

Research Article

First record of *Sphingonotus (Sphingonotus) savignyi savignyi* Saussure, 1884 (Orthoptera: Acrididae: Oedipodinae) from Mongolia

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Abstract

Here, we present the first record of *Sphingonotus (Sphingonotus) savignyi savignyi* Saussure, 1884, for Mongolia, collected from the Gobi area. This collection location defines the currently most north-eastern collection location of the species.

Key Words

band-winged grasshopper, field research, Gobi, new record

Introduction

With 51 recorded species, the Oedipodinae represent the second largest Acrididae subfamily in Mongolia (Gankhuyag et al. 2023). While the genus *Sphingonotus* Fieber, 1852 was extensively studied by Russian scientists in the 20th century (peak 1950–1989; e.g. Nasekomye Mongolii [Insects of Mongolia] volume 1 (1972) - volume 11 (1990)), research activity declined dramatically after the collapse of the Soviet Union in 1991. Only a couple of years ago, Mongolian and German scientists started working intensively on the Orthoptera fauna again. The works of Gantigmaa and Myagmar (2022), Gankhuyag et al. (2023) and Myagmar (2024) remain milestones of modern Orthoptera research in Mongolia. Dey et al. (2021) expanded the knowledge of the distribution of Oedipodinae grasshoppers in Mongolia, based on collection material and field trips from 1962 to 2017. In June/July 2025, the German-Mongolian Expedition team visited the old Soviet field station “Ekhiin Gol” (Fig. 1; Stubbe et al. (2025)), which is now only rarely used for entomological research. Even though the area was intensively studied before, the subspecies *Sphingonotus (Sphingonotus) savignyi savignyi* Saussure,

1884 was not recognised by any entomologist in the past, including Dey (2021), Gantigmaa and Myagmar (2022) and Gankhuyag et al. (2023). Here, we present the first record of *S. (S.) savignyi savignyi* for Mongolia, from the Gobi area.

The subspecies *S. (S.) savignyi savignyi* is known to have a very broad distribution, ranging from the Canary Islands (Husemann and Hochkirch 2007, 2008) over northern Africa (Moussi et al. 2018; Zergoun et al. 2018) and the Maltese Islands (Cassar 1990; Cassar et al. 2020) to Kazakhstan (Tishechkin 2024) and Mongolia (this study), spanning a distribution range of more than 8,000 km. Conversely, the subspecies *Sphingonotus (Sphingonotus) savignyi obscuripes* Chopard, 1949 is only recorded from Mauretania, but has not been recorded since its description. Mestre and Chiffaud (2006) recommend a clarification of the status of this subspecies.

Materials and methods

Specimens were collected by hand or using sweep nets during daylight and within temperatures around 45 °C from 26.06.2025 to 03.07.2025. The specimens were pinned in

the field and one hind leg was stored in 96% ethanol to preserve material for further genetic and genomic studies. Furthermore, one individual was preserved in RNAlater for future transcriptomic analyses. A first identification was performed in the field (based on knowledge of the species by LSD) and afterwards at the Senckenberg German Entomological Institute, Germany (SDEI) using the original description by Saussure (1884) and identification keys by Mistshenko (1936) and Dey et al. (2018). We also compared the individuals with several specimens from north Africa housed in the collection of State Museum of Natural History Karlsruhe, Germany (SMNK) and the collection of the SDEI. Furthermore, pictures of one of the two potential syntypes (assigned by Hollier (2012); images available at Cigliano et al. (2026)), housed at Museum d'Histoire Naturelle, Geneva, Switzerland (MHNG), were used as reference.

Distribution maps were created in QGIS v. 3.40.6 (QGIS.org 2026) using the background map HYP_HR_SR_W_DR v. 2.0.0 (naturalearth.com) and administrative area layer of Mongolia (MNG_adm1; GADM v. 2.5; gadm.org).

Furthermore, specimens were imaged and processed using a Nikon D7200 and AF-S Micro Nikkor 105 mm 1:2.8G ED lens. We used the software ControlMyNikon v. 5.3.0.9.3 Pro (2010–2026, Tetherscript Technology Corp.; controlmynikon.com) for camera control, Zerene Stacker v. 1.04 (Zerene Systems 2009–2017) to stack the serial photos and ImageJ v. 1.51S (imagej.net; Schneider et al. (2012); Rasband, (2017)) to add scale bars. Pictures were edited in Adobe Photoshop v. 27.3.1 (Adobe 1990–2026) and Adobe Illustrator v. 30.2.1 (Adobe 1987–2026).

