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A new species of *Gnamptodon* (Hymenoptera: Braconidae: Telengaiinae) from Israel

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ABSTRACT

A new species of parasitoid wasp, *Gnamptodon avigail* Pisanty sp. n. (Braconidae: Telengaiinae), is described from northern Israel, its distribution presumably extending south to Saudi Arabia based on genetic barcodes and photographs. The species is associated with Christ's thorn jujube, *Ziziphus spina-christi* (L.) Desf. (Rhamnaceae), a drought-tolerant tree, and most likely attacks nepticulid leaf-mining moths feeding on the tree's foliage. This is the first species of subfamily Telengaiinae to be reported from the region of the Levant.

KEYWORDS: Afro-Arabian Rift Valley, biodiversity, Braconidae, Lepidoptera, Nepticulidae, new species, parasitoid wasps, Israel, Saudi Arabia, Telengaiinae.

INTRODUCTION

Telengaiinae Tobias, 1962 (including the former Gnamptodontinae) is a small cosmopolitan subfamily of small-sized braconid wasps, with around 100 species in seven genera (ITIS 2023; Sharkey 2025). The biology of the subfamily is poorly known, but most species are presumably parasitoids of leaf-mining moth larvae of the families Nepticulidae and Gracillariidae (Chen & van Achterberg 2019; Sharkey 2025). The subfamily remains poorly studied also in terms of molecular genetic markers, and the great majority of identified species are not associated with DNA sequences in online databases. A detailed molecular phylogeny of the subfamily is similarly lacking, casting some doubt on the clear limits of generic concepts (but see Jasso-Martínez *et al.* 2022 for a preliminary analysis of mitochondrial markers).

In the Middle East, Telengaiinae are represented by six species from the single genus, *Gnamptodon* Haliday, 1833, reported from Iran, Turkey and Saudi Arabia (Farahani *et al*. 2014; Gadallah *et al*. 2016, 2022, 2024; Beyarslan 2021). This is the largest genus in the subfamily with over 50 species worldwide, and its greatest diversity is in the Holarctic Region (Yu *et al*. 2016; Gadallah *et al*. 2022; ITIS 2023). However, specifically in the Levant (Israel, Jordan, Lebanon and Syria), telengaiine braconids remain essentially unknown. A single record of an unidentified species of *Gnamptodon* from Israel, with a likely wrong host (Coleoptera: Cerambycidae), was mentioned by Halperin (1986) as *Gnaptodon* sp. n. This partial and problematic

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record was overlooked or disregarded in all the literature dealing with Telengaiinae that followed (e.g. Yu *et al*. 2016; Gadallah *et al*. 2022). In the Barcode of Life Database (BOLD) (Ratnasingham & Hebert 2007), Telengaiinae are represented by 1227 sequences, only seven of which are associated with a clear species identification. Another seven Telengaiinae sequences in the database originate from the Levant, all of them *Gnamptodon* spp. collected in central Lebanon and represented by the same barcode index number (BIN). The current study gives the first detailed published record of Telengaiinae from the Levant, based on a generous series of specimens constituting a species new to science, collected from Christ's thorn jujube trees in northern Israel.

MATERIALS AND METHODS

Specimens were collected as part of a survey of parasitoid wasp assemblages inhabiting Christ's thorn jujube trees (*Ziziphus spina-christi* (L.) Desf., Rhamnaceae) in northern Israel. Field work was conducted during July 2024, when the trees were in full bloom. Specimens were collected from trees using a Vortis insect suction sampler (Burkard Manufacturing Co. Ltd, Rickmansworth, UK), and stored in ethanol.

Morphological terms follow van Achterberg (1993) and van Achterberg & Shaw (2016). Measurements were made using an ocular micrometer. Photographs of type series specimens were taken using a ToupTek XCAM4K8MPB colour camera through a Leica M125 stereomicroscope with a Leica Plan APO 1.0× M Series objective and a Leica LED5000 HDI dome illuminator. Additional photographs of non-type specimens collected in Saudi Arabia were obtained from BOLD. Raw photographs were stacked using Helicon Focus 8.2.15 (Helicon Soft Ltd., Ukraine) and edited in Adobe Photoshop 24.6.0.

