



UK Health
Security
Agency

Laboratory reports of hepatitis A infections in England and Wales: 2024

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Enhanced surveillance of hepatitis A

Laboratory reports

There were a total of 889 laboratory reports of new patients who tested positive for acute hepatitis A infection in England and Wales in 2024. This excludes the known false positive reports and those not confirmed, and includes 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 one or more of the following:

- 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
- 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
- samples which the VRD identified as laboratory quality controls

A total of 242 false positive reports were identified, which included 223 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 165 patients that were not reported through SGSS. A total of 724 cases were reported through SGSS, after excluding laboratory quality controls, false positives and cases who were not confirmed.

The greatest number of reports were among those aged between 25 and 34 years (160, 18%) followed by those in the 5 to 9 years age group (153, 17%) and those in the 15 to 24 years age group (137, 15%). More reports were received for males than females in the second, third and fourth quarter of 2024, and more reports were received for females in the first quarter ([Table 1](#)).

The number of laboratory reports by UKHSA centre is presented in [Table 2](#). Reports were assigned to a UKHSA centre according to either the: 1) patient's place of residence; 2) postcode of the patient's registered GP practice; or 3) postcode of the source laboratory.

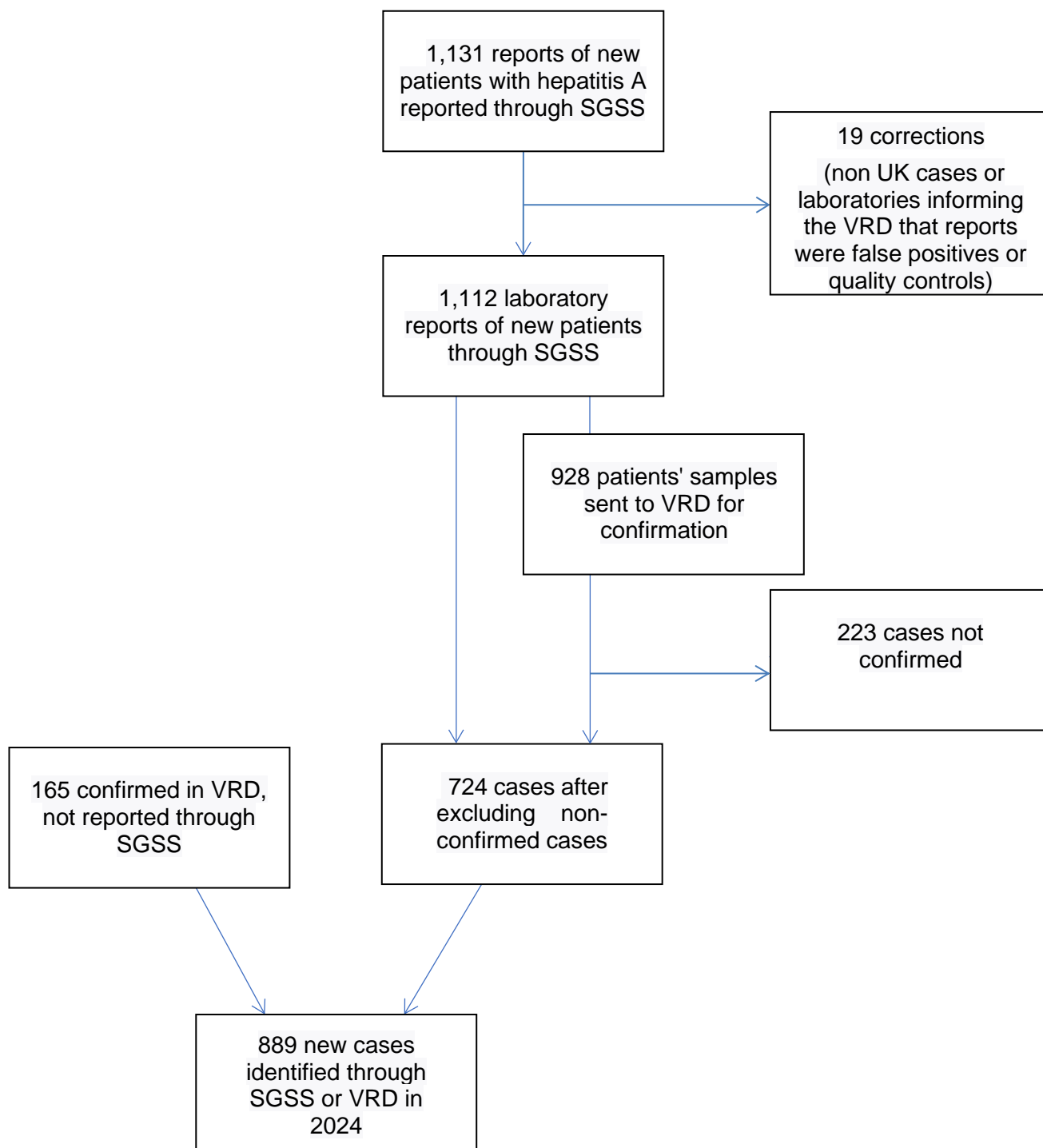
In 2024, the greatest number of hepatitis A reports were from the London region (227, 26%) followed by the North West (117, 13%) and South East (113, 13%). The large number of reports from London compared to other regions is consistent with previous years. Most cases from Wales were reported through SGSS (16, 84%).

Table 1. Laboratory reports of hepatitis A by age, sex, and quarter, England and Wales, 2024

In the following table Q1 = January to March, Q2 = April to June, Q3 = July to September, Q4 = October to December. NK = not known.

Age group (years)	Q1: Female	Q1: Male	Q1: NK	Q2: Female	Q2: Male	Q2: NK	Q3: Female	Q3: Male	Q3: NK	Q4: Female	Q4: Male	Q4: NK	Total
Under 1	0	0	0	0	0	1	0	0	0	0	0	0	1
1 to 4	8	8	0	6	4	0	13	16	0	9	9	1	74
5 to 9	15	15	0	16	13	0	21	24	0	23	26	0	153
10 to 14	7	11	0	7	8	0	19	14	0	9	15	0	90
15 to 24	19	16	0	10	15	1	18	28	0	15	14	1	137
25 to 34	26	25	1	12	28	0	14	19	0	15	20	0	160
35 to 44	19	12	0	10	15	0	8	9	0	11	15	0	99
45 to 54	11	6	0	11	12	0	4	4	0	4	2	0	54
55 to 64	8	7	0	10	9	1	7	4	0	8	7	0	61
65 or over	15	6	0	6	8	0	7	4	1	7	5	0	59
NK	0	0	1	0	0	0	0	0	0	0	0	0	1
Total	128	106	2	88	112	3	111	122	1	101	113	2	889

