Recent advances in molecular characterization of *Sarcocystis* species in some meat producing animals: an updated review

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Abstract

Sarcocystosis is a parasitic disease caused by *Sarcocystis* species that infect humans and animals. It is prevalent in small ruminants like sheep and goats worldwide and causing pathogenic impacts that lead to economic losses owing to carcass condemnation, abortion, and death. Recently, several molecular and phylogenetic analyses have been developed to differentiate *Sarcocystis* species including, the 18S rRNA, 28S rRNA, 18S rDNA, and ITS-1 region. In recent years, the mitochondrial cytochrome c oxidase subunit 1 (cox-1) was successfully used for this purpose. The DNA barcoding using the *cox*1 gene is a reliable tool to distinguish and identify the main *Sarcocystis* genotypes. Therefore, several studies confirmed that the *cox*1 gene is a promising DNA marker for studying the genus *Sarcocystis*. The current review aims to highlight the molecular methods that exist for the identification of *Sarcocystis* species. The results showed that the *Sarcocystis* species of sheep and goats were genetically close related and may be considered as sibling strains, as well as the cross-infection may happen among them. Consequently, the host specificity of several *Sarcocystis* species is questionable. The findings additional emphasized that experimental transmission investigations within the proposed definitive host are required to confirm the characteristics and host ranges of the *Sarcocystis* spp. in sheep and goats. The current review represents updated knowledge about molecular discrimination of *Sarcocystis* species in small ruminants by reviewing and analyzing the recent articles in this aspect.

Keywords: *Sarcocystis* species, Small ruminants, Molecular identification, PCR

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Introduction

*Sarcocystis* is a coccidian parasite related to the phylum Apicomplexa, class Sporozoasida, order Eucoccidiorida, family Sarcocystidae and subfamily Sarcocystina (Levine, 1986; Dubey et al., 2016). *Sarcocystis* was firstly recorded by Friedrich Miescher in 1843 as a white thread-like structure within the skeletal muscular tissue of a deer mouse from his house in Switzerland, therefore, it is called
Miescher’s tubules. The name of *Sarcocystis* derived from Greek, Sarkos means flesh and Kystis meaning bladder, which refers to the encysted stage in mammalian muscular tissue (Dubey et al., 2016). Approximately 196 *Sarcocystis* species are valid, but just 26 of them have a well-known life cycle. *Sarcocystis* have a wide range of animals that can serve as final hosts and the types of animals that can act as intermediate hosts, which distinguish it from *Neospora caninum* and *Toxoplasma gondii* (Dubey et al., 2016; Lindsay and Dubey, 2020). Sarcocystosis is a world-widely distributed protozoan disease that infects different kinds of mammals, birds, and reptiles. Several species of *Sarcocystis* are pathogenic that result in a severe disease, which can lead to abortion and carcasses condemnation in meat-producing animals, also some species are described as zoonotic (Dubey et al., 2015). Small ruminants as meat-producing animals are one of the main divisions of the food supply chain for humans in most countries and infected with various economically significant parasitic diseases, including sarcocystosis and *Eimeria* spp. infection (Latif et al., 1999; Hassanan et al., 2020).

Globally, a high prevalence of sarcocystosis was recorded in sheep such as 96.1, 86.5, 81.5-90, 100 and 95.3% in Brazil, Izmir-Turkey, Saudi Arabia, Iran, and Egypt, respectively (Beyazit et al., 2007; Dehaghi et al., 2013; Al-Quraishy et al., 2014; Elmishmishy et al., 2018; Minuzzi et al., 2019). Also, Morsy et al. (2011) showed that 79.4% of goats were infected with microsarcocysts in Egypt. In Iraq, Latif et al. (1999) recorded a percentage of infection in sheep and goats as 97 and 97.4%, respectively. Also, in the north of Iraq, the percentage of infection with microsarcocysts reached 97% in sheep and 100% in goats (Zangana and Hussein, 2017), whereas the infection with macrosarcocystis recorded as 9.5 and 8.8% in both sheep and goats, respectively (Swar and Shnawa, 2020).

