Egypt. J. Vet. Sci. **Vol. 55,** No. 5, pp. 1295-1306 (2024)

Egyptian Journal of Veterinary Sciences

https://ejvs.journals.ekb.eg/

Morphology and Phylogenetic Variation in Some Flesh Flies of the Genus *Sarcophaga* (Diptera: Sarcophagidae) from Egypt

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Abstract

FLESH FLIES are important in forensic investigations as their larvae can estimate the post-mortem interval (PMI) in human remains. However, before using life-history traits as evidence, correct species identification is necessary. Flesh flies also transmit enteropathogens to humans as diarrheal diseases and cause myiasis in cattle. Identifying adult flesh flies is challenging due to their similar appearance, and it is primarily based on male genitalia morphology. Therefore, studying the phylogenetic relationships within this group is necessary. In this study, a phylogenetic analysis of 23 species representing 9 subgenera of the genus *Sarcophaga* from Egypt was conducted. It involved 56 external morphological and male genitalia characteristics. The results revealed that *Helicophagella* and *Heteronychia* clades are monophyletic groups, while *Liopygia* and *Liosarcophaga* clades are paraphyletic groups. The remaining subgenera consist of a single species each, known as monotypic groups. The study also supported sister group relationships between *Sarcophaga* and *Helicophagella* subgenera, *Liopygia* and *Phytosarcophaga* subgenera, and *Bercaea* and *Liosarcophaga* subgenera. The results revealed different groupings and supported sister group relationships between certain subgenera. Morphological and male genitalia characteristics played a significant role in species differentiation. Overall, these traits serve as reliable indicators for studying variation among *Sarcophaga* species.

Keywords: Flesh flies, Phylogenetic analysis, systematics, Egypt.

Introduction

The Family Sarcophagidae comprise a large and diverse group of flies, consisting of 173 genera and over 3094 described species worldwide [1-2]. These flies primarily distributed across tropical or temperate regions, with a rapid decrease in species number in the latitude region. Few subarctic species of Sarcophagidae are known, and none are found in the treeless tundra [2-3]. The largest subfamily of Sarcophagidae is Sarcophaginae, which contains over 2200 species arranged into 51 genera [1]. Globally, the genus *Sarcophaga* is a diverse group containing approximately 800 species arranged into 133 subgenera [2, 4-5]. In Egypt, there are 28 species of *Sarcophaga* flies belonging to 9 subgenera [5].

Some species of Sarcophagidae are suitable for monitoring pollutant groups [6]. Additionally, these flies have been implicated in disseminating human enteropathogens, which are responsible for gastrointestinal illnesses such as diarrheal diseases caused by some protozoans such as *Cryptosporidium parvum* [7]. Also, some species can cause myiasis in humans and cattle [8]. However, the majority of *Sarcophaga* species have forensic importance, because they are drawn to and may feed on rotting vertebrate carcasses, including those of humans. This makes them useful in forensic investigations involving human remains [9-10].

Forensic entomologists can use evidence from *Sarcophaga* flies found on carcasses to determine the Post-Mortem Interval (PMI), or the shortest period

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(Received 07/12/2023, accepted 18/01/2024)
DOI: 10.21608/EJVS.2024.249158.1707

since death [11-12]. They can provide a more accurate determination of PMI based on differences in the lifecycle of these flies [13]. However, because morphological species-level identification is notoriously difficult, especially for female flies, the use of Sarcophagid specimens in forensic casework has been difficult [12].

The phylogeny of Diptera have been reconstructed by using the morphological characters and the molecular characters widely [14]. Diptera male terminalia have high differences in shape, size, and colour at the species level [15-16]. So, it has higher helpful in determining the species than any other source of morphological characters [16]. The Sarcophagid male's terminalia characteristics are regarded as a rich source of diagnostic traits for accurately determining the species level [16, 17–18].

Roback [19] put forward his phylogenetic hypothesis according to the morphological study of Sarcophagides terminalia. Also, he created generic evolutionary relationships within the subfamily Sarcophaginae based on differences between homologies structures in the male terminalia. Despite the fact that Roback's [19] study was a great benefit to constructing new terms of Sarcophaginae morphology still used.

Several studies have been conducted on the phylogenetic analysis of some genera within the subfamily Sarcophaginae, of which relied on morphological characters to analyze the relationships between different genera within the subfamily [20, 21, 22, 23–24]. More studies have been added on the phylogenetic analysis of some genera within the subfamily Sarcophaginae, that focusing on the infra-generic level relationships within the mega-diverse genus *Sarcophaga* [16, 25-27].

Currently, there are large number of available morphological characters, particularly those of male terminalia that can be used to improve the phylogenetic analysis of Sarcophaginae species. By analyzing these informative characters using modern phylogenetic methods, researchers can better understand the relationships between different species and populations within this diverse group of flies [16].

