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Review

Blastocystis in domestic mammals and poultry:
from prevalence patterns to gut physiologyZuzana Pavlíčková ^{1,*}, Kateřina Jirků ¹, Eliška Zimmelová¹, Laura Hernández Hurtado ^{2,3},
Eleni Gentekaki ⁴, and Anastasios D. Tsousis ⁵

Blastocystis is a common intestinal protist in humans and animals, yet its ecological role and clinical significance remain debated. Companion animals and livestock are of particular interest due to their close contact with humans and potential reservoir roles. This review synthesizes current knowledge on *Blastocystis* occurrence and diversity in these animal groups, reframing the discussion through the lens of host digestive physiology and microbiome ecology. Rather than a taxonomic inventory, we group animals as carnivores, omnivores, or herbivores to highlight how gastrointestinal physiology and diet might shape colonization. Carnivores show low prevalence, herbivores exhibit high subtype richness, and omnivores display intermediate patterns. Growing evidence links *Blastocystis* to gut eubiosis, highlighting the need for broader, integrative research across hosts and environments.

Why is a veterinary perspective important for *Blastocystis*?

Blastocystis is one of the most frequently detected intestinal protists in humans and animals, yet its role within the gut ecosystem remains poorly understood [1]. Once regarded primarily as a pathogen, growing evidence suggests that *Blastocystis* is often a **commensal** (see [Glossary](#)) or even a beneficial member of the intestinal community. In humans, its prevalence is strongly associated with plant-based diets and high gut microbial diversity [2], prompting a re-evaluation of its ecological role, including whether it contributes to maintaining gut homeostasis, interacts with the resident microbiota, or simply occupies a stable niche without causing disease.

Understanding *Blastocystis* colonization from a veterinary perspective is essential for several reasons. First, domestic animals, whether companion species such as dogs and cats or livestock including pigs, cattle, sheep, and poultry, are in close contact with humans and may act as reservoirs for zoonotic subtypes [3,4]. Second, the colonization of these animals provides valuable comparative models for investigating how host digestive physiology and diet shape bacterial and protist communities [5]. Finally, animals themselves may benefit or suffer from the presence of *Blastocystis*, although its clinical significance in veterinary medicine remains uncertain ([Box 1](#)).

Rather than cataloging *Blastocystis* prevalence by host species, this review adopts a functional ecological framework. We classify animals by digestive strategies – carnivores, omnivores, and herbivores – and explore how differences in gastrointestinal physiology and microbial ecology influence the occurrence, diversity, and stability of *Blastocystis* colonization. By integrating veterinary parasitology and microbiome research, we aim to offer a **One Health** perspective on the ecological role and zoonotic potential of *Blastocystis* in companion and farm animals. To maintain consistency and comparability across prevalence studies, we included only those that used molecular diagnostic methods for detecting *Blastocystis* (see Table S1 in the supplemental information online).

Highlights

Diet and digestive physiology strongly shapes *Blastocystis* colonization across animals: herbivores show the highest prevalence and subtype diversity, while carnivores remain transient or incidental hosts.

The acidic and fast-transit gastrointestinal tracts of carnivores limit *Blastocystis* persistence, underscoring how digestive physiology constrains protist–host compatibility.

The high prevalence and subtype diversity observed in healthy animals may indicate a commensal role linked to gut eubiosis and microbial diversity, although potential subtype-specific effects cannot be excluded.

Understanding how host digestive strategies modulate *Blastocystis* colonization provides a framework for interpreting its ecological roles in human and animal microbiomes.

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Box 1. Veterinary implications of *Blastocystis* research

The study of *Blastocystis* in animals extends beyond prevalence data, with direct implications for veterinary medicine and One Health. It underscores the protist's practical significance, not just its ecological role.

- Zoonotic potential: companion and livestock species may harbor subtypes shared with humans (ST1–ST4), emphasizing the need to assess interspecies transmission risks in close-contact and agricultural settings.
- One Health relevance: veterinary surveillance can elucidate how *Blastocystis* circulates among animals, humans, and the environment, particularly in farming systems where cross-contamination is likely.
- Animal health: colonization is largely asymptomatic, but findings in calves suggest possible links to microbial diversity, raising questions about its clinical significance.
- Comparative models: species such as pigs and rodents provide tractable experimental systems for studying host–microbiota–protist interactions, offering translational value for human research.