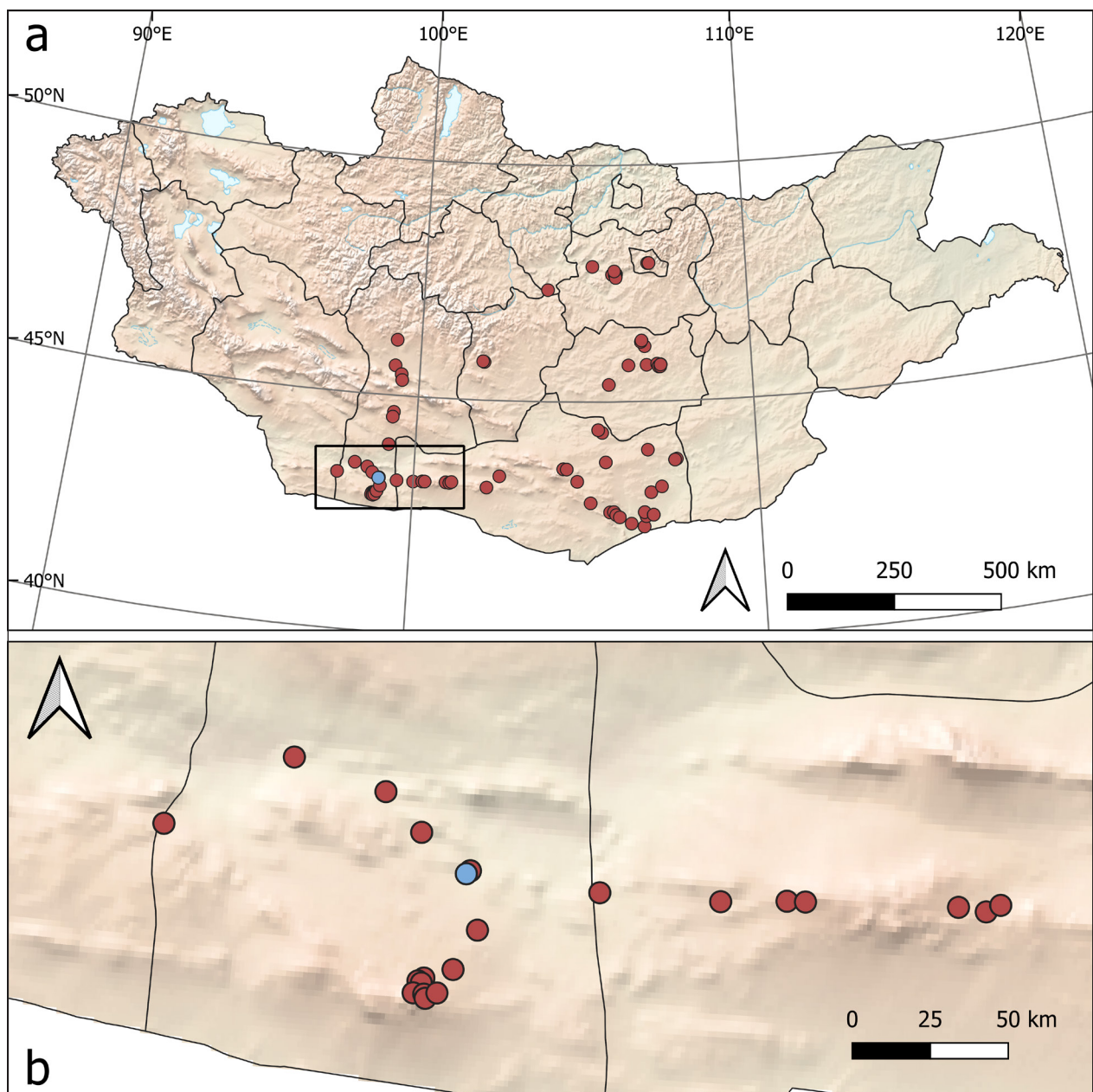


Figure 1. Sampling location of *S. (S.) savignyi savignyi* in Mongolia (blue point). Red points show all visited locations in 2025 (a). The focus map (b) shows visited locations with similar habitats, which were specifically checked for *S. (S.) savignyi savignyi*.

