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Research Article

The Sarcophagidae (Diptera) of Kermanshah, Western Iran, with the First Record of *Sarcophaga* (*Helicophagella*) *bellae* Lehrer from Iran

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Abstract. Despite previous studies on necrophagous flies in Iran, the diversity and distribution of Sarcophagidae species in the country's western regions remain underreported. This study examines Sarcophagidae in Kermanshah city, western Iran, in 2018 through morphological and molecular analysis of 142 male flesh fly specimens. Eight *Sarcophaga* species were identified, all representing new provincial records. *Sarcophaga variegata* was the most prevalent species. In contrast, *Sarcophaga flagellifera* and *Wohlfahrtia nuba* were rare. Notably, *Sarcophaga (Helicophagella) bellae* was documented for the first time in Iran, with its presence confirmed by morphological examination and mtDNA-COI DNA barcoding. Phylogenetic analysis placed *S. bellae* within a distinct clade alongside *Sarcophaga noverca*, *Sarcophaga rosellei*, and *Sarcophaga agnata*, highlighting its close relationship with other *Helicophagella* subgenus. The addition of *S. bellae* provides a medically important species for Iran's insect fauna, as its potential to cause myiasis and aid in forensic entomology investigations. This study broadens our understanding of Sarcophagidae diversity in western Iran, contributing a valuable baseline for forensic entomology and underscoring the importance of faunistic surveys in previously unexplored regions.

Keywords: Flesh flies, mtDNA-COI, phylogenetic, forensic entomology

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Introduction

The flesh fly family, Sarcophagidae, is one of the most diverse families in the order Diptera. Systematically, Sarcophagidae belongs to the Calyptrata group within the Schizophora, infraorder Cyclorrhapha (Moscomorpha), and suborder Brachycera (Pape *et al.*, 2011; Buenaventura & Pape, 2013; Khosravi *et al.*, 2024). Members of this family are relatively large compared to the housefly, *Musca domestica* Linnaeus, 1758, with a body coloration that is predominantly gray, especially in the genus *Sarcophaga* Meigen, 1826. Like many families within Cyclorrhapha, Sarcophagidae exhibits diverse physiological and developmental strategies. Notably, their feeding behaviors underscore their medical, veterinary, and forensic importance (Byrd, 2002). Sarcophagidae flies deposit either first-instar larvae or eggs, depending on the availability of resources (Hediyeloo *et al.*, 2024). They typically follow the family Calliphoridae as the second wave of colonizers on carcasses (Haskell, 1997). The maggots primarily feed on cadavers or exposed meat, but some also consume excrement in varied ecological niches. Feeding behaviors can be species-specific, with certain species exhibiting indoor or outdoor activity preferences while others are active in decomposing buried bodies. In a previous study from Tehran, *Sarcophaga argyrostoma* Robineau-Desvoidy, 1830 maggots were collected exclusively from human cadavers, indicating an indoor association for this species (Haskell, 1997; Talebzadeh *et al.*, 2017; Jafari *et al.*, 2019, Mirzakhanlou *et al.*, 2025).

Alongside postmortem interval estimation, determining the place of death can be a valuable contribution of entomological data to forensic investigations, sometimes providing unique clues for cadaver tracking. Forensic entomologists can identify region-specific species as biomarkers, which may indicate geographical origins and support the repositioning of cadavers (Matuszewski *et al.*, 2013). Some fly species are restricted to specific regions or environmental conditions; for example, *Chrysomya marginalis* Wiedemann, 1830 (Diptera: Calliphoridae) and *Sarcophaga ruficornis* Fabricius, 1794 (Diptera: Sarcophagidae) have been recorded only in southern Iran (Sanei-Dehkordi *et al.*, 2020). A comprehensive database documenting fly diversity by locality is essential for accurate cadaver relocation analysis. The Sarcophagidae family comprises around 2,828 species across 118 genera and 221 subgenera (Pape *et al.*, 2025). These flies are medically significant due to their potential to cause myiasis in humans and animals (Najjari *et al.,* 2020; Ren *et al.*, 2013). In Iran, human myiasis is considered an occupational disease (Akbarzadeh *et al.*, 2012; Alizadeh *et al.*, 2014), with 68 species of the genus *Sarcophaga* reported. The diversity of this family remains unexplored in many parts of Iran, suggesting the possibility of new species records for the Iranian fly fauna (Akbarzadeh *et al.*, 2018).

