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Unlocking the genetic diversity of Scorpions (Arachnida: Scorpiones) in a lowland area of Sistan: a DNA barcoding study

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Abstract

The identity of the scorpions (Arachnida: Scorpiones) in the Sistan region, southeast Iran, was explored using a molecular marker. The list of identified species is as follows: *Androctonus rostami* Barahoei, 2025, *Androctonus sistanus* Barahoei & Mirshamsi, 2022, *Kraepelinia palpator* (Birula, 1903), *Mesobuthus rakhshanii* Barahoei, 2022, *Odontobuthus tigrari* Mirshamsi et al., 2013, *Orthochirus persa* (Birula, 1900), and *Sassanidotus gracilis* (Birula, 1900). Initially, at least five fresh specimens of *Mesobuthus rakhshanii* and *Orthochirus persa* were selected from different populations of each species. The Cytochrome Oxidase Subunit I gene was extracted, amplified, and sequenced using specific primers to evaluate the genetic variations among different genera and species. Sequences of other species were derived from GenBank. Phylogenetic trees were reconstructed using the Maximum Likelihood method and Bayesian Inference and analyzed. Specimens of *Mesobuthus rakhshanii* and *Orthochirus persa* were sequenced for the first time. *Sassanidotus gracilis*, *Mesobuthus rakhshanii*, and *Kraepelinia palpator* are morphologically similar and, as expected, are placed together in a clade as sister groups. The validity of all taxa was confirmed.

Keywords: Buthidae, Iran, phylogenetic tree, Sistan, systematics, taxon validity.

Introduction

Sistan is a lowland desertic plain located in southeastern Iran, characterized by its arid climate and minimal rainfall. This region features vast stretches of sandy and gravelly terrain, shaped by its unique geographical conditions (Mortazavi et al., 2015). It provides a suitable environment for the occurrence of scorpions from various groups (Barahoei, 2022). So far, seven species belonging to six genera of scorpions have been reported in the fauna of the Sistan region, four of which have had their identities confirmed using molecular data (Barahoei, 2022, 2024a, 2024b; Barahoei et al., 2022a, 2025). The results of faunistic studies (Barahoei, 2022; Barahoei et al., 2020, 2022a, 2022b) revealed the existence of seven species belonging to six genera of Buthidae in Sistan region, including *Androctonus rostami* Barahoei, 2025, *Androctonus sistanus* Barahoei & Mirshamsi, 2022, *Kraepelinia palpator* (Birula, 1903), *Mesobuthus rakhshanii* Barahoei, 2022, *Odontobuthus tigrari* Mirshamsi et al., 2013, *Orthochirus persa* (Birula, 1900), and *Sassanidotus gracilis* (Birula, 1900). Identifying species based solely on morphological characteristics has its limitations. These include factors such as phenotypic flexibility and genetic variation among individuals, which can complicate accurate identification. Additionally, the existence of cryptic species is often overlooked in this process (Jarman & Elliott, 2000); Morphological keys are typically applicable only to specific life stages or genders, and their use often requires a high level of expertise (Hebert et al., 2003). Most species are still primarily described based on morphological characters, making morphology the preferred method for taxonomists. Incorporating additional techniques, such as a partial sequence of the genome alongside morphological data, can enhance the accuracy of species identification. One of the most effective methods for rapid and reliable identification and classification of animals is DNA Barcoding, which utilizes small segments of mitochondrial DNA (mtDNA) sequences for species identification and classification. As a result, DNA Barcoding is advantageous for taxonomic research, population genetics, and constructing phylogenetic trees (Mohajeri et al., 2019). Scorpions play a crucial role in both the environment and medicine. They are among the most ancient animal groups on Earth

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(Howard et al., 2019). This study was conducted to verify the validity of known scorpion species in Sistan by determining genetic variations among species, assessing variations between populations of each species, and constructing phylogenetic trees.