Results

The collecting area was defined by very sparse vegetation and pebbly ground (Fig. 2). While the site was mainly occupied by *Sphingonotus (Sphingonotus) obscuratus latissimus* Uvarov, 1925 in a very high abundance (hundreds of specimens per 100 m × 100 m), *S. (S.) savignyi savignyi* was scarcely found (approximately one individual per 20 m × 20 m) and only present in a specific type of micro-habitat: a light coloured soil with dark pebbles. Due to its fast, agile and long flight to escape the net, we only recognised the species by chance at the beginning. The characteristics recognised were the whitish, light sulphur-coloured hind tibia and inner femora, combined with the characteristic hind wing band pattern: darkened apex of the hind wing and a medium broad dark fascia from the upper wing base reaching almost the lower margins of the hind wing disc in a semi-circular shape. Furthermore, the typical structure of the intercalary vein (no nodes, no teeth, no combination of both) for *Sphingonotus (Sphingonotus)* defined after Husemann et al. (2011) is present.

Sphingonotus (Sphingonotus) savignyi savignyi
Saussure, 1884

Mongolia.
Bayan-Khongor Aimag.
Shinejinst.

Close to Ekhiin Gol oasis.

43.246°N, 99.007°E.

Collecting event: 26.06.2025 – 03.07.2025.

Females: 1 (DEI Hemimetabola #100641; Fig. 3).

Males: 5 (DEI Hemimetabola #100642; DEI Hemimetabola #100643; DEI Hemimetabola #100644, Fig. 4; DEI Hemimetabola #100645) + 1 in RNAlater (TT25).

Preservation method: 1 f and 4 m as dried pinned insects; 1 f 4 m hind legs stored in 96% ethanol (-20 °C); 1 m in RNAlater (-80 °C).

Deposit: Senckenberg German Entomological Institute, Müncheberg, Germany.

Discussion

In total, six specimens of *S. (S.) savignyi savignyi* were collected around the field station in Ekhiin Gol. Based on the findings of the species in Ekhiin Gol, we investigated several collecting sites more thoroughly within the area, but without any further findings (Fig. 1). *Sphingonotus savignyi savignyi* was only distributed in specific micro-habitats (dark pebbles on lighter ground) and occurred at the collection location only in low abundance. Due to its very fast and long flight, it seems like the species has the potential for high dispersal. Oedipodinae grasshoppers are known to have high flight capacities, which is mentioned for *Oedipoda caerulescens* (Linnaeus, 1758), which can move and colonise new areas in the Netherlands, by huge distances, even during the night



Figure 2. Habitat around Ekhiin Gol field station (43.246°N, 99.007°E), Bayan-Khongor Aimag, Mongolia.

