Public Health England

Protecting and improving the nation's health

Laboratory reports of hepatitis A infections in England and Wales, 2017

Health Protection Report
Volume 12 Number 27
27 July 2018

Laboratory reports of hepatitis A infections: 2017

During 2017, there were 942 confirmed laboratory reports of hepatitis A virus (HAV) infection in England and Wales (Table 1). The greatest number of reports were among the 25 to 34 age group (n=292), followed by the 65 and over age group (n=121); no cases of hepatitis A were reported in the under 1 year age group. More reports were received for males than females during every quarter of 2017 (Table 1).

Table 1: Laboratory reports of hepatitis A by age, sex, and quarter, England and Wales, 2017*

Age group (years)	Q1			Q2			Q3			Q4			Total
	Jan-Mar			Apr-Jun			Jul-Sep			Oct-Dec			
	Female	Male	NK	Female	Male	NK	Female	Male	NK	Female	Male	NK	
<1	0	0	0	0	0	0	0	0	0	0	0	0	0
1 to 4	2	2	0	1	2	0	1	0	0	3	4	0	15
5 to 9	5	0	0	3	3	0	2	0	0	9	2	0	24
10 to 14	2	1	0	2	0	0	1	3	0	8	4	0	21
15 to 24	6	20	0	5	33	0	5	21	0	10	11	0	111
25 to 34	6	82	0	14	94	0	13	58	0	12	13	0	292
35 to 44	7	31	0	8	56	0	5	37	0	3	22	0	169
45 to 54	2	23	0	5	29	1	3	26	0	8	20	0	117
55 to 64	7	10	0	4	10	0	6	14	0	2	17	0	70
≥65	11	17	0	12	18	0	17	15	0	18	13	0	121
NK	0	0	0	0	0	0	0	0	0	0	0	2	2
Total	**48**	**186**	**0**	**54**	**245**	**1**	**53**	**174**	**0**	**73**	**106**	**2**	**942**

* Due to late reporting, numbers for each quarter may have changed slightly since their HPR quarterly reports.

The number of laboratory reports by PHE Centre is presented below. Reports were assigned to a PHE Centre according to either i) the patient's place of residence ii) the postcode of the patient's registered GP practice, or the iii) the postcode of the source laboratory. In 2017, the greatest number of hepatitis A reports were from the London (n=414) and West Midlands (n=99) regions (Table 2). The comparatively high number of reports from London were linked to the outbreak of hepatitis A amongst men who have sex with men (MSM) (1).

Overall, there was a 112.2% increase in the number of reports received during 2017 (n=942) compared to 2016 (n=444). Prior to 2012, the overall trend had been a decline in the number of reports since 2007. The increased number of reports during 2017 was due to the outbreak of hepatitis A in MSM. Cases of hepatitis A linked to this outbreak were also seen in non-MSM.

Between July 2016 and December 2017, outbreak clusters of HAV were being investigated nationally by PHE and a PHE standard incident response was declared in December 2016. As the outbreak progressed the standard incident response was escalated to an enhanced incident response in April 2017. The outbreak cases were initially reported from geographically distinct clusters. However as the outbreak progressed MSM were identified nationally as the main risk group and a recent travel history to Spain was also noted in some cases (1). The enhanced surveillance of hepatitis A programme had confirmed these outbreak cases to be of genotype IA with identical RNA sequences. These three distinct outbreak strains reported as Event 1, 2 and 3 by the European Centre for Diseases Prevention and Control (ECDC) were investigated in a number of European countries including the United Kingdom (2). The incident response was de-escalated to a standard incident in January 2018.

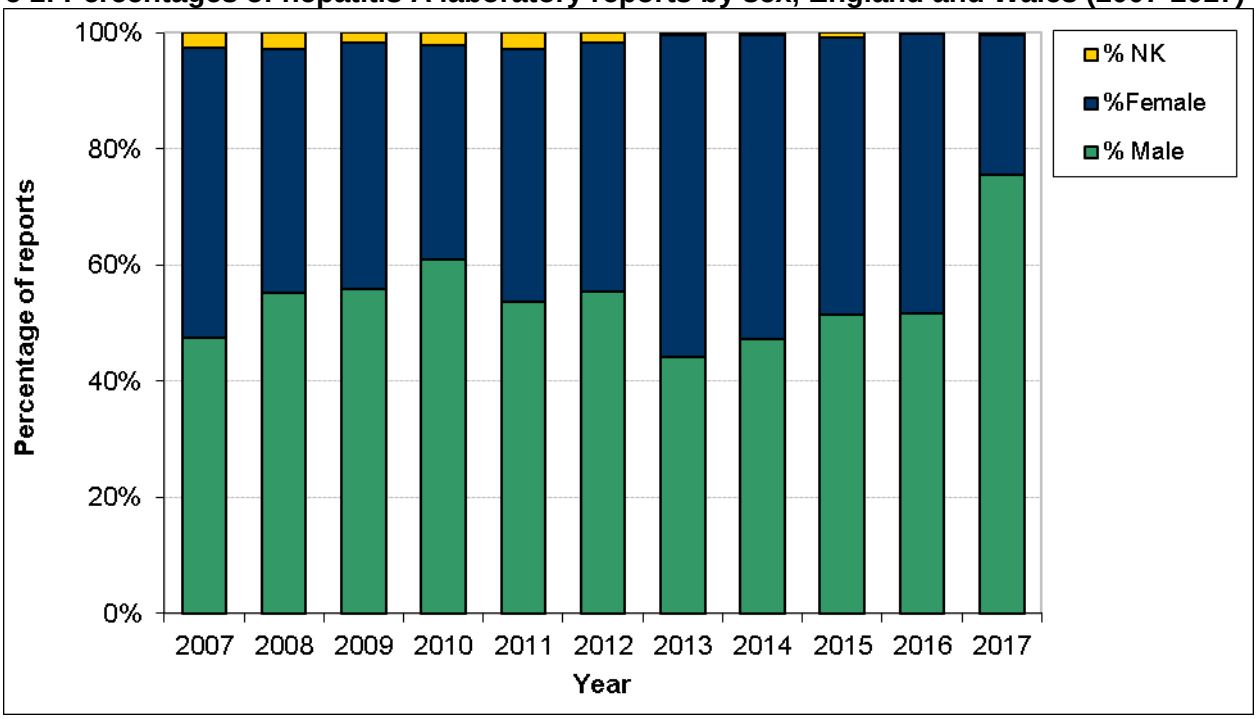
Table 2: Laboratory reports of hepatitis A by PHE Centre (England) and Wales (2007-2017)