Materials and methods

Scorpion specimens were collected from all counties in the Sistan region. After species identification, based on diagnostic characters outlined in key references (Barahoei, 2022, 2024a, 2024b; Barahoei et al., 2020, 2022a, 2022b, 2025). The most appropriate specimens (fresh, stored in 96% ethanol in a refrigerator) were selected for DNA sequencing. DNA was extracted from the pedipalps using a DNA extraction kit for animal tissue (FAVORGEN Co., Taiwan). The quality and concentration of the DNA samples were checked with the Nanodrop, and the samples with the required conditions were selected for the subsequent steps. The mitochondrial gene COI (Cytochrome Oxidase Subunit I) was amplified using standard primers (Folmer et al., 1994). The PCR temperature cycling was conducted as follows: Step 1- 95°C for 3 minutes (one cycle); step 2- 95°C for 45 seconds, 52°C for 45 seconds, 72°C for 45 seconds (35 cycles); Step 3- 72°C for 7 minutes (one cycle); Step 4- 4°C for unlimited time. The presence of amplified DNA in the PCR products was verified using gel electrophoresis. The products were then lyophilized and sent to Noor Comprehensive Medical Genetics Center in Tehran, Iran, for sequencing. The Clustal W version 2.0. was used to assess the quality of the refinement of the sequences, and generate the alignment matrix (Larkin et al., 2007) embedded in BioEdit 7.0.5.3 (Hall, 1999). Genetic distance between and within species was determined with MEGA 7.0 (Kumar et al., 2016). A Maximum Likelihood tree (with a bootstrap of 10,000 replicates and the GTR+I substitution model) was constructed on the Montpellier Bioinformatics platform website (Guindon et al., 2010), and Bayesian inference (with 50,000,000 generations and a burn-in of 5,000) on the CIPRES website (Miller et al., 2010). The generated trees were viewed using FigTree v1.4.0 and finally edited in Adobe Photoshop CC2014.

Results

Twenty-six sequences were used to construct phylogenetic trees, 21 of which were retrieved from GenBank, and seven of which are new. These include three sequences of *Orthochirus persa* and four sequences of *Mesobuthus rakshanii* (Table 1). The sequence of *Apistobuthus pterygocercus*, one of the basal lineages in the family Buthidae (Fet et al., 2003), was considered an outgroup (Fig. 1).

Table 1. Scorpion specimens of the family Buthidae used for constructing phylogenetic trees. Specimens were collected from the Sistan region in Southeast Iran.

| Species | Locality | Accession no. (NCBI) | Reference |
|-------------------------------|---|----------------------------------|-------------------------|
| <i>Androctonus rostami</i> | Sistan & Baluchestan, Nimruz, Sefidabeh (30°58'18.66''N, 60°31'48.27''E) | PP535679 PP535681 PP535682 | Barahoei et al. (2025) |
| | Sistan & Baluchestan, Mirjaveh (29°00'30.46''N, 61°27'03.25''E) | PP535689 | |
| <i>Androctonus sistanus</i> | Sistan & Baluchestan, Zabol, Hasan Abad (31°00'11.11''N, 61°30'05.70''E) | PP535690 | Barahoei (2024a) |
| | Sistan & Baluchestan, Hamun, Kusheh village (30°57'34.51''N, 61°29'28.00''E) | PP535691 | |
| | Sistan & Baluchestan, Hamun, Peere Sabz village (30°50'35.89''N, 61°20'19.82''E) | PP529594 PP529595 PP529596 | |
| <i>Kraepelinia palpator</i> | Sistan & Baluchestan, Zahak, Chah Nimeh (30°50'22.34''N, 61°43'01.45''E) | PP529597 | current study |
| | Sistan & Baluchestan, Hamun, Lootak, Rahmatabad village (30°45'33.16''N, 61°21'09.95''E) | PP529598 | |
| | Sistan & Baluchestan, Hamun, Kusheh village (30°57'34.51''N, 61°29'28.00''E) | PP392845 | |
| <i>Mesobuthus rakshanii</i> | Sistan & Baluchestan, Hamun, Peere Sabz village (30°50'35.89''N, 61°20'19.82''E) | PP392846 | Barahoei et al. (2022a) |
| | Sistan & Baluchestan, Zabol, Hasan Abad (31°00'11.11''N, 61°30'05.70''E) | PP392851 | |
| <i>Odontobuthus tigrari</i> | Sistan & Baluchestan, Zabol, Hasan Abad (31°00'11.11''N, 61°30'05.70''E) | PP392852 | current study |
| | Sistan and Baluchestan, Zabol-Zahedan road (30°09'N, 60°45'E) | MW655765 MW655771 MW655794 | |
| <i>Orthochirus persa</i> | Sistan & Baluchestan, Hamun, Peere Sabz village (30°50'35.89''N, 61°20'19.82''E) | PP574852 PP574853 PP574854 | Barahoei (2024b) |
| | Sistan & Baluchestan, Hamun, Gharib village (30°50'17.83''N, 61°23'02.60''E) | PP461698 | |
| <i>Sassanidothus gracilis</i> | Sistan & Baluchestan, Hamun, Peere Sabz village (30°50'35.89''N, 61°20'19.82''E) | PP461699 PP461700 PP461701 | |



