Cryptosporidium Reference Unit for England and Wales.

Annual report of referrals and Cryptosporidium genotyping, England and Wales, 2024.

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

Cryptosporidium Reference Unit

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Report prepared by the national Cryptosporidium Reference Unit and the Communicable Disease Surveillance Centre.

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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 2024, a total of 5249 specimens were referred to the national Cryptosporidium Reference Unit by clinical diagnostic laboratories in England and Wales.
- The region (by location of referring laboratory) that referred the highest number of specimens was North West England (n = 926), followed by West Midlands (n = 819).
- The region that referred the lowest number of specimens was London (n = 153).
- Of the 5249 specimens referred nationally, 394 (7.5%) were either not confirmed or not typable.
- Of the genotyped specimens, 4477 were referred from laboratories in England, representing 78% of the 5708 Cryptosporidium cases reported to national surveillance in England.
- Of the genotyped specimens, 612 were referred from laboratories in Wales, representing 99% of the 620 Cryptosporidium cases reported to national surveillance in Wales.
- Of the total 4855 genotyped specimens, 3348 (69%) were identified as *Cryptosporidium parvum* and 1399 (29%) were identified as *Cryptosporidium hominis*. 15 were both *C. parvum* and *C. hominis*, and 93 were other *Cryptosporidium* species.
- 583 (12%) of the genotyped specimens reported international travel and 271 (46%) 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 to laboratories, 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 for referrals can be found here: https://phw.nhs.wales/services-and-teams/cryptosporidium-reference-unit/specimen-submission-form/

In 2024, a total of 5249 specimens were referred and accepted at the national Cryptosporidium Reference Unit for confirmation, specialist testing or genotyping.

- Of the genotyped specimens, 4477 were referred from laboratories in England, representing 78% of the 5708 Cryptosporidium cases reported to national surveillance in England. This is an increase on 2023 when 72% of specimens from reported cases were referred.

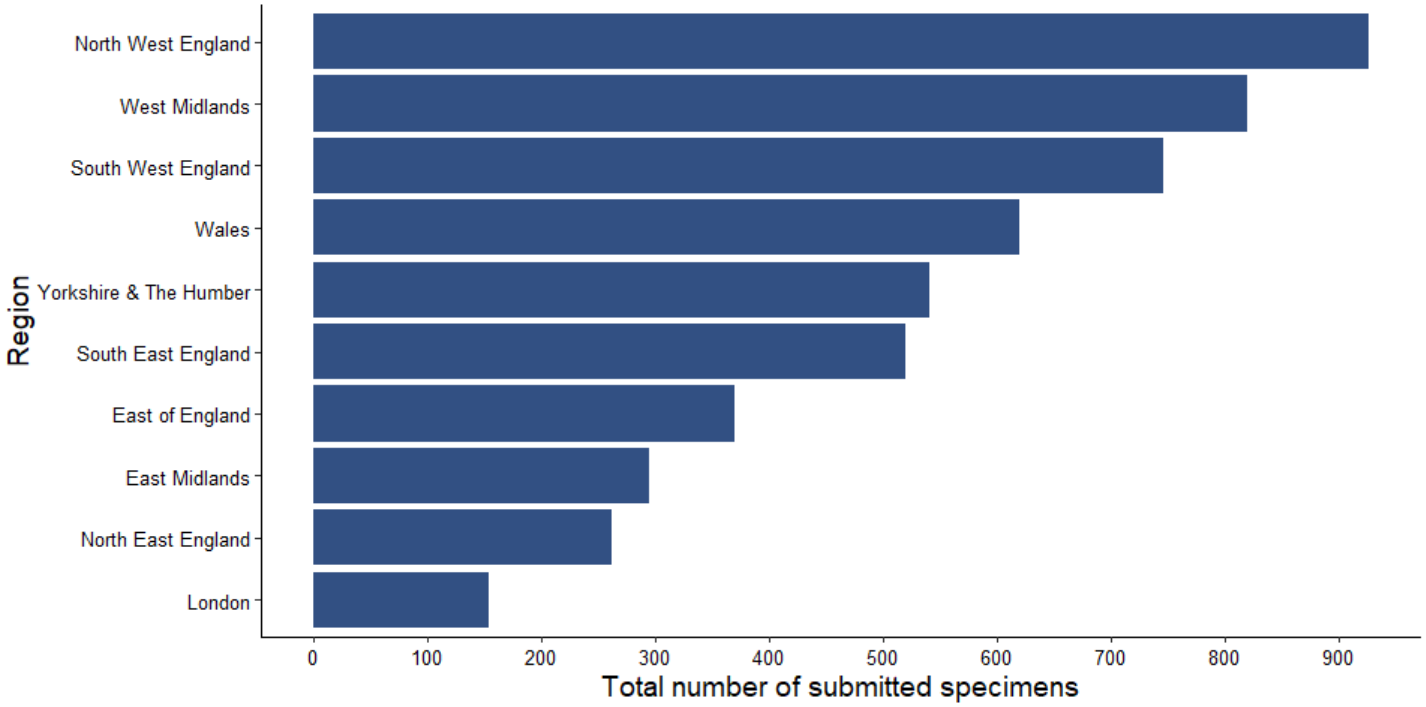
- Of the genotyped specimens, 612 were referred from laboratories in Wales, representing 99% of the 620 Cryptosporidium cases reported to national surveillance in Wales. This is an increase on 2023 when 93% of specimens from reported cases were referred.