Moreover, Barham et al. (2005) observed 97 and 34% of goats were infected with microcysts and macrocysts respectively, in Al-Sulaimany province-Iraq. Several methods have been developed for the diagnosis of sarcocystosis. These methods can be categorized into the macroscopic and microscopic examination, serology, and molecular. This review aims to address the current situation of the recent publications that achieved various molecular analyses to confirm the characterization of *Sarcocystis* species and to highlight the gap in the information regarding sarcocystosis.

**Life cycle stages**

The life cycle of *Sarcocystis* remained unidentified till 1972 when some investigations ultra-structurally investigated the gametogenic and oocyst production of *S. falcula* in poultry within in vitro model (Fayer, 1972; Rommel et al., 1972). The life cycle of *Sarcocystis* requires two obligatory prey-predator hosts for its completion, intermediate host and final host, followed one another successively and described as diheteroxenous parasite (Odening, 1998) (Figure 1). The events occurring in the life cycle are as follows:

![Life cycle of Sarcocystis spp. of small ruminants by schematic line-draw (Modified from Lindsay and Dubey, 2020).](image-url)
Asexual stages

It is found only in the intermediate host, which is mostly a prey animal. Infection begins when *Sarcocystis* oocysts or sporocysts from feces of the final host are ingested by these animals with contaminated food or water. Sporozoites are liberated from the oocysts under the effect of trypsin and bile. These sporozoites invade the gut wall and lodge primarily in the endothelial cells of the small arteries. Four cycles of asexual development, called merogony and schizogony are known (Fayer et al., 2015). During the first three stages of development, sporozoites undergo many nuclear divisions followed by segmentation to generate merozoites, which are motile and crescent in shape. Following these cycles of schizonts, the *Sarcocystis* encysts in the muscles and initially forming metrocytes and then transform to bradyzoites. Sarcocysts having bradyzoites refer to the last encysted stage in the skeletal, cardiac, and smooth muscles of herbivores infected animals, which is infectious for carnivorous animals as definitive hosts (Fayer et al., 2015; Dubey, 2015; Dubey et al., 2016; Khater et al., 2020). Two types of sarcocysts can be found in sheep and goats, including microsarcocyst and macrosarcocyst, which related to different species of *Sarcocystis* as shown, in Figure 2 and 3. Till now, there are seven *Sarcocystis* spp. have recorded from domestic sheep, four of them (*S. tenella, S. arieticanis, S. microps*, and *S. mihoensis*) found to use dogs as definitive hosts. Besides the other three (*S.gigantea, S.medusiformis*, and *S. moulei*) that transmitted by felids (Al-Hoot et al., 2005; Kalantari et al., 2016; Gjerde et al., 2020). Goats are intermediate hosts for three common species of *Sarcocystis* (*S. capracanis, S. moulei*, and *S.hircicanis*) (Lindsay and Dubey, 2020). Moreover, *S. gigantea* and *S. tenella* species that commonly infect sheep have identified in goats also (Ghaffar et al., 1989; Hong et al., 2016). All the mentioned species of goats were able to form microsarcocysts and utilize dogs as definitive hosts except *S. moulei* and *S gigantea* form macrosarcocysts and use cats as definitive hosts for completing their life cycles. These findings suggest sheep and goats can probably serve as alternative hosts for several closely related *Sarcocystis* spp.

A and B: thick-walled sarcocyst with radial striations of *S. tenella* in sheep esophagi, scale bar= 500 nm. C: Heavily infected esophagus of goat showed three different sizes of sarcocysts with inflammation, scale bar = 5 μm. D, E, and F: morphologic features of sarcocysts in the esophagus of goats. Showing a thick wall sarcocysts related to *S. capracanis*. All sections were stained with hematoxylin and eosin. D Scale bar = 500, E= Scale bar = 2 μm, and F Scale bar = 500 nm. (Swar, 2020; unpublished results).