Various methods are available for identifying Sarcophagidae flies, with male genitalia being the most critical morphological characteristic (Szpila *et al.*, 2015; Brown, 2009). Molecular markers, due to their reliability, cost-effectiveness, and ease of use, have become popular tools for species identification, genetic analysis, phylogenetic studies, and forensic investigations. These molecular techniques are now used to support the morphological identification of Sarcophagidae species (Jafari *et al.*, 2019; Talebzadeh *et al.*, 2020). While some studies on necrophagous flies in Iran exist (Jafari *et al.*, 2019), the fauna in the western parts of the country remains undocumented. This study investigates the diversity of the Sarcophagidae family in Kermanshah city, Kermanshah province, Western Iran. As part of this effort, we document the species *Sarcophaga bellae* as a new record for the Iranian Sarcophagidae diversity database.

Materials and methods

Study site: Kermanshah Province, Kermanshah City

Kermanshah (34.31° N, 47.07° E, avg. elev. 1,391 m) is the largest city in western Iran and the capital of Kermanshah province (Fig. 1). Located along the Qarahsoo River, it lies between Farokhshad and Paraw Mountains (north), Teq Bostan (northwest), and Sefidkuh (south). The region borders Kurdistan (north), Ilam and Lorestan (south), Hamedan (east), and Iraq (west). Kermanshah experiences hot, arid summers and cold, partly cloudy winters, with temperatures ranging from -3°C to 38°C, rarely falling below -8°C or exceeding 40°C.

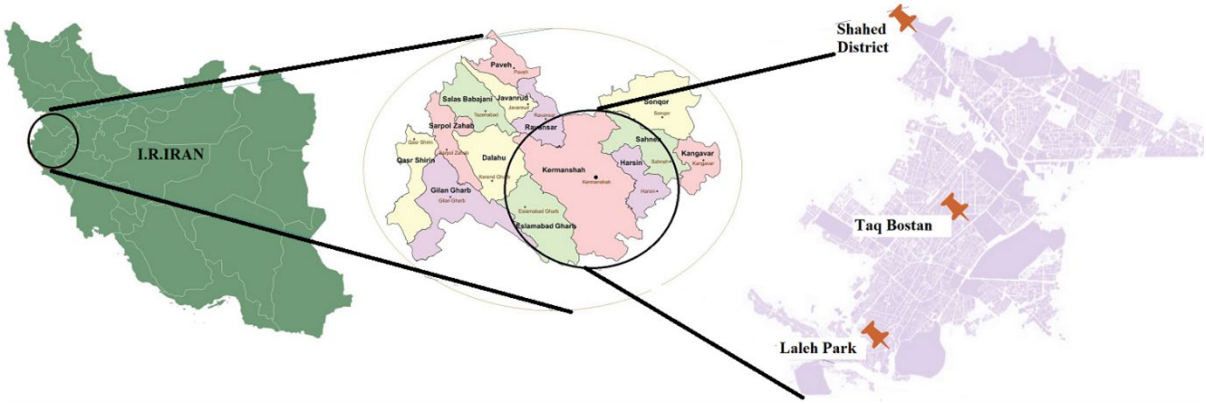

Fig. 1. Map of districts in Kermanshah, western Iran, surveyed for Sarcophagidae fly collection in 2018.

Sample Collection

Members of the family Sarcophagidae were collected using a standard fly net from three regions of Kermanshah city during the summer of 2018 (Table 1, Fig. 1). Samples were collected bi-weekly over a three-month period. To maintain consistency, all collections were conducted by the same researcher. Each specimen was placed in a 1.5 mL microtube with a small hole in the lid to allow air circulation, preserving the flies' morphological integrity until arrival at the laboratory. Specimens were transported to the lab at the end of each collection session. Male flies were killed by freezing, after which their external genitalia were dissected. Species identification was performed by comparing the morphology of genital structures with previously validated keys (Pape, 1996; Povolny, 1997; Pape, 2025). Some specimens were mounted on pins and stored in collection boxes, while others were preserved for molecular identification. Fresh samples were stored in 70% ethanol at -20°C prior to DNA extraction (Jafari *et al.*, 2019).