- We thank the diagnostic laboratories for this improvement and encourage continued referral of specimens for genotyping.

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 centres on lab practice), the region that referred the highest number of specimens was the North West England (n = 926), followed by West Midlands (n = 819). The region that referred the lowest number of specimens was London (n = 153). 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, 2024



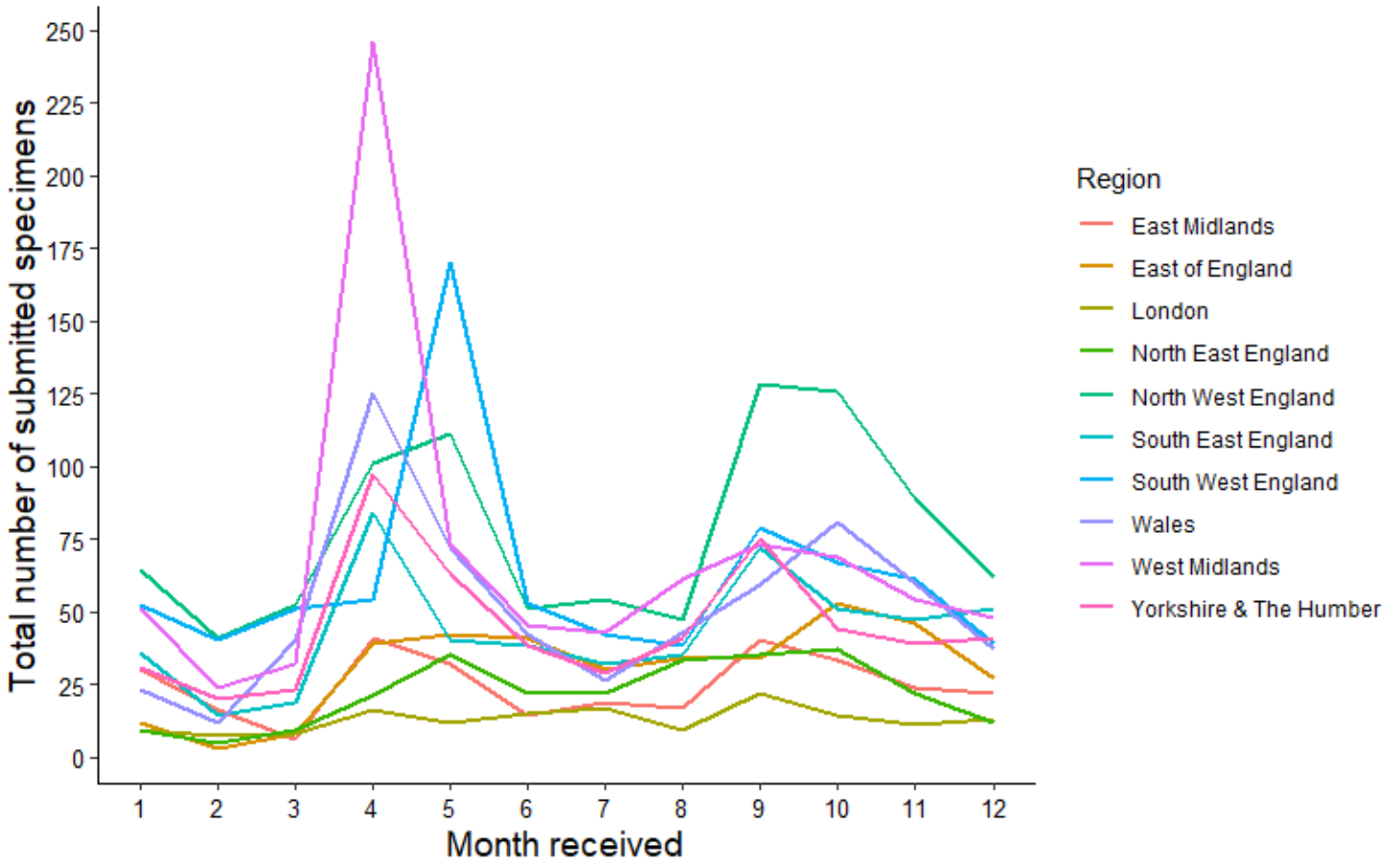
Summary of referrals by region and month, 2024

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 their highest peak in the number of specimens referred in April and a smaller peak in September. This is unusual as the autumn peak is usually higher than the spring peak. However, several large farm-related outbreaks occurred in spring 2024.

The highest monthly number of specimens referred was the West Midlands in April (n = 246), followed by the South West England region in May (n= 170) and North West England in September (n = 128).

Total number of specimens referred per month by region, 2024



Part 2: Cryptosporidium genotyping of referred specimens from England and Wales, 2024

Genotyping to identify *Cryptosporidium* species helps to understand the epidemiology and transmission, 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., 2026a.

Summary of *Cryptosporidium* species identified

Of the 5249 referred specimens in 2024, 394 (7.5%) were either not confirmed as *Cryptosporidium* or were not typable.

Of the 4855 genotyped specimens, 3348 (69%) were identified as *C. parvum* and 1399 (29%) were identified as *C. hominis*. Both *C. parvum* and *C. hominis* were detected in 15 specimens. Other *Cryptosporidium* species were detected in 93 (2%) specimens.

