

Annual Epidemiological Report

December 2023

Hepatitis A in Ireland, 2022

Key Facts

Number of cases, 2022: 66

Crude notification rate, 2022: 1.3/100,000 population

The number of notifications of hepatitis A decreased in 2022 compared to 2021 (n=82), but was relatively high compared to other recent years. The notification rate in 2021 was higher than usual due to two large outbreaks associated with the Irish travelling community.

In 2022, one third of cases were likely to have been infected outside Ireland or were contacts of travel-related cases. Almost one third of cases infected in Ireland were part of a large extended family/local community outbreak. The remaining cases were a mix of sporadic cases and cases linked to smaller outbreaks.

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Background

Hepatitis A is an acute self-limiting disease of the liver caused by the hepatitis A virus. The most common symptoms are fever, loss of appetite and nausea, followed within a few days by jaundice. Disease severity varies, with some people having a relatively mild disease course lasting one to two weeks and others having more severe and prolonged symptoms lasting several months. Many infected children are asymptomatic. Chronic infection does not occur. The virus is shed in the faeces of infected people and is primarily spread from person to person through the faecal-oral route (via hands or other objects or through food or water that has been contaminated with the faeces of an infected person, or directly through oral-anal contact).¹

Hepatitis A infection occurs worldwide, but the risk of infection varies with levels of sanitation and personal hygiene. Ireland is considered a low incidence country. A high proportion of cases notified in Ireland have a history of recent travel, or are part of small family outbreaks, often including an index case who has travelled outside Ireland.

Occasionally, larger outbreaks involving extended family members and wider community contacts are reported. These are often associated with person-to-person spread within family and community networks over an extended period of time rather than a common food source. Food and waterborne outbreaks can also occur, in addition to outbreaks with links to childcare facilities and outbreaks in gay and bisexual men, and other men who have sex with men (gbMSM).¹

There is a safe, effective vaccine for hepatitis A and immunisation is recommended for travellers to endemic areas (Africa, Asia, central and south America, eastern Europe and the Middle East), household, sexual and other close contacts of cases and other people at higher risk of infection, or more severe disease, such as gbMSM, people who inject drugs (PWID) and people with chronic liver disease.¹

Methods

The figures presented in this summary are based on data extracted from the Computerised Infectious Disease Reporting (CIDR) System on 4th December 2023. These figures may differ from those published previously due to ongoing updating of notification data on CIDR. Notification rates are expressed per 100,000 population and were calculated using the 2022 census (www.cso.ie). The National Virus Reference Laboratory (NVRL) carried out genetic sequencing of suitable specimens, on request.

Epidemiology

Number of notifications and notification rates

The incidence of hepatitis A in Ireland has been low over the last decade, ranging from 21 to 82 cases per year (0.4 to 1.6/100,000 population). 2022 was an above average year, with 66 cases of hepatitis A notified (1.3/100,000 population) (figure 1).

