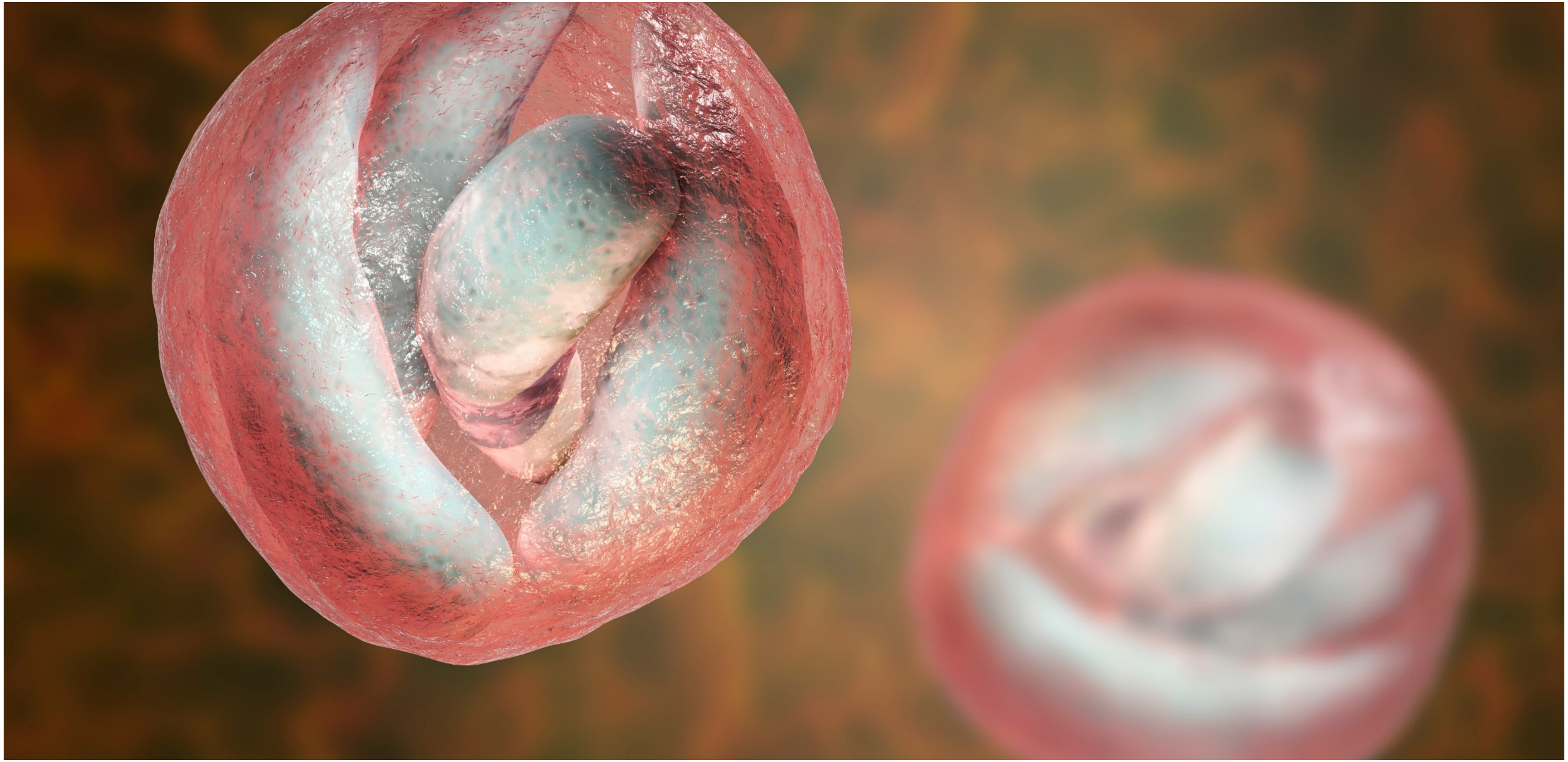
Cryptosporidium

- Working group
  - **Simone Cacciò, Rachel Chalmers**, Peter Deplazes, Brecht Devleesschauwer, Elisabeth Innes, Lucy Robertson, Thomas Romig, Joke van der Giessen

- BIOHAZ Panel
  - Kostas Koutsoumanis, Ana Allende, Avelino Alvarez-Ordóñez, Declan Bolton, Sara Bover-Cid, Marianne Chemaly, Robert Davies, Alessandra De Cesare, Lieve Herman, Friederike Hilbert, Roland Lindqvist, Maarten Nauta, Luisa Peixe, Lucy Robertson, Giuseppe Ru, Marion Simmons, Panagiotis Skandamis, Elisabetta Suffredini

