

# Cryptosporidium Reference Unit for England and Wales.

## Annual report of referrals and *Cryptosporidium* genotyping, England and Wales, 2023.

### National report for England and Wales

<https://phw.nhs.wales/services-and-teams/cryptosporidium-reference-unit/>

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## Summary

- Diagnostic laboratories may refer stools for confirmation of equivocal findings or specialist testing of high-risk patients.
- All diagnostic laboratories are asked to send all *Cryptosporidium* positive stools for genotyping.
- In 2023, a total of 5850 specimens were referred to the national *Cryptosporidium* Reference Unit.
- The region (by location of referring laboratory) that referred the highest number of specimens was the North West (n = 1211), followed by West Midlands (n = 840).
- The region that referred the lowest number of specimens was London (n = 170).
- Referrals largely reflect the regional variation in *Cryptosporidium* notifications but not all laboratories refer all specimens.
- Of the 5850 specimens referred nationally, 343 were either not confirmed or not typable.
- Of the genotyped specimens, 4891 were referred from laboratories in England, representing 72% of the 6837 *Cryptosporidium* cases reported to national surveillance in England.
- Of the genotyped specimens, 613 were referred from laboratories in Wales, representing 93% of the 657 *Cryptosporidium* cases reported to national surveillance in Wales.
- Of the total 5504 genotyped specimens, 2379 (43%) were identified as *Cryptosporidium parvum* and 2991 (54%) were identified as *Cryptosporidium hominis*. 8 were both *C. parvum* and *C. hominis*, and 126 were other *Cryptosporidium* species.
- 784 (14%) of the genotyped specimens reported international travel and 577 (74%) of these were *C. hominis*.

## Part 1. Referrals to the National *Cryptosporidium* Reference Unit

Diagnostic laboratories may refer stools for confirmation of equivocal findings or specialist testing of high-risk patients.

All diagnostic laboratories in England and Wales are asked to send all *Cryptosporidium* positive stools for genotyping. This is actively encouraged; there is no charge and our aim is to achieve unbiased molecular surveillance as well as to support cluster / outbreak identification and investigations; please see the section "Subtyping, clusters and outbreak investigations". Repeat specimens from the same patient within one month are not usually accepted for genotyping, and are excluded from the analysis presented here.

If individual laboratories have trouble sending specimens, please talk to the reference unit about facilitating this.

Our submission form can be found here: <https://phw.nhs.wales/services-and-teams/cryptosporidium-reference-unit/specimen-submission-form/>

In 2023, a total of 5850 specimens were referred and accepted at the national *Cryptosporidium* Reference Unit for confirmation, specialist testing or genotyping.

Overall 5504 genotyped specimens represented 73% of those reported to national surveillance systems in England and Wales.

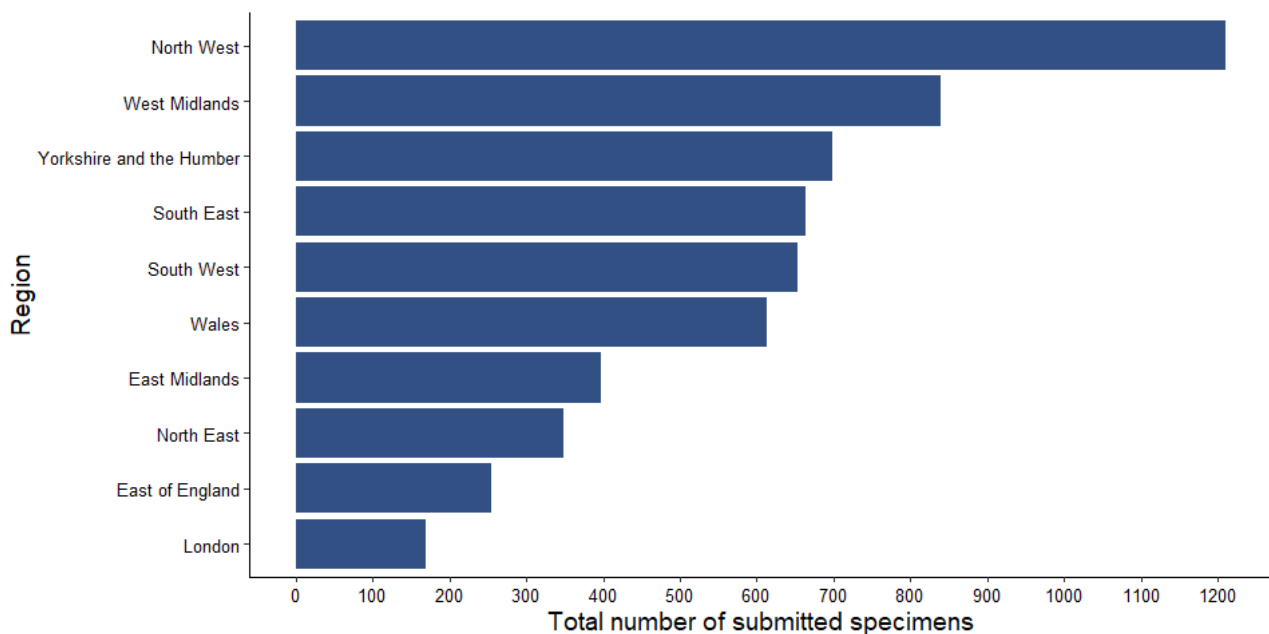
Of the genotyped specimens, 4891 were referred from laboratories in England, representing 72% of the 6837 *Cryptosporidium* cases reported to national surveillance in England.

