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Genomics of Apicomplexa

Fernando Martínez-Ocampo

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Abstract

Apicomplexa is a eukaryotic phylum of intracellular parasites with more than 6000 species. Some of these single-celled parasites are important pathogens of livestock. At present, 128 genomes of phylum Apicomplexa have been reported in the GenBank database, of which 17 genomes belong to five genera that are pathogens of farm animals: *Babesia*, *Theileria*, *Eimeria*, *Neospora* and *Sarcocystis*. These 17 genomes are *Babesia bigemina* (five chromosomes), *Babesia divergens* (514 contigs) and *Babesia bovis* (four chromosomes and one apicoplast); *Theileria parva* (four chromosomes and one apicoplast), *Theileria annulata* (four chromosomes), *Theileria orientalis* (four chromosomes and one apicoplast) and *Theileria equi* (four chromosomes and one apicoplast); *Eimeria brunetti* (24,647 contigs), *Eimeria necatrix* (4667 contigs), *Eimeria tenella* (12,727 contigs), *Eimeria acervulina* (4947 contigs), *Eimeria maxima* (4570 contigs), *Eimeria mitis* (65,610 contigs) and *Eimeria praecox* (53,359 contigs); *Neospora caninum* (14 chromosomes); and *Sarcocystis neurona* strains SN1 (2862 contigs) and SN3 (3191 contigs). The study of these genomes allows us to understand their mechanisms of pathogenicity and identify genes that encode proteins as a possible vaccine antigen.

Keywords: Apicomplexa, genomics, parasitic protists, *Babesia*, *Theileria*, *Eimeria*, *Sarcocystis*, *Neospora*

1. Introduction

Apicomplexa (also called Apicomplexia) is a group of protists comprising a eukaryotic phylum of obligate intracellular parasites with more than 6000 described species [1]. Many of these cell single parasites are important pathogens of humans, domestic animals and livestock, with a health and economic relevance worldwide [2–5]. Apicomplexa microorganisms are intracellular eukaryotes thriving within another eukaryotic cell [6].

This phylum includes *Plasmodium falciparum* and four other *Plasmodium* species, the etiological agents for malaria in humans, a mosquito-transmitted and potentially deadly disease [6]. *Toxoplasma gondii* is a source of toxoplasmosis disease and congenital neurological birth defects (for example, encephalitis and ocular disease) in humans [7–9]. *Cryptosporidium* and *Cyclospora* parasites cause opportunistic human infections associated with immunosuppressive conditions (including AIDS) through contaminated food or water supplies [10, 11], while the invertebrate parasites of genus *Gregarina* are used as models for studying Apicomplexa motility [12].

Apicomplexa parasites infect a wide range of animals from mollusks to mammals [13]. Their life cycles involve only a single host, whereas others require sexual recombination in a vector species for transmission. The life cycle of these parasites has three stages: sporozoite (infective stage), merozoite (a result of asexual reproduction) and gametocyte (germ cells) [12]. These parasites are characterized by the presence of specific organelles (including rhoptries, micronemes and dense granules) involved in the establishment of an intracellular parasitophorous vacuole within the host cell [12].

A defined feature of these microorganisms is the presence of extracellular zoite forms that are usually motile and include an apical complex that gives the phylum its name [14]. With the exception of the genera *Cryptosporidium* and *Gregarina*, all species of the phylum Apicomplexa possess an apicoplast [12, 15–17].

The Apicomplexa parasites causing diseases of veterinary importance are *Babesia*, *Theileria*, *Eimeria*, *Neospora* and *Sarcocystis* [11, 18, 19]. This chapter focuses on genomics of these five genera.

2. Apicomplexa genome

2.1. Apicoplast genome

Twenty years ago, a remnant chloroplast, known as apicoplast, was discovered in *Plasmodium* [20–23]. This apicoplast lost the ability to perform photosynthesis, however, is an essential organelle, and its inhibition is lethal. The apicoplast arose from a secondary endosymbiosis event occurred where an ancestor to *Plasmodium* engulfed a photosynthetic alga [24–26]. This organelle is involved in critical metabolic pathways such as the biosynthesis of fatty acids and heme group degradation [27, 28]. Some of these metabolic pathways are considered as potential targets for antiparasitic drug designs [29, 30].

Like mitochondria, the apicoplast possesses its own genome [29, 31–37]. The apicoplast genome is ~35 kbp smaller than chloroplasts due to the absence of genes encoding proteins involved in photosynthesis. The genome of this plastid has been reduced and contains ribosomal (rRNA) and transfer RNA (tRNA) genes that play an important role in organelle replication [24]. The characteristics of the structure of apicoplast genomes have difficult comparisons with other plastids [20].

2.2. Apicomplexa genomes in GenBank

New drug targets identification, and novel antiparasitic therapeutics are necessary due to the emergence of parasite strains resistant to treatments available today [12, 38–40]. With the recent advancements in genome sequencing technologies, the research of new drug targets can be the focus on genomics analyses.

At present (August 2016), 128 complete and draft genomes of phylum Apicomplexa have been reported in the GenBank database (http://www.ncbi.nlm.nih.gov/genbank/), of which 17 genomes belong to five genera that are pathogens of farm animals: *Babesia*, *Theileria*, *Eimeria*, *Neospora*, and *Sarcocystis* (3, 4, 7, 1, and 2 genomes, respectively). The study and comparison of these genomes will allow us to understand pathogenicity mechanisms and identify genes and proteins with potential drug targets in order to develop novel antiparasitic compounds of veterinary importance.