The proportion of *C. parvum* to *C. hominis* specimens was unusually high and most likely linked to outbreaks in the Spring and to an unseasonal contribution in the autumn.

Other *Cryptosporidium* species identified

Cryptosporidium species	Total	Main reservoir hosts
Cryptosporidium ubiquitum	33	Ruminants, rodents, carnivores, primates
Cryptosporidium cuniculus	26	Rabbits
Cryptosporidium meleagridis	21	Birds, mammals
Cryptosporidium felis	4	Cats
Cryptosporidium occultus	3	Rodents
Cryptosporidium canis	1	Dogs
Cryptosporidium erinacei	1	Hedgehogs
Cryptosporidium sciurinum	1	Squirrels

Cryptosporidium species	Total	Main reservoir hosts
Cryptosporidium Skunk genotype	1	Mustelids
Cryptosporidium tyzzeri	1	Rodents
Cryptosporidium viatorum	1	Humans, rodents

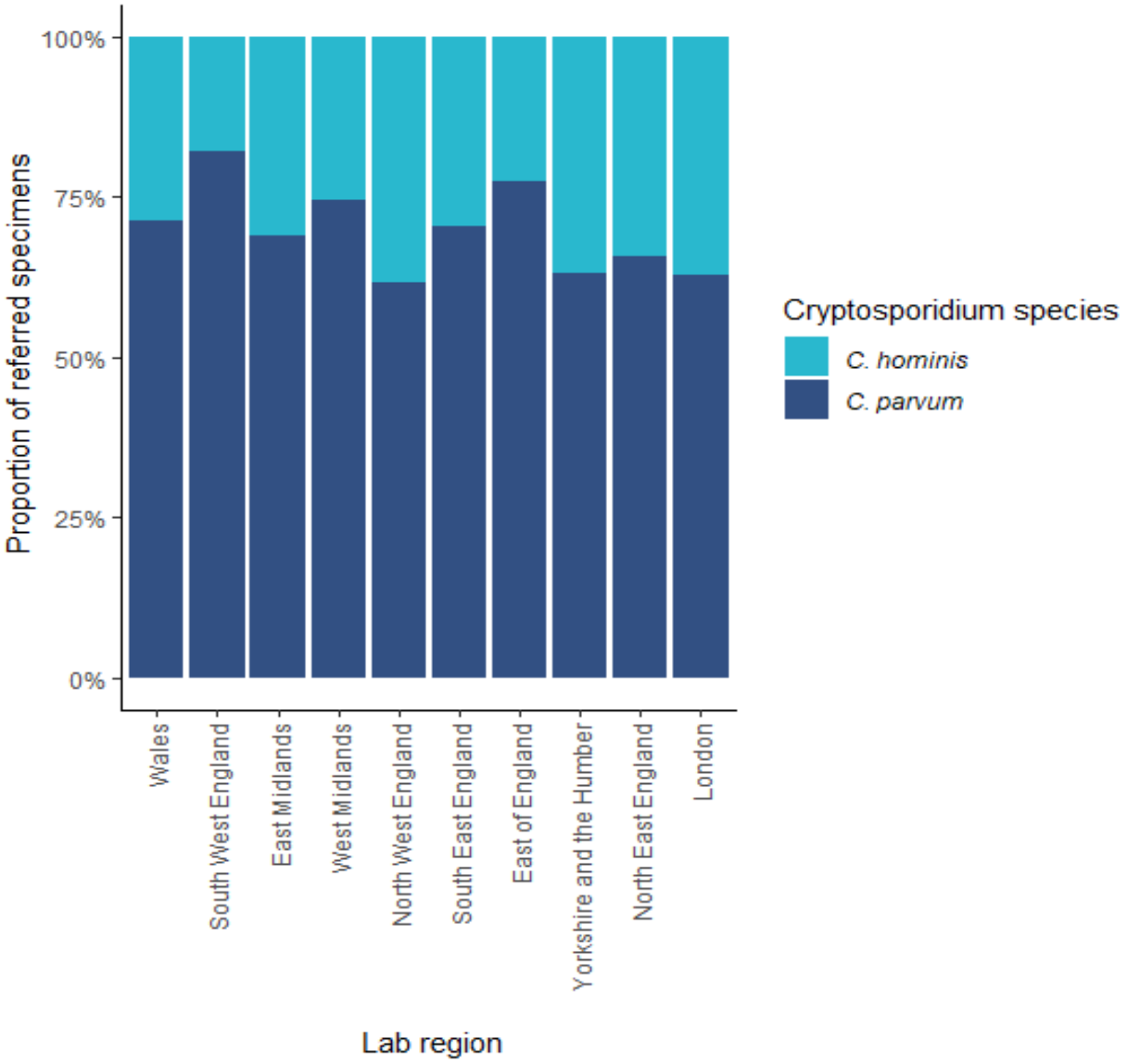
Spatial distribution by *Cryptosporidium* species and region 2024

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 England had the highest frequency of *C. parvum* specimens (82%) compared to *C. hominis* (18%), whereas North West England had the lowest frequency of *C. parvum* specimens (62%) compared to *C. hominis* (38%). Note that an important outbreak of *C. parvum* occurred in the South West in the Spring.