Sexual stages

The final host acquires the infection by ingesting mature sarcocysts within the muscles of infected animals (Lindsay and Dubey, 2020). The Sarcocysts are digested in the digestive system of the definitive host and release the bradyzoites, which invade the mucosa of the small intestine. Then, they are changed into both male and female gametes, namely, microgametes and macrogametes, respectively. These
gametes undergo fertilization to form a zygote, which leads to the formation of the non-motile oocysts. The sexual cycle and fertilization need to be completed within one day. The oocysts of this parasite sporulate in the small intestine. The sporulated oocysts are thin-walled contain two sporocysts, each with four sporozoites. Then, it ruptures, releasing the sporocysts into the intestinal lumen that are excreted with the feces. The prepatent and patent periods differ according to Sarcocystis spp., but in most of them, oocysts are first to shed in the feces after 7 to 14 days post acquiring Sarcocysts (Lindsay and Dubey, 2020).

Species infecting sheep and goats

Several species of Sarcocystis infect sheep (Table 1), some of them transmitted by canids and others by feline (cat). The species transmitted by dogs are mainly pathogenic and cause microsarcocyst in skeletal and cardiac muscles of infected animals. These species, like S. tenella, can cause pathologic effects in sheep including, anorexia, anemia, weight loss, abortion, neural symptoms, and death (Dubey et al., 1988; Abdel-Baki et al., 2009). While the species transmitted by cats, for example, S. gigantea, and S. medusiformis produce macrosarcocyst in the muscular tissue like the esophagus, tongue, and larynx also, they are less pathogenic than the microsarcocysts (Collins et al., 1979; Dubey et al., 2016). There are three common species of this parasite in domestic goats: S. caprafelis (synonym S. moulei), S. hiricanis, and S. capracanis (Table 1). Commonly, S. hiricanis and S. capracanis appear as microscopic sarcocysts, whereas S. moulei forms macroscopic cysts (Dubey et al., 2016). Clinically, S. capracanis is more pathogenic than other species (Collins and Charleston, 1979), the infected goats show fever, weakness, anorexia, weight loss, tremors, abortion, and also lead to death in heavy infection (Dubey et al., 1981).

Nowadays, several publications pointed out that the infection of sheep and goats with species of Sarcocystis that are uncommon in these hosts, as the infection of sheep with S. moulei that normally infect goats in Saudi Arabia and Iran (Al-Hoot et al., 2005; Kalantari et al., 2016). Also, the infection of goats with S. gigantea that commonly infects sheep (Ghaffar et al., 1989) and concluded that the goats can be a host of three species of Sarcocystis that are previously classified as S. moulei, including S. ovifelis (S. gigantea). Also, Hong et al. (2016) proved the infection of goats with S. tenella which is commonly known as sheep specific by molecular and ultrastructural investigation in Korea.

Molecular diagnosis of Sarcocystis spp.

Recently, researchers achieved great success in several molecular techniques for identifying different Sarcocystis species that infect livestock animals and are known to be host-specific. Among them, the 18S rRNA, 28S rRNA, 18S r DNA, mitochondrial cytochrome C oxidase subunit 1 gene (cox1), and ITS-1 region (Dubey et al., 2014; Blazejewski et al., 2015; Ng et al., 2015; Hu et al., 2017; El-Morsey et al., 2019) as shown in Table 2.