In this study, we utilized morphological characters, particularly male genitalia characters, to analyze the phylogenetic relationships between subgenera and species of the genus *Sarcophaga* from Egypt. By conducting this analysis, we aim to gain a better understanding of the evolutionary relationships between different species and populations within this genus. Additionally, this study will provide important signals to facilitate the identification of species-level taxa within the genus *Sarcophaga*

Material and Methods

Source and preparing of specimen

Most of the specimens were collected through field trips to different localities representing most of the Egyptian ecological regions from January 2021 to March 2023 by using decayed meat bait traps and aerial nets. The authors also obtained specimens from their own collection and/or from materials preserved in the main Egyptian insect collections, particularly the Efflatoun Collection at Cairo University and the Entomology Department Collection at Ain Shams University. The collected specimens were immediately pinned and dissected to clearly observe the male genitalia using an entomological pin. Those that were not dissected were preserved by drying and stored in the authors' collection or in one of the Egyptian collections. To clarify the genitalia parts from the dry soft tissue, the terminal part of the abdomen was carefully cut out and placed in hot 10% KOH for approximately 5 minutes. The terminalia were then washed in distilled water, 70% ethanol, and absolute ethanol, respectively. Finally, the male terminalia were pasted to a card beneath the specimen that is pinned.

Examination, identification, and illustration of morphological characters and male genitalia of specimens were conducted using a NOVEL stereo-binocular microscope. At the Zoology and Entomology Department, Faculty of Science, Al-Azhar University, photographic images were taken using a Canon EOS 6D camera that was mounted. The enhanced depth of field software Helicon Focus v6.22 (Helicon Soft Ltd) was then used to stack various source photos.

Nomenclature and terminology

The taxonomy and nomenclature of the genus *Sarcophaga* and the male genital terminology used in this study follow the guidelines set by Pape [1] and El-Ahmady *et al*. [5]. The morphological terminology used in this study is based on the works of Shewell [3], McAlpine [28], and El-Ahmady *et al*. [5]. The identification of the Egyptian flesh fly species in this study were carried out based on the works of Lehrer [29] and El-Ahmady *et al*. [5].

Character Matrix and Cladistic Analysis

In current study, a total of 56 characters were analyzed, including 37 binary and 19 multistate characters. Of these, 35 characters were related to male morphology (Figures 1-4), while 21 characters were related to male genitalia (Figures. 5–6). The data matrix (Table 2 was compiled using the Mesquite software program version 2.75 [30] Phylogenetic analyses were conducted using the TNT software program version 1.6, 2022 [31], based on the parsimony criterion. The phylogenetic trees

were searched using the Technology search option with various parameters, and the parsimonious trees were summarized in a strict consensus tree. To evaluate the support for the groups recovered in the phylogenetic analysis, various measures were calculated, including Absolute Bremer support (aBS), bootstrap (BS) values, and jackknife (JK) values. The aBS was calculated from TBR from existing trees at suboptimal length to 20 extra steps to find the upper limit of supports based on 30,000 suboptimal trees [32]. The BS values were calculated from 3000 bootstrap replicates, while the JK values were calculated from 1000 JK replicates with 36%-character deletion as recommended by Farris *et al.* [33]. Estimating support for groups recovered in the weighted analysis also employed relative Bremer support percentages [34].

Results and Discussion

Revision of genital homologous characters:

Male terminalia **(**Figures. 5–6**)** Relatively large in the Sarcophagides. Sternite 5 has a deep V-shaped emargination posteriorly and the margins are often equipped with long hairs or pads of spiny bristles. A cerci is a long protuberance largely straight or gently curving anteriorly. Surstylus is a broad plate always markedly shorter than the cerci and with long hair-like setae apically. Pregonite is a long protuberance variously developed; with setulae along the dorsal ridge.

Phallus without an epiphallus. The acrophallus is always situated apico-ventrally on the phallic tube, often partly or entirely concealed between sclerotized extensions or appendages from the phallic wall. Phallus in Sarcophagides is distinctly separated into a basiphallus articulating with a distiphallus, and the latter subapically with a transverse desclerotized strip separating the apical plate or juxta, which may be membranous or sclerotized. The distiphallus is further equipped with a median, often swollen and bi- or multilobed structure (vesica) proximal to the acrophallus, and in *Sarcophaga* with a pair of lateral, plate-like structures (harpes) contiguous with the sclerotized part of the phallic tube.

Acrophallus consists of a curved median stylus fused to juxta at one end and usually bifurcated at the other (free) end; and a pair of lateral styli, which are grooved structures, often with lateral margins adpressed so as to build tubular structures, and base distinctly coiled.

Tree topology and branch support

The analytical data of the current study resulted in 42 parsimonious trees with238 best score hits each. The most parsimonious trees vary only in the arranging of some nodes within the genus *Sarcophaga*. Absolute Bremer support values were generally low, but BS and JK values are slightly low as well. These values indicated the amount of homoplasy in the character matrix.

