

# DNA barcoding reveals the Palaearctic species *Histeromerus mystacinus* (Hymenoptera: Braconidae: Rhyssalinae) in eastern North America

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**Abstract**—DNA barcode analysis of specimens belonging to the genus *Histeromerus* Wesmael, 1838 (Hymenoptera: Braconidae) reveals the presence of two species in North America. One is identified as *H. canadensis* Ashmead, 1891, which is widely recorded in North America, while the other is *H. mystacinus* Wesmael, 1838, a species formerly known only from the western Palaearctic.

*Histeromerus* Wesmael, 1838 (Hymenoptera: Braconidae) is a highly distinctive, small genus of cyclostome braconid parasitoid wasps with an unusual-shaped head, highly spinose protibia, and a very elongate and tapering basal metatarsomere (van Achterberg 1976). The taxonomic history of this genus is complex, having variously been classified in the Doryctinae (e.g., Shenefelt and Marsh 1976), Braconinae (van Achterberg 1976), and Histeromerinae (van Achterberg 1984; Shaw and Huddleston 1991). *Histeromerus* is now regarded as a monotypic tribe in the subfamily Rhyssalinae (Zaldívar-Riverón *et al.* 2006; Sharanowski *et al.* 2011).

Only four species have been described (Yu *et al.* 2012): *Histeromerus mystacinus* (Wesmael, 1838) from western Europe as far east as western Russia; *H. canadensis* Ashmead, 1891 originally described from Canada and occurring down the eastern side of the United States of America as far south as North Carolina, but subsequently discovered in western Europe (but so far only in the Netherlands) (van Achterberg 1992); *H. orientalis* Chou and Chou, 1991 from China, Taiwan, and Japan; and most recently, *H. clavatus* Austin and Wharton, 1992 from Australia. They are encountered more frequently by coleopterists than hymenopterists because

females spend much of their lives with their host beetle (Coleoptera) larvae rather deep inside dead wood through which they can bore using their modified head and prothoracic legs (Shaw 1995).

Using DNA barcoding sequence data we show here that two species of *Histeromerus* occur in Canada, one of them being *H. canadensis* as expected, while the second possesses sequences that cluster with *H. mystacinus* to which we assign them.

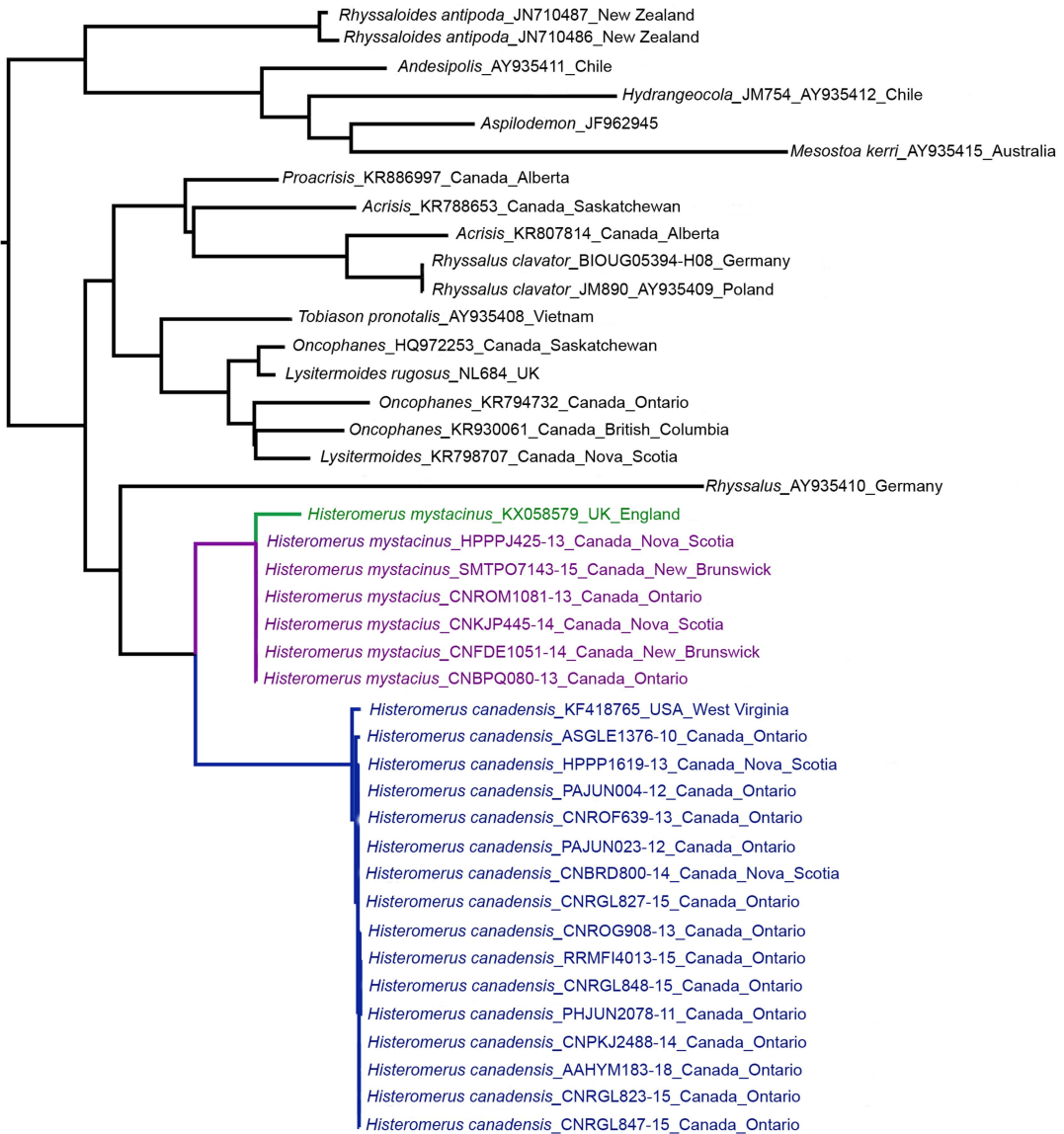
Specimens were predominantly collected in Malaise traps as part of the International Barcode of Life Project (<http://ibol.org/phase1>). They were sequenced for the 648 base pair barcode fragment of the mitochondrial cytochrome *c* oxidase subunit 1 gene using standard protocols (Ivanova *et al.* 2006; deWaard *et al.* 2008; Hebert *et al.* 2013). Additional sequences were included from the first author's publications that are deposited on Genbank ([www.ncbi.nlm.nih.gov/genbank](http://www.ncbi.nlm.nih.gov/genbank)), Barcode of Life Data System (BOLD; [www.boldsystems.org](http://www.boldsystems.org)) or GenBank accession numbers are given on the tree (Fig. 1). Specimens are deposited in the collection of the Centre for Biodiversity Genomics, Guelph, Ontario, Canada. Sequences were analysed using RAXML v8.2.X (Stamatakis 2014), using a GTR + G rate model with the three codons as separate data partitions.

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**Fig. 1.** Maximum likelihood tree based on a 658 base pair segment of near the 5', terminus of the CO1 gene. This tree includes all available *Histeromerus* sequences as well as several other Rhyssalinae species. It is rooted with representatives of the more basal subfamily Mesostoinae.



Sequences from specimens of *Histeromerus* from North America form two discrete clusters, which differ consistently at 48 of the 658 base pairs (7.3%) suggesting a long period of separation (Fig. 1). The larger cluster corresponds to *H. canadensis* and includes specimens from Ontario (Canada), