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Annual Epidemiological Report

September 2018

Hepatitis A in Ireland, 2017

Key Facts

Number of cases, 2017: 66

Crude notification rate, 2017: 1.4/100,000 population

The number of notifications of hepatitis A increased significantly in 2017 compared to 2016 (n=38). This was due to Irish cases linked to a very large European-wide outbreak of hepatitis A, which was mostly associated with men who have sex with men.

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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. Most 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. Common source foodborne outbreaks can also occur, in addition to outbreaks with links to childcare facilities and outbreaks in men who have sex with men (MSM) and people who inject drugs (PWID).[1]

There is a safe, effective vaccine for hepatitis A and vaccination is recommended for travellers to endemic areas (Africa, Asia, Central and South America, Eastern Europe and the Middle East) and people at higher risk of infection, or more severe disease, such as MSM, PWID and people with chronic liver disease.[1]

Methods

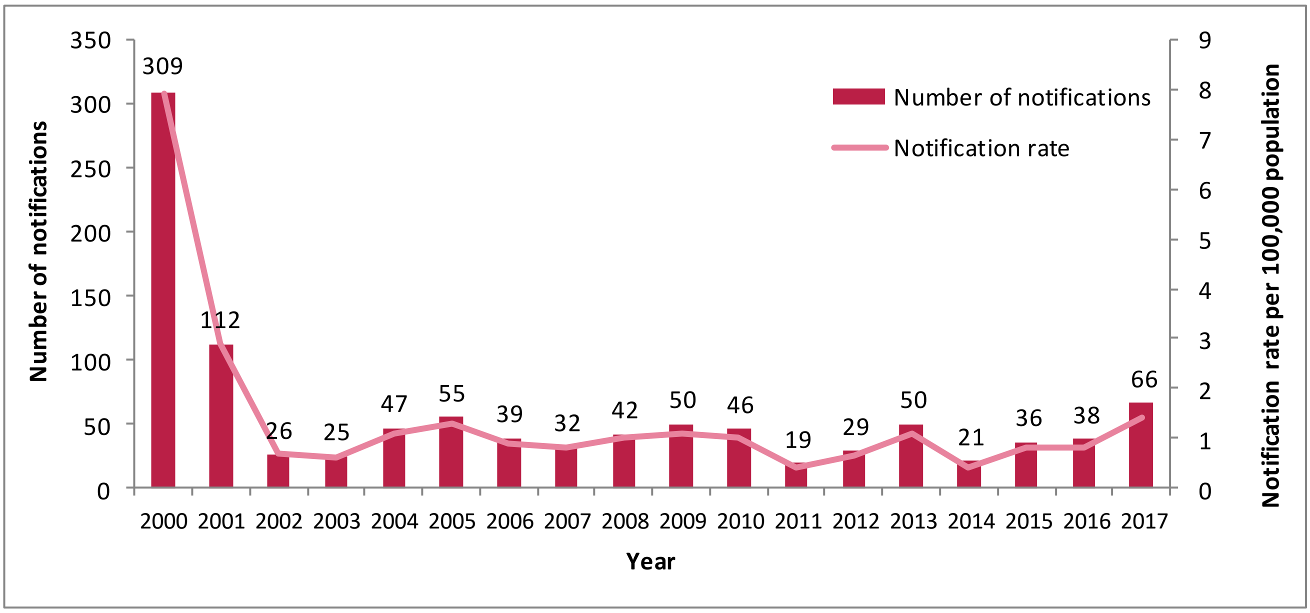
The figures presented in this summary are based on data extracted from the Computerised Infectious Disease Reporting (CIDR) System on 17th September 2018. These figures may differ from those published previously due to ongoing updating of notification data on CIDR. Notification rates are expressed per 100,000 population and are calculated using the 2016 census. The National Virus Reference Laboratory (NVRL) carried out genetic sequencing on all hepatitis A specimens that were available to them and were suitable for sequencing.

