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### Food safety and Public health

# Prevalence, Histopathology and Molecular Characterization of *Sarcocystis* species Infecting Buffaloes in Menoufia Governorate, Egypt

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## ABSTRACT

The present study was done to assess the infection rate, histopathological and molecular characterization of *Sarcocystis* species infecting buffaloes in Menoufia governorate, Egypt. Different muscles of 3513 slaughtered buffaloes in three abattoirs from Menoufia governorate were inspected by naked eye. Histopathological examination was applied on infected muscles with cysts. The DNA from each individual sarcocysts was extracted, amplified and sequenced. The results indicated that the total infection rate of sarcocystosis in examined buffaloes was (12.87 %). The prevalence in females was higher (20.23%) than males was (10.42%). The most affected muscles with *Sarcocystis* spp. cysts were esophagus. There was slight variation in the prevalence of sarcocystosis between the three abattoirs. The occurrence of sarcocystosis was slightly higher in winter and spring seasons than Autumn and Summer seasons. The amplified DNA was yielded the expected band size. The sequence of Sarcocystis cyst in this study was aligned with similar sequences of Sarcocystis spp. which was deposited in gene bank. The sequence of 18S rRNA was highly identical (94-99%) to sequences of Sarcocystis fusiformis from Egypt and other countries. The phylogenetic tree revealed that *Sarcocystis* in the current study was founded in the same genetic clade with the gene bank sequences of *Sarcocystis fusiformis*. In conclusion, the infection rate of sarcocystosis was low in current study compared with previous studies may be due to the enhanced or proper disposal of carnivores and human feces.

**Keywords:** *Sarcocystis* spp., Buffaloes. Prevalence, histopathology, molecular characterization, Egypt.

#### INTRODUCTION

*Sarcocystis* species were a coccidian protozoan which caused cyst in tissues, its life cycle had two hosts, including herbivorous (intermediate host) and carnivorous (definitive host) (Soulsby, 1982). Sarcocystis spp. were host specific and very common in animals (Dubey et al., 1989). Several species could infect the same host (Dubey et al., 1996; and Bhatia, 2000). Sarcocystosis disease was parasitic and zoonotic which was frequently common in cattle and buffaloes. S. hominis was one of the parasitic diseases that was significantly affects public health. Human infections were commonly caused by meats and meat products and infect people when they tissue cysts consume contain bradyzoites (Juyal and Bhatia 1989). Buffaloes were identified as an intermediate host S. dubeyi, dogs were a definitive host for S. levinei and cats were definitive hosts for S. fusiformis and S. buffalonis (Hilali et al., 2011). Bovine eosinophilic myositis (BEM) was an inflammatory response which caused degenerated muscle fibers and condemnation of meat could be resulted from Sarcocystis species. Concerned to macroscopic cysts of S. hirsute, it caused financial losses during the process of meat detection (Dubey and Rosenthal 2023). Concerned histopathological to examination there was fibrosis which caused the white color, degradation of and the concentration tissue of eosinophil granulocytes was produced the green color of the infected muscles (Dubey and Rosenthal 2023). Sarcocystis could be examined in through macroscopic muscle identification of sarcocysts or through the histological study (Urghurt et al., 1996). Customary meat inspection ways in abattoirs were not accurate for determination of the parasite prevalence due to there was small So, strongly sarcocysts. it was recommending the need to use microscopical identification in the serological (ELISA) and postmortem for identification of the disease in Egypt (Metwally et al., 2014). Meat may be detected by cutting meat itself in hydrochloric acid, pepsin and then concentrated the content for presence of bradyzoites (Fayer, 2004). Detection of sporocysts in dogs faces or cats could be helpful in the diagnosis (Urqhurt et al., 1996). The application

of control measures of sarcocystosis on animals' food, hygiene, farm pets and control of uncooked meat all help limitation of the infection (Urghurt et al., 1996; and Fayer, 2004). PCR had been applied for identification of the Sarcocysts. S. cruzi and S. hominis from cattle depending on 18S rRNA gene (Fischer and Odening 1998). Using 18S ribosomal RNA on sarcocystis from buffalo gave nearly identical sequence to S. hominis and this was mean that multiple species that affect ruminant were served as an intermediate host and also a potential source for human infection by this parasite (Yang et al., 2001). This study was focused on the infection rate. histopathology and molecular study of sarcocystis spp. in slaughtered buffaloes in Menoufia province, Egypt. MATERIAL AND METHODS