PHE Centre	Year										
	2007	**2008**	**2009**	**2010**	**2011**	**2012**	**2013**	**2014**	**2015**	**2016**	**2017**
East Midlands	13	19	14	9	6	7	8	10	11	30	29
East of England	31	34	38	36	24	25	23	15	24	47	86
London	50	54	53	72	69	71	91	118	79	180	414
North East	14	5	8	12	10	13	10	9	11	17	25
North West	63	48	64	56	24	28	34	22	43	22	50
South East	32	66	50	28	44	38	29	55	27	51	91
South West	33	30	24	48	11	18	29	14	15	22	71
West Midlands	71	67	59	61	41	44	29	32	47	46	99
Yorkshire and Humber	36	27	34	40	23	36	19	17	69	24	34
Wales*	20	10	12	9	5	8	11	8	4	5	43
Total	**363**	**360**	**356**	**371**	**257**	**288**	**283**	**300**	**330**	**444**	**942**

*non PHE Centre

Age and sex were well completed each year (>97% complete) (Figure 1). Where known, males accounted for 75% (711/942) of reports during 2017 (Figure 1). Since 2008, the majority of reports were among males for all years, excluding 2013 and 2014 (Figure 1). The proportion of reports among males has varied each year; overall males have accounted for 60% of hepatitis A laboratory reports during this period (range 44-75%).

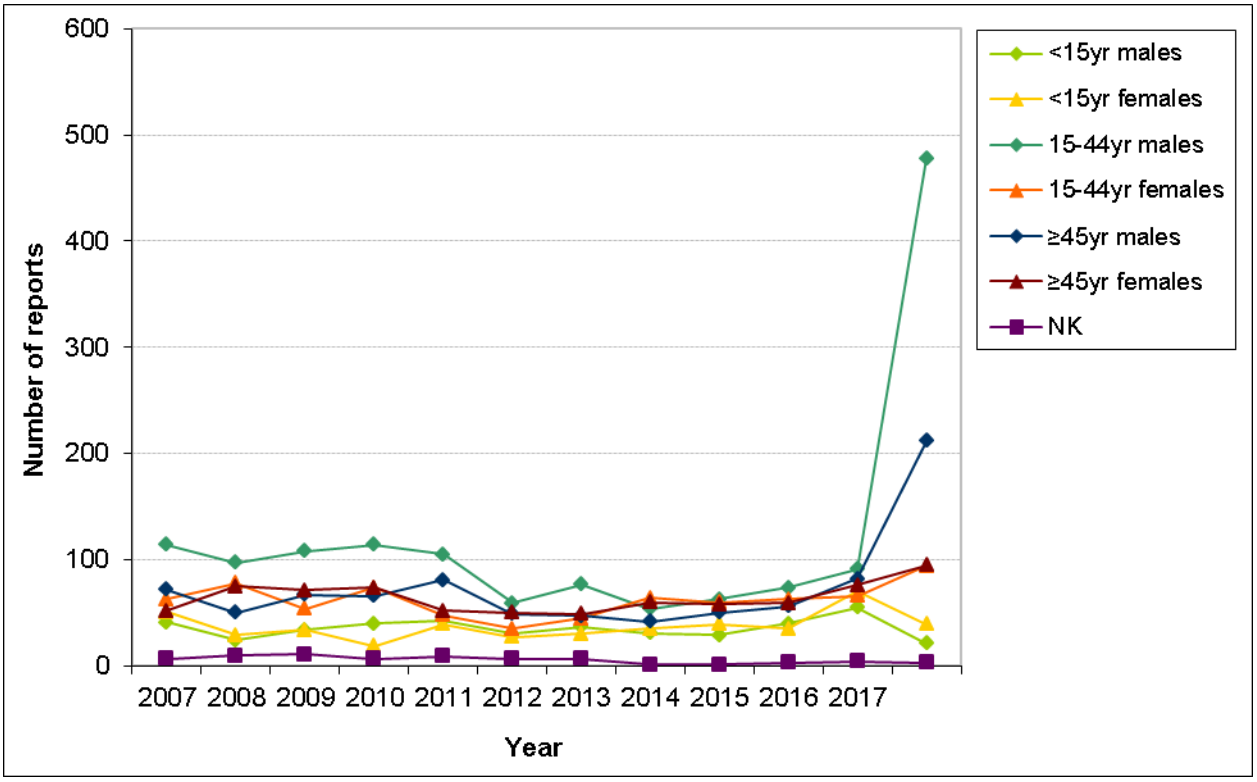
Figure 1: Percentages of hepatitis A laboratory reports by sex, England and Wales (2007-2017)



In 2017, excluding the under 15 years and NK age group, the number of reports received for all other age groups from both males and females increased compared to 2016, (Figure 2).