3. Classification of phylum Apicomplexa

The National Center for Biotechnology Information (NCBI; http://www.ncbi.nlm.nih.gov/) divides the phylum Apicomplexa into two classes: Aconoidasida and Conoidasida (**Figure 1**). The class Aconoidasida is divided into two orders: Haemosporida and Piroplasmida
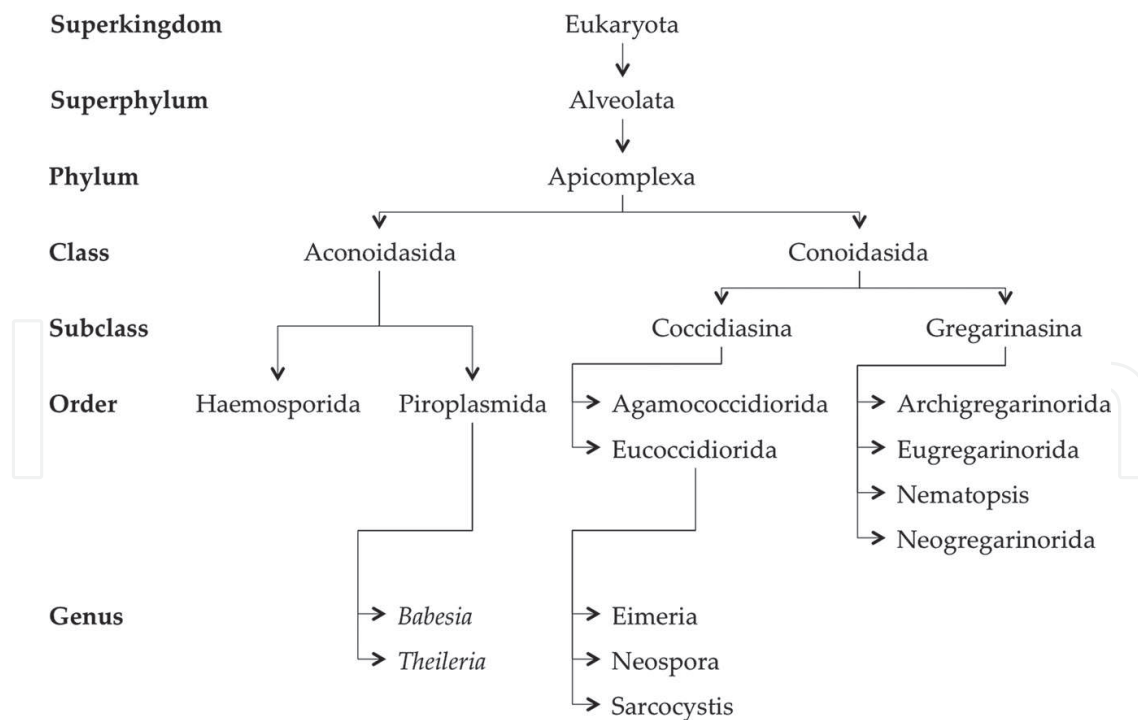

Figure 1. Classification of phylum Apicomplexa. Taxonomic categories are shown in bold (left). Only genera with veterinary importance are shown. The genera *Babesia* and *Theileria* belong to order Piroplasmida. The genera *Eimeria*, *Neospora* and *Sarcocystis* belong to order Eucoccidiorida.

(containing the genera *Babesia* and *Theileria*), while the class Conoidasida is divided into two subclasses: Coccidiasina (containing the genera *Eimeria*, *Neospora* and *Sarcocystis*, that belong to order Eucoccidiorida) and Gregarinasina (**Figure 1**).

It is estimated that subclass Coccidiasina separated from the class Aconoidasida ~705 million years ago [41, 42]. Moreover, in 2004, Douzery et al. calculated it as 495 million years ago [41–43].

4. *Babesia*

Babesia is a genus of intracellular protozoa that cause babesiosis. These parasites are transmitted by ticks and infect erythrocytes in their mammalian hosts. Babesiosis was first described in sheep and cattle in 1888 by Victor Babes, in honor of which is called the genus [44] and is characterized by hemolytic anemia and fever, with occasional hemoglobinuria and death [45].

The genus *Babesia* includes over 100 species that are highly specific for their hosts. Only a few *Babesia* species cause infections in humans, especially immunocompromised individuals. Most cases identified in humans are caused by *Babesia microti* and *Babesia divergens*, parasites of rodents and cattle, respectively [44, 46, 47].

Species affecting animals are: *Babesia bigemina*, *Babesia major*, *Babesia divergens* and *Babesia bovis* that infect cattle [44, 48–51]; *Babesia ovis* and *Babesia motasi* cause infections in sheep [44, 52, 53]; and *Babesia equi* and *Babesia caballi* cause infections in horses [44, 54].

Three genomes of *Babesia* species have been reported in the GenBank database. The *B. bigemina* strain Bond genome is 13,840,936 bp of total length divided into five chromosomes (2.5, 2.8, 3.5, 0.9 and 0.5 Mbp; GenBank accession number from NC_027216.1 to NC_027220.1, respectively). The *B. divergens* strain Rouen 1987 genome is 10,797,556 bp divided into 514 contigs (GenBank accession number CCSG00000000.1).

B. bovis strain T2Bo genome is 8,179,706 bp divided into four chromosomes (1.2, 1.7, 2.6 and 2.6 Mbp, respectively) and one apicoplast (35,107 bp, GenBank accession number NC_011395.1). The chromosomes I and IV of *B. bovis* genome are divided into seven and three contigs, respectively; chromosomes II and III GenBank accession numbers are NC_010574.1 and NC_010575.1, respectively.

4.1. *Babesia bovis* genome

In 2007, Brayton et al. reported the analysis of comparative genomic between *B. bovis*, *Theileria parva* and *P. falciparum* genomes [33]. The *B. bovis* genome has 3671 protein-coding genes and 41.8% of GC content, an analysis of enzymatic pathways revealed a reduced metabolic potential. The results of comparative genomic showed that *B. bovis* genome (8.2 Mbp) is similar in size to that of *T. parva* (8.3 Mbp) [34] and *Theileria annulata* (8.35 Mbp) [55], the smallest Apicomplexa genomes sequenced to date.

In contrast, *B. bovis* and *P. falciparum*, which have similar clinical and pathological features, have major differences in genome size (8.2 and 22.8 Mbp, respectively) and chromosome number (4 and 14, respectively). Additionally, many stage-specific and immunologically important genes from *P. falciparum* are absent in *B. bovis* [33]. The *B. bovis* genome sequence has allowed analyses of the polymorphic variant erythrocyte surface antigen protein (*ves1* gene and discovery of the novel *smorf* gene family) that are postulated to play a role in cytoadhesion and immune evasion (similar to *var.* genes of *P. falciparum*). The ~150 *ves1* genes are distributed in clusters throughout each chromosome [33]. Finally, comparative analyses have identified several novel vaccine candidates into B. bovis genome, including homologs of p36 and Pf12 (*P. falciparum*); p67 and four of six proteins (*T. parva*) targeted by CD8+ cytotoxic T cells [33].

Brayton et al. also reported that the *B. bovis* apicoplast genome is 33 kbp of total length and encodes 32 putative protein coding genes, 25 tRNA genes, and small and large subunit rRNA genes. This organelle genome displays similarities in size and gene content to apicoplasts of *Eimeria tenella*, *P. falciparum*, *T. parva* and *T. gondii* [33, 35, 56]. The *B. bovis* apicoplast genome has 78.2% of AT content (21.8% of GC content) [33].