# 1. Sample collection and study area

This work was brought through the year of 2022 from January to December in Menoufia governorate, Egypt, to conclude the prevalence of Sarcocysts in buffaloes at 3 abattoirs (Ashmoun, El-Shohada and Quisna) in Menoufia, Egypt.

A total of 3513 buffaloes (875 females and 2638 males) were examined macroscopically by naked eye for the immediacy of the parasite. The examined buffaloes were divided into two groups (1st group from 2 to 3 years and 2nd group over 5 years).

The esophagus, pharyngeal, diaphragm, neck, heart, masseter, tongue, thigh and other muscles were investigated grossly for presence of macroscopic sarcocysts.

For microscopic finding of the sarcocystis cysts, specimens of infected tissue were putted and compressed between two slides then were examined under microscope (Mowafy, 1993).

2. Histopathological examination

Infected muscle samples were fixed in formalin (10%). After three days, the muscular tissues were dehydrated, embedded in paraffin. and sectioned to  $(3\mu m)$  for staining by hematoxylin and eosin stain (H&E) (Bancroft and Gamble 2002).

# 3. Sample preparation and DNA extraction

The recovered sarcocysts were washed at first several times with Phosphate Buffer Saline. DNA was pried from each individual sarcocysts from infected buffaloes by using Qiagen DNeasy Tissue and Blood kit® according to manufacturer guidance.

## 4. PCR analysis

Partial gene sequence of 18S rRNA of *Sarcocystis fusiformis* was amplified by using the forward primer (5<sup>-</sup>-CGCCCTTTTAGTGAGGGTGT3<sup>-</sup>)

(5` and primer reverse TACGAATGCCCCCAACTGTC 3`) (El-Seify et al., 2014). The PCR reactions were concluded in 25 µl volume which was contained 12 µl of Emerald Amp® GT PCR Master Mix [Takara Biotechnology], 1 µl of the DNA genome, 10 µl of sterile distilled water (DW) and 1 µl from each primer. The annealing was done at 55 °C for 40 sec. and extension was at 72 °C for 45 sec. An initial denaturation step at 94 °C for 5 min and 35 cycles of final denaturation at 94 °C for 45 sec. and a final extension step at 72 °C for 10 min. Products were screened by electrophoresis in 1.5 % agarose gels.

#### <u>5. DNA Sequencing, Sequence</u> <u>Alignment and phylogenic Analysis</u>

The expected band size was at (600 bp), DNA was purified by using extraction kit gel and sequenced. The18S rRNA sequences were blasted with the NCBI BLAST methods and the sequence was aligned in GenBank. The phylogenetic tree was premediated by the neighbor-joining. The 18S rRNA gene sequence of the parasite

from Menoufia, Egypt was used to create a tree with other sequences from the GenBank.

## RESULTS

# <u>1. Infection rate of Sarcocystis in buffaloes:</u>

A total number of 3513 buffalo carcasses (875 females and 2638 males) were all examined grossly through three abattoirs from Menoufia governorate, Egypt throughout one year to detect the prevalence of *Sarcocystis* species.

The overall prevalence with *Sarcocystis* spp. in buffaloes was 12.87% (452 out of 3513). The prevalence in males was 10.42 % (275 out of 2638), while the prevalence in females was 20.23 % (177 out of 875) (Table 1).