Table 1. Species infecting sheep and goats according to references

<table>
<thead>
<tr>
<th>Intermediate host</th>
<th>Sarcocystis species</th>
<th>Type of Sarcocyst</th>
<th>Definitive host</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sheep</td>
<td>S. tenella</td>
<td>Microsarcocyst</td>
<td>Dogs, coyote, red fox</td>
<td>Dubey et al., 2016; Lindsay and Dubey, 2020</td>
</tr>
<tr>
<td>Sheep</td>
<td>S. arieticanis</td>
<td>Microsarcocyst</td>
<td>Dogs</td>
<td>=</td>
</tr>
<tr>
<td>Sheep</td>
<td>S. gigantea</td>
<td>Macro-sarcocyst</td>
<td>Cats</td>
<td>=</td>
</tr>
<tr>
<td>Sheep</td>
<td>S. medusiformis</td>
<td>Macro-sarcocyst</td>
<td>Cats</td>
<td>=</td>
</tr>
<tr>
<td>Sheep</td>
<td>S. moulei</td>
<td>Macro-sarcocyst</td>
<td>Cats</td>
<td>Al-Hoot et al., 2005; Kalantari et al., 2016</td>
</tr>
<tr>
<td>Sheep</td>
<td>S. mihoensis</td>
<td>Macro-sarcocyst</td>
<td>Dogs</td>
<td>Saito et al., 1997</td>
</tr>
<tr>
<td>Sheep</td>
<td>S. microps</td>
<td>Macro-sarcocyst</td>
<td>Dogs</td>
<td>Wang et al., 1988</td>
</tr>
<tr>
<td>Goats</td>
<td>S. capracanis</td>
<td>Microsarcocyst</td>
<td>Dogs, coyote, red fox</td>
<td>Dubey et al., 2016; Lindsay and Dubey, 2020</td>
</tr>
<tr>
<td>Goats</td>
<td>S. hiricanis</td>
<td>Microsarcocyst</td>
<td>Dogs</td>
<td>=</td>
</tr>
<tr>
<td>Goats</td>
<td>S. moulei</td>
<td>Macro-sarcocyst</td>
<td>Cats</td>
<td>=</td>
</tr>
<tr>
<td>Goats</td>
<td>S. gigantea</td>
<td>Macro-sarcocyst</td>
<td>Cats</td>
<td>Ghaffar et al., 1989</td>
</tr>
<tr>
<td>Goats</td>
<td>S. tenella</td>
<td>Microsarcocyst</td>
<td>Dogs</td>
<td>Hong et al., 2016</td>
</tr>
</tbody>
</table>
Table-2. Some recent publications in molecular diagnosis of *Sarcocystis* spp from sheep and goats