Digestive system diversity across animal hosts: implications for *Blastocystis* colonization

The digestive system is a flexible structure shaped by evolutionary pressures and the demands of various diets. Differences in gut length, compartmentalization, and reliance on enzymatic versus fermentative digestion reflect how animal species process nutrients and directly influence the composition, density, and stability of their gut microbiome.

Herbivores typically have longer intestines with specialized compartments for microbial fermentation, supporting diverse and metabolically active communities. Carnivores, by contrast, possess shorter and simpler tracts adapted for rapid enzymatic digestion and host lower microbial diversity; in domestic cats and dogs, however, the inclusion of plant-based ingredients in commercial diets introduces microbial features that differ from those of strict carnivores [6]. Omnivores display an intermediate strategy, combining features of both herbivorous and carnivorous digestion.

These distinct digestive anatomies and their associated microbial environments shape the gut's ecological landscape and can influence the colonization success of intestinal protists (Box 2). *Blastocystis*, an anaerobic protist, appears to thrive under conditions associated with fiber-rich diets and stable, microbially dense gut environments. In humans, it is more commonly detected in individuals consuming plant-based, high-fiber diets – such as vegetarians and vegans – than in those with diets rich in animal-based products [2]. A similar trend is observed in animals (Figure 1): *Blastocystis* is frequently found in herbivorous species like cattle and sheep but occurs much less often in carnivores [7].

Box 2. Fermentation 101 and the *Blastocystis* niche

Who does the work?

Dense anaerobic consortia drive both foregut and hindgut fermentation. Key functional groups include fiber degraders (e.g., *Ruminococcus*, *Fibrobacter*, *Prevotella*), starch and oligosaccharide fermenters (e.g., *Bacteroides*, *Lactobacillus*), and cross-feeders that consume lactate and hydrogen. These microbial communities produce SCFAs (acetate, propionate, butyrate) and maintain low redox potential in compartments with buffered pH.

Why does this matter for *Blastocystis*?

Blastocystis thrives in stable, anoxic, and microbially dense environments with sufficient digesta retention time – conditions typical of the rumen, herbivore hindgut, and, to a lesser extent, the large intestine of omnivores. By contrast, the short, acidic, and fast-transit gastrointestinal tracts of carnivores offer fewer opportunities for persistent colonization.

Function over taxonomy

Differences in diet, pH, transit time, and buffering capacity can alter which bacterial guilds dominate. Functional redundancy means that different microbial taxa can create similar niches, helping explain colonization in some omnivores and its rarity in carnivores (cross-referenced in text).

Glossary

Commensal: a microorganism that lives in or on a host without causing harm and may provide context-dependent benefits.

Foregut fermenters: herbivorous animals (e.g., cattle, sheep) that rely on microbial fermentation in a multi-chambered stomach before the small intestine.

Gut microbiota: the community of microorganisms residing in the gastrointestinal tract that influences host digestion, immunity, and colonization by eukaryotes such as *Blastocystis*.

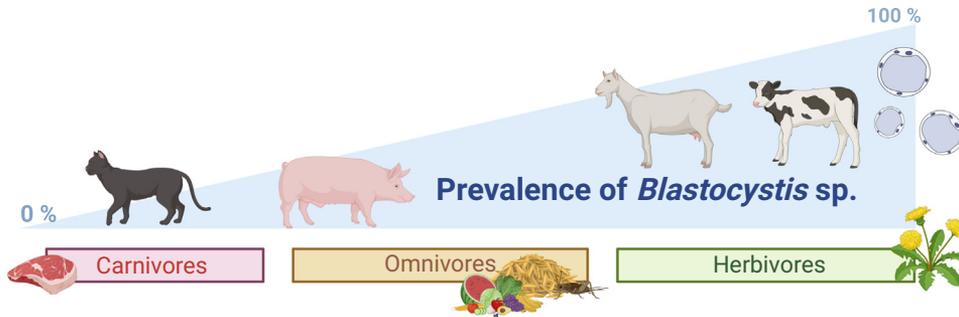
Healthy animals: (in context of *Blastocystis*); clinically normal at sampling ('healthy'). Animals reported by the original study as free of gastrointestinal signs at the time of sampling (e.g., no diarrhea, in normal condition). This label does not exclude subclinical disease, concurrent infections, or future illness. We therefore use 'clinically normal at sampling' or 'apparently healthy', not 'disease-free'.

