2	0	5	5	0	26
5 to 9	8	2	0	4	1	0	6	7	0	9	9	0	46
10 to 14	7	3	0	6	9	0	6	7	0	8	4	0	50
15 to 24	12	14	0	15	12	0	6	7	0	6	13	0	85
25 to 34	8	16	0	4	11	0	11	10	0	8	15	0	83
35 to 44	13	6	0	6	8	0	3	6	0	3	4	0	49
45 to 54	11	6	0	7	6	0	5	2	0	8	7	0	52
55 to 64	3	6	1	3	5	0	3	5	0	8	9	0	43
≥65	15	19	0	4	4	0	6	1	0	11	6	0	66
NK	0	0	0	0	0	1	1	0	0	0	0	0	2
Total	78	73	1	53	63	1	49	47	0	66	72	0	503**

^{*} Due to late reporting, numbers for each quarter may have changed slightly since their HPR quarterly reports. Reports from Wales for Q1 and Q2 were not received via SGSS due to reporting issues, however some cases for that period were identified through the VRD.

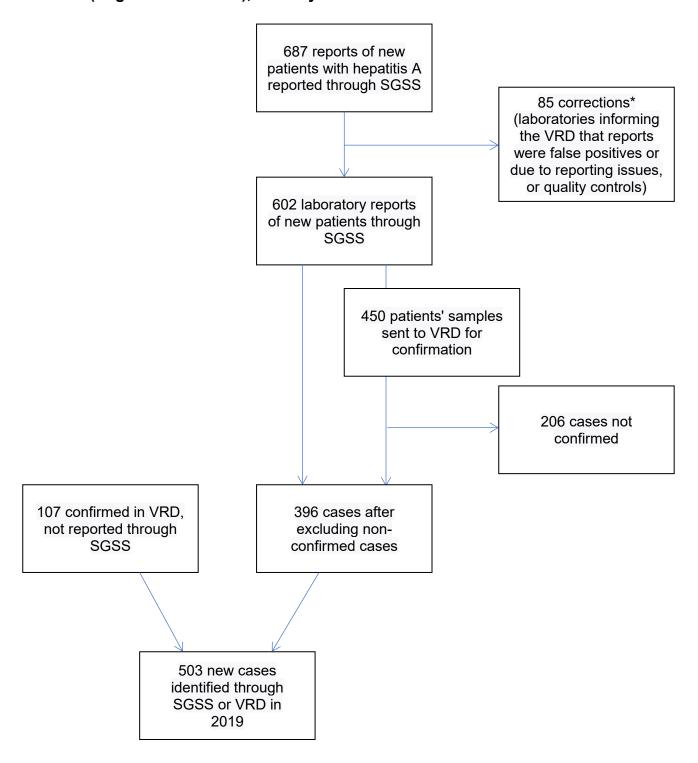
^{**} Provisional numbers.

The number of laboratory reports by PHE centre is presented below (Table 2). Reports were assigned to a PHE centre according to either the:

- 1. Patient's place of residence.
- 2. Postcode of the patient's registered GP practice.
- 3. Postcode of the source laboratory.

In 2019, the greatest number of hepatitis A reports were from the London region (160, 31.8%) followed by the North West, East of England and Yorkshire and Humber with a similar number of reports (66 to 56, 13.1% to11.1%) (Table 2). The large number of reports from London compared to other regions is consistent with previous years. Due to reporting issues, laboratory reports from Wales for the latter half of 2018 and first half of 2019 have not been received – however, 7 cases from Wales from the first half of 2019 have been reported through the VRD.

Figure 1. Flowchart of laboratory reports of hepatitis A and confirmation status by the VRD (England and Wales), January to December 2019



^{* 62} of the corrections were due to a reporting issue by a laboratory in the South East.

Table 2. Laboratory reports of hepatitis A by PHE centre (England) and Wales (2009 to 2019)

PHE centre	Year											
PHE Centre	2009	2010	2011	2012	2012	2013	2014	2015	2016	2017	2019	
East Midlands	14	9	6	7	8	10	11	30	29	22	18	
East of England	38	36	24	25	23	15	24	47	86	49	59	
London	53	72	69	71	91	118	79	180	414	150	160	
North East	8	12	10	13	10	9	11	17	25	7	7	
North West	64	56	24	28	34	22	43	22	50	41	66	
South East	50	28	44	38	29	55	27	51	91	54	50	
South West	24	48	11	18	29	14	15	22	71	34	28	
West Midlands	59	61	41	44	29	32	47	46	99	50	42	
Yorkshire and Humber	34	40	23	36	19	17	69	24	34	26	56	
Wales*	12	9	5	8	11	8	4	5	43	19	17	
Total	356	371	257	288	283	300	330	444	942	452	503**	

^{*} Non PHE centre.

Reports from Q3 and Q4 2018 currently outstanding.

Reports from Q3 and Q4 2018 and Q1 and Q2 2019 were not received through SGSS however some cases from Q1 and Q2 2019 were identified through the VRD.

Overall, there was an 8.9% decrease in the number of reports in 2019 (n=503) compared to 2018 (n=552) when including non-SGSS cases identified by the VRD for both years. The number of reports in 2019 decreased from quarter 1 (152, 30.2%) to quarter 3 (96, 19.1%), before increasing in quarter 4 (138, 27.4%)(Table 1). The number of reports in the first 3 quarters was lower compared to the corresponding quarters in 2018, with decreases of 4% to 32%, but greater in the fourth quarter of 2019 compared to 2018 with an increase of 26% (2018 data including additional non-SGSS cases not shown).

The annual number of HAV reports decreased from 2005 to 2013, followed by a slight increase from 2013 to 2015, and larger increases in 2016 and 2017 coinciding with the start and peak of the national HAV outbreak largely associated with men who have sex with men (MSM). The number of reports fell in 2018, in line with the end of the MSM

^{** 2019} data includes confirmed cases identified by the VRD that were not reported through SGSS.

outbreak, and continued to fall in 2019. However, numbers did not return to pre-2016 levels.

A total of 797 confirmed or probable cases associated with the national 2016 to 2018 MSM outbreak were identified between July 2016 and June 2018. Three distinct outbreak strains reported as Event 1, 2 and 3 by the European Centre for Disease Prevention and Control (ECDC) were associated with this outbreak [1, 2, 3, 4]. This incident was declared over in June 2018 [5]. A number of incidents of the outbreak spilling over into the community were also identified.

A number of clusters were identified in 2019 and one outbreak in the Yorkshire and Humber region involving 33 confirmed cases took place in a school in the second quarter of 2019, of which 20 cases were students and staff.

Age and sex reported through the laboratory reporting systems have been well completed every year over the past decade (>97% complete) (Figure 2), including in 2019 (99.4% complete). Where known, males accounted for a slim majority of reports (50.9%, 255 out of 501) during 2019 (Figure 2).

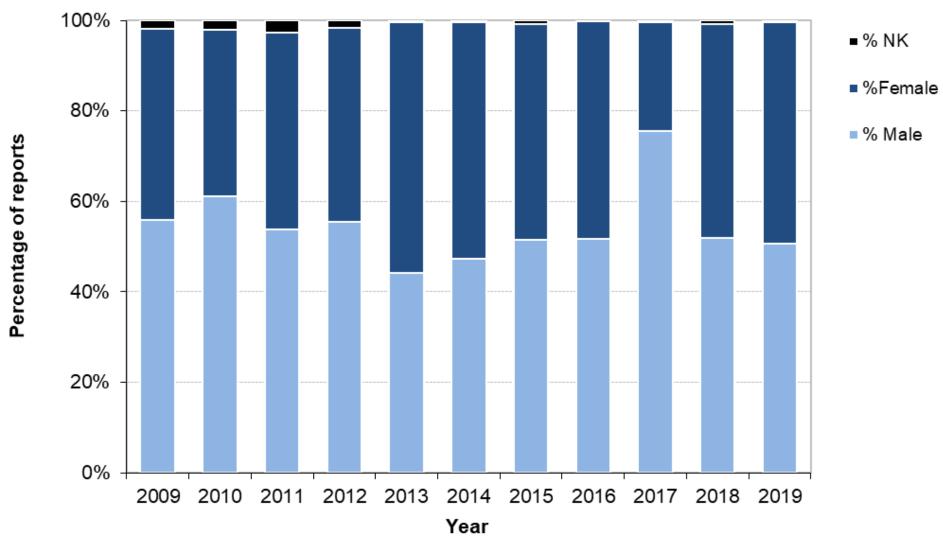


Figure 2. Percentages of hepatitis A laboratory reports by sex, England and Wales* (2009 to 2019**)