5. *Theileria*

The genus *Theileria* infects leukocytes [57], and they are the only eukaryotic pathogens known to transform lymphocytes [11]. These parasites infect a wide range of both domestic and wild animals and are transmitted by Ixodid ticks of the genera *Amblyomma*, *Haemaphysalis*, *Hyalomma* and *Rhipicephalus* [58, 59]. *Theileria* parasites can be grouped into schizont transforming (*T. parva*, *T. annulata* and *Theileria lestoquardi*) [60–62] and nontransforming (*Theileria orientalis*) species [63, 64]. The uncontrolled proliferation of schizonts results in the pathologies associated with corridor disease and East Coast fever (*T. parva*), tropical theileriosis (*T. annulata*) in cattle and malignant theileriosis (*T. lestoquardi*) in goats and sheep [59, 65].

T. orientalis (frequently been referred to as *T. sergenti* [66]) causes bovine piroplasmosis [67–69] and can generate anemia and icterus in cattle but rarely cause fatal disease [64]. *T. orientalis* is classified into two major genotypes: the Chitose (throughout the world) and Ikeda (eastern Asian countries) types [70]. Finally, equine piroplasmosis of horses, mules, donkeys, and zebras is caused by *Theileria equi* [71]. *T. equi* has been renamed several times [72], and molecular phylogenetic analyses indicate an intermediate position between *B. bovis* and *Theileria* spp. [73, 74].

Four genomes of *Theileria* species have been reported in the GenBank database. The *T. parva* strain Muguga genome is 8,347,606 bp divided into four chromosomes (2.5, 2.0, 1.9 and 1.9 Mbp) and one apicoplast (39,579 bp, GenBank accession number NC_007758.1). The chromosomes I and II of *T. parva* genome have the GenBank accession number NC_007344.1 and NC_007345.1, respectively, while the chromosomes III and IV are divided into four and two contigs, respectively. The *T. annulata* strain Ankara isolate clone C9 genome is 8,358,425 bp divided into four chromosomes (2.6, 2.0, 1.9 and 1.8 Mbp; GenBank accession number

NC_011129.1, NC_011099.1, NC_011100.1 and NC_011098.1, respectively). The *T. orientalis* strain Shintoku (Ikeda type) genome is 9,010,364 bp divided into four chromosomes (2.7, 2.2, 2.0 and 2.0 Mbp; GenBank accession number from NC_025260.1 to NC_025263.1, respectively) and one apicoplast (24,173 bp into one contig).

Finally, the *T. equi* strain WA genome is 11,674,479 bp divided into four chromosomes (3.7, 2.3, 2.1 and 3.5 Mbp) and one apicoplast (47,880 bp into one contig). The chromosomes I and III of *T. equi* genome have the GenBank accession number NC_021366.1 and NC_021367.1, respectively, while the chromosomes II and IV are divided into two and six contigs, respectively.

5.1. *Theileria parva* genome

The complete genome sequence of *T. parva* was reported in 2005 [34]. *T. parva* genome has 4035 protein encoding genes (20% fewer than *P. falciparum*) and 34.1% of GC content. Putative functions were assigned to 38% of the predicted proteins. Like *P. falciparum*, the four chromosomes of *T. parva* contain one extremely A + T-rich region (>97%) about 3 kbp in length that may be the centromere [34]. Unlike *P. falciparum*, *T. parva* genome contains two identical, unlinked 5.8S-18S-28S rRNA units, which suggest that it does not possess functionally distinct ribosomes [75]. The infection of T and B lymphocytes by *T. parvum* results in a reversible transformed phenotype with uncontrolled proliferation of host cells that remain persistently infected. Parasite proteins that may modulate host cell phenotype are described by [55]. Telomeres of *T. parvum* have a conserved (~140 bp) sequence adjacent to the telomeric repeat and several subtelomeric regions exhibit 70–100% sequence similarity [34, 76]. The apicoplast genome of *T. parva* differs from *P. falciparum* in that all of its genes are transcribed in the same direction, and 26 of the 44 protein-coding genes share 27–61% sequence similarity with proteins encoded by the *P. falciparum* apicoplast genome [34].

5.2. *Theileria annulata* genome

The *T. annulata* genome sequence was also reported in 2005 [55]. The nuclear genome of *T. annulata* is similar in size (8.35 Mbp) to that of *T. parva* (8.3 Mbp). *T. annulata* genome has 3792 protein encoding genes (243 genes fewer than *T. parva*), 49 tRNA and 5 rRNA genes, and 32.54% of GC content. In addition, 3265 orthologous genes were predicted between *T. annulata* and *T. parva* genomes. Pain et al. predicted 3265 orthologous genes between the *T. annulata* and *T. parva* genomes. Additionally, 34 (*T. annulata*) and 60 (*T. parva*) genes are single-copy genes and their functions have been not described [55].

The parasite genes involved in host-cell transformation require a signal peptide or a specific host-targeting signal sequence. Some candidates include TashAT and SuAT protein families in *T. annulata* [77, 78] and related host nuclear proteins (TpHNs protein family) in *T. parva*. A cluster of 17 SuAT1 and TashAT-like genes was identified in the *T. annulata* genome [55].

5.3. *Theileria orientalis* genome

In 2012, Hayashida et al. reported the comparative genomic analyses between *T. orientalis*, *T. parva*, *T. annulata* and *B. bovis.* The genome size of *T. orientalis* (9 Mbp) is approximately

8% larger than the reported genome sizes of *T. parva* (8.3 Mbp), *T. annulata* (8.35 Mbp) and *B. bovis* (8.2 Mbp). The number of predicted protein-coding (3995) genes identified in *T. orientalis* is similar to that found in *T. parva* (4035). The GC content of the *T. orientalis* genome (41.6%) is higher than *T. parva* and *T. annulata* (34.1 and 32.5%, respectively) but similar to *B. bovis* (41.8%). Unlike *T. parva* and *T. annulata, T. orientalis* does not induce uncontrolled proliferation of infected leukocytes and multiplies predominantly within infected erythrocytes [79]. *T. orientalis* is the first genome sequence of a nontransforming *Theileria* species that occupies a phylogenetic position close to that of the transforming species [79].

5.4. *Theileria equi* genome

The *T. equi* genome sequence was reported in 2012 [80]. *T. equi* genome size (11.6 Mbp) is larger than *T. parva* (8.3 Mbp), *T. annulata* (8.35 Mbp), *T. orientalis* (9 Mbp) and *B. bovis* (8.2 Mbp). *T. equi* genome has two rRNA operons, 46 tRNA genes and 5330 nuclear protein coding genes, ~25% greater than found for *T. parva*, *T. annulata* and *B. bovis*. Furthermore, *T. equi* genome contains 1985 unique genes, and 366 and 137 homologs of genes found only in the two *Theileria* spp. or *B. bovis*, respectively. The apicoplast genome of *T. Equi* has 43 unidirectionally coding sequences, which includes each of the 20 tRNA, and two rRNA genes are present [80].