Of the genotyped specimens, 613 were referred from laboratories in Wales, representing 93% of the 657 *Cryptosporidium* cases reported to national surveillance in Wales.

## Summary of referrals by region and laboratory

Using the location of the diagnostic laboratory (as the patient postcode is not always provided and this analysis focusses on lab practice), the region that referred the highest number of specimens was the North West (n = 1211), followed by West Midlands (n = 840). The region that referred the lowest number of specimens was London (n = 170). Referrals largely reflect the regional variation in *Cryptosporidium* notifications but not all laboratories refer all specimens. Providing postcode information is helpful for spatial analysis as well as liaising with Health Protection Teams and there is space on our submission form for this.

### *Cryptosporidium* specimens referred to the reference unit by laboratory region, 2023



## Summary of referrals by region and month, 2023

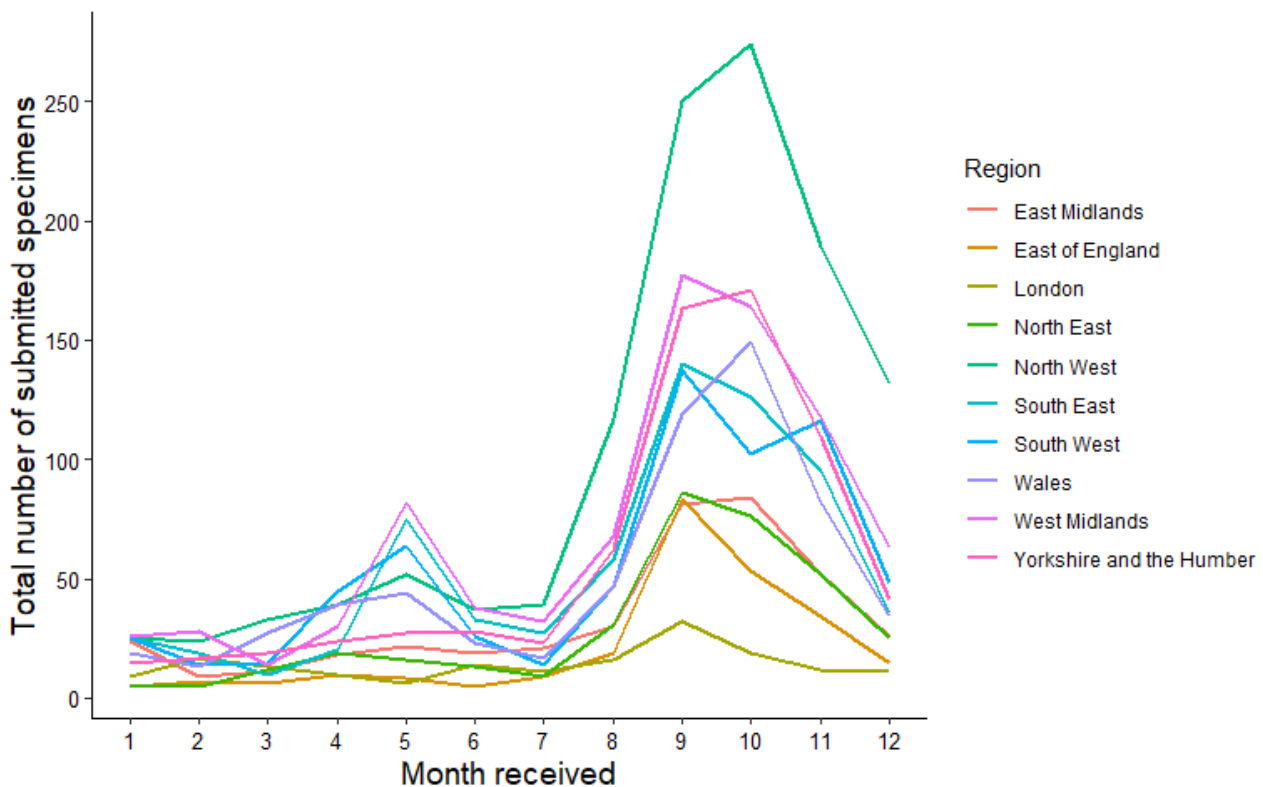
Temporal data are analysed here by month of specimen receipt, as specimen collection dates are not always provided. There is a place for this information on our submission form.

Most regions experienced a small peak in the number of specimens referred in May and their highest peak in September. The highest monthly number of specimens referred was the North West but this was in October (n = 274).

Yorkshire and the Humber region and Wales also had their highest number of specimens referred in October (Yorkshire and the Humber n= 171, Wales n = 149).

There is usually a small spring peak and a larger autumn peak in *Cryptosporidium* cases, so this temporal pattern was not unexpected, but the size of the autumn peak was larger than expected and the exceedance was investigated (Peake et al., 2023; Williams et al., 2025). The increase was mostly in *C. hominis* and the reasons included potential travel-related and recreational water exposures (Peake et al., 2023; Williams et al., 2025). The trend was also observed in other European countries (ECDC [Communicable disease threats report, 22-28 October 2023, week 4](#)).

### Total number of specimens referred per month by region, 2023



## Part 2: *Cryptosporidium* genotyping of referred specimens from England and Wales, 2023

Genotyping to identify *Cryptosporidium* species helps to understand the epidemiology and transmission of *Cryptosporidium*, and thus interventions.