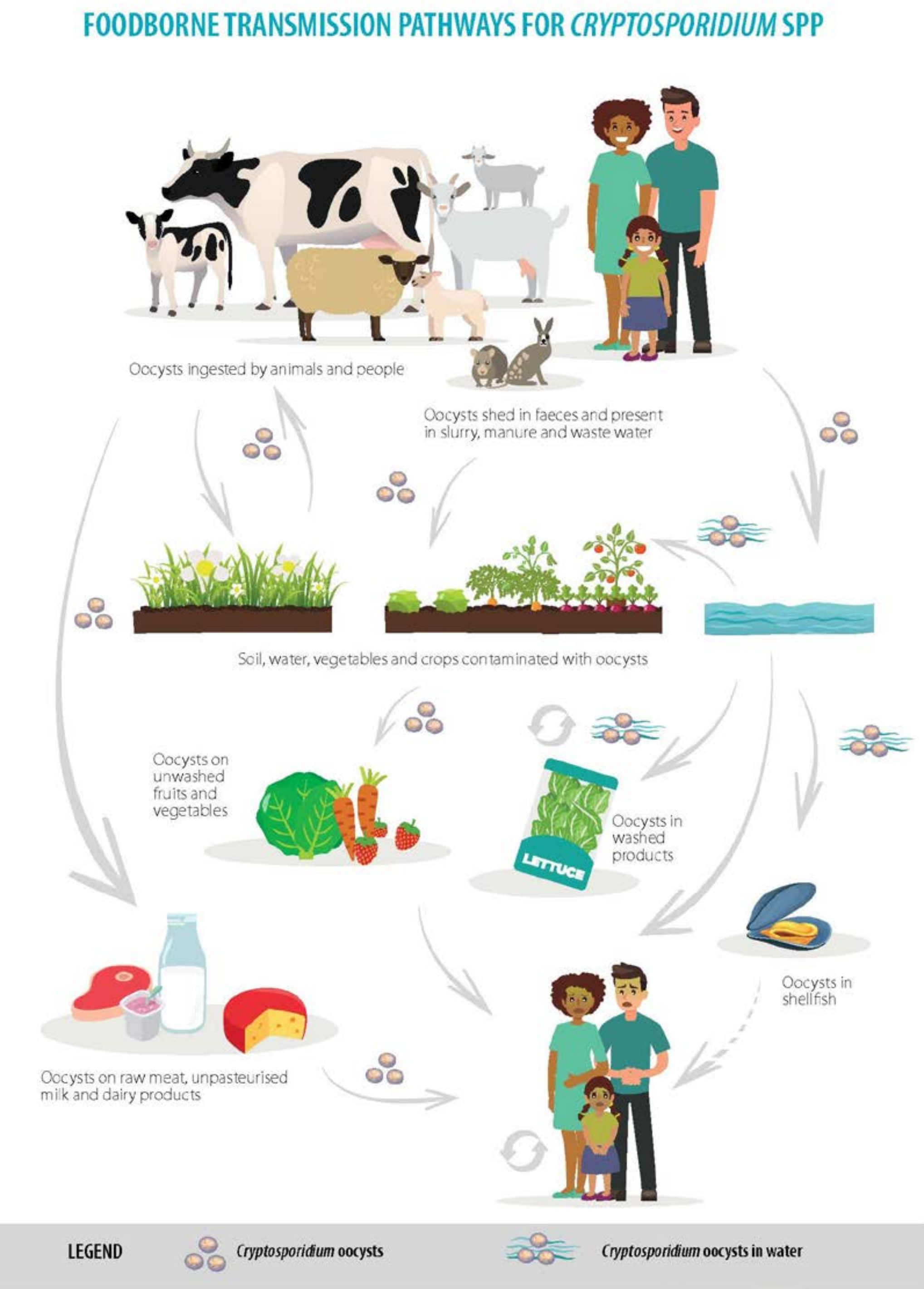
Cryptosporidium spp.



Cryptosporidium spp.