Epidemiology

Number of notifications and notification rates

The incidence of hepatitis A in Ireland has been low over the last decade, ranging from 19 to 50 cases per year (0.4 to 1.1/100,000 population). However, the notification rate increased significantly in 2017, with 66 cases notified (1.4/100,000 population) compared to 38 in 2016 (0.8/100,000 population) (figure 1). This was mainly due to a very large European-wide outbreak in MSM. This outbreak involved three different strains of genotype IA hepatitis A (VRD_521_2016, RIVM-HAV16-090 and V16-25801) and included almost 4,500 confirmed cases in 22 EU/EEA countries. The outbreak started in mid-2016 and peaked in the summer of 2017. No cases of hepatitis A were reported in MSM in Ireland in 2016, but twenty of the cases notified in 2017 were identified as MSM, one additional case was a household contact of an MSM case and nine additional cases were infected with one of the three MSM outbreak strains of hepatitis A. Although the number of outbreak cases began to decline in Europe and in Ireland towards the end of 2017, some cases continued to be identified in 2018.[2]

Figure 1. Number of hepatitis A notifications in Ireland, 2000-2017



Geographic distribution

The notification rates in each HSE area for the past four years are shown in figure 2. Sixty two percent (n=41) of the 2017 cases were notified by HSE East and the notification rate (2.4/100,000 population) in the East was almost twice that of the next highest area. The increased notification rate in the East was mostly due to cases associated with the MSM outbreak.

Age and sex

There was no significant difference in the number of hepatitis A cases in male and females between 2000 and 2016 (male:female ratio:1.1). However, in 2017 almost three quarters of hepatitis A notifications were male (73%, n=48) and 27% (n=18) were female, giving a male to female ratio of 2.7.

The highest notification rates for hepatitis A are usually in children and young to middle-aged adults, reflecting lack of immunity and travel history. However, in 2017 there was an increase in hepatitis A cases in adult males due to the MSM outbreak. The notification rate for males aged between 20 and 44 years was 4.1/100,000 population (n=34, 71% of male cases) compared to a rate of 1.1/100,000 population for females in the same age group (n=9, 50% of female cases) (figure 3). The notification rate for children aged less than 10 years (n=11, 1.6/100,000 population) was similar to other recent years.

Figure 2. **Notification rates for hepatitis A by HSE area in Ireland, 2014-2017**