Figure 1. Flowchart of laboratory reports of hepatitis A and confirmation status by the VRD (England and Wales), January to December 2024



Text version of Figure 1: Flowchart of laboratory reports of hepatitis A and confirmation status by the VRD

There were 1,131 reports of new patients with hepatitis A notified through SGSS in 2024 – of which 19 reports were known incorrect reports and excluded (non-UK cases or laboratories informing the VRD that reports were false positives or quality controls etc). Of the remaining 1,112 laboratory reports of new patients notified through SGSS, 928 patients had samples sent to the VRD for confirmation, with 223 of these not VRD-confirmed. In addition to the 724 new patients notified through SGSS that were VRD-confirmed or did not have a sample sent to the VRD for confirmation, 165 new patients were VRD-confirmed – creating a total of 889 new patients with hepatitis A recorded in England and Wales in 2024 that were VRD-confirmed or SGSS-reported without a sample sent to the VRD for confirmation.

Table 2. Laboratory reports of hepatitis A by UKHSA centre (England) and Wales (2015 to 2024)

UKHSA centre	2015	2016	2017	2018	2019 [note 1]	2020 [note 1]	2021 [note 1]	2022 [note 1]	2023 [note 1]	2024 [note 1]
East Midlands	11	30	29	22	18	17	26	15	28	49
East of England	24	47	86	49	59	28	36	68	74	87
London	79	180	414	150	160	69	86	132	141	227
North East	11	17	25	7	7	1	6	5	10	21
North West	43	22	50	41	66	24	36	65	72	117
South East	27	51	91	54	50	31	34	54	42	113
South West	15	22	71	34	28	28	29	58	23	62
West Midlands	47	46	99	50	42	23	45	60	56	96
Yorkshire and Humber	69	24	34	26	56	18	21	39	46	98
Wales [note 2]	4	5	43	19	17	15	8	9	4	19
Total	330	444	942	452	503	254	327	505	496	889

Note 1: 2019 to 2024 data includes confirmed cases identified by the VRD that were not reported through SGSS.

Note 2: Non-UKHSA centre.

Overall, there was a 79% increase in the number of reports in 2024 (n=889) compared to 2023 (n=496), including non-SGSS cases identified by the VRD for both years.

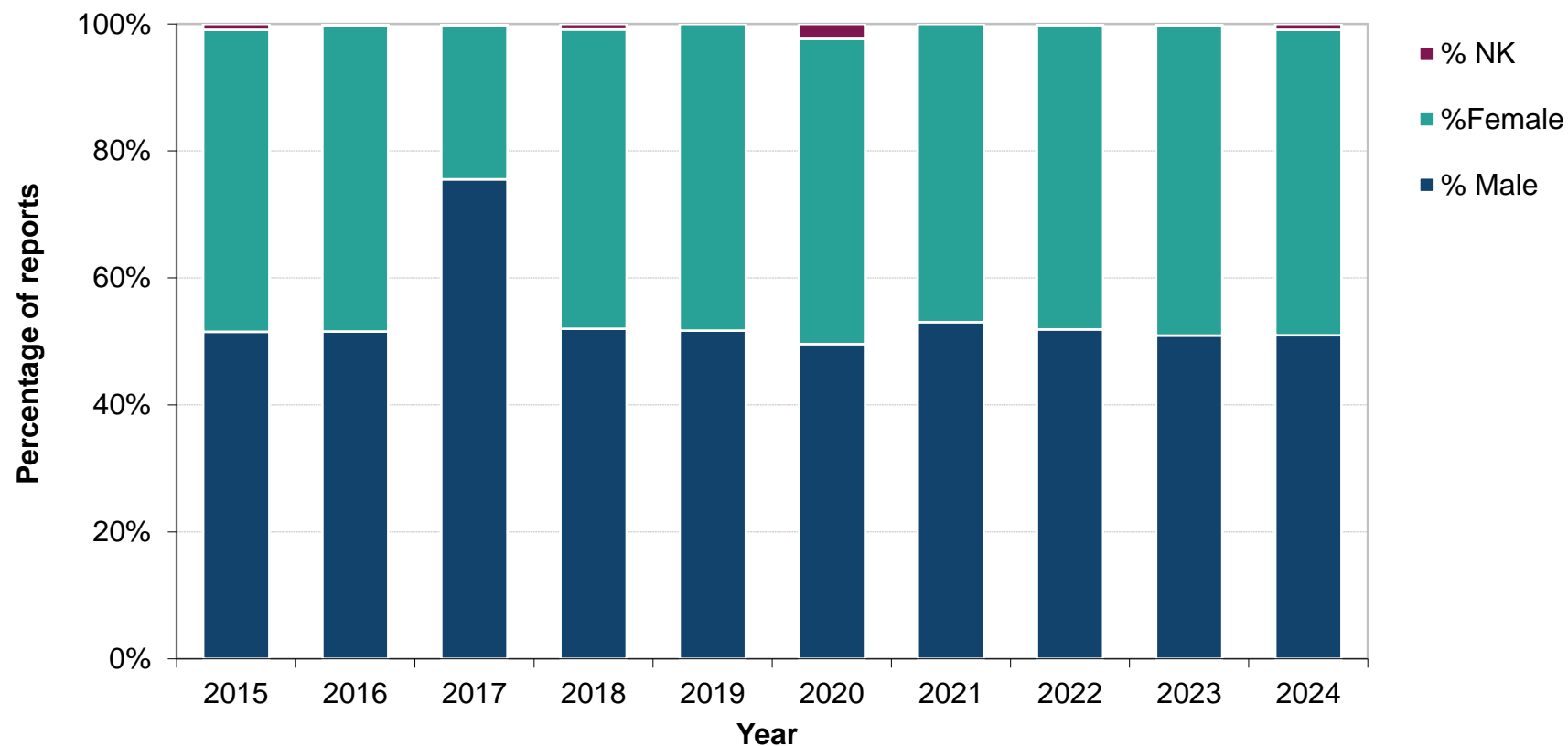
The number of reports in 2024 were greatest in quarter 1 (236, 27%) and quarter 3 (234, 26%) followed by quarter 4 (216, 24%) and quarter 2 (203, 23%) ([Table 1](#)). The number of reports for all quarters was greater compared to the corresponding quarter in 2023 (2023 data by quarter not shown), with the largest increases in quarters 2, 3 and 1 (103%, 100%, 89% increase respectively) and the smallest increase in quarter 4 (40% increase).