DNA Extraction and PCR

Among the 35 *S. bellae* specimens, three males were randomly selected for molecular analysis, focusing on the COI gene. Genomic DNA was extracted from the thoracic muscles of identified adult male sarcophagid specimens using a Qiagen DNeasy Blood & Tissue Kit (Qiagen, Hilden, Germany) according to the manufacturer's protocol. The DNA was resuspended in 30 µl of TE buffer (1 mM Tris–HCl, pH 8; 0.1 mM EDTA) and stored at 4°C. The COI gene was amplified with the primer pair LCO1490 (5'-GGTCAACAAATCATAAAGATATTGG-3') and HCO2198 (5'-TAAACTTCAGGGTGACCAAAAAATCA-3') (Folmer *et al.*, 1994) following the thermal cycling conditions described by Hashemi-Aghdam *et al.* (2017), yielding a product of approximately 711 bp. PCR products were visualized on a 1.2% agarose gel stained with ethidium bromide under a UV transilluminator. All PCR reactions were conducted in a total volume of 25µL, using the Taq DNA Polymerase 2x Master Mix RED, Ampliqon (Denmark), with the following reagents: 1–2µL of DNA extract (10–25 ng), 12.5µL of Master mix, 1µL of each primer (10mM), and 8.5–9.5µL of sterile water. For COI regions, the PCR thermal profile was 2 min at 94°C, followed by 5 cycles of 94°C (30s), 45°C (40s), and 72°C (60s), and then 35 cycles of 94°C (30s), 51°C (40s), and 72°C (60s), with a final extension at 72°C for 10 min.

PCR amplicons from the three male specimens, which were initially identified morphologically, were purified using the MRN-10 GenElute PCR Purification Kit to remove unincorporated dNTPs and primers. Briefly, the protocol involved binding DNA to a spin column, washing with a supplied buffer, and eluting the purified DNA in nuclease-free water. The purified products were sequenced on an automated sequencer (Seqlab, Goettingen, Germany). Bidirectional sequences were edited with ChromasPro (Version, 1.33; www.technelysium.com.au/ChromasPro.html) and aligned using ClustalW2 (Larkin, 2007). Homology was assessed using the FASTA search tool (http://www.ebi.ac.uk/fasta33/). The consensus COI sequences were submitted to GenBank, with unambiguous sequences trimmed to a length of 635 to 673 bp.

Phylogenetic Analysis

Due to the identical sequences of the three specimens obtained in this study, a single sequence was used as a representative for Iranian *S. bellae*. This representative sequence was combined with 44 previously reported sarcophagid sequences from GenBank (Table 2). *Chrysomya albiceps* (GenBank ID: MW200912) was designated as the outgroup. Phylogenetic analysis was conducted using MEGA X software (version 11; Kumar *et al.*, 2018). Trees were reconstructed using Maximum Likelihood (ML) method. The evolutionary distances were computed using the Kimura 2-parameter (K2P) model (Kimura, 1980).

Table1. Sample sites for collecting members of family Sarcophagidae, Kermanshah city, 2018.

Collection site	No of Sarcophagidae (all)	No. of *Sarcophaga bellae*	Longitude	Latitude	Altitude (meter above sea level)
Laleh Park	37	0	34º 17' 47.44''	47º 03' 20.21''	1438
Shahed district	64	35	34º 21' 02.29''	47º 06' 28.20''	1307
Taq Bostan district	41	0	34º 23' 10.38''	47º 07' 52.36''	1320