During 2017, females accounted for 65% of reports in the under 15 year old age group, males accounted for 84% of reports in the 15 to 44 age group, and 69% of reports among the 45 years and over age group. In comparison in 2016, females accounted for 56% of reports in the under 15 year's age group, males accounted for 58% of reports in the 15 to 44 age group, and 52% of reports among the 45 years and over age group.

Figure 2: Laboratory reports of hepatitis A by age and sex, England and Wales (2007-2017)



Risk factor information was poorly reported however as part of the outbreak investigation enhanced surveillance enabled identification of MSM as the main risk group associated with the outbreak strains. Travel history was available for 15.6% of reported cases; compared to 2016 when 23% had a known travel history (Table 3). Overall, despite the identification and reporting of MSM as a risk factor during the outbreak investigation as part of the enhanced surveillance, risk factor information 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 (2007-2017)

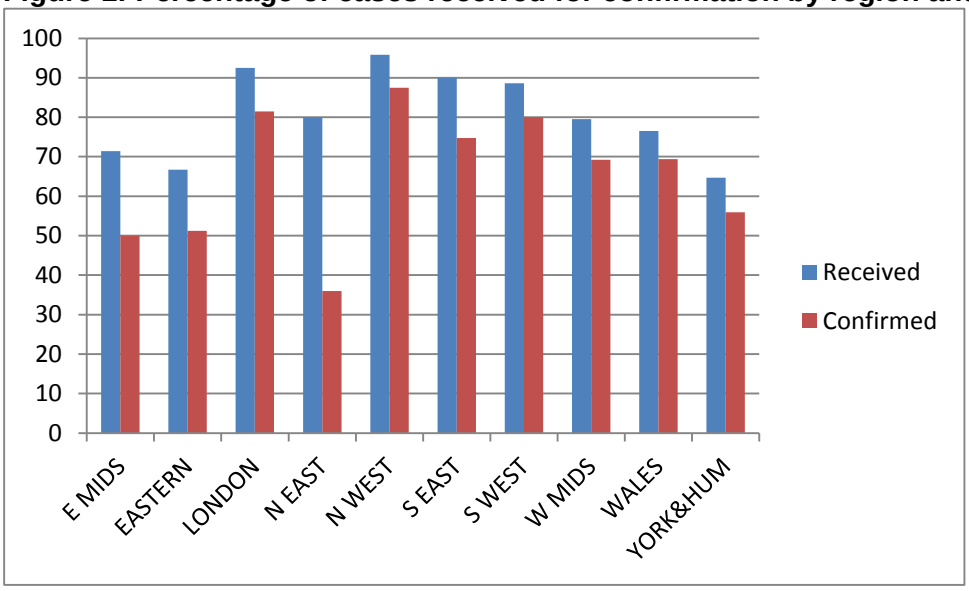
Year	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017
Number of reports	**363**	**360**	**356**	**371**	**257**	**288**	**283**	**300**	**330**	**444**	**942**
Number (%) aged 15-44 years	178 (49%)	167 (46%)	190 (53%)	157 (42%)	96 (37%)	122 (42.4%)	118 (42%)	123 (41%)	138 (41%)	157 (35%)	572 60.7%)
Number (%) male	172 (47%)	209 (55%)	220 (56%)	230 (61%)	138 (54%)	162 (55%)	127 (44%)	142 (47%)	170 (51.5%)	229 (52%)	711 (75.5%)
Number (%) with travel history	53 (14.6)	60 (16.7)	64 (18.0)	66 (17.8)	43 (16.7)	62 (21.5)	43 (15.2)	50 (16.7)	61 (18.5%)	101 (23%)	147 (15.6%)
Number (%) travelled abroad	23 (6.3)	18 (5.0)	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%)

Reference laboratory confirmation and phylogeny of hepatitis A infection: 2017

Of the 942 laboratory reports of acute HAV infection during 2017, 723 (76.8%) had samples forwarded to the Virus Reference Department (VRD) for confirmation which is an increase of 14.3% from 2016. Of the 219 (23.2%) cases who did not have a sample forwarded to VRD for HAV confirmation, 10 cases had no sample remaining, 31 cases had samples forwarded for HEV testing, one case was tested in 2016 and three cases were tested in 2018.

Acute HAV infection was not confirmed in 14.4% (104/723) of the forwarded samples. The remaining 619 (85.6%) cases were confirmed to have acute HAV infection. In addition 238 cases were confirmed to have acute HAV infection that had not been reported through the laboratory reporting system and with the exception of 19 cases they were all recorded in HPzone (eight from Wales and 11 from England). The breakdown of samples received per region can be seen in Figure 1.

Figure 1: Percentage of cases received for confirmation by region and the percentage confirmed.



Twenty seventeen saw a large increase in cases compared to 2016 which was due to a nationwide outbreak which was mostly seen in men who have sex with men (MSM) and for the purposes of this review these cases have been separated out.

Non-outbreak cases

Of the 201 non-outbreak confirmed cases, 113 (56.2%) reported a travel history, 83 (41.3%) had no travel history and five (2.5%) had no information. For the majority of regions travel cases predominated (Figure 2).

The age of the cases ranged from 1 to 84 years of age with travel being the main risk between the ages of 1 and 24 (Figure 3). There has been a decrease in cases confirmed in all age brackets except 1-4 compared to 2016 (Figure 4).

