

# First record of the genus *Sathon* Mason, 1981 (Hymenoptera, Braconidae, Microgastrinae) in China

Zhen Liu<sup>1,2</sup>, Jia-Jun Liu<sup>3</sup>, Jun-Hua He<sup>2</sup>, Xue-Xin Chen<sup>2</sup>

**1** Zoology Key Laboratory of Hunan Higher Education College of life and environmental sciences, Hunan University of Arts and Science, Changde 415000, China **2** Institute of Insect Sciences, Zhejiang University, Hangzhou 310058, China **3** Hunan Applied Technology University, Changde 415000, China

Corresponding author: Zhen Liu ([qingniao8.27@163.com](mailto:qingniao8.27@163.com))

Academic editor: Jose Fernandez-Triana | Received 28 September 2022 | Accepted 13 December 2022 | Published 17 February 2023

<https://zoobank.org/64EBC59C-DCAB-41FA-B34A-6E432820F4BF>

**Citation:** Liu Z, Liu J-J, He J-H, Chen X-X (2023) First record of the genus *Sathon* Mason, 1981 (Hymenoptera, Braconidae, Microgastrinae) in China. *Journal of Hymenoptera Research* 95: 85–94. <https://doi.org/10.3897/jhr.95.95646>

## Abstract

*Sathon* Mason, 1981 is reported for the first time from China through providing a diagnosis, description, and images of *Sathon falcatus* (Nees, 1834). The mitochondrial genome of *S. falcatus* was sequenced, annotated and analysed.

## Keywords

China, Microgastrinae, mitogenomics, *Sathon*

## Introduction

The genus *Sathon* was erected in the tribe Microgastrini by Mason (1981) based on some species from the *vitripennis*- and *falcatus*-groups of *Apanteles* s.l. (Nixon, 1965). Williams (1985) separated three species from *Sathon* Mason and erected a new genus, *Lathrapanteles* Williams, from the New World sooner after its determination. And later, Williams (1988) revised *Sathon* while reporting five new species from the New World. Austin & Dangerfield (1992) added two new species and three new combinations to this genus when reviewing species from the Australasian region. Recently, Fagan-Jeffries et al. (2019) reported one new species from Australia and Fernandez-Triana et al.

(2020) transferred six species from Ethiopian *Microgaster* Latreille to *Sathon* in sorting the world checklist of Microgastrinae parasitoid wasps.

So far, 23 species (Fernandez-Triana et al. 2020) have been described under this genus worldwide. It was strange that none had ever been reported from China before this study, not to speak of *Sathon falcatus* (Nees, 1834), typical representative of Williams's (1988) *S. falcatus*-group in the Old World which is distributed in 42 countries, including some neighboring countries of China, e.g., Japan, Korea, Mongolia, and Russia. We luckily found this species which represents a new genus record of China in Inner Mongolia during our ongoing revision of the Chinese Microgastrinae.

The status of the genus *Sathon* has been discussed by some taxonomists since it was established. Whitfield et al. (2002, 2009) and Arias-Penna et al. (2019) suggested that *Sathon* should likely be subsumed within *Glyptapanteles* Ashmead because they shared many characters. Plus, van Achterberg (2003) and Fernandez-Triana (2010) suggested that *Sathon* and *Glyptapanteles* should be part of an expanded *Protapanteles* Ashmead. It also has complicated relationships with the genera *Choeras* Mason and *Lathrapanteles* (Fagan-Jeffries et al. 2019; Austin and Dangerfield 1992; Fernandez-Triana et al. 2020).

Microgastrine is considered as the most species-rich subfamily of animals on Earth and has become a key group of organisms for studying parasitism, parasitoid genomics, and mating biology (Whitfield et al. 2018). Nuclear genes (Banks et al. 2006), mitochondrial COI, 16S, and 28S genes, along with morphological characters (Mardulyn et al. 1999; Whitfield et al. 2002) and anchored hybrid enrichment data (Parks et al. 2020) had been applied in earlier molecular studies. Here, we present the mitochondrial sequence of *S. falcatus*, which we hope it will be useful for subsequent phylogenetic studies in the subfamily.