The sequence length was 630 nucleotides, including 456 conserved nucleotides (72.38%), 174 variable nucleotides (27.62%), and 164 parsimonious nucleotides (26.03%). The Maximum Likelihood and Bayesian Inference analyses showed that Clade A, which includes members of *Orthochirus*, was placed at the base of the tree, forming a sister group to Clade B (comprising all other species). Clade B1, comprising *Odontobuthus* and *Androctonus*, was placed as the sister group to a clade consisting of *Sassanidothus*, *Mesobuthus*, and *Kraepelinia*. Within Clade B, *Kraepelinia* was placed at the top of the tree, representing the most recent genus in the Sistan region (Fig. 1).

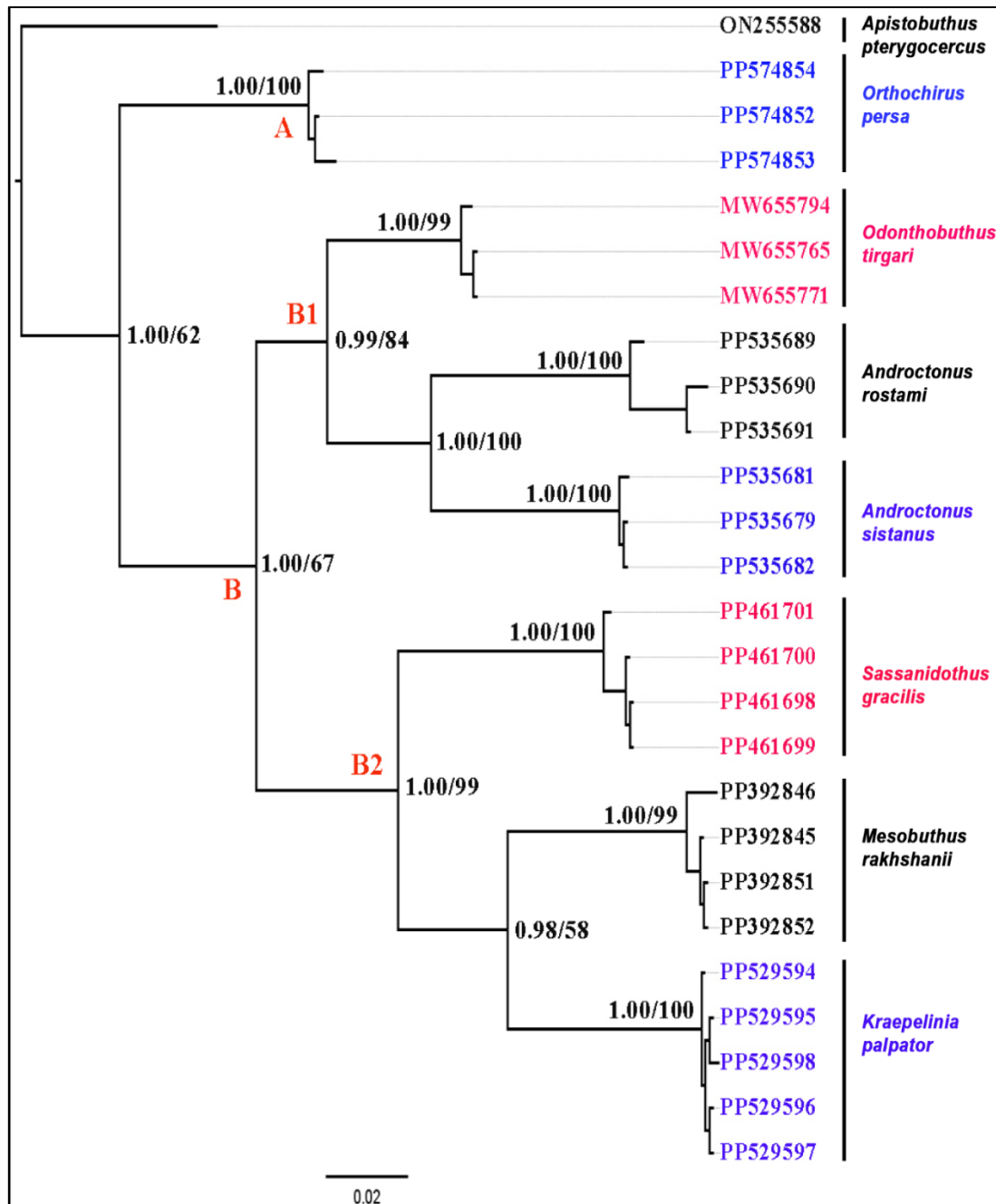


Figure 1. A consensus tree of Bayesian Inference (50,000,000 generations) and Maximum Likelihood (10,000 replicates) constructed based on 25 sequences of the COI gene of scorpions from the Sistan region, southeast Iran. *Apistobuthus pterygocercus* was used as the outgroup. Numbers on the nodes indicate the posterior probabilities from Bayesian Inference (BI) and bootstrap values from Maximum Likelihood (ML), respectively.