DNA was extracted from two ethanol-preserved samples using the Genomic DNA Mini Kit (Tissue) (GT100, Geneaid). Samples were digested overnight in the extraction buffer with proteinase K at 60°C. One sample was homogenized in the tube using a pestle provided in the kit, and the second sample was only soaked in the buffer, leaving the chitinous body parts intact. The extraction continued in the morning following the manufacturers' protocol. A fragment of 1222 bp of the mitochondrial cytochrome c oxidase I (COI) was amplified and sequenced in two different PCR reactions. The barcode region of 658 bp was amplified and sequenced with the LCO1490 and HCO2198 primers (Folmer et al. 1994). Downstream, a second fragment of 553 bp was amplified and sequenced with Cl-J-2183 (alias Jerry) (5'-CAACATYTATTYTGATTYTTTGG-3') (Simon *et al*. 1994) and Cox_Calc_R1 (Belinky *et al*. 2012). Amplification of the full-length 1222 bp fragment with LCO1490 and Cox_Calc_R1 failed, therefore there are 11 nucleotides that are missing in the middle of the sequence where primers "Jerry" and HCO2198 overlap. The resulting sequences were deposited in the Barcode of Life Database, and a query was run through the database to identify related sequences.

Specimen depositories are listed under the following acronyms:

BIOUG – Centre for Biodiversity Genomics, University of Guelph, Ontario, Canada;
BMZC – Beit Margolin Zoological Collection, Oranim Academic College, Tiv'on, Israel;
RMNH – Naturalis Biodiversity Center, Leiden, the Netherlands;
SMNHTAU – The Steinhardt Museum of Natural History, Tel Aviv, Israel.

TAXONOMY

Genus *Gnamptodon* Haliday, 1833

Gnamptodon avigail Pisanty, sp. n.

LSID: urn:lsid:zoobank.org:act:91938EF3-FCAC-490B-9443-80D56FB75318.

Etymology: In the Bible, Avigail was the third wife of King David, noted for her beauty and wisdom (1 Samuel 25:3). The species is named in honour of the author's beloved sister, Avigail Lapin Gera. The species epithet is a noun in apposition.

Diagnosis: *Gnamptodon avigail* is easily diagnosed against all other western Palaearctic and Afrotropical members of the genus, by the combination of low number of antennal flagellomeres (Fig. 1A, D), extremely short marginal cell (Fig. 1F), and weakly differentiated basal area of tergite 2 (Fig. 1E). All western Palaearctic members of the genus have antennae with ≥15 flagellomeres, and the closest members with ≤14 flagellomeres are known from India (*G. indicus* Narendran & Rema, 1996, *G. topali* Papp, 1997) and East Africa (*G. bini* van Achterberg, 1983, *G. unifossa* Fischer, 1963). Of these, *G. bini*, *G. indicus* and *G. topali* are easily excluded by the much larger marginal cell. The closest species is *G. unifossa* described from Tanzania, which shares a short marginal cell and a weakly differentiated basal area of tergite 2, but differs by the yellow distal tergites and the 14 antennal flagellomeres of the female (12–13 in the female of *G. avigail*; the male of *G. unifossa* is unknown). The closest species with 15 flagellomeres (*G. breviradialis* van Achterberg, 1983, *G. isoplasticus* Fischer, 1971, *G. nieukerkeni* van Achterberg, 1983, *G. similis* van Achterberg, 1983, *G. simulans* Ahmad, 2008) also all have longer marginal cells.

Description: ***Female.*** Body length 1.3–1.4 mm. Fore wing length 1.1–1.2 mm.

Head: 1.5× broader than long. Face, vertex and gena smooth and shiny, with short and sparse, semi-erect whitish setae (Fig. 1C, D). Antenna with 12–13 flagellomeres, relative lengths of F1, F2 and penultimate segment 1.3:1.15:1. F1, F2 3×, 3.5× as long as broad (Fig. 1A, D). Stemmaticum slightly elevated, ocelli arranged in equilateral triangle, POL:OD:OOL = 1:1:1.5 (Fig. 1C). Compound eye 1.2× as long as broad, 1.7× as broad as temple in lateral view. Malar space 0.4× as long as compound eye. Vertex and gena posteriorly almost rounded, with only hint of carina (Fig. 1A, C).