The annual number of HAV reports decreased from 2005 to 2013 (data not presented), 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 gay and bisexual men who have sex with men (GBMSM). The number of reports fell in 2018, in line with the end of the GBMSM outbreak, and continued to fall in 2019. However, numbers did not return to pre-2016 levels. In 2020, numbers registered a further fall, most likely attributable to the COVID-19 pandemic disease control measures and the associated reduction in travel. The annual number of reports increased between 2020 and 2024, and in 2024 exceeded the number of reports in 2019.

A total of 797 confirmed or probable cases associated with the national 2016 to 2018 GBMSM 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 cases with these incident strains were identified in community settings.

Age and sex reported through the laboratory reporting systems have been well completed every year over the past decade (over 97% complete) ([Figure 2](#)), including in 2024 (99% complete). Males accounted for a slim majority of reports (51%, 453 of 881 with information) during 2024 ([Figure 2](#)).

Figure 2. Percentages of hepatitis A laboratory reports by sex, England and Wales [note 1] (2015 to 2024 [note 2])



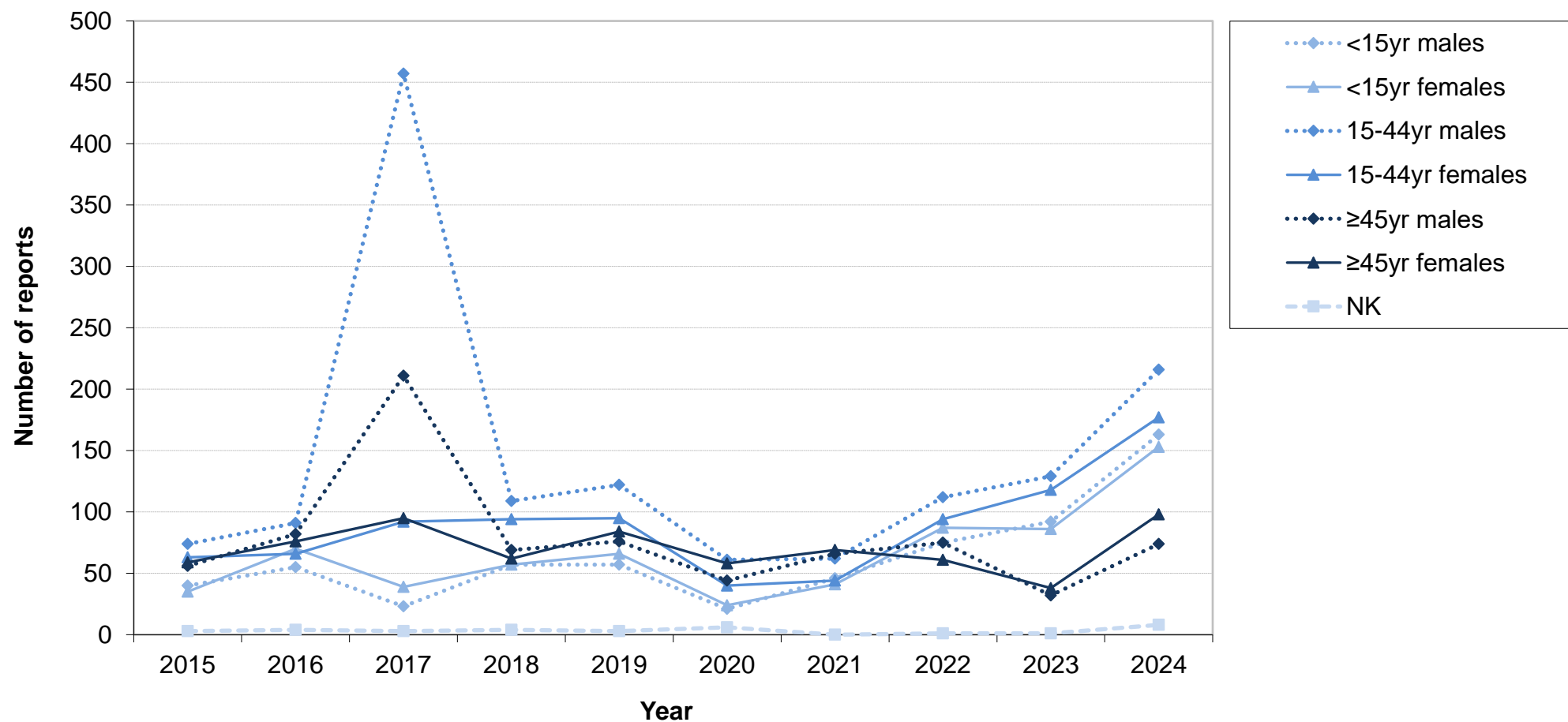
Note 1: Reports from Wales from Q3 and Q4 2018 and Q1 and Q2 2019 were not received through SGSS however some cases from Q1 and Q2 2019 were identified through the VRD.

Note 2: 2019 to 2024 data includes confirmed cases identified by the VRD that were not reported through SGSS.

In 2024, the number of reports increased in all age-sex groups, when compared to 2023 and including non-SGSS cases identified by the VRD for both years ([Figure 3](#)). All age-sex groups increased by 50 percent or more, with age-sex groups aged under 15 years and between 15 and 44 years of age increasing between 50 and 78 percent. The largest relative increase was seen for females aged 45 years and over where 98 reports were received compared to 38 in 2023 (158% increase), followed by males aged 45 years and over where 74 reports were received compared to 32 in 2023 (131% increase).

There was an increase in cases confirmed in all age groups compared to 2023 ([Figure 4](#)).