Table 2. Sarcophagidae nucleotide sequences used for phylogenetic analysis

No	Species	Series (subgenus)	Genbank ID	Origin	Reference
1	*S. bellae*	Helicophagella	OL589153- OL589155	Iran	This study
2	*S. bellae*	Helicophagella	KU746540	Türkiye	Direct submission
3	*S. noverca*	Helicophagella	KU746545	Italy	Direct submission
4	*S. rosellei*	Helicophagella	KU746547	Croatia	Direct submission
5	*S. agnata*	Helicophagella	KU746539	Croatia	Direct submission
6	*S. melanura*	Helicophagella	KX161497	Spain	Direct Submission
7	*S. mimoris*	Bercaeopsis	GQ223325	Spain	Direct Submission
8	*S. dux*	Liosarcophaga	JQ319785	China	Direct Submission
9	*S. aegyptica*	Liosarcophaga	JQ582054	NA	Jordaens *et al.*, 2013
10	*S. marshalli*	Liosarcophaga	KX161490	Spain	Direct Submission
11	*S. jacobsoni*	Liosarcophaga	JQ582057	NA	Jordaens *et al.*, 2013
12	*S. brevicornis*	Liosarcophaga	KF724930	China	Direct Submission
13	*S. carnaria*	Sarcophaga	GQ223342	NA	Direct Submission
14	*S. caerulescens*	Sarcophaga	JQ582069	NA	Direct Submission
15	*S. croatica*	Sarcophaga	JQ582068	NA	Jordaens *et al.*, 2013
16	*S. subvicina*	Sarcophaga	JQ582075	NA	Jordaens *et al.*, 2013
17	*S. variegata*	Sarcophaga	KX161478	Spain	Direct Submission
18	*S. lehmanni*	Sarcophaga	KX161482	Spain	Direct Submission
19	*S. sushkini*	Sarcophaga	KX094928	China	Direct Submission
20	*S. jeanleclercqi*	Sarcophaga	JQ582069	NA	Jordaens *et al.*, 2013
21	*S. pyrenaica*	Sarcophaga	JQ582073	NA	Jordaens *et al.*, 2013
22	*S. cf. bergi*	Sarcophaga	KU746612	Croatia	Direct Submission
23	*S. utilis*	Wohlfahrtiopsis	GQ223327	NA	Direct Submission
24	*S. triplasia*	Heteronychia	JQ582048	NA	Direct Submission
25	*S. vicina*	Heteronychia	JQ582048	NA	Jordaens *et al.*, 2013
26	*S. gravelyi*	Phallosphaera	KC113626	NA	Direct Submission
27	*S. barioensis*	Phallosphaera	KC174711	Malaysia	Direct Submission
28	*S. javana*	Parasarcophaga	FJ479732	NA	Direct Submission
29	*S. taenionota*	Parasarcophaga	KM279656	China	Direct Submission
30	*S. albiceps*	Parasarcophaga	MG913300	Iran	Jafari *et al.*, 2019
31	*S. similis*	Pandelleisca	KX161500	Spain	Direct submission
32	*S. sexpunctata*	Mehria	JQ582074	NA	Jordaens *et al.*, 2013
33	*S. aratrix*	Rosellea	JQ582067	NA	Jordaens *et al.*, 2013
34	*S. aldrichi*	Arachnidomyia	GQ223323	NA	Direct Submission
35	*S. schuetzei*	Kramerea	KF038009	China	Direct Submission
36	*S. argyrostoma*	Liopygia	MG913301	Iran	Jafari *et al.*, 2019
37	*S. cultellata*	Liopygia	JX987057	Spain	Direct Submission
38	*S. princeps*	Seniorwhitea	EF405948	NA	Tan *et al.*, 2010
39	*S. anaces*	Krameromyia	JQ582051	NA	Jordaens *et al.*, 2013
40	*S. subulate*	Bellieriomima	KU746565	Croatia	Direct Submission
41	*S. uliginosa*	Varirosellea	JQ582078	NA	Jordaens *et al.*, 2013
42	*S. peregrina*	Boettcherisca	KT353007	India	Direct Submission
43	*S. seniorwhitei*	Sarcorohdendrofia	KM497352	China	Direct Submission
44	*S. mehadiensis*	Stackelbergeola	KU746525	Croatia	Direct Submission
45	*S. soror*	Myorhina	KU746590	Croatia	Direct Submission
46	*Chrysomya albiceps*	outgroup	MW200912	Ecuador	Direct Submissio

Results

Morphological Species Identification

In this study, 142 male flesh fly specimens from various parts of the city were examined, comprising eight Sarcophagidae species identified using taxonomic keys specific to sarcophagid males (Table 3). *Sarcophaga variegata* Scopoli, 1763 was the most commonly observed species in the area. Identifications were based on sarcophagid morphological characteristics, focusing on male genitalia, which were the only reliable feature for species-level identification. Among the specimens, 35 were identified as *Sarcophaga bellae* Lehrer, 2000. The theme of the adults is gray with obvious checker pattern on abdomen and three conspicuous dark strips on the thorax. The adult can be categorized as big Sarcophagidae with a length about 8 – 12 mm. All parts the external genitalia such as epandrium, cercus, surstylus and phallic tube are blackish brown and have condensed hairs. The aedeagous is curved with a circular end (Z).

Table 3: Species and counts of identified Sarcophagidae fly specimens from Kermanshah city, Iran, 2018.

No.	Species	No. of specimens collected
1	*Sarcophaga aegyptica* Salem, 1935	6
2	*Sarcophaga argyrostoma* Robineau-Desvoidy, 1830	7
3	*Sarcophaga africa* Wiedemann, 1824	20
4	*Sarcophaga variegata* Scopoli, 1763	66
5	*Sarcophaga crossipalpis* Macquart, 1839	6
6	*Sarcophaga flagelifera* Meigen, 1826	1
7	*Sarcophaga bellae* Lehrer, 2000	35
8	*Wohlfahrtia nuba* Wiedemann, 1830	1
	Total	142

Sequence Analysis

We successfully amplified and sequenced a 711 bp fragment of the COI gene of the three selected male specimens, obtaining reliable sequences of approximately 635, 668, and 673 bp, which were deposited in GenBank (accession numbers OL589153–OL589155). The average A+T content for the COI region was 68.5%. Blast search confirmed a 100% identity between the Iranian *S. bellae* specimens and *S. bellae* from Türkiye (GenBank ID: KU746540).