6. *Eimeria*

Eimeria is a genus that includes species capable of causing the disease coccidiosis in cattle and poultry. *Eimeria* parasites exhibit immense diversity in host range including mammals, birds, reptiles, fish and amphibians [81–86]. It is estimated that there are many thousands of *Eimeria* species [87]. Coccidiosis is primarily associated with enteric disease with few exceptions [88–90]. The avian coccidiosis can be subdivided into hemorrhagic and malabsorptive pathologies related to *Eimeria brunetti*, *Eimeria necatrix* and *Eimeria tenella*; or *Eimeria acervulina*, *Eimeria maxima*, *Eimeria mitis* and *Eimeria praecox*, respectively [91]. *E. tenella* is among the most pathogenic avian parasites causing weight loss, reduced feed efficiency, reduced egg production and death [92]. The total loss is estimated at around USD 2.4 billion annually [93], including the costs of control and prevention worldwide.

Seven genomes of *Eimeria* species have been reported in the GenBank database. The *E. brunetti* strain Houghton genome is 66,890,165 bp divided into 24,647 contigs (GenBank accession number CBUX000000000.1). The *E. necatrix* strain Houghton genome is 55,007,932 bp divided into 4667 contigs (GenBank accession number CBUZ000000000.1). The *E. tenella* strain Houghton genome is 51,859,607 bp divided into 12,727 contigs (GenBank accession number CBUW000000000.1). The *E. acervulina* strain Houghton genome is 45,830,609 bp divided into 4947 contigs (GenBank accession number CBUS000000000.1). The *E. maxima* strain Weybridge genome is 45,975,062 bp divided into 4570 contigs (GenBank accession number CBUY000000000.1). The *E. mitis* strain Houghton genome is 60,415,144 bp divided into 65,610 contigs (GenBank accession number CBUT000000000.1). *E. praecox* strain Houghton genome is 60,083,328 bp divided into 53,359 contigs (CBUU000000000.1).

E. tenella strain Houghton was isolated in the United Kingdom in 1949. The *E. tenella* genome size is ~60 Mbp with a GC content of ~53%. Its molecular karyotype comprises 14 chromosomes of between 1 and >6 Mbp, and the genome is available in http://www.sanger.ac.uk/Projects/E_tenella/. Moreover, parallel projects have been undertaken to generate the complete sequences of chromosomes I (~1 Mbp) and II (~1.2 Mbp), which are associated with resistance to the anticoccidial drug arprinocid and precocious development, respectively [94]. In 2007, Ling et al. reported the sequencing and analysis of the first chromosome of *E. tenella* [95]. The chromosome I of *E. tenella* is 1,347,714 pb of total length and has the GenBank accession number AM269894.1.

7. *Neospora*

The genus *Neospora* is constituted by only two species: *Neospora caninum* and *Neospora hughesi*. *N. caninum* is the etiologic agent of the disease neosporosis and is a close relative of *T. gondii* [96]. They share many common morphological and biological features [97]. *Neospora* parasite appears not to be zoonotic, having a more restricted host range [98, 99], and shows a striking capacity for highly efficient vertical transmission in bovines [100]. *N. caninum* is one of the leading causes of infectious bovine abortion [101, 102].

Only one genome of *N. caninum* strain Liverpool has been reported in the GenBank database. This genome has 57,547,420 bp of total length divided into 14 chromosomes: Ia (2,288,409 bp), Ib (1,908,326 bp), II (2,170,133 bp), III (2,139,717 bp), IV (2,317,323 bp), V (2,735,753 bp), VI (3,360,651 bp), VIIa (3,947,736 bp), VIIb (4,923,984 bp), VIII (6,723,156 bp), IX (5,490,906 bp), X (6,985,512 bp), XI (6,081,843 bp) and XII (6,473,971 bp); GenBank accession number from NC_018385.1 to NC_018398.1.

8. *Sarcocystis*

More than 150 species of *Sarcocystis* have an indirect life cycle. They require both an intermediate and a final host, usually a herbivorous and a carnivorous vertebrate animal, respectively [103]. For this transition, *Sarcocystis* species produce infectious tissue cysts surrounded by glycosylated cyst walls that are largely restricted to muscle. Ingestion of tissue cysts through predation by the final hosts propagates the life cycle [104]. All vertebrates, including mammals, some birds, reptiles and possibly fish, are intermediate hosts to at least one *Sarcocystis* species [105, 106]. Final hosts include carnivores or omnivores, such as humans, some reptiles and raptorial birds [107].

Sarcocystis species are the causal agents of Sarcocystosis, a disease typically asymptomatic but can be associated with myositis, diarrhea or infection of the central nervous system [104]. Some species of *Sarcocystis* that infect farm animals (such as cattle, sheep and horses) cause fever, lethargy, poor growth, reduced milk production, abortion and death [107].

Sarcocysti cruzi, *Sarcocysti hirsuta* and *Sarcocysti hominis* used cattle as intermediate hosts, and canids, felids and humans as final hosts, respectively [108]. Additionally, *Sarcocysti sinensis* also used cattle as intermediate host [109], but its final host remains to be elucidated [110]. *S. hominis* causes gastrointestinal malaise [108] and *S. sinensis* may also elicit symptoms in humans [111].

Sarcocysti neurona is the causal agent of equine protozoal myeloencephalitis [106]. This disease destroys neural tissue and can be fatal to horses, marine mammals and several other mammals. *S. neurona* also infects many mammals asymptomatically [104]. Furthermore, three *Sarcocystis* species have been identified from pigs: *Sarcocysti miescheriana*, *Sarcocysti porcifelis* and *Sarcocysti suihominis* [112]. In 2015, Blazejewski et al. reported the first genome sequence of *S. neurona* strain SN1 [104].

Two genomes of *S. neurona* strains have been reported in the GenBank database. The *S. neurona* strain SN3 clone E1 genome is 124,404,968 bp divided into 3191 contigs (GenBank accession number JAQE00000000.1). *S. neurona* strain SN1 genome is 130,023,008 bp divided into 2862 contigs (GenBank accession number JXWP00000000.1). *S. neurona* strain SN1 was isolated from an otter that died of protozoal encephalitis [113]. The apicoplast genome architectures of *S. neurona* strains SN1 and SN3 are highly similar to those of *Toxoplasma gondii* and *Plasmodium falciparum* [104]. *S. neurona* strains SN1 and SN3 are the first genomes reported in the genus *Sarcocystis*. These genomes are more than twice the size of other sequenced coccidian genomes.