## Material and methods

### Collection, Identification and DNA extraction

This work is based on specimens in the collections of the Parasitic Hymenoptera Collection of Zhejiang University, Hangzhou, China. Materials were all collected by hand netting in Helan Mountain, Inner Mongolia (E105°49'–106°41', N38°19'–39°22'). Each dried specimen was tagged with a unique number.

Descriptions and measurements were made using a stereomicroscope (Zeiss Stereo Discovery V8). All photographs of the wasps were taken and processed using a digital camera KEYENCE VHX-2000C. The images were further processed using Adobe Photoshop CS6. Morphological terms for body structures and measurements follow Nixon (1965) and Mason (1981). The veins follow the modified Comstock-Needham system (van Achterberg 1993). The terminology of the cuticular sculpture follows Harris (1979).

Genomic DNA was extracted from the legs of a single specimen (No. 201006962) using a Ezup Column Animal Genomic DNA Purification Kit (Sangon Biotech,

China) following the manufacturer's protocols. Extracted genomic DNA were qualified by NanoPhotometer (IMPLEN, CA, USA) and Qubit 3.0 (Invitrogen, Life Technologies, Carlsbad, CA, USA) and a Nanodrop 2000c Spectrophotometer (Thermo Scientific, Wilmington, DE, USA). All residual DNAs are archived ( $-30\text{ }^{\circ}\text{C}$ ) in the molecular laboratory of Hunan University of Arts and Science, Changde, China, and are available for further study upon request.

## Genome sequencing, assembly and annotation

The extracted genomic DNA of the specimen was sheared into fragments of approximately 350 bp in length using the Ultrasonic Processor Covaris S220 (Covaris, Inc. MS, USA). High-throughput sequencing libraries were constructed using the Illumina TruSeq DNA PCR-Free HT Kit and sequenced using an Illumina Novaseq6000 with the strategy of producing 150 bp paired-ends by the Annoroad Gene Tech. (Beijing) Co., Ltd. Quality of raw sequencing reads was checked by FastQC version 0.11.3 (Andrews 2010), and low-quality reads and sites were filtered by Trimmomatic version 3.2.57 (Bolger et al. 2014).

The target mitochondrial reads were filtered out using BLAST (BLASTn with E value:  $1 \times 10^{-5}$ ) against a reference data set containing Braconidae mitochondrial genomes via the FastqExtract script (Crampton Platt et al. 2015). The mitochondrial genome of *Sathon falcatus* was assembled by IDBA\_UD version 1.1.3 (Peng et al. 2012) and SPAdes version 3.15.2 (Bankevich et al. 2012) with default parameters.

Annotation of the assembled genome was performed by using MITOS Web Server (Bernt et al. 2013). Start and stop codons of protein-coding genes (PCGs) were manually adjusted in Geneious Prime v11 by referencing to the published mito-genomes of Microgastrinae. Gene rearrangements were analyzed by comparing with the putative ancestral type of *Drosophila melanogaster* (Diptera: Drosophilidae).

## Results

### Taxonomy

#### Genus *Sathon* Mason, 1981

*Sathon* Mason, 1981: 78. Williams 1988: 540; Austin and Dangerfield 1992: 52; Fagan-Jeffries et al. 2019: 427. Fernandez-Triana et al. 2020: 945.

**Type species.** *Apanteles neomexicanus* Muesebeck, 1920, by original designation.

**Diagnosis.** Areolet of fore wing present or absent; metanotum with sublateral lobes slightly setose, exposing postero-lateral phragma of scutellum; propodeum with median carina present over most of length or almost completely absent, but marked by at least a trace of rugosity; tergite I somewhat narrow, length at least  $3.0\times$  longer than

apical width; tergite II subtriangular; hypopygium evenly sclerotized, without striae mid-ventrally; ovipositor sheaths at least half as long as hind tibia; often with large external genitalia in male.