Phylogenetic Relationships

With a few exceptions, phylogenetic analysis using either Neighbor-Joining or Maximum Likelihood produced similar topology and grouped the Sarcophagidae species into distinct clades corresponding to their taxonomic series or subgenera (Fig. 3). The Iranian *S. bellae* formed a clade with *S. bellae* from Türkiye, and this combined group was sister to a clade containing *S. noverca, S. rosellei*, and *S. agnata*, all within the Helicophagella subgenus.

Discussion

This study documented eight *Sarcophaga* species in Kermanshah city; all newly recorded for this area in western Iran. These findings emphasize the diversity of necrophagous flies in the region and highlight the influence of varied biogeographical zones on Iran's fauna. Although Iran is part of the Eastern Mediterranean Region, it is classified within the southern Palearctic zone according to international biogeographical categorizations.

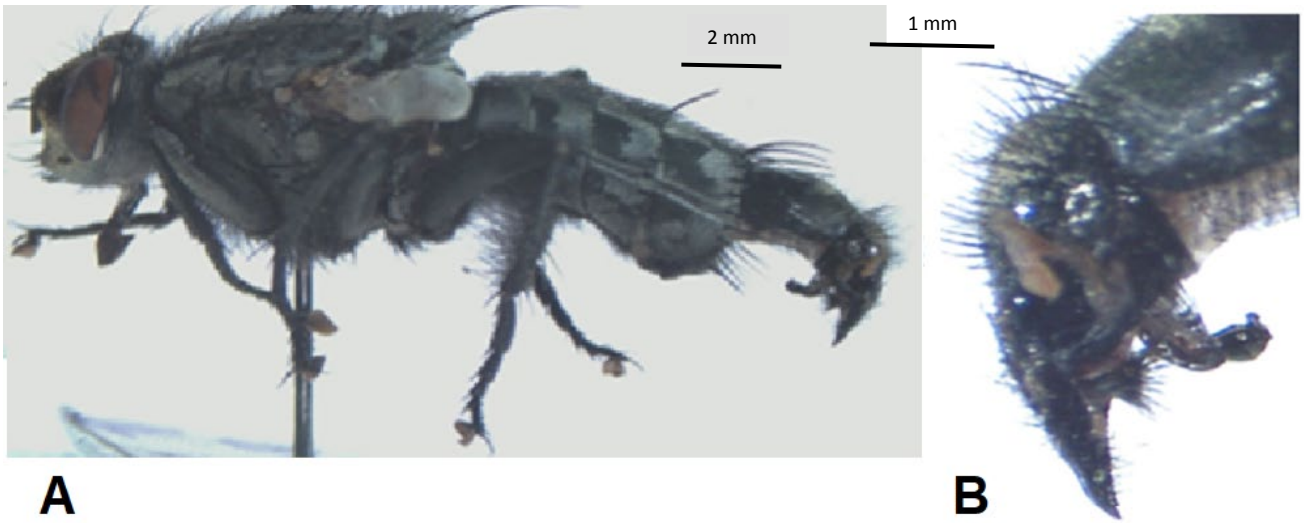

Fig. 2. General appearance (A) and male genitalia (B) of *Sarcophaga (Helicophagella) bellae* (Sarcophagidae: Diptera), collected in Kermashah, Iran, 2018.