The extensive homoplasy in Sarcophagides morphological characters, like other genera of the family Sarcophagidae, is considered a weakness of the data matrix characters of the genus *Sarcophaga* (Table 1). So, it is challenging to gain powerful branch support. According to the BS and JK values in cladistic analyses. However, despite this challenge, the obtained trees have high accuracy based on morphological and genitalia characteristics.

Relationships and diagnosis of Subgenera and species.

The genus *Sarcophaga* is considered to be a monophyletic group and a sister-group of the genus *Lepidodexia*. The juxta fused with the median stylus and the presence of herpes are two specifically derived apomorphies that serve as the basis for this classification, as well as one homoplasious character state, which is pointed harpes [14]. In terms of subgenera, the genus *Sarcophaga* has four polytypic subgenera that are represented by multiple taxa, and five monotypic subgenera that are represented by a single taxon (Table 1). Our phylogenetic analysis supported all monophyletic subgenera except for subgenera *Liopygia* and *Liosarcophaga*, which were found to be paraphyletic.

Overall, these findings provide important insights into the evolutionary relationships within the genus *Sarcophaga*. The presence of derived apomorphies and homoplasious character states can help to clarify the evolutionary history of this group and shed light on its diversification over time. Additionally, the identification of monophyletic and paraphyletic subgenera can inform taxonomic revisions and help to refine our understanding of the diversity and distribution of *Sarcophaga* species.

Subgenus *Helicophagella* clade

The monophyly of *Helicophagella* and *Sarcophaga* and a sister group relationship between two subgenera were supported in all trees analyzed by two apomorphies' unique characters: Protandrial segment colour is black) (27:0) and harpes is narrow and pointed apically (51:8) (Figure 7). In spite of the BS and JK values were low. The relationship between the two subgenera was confirmed by Giroux's [14] phylogenetic analysis.

Helicophagella subgenus is a polytypic group. It represented by two species *S. (Helicophagella) maculata* that distinguished by two uniquely apomorphies characters: Cerci is narrow without punctuation or prominence (33:2) and juxtal arm is with spin ventrally (43:3), and three homoplasious characters (8:0, 50:1 & 52:0) (Figure 7). Also, *S.*

(Helicophagella) melanura which has two uniquely apomorphies characters: Head capsule is black (12:2) and vesical apex with an antero-inferior spine (55:5) and six homoplasious characters (17:0, 18:0, 20:1, 41:1, 53:4 & 54:3) (Figure 7).

Sarcophaga is a monotypic subgenus that represented by *S. (Sarcophaga) lehmanii*. So, it was unresolved in our analysis. But it separated from a sister group for subgenus *Helicophagella* by one apomorphies unique character: Cerci an excavation is present (Figure 7) (34:1) and seven homoplasious characters (Figure 7).

The monophyly of subgenus *Helicophagella* was supported by three homoplasious characters our analysis. This clade contains two monophyly species relationship *S. (Helicophagella) maculata* that are distinguished by two apomorphies unique characters (33:2, 43:4) and three homoplasious characters (8:0, 50:1, 52:0) (Figure 7) from *S. (Helicophagella) melanura* by two apomorphies unique characters (12:2, 55:5) (Figure 7) and six homoplasious characters (17:0, 18:0, 20:1, 41:1, 53:4, 54:3) (Figure **7**).

Subgenus *Pseudothyrsocnema*

It is a monotypic subgenus represented by *S. (Pseudothyrsocnema) spinose.* It has a monophyly relationship to the *Helicophagella* clade in the majority of the analyzed phylogenetic trees. Which was supported by three homoplasious characters (33:1, 36:0, 38:0). It is distinguished by two apomorphies unique characters: the vesical internal part is membranous and the external part is sclerotized (53:5), and the vesical is transparent internally and dark externally (54:4), and five homoplasious characters (13:1, 21:1, 28:0, 30:1, 39:1) (Figure 7).

Subgenus *Heteronychia* clade

The monophyly of subgenus *Heteronychia* was supported by three homoplasious characters). Whitmore *et al*. [26], mentioned the *Heteronychia* clade is a monophyletic group. Also, *Heteronychia* is a sister group to *Sarcophaga* [14] according to our study. This clade contains two monophyly species relationship *S. (Heteronychia) fertoni* that are distinguished by one apomorphies character: Styli is teeth ventrally (48:2) from *S. (Heteronychia) ferox* by three homoplasious characters (35:1, 42:0, 56:1) (Figure 7)