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



Age-sex distribution of confirmed cases

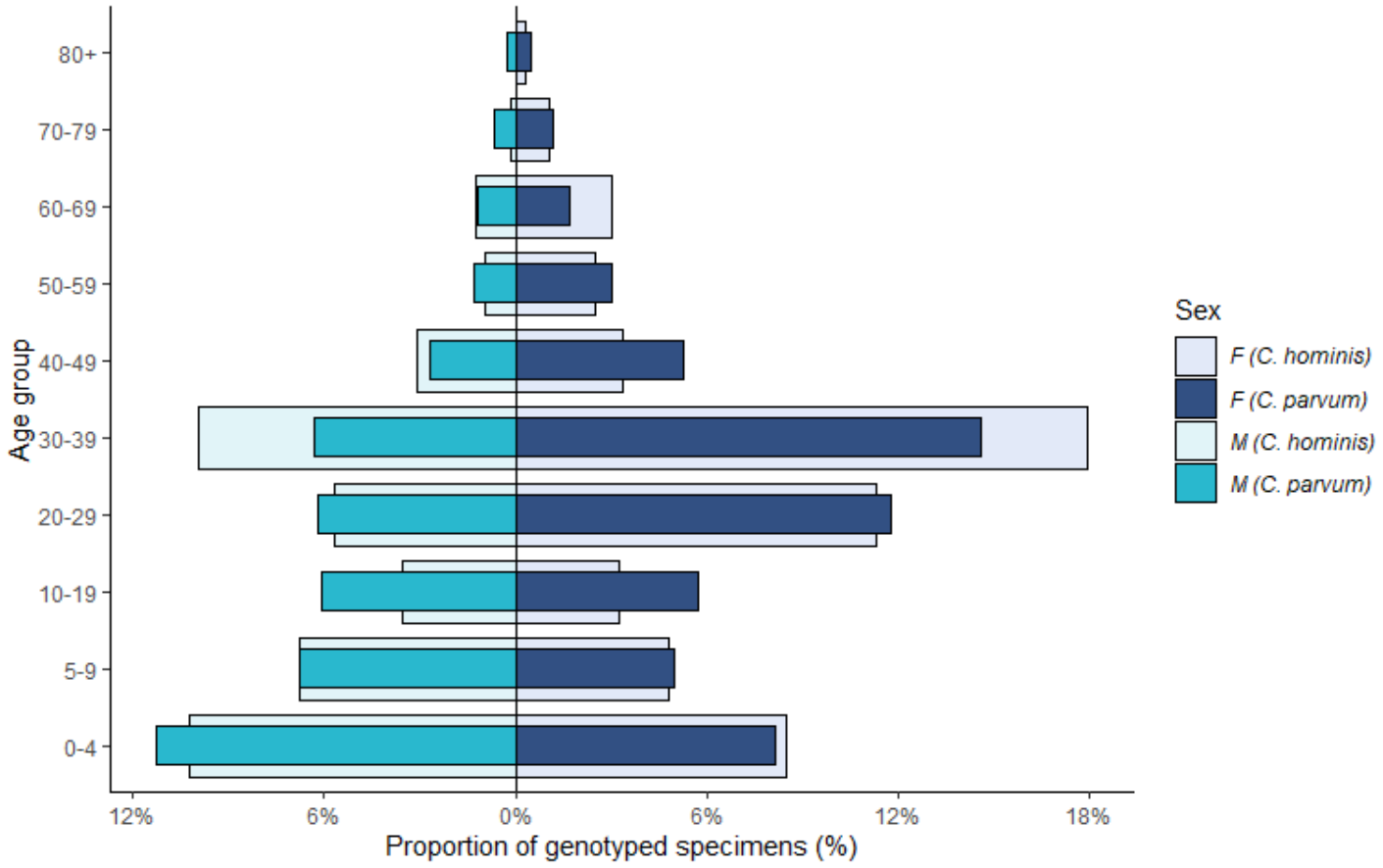
Age and sex information was available for 4672/4748 (98%) *C. parvum* and *C. hominis* specimens.

Most genotyped specimens were from the 30-39 years age group (n = 1083) and 0-4 years age group (n = 905).

There was no difference overall between the distribution of *C. parvum* and *C. hominis* by sex, as for *C. parvum* 1894/3316 (57%) specimens were from females and 1422 (43%) from males, and for *C. hominis* where 779/1356 (57%) were from females and 577 (43%) from males.

When age was also considered, the distribution differed; there were more *C. parvum* and *C. hominis* specimens in boys under 4 years of age, and in women aged 20-39 years than other ages. *C. parvum* predominated in young boys and was almost equal to *C. hominis* in girls. Interestingly, the predominance of *C. hominis* in women of childbearing age usually seen was not as evident in 2024, as *C. parvum* predominated in the 20-29 year age group and was present in a high proportion of the 30-39 age group.