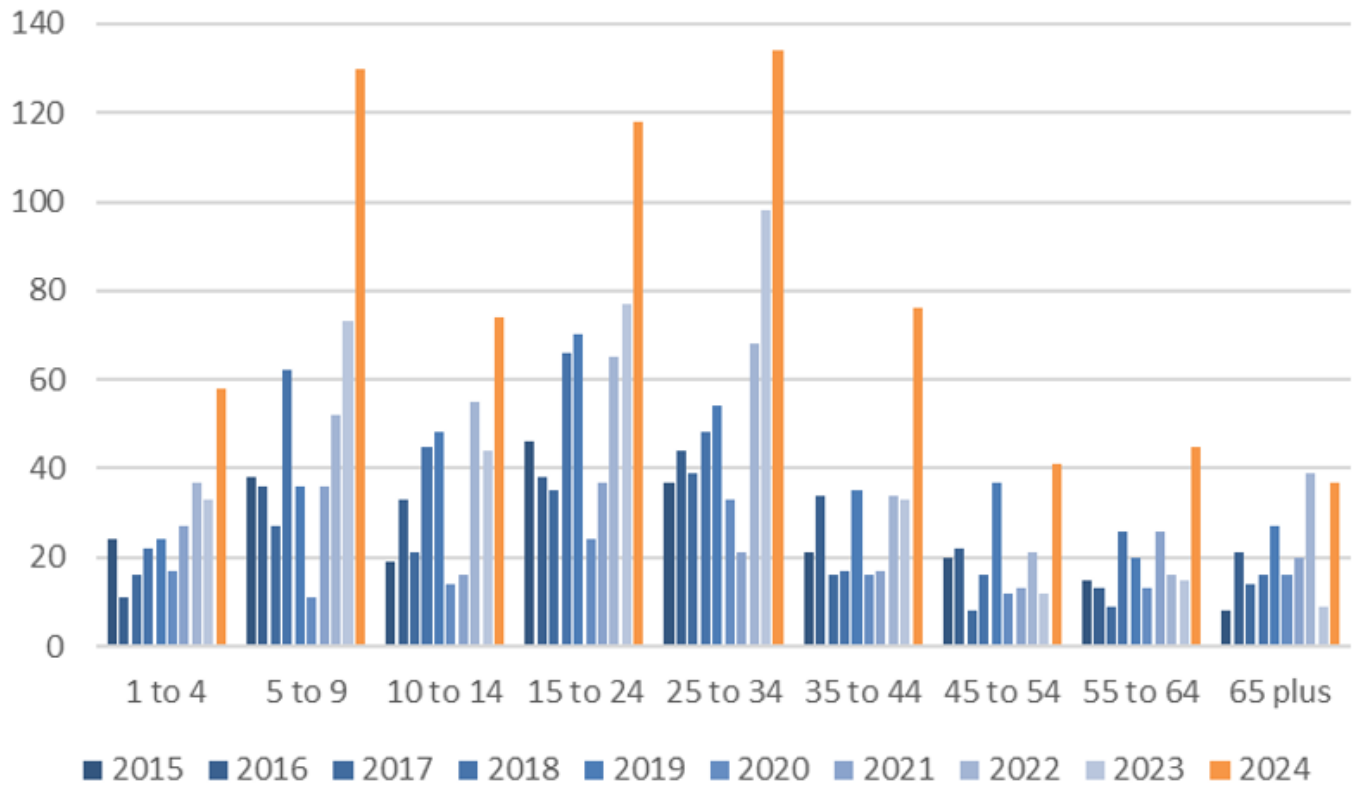
Figure 3. Laboratory reports of hepatitis A by age and sex, England and Wales [note 1] (2015 to 2024 [note 2])



Note 1: 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.

Note 2: 2019 to 2024 data includes confirmed cases identified by the VRD that were not reported through SGSS.

Figure 4. Comparison of confirmed HAV infections by age 2015 to 2024 [note 1]



Note 1: confirmed cases with the MSM outbreak sequences in 2016-2018 excluded from figure

Reference laboratory confirmation

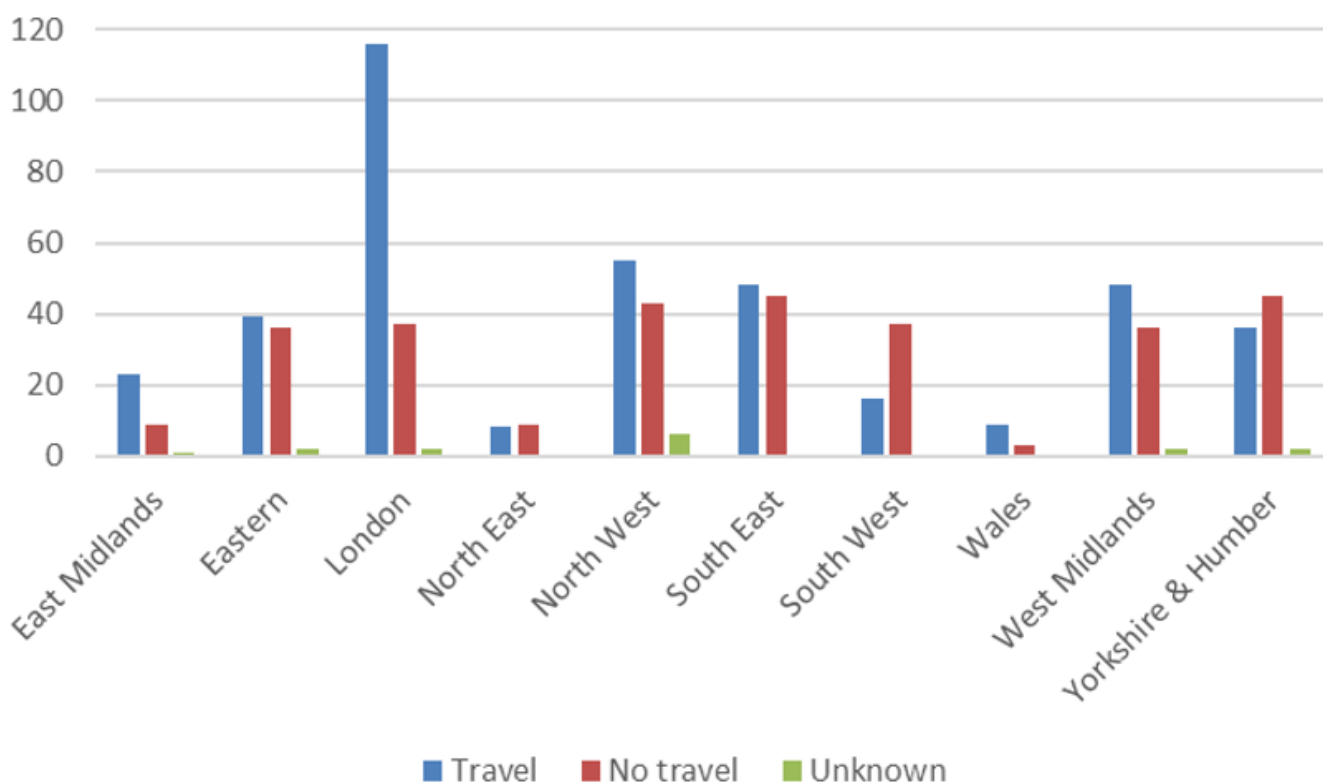
Of the 724 laboratory reports of acute HAV infection during 2024, 547 (75.6%) cases had samples forwarded to the Virus Reference Department (VRD) for genotyping. Of the 177 (24.4%) cases who did not have a sample forwarded to VRD, eight cases had no sample remaining, two cases had samples referred for HEV testing, and 1 case had a sample referred for HBV testing.