Result recorded in Table (2) revealed the prevalence of sarcocystosis (three abattoirs) in Menoufia province. Prevalence of *Sarcocystis* spp. was 10.9%, 14.38 % and 11.38 % in Ashmoun, El shohada and Quesna abattoirs, respectively. Females showed higher infection rates than males in different three abattoirs.

The distribution of the *Sarcocystis* species in slaughtered male buffaloes was 145 (52.72%) in esophagus and pharyngeal muscles, and 130 (47.27%) in the tongue, while in females were 135 (48.74%) in esophagus and pharyngeal muscles 142 (51.26%) in the tongue (Table 3).

Regarding to seasonal prevalence in Table (4), the females in different seasons recorded higher infection rate with sarcocystosis than males. The prevalence of sarcocystosis was higher in winter (14.82 %) and spring (14.27%) than Autumn (10.67%) and summer (10.27 %), respectively.

**Table 1.** Overall prevalence of *Sarcocystis* species cysts in buffaloes carcasses at 3 abattoirs in Menoufia governorate

sex	No. examined	No. infected	percent of infection
Male	2638	275	10.42 %
Female	875	177	20.23 %
Total	3513	452	12.87 %

**Table 2.** The infection rate of *Sarcocystis* spp. cysts in examined buffaloes carcasses of 3 abattoirs in Menoufia governorate.

Abattoir	Examined carcasses			Infected carcasses				Total		
	Males	Females	Total	Males		Females		Infected non		
				Ν	%	Ν	%		infected	%
Ashmoun	637	116	753	55	8.63	21	18.1	76	677	10.09
										%
El-	811	579	1390	120	14.7	100	17.27	220	1170	14.38
shohada					9					%
Quesna	1100	270	1370	100	9.09	56	20.74	156	1214	11.38
										%
Total	2538	975	3513	275	10.4	177	19.48	452	3061	12.87
					2					%

Table 3. The distribution of *Sarcocystis* spp. cysts in different muscles of infected buffaloes carcasses.

Infected organ	Male	Female	Total
Esophagus and Pharyngeal muscle	145 (52.72%)	135 (48.74% )	280
Tongue	130 (47.27%)	142 (51.26%)	272
Total	275	277	552

Season	Genus Male F			emale Total			Percent of infection	
	Infected	Non infected	Infected	Non infected	Infected	Non infected	total	
Autumn	45	454	26	140	71	594	665	10.67%
Winter	85	620	57	196	142	816	958	14.82%
Spring	95	764	65	197	160	961	1121	14.27%
Summer	50	524	29	166	79	690	769	10.27%
Total	275	2362	177	699	452	3061	3513	12.87%

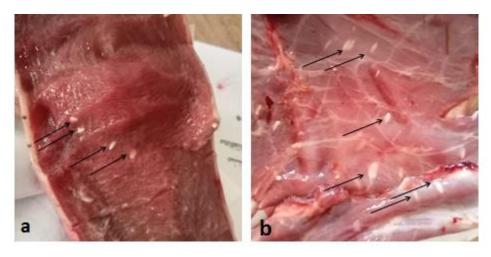
**Table 4.** Seasonal infection rate of *Sarcocystis* spp. cysts in buffaloes carcasses at 3 abattoirs in Menoufia governorate.

#### <u>2. Morphological and histopathological examination of Sarcocystis spp. in</u> <u>buffaloes:</u>

The macroscopic *Sarcocystis* cyst appeared grossly as a spindle shape cyst, white colored and distributed under the serosal membrane between the muscle bundles parallel to the longitudinal axis of the muscle fiber, their measurements were ranged from  $0.3-2.5 \times 0.2-0.7$  cm. The most infected muscles were esophagus and tongue muscle (Fig.1).