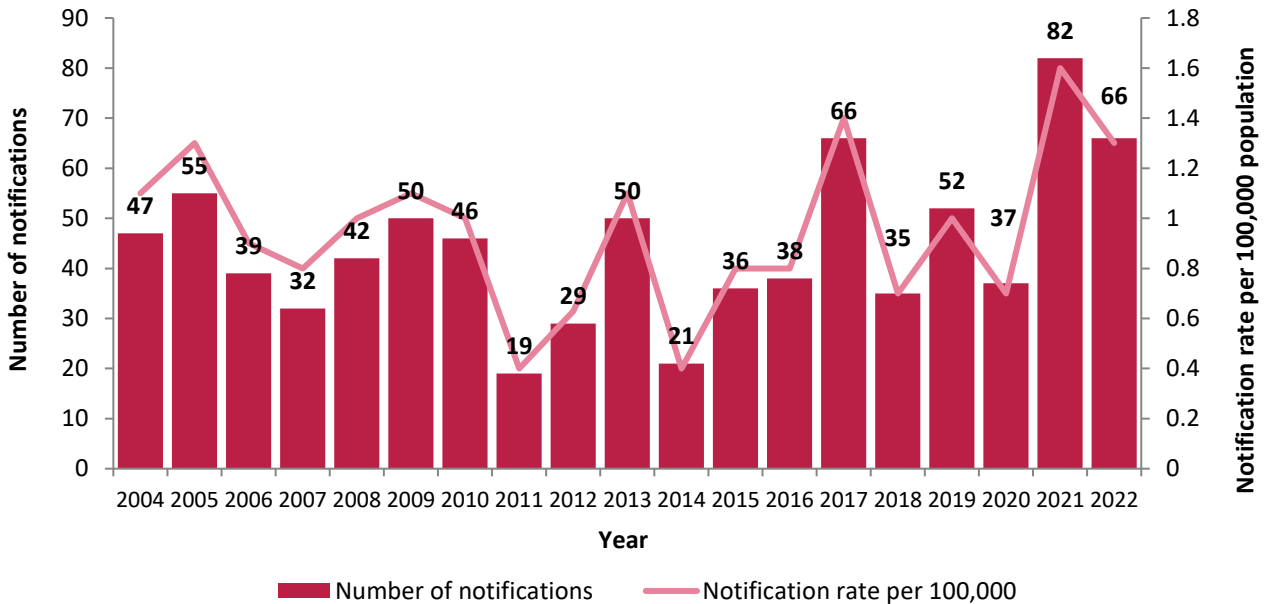


Figure 1. Number of hepatitis A notifications in Ireland, and notification rate per 100,000 population, 2004-2022

Geographic distribution

The notification rates in each HSE public health area for the past four years are shown in figure 2. The highest rates in 2022 were in HSE Dublin and Midlands and HSE Midwest. In the Dublin and Midlands area this was mostly due to a large extended family and local community outbreak with 11 linked cases and 3 further tentatively linked cases, but a family outbreak and a travel associated outbreak were also reported in this area. Three outbreaks were reported in the Midwest; two family/extended family outbreaks and one workplace outbreak. Two involved an index case who had travelled outside Ireland.

Age and sex

The highest notification rates in 2022 were in children and young adults (<35 years) (figure 3). This is a fairly typical pattern for hepatitis A in Ireland and reflects lack of immunity, travel and family outbreaks.

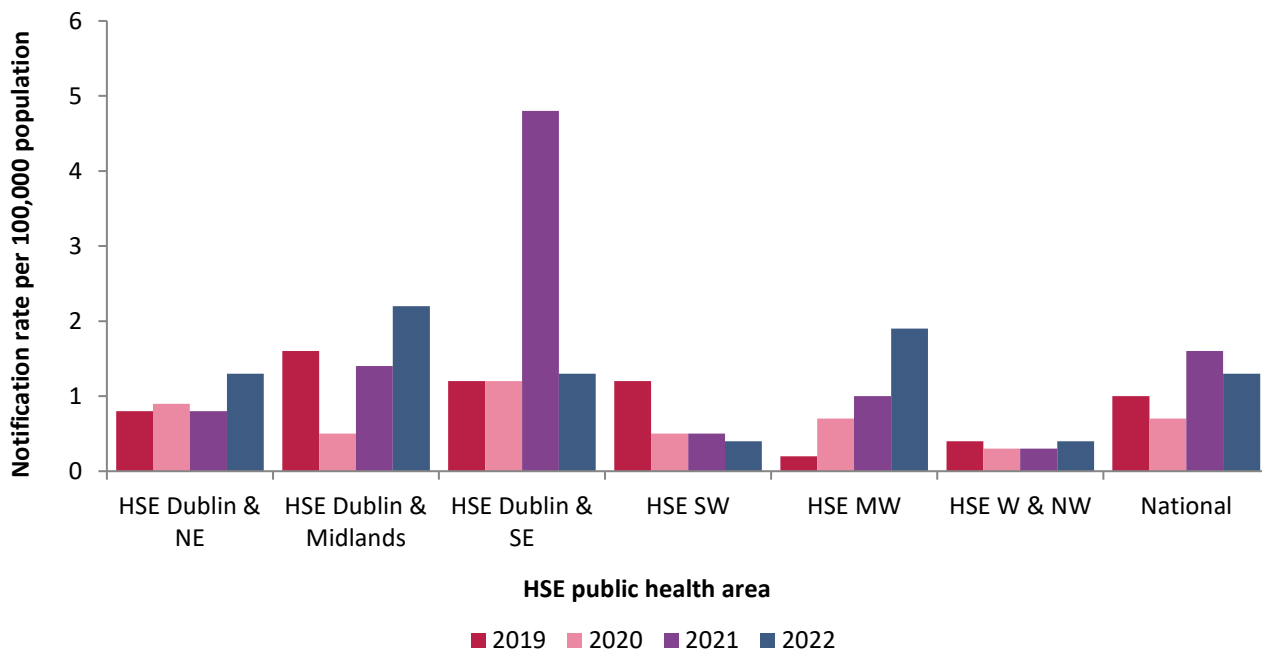


Figure 2. Notification rates for hepatitis A by HSE public health area in Ireland, 2019-2022