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References

[1] Adl SM, Leander BS, Simpson AGB, Archibald JM, Anderson OR, Bass D, et al. Diversity, nomenclature, and taxonomy of protists. Systematic Biology(England). 2007 Aug;**56**(4): 684-689

[2]   Battle KE, Gething PW, Elyazar IRF, Moyes CL, Sinka ME, Howes RE, et al. The global public health significance of Plasmodium vivax. Advances in Parasitology(England). 2012;**80**:1-111

[3]   Checkley W, White ACJ, Jaganath D, Arrowood MJ, Chalmers RM, Chen X-M, et al. A review of the global burden, novel diagnostics, therapeutics, and vaccine targets for cryptosporidium. The Lancet Infectious Diseases (United States). 2015 Jan;**15**(1):85-94

[4]   Morrison WI. The aetiology, pathogenesis and control of theileriosis in domestic animals. Revue Scientifique Et Technique (France). 2015 Aug;**34**(2):599-611

[5]   Torgerson PR, Mastroiacovo P. The global burden of congenital toxoplasmosis: A systematic review. Bulletin of the World Health Organization (Switzerland). 2013 Jul;**91**(7):501-508

[6]   Seeber F, Steinfelder S. Recent advances in understanding apicomplexan parasites. F1000Research (England). 2016;**5**

[7]   Belanger F, Derouin F, Grangeot-Keros L, Meyer L. Incidence and risk factors of toxoplasmosis in a cohort of human immunodeficiency virus-infected patients: 1988-1995. HEMOCO and SEROCO Study Groups. Clinical Infectious Diseases (United States). 1999 Mar;**28**(3):575-581

[8]   Schluter D, Daubener W, Schares G, Gross U, Pleyer U, Luder C. Animals are key to human toxoplasmosis. International Journal of Medical Microbiology (Germany). 2014 Oct;**304**(7):917-929

[9]   Havelaar AH, Kirk MD, Torgerson PR, Gibb HJ, Hald T, Lake RJ, et al. World health organization global estimates and regional comparisons of the burden of foodborne disease in 2010. PLoS Med (United States). 2015 Dec;**12**(12):e1001923

[10]   Hunter PR, Nichols G. Epidemiology and clinical features of Cryptosporidium infection in immunocompromised patients. Clinical Microbiology Reviews (United States). 2002 Jan;**15**(1):145-154

[11]   Roos DS. Genetics. Themes and variations in apicomplexan parasite biology. Science. (United States). 2005 Jul;**309**(5731):72-73

[12]   Wasmuth J, Daub J, Peregrin-Alvarez JM, Finney CAM, Parkinson J. The origins of apicomplexan sequence innovation. Genome Research (United States). 2009 Jul;**19**(7):1202-1213

[13]   Cavalier-Smith T. Kingdom protozoa and its 18 phyla. Microbiological Reviews (United States). 1993 Dec;**57**(4):953-994

[14]   Sibley LD. Intracellular parasite invasion strategies. Science (United States). 2004 Apr; **304**(5668):248-253

[15]   Zhu G, Marchewka MJ, Keithly JS. Cryptosporidium parvum appears to lack a plastid genome. Microbiology (England). 2000 Feb;**146**(Pt 2:315-321)

[16] Fast NM, Kissinger JC, Roos DS, Keeling PJ. Nuclear-encoded, plastid-targeted genes suggest a single common origin for apicomplexan and dinoflagellate plastids. Molecular Biology and Evolution (United States). 2001 Mar;**18**(3):418-426

[17] Toso MA, Omoto CK. Gregarina niphandrodes may lack both a plastid genome and organelle. The Journal of Eukaryotic Microbiology (United States). 2007;**54**(1):66-72

[18] Graat EA, Ploeger HW, Henken AM, De Vries Reilingh G, Noordhuizen JP, Van Beek PN. Effects of initial litter contamination level with Eimeria acervulina on population dynamics and production characteristics in broilers. Veterinary Parasitology (Netherlands). 1996 Oct;**65**(3-4):223-232

[19] Dubey JP. Recent advances in Neospora and neosporosis. Veterinary Parasitology (Netherlands). 1999 Aug;**84**(3-4):349-367

[20] Wilson RJ, Denny PW, Preiser PR, Rangachari K, Roberts K, Roy A, et al. Complete gene map of the plastid-like DNA of the malaria parasite Plasmodium falciparum. Journal of Molecular Biology(England). 1996 Aug;**261**(2):155-172

[21] Gardner MJ, Williamson DH, Wilson RJ. A circular DNA in malaria parasites encodes an RNA polymerase like that of prokaryotes and chloroplasts. Molecular and Biochemical Parasitology (Netherlands). 1991 Jan;**44**(1):115-123

[22] Howe CJ. Plastid origin of an extrachromosomal DNA molecule from Plasmodium, the causative agent of malaria. Journal of Theoretical Biology (England). 1992 Sep;**158**(2):199-205

[23] McFadden GI, Reith ME, Munholland J, Lang-Unnasch N. Plastid in human parasites. Nature (England). 1996;**381**:482

[24] Nisbet RER, McKenzie JL. Transcription of the apicoplast genome. Molecular and Biochemical Parasitology. 2016 Jul

[25] Kohler S, Delwiche CF, Denny PW, Tilney LG, Webster P, Wilson RJ, et al. A plastid of probable green algal origin in Apicomplexan parasites. Science (United States). 1997 Mar;**275**(5305):1485-1489

[26] Janouskovec J, Horak A, Obornik M, Lukes J, Keeling PJ. A common red algal origin of the apicomplexan, dinoflagellate, and heterokont plastids. Proceedings of the National Academy of Sciences of the United States of America (United States). 2010 Jun;**107**(24):10949-10954

[27] Ralph SA, van Dooren GG, Waller RF, Crawford MJ, Fraunholz MJ, Foth BJ, et al. Tropical infectious diseases: Metabolic maps and functions of the Plasmodium falciparum apicoplast. Nature Reviews. Microbiology 2004 Mar;**2**(3):203-216

[28] Waller RF, McFadden GI. The apicoplast: A review of the derived plastid of apicomplexan parasites. Current Issues in Molecular Biology (England). 2005 Jan;**7**(1):57-79

[29] Huang Y, He L, Hu J, He P, He J, Yu L, et al. Characterization and annotation of Babesia orientalis apicoplast genome. Parasites and Vectors (England). 2015;**8**:543

[30] Aboulaila M, Munkhjargal T, Sivakumar T, Ueno A, Nakano Y, Yokoyama M, et al. Apicoplast-targeting antibacterials inhibit the growth of Babesia parasites. Antimicrobial Agents and Chemotherapy (United States). 2012 Jun;**56**(6):3196-3206

[31] Imura T, Sato S, Sato Y, Sakamoto D, Isobe T, Murata K, et al. The apicoplast genome of Leucocytozoon caulleryi, a pathogenic apicomplexan parasite of the chicken. Parasitology Research (Germany). 2014 Mar;**113**(3):823-828