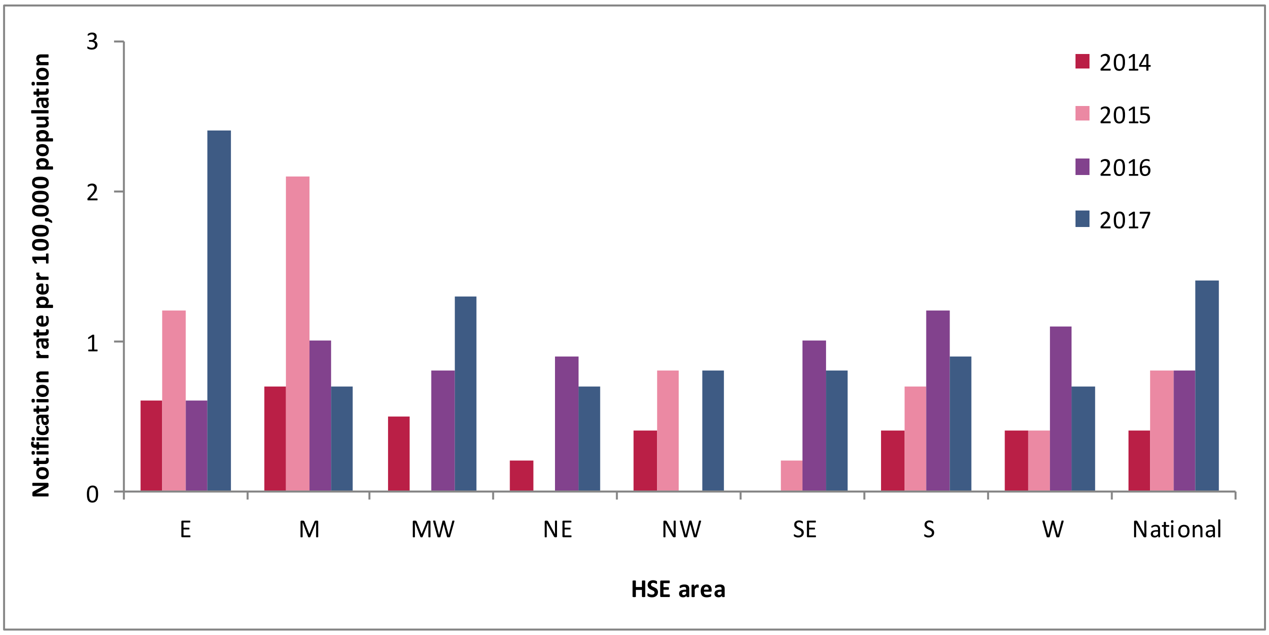
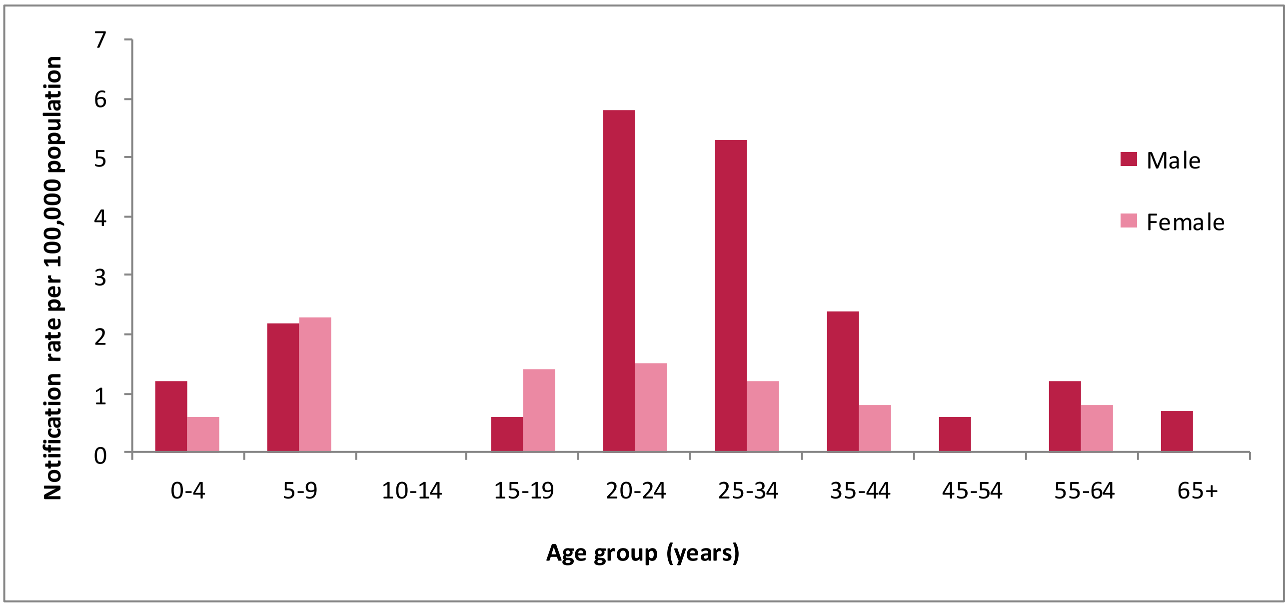


Figure 3. **Hepatitis A age and sex-specific notification rates/100,000 population in Ireland, 2017**



Country of infection

The most likely country of infection was reported for 96% (n=63) of hepatitis A notifications in 2017. Of these, almost half (48%, n=30) were infected in Ireland. Aside from Ireland, the most common countries of infection were India (n=4), Spain (n=4), Germany (n=3), Pakistan (n=3) and Romania (n=3).