*C. hominis* is host-adapted to humans and transmission is anthroponotic. *C. parvum*, in addition to humans, has a wide range of animal hosts and zoonotic transmission is especially linked to young livestock.

At the national reference unit, genotyping is undertaken in the first instance by duplex real-time PCR to detect *C. parvum* and *C. hominis*. If these predominant species are not detected, a real-time PCR that detects all *Cryptosporidium* species is used and the amplicon is sequenced to confirm which species is present.

These methods are described in Robinson et al., 2020 and Elwin et al., 2022.

### Summary of *Cryptosporidium* species identified

Of the 5850 referred specimens in 2023, 343 were either not confirmed as *Cryptosporidium* or were not typable (species not identified).

Of the 5504 genotyped specimens, representing 73% of those reported to national surveillance, 2379 (43%) were identified as *C. parvum* and 2991 (54%) were identified as *C. hominis*.

Both *C. parvum* and *C. hominis* were detected in 8 specimens.

Other *Cryptosporidium* species were detected in 126 (2%) specimens.

## Other *Cryptosporidium* species

<b><i>Cryptosporidium</i> species (number detected in 2023)</b>	<b>Total</b>	<b>Main reservoir hosts</b>
<i>C. cuniculus</i>	33	Rabbits
<i>C. ubiquitum</i>	33	Ruminants, rodents, carnivores, primates
<i>C. meleagridis</i>	21	Birds, mammals
<i>C. felis</i>	16	Cats
<i>C. canis</i>	4	Dogs
<i>C. viatorum</i>	4	Humans, rodents
<i>C. sciurinum</i>	4	Squirrels
<i>C. occultus</i>	3	Rodents
<i>C. ditrichi</i>	2	Rodents
<i>C. erinacei</i>	2	Hedgehogs
<i>C. equi</i>	1	Horses
<i>C. novel genotype</i>	1	Unknown
<i>C. parvum</i> & possible other spp.	1	Unknown
<i>C. skunk genotype</i>	1	Mustelids

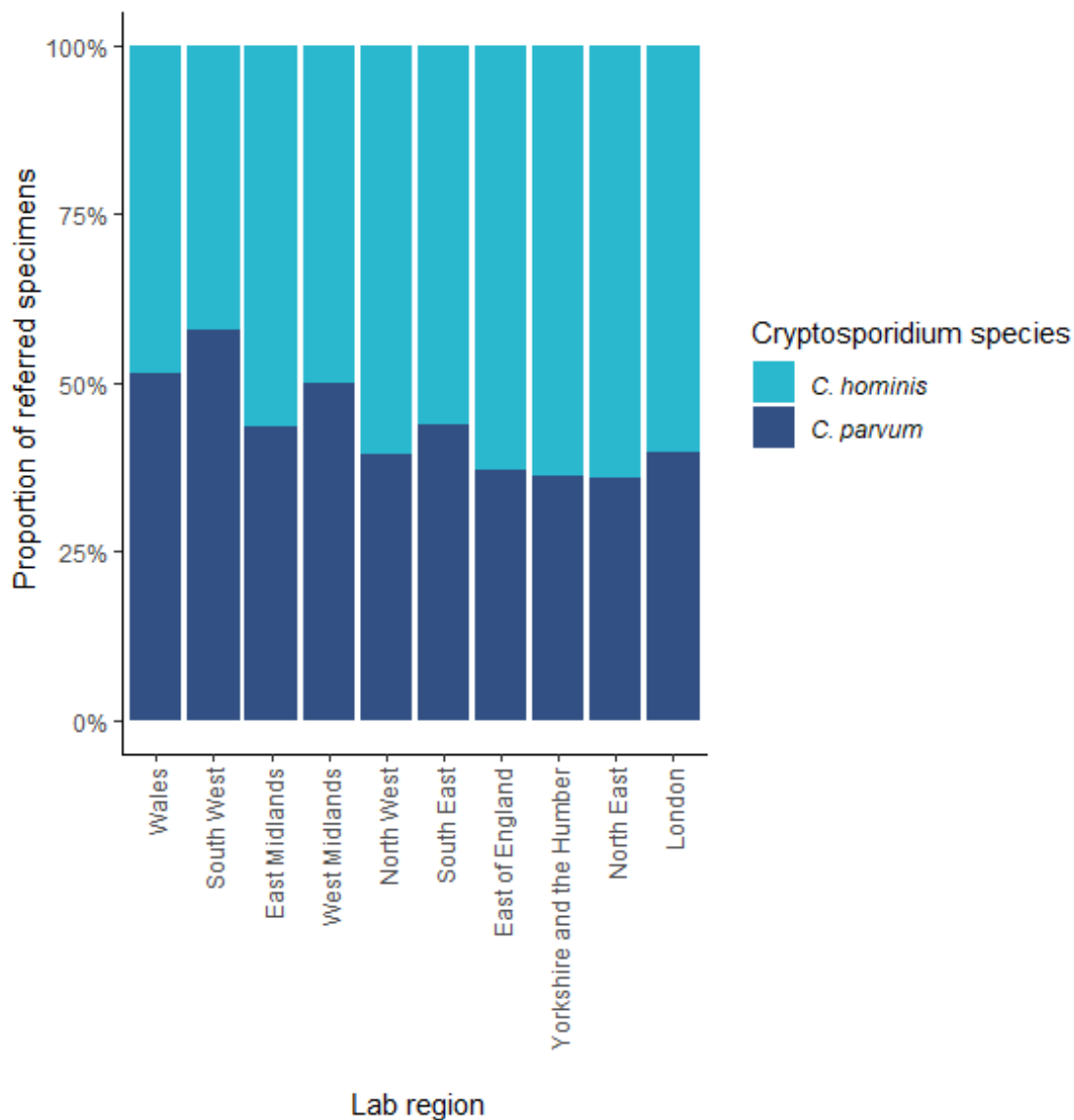
## Spatial distribution by *Cryptosporidium* species and region 2023