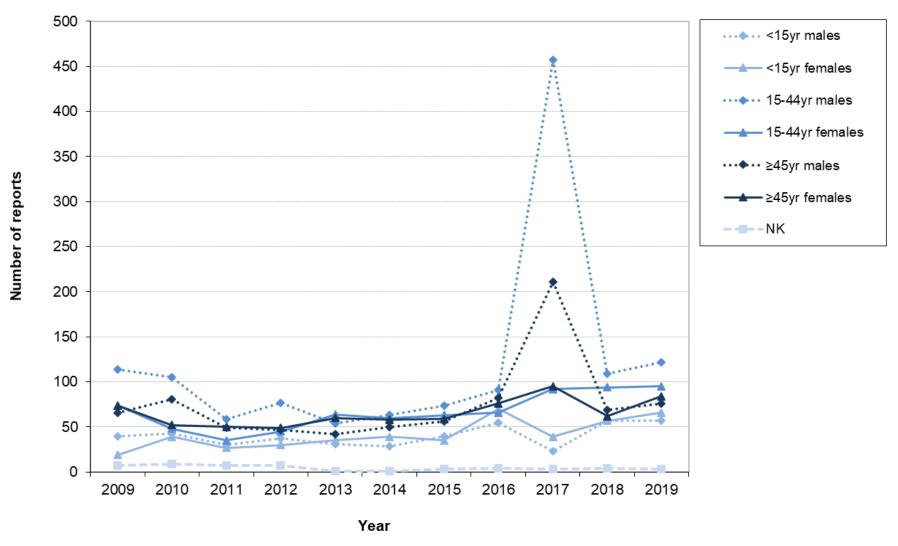
^{*} Reports from Wales from Q3 and Q4 2018 and Q1 and Q2 2019 were not received through SGSS however some cases from Q1 and Q2 2019 were identified through the VRD.

^{** 2019} data includes confirmed cases identified by the VRD that were not reported through SGSS.

In 2019, the number of reports decreased in all age-sex groups except for in females aged 45 years and over, when compared to 2018 and including non-SGSS cases identified by the VRD for both years (Figure 3, 2018 figures including additional non-SGSS cases not shown). The largest decrease was seen for males under 15 years of age where 57 reports were received compared to 76 in 2018 (difference=19, 25.0% decrease). The number of reports in males aged 15 to 44 years decreased from 134 in 2018 to 122 (difference=12, 9.0% decrease) in 2019. In females aged 45 years and over, the number of reports received increased to 84 compared to 69 in 2018 (difference=15, 21.7% increase).

During 2019, females accounted for a small majority of reports in the under 15 years and 45 years and over age groups (53.7% and 52.5% respectively), and males accounted for a small majority of reports in the 15 to 44 year age group (56.2%).

Figure 3. Laboratory reports of hepatitis A by age and sex, England and Wales* (2009 to 2019**)



^{*} Reports from Wales from Q3 and Q4 2018 and Q1 and Q2 2019 were not received through SGSS however some cases from Q1 and Q2 2019 were identified through the VRD.

^{** 2019} data includes confirmed cases identified by the VRD that were not reported through SGSS.

Risk factor information was poorly reported through the laboratory reporting system. Travel history was available for 16.9% (67 out of 396) of reported SGSS cases; compared to an average of 17.7% (range 14.6% to 22.7%) from 2009 to 2019 (Table 3). Of these, 13.4% (9 out of 67) were reported to have travelled abroad. Risk factor information reported through the laboratory reporting system including travel history remains rare, which limits the conclusions that can be drawn from these data.