Figure 2: Confirmed HAV infections by region and travel history

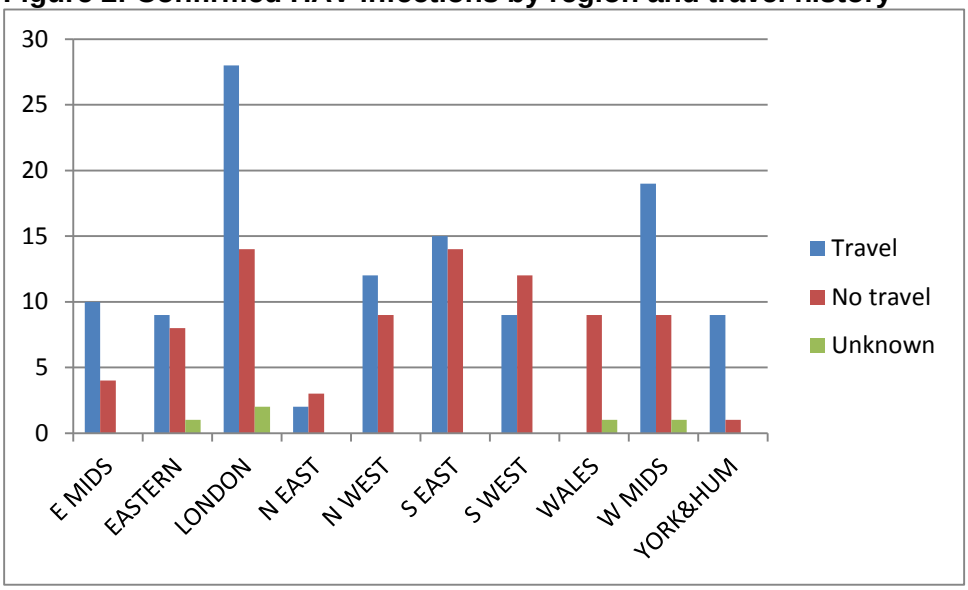


Figure 3: Confirmed HAV infections by age and travel history

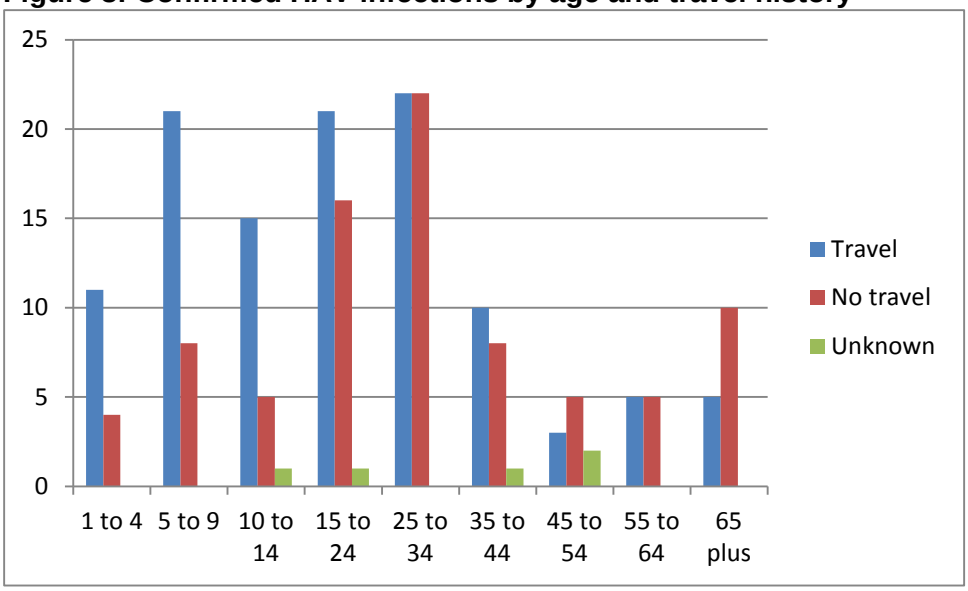
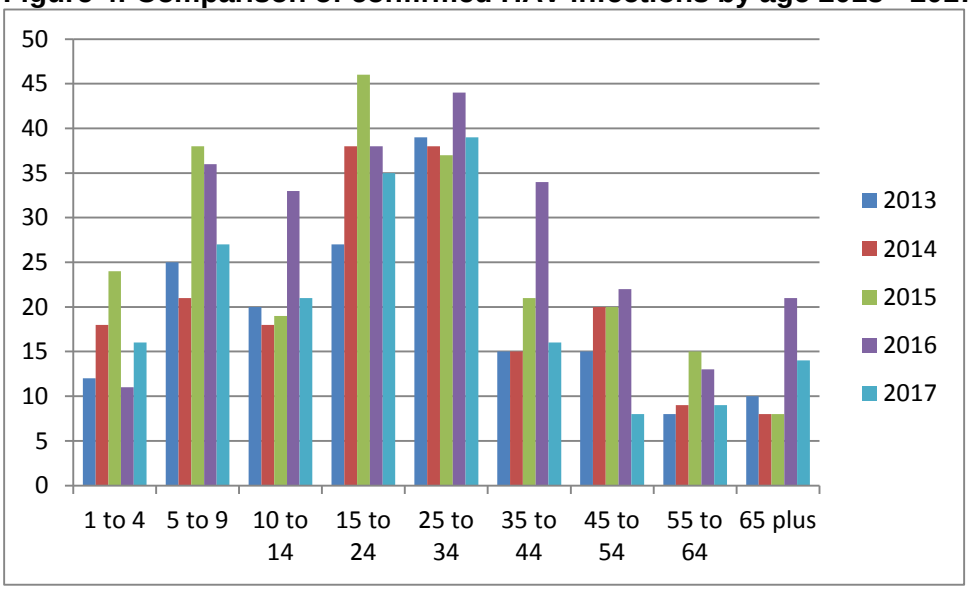


Figure 4: Comparison of confirmed HAV infections by age 2013 - 2017



Outbreak cases

The outbreak was associated with three distinct sequences: VRD_521_2016 (Event 1 – strain 1), RIVM-HAV16-090 (Event 2 – strain 2) and V16-25801 (Event 3 – strain 3). The peak of sampling was in week 10 (Figure 5) with the majority of cases being seen in London (Figure 6) and the most affected age group being 25 to 34 year olds (Figure 7).