The spatial distribution of *C. parvum* and *C. hominis* is influenced by socio-economic and environmental risk factors. For *C. hominis* these include living in an urban area where high population density facilitates person-to-person spread. For *C. parvum* these include living in a rural area, or where ruminant livestock density is high.

The occurrence of *C. parvum* and *C. hominis* differed between regions.

South West had the highest frequency of *C. parvum* specimens (58%) compared to *C. hominis* (42%), whereas the North East reported the lowest frequency of *C. parvum* specimens (36%) compared to *C. hominis* (64%).

### Proportion of *C. hominis* / *C. parvum* by region of referring laboratory



## Age-sex distribution of confirmed cases

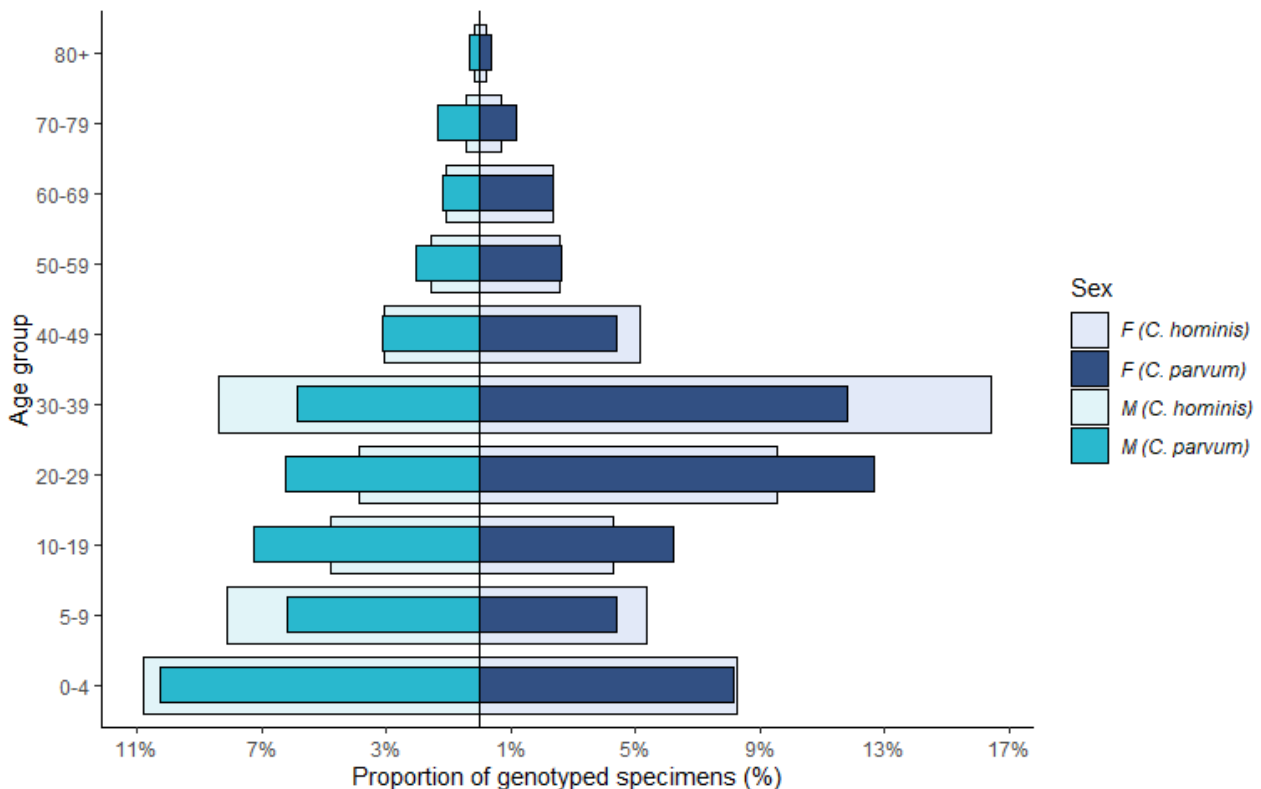
Age and sex information was available for 5162/5370 (96%) *C. parvum* and *C. hominis* specimens.

Most genotyped specimens were from the 30-39 age group (n = 1143) and the 0-4 age group (n = 993).

There was a small difference overall between the sex distribution of *C. parvum* where 1278/2312 (55%) specimens were from females and 1034 (45%) from males, and *C. hominis* where 1612/2850 (57%) were from females and 1238 (43%) from males.

The age and sex distribution differed; there were more *C. parvum* and *C. hominis* specimens from boys under 4 years of age, and from women aged 20-39 years. An expected predominance of *C. hominis* in young children was absent. Interestingly, the predominance of *C. hominis* in women of childbearing age usually seen was evident in the 30-39 age group but this year also in males, and in the 20-29 age group there was a greater proportion of *C. parvum*.