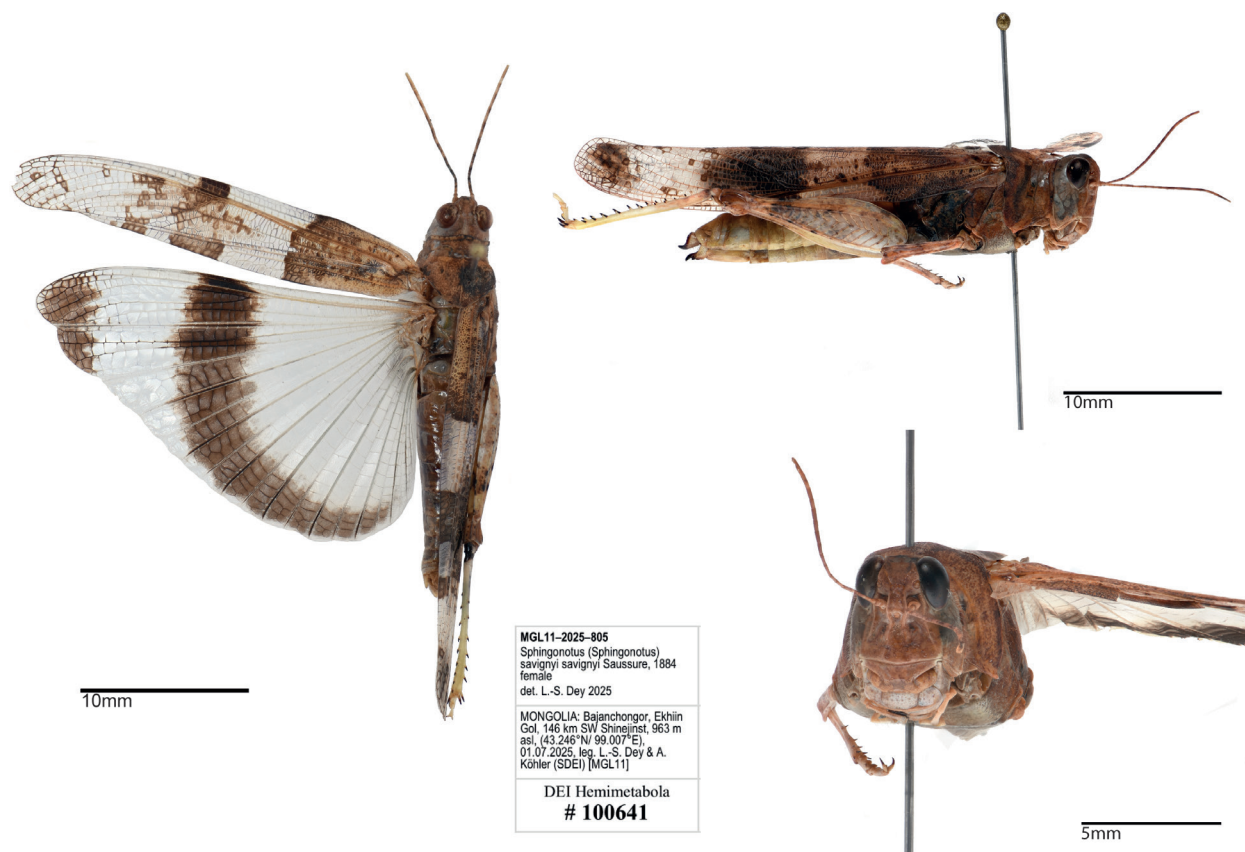


Figure 3. Dorsal, lateral, and frontal view of female *S. (S.) savignyi savignyi* (DEI Hemimetabola #100641).

