

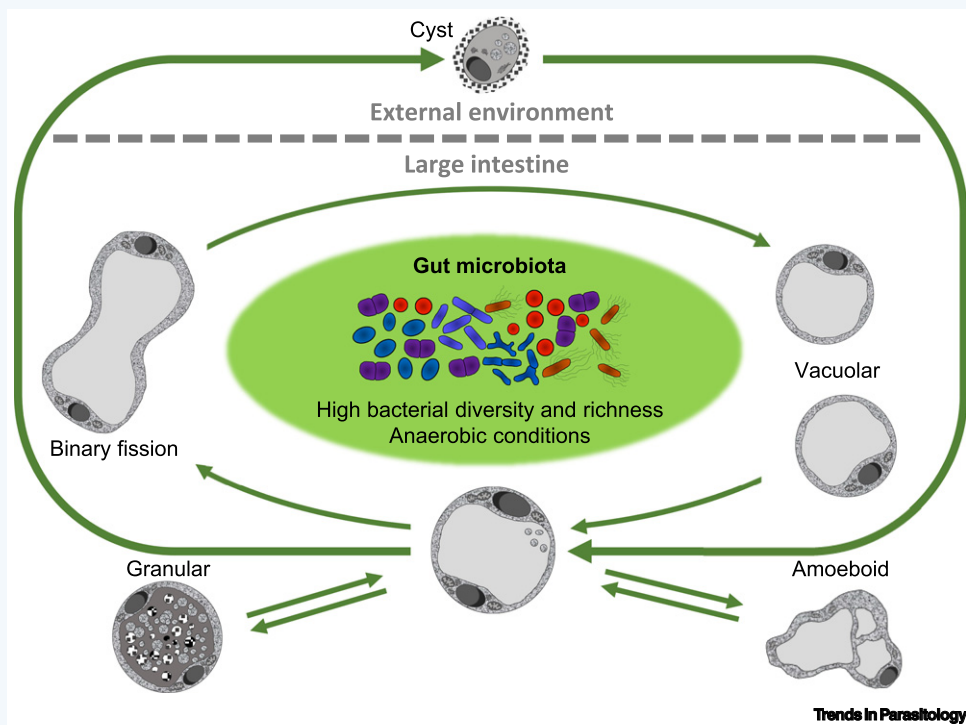
# Blastocystis

Christen Rune Stensvold,<sup>1,\*</sup> Kevin S.W. Tan,<sup>2</sup> and C. Graham Clark<sup>3</sup>

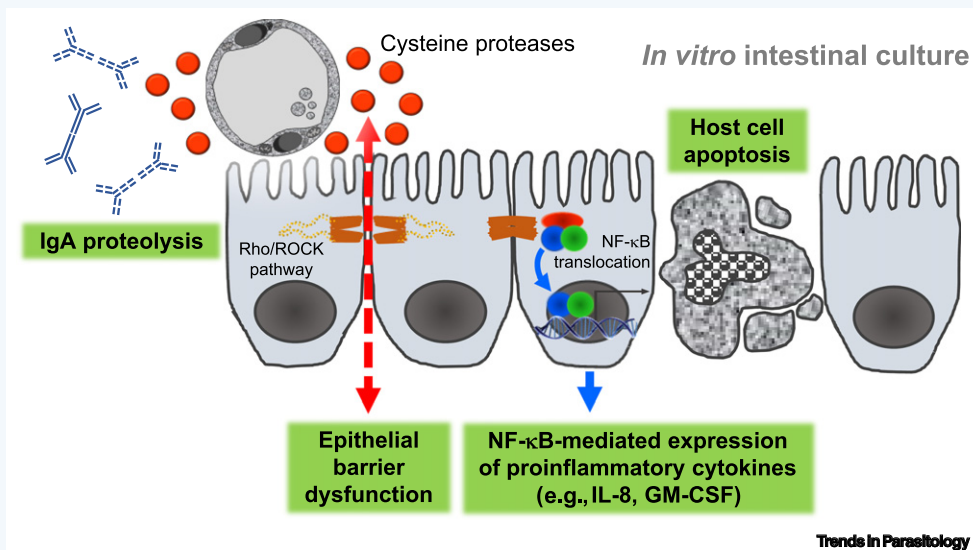
<sup>1</sup>Statens Serum Institut, Copenhagen, Denmark