Figure 5: Chronology of Events 1, 2 & 3 during 2017

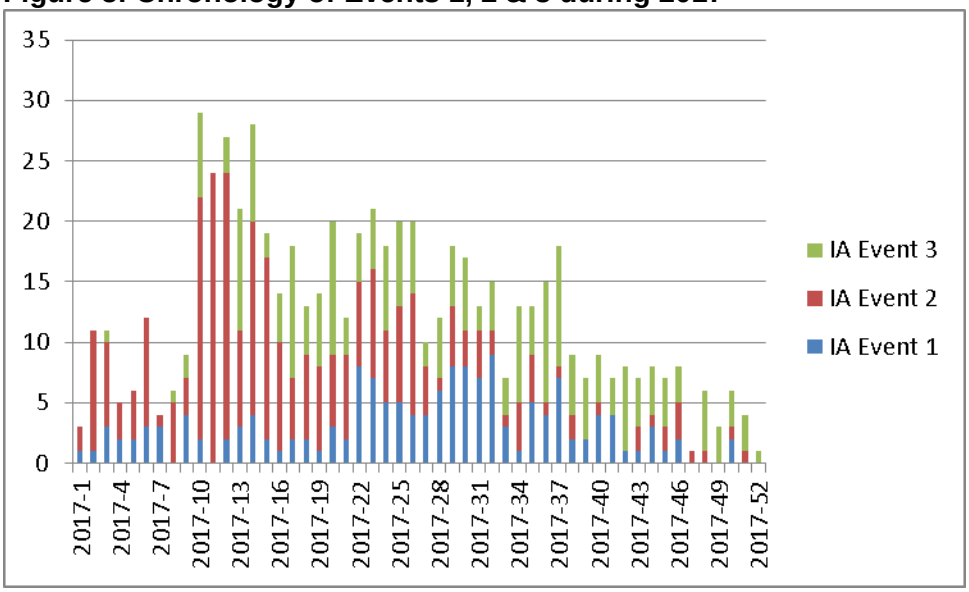


Figure 6: Regional breakdown of cases with Events 1, 2 and 3.