In addition, 165 cases were confirmed to have acute HAV infection that had not been reported through the laboratory reporting system, however, all English cases were recorded in HPZone or CIMS.

Travel history

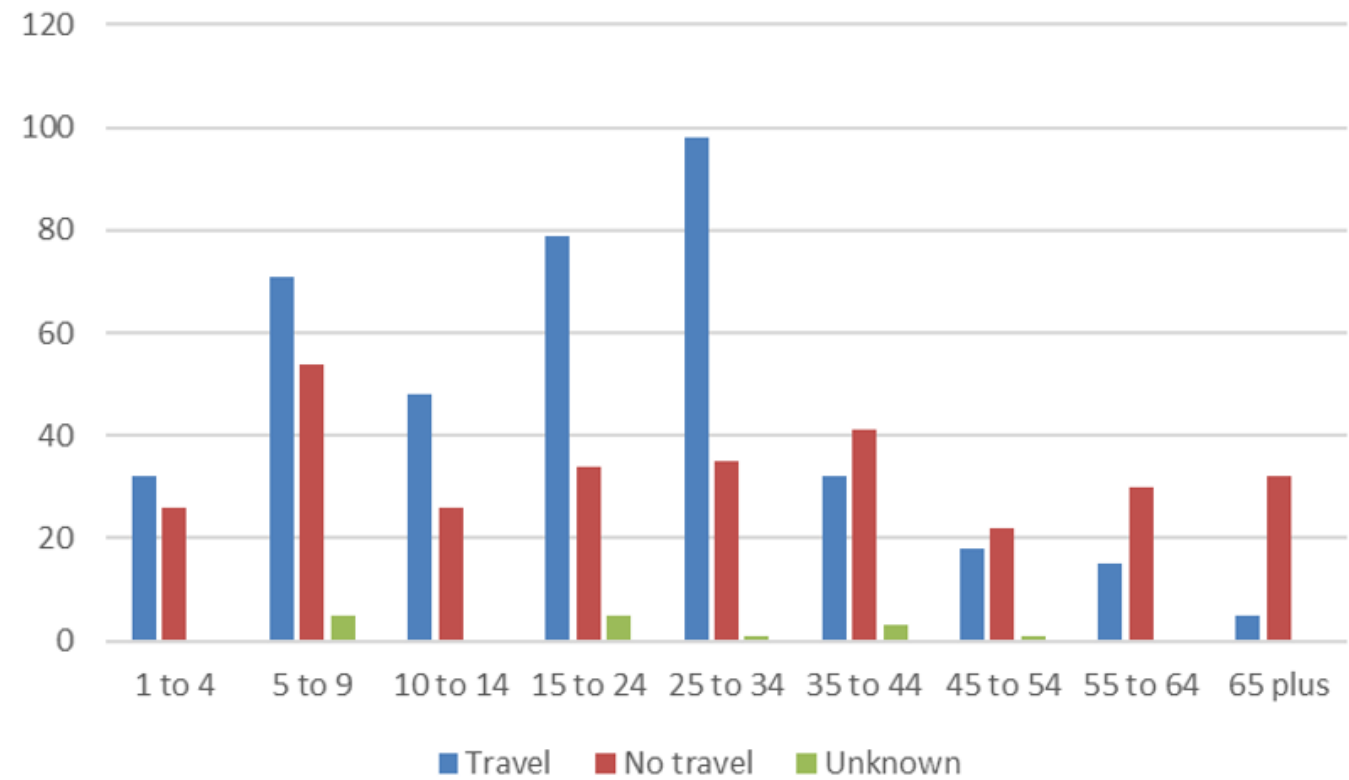
Of the 713 confirmed cases, 403 (56.5%) reported a travel history, 296 (41.5%) had no travel history and 14 (2%) had no information. Most of the cases were reported in London, and this was also where the largest number of travel-related cases were reported ([Figure 5](#)).

Figure 5. Confirmed HAV infections by Wales, English region and travel history



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 34 ([Figure 6](#)).