### Age and Sex of submitted *C. parvum* and *C. hominis* specimens 2023



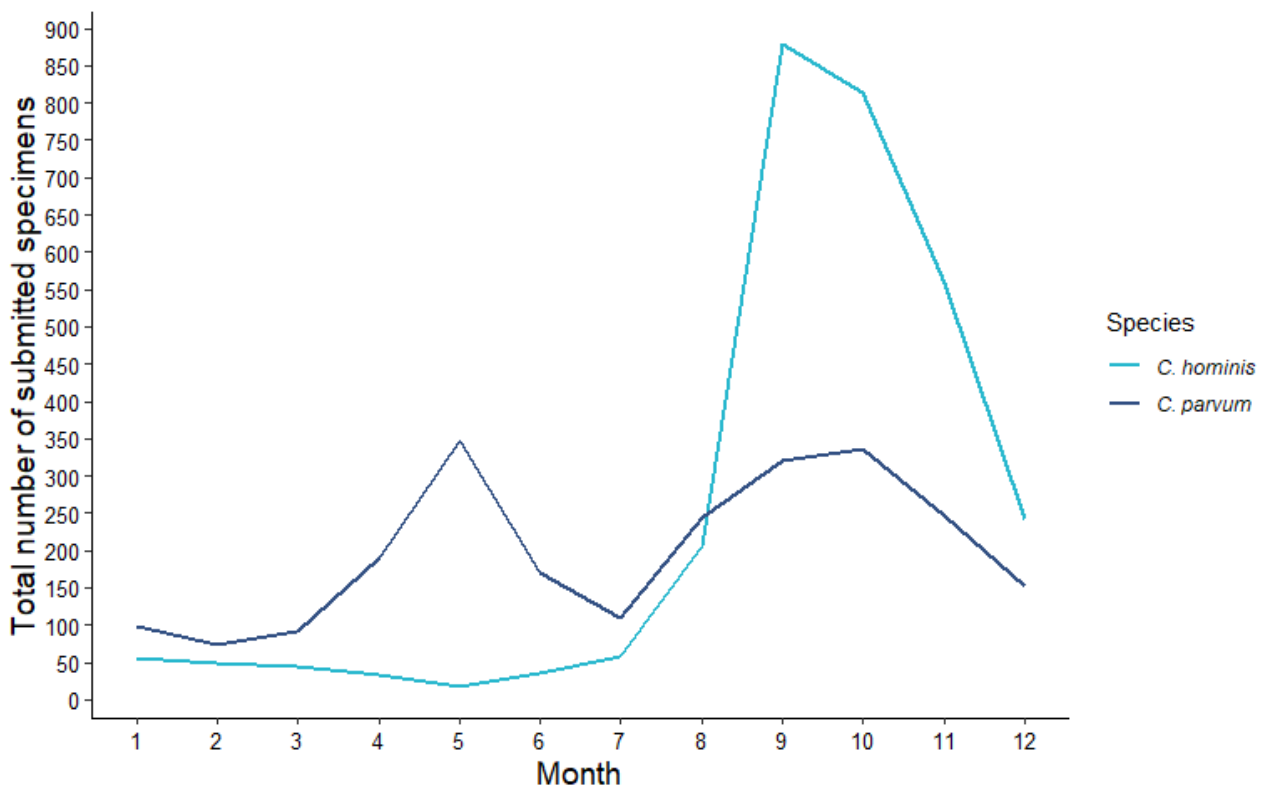
## Temporal distribution of referred specimens, 2023

The temporal distribution of *Cryptosporidium* species is influenced by environmental factors and human behaviour such as seasonal visits to open farms and international travel to see friends and family or for holidays.

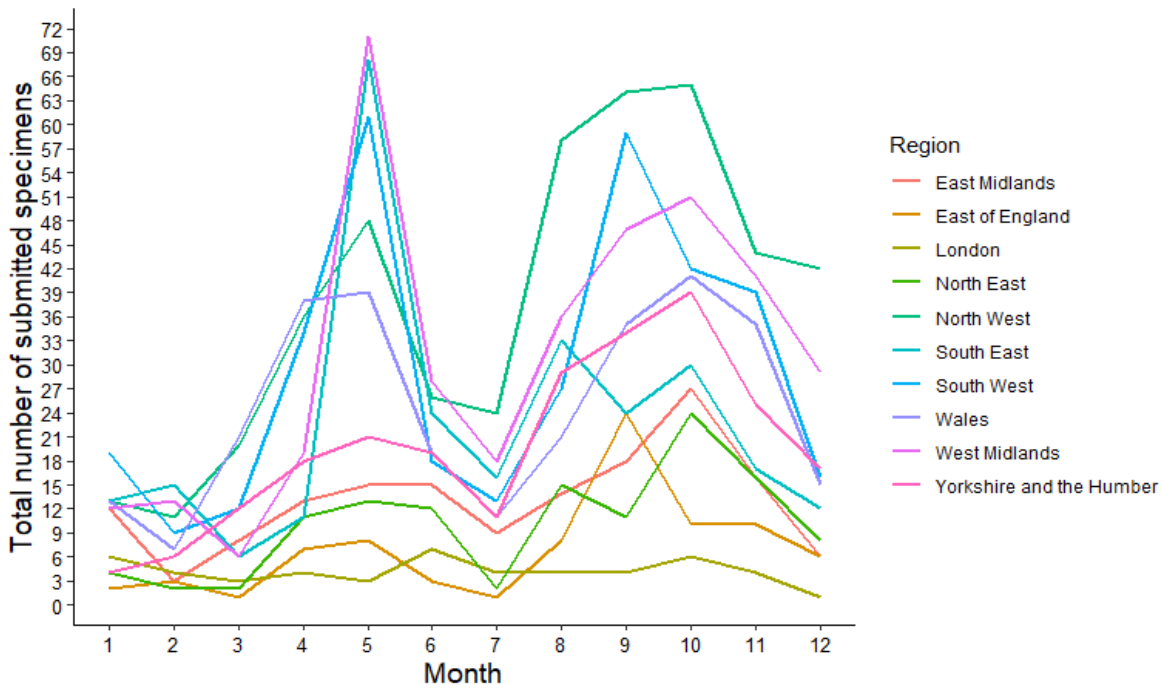
The number of *C. parvum* specimens peaked in May ( $n = 347$ ) and again with an unexpected peak of a similar size in October ( $n = 335$ ).