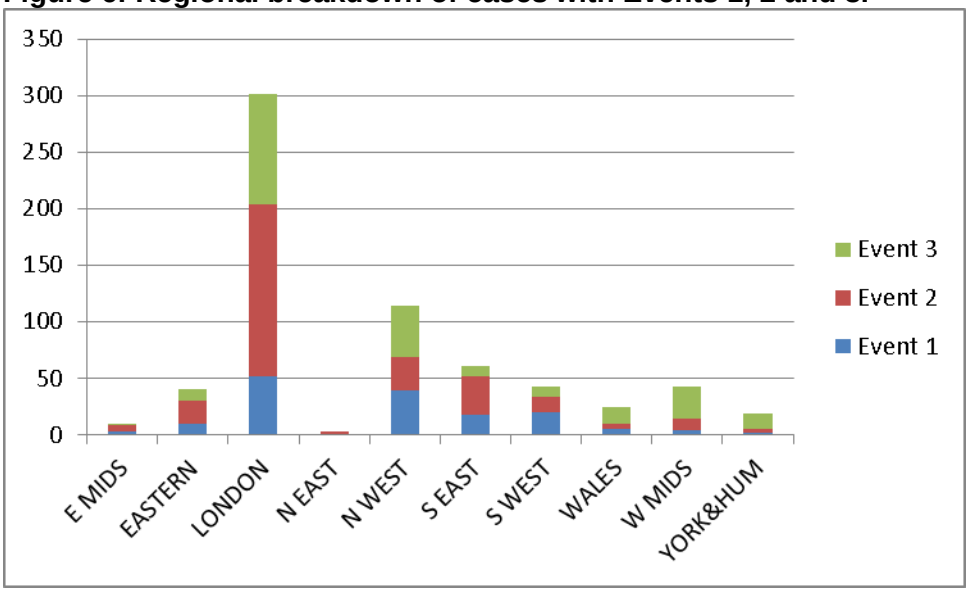
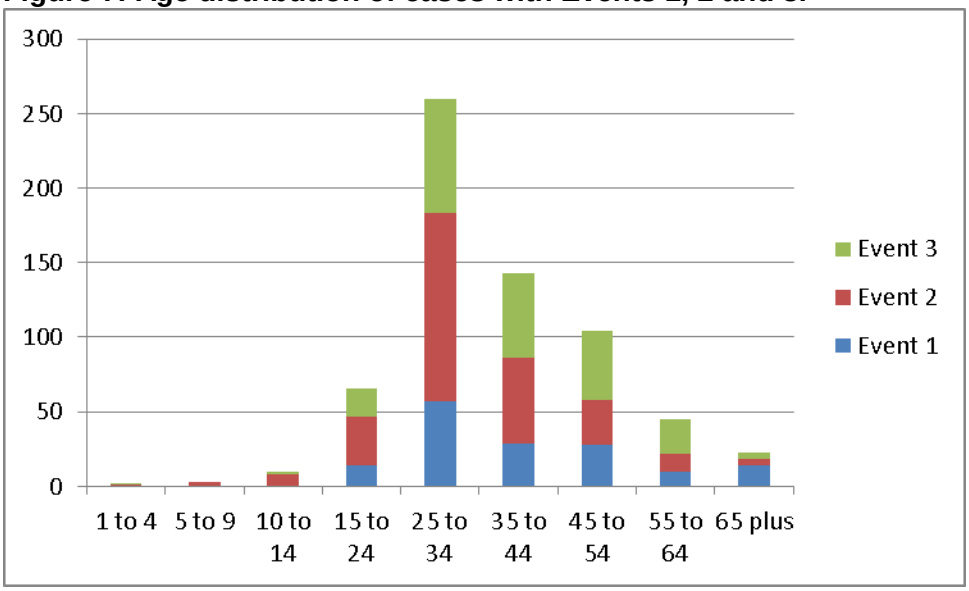
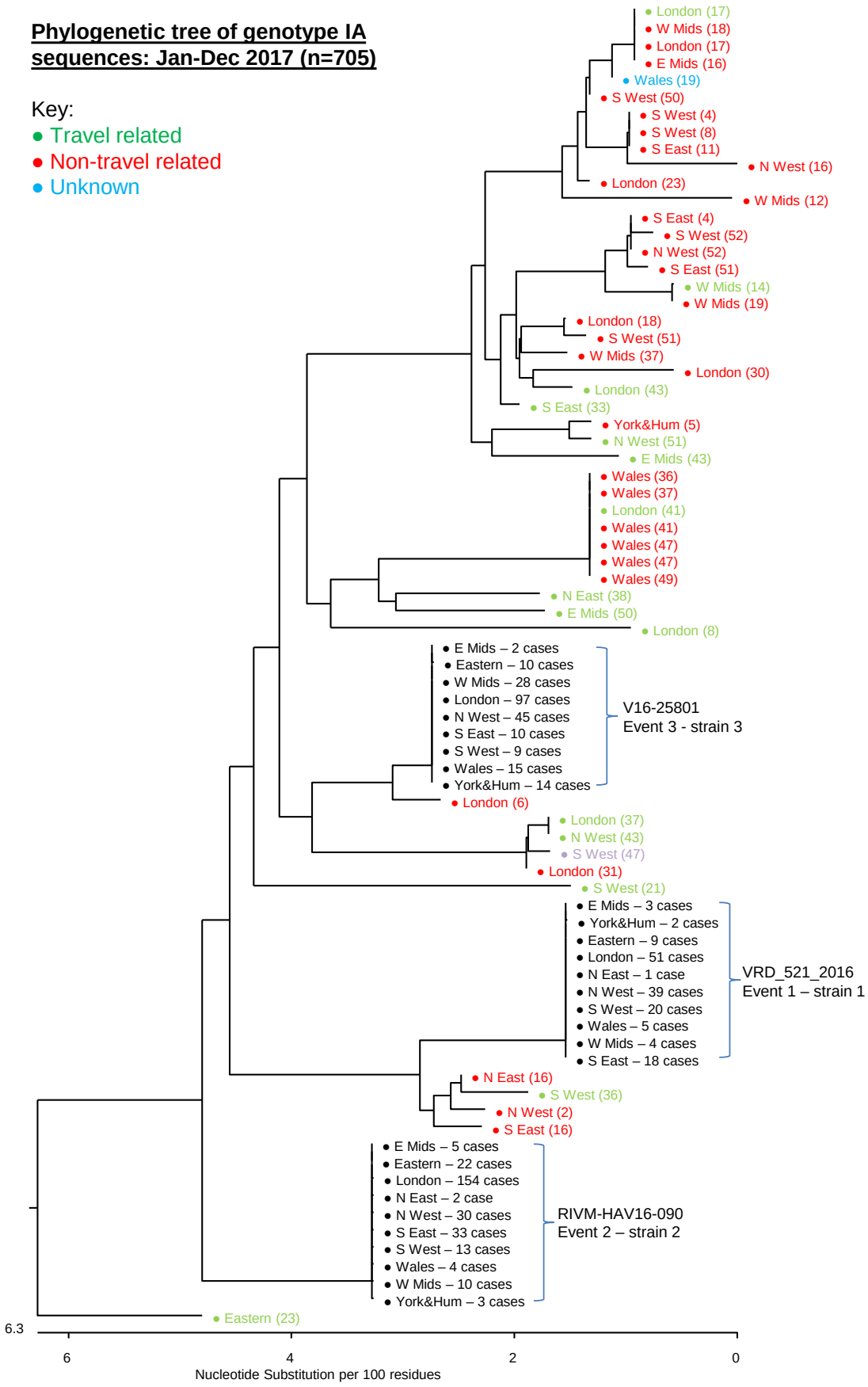