Microscopically, the cyst had a thick prominent wall (Fig.2). Numerous thin

septa were attached from the wall of cyst which was separated the cyst into irregular several chambers filled with oval, elongated and other large organisms, which were found as bradyzoites. The bradyzoites were crowded peripherally, while in the central part of the sarcocysts, there was a small area where the septa inhibited very few bradyzoites, moreover there was no inflammatory response around the sarcocysts was associated.



**Fig. 1.** Photograph of several macroscopic *Sarcocystis* spp. cysts in Tongue (a) and esophagus (b) of infected buffalo carcass

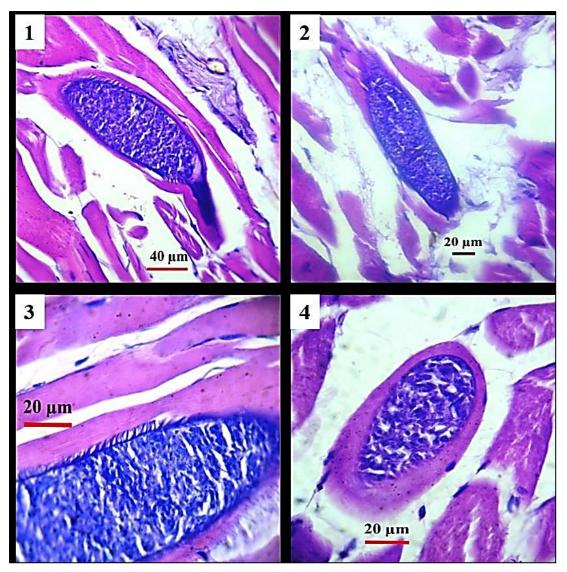


Fig. 2. Micrograph of *Sarcocystis* species cyst in muscle of infected buffalo (H & E stained)

#### <u>3. Molecular characterization of</u> <u>Sarcocystis species</u>

The DNA which extracted was then amplified from each macroscopic cyst by using forward and reverse primers of targeted 18S ribosomal RNA (18S rRNA). The amplified DNA was yielded band at 600 bp as in (Fig. 3).

Sequences of Sarcocystis cyst in current study was aligned with the

sequences of similar Sarcocystis species. which deposited in gene bank. The sequence of 18S rRNA was highly (about 94-99%) identical with sequences of Sarcocystis fusiformis from Egypt and other countries. The phylogenetic tree revealed that Sarcocystis in the current study was founded in the same genetic clade with the Sarcocystis fusiformis in gene bank (Fig.4).

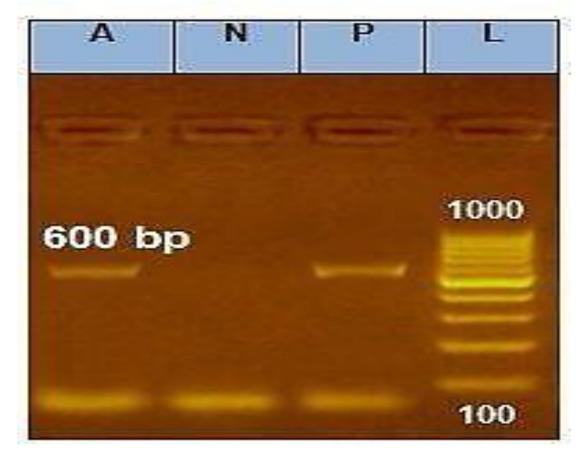


Fig. 3. Gel electrophoresis of the 18S rRNA gene of *S. fusiformis*. DNA size marker of 100bp.