Subgenera *Parasarcophaga* and *Phytosarcophaga*

These genera form a pectinate chain of clades basal to the subgenus *Liopygia* clade. Sister group relationships in these subgenera were each supported by three homoplasious character states (Figure 7). Subgenus *Parasarcophaga* is a monotypic subgenus that is represented by *S. (Parasarcophaga) hirtipes* that are defined by one apomorphic character: lower calypter broadly expanded and more angular (26:0) (Figure 7) and nine homoplasious characters (Figure 7). Subgenus *Phytosarcophaga* has a monophyletic relationship with subgenus *Liopygia* in most analyzed trees that is supported by one homoplasious character: cerci is broad with punctuation or prominence (33:0) (Figure 7), It is a monotypic subgenus that was represented by *S. (Phytosarcophaga) destructor* from Egypt. On contrary, Giroux, [14] revealed that the subgenera *Parasarcophaga* and *Phytosarcophaga* not sister group. However, pending a more comprehensive analyses with a larger and more representative species should be conducted.

Subgenus *Liopygia* clade

According to traditional taxonomy of the subgenus *Liopygia* is monophyletic group [1]. But in our phylogenetic analysis it is obtain a paraphyletic group in all the analyzed trees. Subgenera *Liopygia* and *Bercaea* are a sister group [14]. Our analysis the subgenera *Liopygia* and *Parasarcophaga* are a sister group. Due to the existence of *S. (Liopygia) ruficornis* away from the *Liopygia* clade in most the trees analyzed. The remaining species are supported a monophyly group by one apomorphic character: Protandrial segment is orange (27:1) and one homoplasious character (46:1) *S. (Liopygia) crassipalpes* is distinguished from other species by one homoplasious character: Surstylus are oval (36:3) (Figure 7). *S. (Liopygia) argyrostoma* and *S. (Liopygia) surcofi* are monophyletic and a sister-species relationship.

Subgenus *Bercaea*

It is a monotypic subgenus that represented in Egypt by *S. (Bercaea) Africa*. It is a sister group to subgenus *Liopygia* [14]. At our analysisit is a sister group and monophyletic relationship with subgenus *Liosarcophaga* in all analyzed trees by four homoplasious character (17:1, 21:1, 50:1, 55:0) (Figure 7). Especially *S. (Liosarcophaga) tibialis* that supported by appropriate values of the BS and JK.

Subgenus *Liosarcophag* clade

Because *S.* (*Liosarcophaga*) *pharaonis* broke away from this clade in all analyzed trees. So, the *Liosarcophaga* clade is a paraphyletic group. The remaining species are supported a monophyletic group in most analyzed trees by Protandrial segment is grey (27:1) and one homoplasious character (38:0). It is divided into two monophyletic group: *S. (Liosarcophaga) marshalli, S. (Liosarcophaga) rohdendorfi* and *S. (Liosarcophaga) tibialis* are obtain a monophyletic and a sister species relationship by one homoplsious character: (28/2).

And *S. (Liosarcophaga) aegyptiaca, S.* (*Liosarcophaga*) *Parkeri, S. (Liosarcophaga) dux, S.* (*Liosarcophaga*) *redux, S.* (*Liosarcophaga*) *jacobsoni* and S. (*Liosarcophaga*) *mennae* are supported a monophyletic and a sister group by three homoplsious characters (8:2, 17:1, 21:1) (Figure 7). Also BS and JK values corroborative the relationships in this clade.

In the first group, *S.* (*Liosarcophaga*) *marshalli* is distinguished by one uniquely apomorphy character: Cerci an excavation present (34:1) and three homoplasious characters (37:0, 53:2 & 54:2). *S.* (*Liosarcophaga*) *rohdendorfi* is separated by two homoplasious characters (23:1 & 39:1). And *S.* (*Liosarcophaga*) *tibialis* has two uniquely apomorphies characters: Postgenal setae grey (7:2) and juxtal arm with spin ventrally (43:3) and four homoplasious characters (Figure 7).

The second group contains *S. (Liosarcophaga) aegyptiaca* and *S.* (*Liosarcophaga*) *parkeri* that are very close sister species that are supported by one uniquely apomorphy character: The posterior margin of the lower calypter is rounded (26:1) and three homoplasious characters (10:1, 22:0 & 23:1) (Figure 7) and with high values of BS and JK (Figure 7).

S. (*Liosarcophaga*) *redux* was separated by a weak node that has two homoplasious characters (Also, *S.* (*Liosarcophaga*) *dux* was separated by five homoplasious characters (Finally, *S. (Liosarcophaga) mennae* and *S. (Liosarcophaga) jacobsoni* are a close sister species that supported by three homplasious characters) and high BS and JK values (Figure 7)

Conclusions

The phylogenetic analysis of the Egyptian Sarcophagides conducted by our study is the first attempt to utilize a range of external morphological and male genitalia characteristics. The complex structure of the male genitalia was considered a source of phylogenetic characters that produced important apomorphic characters for most nodes in the phylogenetic tree.