**Host.** Bombycidae: *Bombyx mori* (L., 1758); Limacodidae: *Cheromettia lohor* (Moore, 1859), *C. sumatrensis* (Heylaerts, 1884); Noctuidae: *Actinotia polyodon* (Clerck, 1759), *Apamea lateritia* (Hufnagel, 1766), *Apamea monoglypha* (Hufnagel, 1766); Papilionidae: *Papilio zelicaon* Lucas, 1858; Pterophoridae: *Adaina microdactyla* (Hübner, 1813), *Emmelina monodactyla* (L., 1758); Psychidae: *Hyalarcta huebneri* (Westwood, 1854); *H. nigrescens* (Doubleday, 1845), *Narycia* Stephens, 1836; Sesiidae: *Synanthedon tipuliformis* Clerck, 1759, *Zeiraphera griseana* (Hübner, 1799); Tortricidae: *Rhyacionia buoliana* (Denis & Schiffermüller, 1775) (Yu et al. 2016; Fernandez-Triana et al. 2020). This list of hosts records was compiled in a non-critical way by Yu et al. (2016) from the literature and it is very likely that several (perhaps many) records are inaccurate or erroneous.

**Distribution.** Worldwide.

### *Sathon falcatus* (Nees, 1834)

*Microgaster falcatus* Nees von Esenbeck 1834: 175; type lost, Neotype designated by Wilkinson 1945: 113, ♀ – Germany: Zoologisches Museum, Hamburg University.

*Microgaster equestris* Haliday, 1834. Synonymized by Curtis 1837: 116.

*Apanteles equestris*; Hincks, 1944: 20.

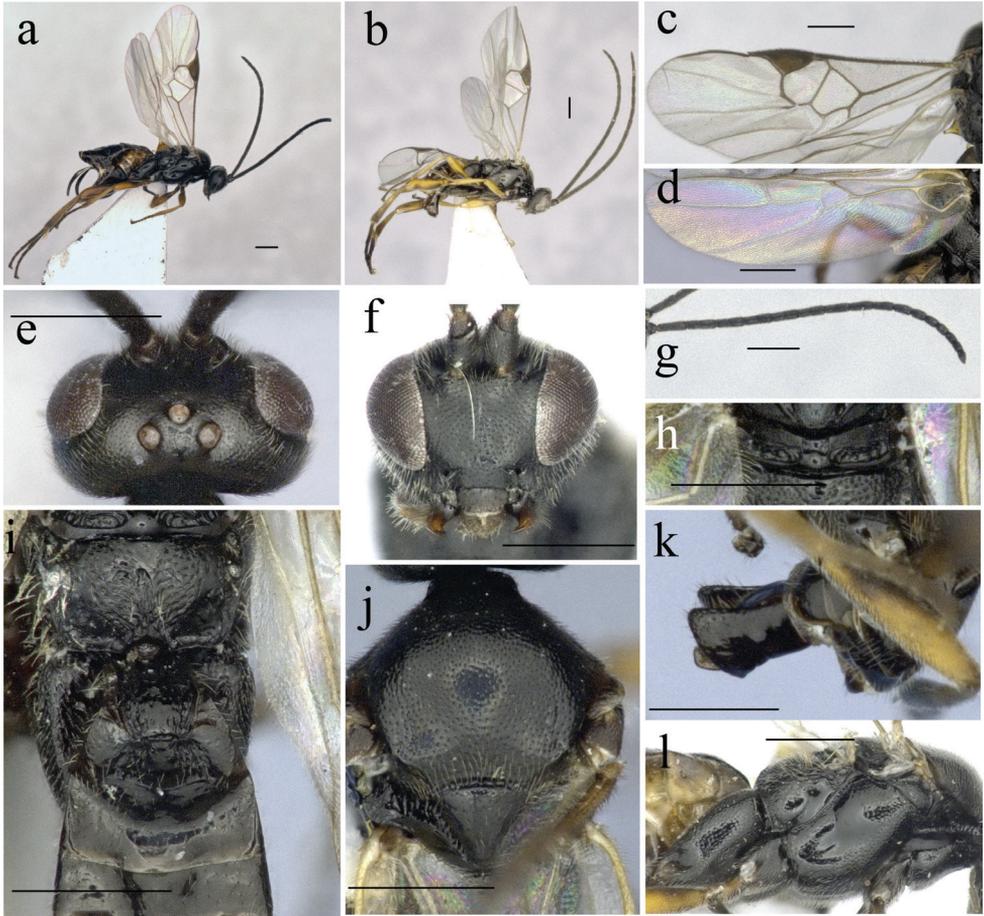
*Apanteles priapus* Gautier & Cleu, 1927. Syn. by Wilkinson 1945: 133.