Table 3. Trends in hepatitis A laboratory reports, England and Wales* (2009 to 2019)

Year	2009	2010	2011	2012	2012	2013	2014	2015	2016	2017	2019**
Number of reports	356	371	257	288	283	300	330	444	942	452	503
Number (%) aged 15 to 44 years	190 (53.4)	157 (42.3)	96 (37.4)	122 (42.4)	118 (41.7)	123 (41.0)	138 (41.8)	157 (35.4)	572 (60.7)	203 (44.9)	217 (43.1)
Number (%) male	220 (61.8)	230 (62.0)	138 (53.7)	162 (56.3)	127 (44.9)	142 (47.3)	170 (51.5)	229 (51.6)	711 (75.5)	235 (52.0)	255 (50.7)
Number (%) with travel history	64 (18.0)	66 (17.8)	43 (16.7)	62 (21.5)	43 (15.2)	50 (16.7)	61 (18.5)	101 (22.7)	147 (15.6)	66 (14.6)	67*** (16.9)
Number (%) travelled abroad	13 (3.7)	29 (7.8)	7 (2.7)	20 (6.9)	10 (3.5)	4 (1.3)	11 (3.3)	11 (2.5)	3 (0.3)	3 (0.7)	9*** (2.3)

^{*} Reports from Wales from Q3 and Q4 2018 and Q1 and Q2 2019 were not received through SGSS however some cases from Q1 and Q2 2019 were identified through the VRD.

^{** 2019} data includes confirmed cases identified by the VRD that were not reported through SGSS.

^{***} Travel data is from SGSS and hence only refers to the 396 SGSS cases in 2019.

Reference laboratory confirmation and phylogeny of hepatitis A infections: 2019

Of the 396 SGSS laboratory reports of acute HAV infection during 2019, 244 (61.6%) cases had samples forwarded to the Virus Reference Department (VRD) for HAV genotyping. Of the 152 (38.4%) cases who did not have a sample forwarded to VRD for HAV genotyping, 5 cases had no sample remaining, 14 cases had samples forwarded for HEV testing, 1 case had a sample forwarded for HCV testing, 1 case had a sample forwarded for HBV testing and there was no additional information for samples of the remaining cases.

In addition, 107 cases were confirmed to have acute HAV infection that had not been reported through the laboratory reporting system, however, all English cases were all recorded in HPZone. The breakdown of samples received per region can be seen in Figure 4.

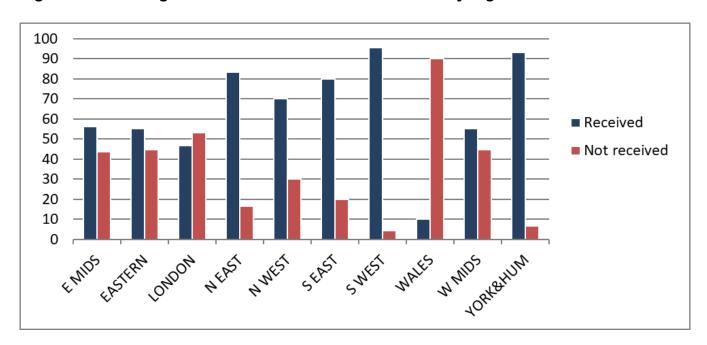


Figure 4. Percentage of cases received for confirmation by region

Of the 351 (107+244) confirmed cases, 168 (47.9%) reported a travel history, 175 (49.9%) had no travel history and 8 (2.2%) had no information (Figure 6).

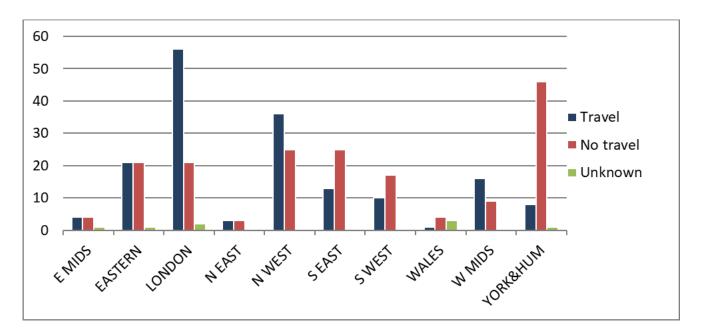


Figure 5. Confirmed HAV infections by region and travel history

The age of the cases ranged from 1 to 86 years of age with travel being the main risk between the ages of 1 and 34 (Figure 3).