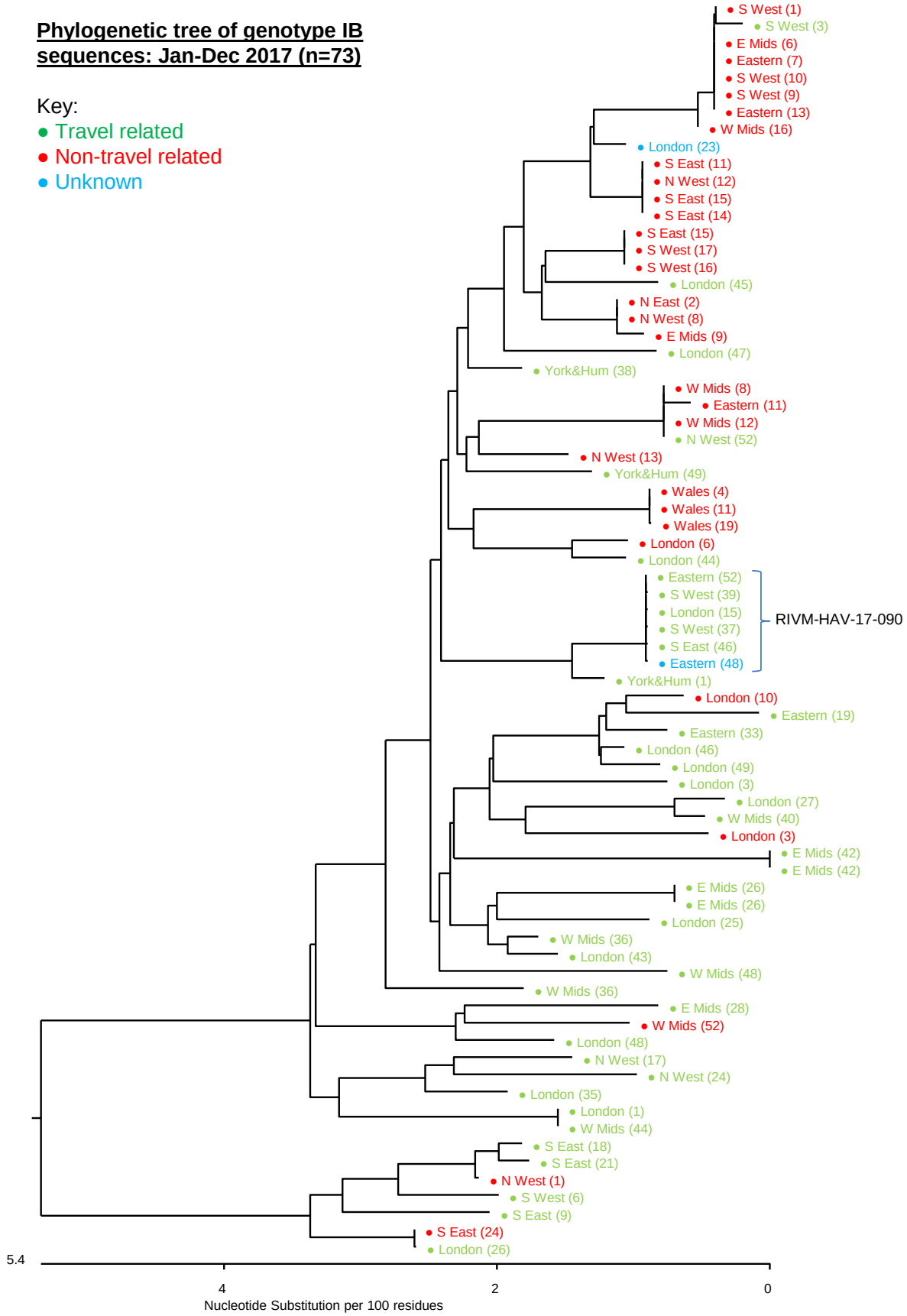
Figure 7: Age distribution of cases with Events 1, 2 and 3.



It was possible to genotype 851 of the confirmed cases (samples from laboratory reports on SGSS and those not reported through SGSS)) ; 705 (82.8%) were genotype IA, 73 (8.6%) were genotype IB, one (0.1%) were genotype IIA and 73 (8.6%) were genotype IIIA. This sequence information for each genotype is presented as phylogenetic trees with each sequence represented by a dot with the patient region and the week of sampling in brackets with the exception of sequences VRD_521_2016 (Event 1 – strain 1), RIVM-HAV16-090 (Event 2 – strain 2) and V16-25801 (Event 3 – strain 3) which have been represented in the tree by region and the number of cases observed due the large numbers of cases. No phylogenetic tree has been compiled for genotype IIA only one case being seen in 2017 and was associated with travel to Cameroon.



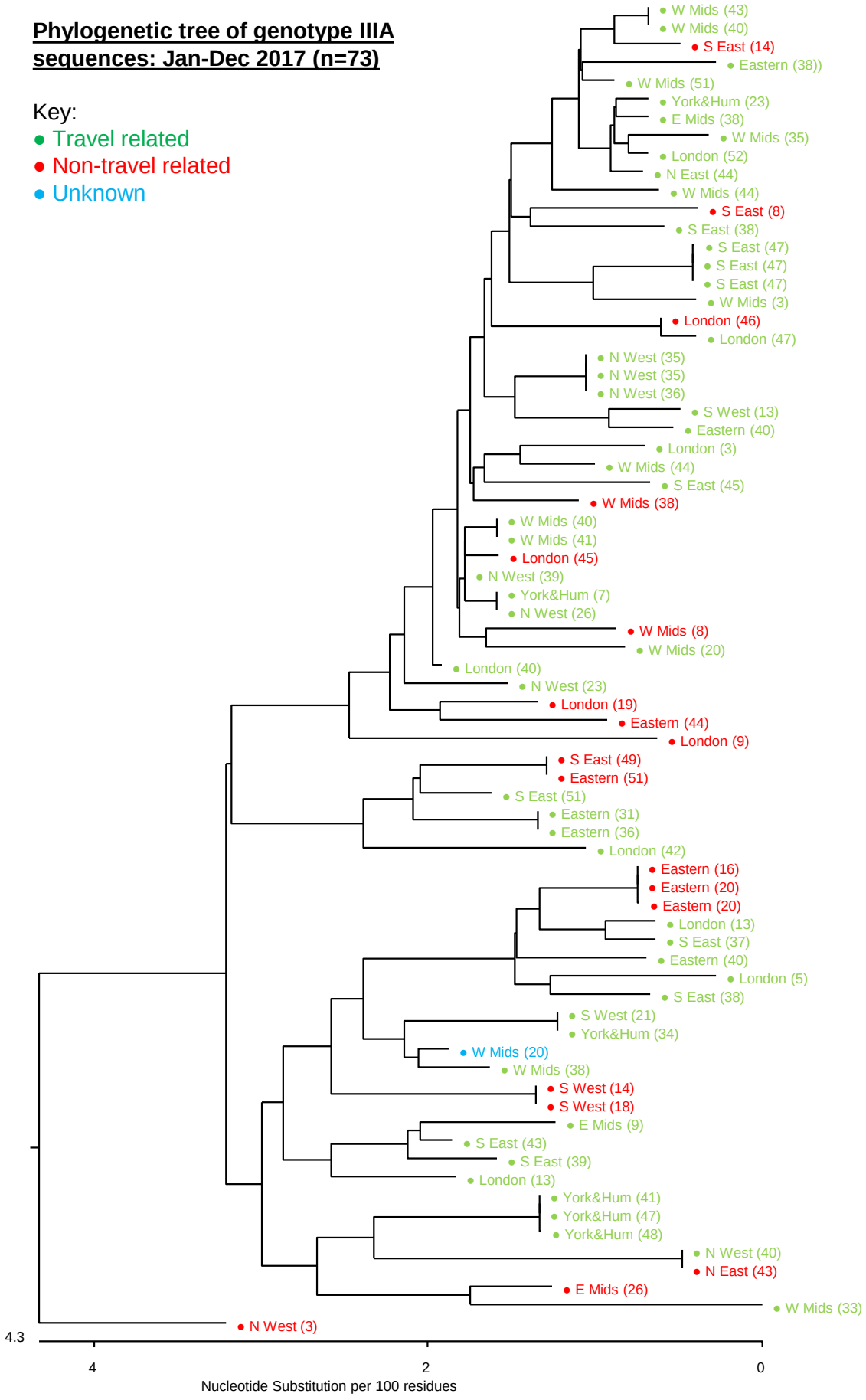
The large majority of cases with genotype IA were associated with three distinct outbreak strains VRD_521_2016 (Event 1 – strain 1), RIVM-HAV16-090 (Event 2 – strain 2) and V16-25801 (Event 3 – strain 3) and they predominantly affected the MSM community (1, 2, 3); Events 1, 2 and 3 had 152, 274 and 230 cases respectively. Outside of the outbreak the majority of cases with genotype IA had no travel history 29/48 (60.4%).