*Apanteles gladiator* Szepligeti, 1901. Syn. by Tobias 1971: 246.

*Sathon falcatus*: Mason 1981: 78; Williams 1988: 560.

**Diagnosis.** Body length 3.3–3.5 mm, fore wing length 3.6–3.8 mm. Antenna nearly 1.1× longer than body length, preapical segment of antenna 1.3× longer than wide. Scutellar sulcus curved, narrow with sparse carinae in between. Propodeum 1.8× wider than long, not shiny, densely longitudinally rugose medially, with punctate-rugose aside, largely polished on anterior-medial part and posterior corners. Pterostigma 2.3× as long as its widest part. Tergite I slightly narrowing towards posterior margin, 2.2× longer than hind width, turned-over part as long as wide, shallowly and independently punctate, weakly rugulose-punctate laterally. Tergite II weakly striate laterally, polished medially, strongly curved apically. Ovipositor sheath 0.8× length of hind tibia, falcate.

**Head.** Transverse in dorsal view, 1.9× as wide as long, 1.1× wider than mesoscutum. Eyes 1.6× longer than temple dorsally. Gena slightly dull with poorly defined, shallow punctures, constricted behind eyes from dorsal view (Fig. 1e). Face (Fig. 1f) a little shiny with fine, sparse punctures with intervals 2–4 times of a puncture diameter, transverse, 0.8× as high as wide, sparsely pubescent. Ocelli big, posterior tangent to anterior ocellus just touching posterior pair of ocelli, distance between fore and a hind ocelli shorter than diameter of an hind ocellus, hind ocelli separated from one another



**Figure 1.** *Sathon falcatus* (Nees, 1834) (new record to China) **a** ♀, habitus, lateral view **b** ♂, habitus, lateral view **c** fore wing **d** hind wing **e** head, dorsal view **f** head, frontal view **g** antenna **h** metanotum **i** propodeum and terga I–III **j** mesosoma, dorsal view **k** male external genitalia **l** mesopleuron, lateral view. Scale line: 0.5 mm.

by 1.5× their own diameter and from eye by 1.4× their own diameter. Antenna nearly 1.1× longer than body length, preapical segment of antenna 1.3× longer than wide (Fig. 1g).

**Mesosoma.** Length:width:height = 29.0:17.5:20. Mesoscutum (Fig. 1j) shiny, no notaulic courses, punctures fine, intervals 2–3× of a puncture diameter, a little sparser posteriorly. Scutellar sulcus curved, narrow with sparse carinae in between. Scutellum shiny, with sparse punctures, intervals 2–4× of a puncture diameter. Propodeum (Fig. 1i) 1.8× wider than long, not shiny, densely longitudinally rugose medially, with punctate-rugose aside, largely polished on anterior-medial part and posterior corners. Mesopleuron (Fig. 1l) highly shiny, largely polished, except anterior part shallowly punctate, intervals 2–3× of a puncture diameter.

**Legs.** Hind coxa shallowly punctate dorsally. Inner spurs of hind tibia half-length of hind basitarsus, outer spur 2/5. Basitarsus of hind leg as long as tarsomeres 2–4.