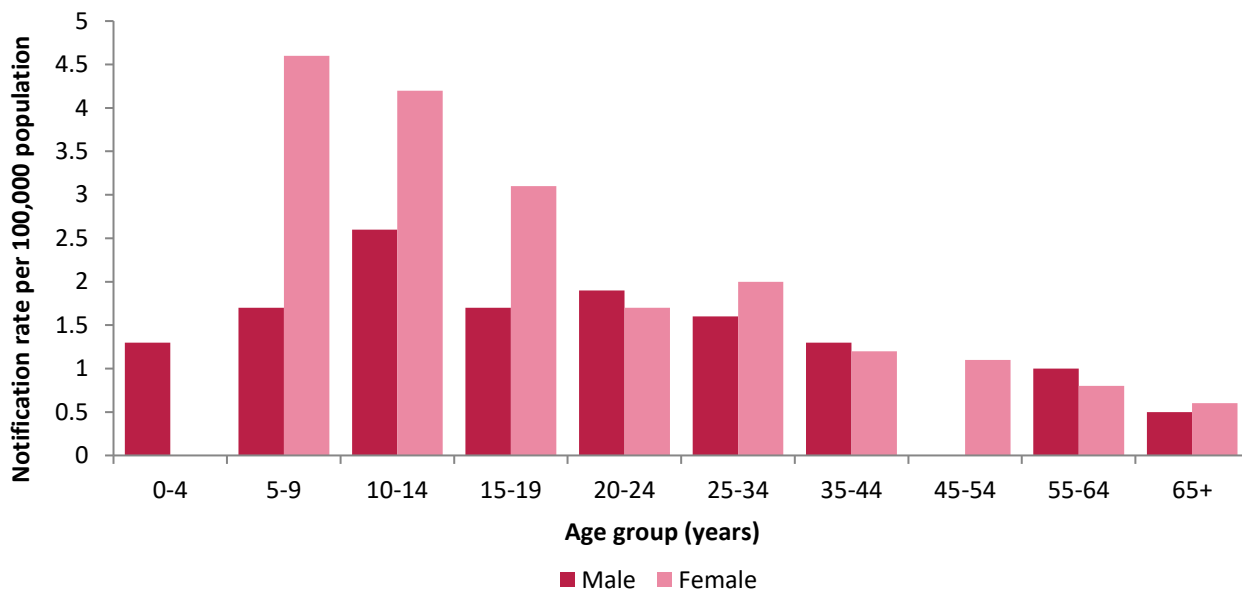


Figure 3. Hepatitis A age and sex-specific notification rates/100,000 population in Ireland, 2022

Country of infection

The most likely country of infection was reported for 79% (n=52) of hepatitis A notifications in 2022. Of these, 29% (n=15) were associated with travel outside Ireland and the remaining 71% (n=37) were infected in Ireland. The most common regions of infection were western Europe (including Ireland) (n=42) and south & south-east Asia (n=7).

Five of the cases who were infected in Ireland were part of outbreaks where the index case was infected outside of Ireland. Two additional cases, for whom country of infection was not reported, were linked to an outbreak involving an index case who had travelled to south/south east Asia. Overall, one third of hepatitis A notifications in 2022 had either travelled outside Ireland or were contacts of a travel related case.

The remaining two thirds of cases were infected in Ireland and not linked to travel-related cases (n=32) or country of infection was not reported (n=12). Sixteen of these were reported as sporadic cases with no known links to other cases. The remaining twenty eight were either reported to be part of an outbreak or suspected to be linked to other cases.

Outbreaks and sequencing data

The NVRL carried out genetic sequencing for 23% (n=15) of hepatitis A cases notified in 2022. These related to four outbreaks, some with cases spanning other years. The sequenced cases and associated cases are shown in figure 4.

Of the twenty two cases linked to travel in 2022, twelve were associated with five outbreaks (four family outbreaks and one workplace outbreak) and the remaining cases were sporadic. Sequencing information was available for one of these outbreaks, with subgenotype IIIA detected in one case.

Five further outbreaks were reported with no known links to travel. Twenty two cases were definitively linked to these outbreaks and tentative associations were reported for a further six cases.

The largest was an extended family and local community outbreak with twelve definitively linked and seven tentatively linked cases. Fourteen of these were in 2022 and five were in 2023. Eleven of these cases were sequenced and found to have the same sequence (genotype IB, V22-000241-GER) as that shared in an epipulse query posted by Germany in relation to three unrelated cases with no obvious source of infection. Two further sporadic cases with this sequence were identified in Ireland, but no epidemiological links were identified between these cases and the other cases involved in the outbreak and they were considered to have been infected independently. Where food history was completed, berry consumption was reported by the early Irish cases, but no definitive link to berries or other food items were identified. The onset dates indicate that onward transmission was likely to have been through person to person spread over an extended period of time. In response

to the epipulse query, Sweden reported one 2021 case with an identical sequence. This case had consumed a smoothie with frozen strawberries. Cases were also reported by Norway (n=3) and Hungary (n=2), but the exposure sources were not identified.