Genetic distances between species, obtained from COI gene sequences, confirmed the validity of all species and genera (Table 2). Among the scorpions of Sistan, the lowest genetic difference (0.099) was observed between *Kraepelinia palpator* and *Mesobuthus rakhshanii*, while the highest (0.176) was found between *Androctonus sistanus* and *Sassanidothus gracilis* (Table 2).

Table 2. Genetic distances between scorpion species based on COI gene sequences collected from the Sistan region in Southeast Iran. Bold values indicate intraspecific distances.

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 |
|---|--------------|--------------|--------------|--------------|--------------|--------------|--------------|
| 1. <i>Androctonus rostami</i> | 0.000 | | | | | | |
| 2. <i>Androctonus sistanus</i> | 0.119 | 0.012 | | | | | |
| 3. <i>Kraepelinia palpator</i> | 0.155 | 0.167 | 0.001 | | | | |
| 4. <i>Mesobuthus rakhshanii</i> | 0.141 | 0.160 | 0.099 | 0.004 | | | |
| 5. <i>Odontobuthus tigrari</i> | 0.115 | 0.109 | 0.137 | 0.147 | 0.001 | | |
| 6. <i>Orthochirus persa</i> | 0.128 | 0.153 | 0.154 | 0.164 | 0.120 | 0.005 | |
| 7. <i>Sassanidotus gracilis</i> | 0.150 | 0.176 | 0.134 | 0.110 | 0.132 | 0.159 | 0.002 |
| 8. <i>Apistobuthus pterygocercus</i> | 0.142 | 0.136 | 0.143 | 0.149 | 0.116 | 0.107 | 0.154 |