**Wings.** Pterostigma 2.3× as long as its widest part (Fig. 1c). Vein 1-R1 1.4× length of pterostigma, nearly 4.0× longer than its distance from apex of marginal cell. Vein r arising from apex of pterostigma, nearly perpendicular to and 0.8× as long as width of latter, r 1.2× longer than 2-SR, distinctly angled at meeting, 2-M 4/5 length of 2-SR. First discal cell of fore wing nearly 1.2× wider than high. Second submarginal cell of hind wing 1.5× wider than high, vein cu-a of hind wing a little incurved (Fig. 1d).

**Metasoma.** 1.4× longer than mesosoma. Tergite I (Fig. 1i) slightly narrowing towards posterior margin, 2.2× longer than hind width, basal width 1.4× longer than apical width, basal 2/5 concave, turned-over part as long as wide, shallowly and independently punctate, weakly rugulose-punctate laterally, no longitudinal channel. Tergite II weakly striate laterally, polished medially, 1.9× wider than long in middle, strongly curved apically. Tergite III 1.6× longer than tergite II. Tergites posterior to tergite II polished, shiny, and sparsely pubescent. Hypopygium a little shorter than apex of metasoma. Ovipositor sheath 0.8× length of hind tibia, falcate.

**Colour.** Black (Fig. 1a). Tegula brown. Palpi blackish brown and spurs pale yellow. Flagellum of antenna dark brown. Mandible yellowish brown. Legs mainly reddish yellow, except sometimes hind femur, apical fourth and all tarsi fulvous. Wing membrane hyaline, vein and pterostigma brown.

**Male.** Similar to female, except preapical segment of antenna much longer, 2.5× longer, colouration of legs lighter (Fig. 1b).

**Hosts.** Noctuidae: *Actinotia polyodon* (Clerck, 1759), *Apamea lateritia* (Hufnagel, 1766), *Apamea monoglypha* (Hufnagel, 1766); Pterophoridae: *Adaina microdactyla* (Hübner, 1813); Sesiidae: *Synanthedon tipuliformis* Clerck, 1759; *Zeiraphera griseana* (Hübner, 1799); Tortricidae: *Rhyacionia buoliana* (Denis & Schiffermüller, 1775) (Yu et al. 2016; Fernandez-Triana et al. 2020, see comments above).

**Material examined.** (ZJUH). 15♀♀5♂♂, Luanchaigou, Helan Mountain, Inner Mongolia, 26.VII.2010, Jie Zeng, Nos. 201006962, 201007079, 201006956, 201006892, 201006933, 201007110, 201006901, 201006900, 201007014, 201007015, 201007019, 201007020, 201007022, 201007013, 201007113, 201006895, 201006946, 201006913, 201007100, 201006910; 108♀♀29♂♂, Dayanggou, Helan Mountain, Inner Mongolia, 27.VII.2010, Hongfei Chai, Nos. 201007246, 201007253, 201007262, 201007316, 201007391, 201007216, 201007397, 201007399, 201007404, 201007401, 201007396, 201007395, 201007394, 201007380, 201007388, 201007402, 201007406, 201007400, 201007389, 201007390, 201007418, 201007414, 201007332, 201007331, 201007430, 201007429, 201007431, 201007433, 201007435, 201007255, 201007282, 201007434, 201007387, 201007386, 201007385, 201007341, 201007343, 201007359, 201007357, 201007377, 201007344, 201007345, 201007333, 201007348, 201007360, 201007371, 201007378, 201007213, 201007265, 201007252, 201007312, 201007314, 201007315, 201007352, 201007330, 201007327, 201007326, 201007325, 201007324, 201007322,