The morphology relationships were supported by male genitalia apomorphies within the *Helicophagella* clade, and within the species of *Liopygia* and *Liosarcophaga* clades. However, the majority of the morphological characters were considered homoplasious characters.

The results of our study provide a preliminary hypothesis of the relationship of subgenera and species of the genus *Sarcophaga*. It was found that the *Helicophagella* and *Heteronychia* clades are monophyletic groups, while the *Liopygia* and *Liosarcophaga* clades are paraphyletic groups. The remaining subgenera are monotypic groups. It is important to note that future research should use molecular character sets to test this phylogenetic hypothesis. While our study provides valuable insights into the evolutionary relationships within the genus *Sarcophaga*, further research is needed to confirm and refine these findings.

Overall, the present study demonstrates the value of utilizing a range of external morphological and male genitalia characteristics in phylogenetic analyses of Sarcophagides. By identifying important apomorphic characters and supporting monophyletic relationships within certain clades, this research provides a foundation for future studies on this important group of insects.

Characters used in phylogenetic analysis

1. Abdomen appearance: (0) dark spots, (1) checkerboard pattern.
2. Coxapleuron steak: (0) absent, (1) present.
3. Distiphallus parts: (0) nondeveloped, (1) developed.
4. Hind coxa setose posteriorly: (0) bare, (1) present.
5. Male abdominal sternites 3 – 4: (0) partly concealed by margins of corresponding tergites, (1) exposed and overlapping margins of corresponding tergites.
6. Gena setae, colour: (0) black, (1) anterior part of gena with black hairs and posterior part with white hairs, (2) white.
7. Postgenal setae, colour: (0) black, (1) white, (2) grey.
8. Occipital setae, colour: (0) black; (1) Occipital foramen setae are white or yellowish, with black outside setae; (2) white or yellowish.
9. Median occipital sclerite, setosity: (0) setae never extending below paravertical setae; (1) setae extending below paravertical setae.
10. Supracervical setae, colour: (0) black; (1) white, yellow or golden yellow
11. Parafacial setae: (0) Scattered; (1) arranged at one a row.
12. Head capsule colour: (0) brown, (1) grey, (2) black.
13. Head capsule colour reflection with light: (0) silver, (1) gold.
14. Width of frontal vitta of eye width at narrowest part: (0) > 0.7, (1) < 0.7.
15. Frontal setae number: (0) > 10 pairs, (1) = 10 pairs, (2) < 10 pairs.
16. Pedical colour: (0) brown, (1) grey, (2) black.
17. Flagellomere colour: (0) brown, (1) grey.
18. Arista colour: (0) brown, (1) grey.
19. Width of lower facial margin of eye width: (0) > 0.6, (1) < 0.6.
20. Porbocies colour: (0) brown, (1) black.
21. Palps colour: (0) brown, (1) grey.
22. Postalar wall, setosity: (0) bare; (1) setose.

23. Presutural acrostichal seta: (0) absent; (1) present.
24. Postsutural acrostichal seta: (0) absent; (1) present.
25. Male discal scutellar bristles: (0) absent; (1) present.
26. Lower calypter, shape: (0) posterior margin relatively straight, calypter widely expanded and more angular; (1) posterior margin round.
27. Protandrial segment colour: (0) black; (1) grey; (2) orang; (3) brown (4) apical half grey and basal half brown; (5) apical half black and basal half brown.
28. Protandrial setae: (0) absent; (1) present.
29. Epandrium segment colour: (0) black; (1) orang; (2) brown (3) apical half brown and basal half grey.
30. 5^{th} abdominal sternite shape apically: (0) rounded; (1) corrugated.
31. 5^{th} abdominal sternite forman: (0) absent; (1) present.
32. 5^{th} abdominal forman shape: (0) rounded; (1) triangular, (2) oval (3) heart-like.
33. Cerci shape: (0) broad with punctuation or prominence; (1) broad basally, without punctuation or prominence (2) narrow without punctuation or prominence.
34. Cerci an excavation: (0) absent; (1) present.
35. Cerci shape apically: (0) pointed; (1) rounded.
36. Surstylus shape: (0) triangular; (1) trapezoidal; (2) narrow and long; (3) oval.
37. Pregonite shape: (0) straight; (1) slightly curved; (2) curved.
38. Pregonite apex shape: (0) pointed; (1) rounded.
39. Pregonite preapical an excavation: (0) absent; (1) present.
40. Pregonite median suture extended to apex: (0) absent; (1) present.
41. Juxtal arm shape: (0) long and narrow; (1) short and broad; (2) long and broad.
42. Juxtal arm bifidation: (0) bifid; (1) not bifid.
43. Juxtal arm prominence: (0) absent; (1) with spin dorsally, in forward direction; (2) with spin dorsally, in backward direction; (3) with spin ventrally; (4) with microscopic teeth apically.
44. Juxtal tip: (0) absent; (1) present.
45. Juxtal tip shape: (0) Small; (1) large.
46. Styli shape: (0) narrow; (1) broad.
47. Styli prominence: (0) absent; (1) present.
48. Styli prominence type and orientation: (0) teeth apico-ventrally; (1) serrated apico-ventrally and apico-dorsally; (2) teeth ventrally; (3) teeth apico-dorsally; (4) teeth dorsally.
49. Styli apex shape: (0) pointed; (1) rounded.
50. Harpes developing: (0) developed; (1) poorly developed.
51. Harpes shape: (0) broad at base, pointed apically or with spine-like process; (1) narrow, rounded apically; (2) broad, rounded apically; (3) broad, with arm apically; (4) narrow, pointed apically.
52. Vesical shape: (0) elongated; (1) rounded; (2) broad; (3) horn-like.
53. Vesical sclerotization: (0) heavily sclerotized; (1) sclerotized; (2) membranous; (3) internal part sclerotized and external part membranous; (4) dorsal part sclerotized and ventral part membranous; (5) internal part membranous and external part sclerotized.
54. Vesical colour: (0) transparent; (1) dark; (2) dark internally and transparent externally; (3) dark dorsally and transparent ventrally; (4) transparent internally and dark externally.
55. Vesical apex shape: (0) pointed; (1) not pointed with 2 short processes; (2) not pointed with 3 short processes; (3) truncate or dentate apically; (4) rounded apically (5) with an antero-inferior spine.
56. Vesical arm: (0) absent; (1) present.