<sup>2</sup>National University of Singapore, Singapore

<sup>3</sup>London School of Hygiene and Tropical Medicine, London, UK



*Blastocystis* colonizes the large intestine and divides by binary fission. *In vitro*, *Blastocystis* can adhere to intestinal mucin and secrete cysteine proteases that contribute to pathogenesis through degradation of secretory IgA, Rho/ROCK-mediated tight-junction compromise, NF- $\kappa$ B-mediated secretion of inflammatory cytokines, and host cell apoptosis. It is currently unknown whether this occurs *in vivo*. Most gut microbiota studies that include *Blastocystis* report that *Blastocystis* is a common constituent of the healthy gut microbiota and is associated with higher bacterial richness, and that long-term asymptomatic carriage is common. In contrast, a couple of recent studies have suggested that *Blastocystis* decreases beneficial gut bacteria, leading to a dysbiotic state. Such discrepant observations have led to confusion on the clinical relevance of the parasite. *Blastocystis* is relatively rare in patients with inflammatory bowel disease, and its role in irritable bowel syndrome is still controversial.



## KEY FACTS:

*Blastocystis* from mammals and birds can be classified into at least 17 subtypes (STs) currently, based on small subunit (SSU) rRNA genes. STs are as divergent as species or even genera.

Humans can host ST1–9 and 12; more than 90% of human *Blastocystis* strains belong to ST1–4.

Reservoir hosts have been identified for all subtypes except ST9; cryptic host specificity exists for at least some of them.

Two genomes: a nuclear genome of 12.9–18.8 Mb (depending on ST) encoding 5713–6544 proteins, and a mitochondrial genome of 27.7–29.3 kb.

*Blastocystis* can be cultured easily in Jones' and other media with fecal bacteria. A genetic manipulation method for ST7 has been described recently.

Subtype nomenclature was introduced when it became clear that the names of previous species were invalid or represented multiple very distinct entities.

## DISEASE FACTS:

Despite more than 1 billion carriers worldwide, the public health significance remains unknown.

*Blastocystis* has been found more commonly in the gastrointestinal tract of healthy individuals.

Gut bacterial diversity and richness are mostly higher in *Blastocystis*-positive individuals. ST7 has been shown to decrease the levels of beneficial gut bacteria such as *Bifidobacterium* and *Lactobacillus*.

The zoonotic contribution to human *Blastocystis* colonization is probably low.

## TAXONOMY AND CLASSIFICATION:

**KINGDOM:** Sar  
**PHYLUM:** Stramenopiles  
**CLASS:** Bigyra  
**ORDER:** Opalinata  
**FAMILY:** Blastocystidae  
**GENUS:** *Blastocystis*  
**SPECIES:** Currently not applicable

\*Correspondence: [run@ssi.dk](mailto:run@ssi.dk) (C.R. Stensvold).



## Resources

[www.pubmlst.org/blastocystis](http://www.pubmlst.org/blastocystis)

## Literature

1. Stensvold, C.R. *et al.* (2007) Terminology for *Blastocystis* subtypes – a consensus. *Trends Parasitol.* 23, 93–96
2. Adl, S.M. *et al.* (2019) Revisions to the classification, nomenclature, and diversity of eukaryotes. *J. Eukaryot. Microbiol.* 66, 4–119
3. Clark, C.G. *et al.* (2013) Recent developments in *Blastocystis* research. *Adv. Parasitol.* 82, 1–32
4. Tito, R.Y. *et al.* (2019) Population-level analysis of *Blastocystis* subtypes prevalence and variation in the human gut microbiota. *Gut* 68, 1180–1189
5. Denoeud, F. *et al.* (2011) Genome sequence of the stramenopile *Blastocystis*, a human anaerobic parasite. *Genome Biol.* 12, R29
6. Gentekaki, E. *et al.* (2017) Extreme genome diversity in the hyper-prevalent parasitic eukaryote *Blastocystis*. *PLoS Biol.* 15, e2003769
7. Silberman, J.D. *et al.* (1996) Human parasite finds taxonomic home. *Nature* 380, 398
8. Li, F.J. *et al.* (2019) Successful genetic transfection of the colonic protistan parasite *Blastocystis* for reliable expression of ectopic genes. *Sci. Rep.* 9, 3159
9. Yason, J.A. *et al.* (2019) Interactions between a pathogenic *Blastocystis* subtype and gut microbiota: *in vitro* and *in vivo* studies. *Microbiome* 7, 30
10. Beghini, F. *et al.* (2017) Large-scale comparative metagenomics of *Blastocystis*, a common member of the human gut microbiome. *ISME J.* 11, 2848–2863