Figure 6. Confirmed HAV infections by age and travel history

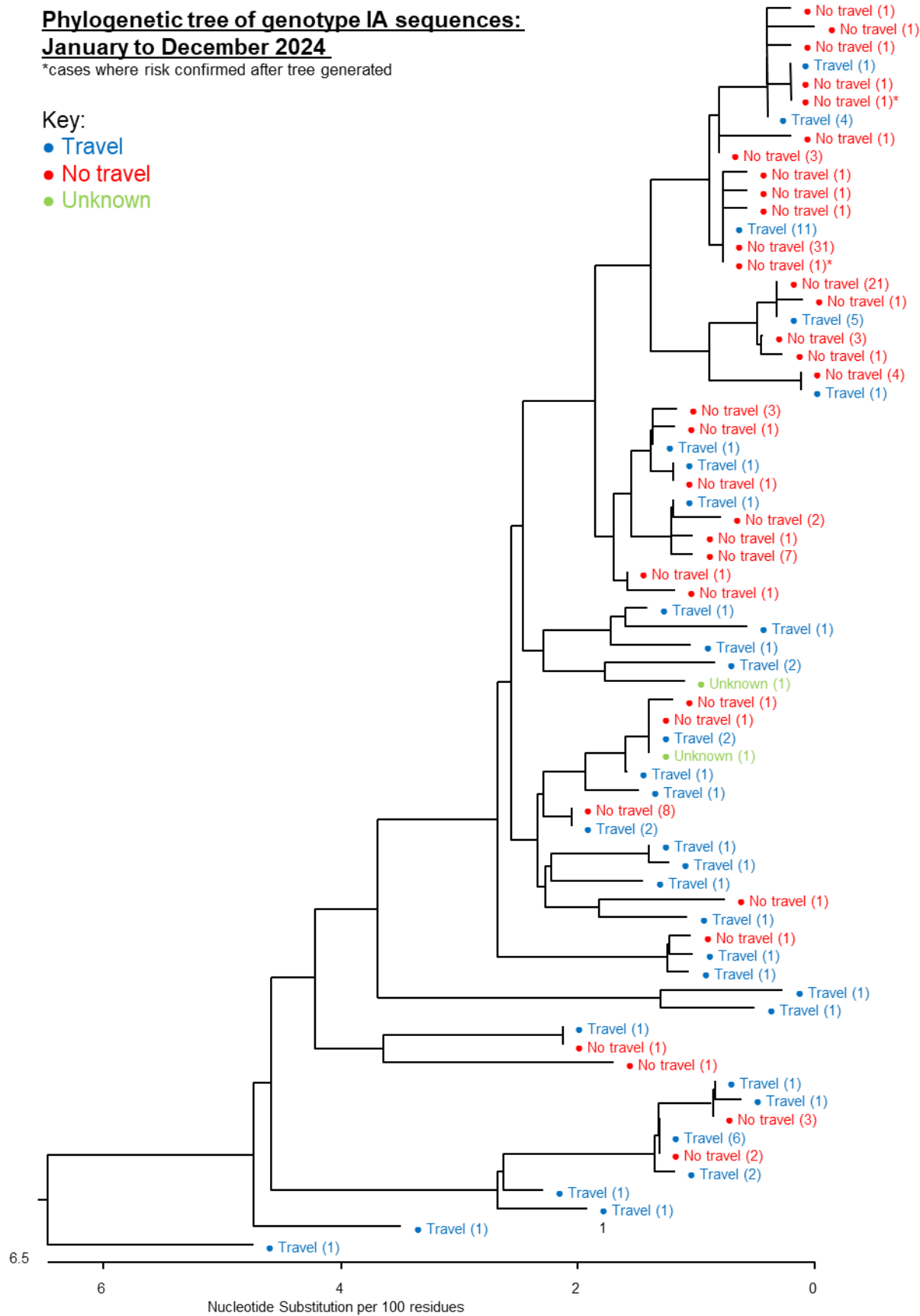


Phylogenetic trees

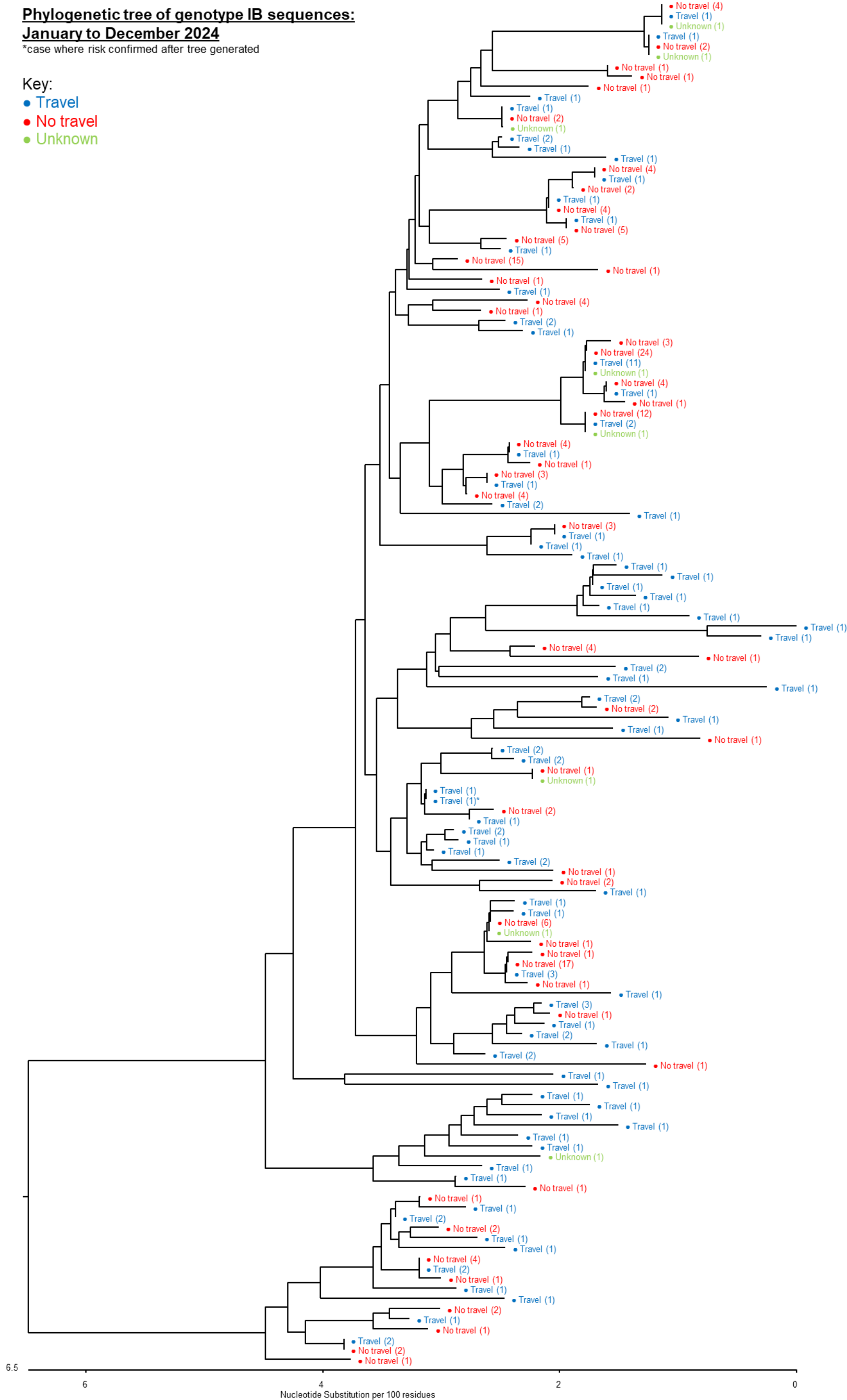
It was possible to genotype 700 of the confirmed cases: 175 (25%) were genotype IA, 273 (39%) were genotype IB, 1 was genotype IIA (0.1%) and 251 (35.9%) were genotype IIIA. The sequences for each genotype (except for genotype IIA) are presented as phylogenetic trees.

Due to the large number of cases in 2024 each sequence is represented by a dot and the number of cases seen with the sequence in brackets for the genotype IA and IB phylogenetic trees. For genotype IIIA the trees are divided into the main travel destinations with each sequence being labelled with the quarter it was observed in (cases with a different destination or no or unknown travel history at the time the trees were generated are not represented).

Most cases with genotype 1A were non-travel related, 111 out of 175 (63.4%), with nearly half associated with 2 sequences (52 cases). Of the travel-related cases, Morocco, Poland and South America were the most common destinations.