The number of *C. hominis* specimens stayed consistently low across the first eight months of the year, peaking sharply in September ( $n = 879$ ), when 577 (66%) of these reported foreign travel (see below). This extraordinarily large exceedance was reported at the time in Eurosurveillance (Peake et al., 2023).

### *C. parvum* and *C. hominis* specimens per month of receipt 2023

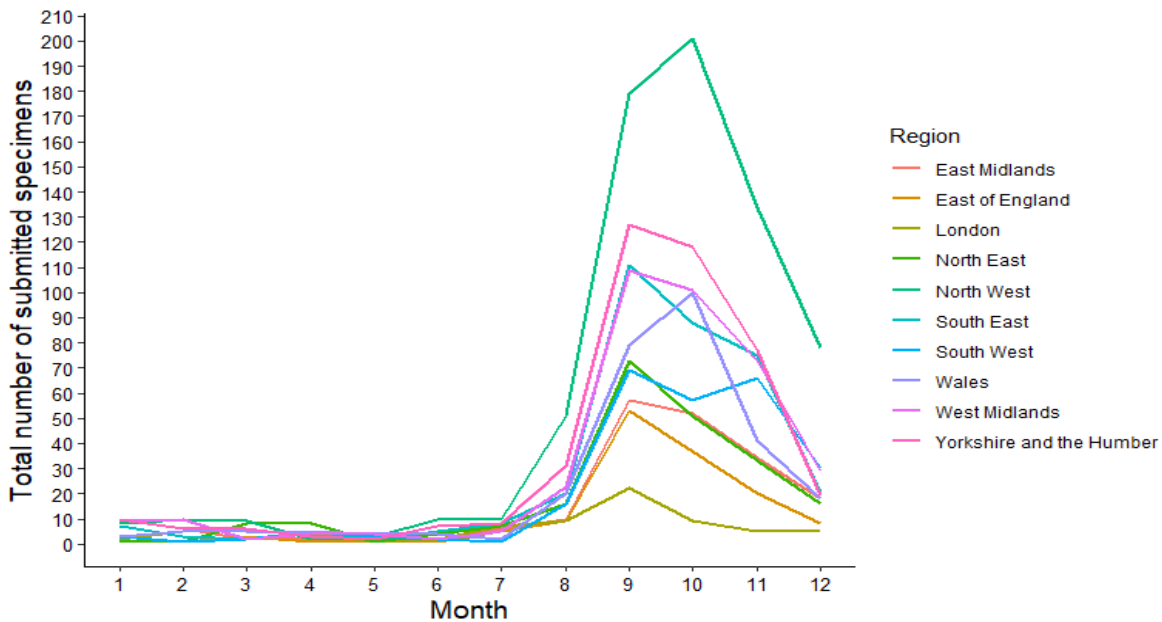


### C. parvum specimens per month of receipt by region in England and Wales 2023



The North West region referred the most specimens that were *C. hominis* in the autumn, peaking slightly later than most regions in October.

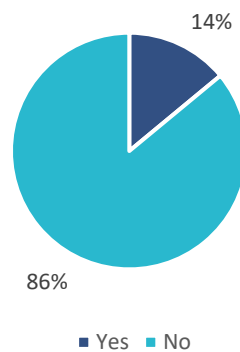
### C. hominis specimens per month of receipt by region in England and Wales 2023