Hindgut fermenters: herbivorous animals (e.g., horses, rabbits) that conduct fermentation in the cecum and colon after enzymatic digestion in the small intestine.

One Health: an integrative approach that recognizes the interconnected health of humans, animals, and the environment and promotes cross-disciplinary collaboration to address complex health challenges at the human–animal–ecosystem interface.

Short-chain fatty acids (SCFAs): metabolites such as acetate, propionate, and butyrate, produced during microbial fermentation of dietary fiber, that serve as energy sources and signaling molecules for the host.

Zoonosis/zoonotic transmission: the transmission of infectious agents, including certain *Blastocystis* subtypes, between animals and humans.



Trends in Parasitology

Figure 1. Diet-linked trends in *Blastocystis* spp. colonization among domestic animals. Schematic representation illustrating the broad trend of lower *Blastocystis* prevalence in carnivores, intermediate levels in omnivores, and higher prevalence in herbivores, reflecting differences in gut physiology and diet. Figure created in BioRender.

Carnivores

Digestive tract and microbiome

Carnivores, specifically cats and dogs (obligate carnivory in cats, facultative in dogs), share a short and anatomically compact gastrointestinal tract adapted to digesting animal-based diets [8]. In both species, the stomach produces a highly acidic environment (pH <2) and secretes proteolytic enzymes, supporting efficient protein breakdown and serves as a strong barrier against microbial colonization. Fermentative activity in the large intestine is limited, especially in cats, which possess a rudimentary cecum and a short colon. Dogs exhibit a slightly greater capacity for processing plant-derived substrates, reflecting their partial shift from strict carnivory.

In terms of microbial composition, the **gut microbiota** in both species is dominated by proteolytic genera such as *Fusobacterium*, *Bacteroides*, and *Clostridium* [9]. Cats tend to harbor a more stable yet overall less diverse microbial community than dogs, whose microbiota respond more readily to dietary changes. Nonetheless, both species maintain relatively low fermentative capacity and rapid gastrointestinal transit time, combined with low buffering capacity and sustained gastric acidity, making the intestinal environment less favorable for colonization by eukaryotic microorganisms. These physiological and microbial traits may contribute to the lower prevalence of intestinal protists, including *Blastocystis* spp., in carnivores compared with herbivores and omnivores.

Blastocystis occurrence

Investigation of *Blastocystis* in carnivores – primarily dogs and cats – has been motivated by their close contact with humans, raising questions about interspecies transmission and the possible role of these animals as reservoirs [10]. A limited number of studies from the past decade showed highly variable prevalence of *Blastocystis* in dogs, ranging from 0% to 60% [11–13]. However, most surveys report rates between 1% and 8%, with an overall mean ~13% across available data (e.g., [12–20]). In cats, prevalence estimates span 0% to 18% [12,17,21], but the majority of studies detect *Blastocystis* in less than 10% of samples (e.g., [11,14,18,22,23]), yielding an average prevalence ~5% – lower than that observed in dogs.

A relatively high subtype diversity of *Blastocystis* has been documented in dogs, with at least 11 subtypes identified to date (ST1–ST8, ST10, ST23, and ST24) [14]. ST1–ST4 occur in both humans and pets, but host associations differ (ST1–3 prevalent in humans; ST4 linked to rodents). Shared environments and contaminated water or feed may act as transmission pathways, and although direct **zoonotic transmission** between pets and owners is possible, it cannot be

assumed without longitudinal evidence [18,24]. In cats, a narrower diversity of subtypes has been reported, with six dominant subtypes reported (ST1, ST3, ST4, ST5, ST10, and ST14), among which ST1 is most frequent, followed by ST3, ST10, and ST14 [14].