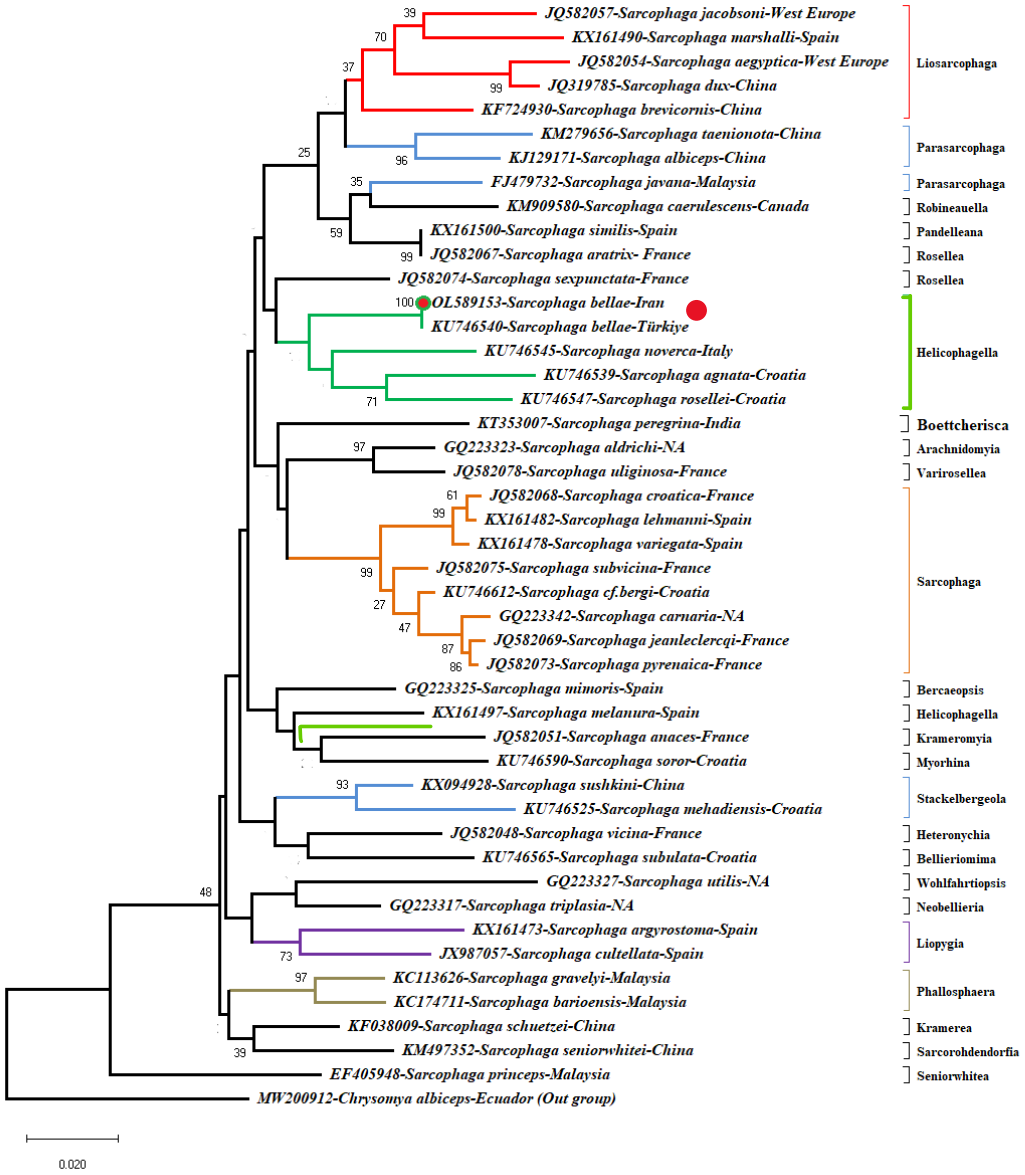

Fig. 3: Maximum Likelihood phylogenetic tree of *Sarcophaga* species based on mtDNA-COI sequences (644 bp). The tree was reconstructed in MEGA X (Kumar *et al.*, 2018) using the Kimura 2-parameter model (Kimura, 1980) and includes a representative Iranian *Sarcophaga bellae* sequence (highlighted with a red circle) along with 44 other *Sarcophaga* sequences from the GenBank. *Chrysomya albiceps* was used as the outgroup. Bootstrap values equal or greater than 25% are shown at the nodes. Taxonomic series (subgenera) are indicated on the right. The final dataset comprised 46 nucleotide sequences.

The country's geographic diversity incorporates influences from both the Oriental zone (in the southeast) and the Afrotropical zone (in the south), contributing to a wide range of species, including those within Arthropoda. Such regional data on necrophagous fly diversity are essential for forensic entomological surveys, as they help establish local species baselines. Akbari *et al.* (2023) reported on the diversity of necrophagous flies in Ilam province, also in western Iran, using pooled data from various families such as Calliphoridae, Sarcophagidae, Muscidae, and Oestridae to calculate species diversity indices. The current study provides preliminary data specifically on the *Sarcophaga* genus (Diptera: Sarcophagidae) in Kermanshah, a province with high religious and historical tourism. This baseline data contributes to a broader understanding of regional fly fauna in Iran. *Sarcophaga* (*Helicophagella*) *bellae* (Lehrer, 2000) (Diptera: Sarcophagidae) is reported here for the first time among Iranian flesh fly fauna. This report expands the known distribution of *S. bellae* in the Palearctic region, extending it from Greece, the Middle East, and Türkiye (Verves & Khrokalo, 2018) to Iran. While Kermanshah does not border