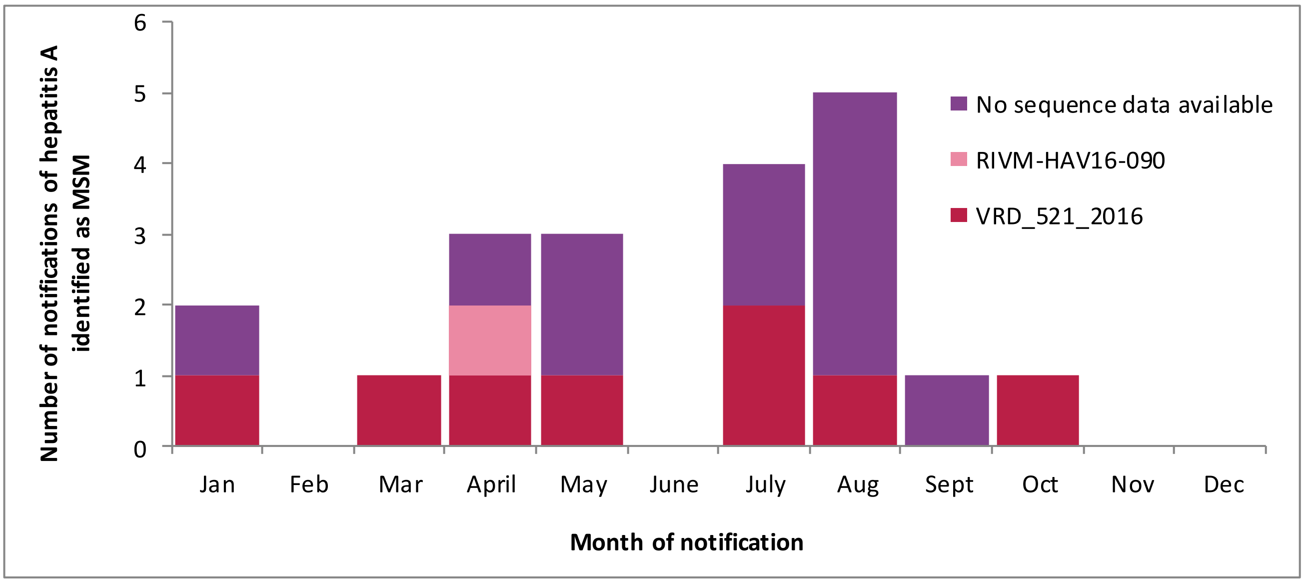
MSM outbreak and linked cases (n=30)

Twenty of the 66 cases of hepatitis A notified in 2017 were identified as MSM. Their ages ranged from 20 to 42 years (median 32.5). Thirteen were infected in Ireland, six were likely to have been infected outside Ireland and no information on travel history was available for the remaining case.

Eighty five percent (n=17) of the MSM cases were reported by HSE E. Thirty percent (n=6) had gonorrhoea, HIV and/or chlamydia coinfections. Samples from nine of the twenty MSM cases were sequenced by the NVRL. Eight were infected with the VRD_521_2016 hepatitis A strain and one with the RIVM-HAV16-090 strain (figure 4).

Two of the MSM cases were definitively linked; one case was a known sexual contact of an earlier case. A further case, who was a household contact of the index case, was also linked to this outbreak. Sequencing data were not available for these three cases. No epidemiological links were identified between the remaining cases in MSM.

Figure 4. Number of hepatitis A notifications identified as MSM, by month of notification and strain of hepatitis A in Ireland, 2017



There were nine additional male adult cases of hepatitis A with one of the three MSM outbreak strains of hepatitis A: four had the V16-25801 strain, three had the VRD_521_2016 strain and two had the RIVM-HAV16-090 strain. Two reported possible sexual exposures, but their sexual orientation was not known, and seven reported no possible sexual exposures. Five of the seven had travelled to countries where the outbreak strains were circulating and the remaining two cases were infected in Ireland.