201007321, 201007318, 201007363, 201007317, 201007335, 201007307,  
 201007306, 201007303, 201007302, 201007301, 201007299, 201007297,  
 201007296, 201007293, 201007287, 201007283, 201007284, 201007278,  
 201007275, 201007272, 201007271, 201007270, 201007267, 201007264,  
 201007261, 201007257, 201007251, 201007249, 201007245, 201007244,  
 201007243, 201007242, 201007239, 201007235, 201007234, 201007229,  
 201007228, 201007227, 201007208, 201007205, 201007206, 201007209,  
 201007211, 201007212, 201007215, 201007392, 201007222, 201007204,  
 201007202, 201007201, 201007198, 201007200, 201007199, 201007196,  
 201007195, 201007194, 201007192, 201007191, 201007187, 201007186,  
 201007184, 201007185, 201007156, 201007160, 201007164, 201007162,  
 201007166, 201007169, 201007172, 201007176, 201007173, 201007174,  
 201007177, 201007179, 201007183, 201007420, 201007419; 1♀, Qianggangling,  
 Helan Mountain, Inner Mongolia, 3.VIII.2010, Dingjie Zhang, No. 201006771; 1♀,  
 Ganshuwan, Helan Mountain, Inner Mongolia, 9.VIII.2010, Yan Li, No. 201006663.

**Distribution.** China: Inner Mongolia; Afghanistan, Austria, Armenia, Azerbaijan, Belarus, Bosnia and Herzegovina, Croatia, Czech Republic, Denmark, Egypt, Estonia, Finland, France, Georgia, Germany, Hungary, Indonesia, Ireland, Italy, Japan, Kazakhstan, Kyrgyzstan, Korea, Latvia, Lithuania, Luxembourg, Macedonia, Mongolia, Montenegro, Netherlands, Poland, Romania, Russia, Serbia, Slovenia, Spain, Sweden, Switzerland, Tajikistan, Turkey, United Kingdom and Uzbekistan.

**Notes.** Characters of the examined specimens from China are mostly in agreement with the description in William (1988), except the legs are lighter (mainly reddish-yellow in female or yellow in male) than what he described (mainly rufo-fulvous in female). Characters combining large inflexible hypopygium, the length of ovipositor with its sheath and the typical large external genitalia in males (Fig. 1k, 1.5× wider than width of hind femur), could be a useful way to distinguish *S. falcatus* from other related genera in China. We treated *Sathon* provisionally as a valid genus for the Chinese fauna, with only one distinguishable representative for now, though the size of genitalia varies in other *Sathon* species.

## Genome characteristic analyses

A total of 5.76 Gb filtered clean data were produced. The incomplete mitochondrial genome of *S. falcatus* is 14,492 bp in length (GenBank accession [OP432054](#)), containing 11 PCGs, 17 tRNA genes. The entire A+T content in the *S. falcatus* mitochondrial genome was 88%, which ranged from 75.60% (cox1) to 91.7% (atp8) with 39.7% of A, 7.1% of G, 48.3% of T, and 4.9% of C. It is common to find such relative high A+T proportion in the mitochondrial genome of Hymenoptera (Oliveira et al. 2008). The sequence of *COI* gene obtained closest match with a *Sathon* sp. sequence (Sample ID: CGTURK-1557, BIN ID: [BOLD:ACE9685](#)) by 99.07% and *Sathon falcatus* sequence (Sample ID: CGTURK-1532, BIN ID: [BOLD:AAB3882](#)) by 98.45% when blasted in the BOLD (Barcode of Life Database, <http://www.boldsystems.org/>), which confirmed the conspecificity of Chinese material with other *S. falcatus* specimens.



**Figure 2.** Gene rearrangement in the mitochondrial genome of *Sathon falcatus* (Nees, 1834).

Gene rearrangements were evident when compared with the ancestral type of *Drosophila melanogaster*: remote and local inversion occurred in *trnH* and *trnY* respectively, *trnK* and *trnD* were translocated, *cox3–nad4* were shuffled (Fig. 2). The rearrangements showed on mitogenomes evidenced the rapid evolution of this group compared to other lineages of Hymenoptera.

## Acknowledgements

We thank the reviewers who critically reviewed the manuscript. Funding for this study was provided by the National Natural Science Foundation of China (32100351), Scientific Research Fund of Hunan Provincial Education Department (20K089) and Hunan Provincial Natural Science Foundation of China (2020JJ5392).