## Travel history and *Cryptosporidium* species

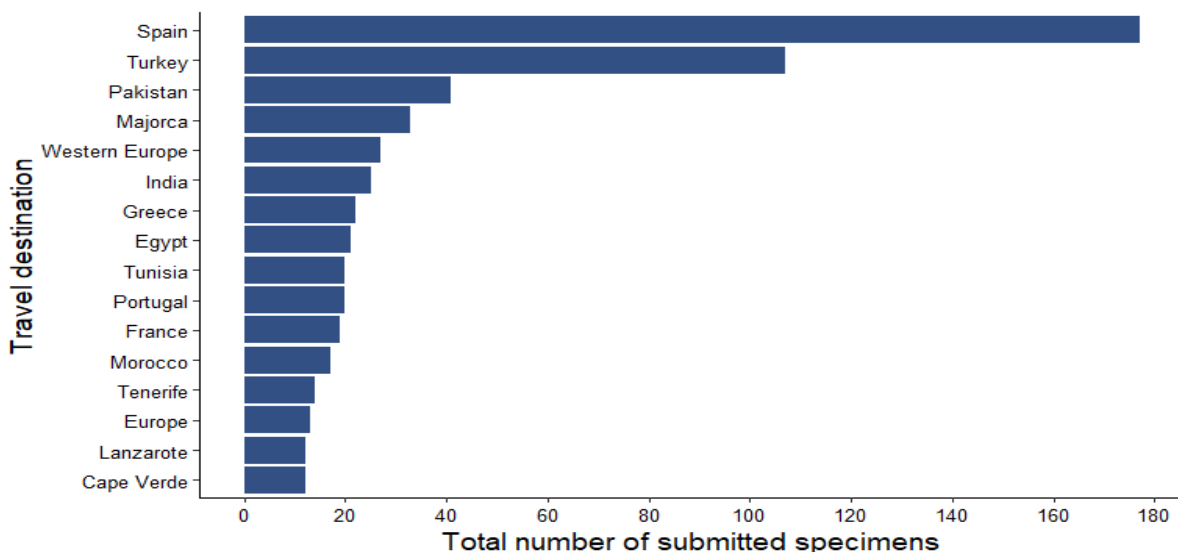
A history of international travel is often associated with *Cryptosporidium* infection but can be underestimated if the history is not recorded. This is why we include a space to record this on our submission form. In 2023, 784 of 5504 (14%) of the genotyped *Cryptosporidium* specimens reported international travel within the incubation period of their infection. However, lack of information does not imply an absence of travel.

### Proportion of genotyped specimens, England and Wales, with international travel report, 2023



The top three travel destinations from genotyped specimens were Spain (n = 177), Turkey (n = 107) and Pakistan (n = 41). Travel to Spain and Turkey was mainly in the summer/autumn.

### International travel destinations of *Cryptosporidium* cases genotyped from England and Wales, 2023 (see Appendix for destinations with <10 reports)



Note: this plot shows the top 16 international travel destinations (more than 10 cases reported visiting during incubation period). See Appendix for a full list of visited destinations with less than 10 reports.

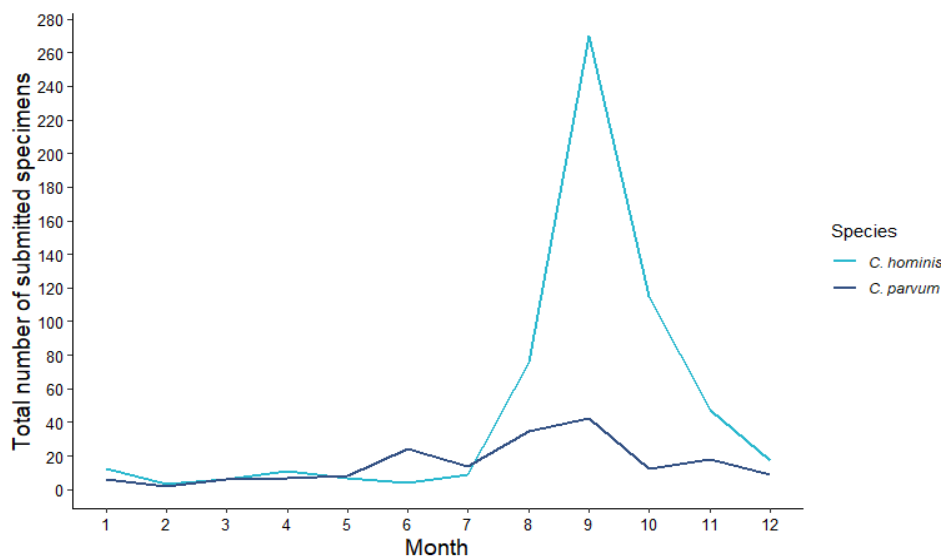
Of the 784 genotyped specimens that reported foreign travel, more were *C. hominis* 577 (74%) than *C. parvum* 183 (23%). These reports contributed to the increase in *C. hominis* in the summer/autumn.

### Summary of international travel destinations and *Cryptosporidium* species

<i>Cryptosporidium</i> species	Total among travellers	Spain	Turkey	Pakistan	Egypt	India	Majorca
<i>C. hominis</i>	577	158	81	21	20	19	31
<i>C. parvum</i>	183	16	25	19	1	4	5
<i>C. hominis</i> and <i>C. parvum</i>	3	1	1	0	0	0	0
<i>C. cuniculus</i>	4	2	0	0	0	0	0
<i>C. meleagridis</i>	9	0	0	1	0	0	0
<i>C. felis</i>	2	0	0	0	0	1	0
<i>C. viatorum</i>	2	0	0	0	0	1	0

The majority (n= 270) of *C. hominis* specimens with international travel history were received in September, similarly the month with the highest frequency of international travel for *C. parvum* specimens was September (n = 42).

### *C. parvum* and *C. hominis* cases reporting international travel by month of receipt from England and Wales, 2023



## Subtyping, clusters and outbreak investigations, England and Wales, 2023

One of the main values of *Cryptosporidium* genotyping and subtyping is for identifying and investigating outbreaks. Without the specimens you refer for genotyping, this would not be possible and the public health response would be compromised. Traditionally, the CRU has used gp60 subtyping by sequencing a hypervariable region of the gp60 gene to investigate outbreaks. More explanation of the gp60 nomenclature and outbreak investigations can be found in Chalmers et al., 2019 and Robinson et al., 2025.