- *Cryptosporidium* spp. are protozoan parasites
- Although as many as 17 species have been associated with human infection, two are responsible for the vast majority of human cases of disease: *C. hominis* and *C. parvum*

Species	Major host(s)	Occurrence in humans (globally)
Cryptosporidium hominis	Humans	Most common species
Cryptosporidium parvum	Ruminants and humans	Most common species
Cryptosporidium meleagridis	Birds and humans	Commonly reported
Cryptosporidium ubiquitum	Ruminants, rodents, primates	Commonly reported
Cryptosporidium canis	Dogs	Less commonly reported
Cryptosporidium cuniculus	Rabbits	Less commonly reported
Cryptosporidium felis	Cats	Less commonly reported
Cryptosporidium muris	Rodents	Less commonly reported
Cryptosporidium viatorum	Humans, Australian swamp rat	Less commonly reported



- Foodborne outbreaks reported to EFSA
  - 2005 to 2016, a total of 53 cryptosporidiosis outbreaks were reported, of which 7 were attributed to food
  - Foodborne outbreaks were mainly linked to fresh produce (n=11), especially more recently, followed by unpasteurised milk and dairy products (n=7).

Cryptosporidium spp. detection in food

European Food Safety Authority

- Most sensitive methods require oocyst separation from the sample matrix and detection either by polymerase chain reaction or by immunofluorescence microscopy
- Quantification and genotyping difficult
- PCR-based methods that have been applied to food provide neither an idea of viability or infectivity
- There is only one standard method: ISO 18744 ‘Microbiology of the food chain — Detection and enumeration of *Cryptosporidium* and *Giardia* in fresh leafy green vegetables and berry fruits’, which makes comparisons of studies difficult

Cryptosporidium spp. occurrence in food

- In large surveys, oocysts have been detected in up to 8% of fresh produce samples
- No data on the occurrence in fruit juice or milk and dairy products in Europe
- The only structured, prospective survey of meat in Europe did not detect oocysts
- Data for molluscan shellfish is indicating that a high proportion of samples may be contaminated and that depuration processes may fail to remove the oocysts

Cryptosporidium spp. foodborne pathways

- Information on relative importance of food versus other transmission pathways for human cryptosporidiosis results mostly from expert knowledge elicitation

Country	Food	Water	Person-to-person	Animal contact	Reference
EUR A	10% (0–39)	38% (3–70)	30% (1–65)	14% (0–44)	Hald et al., 2016
EUR B	11% (0–39)	37% (2–68)	28% (1–64)	16% (0–46)	Hald et al., 2016
EUR C	9% (0–40)	36% (5–70)	29% (1–64)	15% (0–48)	Hald et al., 2016
Canada	11% (1–37)	37% (13–68)	24% (5–61)	23% (5–57)	Butler et al., 2015
Greece	6% (6–8)	N/A[(d)]	N/A	N/A	Gkogka et al., 2011
Netherlands	12% (0–20)	28% (10–39)	27% (10–38)	13% (5–19)	Havelaar et al., 2008

- Foodborne cryptosporidiosis is mainly associated with fresh produce

Cryptosporidium spp. control

- Control of oocysts as faecal contaminants of food and water will decrease the likelihood of transmission, e.g. by minimising access of animals, providing sanitation and hand hygiene for food workers, using potable water for irrigation and washing
- Specific treatments: heat treatment (pasteurisation, cooking) and freezing at -80ºC

Major gaps

- Development of validated detection methods, including **survival / infectivity assays and consensus molecular typing protocols**, for the development of quantitative risk assessments and efficient control measures.
- Application of validated methods to **different types of fresh produce** is of particular relevance
- Application of **whole genome sequencing** may provide a solution in some circumstances, but it is hard to apply to low numbers of parasites in a contamination situation
- As the **food-borne route may be overlooked**, inclusion of questions on food consumption within a relevant time span should be encouraged when investigating cases or outbreaks of infection

Future research projects

- **IMPACT**, EFSA grant 2019-2020

(Standardising molecular detection methods to Improve risk assessment capacity for foodborne protozoan Parasites, using *Cryptosporidium* in ready-to-eat salad as a model).

- Responsible Partner: BFR
- Contributing Partners: BIOR, ISS, NMBU, PHW, UL

Keywords:

Validation and standardization of molecular methods for detetcion in salad leaves

Optimisation of the SOP

Validation of the SOP (Ring rial)

- **PARADISE**

(PARAsite Detection, ISolation and Evaluation; submitted to the One Health EJP)

- Responsible Partner: ISS
- Contributing Partners: ANSES, BFR, INIAV, NVI, OKI, PHA, PIWET, RIVM, RKI, SLV, SSI, SVA, University of Surrey, VRI
- External Partners: BIOR, CRU, HZAU, JLU, NMBU, UoM

Keywords:

Genomics and metagenomics

Multi-locus typing schemes

Novel enrichments strategies