Although *Blastocystis* has been detected in both dogs and cats, current evidence does not support a conclusive link between its presence and any clinical or gastrointestinal manifestations in these hosts [10]. Furthermore, critical evaluation of the literature suggests that dogs and cats are unlikely natural hosts of *Blastocystis* but rather short-term carriers that may act as incidental sources of zoonotic transmission [14].

Omnivores

Digestive tract and microbiome

Omnivores, such as pigs, exhibit a more flexible digestive strategy than carnivores. Their monogastric gastrointestinal tract is relatively long and includes a well-developed cecum and colon, which support substantial microbial fermentation [25]. Unlike obligate carnivores, pigs are physiologically adapted to digest both animal- and plant-derived substrates, relying not only on enzymatic breakdown but also on microbial activity in the large intestine. This anatomical configuration enables a longer retention time and the processing of complex carbohydrates and fibers.

Metagenomic and functional studies confirm that the pig gut harbors a diverse and dynamic microbial community, dominated by *Firmicutes*, *Bacteroidetes*, and *Proteobacteria*, with key genera such as *Prevotella*, *Lactobacillus*, *Clostridium*, and *Ruminococcus* [26]. This composition reflects the gut's capacity to ferment a wide array of polysaccharides and proteins. The large intestine serves as the primary fermentation site, producing **short-chain fatty acids (SCFAs)** such as acetate, propionate, and butyrate, which support epithelial integrity, immune modulation, and colonization resistance. Factors such as age, diet, and weaning stress further shape this microbiota, rendering it highly plastic and responsive to nutritional inputs.

This enhanced microbial richness and fermentative capacity likely expand the ecological niches available to anaerobic protists such as *Blastocystis*, which thrive in stable, anoxic environments. Compared with carnivores, omnivorous hosts like pigs provide more favorable niches for eukaryotic colonizers due to their slower intestinal transit time, greater microbial biomass, and broader substrate availability [27].

Blastocystis occurrence

The occurrence of *Blastocystis* spp. in omnivorous animals such as pigs and rats is of particular interest due to their frequent contact with humans – whether as livestock, laboratory animals, or urban synanthropes – and their similar omnivorous diets. Pigs are considered a promising model for studying the human gut microbiota and the epidemiology of *Blastocystis* [28], while rats have been used in experimental models to investigate colonization dynamics and the pathogenicity of different *Blastocystis* subtypes [29,30].

In pigs, the reported prevalence varies considerably from 9% [31] to 100% [4,21], with most studies reporting rates between 35% and 81% and an overall mean of ~53% [4,21,31–39]. Multiple *Blastocystis* subtypes have been identified (ST1–ST5, ST10, and ST15) (e.g., [32,38–40]), with ST5 consistently dominating across studies (e.g., [21,32,36,37]). The persistent dominance of ST5 suggests that pigs may serve as its natural host.

In omnivorous rodents, particularly rats, prevalence is lower, ranging from 4% [41] to 38% [42], with most surveys reporting a range from 4% to 16% and an average of ~15% [17,41–43]. The

most common subtypes include ST1–ST5 and ST7 [42,43], among which ST4 predominates, suggesting a strong association with omnivorous rodents (e.g., [41,44]).

While the relationship between *Blastocystis* colonization and gastrointestinal symptoms in pigs remains unresolved, the consistently high prevalence in both domestic and wild pigs suggests that *Blastocystis* likely constitutes a stable component of the **healthy** porcine gut microbiota.

Herbivores

Digestive tract and microbiome

All mammalian herbivores have evolved specialized gut compartments that house a complex microbial ecosystem, enabling the effective breakdown of fibrous plant material. Herbivores, encompassing both **foregut fermenters** (e.g., cattle, sheep) and **hindgut fermenters** (e.g., horses, rabbits), possess intricate gastrointestinal systems finely tuned for digesting high-fiber diets. Foregut fermenters, such as ruminants, are characterized by multi-chambered stomachs – particularly the rumen – supporting dense microbial consortia responsible for pre-gastric fermentation [45]. By contrast, hindgut fermenters rely on extensive microbial activity in the cecum and colon, where fermentation occurs after enzymatic digestion in the small intestine [46].