Türkiye, its close proximity suggests that *S. bellae* may have migrated from Türkiye into Iran and potentially into Iraq, which shares borders with both Türkiye and Iran. Given the lack of data on Iraqi Sarcophagidae, this finding of *S. bellae* in western Iran (east of Iraq) suggests that it may also be present in Iraq. Our findings significantly expand the known dipteran fauna of Kermanshah province. While *S. bellae* represents a new country record, the seven other species collected, though previously documented in other parts of Iran (Akbarzadeh *et al.*, 2012, 2018; Sanei-Dehkordi *et al.*, 2020; Motevalli Haghi *et al.*, 2021), are all newly recorded for this province. This underscores the substantial gap in regional biodiversity data that this study begins to address.

The species assemblage we observed provides insight into the sarcophagid community in western Iran. The prevalence of widespread species like *S. argyrostoma*, *S. africa*, *S. aegyptica*, and the dominant *S. variegata*—all reported from diverse biogeographical zones across the country—suggests a degree of ecological generality. Their confirmed presence in Kermanshah aligns with their status as common members of Iran's sarcophagid fauna. Of particular forensic significance is *S. argyrostoma*, which to date remains the only species in Iran with confirmed activity on human corpses in indoor settings (Talebzadeh *et al.*, 2017). The ubiquity of these species marks them as key forensically relevant taxa whose life-history patterns warrant further detailed study. In contrast, we also recorded species with more restricted distributions, such as *S. flagellifera* and *S. crassipalpis*. Their presence, previously noted primarily in southern provinces like Fars and Sistan and Baluchestan (Rafinejad *et al.*, 2014; Nateghpour & Akbarzadeh, 2017), indicates a more specialized biogeographical pattern. Such species could become valuable forensic indicators for cases of cadaver relocation once a more comprehensive, nation-wide distribution database is established. Furthermore, our study adds Kermanshah to the known range of *W. nuba*, a species confirmed as a myiasis agent in other parts of the country (Akbarzadeh, 2012; Maleki Ravasan *et al.*, 2012). This new record is crucial for understanding the potential public and animal health risks associated with this fly in western Iran. Finally, the discovery of *S. bellae* is not merely a new provincial record but elevates the total number of documented *Sarcophaga* species in Iran from 20 to 21 (Akbarzadeh *et al.*, 2018). This highlights that even among a relatively well-studied family, significant taxonomic and distributional discoveries remain to be made, particularly in under-surveyed regions like Kermanshah.

The main problem for the low number of reported species of the genus *Sarcophaga* is the limited morphological characters for their identification. The only reliable character is the shape of male genital organ. In almost all studies on the fauna of Sarcophagidae flies, a noticeable number of samples were left unknown because of their gender (Szpila *et al.*, 2015). Identification of female members of the family Sarcophagidae based on external morphology is almost impossible. Due to this issue, most precious samples especially in investigations in the field of forensic entomology, remain unusable (Babapour *et al.*, 2016). In this study, about 17% of the collected flies of the genus *Sarcophaga* were female and unidentified. With sampling in various geographical conditions and approving new methods for identifying such as molecular methods, finding new records could be expected. Cadaver displacement is one of the most important types of information that can be derived from the fauna of flies on the cadavers (Catts, 1992). Knowing the fauna of each locality is needed to locate the origin of flies found on cadavers (Fakoorziba *et al.*, 2017). The results of this study revealed that *S. bellae* can be mentioned as representative of western regions of Iran.

Using molecular studies based on COI has been confirmed to be effective for many groups of insects (Oshaghi *et al.*, 2007; Naddaf *et al.*, 2012; Karimian *et al.*, 2014; Sharma *et al.*, 2015; Hashemi-Agdam *et al.*, 2017; Koosha *et al.*, 2017; Jafari *et al.*, 2019; Khanzadeh *et al.*, 2020) as well as members of family Sarcophagidae (Sharma *et al.*, 2015; Talebzadeh *et al.*, 2020). The 623 bp COI region sequence data used for phylogenetic analysis of the *S. bellae* species in this study showed this marker is a powerful molecular tool for better understanding of the species identification and its geographical distribution. Results of this study suggest that spatial distribution of *S. bellae* has been extended from Türkiye toward western parts of Iran. As a conclusion, this study represents the first documentation of *S.* (*Helicophagella*) *bellae* in Iran, expanding its known distribution in the Palearctic region to include western Iran. Given the geographical proximity of Kermanshah province to Iraq and Türkiye, this finding highlights the need for further studies in Iraq to clarify the species' full range. In addition to *S. bellae*, the study identified seven others *Sarcophaga* species, all newly recorded in Kermanshah province, underscoring the regional diversity of necrophagous flies and the influence of varied biogeographical zones on Iran's fauna. The results further emphasize the utility of COI molecular markers for accurate species identification, particularly for forensic

applications where species differentiation is crucial. Enhanced sampling and molecular techniques are likely to reveal additional species within this genus, aiding both biodiversity assessments and forensic investigations in the region.