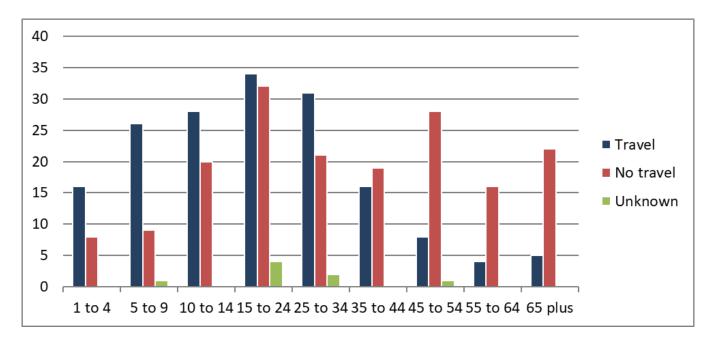
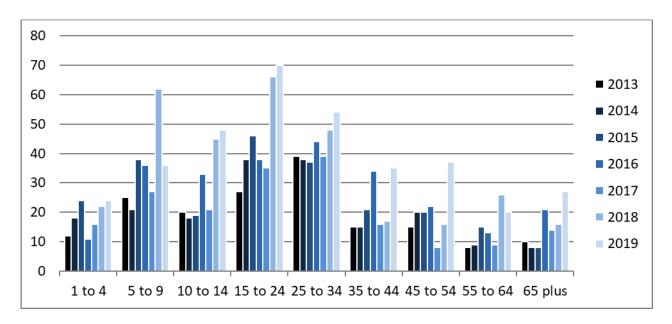


Figure 6. Confirmed HAV infections by age and travel history

There has been an increase in cases confirmed in all age groups compared to 2018, with the exception of 1 to 4; 5 to 9; and 55 to 64. Age groups 10 to 14; 15 to 24; 25 to 34; 35 to 44; 45 to 54; and 65 plus have seen their highest number of cases since the start of the enhanced surveillance (Figure 7).

Figure 7. Comparison of confirmed HAV infections by age 2013 to 2019



Phylogenetic trees

It was possible to genotype 339 of the 351 VRD confirmed cases of acute HAV infection, which fell into the following categories:

- 134 (39.5%) were genotype IA
- 125 (36.9%) were genotype IB
- 80 (23.6%) were genotype IIIA

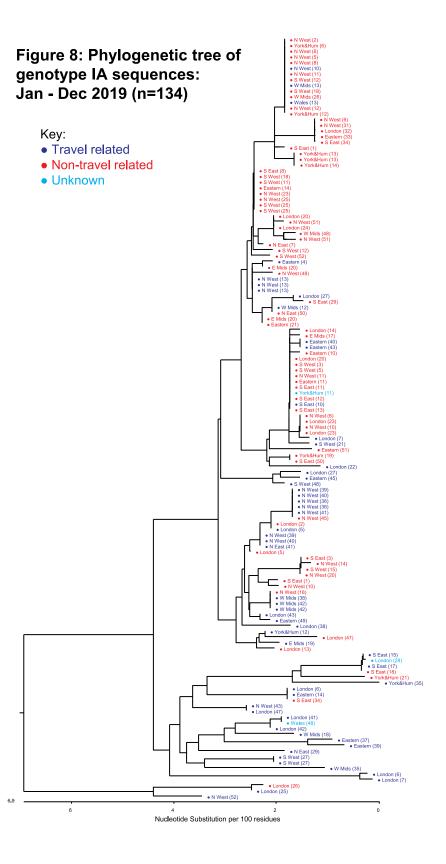
Figures 8, 9 and 10 present sequence information for each genotype as a phylogenetic tree in which each sequenced case is represented by a dot, followed by the PHE region where each case was tested (and the week of testing in brackets). Each case is colour-classified by presumed risk factor (according to whether a travel history was recorded), as follows:

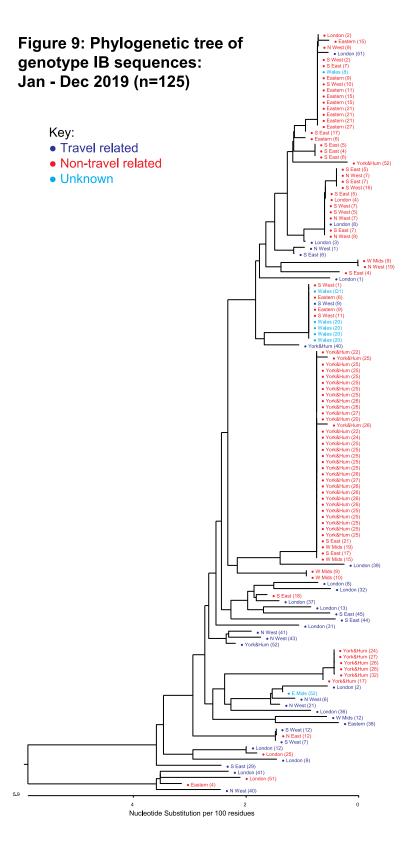
- travel (green)
- non-travel (red)
- unknown (blue)

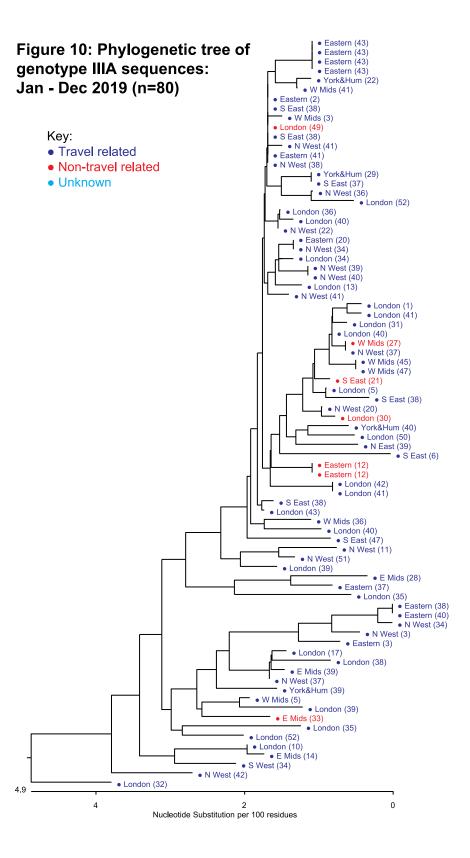
Figure 8 shows the 134 genotype IA sequences generated in 2019. The majority of genotype IA cases had no travel history (75 out of 134, 56%) and were largely associated with Moroccan-like strains [1]. Of the travel-related cases, Morocco and Romania were the most common destinations. Very few cases were seen with the strains associated with the MSM outbreak of July 2016 to June 2018, and all bar one was travel associated.

Figure 9 shows the 125 genotype IB sequences generated in 2019. The majority of cases were non-travel-related (89 out of 125, 71.2%) which was largely due to a community outbreak involving 31 individuals. Of the travel associated cases, the most common area of travel was Africa.

Figure 10 shows the 80 genotype IIIA sequences generated in 2019. As in previous years the majority of cases with genotype IIIA had a travel history (73 out of 80, 91%) with Pakistan being the most commonly visited country (38 cases). Genotype IIIA is geographically associated with South Asia and travellers may not perceive themselves or their family to be at risk if they grew up in an endemic area and are travelling 'home' to visit friends and relatives [7].







Summary of enhanced surveillance

In 2019, 61% of samples associated with laboratory reports of acute HAV infection were forwarded to VRD for genotyping, a drop of 4% compared to 2018. In addition, significant numbers of cases genotyped within VRD have not been reported through the SGSS laboratory reporting system (107 cases) although the majority were notified to their local Health Protection Teams.

Typing of hepatitis A virus remains an invaluable tool in tracking community outbreaks. It has increased our understanding of the molecular epidemiology of the virus and has enabled us to pinpoint the likely country of origin of some viral types of specific outbreaks even when a source cannot be identified. Identification of such community and national outbreaks is only possible by the continued submission of samples by laboratories from both travels associated, and non-travel associated cases.

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