This specialized anatomy results in prolonged retention times and stable, anoxic fermentation chambers. The resultant microbial communities are among the most diverse and active in mammals – in ruminants, the rumen harbors up to 10^{10} – 10^{11} bacteria, archaea, fungi, and protists per ml, dominated by *Firmicutes*, *Bacteroidetes*, cellulolytic bacteria, methanogenic archaea, fungi, and protists that break down cellulose, hemicellulose, and starch into SCFAs such as acetate, propionate, and butyrate [47]. Similarly, equine hindgut fermentation delivers SCFAs in millimolar concentrations, with fiber-degrading consortia of bacteria, fungi, and archaea, such as *Ruminococcus*, *Prevotella*, and *Fibrobacter* [48].

The immense microbial density and compositional stability in herbivores stand in sharp contrast to those of carnivores and omnivores. Comparative analyses demonstrate that both foregut and hindgut fermenters exhibit substantially higher microbial richness.

Blastocystis occurrence in non-ruminants

Non-ruminant herbivores represent a diverse group of potential *Blastocystis* hosts, but available data remain limited compared with ruminants and omnivores. Current evidence highlights marked variability in prevalence across species and geographic regions, together with considerable subtype diversity in certain hosts (Figure 2).

Horses. The prevalence of *Blastocystis* in horses varies widely across regions, with reported rates ranging from 0% to 55% [4,49–51]. However, targeted studies on equine hosts remain scarce and many rely on small sample sizes (Box 3). To date, only one larger molecular study has assessed *Blastocystis* prevalence in horses, reporting a prevalence of 44% [49], while comparable datasets exist for cattle and small ruminants. This contrast underscores that limited number of studies, small sample sizes, and variation in detection methods may partly account for reports of low or zero prevalence.

Subtype diversity in horses appears notably high, with at least 13–14 subtypes identified. Subtype ST10 is consistently dominant, particularly in Colombia, where it occurs in over 80% of positive samples [49], and is also common in other studies worldwide – suggesting possible adaptation to equine and herbivore hosts. Other subtypes reported include ST1–ST7, ST14,

Animal group	Subtypes of <i>Blastocystis</i>
Carnivores	
Cats 	ST1, ST3, ST4, ST5, ST10, ST14
Dogs 	ST1, ST2, ST3, ST4, ST5, ST6, ST7, ST8, ST10, ST23, ST24
Omnivores	
Rats 	ST1, ST2, ST3, ST4 , ST5, ST7
Pigs 	ST1, ST2, ST3, ST4, ST5 , ST10
Herbivores	
Horses 	ST1, ST2, ST3, ST4, ST5, ST6, ST7, ST10 , ST14, ST24, ST25, ST26, ST33, ST34, ST44
Small pet herbivores	ST1, ST3, ST4, ST5, ST7, ST17
Goats 	ST1, ST3, ST4, ST5 , ST6, ST7, ST8, ST10 , ST12, ST14 , ST21, ST26, ST30, ST43, ST44
Sheep 	ST1, ST2, ST3, ST4, ST5, ST6, ST7, ST10 , ST12, ST14 , ST21, ST23, ST24, ST25, ST26, ST30, ST42, ST43, ST44
Cattle 	ST1, ST2, ST3, ST4, ST5, ST6, ST7, ST10 , ST12, ST14 , ST21, ST23, ST24, ST25, ST26 , ST30, ST32, ST43, ST44
Birds	
Poultry 	ST1, ST2, ST3, ST4, ST5, ST6 , ST7 , ST8, ST9, ST10, ST13, ST14, ST25, ST29

Trends in Parasitology

Figure 2. A list of *Blastocystis* subtypes (STs) detected in various animal groups. Overview of *Blastocystis* STs reported in carnivores, omnivores, herbivores, and birds. Bolded STs indicate the most frequently identified subtypes within each host group. Figure created in BioRender.

ST24–ST26, ST33–ST34, and ST44 [4,49,51]. Mixed infections are frequent; up to 55.6% of positive horses in Colombia carried multiple subtypes, with some harboring six STs – highlighting the genetic complexity of *Blastocystis* in equines [49].