In 2023, the CRU provided species-level typing for 15 of the 21 outbreaks reported to national surveillance systems in England and all four of the outbreaks reported in Wales. The outbreaks in England are listed here: [Cryptosporidium data 2014 to 2023 - GOV.UK](#). Exceedances were also investigated, particularly in September-October 2023.

*Cryptosporidium parvum* outbreaks were more commonly related to open, petting or commercial farm settings and some of these outbreaks were very large involving tens or hundreds of cases (Peake et al., 2024).

*Cryptosporidium hominis* outbreaks were more common in swimming pool or other treated recreational water settings.

Sixteen of the twenty-five outbreaks benefitted from gp60 subtyping. A national exceedance in August-October 2023, although not classified as an outbreak, illustrated the emergence of various *C. hominis* subtypes that used to be less common than the previously predominant IbA10G2. There were mainly IfA12G1R5, IdA13, IbA9G3, IbA13G3 and IeA11G3T3. One outbreak in a nursery was caused by IdA16.

For *C. parvum*, which was known to be more variable than *C. hominis*, a multilocus genotyping scheme (using variable number of tandem repeats analysis, or MLVA) was implemented for outbreaks in 2021 (Gopfert et al., 2022). In 2023, ten outbreaks also benefitted from MLVA. In one outbreak in Wales, the cases that drank milk or milkshakes from a farm gate producer-processor vending machine were linked by MLVA profile to the dairy herd that supplied milk.

We have also continued to pilot the routine testing of all *C. parvum* cases in Wales and the North West of England by MLVA initiated in a study supported by pump priming funding from the National Institute for Health and Care Research (NIHR) Health Protection Research Unit in Gastrointestinal Infections (Risby et al., 2023). This work highlighted to Field Epidemiology Services or Health Protection Teams clusters of cases where public health action may be needed.

In summary, MLVA provided evidence to strengthen the links between cases and exposures / settings and can identify outbreaks more rapidly than disease surveillance. This is only possible if laboratories send us specimens; thank you for doing this.

## Genotyping plans for 2024

In 2024 we aimed to develop and trial automation of MLVA clusters and communications for public health actions in Wales with a view to providing a future model for roll out across England.

## Appendix

Number of genotyped *Cryptosporidium* specimens by country of recent travel.

Afghanistan (6)	Jamaica (1)
Africa (3)	Jordan (1)
Algeria (3)	Kenya (4)
America (1)	Kuwait (1)
Antigua (1)	Madagascar (2)
Asia (4)	Madrid (1)
Australia (2)	Malawi (2)
Belgium (3)	Malta (6)
Bulgaria (1)	Mauritius (2)
Canary Islands (2)	Mediterranean (1)
Caribbean (1)	Menorca (9)
Caribbean Cruise (1)	Mexico (5)
Central America + Caribbean (1)	Mexico+Miami+Caribbean (1)
Central and Eastern Europe (1)	Middle East (2)
Central Eastern Europe (1)	Monaco (1)
Congo (1)	Nepal (2)
Corfu (1)	Netherlands and Hungary (1)
Costa Rica (3)	North Africa (1)
Crete (1)	North America (1)
Croatia (6)	Pakistan and Middle East (1)
Cyprus (3)	Philippines and India (1)
Dominican Republic (6)	Poland (3)
Dubai (1)	Rhodes (3)
East Africa (1)	Romania (1)
Eastern Europe (2)	Sicily (1)
Eritrea (3)	South and North America (1)
Ethiopia (2)	South Africa (3)
Europe + Singapore (1)	South Africa and Zimbabwe (2)
Fiji (1)	South Central Asia (1)
Finland (3)	South East Asia (1)
France and Spain (3)	Spain and Turkey (1)
France Brittany (1)	Spain and Western Europe (1)
Gambia (2)	Spain Benidorm (3)
Germany (4)	Sri Lanka (1)
Ghana (1)	Sub Saharan Africa (3)
Gran Canaria (6)	Tajikistan (1)
Guatemala (1)	Tanzania (1)
Holland (4)	Tenerife and Spain (1)
Hungary (1)	Thailand (2)
Ibiza (6)	United Arab Emirates (4)
Indian Subcontinent (2)	USA (2)
Indonesia (1)	Vietnam and Asia (1)
Ireland (1)	Zante (1)
Italy (7)	Zimbabwe (2)
Italy and Lebanon (1)	

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## Acknowledgements

We thank all the laboratories who sent, continue to send, and that have started to send, *Cryptosporidium* positive faeces for genotyping. Without your help, improved understanding of the occurrence, distribution, epidemiology and transmission of *Cryptosporidium* would not be possible. This also enables timely public health actions and targeted interventions. THANK YOU!

Thanks are extended to our colleague Oghogho Orife at the Public Health Wales Communicable Disease Surveillance Centre for data analysis and presentation.

The *Cryptosporidium* Reference Unit team in 2023:

Prof. Rachel Chalmers, Consultant Clinical Scientist and Head of Unit

Dr. Kristin Elwin, Principal Clinical Scientist

Dr. Guy Robinson, Principal Clinical Scientist

Dr. Harriet Risby, Research Scientist

Mr. David Cooper, Biomedical Scientist

Ms. Rahma Mohammed, Biomedical Support Worker