Age and Sex of C. parvum and C. hominis specimens 2024

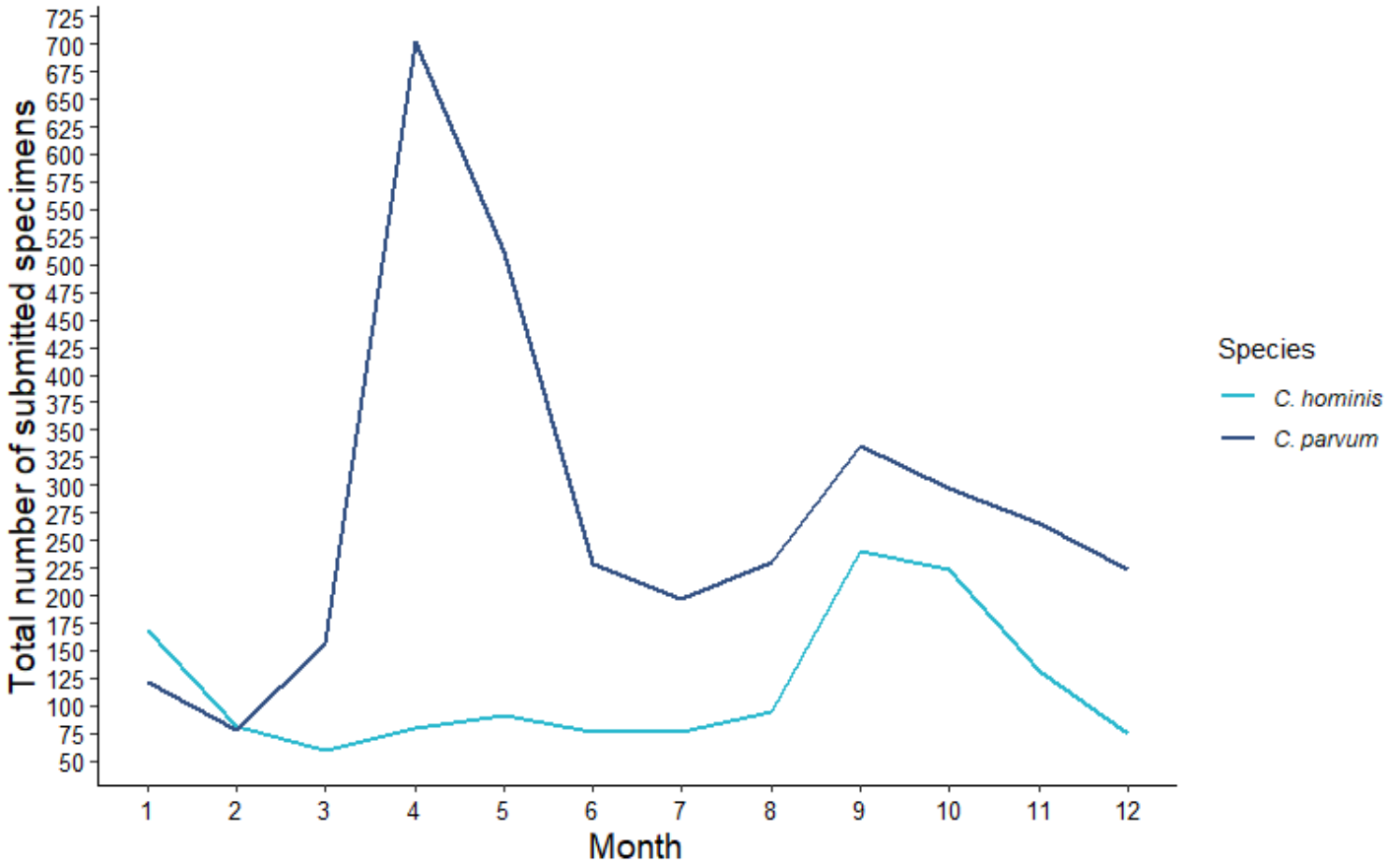


Temporal distribution of referred specimens, 2024

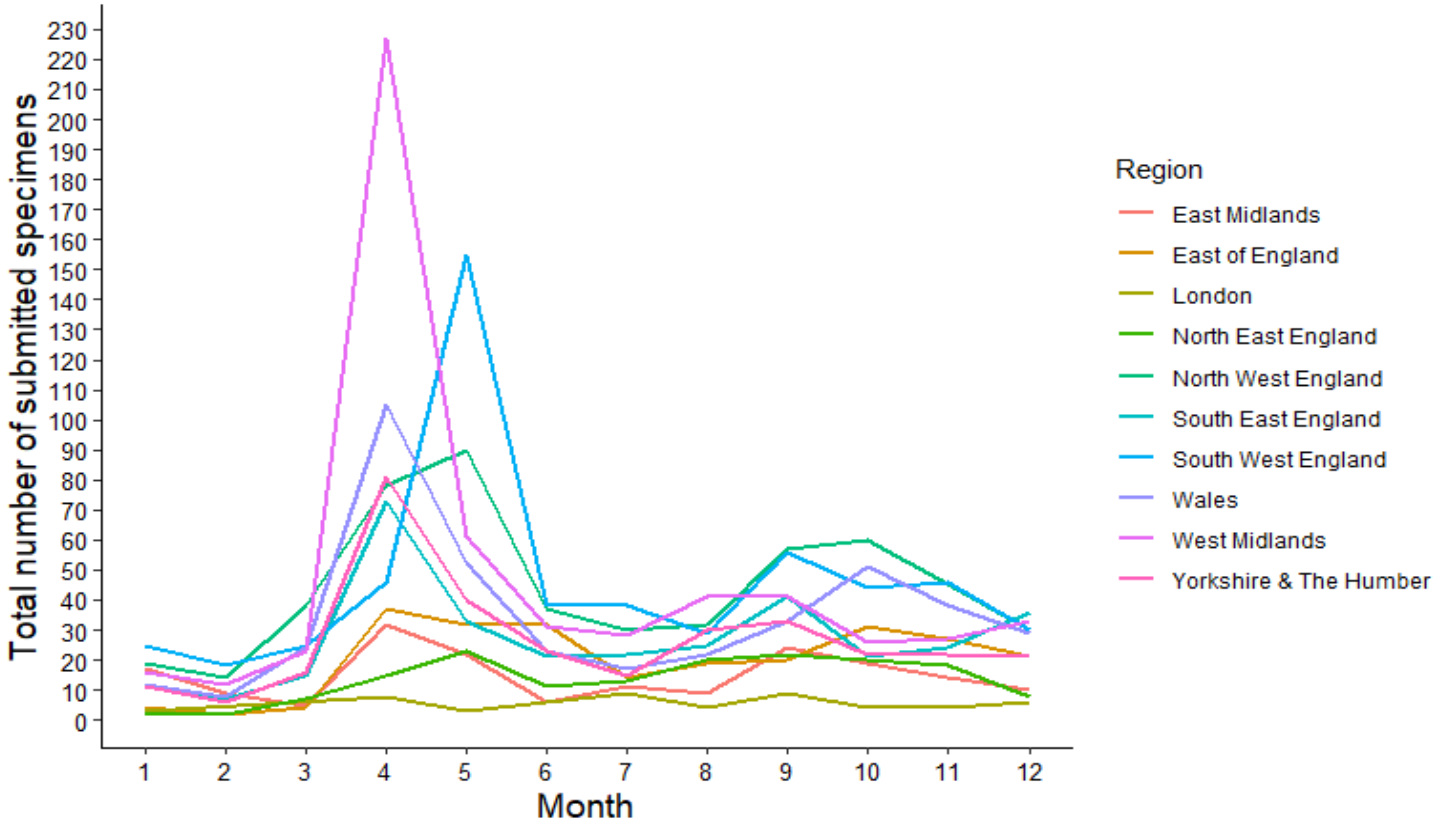
The temporal distribution of *Cryptosporidium* species is influenced by environmental factors and human behaviour such as seasonal visits to open farms and international travel to see friends and family or for holidays.