## References

- Andrews S (2010) FastQC: a quality control tool for high throughput sequence data. <http://www.bioinformatics.babraham.ac.uk/projects/fastqc/>
- Arias-Penna DC, Whitfield JB, Janzen DH, Hallwachs W, Dyer LA, Smith MA, Fernández-Triana JL (2019) A species-level taxonomic review and host associations of *Glyptapanteles* (Hymenoptera, Braconidae, Microgastrinae) with an emphasis on 136 new reared species from Costa Rica and Ecuador. *ZooKeys* 890: 1–685. <https://doi.org/10.3897/zookeys.890.35786>
- Austin AD, Dangerfield PC (1992) Synopsis of Australasian Microgastrinae (Hymenoptera: Braconidae), with a key to genera and description of new taxa. *Invertebrate Systematics* 6(1): 1–76. <https://doi.org/10.1071/IT9920001>
- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Pribelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA (2012) SPAdes: A new genome assembly algorithm and its applications to single-cell sequencing. *Journal of Computational Biology* 19(5): 455–477. <https://doi.org/10.1089/cmb.2012.0021>
- Banks JC, Whitfield JB (2006) Dissecting the ancient rapid radiation of microgastrine wasp genera using additional nuclear genes. *Molecular Phylogenetics and Evolution* 41: 690–703. <https://doi.org/10.1016/j.ympev.2006.06.001>
- Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsche G, Pütz J, Middendorf M, Stadler PF (2013) MITOS: Improved de novo metazoan mitochondrial genome annotation. *Molecular Phylogenetics and Evolution* 69(2): 313–319. <https://doi.org/10.1016/j.ympev.2012.08.023>

- Bolger AM, Lohse M, Usadel B (2014) Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics* 30: 2114–2120. <https://doi.org/10.1093/bioinformatics/btu170>
- Crampton-Platt A, Timmermans MJ, Gimmel ML, Kutty SN, Cockerill TD, Vun Khen C, Vogler AP (2015) Soup to Tree: The Phylogeny of Beetles Inferred by Mitochondrial Metagenomics of a Bornean Rainforest Sample. *Molecular Biology and Evolution* 32: 2302–2316. <https://doi.org/10.1093/molbev/msv111>
- Fagan-Jeffries EP, Cooper SJ, Austin AD (2019) New species of Australian microgastrine parasitoid wasps (Hymenoptera: Braconidae: Microgastrinae) documented through the ‘Bush Blitz’ surveys of national reserves. *Zootaxa* 4560(3): 401–440. <https://doi.org/10.11646/zootaxa.4560.3.1>
- Fernandez-Triana J (2010) Eight new species and an annotated checklist of Microgastrinae (Hymenoptera: Braconidae) from Canada and Alaska. *ZooKeys* 63: 1–53. <https://doi.org/10.3897/zookeys.63.565>
- Fernandez-Triana J, Shaw MR, Boudreault C, Beaudin M, Broad GR (2020) Annotated and illustrated world checklist of Microgastrinae parasitoid wasps (Hymenoptera, Braconidae). *ZooKeys* 920: 1–1089. <https://doi.org/10.3897/zookeys.920.39128>
- Harris RA (1979) Glossary of surface sculpturing. *Occasional Papers in Entomology of the California Department of Food and Agriculture* 28: 1–31.
- Mardulyn P, Whitfield JB (1999) Phylogenetic signal in the COI, 16S, and 28S genes for inferring relationships among genera of Microgastrinae (Hymenoptera: Braconidae). Evidence of a high diversification rate in this group of parasitoids. *Molecular Phylogenetics and Evolution* 12: 282–294. <https://doi.org/10.1006/mpev.1999.0618>
- Mason WRM (1981) The polyphyletic nature of *Apanteles* Foerster (Hymenoptera: Braconidae): A phylogeny and reclassification of Microgastrinae. *Memoirs of the Entomological Society of Canada* No. 115. 147 pp. <https://doi.org/10.4039/entm113115fv>
- Nixon GEJ (1965) A reclassification of the tribe Microgasterini (Hymenoptera: Braconidae). *Bulletin of the British Museum (Natural History), Entomology series Supplement* 2: 1–284. <https://doi.org/10.5962/p.144036>
- Nees von Esenbeck CG (1834) *Hymenopterorum Ichneumonibus affinium monographiae, genera Europaea et species illustrantes, 1. Stuttgartiae et Tubingae.* 320 pp. <https://doi.org/10.5962/bhl.title.26555>
- Oliveira D, Raychoudhury R, Lavrov DV, Werren JH (2008) Rapidly evolving mitochondrial genome and directional selection in mitochondrial genes in the parasitic wasp *Nasonia* (Hymenoptera: Pteromalidae). *Molecular Biology and Evolution* 25: 2167–2180. <https://doi.org/10.1093/molbev/msn159>
- Parks KS, Janzen DH, Hallwachs W, Fernández-Triana J, Dyer LA, Rodriguez JJ, Arias-Penna DC, Whitfield JB (2020) A five-gene molecular phylogeny reveals *Parapanteles* Ashmead (Hymenoptera: Braconidae) to be polyphyletic as currently composed. *Molecular Phylogenetics and Evolution* 150: e106859. <https://doi.org/10.1016/j.ympev.2020.106859>
- Peng Y, Leung HCM, Yiu SM, Chin FYL (2012) IDBA-UD: A de novo assembler for single-cell and metagenomic sequencing data with highly uneven depth. *Bioinformatics* 28(11): 1420–1428. <https://doi.org/10.1093/bioinformatics/bts174>
- Tobias V (1971) Review of the Braconidae (Hymenoptera) of the USSR. *Trudy Vsesoyuznogo Entomologicheskogo Obshchestva* 54: 156–268.