[32] Lau AOT, McElwain TF, Brayton KA, Knowles DP, Roalson EH. Babesia bovis: a comprehensive phylogenetic analysis of plastid-encoded genes supports green algal origin of apicoplasts. Experimental Parasitology (United States). 2009 Nov;**123**(3):236-243

[33] Brayton KA, Lau AOT, Herndon DR, Hannick L, Kappmeyer LS, Berens SJ, et al. Genome sequence of Babesia bovis and comparative analysis of apicomplexan hemoprotozoa. PLoS Pathogens (United States). 2007 Oct;**3**(10):1401-1413

[34] Gardner MJ, Bishop R, Shah T, de Villiers EP, Carlton JM, Hall N, et al. Genome sequence of Theileria parva, a bovine pathogen that transforms lymphocytes. Science (United States). 2005 Jul;**309**(5731):134-137

[35] Cai X, Fuller AL, McDougald LR, Zhu G. Apicoplast genome of the coccidian Eimeria tenella. Gene (Netherlands). 2003 Dec;**321**:39-46

[36] Williamson DH, Denny PW, Moore PW, Sato S, McCready S, Wilson RJ. The in vivo conformation of the plastid DNA of Toxoplasma gondii: implications for replication. Journal of Molecular Biology. 2001 Feb;**306**(2):159-168

[37] Tang K, Guo Y, Zhang L, Rowe LA, Roellig DM, Frace MA, et al. Genetic similarities between Cyclospora cayetanensis and cecum-infecting avian Eimeria spp. in apicoplast and mitochondrial genomes. Parasites & Vectors (England). 2015;**8**:358

[38] Aspinall T V, Joynson DHM, Guy E, Hyde JE, Sims PFG. The molecular basis of sulfonamide resistance in Toxoplasma gondii and implications for the clinical management of toxoplasmosis. The Journal of Infectious Diseases (United States). 2002 Jun;**185**(11):1637-1643

[39] Trouiller P, Olliaro P, Torreele E, Orbinski J, Laing R, Ford N. Drug development for neglected diseases: a deficient market and a public-health policy failure. Lancet (London, England). 2002 Jun;**359**(9324):2188-2194

[40] White NJ. Antimalarial drug resistance. The Journal of Clinical Investigation. 2004;**113**:1084-1092

[41] Shanmugasundram A, Gonzalez-Galarza FF, Wastling JM, Vasieva O, Jones AR. Library of Apicomplexan Metabolic Pathways: a manually curated database for metabolic pathways of apicomplexan parasites. Nucleic Acids Research (England). 2013 Jan;**41**(Database issue):D706-D713

[42] Hedges SB, Dudley J, Kumar S. TimeTree: A public knowledge-base of divergence times among organisms. Bioinformatics (England). 2006 Dec;**22**(23):2971-2972

[43] Douzery EJP, Snell EA, Bapteste E, Delsuc F, Philippe H. The timing of eukaryotic evolution: Does a relaxed molecular clock reconcile proteins and fossils? Proceedings of the National Academy of Sciences of the United States of America (United States). 2004 Oct;**101**(43):15386-15391

[44] Beugnet F, Moreau Y. Babesiosis. Revue Scientifique Et Technique (France). 2015 Aug; **34**(2):627-639

[45] Mosqueda J, Olvera-Ramirez A, Aguilar-Tipacamu G, Canto GJ. Current advances in detection and treatment of babesiosis. Current Medicinal Chemistry (Netherlands). 2012;**19**(10):1504-1518

[46] Hunfeld K-P, Hildebrandt A, Gray JS. Babesiosis: Recent insights into an ancient disease. International Journal for Parasitology (England). 2008 Sep;**38**(11):1219-1237

[47] Cassini R, Bonoli C, Montarsi F, Tessarin C, Marcer F, Galuppi R. Detection of Babesia EU1 in Ixodes ricinus ticks in northern Italy. Veterinary Parasitology (Netherlands). 2010 Jul;**171**(1-2):151-154

[48] Doyle RL, Da Silva AS, Oliveira CB, Franca RT, Carvalho FB, Abdalla FH, et al. Cholinesterases as markers of the inflammatory process associated oxidative stress in cattle infected by Babesia bigemina. Comparative Immunology, Microbiology & Infectious Diseases (England). 2016 Jun;**46**:1-6

[49] Purnell RE, Brocklesby DW, Stark AJ. Protection of cattle against Babesia major by the inoculation of irradiated piroplasms. Research in Veterinary Science (England). 1978 Nov;**25**(3):388-390

[50] Cuesta I, Gonzalez LM, Estrada K, Grande R, Zaballos A, Lobo CA, et al. High-Quality Draft Genome Sequence of Babesia divergens, the Etiological Agent of Cattle and Human Babesiosis. Genome Announcements (United States). 2014;**2**(6)

[51] Yang C, Liu J, Li A, Li Y, Liu A, Xie J, et al. Evaluating the Babesia bovis infection of cattle in China with enzyme-linked immunosorbent assay (ELISA). Acta Parasitologica (Poland). 2015 Dec;**60**(4):721-726

[52] Erster O, Roth A, Wollkomirsky R, Leibovich B, Savitzky I, Zamir S, et al. Quantitative analysis of Babesia ovis infection in sheep and ticks. Veterinary Parasitology (Netherlands). 2016 May;**221**:39-45

[53] Alani AJ, Herbert I V. The pathogenesis of Babesia motasi (Wales) infection in sheep. Veterinary Parasitology (Netherlands). 1988 Mar;**27**(3-4):209-220

[54] Xu Y, Zhang S, Huang X, Bayin C, Xuan X, Igarashi I, et al. Seroepidemiologic studies on Babesia equi and Babesia caballi infections in horses in Jilin province of China. The Journal of Veterinary Medical Science (Japan). 2003 Sep;**65**(9):1015-1017

[55] Pain A, Renauld H, Berriman M, Murphy L, Yeats CA, Weir W, et al. Genome of the host-cell transforming parasite Theileria annulata compared with T. parva. Science (United States). 2005 Jul;**309**(5731):131-133

[56] Williamson DH, Gardner MJ, Preiser P, Moore DJ, Rangachari K, Wilson RJ. The evolutionary origin of the 35 kb circular DNA of Plasmodium falciparum: new evidence supports a possible rhodophyte ancestry. Molecular Genetics and Genomics (Germany). 1994 Apr;**243**(2):249-252

[57] Uilenberg G. Babesia. A historical overview. Veterinary Parasitology (Netherlands). 2006 May;**138**(1-2):3-10

[58] Mans BJ, Pienaar R, Latif AA. A review of Theileria diagnostics and epidemiology. International Journal for Parasitology: Parasites and Wildlife (England). 2015 Apr; **4**(1):104-118