Cases with no identified links to the MSM outbreak (n=36)

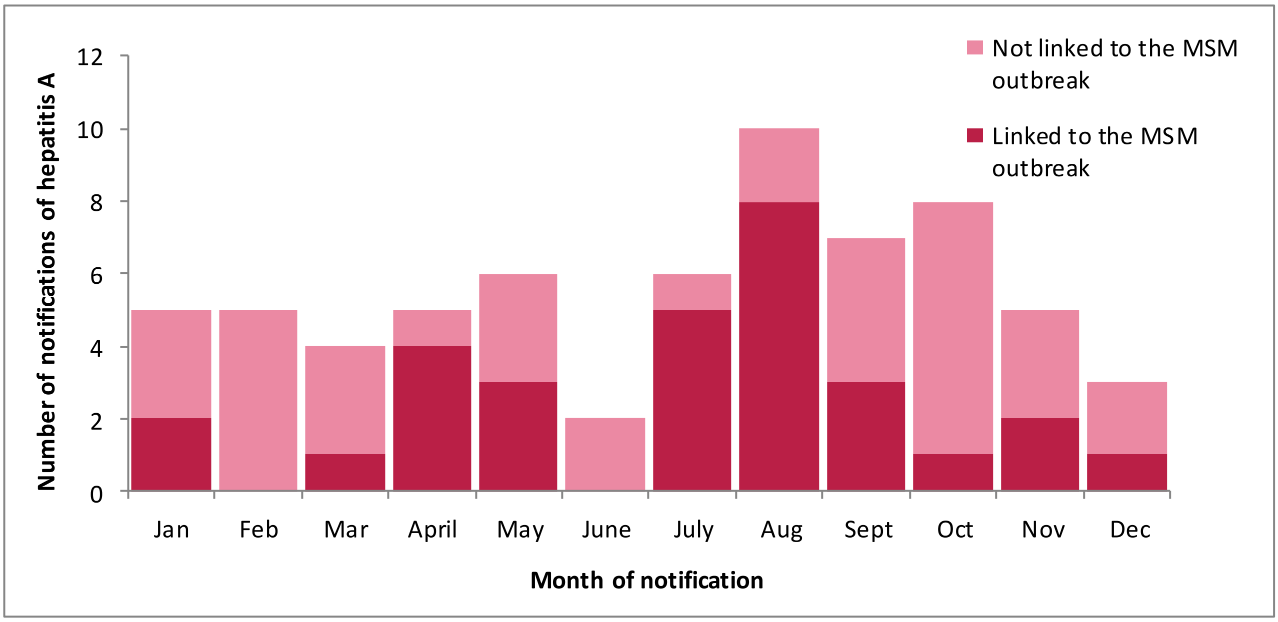
Aside from cases linked to the European-wide MSM outbreak, there were 26 sporadic cases of hepatitis A in 2017 and 10 cases associated with five distinct outbreaks.

Seventeen of the sporadic cases were likely to have been infected outside Ireland, eight were infected in Ireland and country of infection was not known for the remaining case. Sequencing data were available for eight: four were genotype IB, three were genotype IA (but not one of the MSM outbreak strains) and one was genotype IIIA.

The index cases in three of the five outbreaks were infected outside Ireland (Sudan, Pakistan and Romania). The two outbreaks that were not associated with travel were both family outbreaks of genotype IB hepatitis A. The source of infection was not identified for either.

Figure 5 shows the month of notification for all cases of hepatitis A in 2017, by whether or not they were linked to the MSM outbreak.

Figure 5. Month of notification for cases of hepatitis A in Ireland, by whether they were linked to the European-wide MSM outbreak, 2017



Discussion

Genetic sequencing has greatly facilitated the linking and investigation of cases of hepatitis A. Sequencing data were particularly important in Ireland, and in Europe, in terms of identifying and monitoring the recent hepatitis A outbreak in MSM. Significant work was subsequently done to raise awareness of the risk of hepatitis A in MSM, to encourage vaccination and promote hygiene and safe-sex measures to reduce the risk of infection. There was some spillover of the MSM outbreak strains into the general population in Europe, with increased numbers of females and older cases identified in some European countries as the outbreak progressed. However, the number of cases identified decreased significantly in the second half of 2017 and this outbreak has been largely controlled.

Further information available on HPSC website

http://www.hpsc.ie/a-z/hepatitis/hepatitisa/guidancepublications/

http://www.hpsc.ie/a-z/hepatitis/hepatitisa/factsheets/

Acknowledgements

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