<table>
<thead>
<tr>
<th>Sarcocystis species and method</th>
<th>Molecular findings</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>Six <em>Sarcocystis</em> spp. Ribosomal RNA sequences.</td>
<td>Two groups of <em>Sarcocystis</em> spp. were identified molecularly. The first group contains two species that need cats as definitive hosts, and the second one has <em>Sarcocystis</em> spp. that the dogs act as definitive hosts for them. Also, <em>Sarcocystis</em> was separated from <em>Toxoplasma</em> and the classification of them as two genera into different subfamilies of the Sarcocystidae was refuted.</td>
<td>Tenter et al., 1992</td>
</tr>
<tr>
<td><em>S. tenella</em> RFLP-PCR genotyping for the 18S rRNA</td>
<td>Twenty-two of 602 Brazilian sheep were positive for <em>Sarcocystis</em> species. Identification of the 18S rRNA gene of <em>S. tenella</em> (GenBank accession number L24383-1).</td>
<td>da Silva et al., 2009</td>
</tr>
<tr>
<td><em>S. gigantea</em> and <em>S. tenella</em> Mitochondrial cytochrome c oxidase subunit I gene (cox1) and the nuclear ssrRNA gene sequences</td>
<td>For the first time established cox1 as a new genetic marker for the identification of <em>Sarcocystis</em> spp. Also, it presented the first molecular characterization of <em>S. gigantea</em> (KC209733) besides <em>S. tenella</em> of sheep in Norway. Results of ssrRNA gene sequences showed that three of the four sequences of microscopic sarcocysts isolated from sheep were indistinguishable (KC209734–KC209736), one nucleotide was incompatible with the fourth sequence (KC209737). Sequence identity in BLAST showed sequences were most similar (99.1% identity) to <em>S. capracanis</em> (L76472), whereas had 96.4% similarity with <em>S. tenella</em> (L24383).</td>
<td>Gjerde, 2013a</td>
</tr>
<tr>
<td><em>S. tenella</em> proved by 18S rRNA gene sequence with PCR-RFLP technique.</td>
<td>RFLP-PCR analysis explained that microscopic cysts were <em>S. tenella</em> in 70% of the tested specimens of sheep from Iran.</td>
<td>Shabhazi et al., 2013</td>
</tr>
<tr>
<td><em>S. gigantea</em> and <em>S. tenella</em> in sheep by the 18s rRNA gene sequence</td>
<td>Genotyping of ten sarcocysts revealed that the pattern of macrosarcocyst identified as <em>S. gigantea</em> and the microsarcocyst is <em>S. tenella</em> in Iranian sheep.</td>
<td>Bahari et al., 2014</td>
</tr>
<tr>
<td><em>S. gigantea</em> and <em>S. medusiformis</em> by the PCR and RFLP techniques.</td>
<td>The results proved that fat macrosarcocysts were <em>S. gigantea</em> as 29.31% and thin macro-sarcocysts were <em>S. medusiformis</em> in 7.52%.</td>
<td>Farhang-Pajuh et al., 2014</td>
</tr>
<tr>
<td><em>S. neurona</em> strain SO SN1 RNA and Genomic DNA Were sequenced</td>
<td>Identified the first genome sequence of <em>S. neurona</em>. The accession number of the nucleotide sequence was SRP052925 in the National Center for Biotechnology Information (<a href="http://www.ncbi.nlm.nih.gov/bioproject/252030">http://www.ncbi.nlm.nih.gov/bioproject/252030</a>)</td>
<td>Blazejewski et al., 2015</td>
</tr>
<tr>
<td><em>S. capracanis</em> by 18S RNA sequences</td>
<td>Microsarcocysts in goats skeletal muscles were characterized as <em>S. capracanis</em></td>
<td>Kutty et al., 2015</td>
</tr>
<tr>
<td><em>S. tenella</em> by 18S rRNA method.</td>
<td>Sequence findings of Sarcocystis spp. in sheep confirmed the presence of <em>S. tenella</em> only in Italy.</td>
<td>Bacci et al., 2016</td>
</tr>
<tr>
<td><em>S. arieticanis</em> and <em>S. capracanis</em> in sheep and goats respectively by 18S ribosomal DNA(r DNA)</td>
<td>Molecular and ultrastructural results proved the first confirmation of <em>S. tenella</em> and <em>S. arieticanis</em> in sheep and <em>S. capracanis</em> in goats in Brazil.</td>
<td>Bittencourt et al., 2016</td>
</tr>
<tr>
<td><em>S. tenella</em> in goats With 18S r DNA sequence</td>
<td>First molecular and ultrastructural documentation of <em>S. tenella</em> in domestic goats in Korea.</td>
<td>Hong et al., 2016</td>
</tr>
<tr>
<td>18S rRNA gene of <em>S. tenella</em></td>
<td>Molecular characterization and phylogeny of <em>S. tenella</em> in sheep in Baghdad-Iraq.</td>
<td>Whaeeb and Faraj, 2016</td>
</tr>
</tbody>
</table>
The first sequenced genome in the genus *Sarcocystis* was related to *S. neurona*. The genome has 127-Mbp and it is more than double the size of other sequenced coccidian genomes (Blazejewski et al., 2015). Tenter et al. (1992) identified two monophyletic groups of *Sarcocystis* species; one of them represents the species that uses the cat as the definitive host, while the second includes the species that require dogs as final hosts for completing their life cycles. Initially, *Sarcocystis spp.* were described as largely host-specific; however, over the last few years, numerous *Sarcocystis* species employing different animals as intermediate hosts were confirmed. As a result, host specificity became questionable.