The number of *C. parvum* specimens peaked in April (n = 702). The number of *C. hominis* specimens stayed consistently low across the first eight months of the year, with a much smaller than expected peak in September (n = 241). Previously, the autumn peak was driven by *C. hominis* but in 2024 there were fewer *C. hominis* specimens than *C. parvum*. The change in predominance of *C. parvum* over *C. hominis* in the autumn is subject to ongoing investigation and the reasons are likely to be multi-factorial. There were also fewer *C. hominis* outbreaks and fewer linked to swimming pools (which usually occur in the late summer-autumn) than usual.

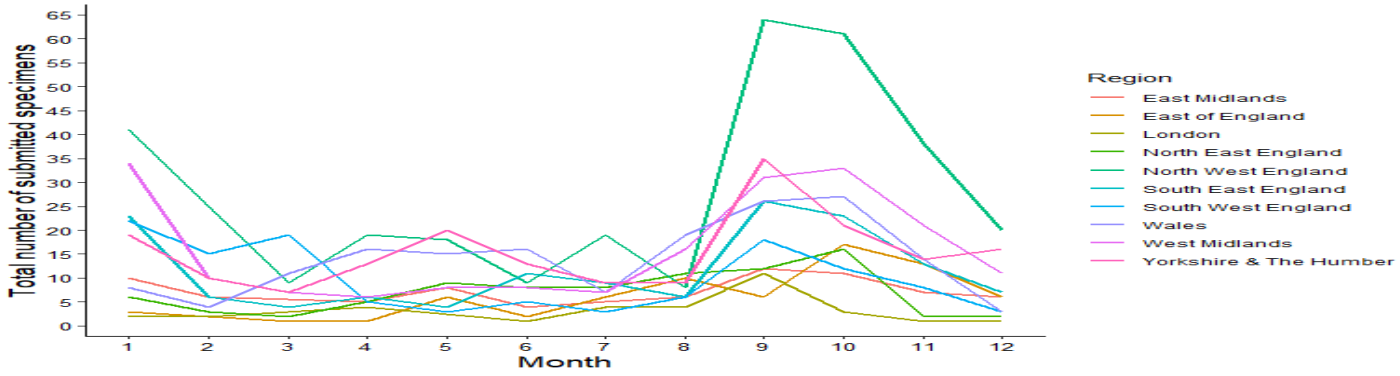
C. parvum and C. hominis specimens per month of receipt in England and Wales 2024



C. parvum specimens per month of receipt by region in England and Wales 2024



C. hominis specimens by month of receipt by region in England and Wales 2024

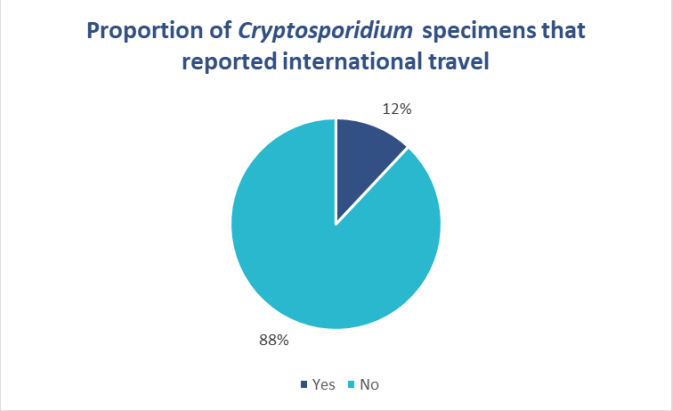


Travel history and *Cryptosporidium* species

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.