In contrast to humans, clinical data on *Blastocystis* in domestic animals are scarce, as most studies focus on occurrence and subtype distribution rather than clinical relevance. To date, no studies have specifically examined the impact of *Blastocystis* on the health of equine hosts. However, the available research has been conducted on healthy animals, suggesting that this protist likely constitutes a stable component of the herbivore intestinal ecosystem.

Small pet herbivores. In small herbivores (e.g., rabbits, guinea pigs, chinchillas) *Blastocystis* spp. occurs less frequently than in large herbivores, particularly ruminants. For instance, the prevalence in rabbits ranges from 1% to 15% [52–54]. Several subtypes have been identified in pet rabbits, most notably ST1, ST3, ST4, ST7, and ST17, with ST1 being the most prevalent [52–54].

The prevalence of *Blastocystis* spp. is also relatively low in other small herbivorous species. In a study of 503 pet rodents from southwestern China – including squirrels, chipmunks, chinchillas, guinea pigs, and hamsters – the overall prevalence was only 8% [55]. Subtype ST4 was detected almost exclusively, accounting for 41 of 42 positive cases, with ST17 identified in a single chinchilla [55]. Notably, none of these animals exhibited pronounced clinical signs during sampling.

Box 3. Methodological and diagnostic challenges in veterinary studies

Progress in understanding *Blastocystis* in animals is hampered by technical and design-related issues. Recognizing these constraints is key to interpreting current findings.

- Diagnostic variability: inconsistent PCR targets and sequencing protocols limit comparability of prevalence and subtype data.
- Sampling limitations: many studies involve small cohorts or single regions, masking true host- and region-specific patterns.
- Temporal gaps: few longitudinal studies exist, making it unclear whether colonization is persistent or transient.
- Health associations: clinical relevance is rarely assessed, leaving open the question of whether colonization influences animal health.

Blastocystis has also been detected in other small herbivores, such as the coypus (*Myocastor coypus*). In these animals, the prevalence was 14%, with subtypes ST4 and ST5 identified [56].

Blastocystis occurrence in ruminants

Ruminants are among the most extensively investigated herbivores in *Blastocystis* research. Studies consistently report both high prevalence and remarkable subtype diversity across sheep, goats, and cattle (Figures 2 and 3). The recurrent detection of specific subtypes – particularly ST10 and ST14 – suggests a degree of host adaptation to the ruminant gastrointestinal environment, likely reflecting shared digestive physiology and microbiota composition. These patterns highlight ruminants as important reservoirs for *Blastocystis* and as key models for understanding host–parasite–microbiome interactions.

Sheep. An analysis of data from multiple studies examining the prevalence of *Blastocystis* spp. in sheep reveals substantial variability, with reported rates ranging from 5% to 91% [3,57]. Across the selected studies, the mean prevalence is approximately 30% [51,58–62]. Sheep are known to harbor an exceptionally high diversity of *Blastocystis* subtypes, with 19 distinct subtypes identified to date – ST1–ST7, ST10, ST12, ST14, ST21, ST23–ST26, ST30, and ST42–ST44 [50,62,63]. Of these, ST10 and ST14 are consistently reported as the most common subtypes in ovine hosts, a pattern that reflects subtype-specific adaptation to the ruminant gastrointestinal environment [50,57,64]. It is worth mentioning that recent evidence indicates that ‘ST10 *sensu lato*’ includes multiple genomic clades likely representing separate subtypes [65,66]. Earlier reports are retained but may combine multiple lineages, which should be considered when interpreting host specificity and zoonotic potential. High subtype diversity in sheep suggests that *Blastocystis* is well integrated into the ovine gut microbiota. However, the ecological roles and potential health impacts of these subtypes in ovine populations remain to be fully elucidated.