Discussion

Molecular studies conducted on Iranian scorpions have often confirmed the validity of the studied species and led to the description of new species from various genera, including *Androctonus* (Barahoei et al., 2022b, 2025), *Hemiscorpius* (Shahi & Barahoei, 2024), *Kraepelinia* (Barahoei, 2024a), *Mesobuthus* (Fet et al., 2018; Kovařík et al., 2022), *Odontobuthus* (Mirshamsi et al., 2013; Azghadi et al., 2014; Barahoei et al., 2022a), and *Sassanidotus* (Barahoei, 2024b). In the study of scorpions from the Sistan region, three species were described: *Androctonus rostami*, *A. sistanus*, and *Mesobuthus rakhshanii* (Barahoei, 2022; Barahoei et al., 2022b, 2025). A total of seven species from six different genera within the Buthidae family have been documented in this area (Barahoei, 2022). Phylogenetic trees drawn based on the sequences obtained from the COI mitochondrial gene (Fig. 1) and the genetic distances obtained from these sequences confirm the validity of all species (Table 2). The minimum interspecific genetic distance for separation of two species is 6% (Barahoei et al., 2022a). The mountainous belt of eastern Iran results from the collision of Lut and Afghan blocks in the Middle Eocene (Tirrul et al., 1983). All scorpions, especially members of the *Androctonus* have achieved different morphological and genetic changes based on habitat. The specimens in mountainous areas are dark (*A. rostami*), and those in low-altitude and plain regions are yellow (*A. sistanus*). One reason could be the colour of the habitat substrate, which is effective in camouflage. With the geographical separation of *Mesobuthus* populations, two species have been created on both sides of the eastern mountainous belt of Iran, *M. kirmanensis* in the west and *M. rakhshanii* in the east. In appearance, *M. rakhshanii* is similar to *M. macmahoni* (Barahoei, 2022; Kovařík et al., 2022), and one reason is that they live in the same climatic conditions. *Odontobuthus tigrari*, a species distributed in the mountainous belt of eastern Iran, from the center of Sistan and Baluchestan to North Khorasan province, were studied before and confirmed its validity (Barahoei et al., 2022a). Three species, *Sassanidotus gracilis*, *Mesobuthus rakhshanii*, and *Kraepelinia palpator* are morphologically similar and, as expected, are placed together in a clade as sister groups. *Kraepelinia palpator* and *M. rakhshanii* have the lowest genetic distance (0.099) and are morphologically similar. These two genera are separated by the location of *eb* trichobothrium, which is located on the distal part of the manus of chela in *Kraepelinia* (Lourenço & Leguin 2010) and the fixed finger of chela in *Mesobuthus* (Kovařík et al., 2022), also, small size (less than 45 mm), chela fingers thick and short, and with a chamfered and hairy end, with presence teeth on the ventral surface of metasomal segment II-III in *Kraepelinia* (Barahoei, 2024a). The genetic distance between *Sassanidotus* and *Kraepelinia* was 0.134, while the distance between *Sassanidotus* and *Mesobuthus* was 0.110. Morphologically, *Sassanidotus* is distinguished from *Kraepelinia* and *Mesobuthus* by having four terminal denticles on the movable finger (instead of five) and by the carinae of its tergites, which project beyond the posterior margin as distinct spiniform processes (Barahoei, 2024b).

Conclusion

In this survey, seven valid species of scorpions were identified as being distributed in the Sistan region. These species include *Androctonus rostami*, *A. sistanus*, *Kraepelinia palpator*, *Mesobuthus rakhshanii*, *Odontobuthus tigrari*, *Orthochirus persa*, and *Sassanidotus gracilis*.

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