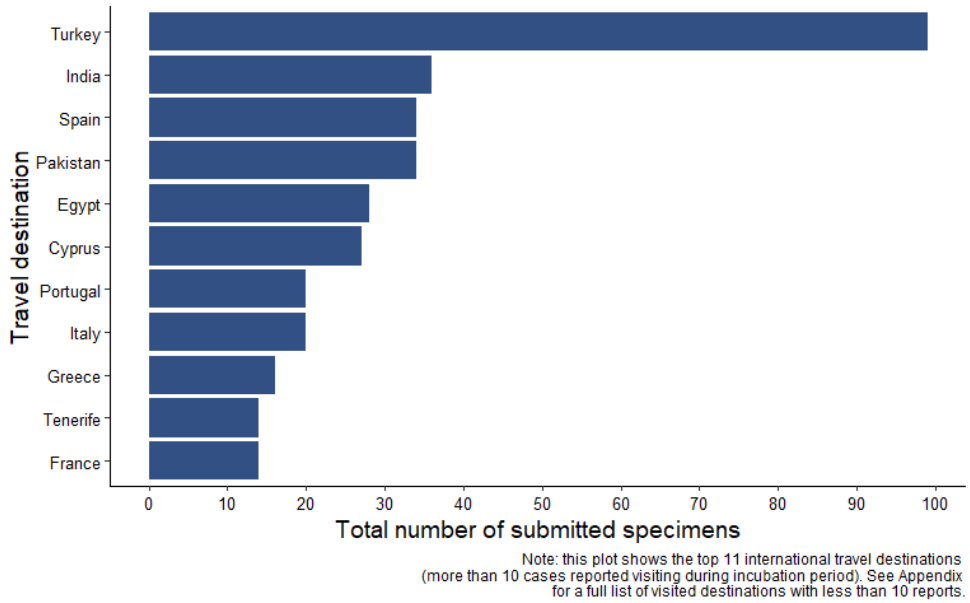
In 2024, 583 of 4855 (12%) of the genotyped *Cryptosporidium* specimens reported international travel within the incubation period of their infection.

Proportion of genotyped specimens, England and Wales, with international travel report, 2024



The top four travel destinations reported for genotyped specimens were Turkey (n = 99), India (n = 36), Spain (n = 34) and Pakistan (n = 34).

International travel destinations of Cryptosporidium cases genotyped from England and Wales, 2024 (see Appendix for destinations with <10 reports)



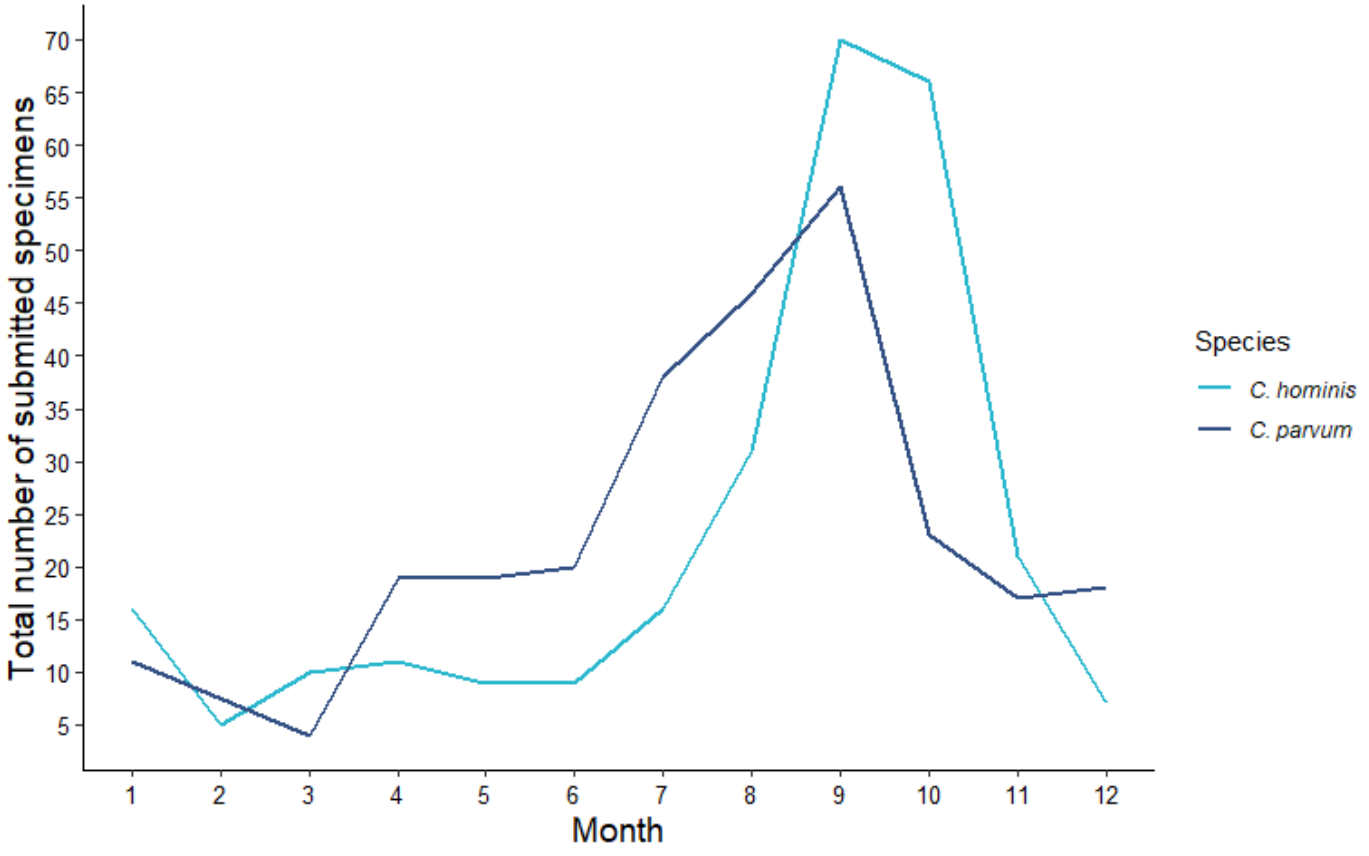
Of the 583 genotyped specimens that reported foreign travel, there were equal numbers of *C. hominis* (n=271, 49%) and *C. parvum* (n=271, 49%). This was unusual as *C. hominis* is normally more frequently associated with foreign travel. The top travel destinations of *C. hominis* cases were Turkey, Pakistan, Egypt and India while for *C. parvum* cases Turkey, Spain, Italy and Portugal.