| S. gigantea and S. moulei in sheep by partial 18S r RNA gene sequences. | Among thirty sequences of DNA sarcocysts, 20 (66.7%), 6 (20%), and 4 (13.3%) specimens were characterized as S. gigantea, S. moulei, and Sarcocystis spp., respectively. The first record of S. moulei in sheep, as well as they, concluded that sheep consider as an alternative host for this species besides goats in Iran. | Kalantari et al., 2016 |
| S. gigantea by analysis of part of 18S r RNA gene sequence | The first documentation of S. gigantea in sheep from Argentina | Gual et al., 2017 |
| Identification of S. tenella, and S. arieticanis by the 18S r RNA gene, 28S r RNA gene, mitochondrial cox1 gene, and ITS-1 region sequences | Genetic characterization of S. tenella, and S. arieticanis by four markers in sheep from China. | Hu et al., 2017 |
| 18S rRNA gene of S. tenella and S. capracanis. | First detection and molecular identification of S. tenella and S. capracanis from sheep and goats in Tunisia | Amairia et al., 2018 |
| 18S RNA gene of S. tenella from sheep | Recorded S. tenella from Egypt in the Gene Bank (accession number KP263759.1.) | Hussein et al., 2018 |
| S. tenella and S. arieticanis Analysis of cox1 gene sequence in sheep. | First molecular confirmation of S. tenella (MH561854) in *Ovis ammon* sheep in China by mitochondrial cox1 gene sequences that consider as an appropriate intermediate host. | Dong et al., 2018 |
| S. tenella and S. capracanis Mitochondrial cox1 sequences | First molecular confirmation of S. tenella and S. capracanis by cox1 gene in sheep and goats respectively, from Saudi Arabia. As well as, they concluded the strong phylogenetic relation between Sarcocystis species from sheep and goats. | Metwally et al., 2019 |
| S. tenella and S. arieticanis in sheep. Sequence by 18S r RNA, 28S r RNA, COX1, and ITS-1 | The first molecular and ultrastructural confirmation of eleven isolates of S. tenella and S. arieticanis from sheep in Egypt under the accession numbers MH413034- MH413040 and MH413045- MH413048 in the Gene Bank. They concluded that COX1 and ITS-1 genes seemed to be the best genetic markers amongst the other tested. Also, this study mentioned to the S. tenella of sheep and S. capracanis the goat’s species as closely related sister species. | El-Morsey et al., 2019 |
| S. tenella, S. arieticanis, S. gigantea, S. medusiformis, and S. mihoensis-like. Cytochrome c oxidase subunit 1 gene (cox1), 18S RNA, and 28S r RNA gene. | Five species of Sarcocystis from sheep were molecularly identified in sheep by three genetic markers. The finding of this study suggested that S. medusiformis, S. gigantea, and S. moulei have genetically sister sequences. All these three species formed macroscocysts in sheep, and utilize the cat as a definitive host for all of them. | Gjerde et al., 2020 |
| S. arieticanis by 18S rRNA gene sequence | First molecular characterization of S. arieticanis in cardiac muscles of sheep in Egypt. Sarcocystis cyst size considered as a significant feature in the classification. | Hussein, 2020 |
Regarding this aspect, in Saudi Arabia, Al-Hoot et al. (2005) identified *S. moulei* from the sheep by ultrastructural study, the species which commonly infect goats. Also, *S. moulei* was confirmed molecularly in sheep by Kalantari et al. (2016) in Iran. In the same regard, *S. capracanis* was recognized in the cerebrospinal fluid of 2 sheep with meningoencephalitis in the United Kingdom (Formisano et al., 2013). Therefore, sheep can serve as an alternative intermediate host for this species besides goats. In addition, in a study regarding sarcocystosis of sheep in Egypt, Elmishmishy et al. (2018) recorded the complete similarity between the isolate of *S. gigantea* from sheep and that of *S. moulei* and suggested the cross-transmission of *S. moulei* between sheep and goats and they are phylogenetically close. Another study also demonstrated that the *S. tenella* of sheep and *S. capracanis* the goat’s species are genetically closely related sister species by ultra-structural