TABLE 1. Data matrix of morphological characters used in the study. ? = missing data

Scientific name	1 1234567890	1111111112 1234567890	2222222223 1234567890	3333333334 1234567890	4444444445 1234567890	5555555 1223456
S. aegyptica	1011121201	1010001000	1011114110	1110011100	0101001110	101110
S. parkeri	1011121201	1100001000	1011114010	1110001000	0101001110	001120
S. dux	1011121210	0010101100	1001103010	1110001000	0001000?10	0211?0
S. redux	1011121210	1100001100	1101101010	1110000010	0001001010	001110
S. jacobsoni	1011121210	0110011000	0101101030	1110001000	0001101010	001100
S. mennae	1011121?0?	0010011110	1??1??1030	1110001000	0001101010	001130
S. marshalli	1011121?0?	1100000000	0??1??1020	1110000000	0111000?10	002230
S. pharaonis	1011120110	1100000000	0101105010	1110001100	0101101200	000030
S. rohdendorfi	1011121110	1100200010	0111104020	1110001010	0100?01210	201130
S. tibialis	1011122110	1100101010	11?1103030	1110001000	0130?00?11	?04300
S. argyrostoma	1011121210	1010011000	0101104010	1?00101101	1101111310	0200?0
S. crassipalpis	1011121?10	1010000000	1101102010	1?00031100	0101011410	010030
S. surcoufi	1011111210	1100101100	1101102010	1000011100	0100?11310	3200?1
S. ruficornis	1011121210	1100000000	0101103110	1000032000	2121001210	101140
S. africa	1011121110	1000121010	1100104121	1110022000	2100?00?11	201101
S. hirtipes	1011121110	0010211001	0111003010	1010002100	0100?00?01	?300?0
S. lehmanni	1011111110	0100221100	1101100100	1011012101	0100221100	422230
S. maculata	1011111000	0000011100	0101100100	1020002000	2140?00?11	401140
S. melanura	1011101107	?201000001	010?100100	1210002000	1100?10?00	424350
S. destructor	1011111110	1011000000	0001103010	1000001100	0100?01410	210030
S. ferox	1011101???	1001001100	0?????3110	1100112100	2000?00?00	321141
S. fertoni	1011101???	1111001100	1?????3131	1310002010	0100?00?00	325430
Wohlfahrtia nuba **(Outgroup)**	0100000010	1100000010	0001103120	0?10031111	??0????????	?0??41