	MN334329.1:749-1262 Sarcocystis silva isolate CcES2.2 small subunit ribosomal RNA gene partial sequence							
	LC481015.1:764-1277 Sarcocystis japonica D248-2 gene for 18S ribosomal RNA partial sequence							
	GQ250970.1:683-1191 Sarcocystis tarandi isolate St3RtN clone 4 18S ribosomal RNA gene partial sequence							
	64 KX643338.1:748-1262 Sarcocystis silva isolate CcLttva2 18S ribosomal RNA gene partial sequence							
	KY019057.1:783-1291 Sarcocystis silva isolate Ccl4.16 clone 2 18S ribosomal RNA gene complete sequence							
	LC481018.1:774-1282 Sarcocystis cf. tarandi D245-3 gene for 18S ribosomal RNA partial sequence							
	MN334328.1:748-1262 Sarcocystis silva isolate CcLT33.3 small subunit ribosomal RNA gene partial sequence							
	OQ507389.1:1-494 Sarcocystis fusiformis strain Sarc3-Bu-AZ-DRC small subunit ribosomal RNA gene partial sequence							
	KR186119.1:734-1296 Sarcocystis fusiformis isolate Bb4.5 clone 2.18S ribosomal RNA gene complete sequence							
	KR186123.1:726-1291 Sarcocystis fusiformis isolate Bb5.1 clone 7 18S ribosomal RNA gene complete sequence							
	KJ778019.1:568-1125 Sarcocystis cafferi isolate 13Z122-Animal 18S ribosomal RNA gene partial sequence							
64	AF176926.1:679-1249 Sarcocystis fusiformis strain 2f1 18S ribosomal RNA gene partial sequence							
-	KF874628.1:529-1086 Sarcocystis sp. 1. ES-2013 18S ribosomal RNA gene partial sequence							
	KR186117.1:734-1293 Sarcocystis fusiformis isolate Bb3.4 clone 3 18S ribosomal RNA gene complete sequence							
	KR186122.1:734-1296 Sarcocystis fusiformis isolate Bb5.1 clone 5 18S ribosomal RNA gene complete sequence							
	U03071.1:734-1297 Sarcocystis fusiformis 18S rRNA							
	SARCOCYST EGYPT 2023							
	KJ778011.1:568-1125 Sarcocystis cafferi isolate 13Z122-2B 18S ribosomal RNA gene partial sequence							
	KR186120.1.731-1296 Sarcocystis fusiformis isolate Bb5.1 clone 1 18S ribosomal RNA gene complete sequence							
	MW324480.1:31-593 Sarcocystis fusiformis isolate SF-buff small subunit ribosomal RNA gene partial sequence							
	OQ507387.1:1-494 Sarcocystis fusiformis strain Sarc1-Bu-AZ-DRC small subunit ribosomal RNA gene partial sequence							
ŝ	KU247912.1:753-1301 Sarcocystis buffalonis isolate Bb18.1 clone 9 18S ribosomal RNA gene complete sequence							
	KU247911.1:759-1307 Sarcocystis buffalonis isolate Bb18.1 clone 8 18S ribosomal RNA gene complete sequence							
	KU247910.1:753-1304 Sarcocystis buffalonis isolate Bb18.1 clone 7 18S ribosomal RNA gene complete sequence.							
	KU247907.1:752-1303 Sarcocystis buffalonis isolate Bb18.1 clone 4 18S ribosomal RNA gene complete sequence.							
	AF176940.1:701-1252 Sarcocystis hirsuta strain 21kmo1 18S ribosomal RNA gene partial sequence							
	KU247906.1:753-1304 Sarcocystis buffalonis isolate Bb18.1 clone 3 18S ribosomal RNA gene complete sequence.							
	KT901160.1:748-1304 Sarcocystis hirsuta isolate B6.3 clone 5 18S ribosomal RNA gene complete sequence							
	KT901162.1:759-1310 Sarcocystis hirsuta isolate B6.3 clone 7 18S ribosomal RNA gene complete sequence							
i	AF176941.1:701-1252 Sarcocystis hirsuta strain 22kmo3 18S ribosomal RNA gene partial sequence							
6	KC209741.1:721-1272 Sarcocystis hirsuta isolate B5.1 18S ribosomal RNA gene partial sequence							

0.0010

Fig. 4. Phylogenetic tree of *Sarcocystis fusiformis* 18S rRNA gene from Menoufia, Egypt.