Three outbreaks were family outbreaks with 10 linked cases in total. One case in one of these outbreaks was sequenced as subgenotype IIIA.

One further case was associated with an outbreak spanning late 2020 to January 2023, which predominantly occurred in the Irish travelling community. Nineteen cases were reported to be linked to this outbreak in total (5 sequenced as subgenotype IA and 14 additional epidemiologically linked cases) (figure 4).

Three other cases in 2022 were found to have matching sequences but no epidemiological links to each other and were not considered to be part of an outbreak in Ireland. However, the sequence (subgenotype IB, 2707092_HUN_P1) matched that involved in a large outbreak in Hungary. At the time of the outbreak Hungary posted an epipulse query to inform other countries and several other countries responded to say that they had identified cases with matching sequences. The outbreak was originally thought to be gbMSM related, but this sequence was subsequently detected in frozen berries in Belgium. The berries had been distributed in several European countries and a recall was issued. The Irish cases were in a child and two adults. Two of the three cases had consumed berries and no enhanced data were available for the third case. <https://www.fsai.ie/news-and-alerts/food-alerts/recall-of-additional-best-before-dates-of-ardo-fro>; <https://webgate.ec.europa.eu/rasff-window/screen/notification/565904>

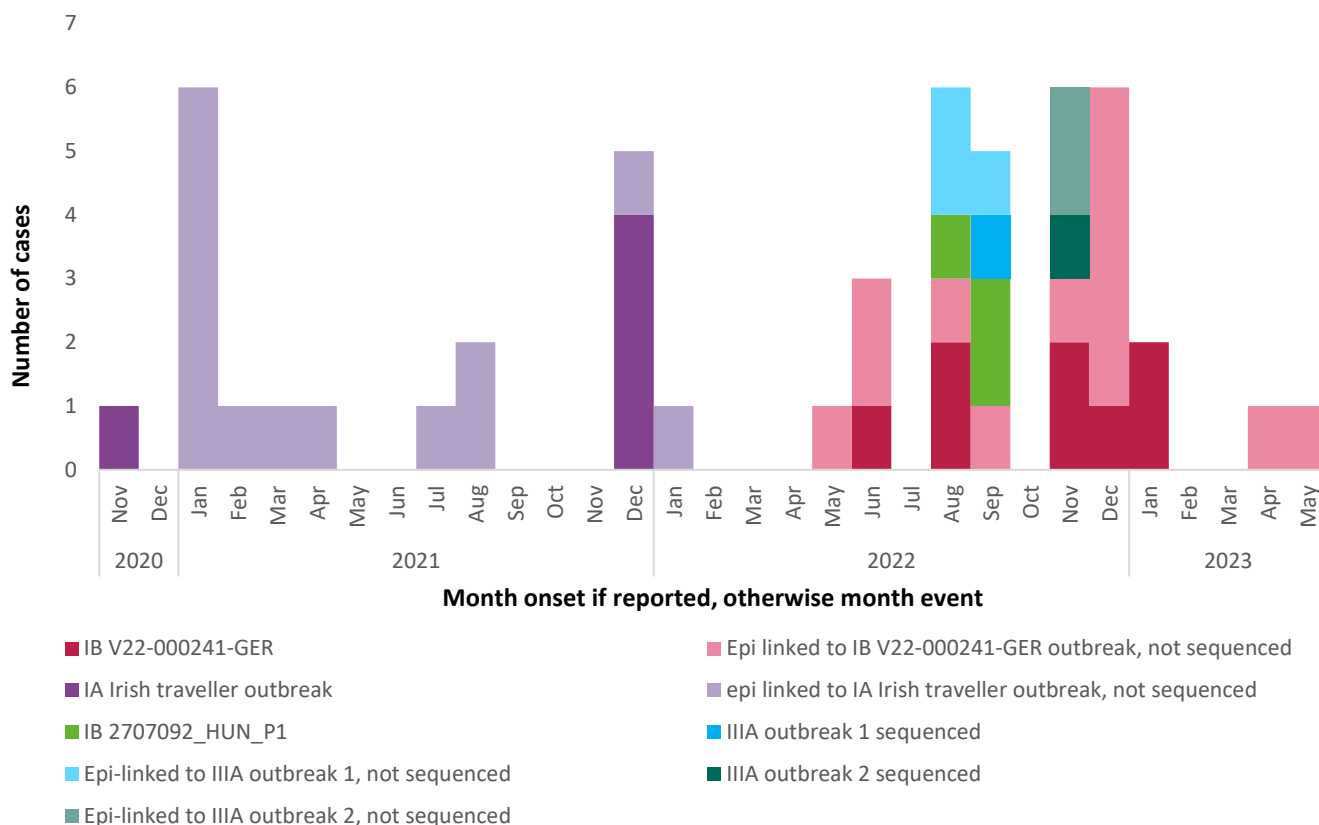


Figure 4. Sequencing results for 2022 and epi-linked cases and related sequences from 2022 and other years

Discussion

In 2022, one third of cases of hepatitis A were infected outside Ireland or were linked to cases who had been infected outside Ireland.

Almost one third of the remaining cases were associated with single extended family and local community outbreak characterised by person to person spread over an extended time period. This outbreak ultimately spanned a 14 month time period and genetic sequencing was important in allowing cases with tentative epidemiological links to be confirmed as part of the same outbreak.

Sequencing data have also been instrumental in the past in linking cases involved in international outbreaks in gbMSM and detecting a number of outbreaks linked to imported frozen berries.²⁻⁷

Further information

<https://www.hpsc.ie/a-z/hepatitis/hepatitisa/surveillancereports/>

<https://www.hpsc.ie/a-z/hepatitis/hepatitisa/guidancepublications/>