and phylogenetic analysis using 18S rRNA, 28S rRNA, COX1, and ITS-1 genetic markers (El-Morsey et al., 2019). In Saudi Arabia, a recent study concluded a strong phylogenetic correlation among Sarcocystis species from sheep and goats (Metwally et al., 2019). Yang et al. (2001) confirmed that morphologically identical species from two different intermediate hosts should be considered the same species. However, many Sarcocystis species seem to have a wider intermediate host option than previously known. Also, more recent findings suggest that *S. medusiformis, S. gigantea, and S. moulei* possess genetically sister sequences. All these species proved to form macrosrccysts in sheep, and the cat is the definitive host for them (Gjerde et al., 2020). This phenomenon has also been observed in the infection of cattle and water buffalo with uncommon Sarcocystis spp. As a result, these investigations lead to the suggestion that Sarcocystis species are non-specific to the host (Jehle et al., 2009; Xiang et al., 2011; Gjerde et al., 2016; Dakhil et al., 2017; El-kady et al., 2018). Gjerde (2013a; 2013b) concluded that cox1 sequences appear to explain better than the ssrRNA gene sequences for characterization of the closely related species of Sarcocystis, and recommended using this novel genetic marker in future studies. Additionally, Gjerde et al. (2016) suggested that the cox1 gene was superior to both 18S and 28S rRNA genes. In the same regard, El-Morsey et al. (2019) confirmed that cox1and ITS-1 genes looked to be the best genetic markers amongst the other tested in the differentiation of the closely related *Sarcocystis* spp. within the intermediate hosts because of their high divergence, as shown in Table 2. Another investigation compared the new sequences of four genetic markers (18S rRNA, 28S rRNA, mitochondrial COX1, and ITS-1) for *S. tenella* and *S. capracanis*, and confirmed that the ITS-1 region could be more useful for distinguishing the closely related *Sarcocystis* spp. owing to its high divergence (Hu et al., 2017). Besides, the same was true for the genetic similarity of sheep and goats infection with *Eimeria* spp., which was recorded by phylogenetic analysis of the ITS-1 sequences of this parasite in Egypt. The sequence of (ITS-1) region of *E. ahsata* was 100% similar to ovine *E. ahsata* and clustered in a single clade with *E. cardinalis* and *E. faurei*. On the other hand, *E. arloingi* was 100% identical to *E. arloingi* of goat and clustered with bovine *E. ellipsoidalis* (Hassanen et al., 2020).

**Conclusion**

In conclusion, the information about *Sarcocystis* spp. is still not highly clarifying. However, several publications related to the biological aspect of sarcocystosis have been achieved, whereas there are numerous ongoing researches on molecular and ultrastructural diagnosis still perform globally. The 18S rRNA ribosomal gene and mitochondrial cytochrome c oxidase subunit I (cox1) genes were the most analysis used for molecular characterization and phylogenetic analysis of Sarcocystis spp. The results of some reviewed articles showed that the Sarcocystis species of sheep and goats were closely related and may consider as sibling strains, as well as the cross-infection, may happen among these animals. Therefore, the host specificity of several Sarcocystis species is questionable. The findings further emphasize that experimental transmission investigations within the proposed definitive host are required to confirm the characteristics and host ranges of the Sarcocystis spp. within these two ruminants.

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**References**


Swar SO, 2020 Molecular and ultrastructural characterization of Sarcocystis species in domestic sheep and goats from Soran city, Erbil-Iraq. Unpublished PhD Thesis. Department of Biology, Faculty of Science, Soran University, Iraq.

Contribution of Authors

Swar SO: Literature review and wrote the first draft of the manuscript
Shnawa BH: Conceived idea, manuscript final writing, editing and approval