[59] Bishop R, Musoke A, Morzaria S, Gardner M, Nene V. Theileria: Intracellular protozoan parasites of wild and domestic ruminants transmitted by ixodid ticks. Parasitology (England). 2004;**129** Suppl:S271–S283

[60] Irvin AD, Brown CG, Kanhai GK, Stagg DA. Comparative growth of bovine lymphosarcoma cells and lymphoid cells infected with Theileria parva in athymic (nude) mice. Nature (England). 1975 Jun;**255**(5511):713-714

[61] Brown CG. Control of tropical theileriosis (Theileria annulata infection) of cattle. Parassitologia (Italy). 1990 Apr;**32**(1):23-31

[62] Hooshmand-Rad P, Hawa NJ. Malignant theileriosis of sheep and goats. Tropical Animal Health and Production. 1973;**5**(2):97-102

[63] Sivakumar T, Hayashida K, Sugimoto C, Yokoyama N. Evolution and genetic diversity of Theileria. Infection, Genetics and Evolution (Netherlands). 2014 Oct;**27**:250-263

[64] Onuma M, Kakuda T, Sugimoto C. Theileria parasite infection in East Asia and control of the disease. Comparative Immunology, Microbiology and Infectious Diseases (England). 1998 Jul;**21**(3):165-177

[65] McKeever DJ. Bovine immunity—A driver for diversity in Theileria parasites? Trends in Parasitology. 2009 Jun;**25**(6):269-276

[66] Uilenberg G. Theileria sergenti. Vol. 175. Netherlands: Veterinary parasitology; 2011 p. 386

[67] Shimizu S, Yoshiura N, Mizomoto T, Kondou Y. Theileria sergenti infection in dairy cattle. The Journal of Veterinary Medical Science (Japan). 1992 Apr;**54**(2):375-377

[68] Uilenberg G, Perie NM, Spanjer AA, Franssen FF. Theileria orientalis, a cosmopolitan blood parasite of cattle: Demonstration of the schizont stage. Research in Veterinary Science. 1985 May;**38**(3):352-360

[69] Fujisaki K, Kawazu S, Kamio T. The taxonomy of the bovine Theileria spp. Parasitology Today (England). 1994 Jan;**10**(1):31-33

[70] Kubota S, Sugimoto C, Onuma M. Population dynamics of Theileria sergenti in persistently infected cattle and vector ticks analysed by a polymerase chain reaction. Parasitology (England). 1996 May;**112** (Pt 5:437-442)

[71] Ueti MW, Palmer GH, Scoles GA, Kappmeyer LS, Knowles DP. Persistently Infected horses are reservoirs for intrastadial tick-borne transmission of the Apicomplexan parasite Babesia equi. Infection and Immunity. 2008;**76**:3525-3529

[72] Mehlhorn H, Schein E. Redescription of Babesia equi Laveran, 1901 as Theileria equi Mehlhorn, Schein 1998. Parasitology Research (Germany). 1998 Jun;**84**(6):467-475

[73] Allsopp MT, Cavalier-Smith T, De Waal DT, Allsopp BA. Phylogeny and evolution of the piroplasms. Parasitology (England). 1994 Feb;**108** (Pt 2:147-152)

[74] Allsopp MTEP, Allsopp BA. Molecular sequence evidence for the reclassification of some Babesia species. Annals of the New York Academy of Sciences (United States). 2006 Oct;**1081**:509-517

[75] Gunderson JH, Sogin ML, Wollett G, Hollingdale M, de la Cruz VF, Waters AP, et al. Structurally distinct, stage-specific ribosomes occur in Plasmodium. Science (United States). 1987 Nov;**238**(4829):933-937

[76] Sohanpal B, Wasawo D, Bishop R. Cloning of telomere-associated DNA using single-specific-primer polymerase chain reaction provides evidence for a conserved sequence directly adjacent to Theileria parva telomeric repeats. Gene (Netherlands). 2000 Sep;**255**(2):401-409

[77] Shiels BR, McKellar S, Katzer F, Lyons K, Kinnaird J, Ward C, et al. A Theileria annulata DNA binding protein localized to the host cell nucleus alters the phenotype of a bovine macrophage cell line. Eukaryotic Cell (United States). 2004 Apr;**3**(2):495-505

[78] Swan DG, Phillips K, Tait A, Shiels BR. Evidence for localisation of a Theileria parasite AT hook DNA-binding protein to the nucleus of immortalised bovine host cells. Molecular and Biochemical Parasitology (Netherlands). 1999 Jun;**101**(1-2):117-129

[79] Hayashida K, Hara Y, Abe T, Yamasaki C, Toyoda A, Kosuge T, et al. Comparative genome analysis of three eukaryotic parasites with differing abilities to transform leukocytes reveals key mediators of Theileria-induced leukocyte transformation. MBio (United States). 2012;**3**(5):e00204-e00212

[80] Kappmeyer LS, Thiagarajan M, Herndon DR, Ramsay JD, Caler E, Djikeng A, et al. Comparative genomic analysis and phylogenetic position of Theileria equi. BMC Genomics (England). 2012;**13**:603

[81] Jirku M, Jirku M, Obornik M, Lukes J, Modry D. A model for taxonomic work on homoxenous coccidia: redescription, host specificity, and molecular phylogeny of Eimeria ranae Dobell, 1909, with a review of anuran-host Eimeria (Apicomplexa: Eimeriorina). The Journal of Eukaryotic Microbiology (United States). 2009;**56**(1):39-51

[82] Gibson-Kueh S, Yang R, Thuy NTN, Jones JB, Nicholls PK, Ryan U. The molecular characterization of an Eimeria and Cryptosporidium detected in Asian seabass (Lates calcarifer) cultured in Vietnam. Veterinary Parasitology (Netherlands). 2011 Sep;**181**(2-4):91-96

[83] Yang R, Fenwick S, Potter A, Elliot A, Power M, Beveridge I, et al. Molecular characterization of Eimeria species in macropods. Experimental Parasitology (United States). 2012 Oct;**132**(2):216-221

[84] Chapman HD, Barta JR, Blake D, Gruber A, Jenkins M, Smith NC, et al. A selective review of advances in coccidiosis research. Advances in Parasitology (England). 2013;**83**:93-171

[85] Jirku M, Kvicerova J, Modry D, Hypsa V. Evolutionary plasticity in coccidia - striking morphological similarity of unrelated coccidia (apicomplexa) from related hosts: Eimeria spp. from African and Asian Pangolins (Mammalia: Pholidota). Protist (Germany). 2013 Jul;**164**(4):470-481

[86] Kvicerova J, Hypsa V. Host-parasite incongruences in rodent Eimeria suggest significant role of adaptation rather than cophylogeny in maintenance of host specificity. PLoS One (United States). 2013;**8**(7):e63601