Author's Contributions

Zohreh Azizi: methodology; investigation; draft preparation; and visualization; **Mohammad Ali Oshaghi**: Conceptualization; methodology; formal analysis; final review and edit; visualization; supervision; and project administration; **Mohammad Mehdi Sedaghat**: Conceptualization; formal analysis; and supervision; **Kamal Azam**: Conceptualization; methodology; and formal analysis; **Nayyereh Choubdar**: methodology; formal analysis; investigation; and draft preparation, and **Kamran Akbarzadeh**: Conceptualization; methodology; formal analysis; investigation; visualization; supervision; project administration and funding acquisition.

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Data Availability Statement

All data supporting the findings of this study are available within the paper. The sequence data obtained in this study were deposited in GenBank database under accession numbers OL589153 to OL589155. The specimens examined in this study are deposited in the last author's collection at the (Tehran University of Medical Sciences, Tehran, Iran) and are available by the curator upon request.

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Ethics Approval and Consent to Participate

Insects were used in this study. All applicable international, national, and institutional guidelines for the care and use of animals were followed. This article does not contain any studies with human participants performed by the authors.

Conflict of Interest

The authors declare that there is no conflict of interest regarding the publication of this paper.

Generative AI statement

The authors declare that no Gen AI was used in the creation of this manuscript.

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Research Article

مگس های گوشت کرمانشاه در غرب ایران، با معرفی گونه *Sarcophaga* (*Helicophagella*) *bellae* Lehrer به عنوان رکورد جدید برای فون مشرات کشور Sarcophagidae (Diptera)

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چکیده: علیرغم مطالعات قبلی در زمینه شناسایی مگس‌های پوسیده‌خوار ایران، تنوع و پراکنش مگس‌های خانواده Sarcophagidae در مناطق غربی کشور گزارش نشده است. در این مطالعه، تنوع مگس های سارکوفاژیده در استان کرمانشاه در غرب ایران با دو روش مرفولوژیک و مولکولی روی ۱۴۲ نمونه صید شده، بررسی شد. نمونه های صید شده شامل هشت گونه از مگس های خانواده سارکوفاژیده بودند که همه آنها برای فون مگس های سارکوفاژیده استان جدید بودند. *Sarcophaga variegata* بعنوان گونه غالب و گونه های *Sarcophaga flagellifera* و *Wohlfahrtia nuba* بعنوان گونه های نادر در این تحقیق بودند. در این مقاله مگس گونه *Sarcophaga* (*Helicophagella*) *bellae* که هویت آن با روش های مرفولوژیک و مولکولی (mtDNA-COI DNA barcoding) تایید شده است، برای اولین بار از ایران گزارش می شود. تصویر اندام تناسلی نر این گونه بعنوان گواهی برای شناسایی این گونه ارائه شده است. روش بارکدینگ DNA، تشابه صد در صدی این نمونه با نمونه های ثبت شده در بانک ژنی از کشور همسایه، ترکیه را نشان می دهد (GenBank ID: KU746540). آنالیز فیلوژنتیک این گونه را در یک کلاد جداگانه به همراه گونه‌های *Sarcophaga noverca*، *Sarcophaga rosellei* و *Sarcophaga agnata* قرار داده، قرابت آن با زیرجنس *Helicophagella* را تایید می کند. به دلیل توانایی این گونه برای ایجاد میازیس و نیز اهمیت آن در علم حشره شناسی قانونی، گونه *Sarcophaga (Helicophagella) bellae* بعنوان یک گونه مهم از نظر پزشکی به فون حشرات ایران اضافه می‌شود. این تحقیق دانش ما را در زمینه تنوع مگس‌های خانواده سارکوفاژیده در غرب ایران بالا برده، گامی در جهت تکمیل اطلاعات پایه‌ای است که مورد نیاز علم حشره شناسی قانونی می‌باشد. این تحقیق تاکیدی است بر اهمیت بدست آوردن اطلاعات پایه‌ای در زمینه فون مگس‌ها در مناطقی است که تاکنون مطالعه ای در آن صورت نگرفته است.

کلمات کلیدی: مگس گوشت، mtDNA-COI، ژنتیک تکاملی، حشره شناسی قانونی

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