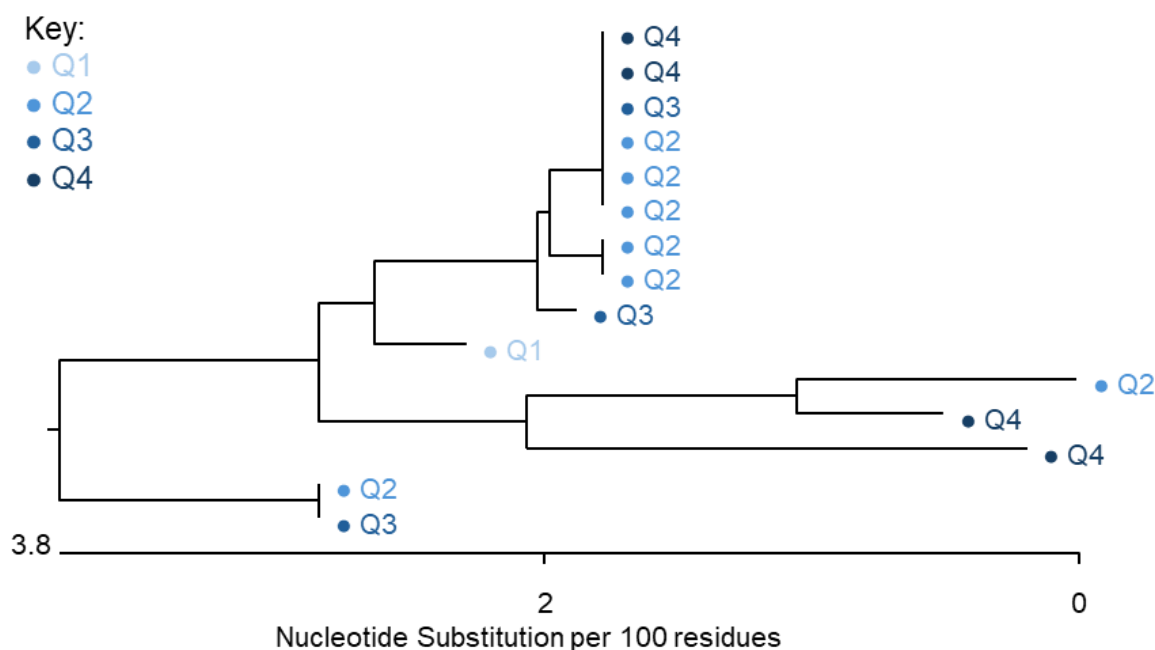


For genotype IB just over half the cases were non-travel related 152 out of 273 (55.7%) with school and community outbreaks contributing to this. Of the travel-related cases, Slovakia, Egypt and East Africa were the most common destinations.



As in previous years most cases with genotype IIIA had a travel history (218 out of 251, 86.9%) with India and Pakistan being the most visited countries (172 cases, 2 not represented in the trees as information received after the trees were generated). 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 (6). A total of 107 (42.6%) cases were under 18 years of age and of these cases 81.3% (87 cases) were in quarters 3 and 4 of the year.

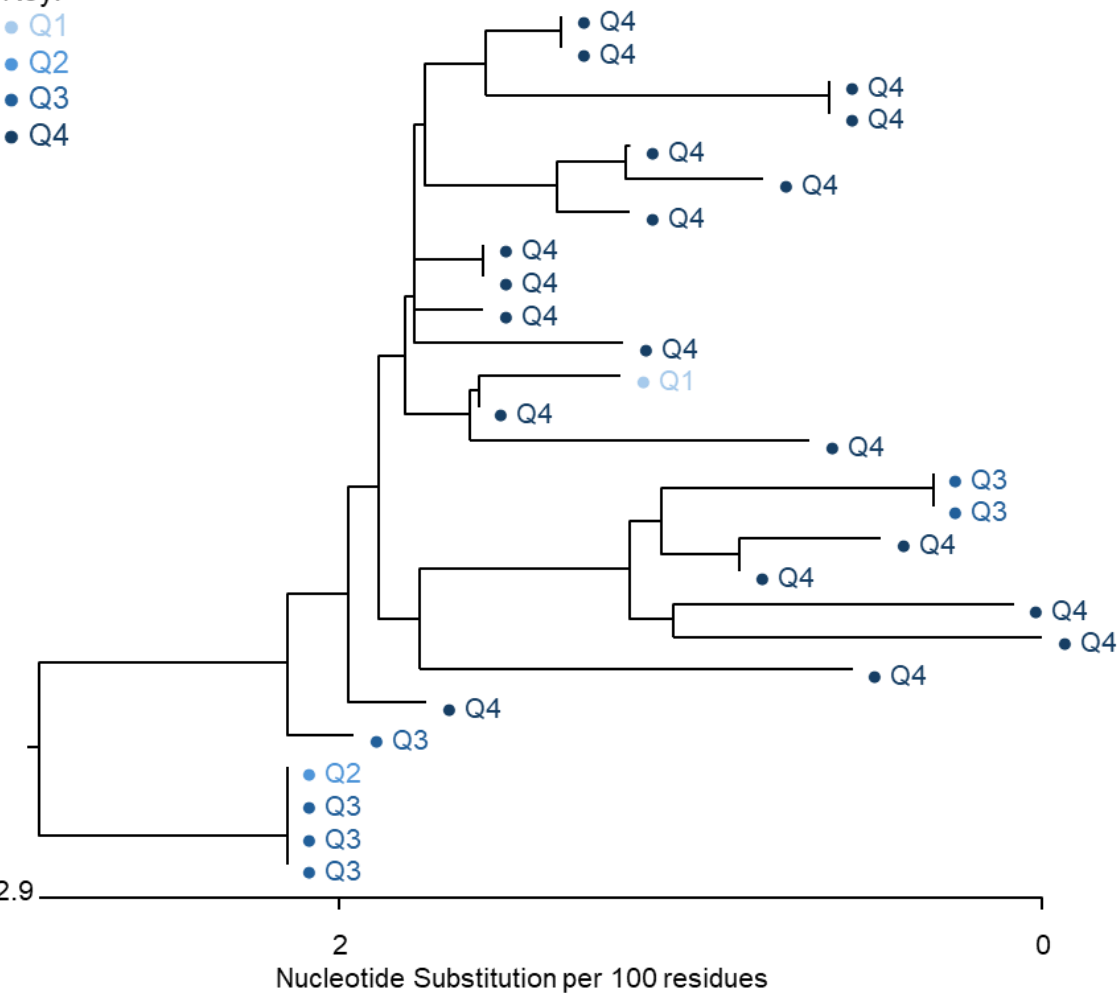
**Phylogenetic tree of genotype IIIA sequences
 from Bangladesh (n=12) & Nepal (n=3): January to December 2024**