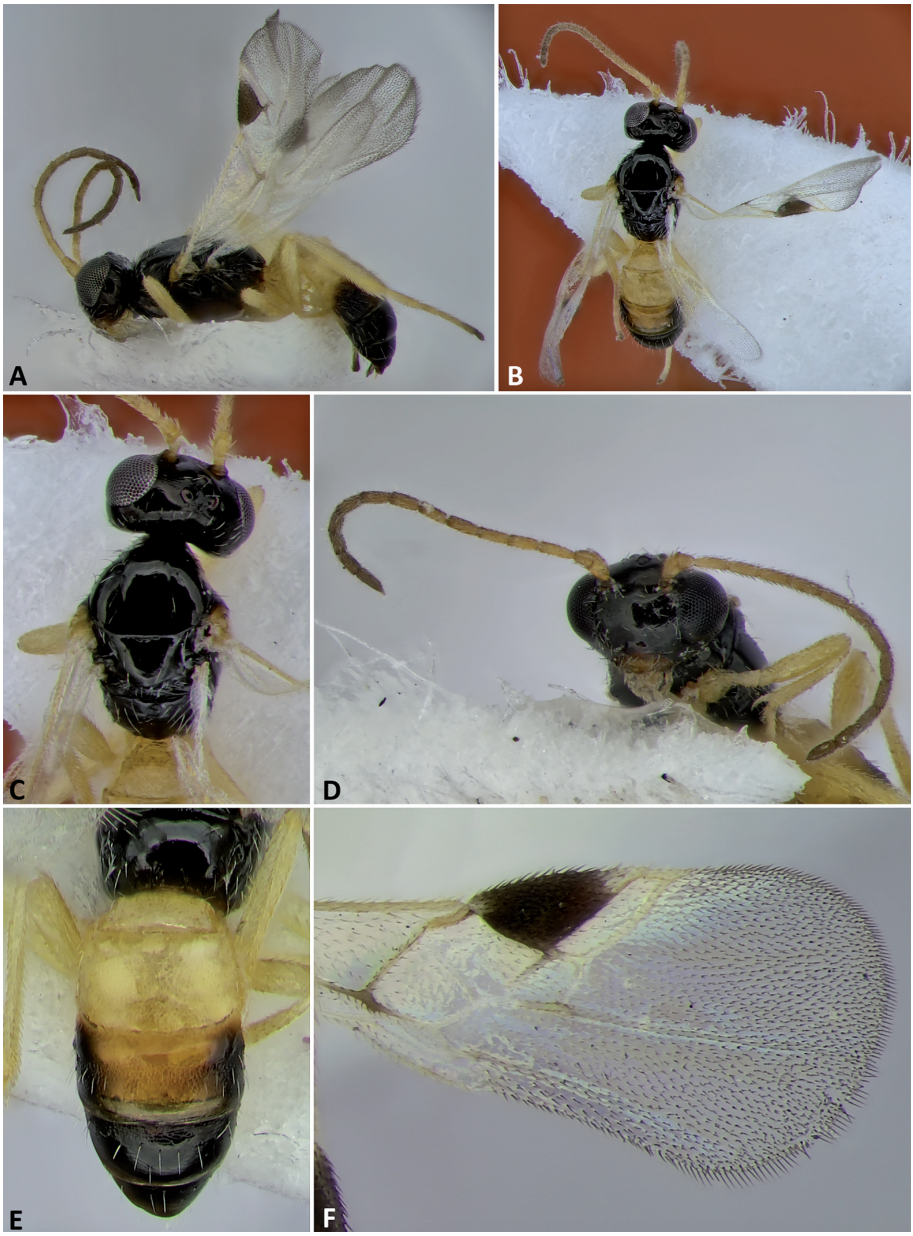

Fig. 1. *Gnamptodon avigail* sp. n., female paratypes: (A) habitus, lateral view; (B) habitus, dorsal view; (C) head and mesosoma, dorsal view; (D) head, frontal view; (E) propodeum and metasoma, dorsal view; (F) fore wing.

Fig. 2. *Gnamptodon avigail* sp. n., barcoded female from Saudi Arabia, dorsal view. Photo credit: CBG Photography Group, Centre for Biodiversity Genomics, 2026.

Mesosoma: Mesoscutum, scutellum, mesopleuron and propodeum smooth and shiny, with short and sparse whitish setae (Fig. 1C). Propodeum with two minute mediolateral longitudinal carinae near apex (Fig. 1E).