#### DISCUSSION

The current study was showed the infection rate and molecular characterization of Sarcocystis fusiformis in Egyptian buffaloes in Menoufia province, Egypt. The total prevalence of *S*. fusiforms in slaughtered buffaloes was (12.87%) and this rate was decrease than that of Mohanty et al., (1995) who found that the infection rates with S. fusiforms was (87%) in India, Said, (1996) who

found the infection rate of *S. fusiforms* was (76.8 %) in Beni-suef, Egypt, Fawaz, (1998) who found that the infection rate of *S. fusiforms* was in Qena (72.6 %). Latif et al., (1999) who found that the prevalence of *S. fusiforms* was (82.9%) in Iraq, and El-Dakhly et al., (2011) who mentioned that the infection rate of *S. fusiforms* was (78.6 %) in Beni-suef, Egypt,

The low infection rate of sarcocystosis in the current study may be due to ways that used in diagnosis of infection that depend on the detection of sarcocysts by using naked eye during meat inspection.

Concerning to the allocation of sarcocysts in variant organs, the Sarcocystis species in the present study were infect different muscles as pharyngeal oesophagus, tongue, muscle and the esophagus was the most infected organs with Sarcocystis spp., this finding agreed with previous studies Huong, (1999); Latif et al., (1999); Orvan et al., (2010); Abdel-Baky's, (2011); Abu-Elwafa et al., (2015b); JyothiSree et al., (2017); El-Bahy et al., (2019); Ardalan (2020) and Gareh et al., (2020) who reported that the most infected organs were oesophagus, heart and tongue.

In this study, there was no parasite cysts were discovered in heart muscles, this finding disagree with El-Dakhly et al. (2011) and Ahmed et al., (2016) who recorded that occurrence of the parasitic *Sarocystis* in variant organs of buffaloes didn't hold a special pattern.

In current study, the prevalence was greater in females (20.23%) than males (10.42%) and this finding agreed with Ahmed et al., (2016); Ibrahim et al., (2018) and El Shanawany et al., (2019) who reported that the prevalence of Sarocystis cysts was affect females more than males, and also agreed with Ghorbanpoor et al., (2007); Oryan et al., (2010) and Ibrahim et al., (2018) who found that female animals was exhibited greater infection rate than males.

The difference between sex in the present study could be due to the stress factors that affect females as pregnancy, lactation and the immune system.

The infection rate of sarcocystosis in the present study was greater in winter (14.82 %) and spring (14.27%) than Autumn (10.67%) and summer (10.27%) seasons and the females were recorded greater prevalence than males, this detection disagreed with Abdel-Baky, (2011) who found that there was no contrast in the infection rate of Sarcocystis parasite species in buffalo carcasses per season.

the current study, molecular In characterization of Sarcocystis parasite by using primers of 18S rRNA gave a band at 600 base pair. The sequence of the primer was highly identical (about 94-99%) with sequences of Sarcocystis fusiformis from Egypt and other countries. The phylogenetic tree revealed that Sarcocystis in the current study was recorded in the same genetic clade with the Sarcocystis fusiformis in gene bank, this finding agrees with Holmdahl et al., (1999); Li et al., (2002) and Jehle et al., (2009) who reported that the18S had targeted gene for the characterization and detection of the related Sarcocystis species and for the phylogenic analysis also, also agreed with Olsen and Woese (1993) who found that the gene regions of 18S rRNA was used to increase the same gene region in similar parasite spp. Because of its structure which allowed the extension in different phylogenic analysis studies, and agreed with Holmdahl et al., (1999) who stated that the 18S primer gene was gave an identity value with other species, it was an important to detect Sarcocystis based on molecular analysis of its gene, and also agreed with Williams et al.. (1990) who found that the molecular techniques had been useful in the determination of Sarcocystis spp., in intermediate hosts. These methods were provided specific and more sensitive ways for diagnosis than conventionally one in the epidemiological.

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