Summary of international travel destinations and Cryptosporidium species

Cryptosporidium species	Total among travellers	Turkey	India	Spain	Pakistan	Egypt	Cyprus	Portugal	Italy	Greece	Tenerife	France
C. hominis	271	64	23	14	27	23	16	5	5	2	9	4
C. parvum	271	35	13	19	7	5	11	15	15	14	5	10

The majority of both *C. hominis* (n= 70) and *C. parvum* (n=56) specimens with international travel history were received in September.

C. parvum and C. hominis cases reporting international travel by month of receipt from England and Wales, 2024



Subtyping, clusters and outbreak investigations, England and Wales, 2024

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 method, *gp60* nomenclature and outbreak investigations can be found in Chalmers et al., 2019, Robinson et al., 2025 and Robinson et al., 2026b.

In 2024, the CRU provided species-level typing for 28 of the 32 outbreaks reported to national surveillance in England (Cryptosporidium data 2015 to 2024 - GOV.UK) and all of the five outbreaks reported in Wales.

Cryptosporidium parvum outbreaks were mostly related to open, petting or commercial farm settings and some of these outbreaks were very large (Cryptosporidium data 2015 to 2024 - GOV.UK; Jones et al., 2025). One outbreak in South West England was related to mains drinking water. *Cryptosporidium hominis* outbreaks were more common in swimming pools and daycare nurseries.

Twenty four outbreaks benefitted from *gp60* subtyping. For *C. parvum*, which has historically been 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 2024, twenty four outbreaks also benefitted from MLVA. This strengthened the links between cases and in some outbreaks with suspected sources.

To provide an additional way of identifying possible outbreaks, supplementing surveillance and epidemiological investigations, we have continued to pilot the routine subtyping of all *C. parvum* cases in Wales and the North West of England by MLVA (Risby et al., 2023). The results are used to highlight to Field Epidemiology Services or Health Protection Teams those clusters of cases where public health action may be needed. In 2024 automated cluster analysis was implemented by CDSC Wales identifying escalation where needed (Chalmers et al., 2025).

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 2025

In 2025 we aim to review and revise the automated cluster analysis in Wales and discuss inclusion of subtyping (gp60 and MLVA) in the UKHSA's Second Generation Surveillance System (SGSS) to help facilitate wider application outside of known outbreaks.

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Appendix

Afghanistan (3)	Malaysia (2)
Africa (7)	Malawi (1)
Albania (2)	Maldives (2)
Angola (1)	Malta (5)
Australia and New Zealand (5)	Majorca (8)
Austria (1)	Mecca (1)
Bali (2)	Mediterranean (2)
Belgium (1)	Menorca (3)
Bosnia and Herzegovina (1)	Mexico (9)
Brazil (2)	Middle East (2)
Bulgaria (1)	Morocco (7)
Canary Islands (3)	Netherlands (1)
Cape Verde (5)	New Zealand (1)
Caribbean (3)	Nicaragua (1)
Central America (4)	Nigeria (1)
Costa Rica (1)	Northern Africa (3)
Crete (1)	Northern America (5)
Croatia (1)	Norway (2)
Crete (1)	Poland (2)
Cuba (3)	Qatar (1)
Czech Republic (1)	Romania (1)
Denmark (1)	Russia (1)
Dubai (6)	Singapore (1)
Dubai, Vietnam, Hong Kong (1)	Somalia (2)
Eastern Asia (1)	South Africa (5)
Eastern Europe (2)	South America (7)
Eritrea (2)	South East Asia (1)
Europe (7)	Sri Lanka (2)
Gabon (1)	Sudan (1)
Germany (1)	Sweden (1)
Ghana (1)	Thailand (6)
Gran Canaria (6)	Tunisia (7)
Holland (1)	Uganda (1)
Ibiza (1)	United Arab Emirates (1)
Iran (1)	USA (10)
Kenya (3)	Uzbekistan (1)
Lanzarote (5)	Western Europe (9)

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 2024:

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. Emma Laddams, Biomedical Support Worker