<https://www.hpsc.ie/a-z/hepatitis/hepatitisa/factsheets/>

<https://www.fsai.ie/consumer-advice/food-safety-and-hygiene/berries-advice-to-boil-imported-frozen-berries>

<https://www.sexualwellbeing.ie/sexual-health/vaccinations/hepatitis-a/>

<https://man2man.ie/vaccines/>

<https://man2man.ie/hepatitis-a/>

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References

1. Health Service Executive. Immunisation Guidelines for Ireland. Hepatitis A. December 2022. Available at: https://rcpi.access.preservica.com/uncategorized/IO_950e5299-ead9-4db1-8c75-e8313f59ad7a/
2. European Centre for Disease Prevention and Control (ECDC). Epidemiological update: Hepatitis A outbreak in the EU/EEA mostly affecting men who have sex with men. Sept 2018. Available at: <https://ecdc.europa.eu/en/news-events/epidemiological-update-hepatitis-outbreak-eueea-mostly-affecting-men-who-have-sex-men-2>

3. Gassowski M, Michaelis K, Wenzel JJ, Faber M, Figoni J, Mouna L et al. Two concurrent outbreaks of hepatitis A highlight the risk of infection for non-immune travellers to Morocco, January to June 2018. *Euro Surveill.* 2018 Jul;23(27).
4. Mollers M, Boxman ILA, Vennema H, Slegers-Fitz-James IA, Brandwagt D, Friesema IH et al. Successful use of advertisement pictures to assist recall in a food-borne hepatitis A outbreak in the Netherlands, 2017. *Food Environ Virol.* 2018; 10(3): 272-277.
5. Severi E, Verhoef L, Thornton L, Guzman-Herrador BR, Faber M, Sundqvist L, et al. Large and prolonged food-borne multistate hepatitis A outbreak in Europe associated with consumption of frozen berries, 2013 to 2014. *Euro Surveill.* 2015;20(29):21192. Available from: <https://www.eurosurveillance.org/content/10.2807/1560-7917.ES2015.20.29.21192>
6. Fitzgerald M, Thornton L, O'Gorman J, O'Connor L, Garvey P, Boland M, Part AM, Rogalska J, Coughlan H, MacDiarmada J, Heslin J, Canny M, Finnegan P, Moran J, O'Flanagan D; Hepatitis A Outbreak Control Team. Outbreak of hepatitis A infection associated with the consumption of frozen berries, Ireland, 2013-linked to an international outbreak. *Euro Surveill.* 2014 Oct 30;19(43). Available from: <https://www.eurosurveillance.org/content/10.2807/1560-7917.ES2014.19.43.20942>
7. Enkirch T, Eriksson R, Persson S, Schmid D, Aberle SW, Löf E et al. Hepatitis A outbreak linked to imported frozen strawberries by sequencing, Sweden and Austria, June to September 2018. *Euro Surveill.* 2018;23(41). Available from: <https://www.eurosurveillance.org/content/10.2807/1560-7917.ES.2018.23.41.1800528>