Phylogenetic tree of genotype IIIA sequences
from Afghanistan: January to December 2024 (n=27)

Key:

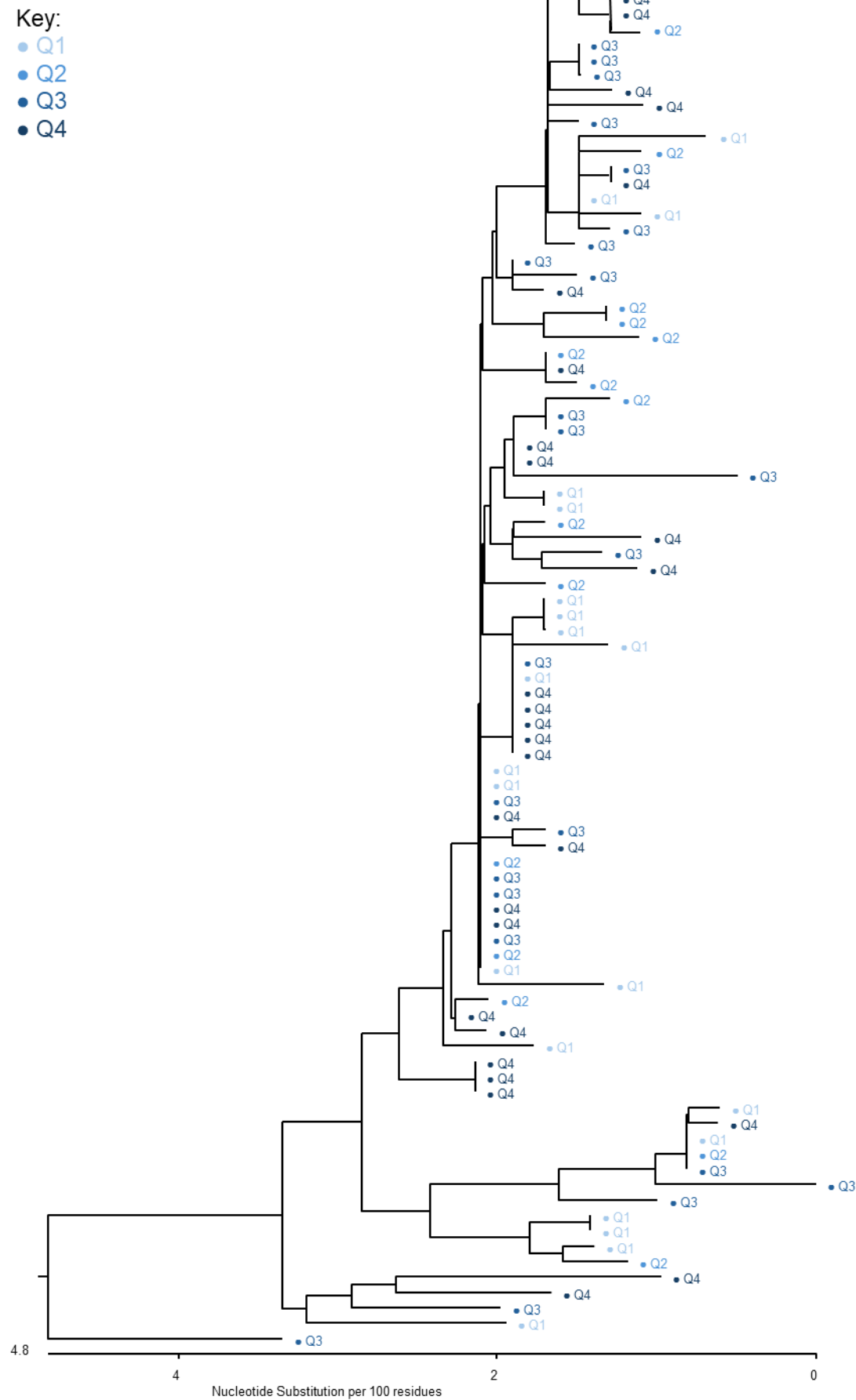
- Q1
- Q2
- Q3
- Q4



**Phylogenetic tree of genotype IIIA sequences
from Pakistan: January to December 2024 (n=78)**



**Phylogenetic tree of genotype IIIA sequences
from India: January to December 2024 (n=92)**



Summary of enhanced surveillance

Compared with 2023, there was an increase in the number of hepatitis A cases reporting a travel history (403 cases in 2024 compared with 278 cases in 2023, an increase of 45%) and for cases with no travel history (296 cases in 2024 compared with 112 cases in 2023, an increase of 164%) as recorded in the case management systems (HPZone or CIMS).

Of the genotyped cases 403 cases reported a travel history. Of these, 64 cases were of genotype IA compared with 25 cases in 2023 (an increase of 156%), 121 cases were of genotype IB compared with 64 cases in 2023 (an increase of 89%), and 218 cases were of genotype IIIA compared with 190 cases in 2023 (an increase of 15%). Across the genotypes the main travel destinations remain the same between 2023 and 2024 with the addition of Poland for genotype IA and Slovakia for genotype IB.

Of the 296 genotyped cases with no travel history, 111 cases were genotype IA compared to 29 cases in 2023 (an increase of 283%), 152 cases were genotype IB compared to 63 cases in 2023 (an increase of 141%), and 33 cases were genotype IIIA compared to 22 cases in 2023 (an increase of 50%). The non-travel related genotype IA cases were mainly associated with Moroccan like sequences (100 cases) of which there were 2 dominant sequences. One was reported through ECDC to have been observed in other European countries and this is reflected in this same sequence being observed in travellers returning from European destinations. There was 1 other dominant non-travel related sequence which was Romanian like. The non-travel related genotype IB cases were mainly associated with Egyptian like sequences (48 cases) with 1 dominant sequence being seen in 15 cases. There were other dominant sequences in the non-travel associated cases: 2 with Slovakian like sequences, 1 of which was the cause of a large community outbreak and was reported by ECDC to be circulating in large European outbreaks and 1 with a West Asian sequence.

The year 2024 saw the largest number of cases since the outbreak in GBMSM in 2016, 2017 and 2018 ([2](#), [3](#)), with 74.8% of samples associated with laboratory reports of acute HAV infection forwarded to VRD for genotyping.

Sequencing of hepatitis A virus remains an invaluable tool in tracking outbreaks. Our increased understanding of the molecular epidemiology of the virus enables the mapping of the likely country of origin of some outbreaks even when a source cannot be identified. Identification of outbreaks is only possible by the continued submission of samples by laboratories from both travel-associated and non-travel associated cases.

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