Wings: Pterostigma 2.3× as long as broad. Marginal cell extremely short, vein 1-R1 0.25× length of pterostigma. 3-SR : SR1 = 1 : 3.5; 2-SR : 3-SR : r-m = 2 : 1 : 1.5 (Fig. 1F).

Legs: Relative lengths of hind femur, tibia and tarsus 1:1.3:1.3. Hind femur and tibia 3.5× and 7× as long as broad. Hind basitarsus 0.35× as long as tarsus, 4× as long as broad (Fig. 1A).

Metasoma: Relative lengths of T1–T3 1.2:1.3:1. T1 1.4× broader than long, mostly smooth centrally, coriaceous laterally, lateral carinae limited to basal ⅓–½ (Fig. 1C, E). T2 1.5× broader than long, coriaceous, basal area weakly elevated, smoother and shinier than rest of tergite, medially occupying 0.35× tergite length. Second metasomal suture distinctly impressed. T3 with basal half smooth and slightly elevated, apical half coarsely coriaceous. T4–5 more or less smooth (Fig. 1E). Ovipositor about half as long as hind tibia.

Colour: Antenna brownish-yellow, becoming slightly darker distally (Fig. 1A, D). Clypeus brownish basally, yellowish apically, mouthparts yellowish (Fig. 1D). Remainder of face, vertex and gena black (Fig. 1A–D). Mesosomal cuticle black,

tegulae yellow (Fig. 1A–C, E, F). Wings opacified by dense setae, veins whitish-translucent to yellowish, pterostigma black (Fig. 1F). Legs yellow, apical tarsomere brownish-yellow, pretarsus black (Fig. 1A–F). T1–2 yellow, T3 brownish-yellow centrally, black laterally, T4–5 mostly black (Fig. 1A–C, E, F).

Male. Similar to female, except: antenna with 13–14 (rarely 15) flagellomeres.

Consensus barcode sequence:
TGTTTTATATTTTTTATATGGTATATGGGCTGGTATAGTAGGTTTATCAATA
AGGTTAATTATTCGATTAGAATTAGGTATACCTGGTAGATTATTAACTAATG
ATCAAATTTATAATAGAATAGTTACAGCTCATGCATTTGTTATAATTTTTTT
TATAGTTATGCCTGTAATAATTGGTGGATTTGGTAATTGATTAGTTCCTTTA
ATATTAGGAGCACCAGATATAGCTTTCCCACGAATAAATAATATAAGATTT
TGACTATTAATTCCTTCATTAATTTTATTATTTTTAAGAGGATTTTTAAATGT
AGGAGTTGGTACAGGGTGAACAATATATCCACCTTTATCTTCTTTAATGGG
TCATAGGGGGTTATCAGTTGATTTAGCTATTTTTTCTTTACATTTAGCTGGT
GCTTCATCGATTATAGGAGCTATTAATTTTATTTCAACAATTTTTAATATAC
GTTTAATTTATTTAAAATTAGATCAAATAAGATTAATAATTTGATCAATTTT
AATTACTGCTTTTTTATTATTATTATCATTACCTGTTTTAGCTGGTGCAATTA
CAATATTATTAACTGATCGAAATTTAAATACTACTTTTTTTGATTTTAGAGG
AGGAGGTGATCCAATTTTATTTCAACATTTATTT

Holotype: ♀ 485679 **Israel:** Reshafim, 32.485°N 35.470°E, –114 m a.s.l., vii.2024, N. Saabna, suction, on *Ziziphus spina-christi* (L.) Desf. (SMNHTAU).

Paratypes: Israel: 14♀, 484621, 485680 to 485692, Reshafim, 32.485°N 35.470°E, –114 m a.s.l., vii.2024, N. Saabna, suction, on *Ziziphus spina-christi* (L.) Desf. (SMNHTAU); 16♂, 485697 to 485712, same data (SMNHTAU); 2♀, 2♂, same data (BMZC); 2♀, 2♂, same data (RMNH); 1♀, 484622, same data, BOLD accession no. GPHYM002-25 (SMNHTAU); 5♀, 485723 to 485727, Tirat Zevi, 32.427°N 35.5245°E, –208 m a.s.l., vii.2024, N. Saabna, suction, on *Ziziphus spina-christi* (L.) Desf. (SMNHTAU); 6♂, 485717 to 485722, same data (SMNHTAU).