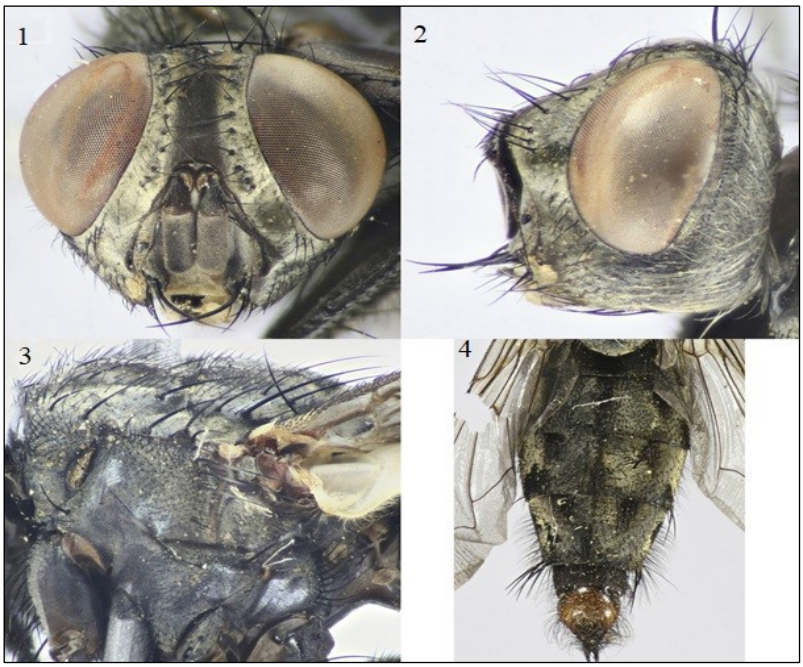

Fig. 1–4. *Sarcophaga* (*Liosarcophaga*) *mennae*: 1. Head (frontal view); 2. Head (lateral view); 3. Thorax (lateral view); 4. Abdomen (dorsal view)

TABLE 2. List of subgenera and species of genus *Sarcophaga* in the current study from Egypt

Subgenus	Scientific name
Bercaea	*S. africa* (Wiedemann, 1824)
Helicophagella	*S. maculata* Meigen, 1835
	S. melanura (Meigen, 1826)
Heteronychia	*S. ferox* Villeneuve, 1908
	S. fertoni Villeneuve, 1911
Liopygia	*S. argyrostoma* Robineau-Desvoidy, 1830
	S. crassipalpis Macquart, 1839
	S. ruficornis Fabricius, 1794
	S. surcoufi Villeneuve, 1913
Liosarcophaga	*S. aegyptica* Salem, 1935
	S. dux Thomson, 1869
	S. jacobsoni Rohdendorf, 1937
	S. marshalli Parker, 1923
	S. mennae Al-Ahmady, 2018
	S. parkeri Rohdendorf, 1937
	S. pharaonis Rohdendorf, 1934
	S. redux Walker, 1849
	S. rohdendorfi Salem, 1936
	S. tibialis Macquart, 1851
Parasarcophaga	*S. hirtipes* Wiedemann, 1830
Pseudothyrsocnema	*S. spinosa* Villeneuve, 1912
Phytosarcophaga	*S. destructor* Malloch, 1929
Sarcophaga	*S. lehmanni* Mueller, 1922

Fig. 5, 6. *Sarcophaga* (*Liosarcophaga*) *mennae*: 5. Male genitalia (lateral view); 6. Distiphallus (lateral view). Scale bar: 0.5 mm