Goats. As in sheep, *Blastocystis* is frequently detected in goats, possibly reflecting the close similarities in their digestive physiology and gut microbiota, which may create favorable conditions for colonization. However, a direct causal relationship has yet to be established. Reported

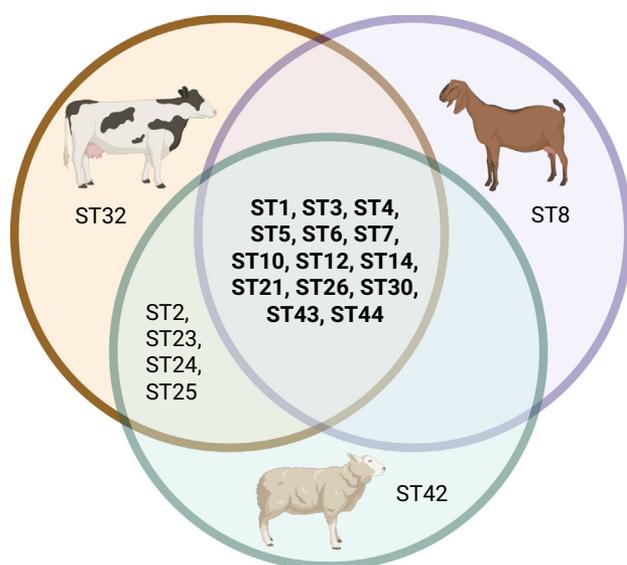


Figure 3. Venn diagram illustrating the distribution of *Blastocystis* subtypes (STs) identified in ruminants (cattle, goats, and sheep). Subtypes shown in the central overlap are shared among all three ruminant species, whereas those in non-overlapping regions were detected only in individual ruminant hosts (although they occur in other animal groups). Figure created in BioRender.

prevalence in goats varies widely, ranging from 24% to 81% [50,51,60,62], with most studies indicating an average prevalence of ~32% [62]. A broad range of subtypes has been identified in goats, including ST1, ST3–ST8, ST10, ST12, ST14, ST21, ST26, ST30, ST43, and ST44 [50,51,62,67,68]; consistent with patterns observed in sheep, ST10 and ST14 are the most common, with ST5 also occurring relatively frequently (e.g., [50,51,68]).

Cattle. Similar to other ruminants, the reported prevalence of *Blastocystis* in cattle varies widely, ranging from 2% to 100% [3,51,62,69,70], with an overall average of ~20% [62,71]. Cattle harbor remarkably diverse subtypes, including ST1–ST7, ST10, ST12, ST14, ST21, ST23–ST26, ST30, ST32, ST43, and ST44 [4,50,62,66]. A large longitudinal study in dairy calves from USA showed that *Blastocystis* prevalence increased with age, reaching a cumulative 100% over 24 months. A broad range of subtypes was identified, including marked diversity within ST10, reinforcing the need to further resolve this subtype into distinct lineages [65,66]. Consistent with findings in sheep and goats, ST10 and ST14 are the most prevalent in bovine hosts [62], while ST26 also occurs frequently [69]. The recurrent detection of these subtypes across multiple ruminant species (Figures 2 and 3) may reflect host-adaptive traits that favor their persistence in the ruminant gastrointestinal environment, potentially linked to shared dietary habits, rumen fermentation, and overall gut microbiome similarity.

A recent study examining the relationship between intestinal protists and gut microbiota in both diarrheic and healthy calves (clinically normal at sampling) found that *Blastocystis* was detected exclusively in healthy individuals [72]. Its presence showed strong positive associations with a broad spectrum of beneficial gut bacteria. Importantly, *Blastocystis* colonization correlated with enhanced overall microbial diversity and compositional evenness, suggesting a potential role in promoting or maintaining intestinal ecological balance. By contrast, pathogenic protists such as *Eimeria*, *Cryptosporidium*, and *Giardia* were associated with disrupted microbial communities and disease states. These findings suggest that, rather than acting as a pathogen, *Blastocystis* may help preserve microbial richness and stability within the calf intestine, thereby positioning it as a potential indicator of gut eubiosis rather than dysbiosis.

Birds

Digestive tract and microbiome

Avian gut microbiota shares core bacterial phyla with mammalian gut microbiota, especially at higher taxonomic ranks. However, the specific functions of the avian intestinal microbiome are thought to be closely linked to evolutionary adaptations unique to birds [73].