For genotype IB the majority of cases were travel related 40/73 (54.8%), the most common areas of travel being Africa and the Middle East. There were also multiple importations of the same sequence from Bulgaria which was also associated with an outbreak in the Netherlands linked to raspberries from Bulgaria, RIVM-HAV17-090 (4).

Phylogenetic tree of genotype IIIA sequences: Jan-Dec 2017 (n=73)

Key:
- Travel related
- Non-travel related
- Unknown



As in previous years the majority of cases with genotype IIIA had a travel history (53/73, 72.6%). 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 (5). Although travel was the main risk for cases with genotype IIIA the percentage of cases with no travel history was higher than previous years. Approximately one third of these non-travel related cases were seen in children under the age of 16 suggesting possible transmission from an asymptomatic child case with travel history.

Summary

In 2017 just over 75% of samples associated with laboratory reports of acute HAV infection were forwarded to VRD for confirmation. Comparison of SGSS reports with data from VRD have shown that less than 15% were not true cases of acute HAV which is lower than in previous years. In addition significant numbers of cases genotyped within VRD have not been reported through the laboratory reporting system –SGSS (238 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 and our increased our understanding of the molecular epidemiology of the virus has enabled us to pin point the likely country of origin of some outbreaks even when a source cannot be identified. Phylogenetic analysis has been invaluable in identifying the monitoring of the national outbreak of hepatitis A amongst MSM that was first identified in 2016. Identification of such community and national outbreaks is only possible by the continued submission of samples by laboratories from both travel associated and non-travel associated cases.

References

1. Beebeejaun K, Degala S, Balogun K, Simms I, Woodhall SC, Heinsbroek E, et al (2017). Outbreak of hepatitis A associated with men who have sex with men (MSM), England, July 2016 to January 2017. *Euro Surveill*. (2 Feb) **22**(5).
2. Werber D, Michaelis K, Hausner M, Sissolak D, Wenzel J, Bitzegeio J, et al (2017). Ongoing outbreaks of hepatitis A among men who have sex with men (MSM), Berlin, November 2016 to January 2017 - linked to other German cities and European countries. *Euro Surveill*. (2 Feb) **22**(5).
3. Freidl GS, Sonder GJ, Bovée LP, Friesema IH, van Rijckevorsel GG, Ruijs WL, et al (2017). Hepatitis A outbreak among men who have sex with men (MSM) predominantly linked with the EuroPride, the Netherlands, July 2016 to February 2017. *Euro Surveill*. (23 Feb) **22**(8).
4. Mollers M, Boxman ILA, Vennema H, Slegers-Fitz-James IA, Brandwagt D, Friesema IH, et al (2018). Successful use of advertisement pictures to assist recall in a food-borne hepatitis A outbreak in the Netherlands, 2017. *Food Environ Virol*. (4 May).
5. Health Protection Agency (2008). Foreign travel-associated illness – a focus on those visiting friends and relatives: 2008 report.

About Public Health England

Public Health England exists to protect and improve the nation's health and wellbeing, and reduce health inequalities. We do this through world-class science, knowledge and intelligence, advocacy, partnerships and the delivery of specialist public health services. We are an executive agency of the Department of Health, and are a distinct delivery organisation with operational autonomy to advise and support government, local authorities and the NHS in a professionally independent manner.

About *Health Protection Report*

Health Protection Report is a national public health bulletin for England and Wales, published by Public Health England. It is PHE's principal channel for the dissemination of laboratory data relating to pathogens and infections/communicable diseases of public health significance and of reports on outbreaks, incidents and ongoing investigations.

Public Health England, Wellington House, 133-155 Waterloo Road, London SE1 8UG
Tel: 020 7654 8000 www.gov.uk/phe
Twitter: @PHE_uk Facebook: www.facebook.com/PublicHealthEngland
Queries relating to this document should be directed to: the Immunisation, Hepatitis and Blood Safety Department, National Infection Service, 61 Colindale Avenue, London NW9 5EQ.
immunisation@phe.gov.uk

Published July 2018
PHE publications gateway number: 2018303