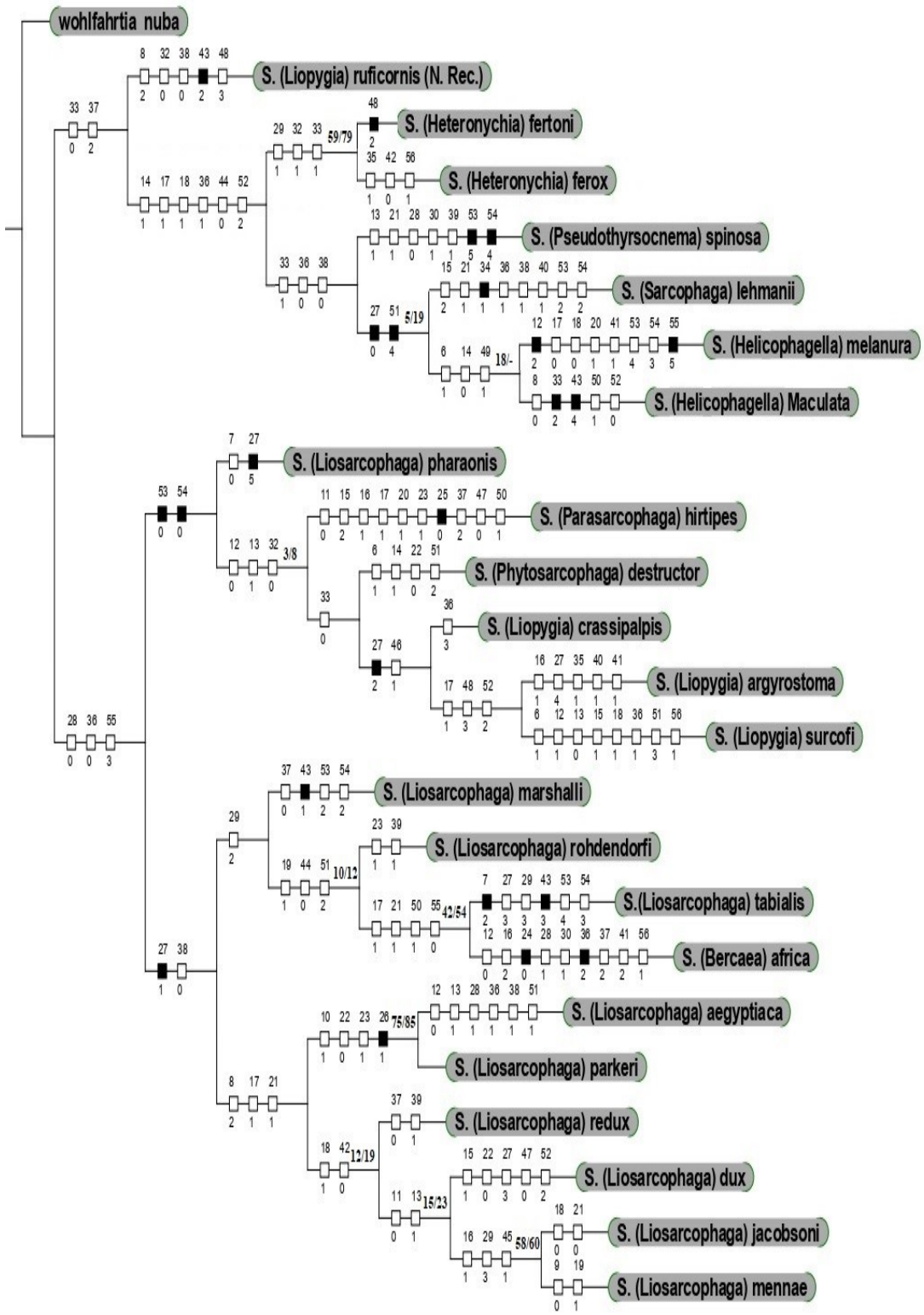

Fig. 7. Strick consensus tree of 42 most parsimonious trees. Black hashmarks represent uniquely apomorphy character; white hashmarks represent homoplasious character. Left = Standard Bootstrap value, and right = jackknife value.

Acknowledgment

The authors would like to thank all the staff of Zoology and Entomology Department, Faculty of Science, Al-Azhar University, Egypt who provided help during the research.

Conflicts of interest

The authors declare no conflict of interest.

Funding statement

This study was self-funded

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الاختلافات المورفولوجية والتطورية في بعض ذباب اللحم من جنس ساركوفاجا (ثنائية الاجنحة: ساركوفاجيدي) من مصر

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عائلة الساركوفاجيدي تعرف بذباب اللحم هي مجموعة كبيرة ومتنوعة من الذباب، تتكون من 173 جنسًا وأكثر من 3094 نوعًا موصوفًا في جميع أنحاء العالم. عالميا، يعتبر جنس ساركوفاجا مجموعة متنوعة تحتوي على ما يقرب من 800 نوع مرتبة في 133 تحت جنس. يوجد في مصر 28 نوعًا من ذباب اللحم تنتمي إلى 9 تحت أجناس. ذباب اللحم له عدة أهميات منها ما يستخدم لرصد مجموعات الملوثات. وهناك بعض الانواع تساعد في نشر مسببات الأمراض المعوية البشرية، المسؤولة عن أمراض الجهاز الهضمي. بالإضافة الي بعض الانواع التى تسبب عملية التدويد للإنسان والماشية. أما غالبية أنواع ذباب اللحم فلها أهمية في الطب الشرعي، لأنها تنجذب إلى جثث الفقاريات المتعفنة، بما في ذلك جثث البشر، وقد تتغذى عليها. وهذا يجعلها مفيدة في تحقيقات الطب الشرعي المتعلقة بالرفات البشرية.ونظرًا لصعوبة تحديد مستوى الأنواع المورفولوجية، خاصة بالنسبة لإناث الذباب، فقد كان استخدام عينات ذباب اللحم في أعمال الطب الشرعي أمرًا صعبًا.

في الدراسة الحالية، جرت محاولة لإجراء التحليل الوراثي الأول لـ 23 نوعًا تمثل 9 تحت أجناس من جنس ساركوفاجا من مصر باستخدام 56 صفة خارجية وصفة تناسلية ذكرية. أظهرت نتائج الدراسة أن تحت جنسى هليكوفاجيلا هيتيرونايكيا عبارة عن مجموعات أحادية العرق، في حين أن تحت جنسى ليوبيجيا وليوساركوفاجا عبارة عن مجموعات شبه عرقية. تتكون كل من الأجيال الفرعية المتبقية من نوع واحد، يُعرف بالمجموعات الأحادية النمط. بالإضافة إلى ذلك، دعمت الدراسة علاقات المجموعات الشقيقة بين تحت أجناس (ساركوفاجا وهليكوفاجيلا) و(ليوبيجيا وفيتوساركوفاجا) و (بيركيا و ليوساركوفاجا).

الكلمات الدالة: ساركوفاجا (ذباب اللحم) ، التحليل التطورى ، علم التصنيف ، مصر.