- Whitfield JB, Benzing A, Ponce F (2002) Review of the *Glyptapanteles* species (Hymenoptera: Braconidae, Microgastrinae) attacking noctuids in field crops in the Neotropical Region, with description of two new species from the Ecuadorian Andes. *Journal of Hymenoptera Research* 11: 152–165.
- Whitfield JB, Rodriguez JJ, Masonick PK (2009) Reared microgastrine wasps (Hymenoptera: Braconidae) from Yanayacu Biological Station and environs (Napo Province, Ecuador): diversity and host specialization. *Journal of Insect Science* 9(1): 31. <https://doi.org/10.1673/031.009.3101>
- Whitfield JB, Austin AD, Fernandez-Triana J (2018) Systematics, Biology, and Evolution of Microgastrine Parasitoid Wasps. *Annual Review of Entomology* 63: 389–406. <https://doi.org/10.1146/annurev-ento-020117-043405>
- Wilkinson DS (1945) Description of palearctic species of *Apanteles* (Hymen., Braconidae). *Transactions of the Royal Entomological Society of London* 95(3): 35–226. <https://doi.org/10.1111/j.1365-2311.1945.tb00436.x>
- Williams DJM (1985) The New World genus *Lathrapanteles* n. gen.: phylogeny and placement in the Microgastrinae (Hymenoptera: Braconidae: Cotesiini). *Canadian Journal of Zoology* 63(8): 1962–1981. <https://doi.org/10.1139/z85-289>
- Williams DJM (1988) Classification, phylogeny and zoogeographic studies of species of *Sathon* Mason (Hymenoptera: Braconidae). *Quaestiones Entomologicae* 24(4): 529–639.
- van Achterberg C (1993) Illustrated key to the subfamilies of the Braconidae (Hymenoptera: Ichneumonoidea). *Zoologische Verhandelingen (Leiden)* 283: 1–189.
- van Achterberg C (2003) Western Palaeartic genera of the subfamily Microgastrinae: A reappraisal of the generic and tribal division (Hymenoptera: Braconidae). In: Melika G, Thuróczy C (Eds) *Parasitic wasps. Evolution, systematics, biodiversity and biological control* (Agroinform Budapest): 19–35.
- Yu DSK, van Achterberg C, Horstmann K (2016) *Taxapad 2016, Ichneumonoidea 2015*. Database on flash-drive. Nepean, Ontario. <http://www.taxapad.com>