[87] Blake DP. Eimeria genomics: Where are we now and where are we going? Veterinary Parasitology (Netherlands). 2015 Aug;**212**(1-2):68-74

[88] Long PL, Millard BJ, Joyner LP, Norton CC. A guide to laboratory techniques used in the study and diagnosis of avian coccidiosis. Folia Veterinaria Latina (Italy). 1976;**6**(3):201-217

[89] Revets H, Dekegel D, Deleersnijder W, De Jonckheere J, Peeters J, Leysen E, et al. Identification of virus-like particles in Eimeria stiedae. Molecular and Biochemical Parasitology (Netherlands). 1989 Oct;**36**(3):209-215

[90] Novilla MN, Carpenter JW. Pathology and pathogenesis of disseminated visceral coccidiosis in cranes. Avian Pathology (England). 2004 Jun;**33**(3):275-280

[91] Reid AJ, Blake DP, Ansari HR, Billington K, Browne HP, Bryant J, et al. Genomic analysis of the causative agents of coccidiosis in domestic chickens. Genome Research (United States). 2014 Oct;**24**(10):1676-1685

[92] Chapman HD, Shirley MW. The Houghton strain of Eimeria tenella: A review of the type strain selected for genome sequencing. Avian Pathology (England). 2003 Apr;**32**(2):115-127

[93] Shirley MW, Smith AL, Tomley FM. The biology of avian Eimeria with an emphasis on their control by vaccination. Advances in Parasitology (England). 2005;**60**:285-330

[94] Shirley MW, Harvey DA. A genetic linkage map of the apicomplexan protozoan parasite Eimeria tenella. Genome Research (United States). 2000 Oct;**10**(10):1587-1593

[95] Ling K-H, Rajandream M-A, Rivailler P, Ivens A, Yap S-J, Madeira AMBN, et al. Sequencing and analysis of chromosome 1 of Eimeria tenella reveals a unique segmental organization. Genome Research (United States). 2007 Mar;**17**(3):311-319

[96]   Dubey JP, Carpenter JL, Speer CA, Topper MJ, Uggla A. Newly recognized fatal protozoan disease of dogs. Journal of the American Veterinary Medical Association (United States). 1988 May;**192**(9):1269-1285

[97]   Dubey JP, Barr BC, Barta JR, Bjerkas I, Bjorkman C, Blagburn BL, et al. Redescription of Neospora caninum and its differentiation from related coccidia. International Journal for Parasitology (England). 2002 Jul;**32**(8):929-946

[98]   McCann CM, Vyse AJ, Salmon RL, Thomas D, Williams DJL, McGarry JW, et al. Lack of serologic evidence of Neospora caninum in humans, England. Emerging Infectious Diseases (United States). 2008 Jun;**14**(6):978-980

[99]   Dubey JP, Schares G, Ortega-Mora LM. Epidemiology and Control of Neosporosis and Neospora caninum. Clinical Microbiology Reviews. 2007;**20**:323-367

[100] Davison HC, Otter A, Trees AJ. Estimation of vertical and horizontal transmission parameters of Neospora caninum infections in dairy cattle. International Journal for Parasitology (England). 1999 Oct;**29**(10):1683-1689

[101] Trees AJ, Davison HC, Innes EA, Wastling JM. Towards evaluating the economic impact of bovine neosporosis. International Journal for Parasitology (England). 1999 Aug;**29**(8):1195-1200

[102] Reid AJ, Vermont SJ, Cotton JA, Harris D, Hill-Cawthorne GA, Konen-Waisman S, et al. Comparative genomics of the apicomplexan parasites Toxoplasma gondii and Neospora caninum: Coccidia differing in host range and transmission strategy. PLoS Pathogens (United States). 2012;**8**(3):e1002567

[103] Hornok S, Mester A, Takacs N, Baska F, Majoros G, Fok E, et al. Sarcocystis-infection of cattle in Hungary. Parasites & Vectors (England). 2015;**8**:69

[104] Blazejewski T, Nursimulu N, Pszenny V, Dangoudoubiyam S, Namasivayam S, Chiasson MA, et al. Systems-based analysis of the Sarcocystis neurona genome identifies pathways that contribute to a heteroxenous life cycle. MBio (United States). 2015;**6**(1)

[105] Cowper B, Matthews S, Tomley F. The molecular basis for the distinct host and tissue tropisms of coccidian parasites. Molecular and Biochemical Parasitology (Netherlands). 2012 Nov;**186**(1):1-10

[106] Dubey JP, Lindsay DS, Saville WJ, Reed SM, Granstrom DE, Speer CA. A review of Sarcocystis neurona and equine protozoal myeloencephalitis (EPM). Veterinary Parasitology (Netherlands). 2001 Feb;**95**(2-4):89-131

[107] Fayer R, Esposito DH, Dubey JP. Human infections with Sarcocystis species. Clinical Microbiology Reviews (United States). 2015 Apr;**28**(2):295-311

[108] Dubey JP, Lindsay DS. Neosporosis, toxoplasmosis, and sarcocystosis in ruminants. Veterinary Clinics of North America: Food Animal Practice. (United States). 2006 Nov;**22**(3):645-671

[109] More G, Pantchev A, Skuballa J, Langenmayer MC, Maksimov P, Conraths FJ, et al. Sarcocystis sinensis is the most prevalent thick-walled Sarcocystis species in beef on sale for consumers in Germany. Parasitology Research (Germany). 2014 Jun;**113**(6):2223-2230

[110] Dubey JP, Fayer R, Rosenthal BM, Calero-Bernal R, Uggla A. Identity of Sarcocystis species of the water buffalo (Bubalus bubalis) and cattle (Bos taurus) and the suppression of Sarcocystis sinensis as a nomen nudum. Veterinary Parasitology (Netherlands). 2014 Sep;**205**(1-2):1-6

[111] Chen X, Zuo Y, Rosenthal BM, He Y, Cui L, Yang Z. Sarcocystis sinensis is an ultrastructurally distinct parasite of water buffalo that can cause foodborne illness but cannot complete its life-cycle in human beings. Veterinary Parasitology (Netherlands). 2011 May;**178**(1-2):35-39

[112] Saito M, Shibata Y, Ohno A, Kubo M, Shimura K, Itagaki H. Sarcocystis suihominis detected for the first time from pigs in Japan. The Journal of Veterinary Medical Science (Japan). 1998 Mar;**60**(3):307-309

[113] Miller MA, Crosbie PR, Sverlow K, Hanni K, Barr BC, Kock N, et al. Isolation and characterization of Sarcocystis from brain tissue of a free-living southern sea otter (Enhydra lutris nereis) with fatal meningoencephalitis. Parasitology Research (Germany). 2001 Mar;**87**(3):252-257