Other material examined: Israel: 1♂, 484623, Reshafim, 32.485°N 35.470°E, –114 m a.s.l., vii.2024, N. Saabna, suction, on *Ziziphus spina-christi* (L.) Desf., BOLD accession no. GPHYM001-25, specimen completely destroyed for DNA analysis (SMNHTAU).

Material examined by photograph: Saudi Arabia: 1♀, Jeddah, Hada Al-Sham Farm and Research Station, 21.7954°N 39.7107°E, 24.iv–1.v.2014, J. Sabir, Malaise trap, BOLD accession no. GMSUD424-14, BIOUG 17673-H07; 1♂, same data, 1–8.v.2014, BOLD accession no. GMSUE157-14, BIOUG 17735-A12; 1♀, same data, 29.v–5.vi.2014, BOLD accession no. GMSUI428-15, BIOUG 18272-D08; 1♂, same data, BOLD accession no. GMSUI467-15, BIOUG 18272-G11; 1♀, same data, 26.vi–3.vii.2014, BOLD accession no. GMSUM231-15, BIOUG 18771-H07.

Material not examined: Saudi Arabia: 1 (sex unknown), Jeddah, Hada Al-Sham Farm and Research Station, 21.7954°N 39.7107°E, 8–15.v.2014, J. Sabir, Malaise trap, BOLD accession no. GMSUF334-14, BIOUG 17880-C03; 1 (sex unknown), same data, BOLD accession no. GMSUF346-14, BIOUG 17880-D03; 1 (sex unknown), same data, BOLD accession no. GMSUF412-14, BIOUG 17881-A10; 1 (sex unknown), same data, 15–22.v.2014, BOLD accession no. GMSUG397-14, BIOUG 18053-F03; 1 (sex unknown), same data, 29.v–5.vi.2014, BOLD accession no. GMSUI512-15, BIOUG 18273-C09; 1 (sex unknown), same data, 19–26.vi.2014, BOLD accession no. GMSUL190-15, BIOUG 18538-D02; 1 (sex unknown), same data, 26.vi–3.vii.2014, BOLD accession no. GMSUM232-15, BIOUG 18771-H08; 1 (sex unknown), same data, BOLD accession no. GMSUM311-15, BIOUG 18772-G04.

Host: *Gnamptodon avigail* sp. n. presumably parasitizes *Stigmella* spp. (Lepidoptera: Nepticulidae), known to feed on *Ziziphus* spp. (Rhamnaceae), the trees on which

the wasps were collected (Halperin & Sauter 1992; van Nieukerken 2010; van Nieukerken *et al.* 2016; Stonis *et al*. 2020). The most likely candidate is *S. birgittae* Gustafsson, 1985, which feeds on *Z. spina-christi* in Israel, the Arabian Peninsula and North Africa (van Nieukerken 2010; van Nieukerken *et al*. 2016).

Remarks: The barcoded specimens from Saudi Arabia closely match the type series in nucleotide sequence (97.6–98.2% identity, data accessed on December 2025) and in morphology (based on photographs, Fig. 2); *Z. spina-christi* trees are known from the Hada Al-Sham (Hindi 2025). This implies a broad distributional range of *Gnamptodon avigail* sp. n. along a part of the Afro-Arabian Rift Valley.

DISCUSSION

The typical morphology of *Gnamptodon avigail* sp. n. (antennae with a few flagellomeres, close affinity to *G. unifossa* from tropical Africa), suggests its tropical evolutionary origin. This is also reflected by the typical tropical and subtropical distributions of the plant host – *Z. spina-christi*, and the presumed larval host: *S. birgittae* belongs to a group of species feeding on Rhamnaceae (van Nieukerken 2010). It is possible that both the wasps and their lepidopteran hosts have evolved in close association with this specific group of plants, and more research on the biology and host relationships of this minute, intriguing group of wasps will shed more light also on its enigmatic evolutionary history. Future studies should examine the life cycle, behaviour, and seasonal activity of *G. avigail* sp. n. to clarify its ecological role, and investigate its association with *Z. spina-christi* trees to inform conservation strategies for maintaining local parasitoid diversity in arid and semi-arid areas.

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