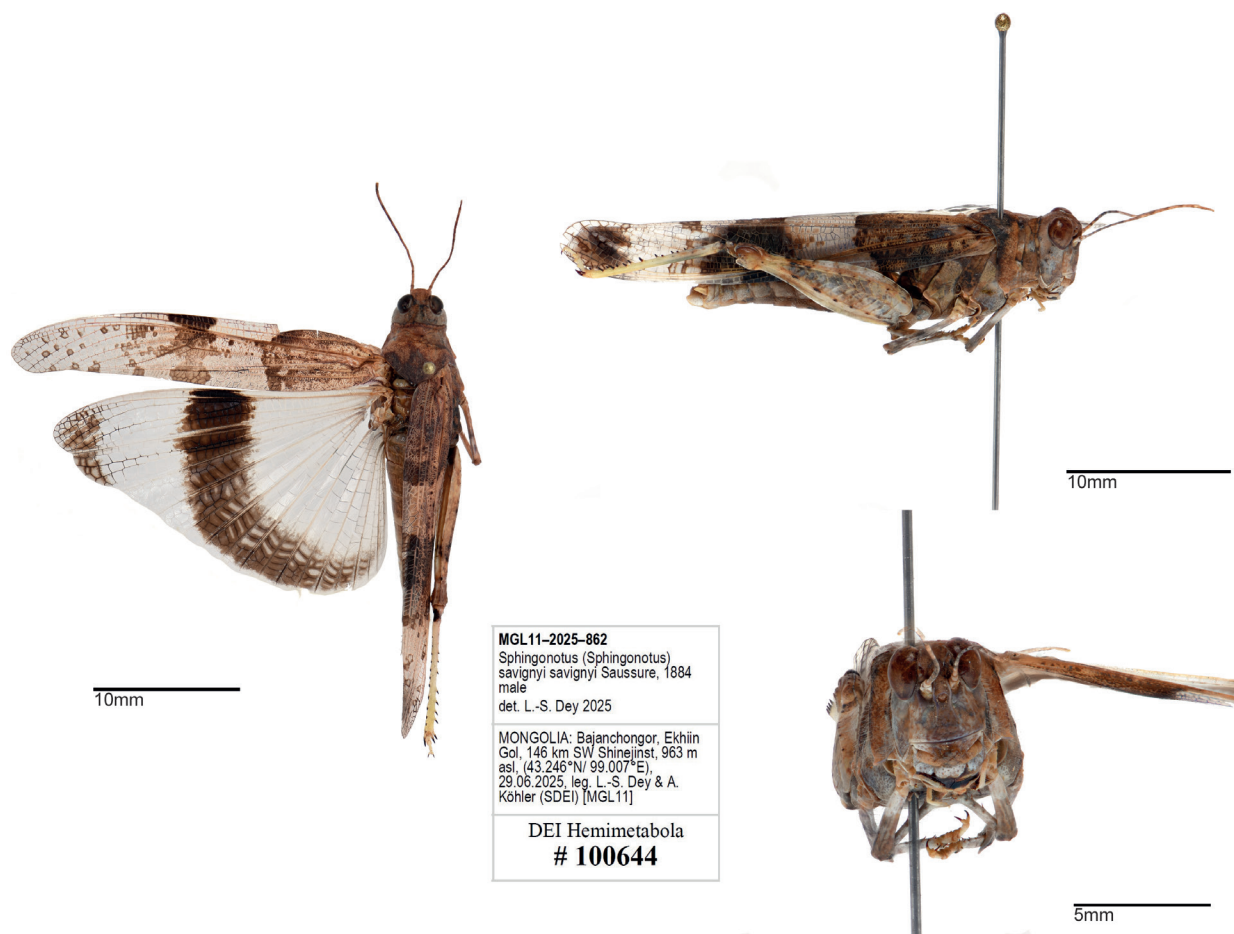


Figure 4. Dorsal, lateral and frontal view of male *S. (S.) savignyi savignyi* (DEI Hemimetabola #100644).

(van Leeuwen et al. 2019). Detzel (1998) documented that individuals of *Oedipoda germanica* (Latreille, 1804) can move up to 514 m and *Sphingonotus caerulans* (Linnaeus, 1767) can pass over forest areas at a height of 20 m. Studies investigating the dispersing capacities of Oedipodinae are still rare, but combining the flight capacity, dispersal ability and sparse abundance might be the reason why no previous study recorded the species in Mongolia yet, even though the region has been studied in the last couple of years. Overall, based on this study, the species appears to have a huge distribution range from the Canary Islands (Husemann and Hochkirch 2007, 2008) to Mongolia. It should be noted that the other records from the eastern part of this subspecies' range – Kazakhstan (Tishechkin 2024) and Xinjiang, China (Li et al. 2025) – were also made within the last five years. Given the high level of research on Mongolian orthopteran fauna, it is unlikely that the species has been overlooked until now. A recent eastwards expansion of its range can therefore be suspected.

Based on its unique morphology, it is easily identifiable even though there are some differences in the specimens compared to the original description and pictures of one potential syntype (ambiguous assignment by Hollier (2012)). The original description of Saussure (1884) does not include a darkened apex of the triangular hind wing, but based on further and ongoing studies on the species, its relatives, the phylogenetic position (e.g. Husemann et al. (2013); Husemann et al. (2014); Moussi et al. (2018); Dey et al. (2020)) and their distribution across Eurasia and Africa, we conclude that this trait is likely variable within the species. Variable hind wing band patterns and colouration are frequently occurring traits in Oedipodinae (Willey and Willey 1967; Dey et al. 2022; Hochkirch et al. 2023). This is also shown in several phylogenetic studies comparing specimens of *S. (S.) savignyi savignyi* across the distribution range (Hochkirch and Husemann 2008; Moussi et al. 2018; Dey et al. 2020). Pattern and colour of the hind wing should not be decisive features for misidentification in this specific case. Even though several studies show the monophyly of the species using only mitochondrial or a combination with nuclear markers (e.g. Husemann et al. (2013); Husemann et al. (2014); Moussi et al. (2018); Dey et al. (2020)), previous mitogenomic studies on the genus recognised several problems regarding the resolution of mitochondrial fragments like nuclear copies of mitochondrial pseudogenes, incomplete lineage sorting or mtDNA introgression (e.g. Hawlitschek et al. (2016); Dey et al. (2020); Ragazzini et al. (2025)). Therefore, future studies on this species should integrate samples from the whole distribution range and should shed light on the evolutionary drivers and phylogenetic/phylogenomic position within the genus using modern genetic and genomic tools.

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