In captivity, avian gut microbiota is shaped by restricted diets, reduced exposure to natural habitats, and human-managed care, often resulting in reduced gut microbiome diversity and stability, which may increase susceptibility to pathogens [74]. Like other vertebrates, the core avian gut microbiota is typically dominated by *Firmicutes*, along with smaller proportions of other phyla such as *Actinobacteria*, *Bacteroidetes*, and *Proteobacteria* [75]. Among the microbial metabolites, SCFAs – produced through the anaerobic fermentation of dietary fiber – play a crucial role in modulating host immune responses. Thus, regulating the abundance and activity of SCFA-producing bacteria in the gut may represent a promising avenue for preventing and controlling enteric pathogens [76].

Blastocystis occurrence in poultry

Blastocystis has been identified in a variety of domesticated avian species worldwide [67]. Poultry, particularly chickens, are recognized as potential reservoirs for zoonotic subtypes due to their proximity to humans and the widespread use of their feces as fertilizer. The prevalence of *Blastocystis* in

poultry typically ranges from 4% to 34% [11,41,59,77,78], varying according to species, geographic location, and sample size. On average, a prevalence rate of approximately 26% has been reported in the literature [62]. Available data indicate that poultry can serve as hosts for several *Blastocystis* subtypes, including ST1–ST10, ST13, ST14, ST25, and ST29 [62,78]. However, most studies have reported the predominance of ST6 and ST7 (e.g., [59,62,77]), which are typically associated with birds, supporting the notion of host specificity for these subtypes.

In poultry and other managed birds, *Blastocystis* is frequently detected in flocks without reported gastrointestinal symptoms [79], indicating that it can form part of the avian eukaryome under typical husbandry conditions.

Concluding remarks and future perspectives

Future research on *Blastocystis* in veterinary parasitology must move beyond prevalence surveys to a deeper understanding of the mechanisms that determine colonization success and stability (see [Outstanding questions](#)). Current evidence highlights the central role of host digestive strategies: species with high fermentative capacity provide favorable conditions for long-term persistence of the protist, while carnivores with short, simple tracts tend to harbor only transient infections [7]. These differences underscore the need to interpret *Blastocystis* within a broader ecological and functional framework, rather than as a parasite tied to individual host species.

To achieve this, standardized protocols for detection and subtyping are essential, along with harmonized metadata collection and longitudinal designs that can distinguish stable colonization from transient passage [80]. Integrating microbiome, metabolome, and immunological data will be crucial for determining whether *Blastocystis* acts as a neutral commensal, an indicator of gut balance, or an active modulator of host–microbiota interactions.

Veterinary models – from pigs to laboratory rodents – offer unique opportunities to explore these dynamics under conditions and at scales not possible in human studies. By connecting parasitology, microbiome science, and veterinary medicine, *Blastocystis* may be reframed not only as a controversial protist but also as a key to understanding the intricate relationships among hosts, microbes, and intestinal eukaryotes within a One Health framework [1].

Acknowledgments

This publication is based upon work from COST Action *Blastocystis under One Health* (CA21105), resulting from discussions and activities during WG4 workshop, supported by COST (European Cooperation in Science and Technology), and also funded by a grant from the Czech Science Foundation (reg. no. 22-04837S) to K.J.

Declaration of interests

The authors declare no competing interests.

Supplemental information

Supplemental information associated with this article can be found online at <https://doi.org/10.1016/j.pt.2025.12.001>.

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Outstanding questions

What determines why some subtypes (e.g., ST5 in pigs, ST14 in ruminants) are host-adapted while others show broad host ranges?

Does *Blastocystis* act as a commensal, a marker of eubiosis, or something more?

How do diet, fiber intake, and fermentation capacity shape colonization success across digestive strategies?

Can veterinary models (e.g., pigs, rats) clarify immunological and microbiome-level consequences of colonization?

What standardization is required to resolve variability in detection and subtyping across studies?

Colonizers or transients? Is *Blastocystis* a true gut colonizer or just passing through – especially in carnivores? Longitudinal studies are key.

Is *Blastocystis* pathogenic in animals? Histology-based studies, particularly in farm animals, could help answer this.

Are zoonotic subtypes truly zoonotic? Longitudinal studies of both human and animal hosts are needed to investigate host specificity and transmission dynamics.

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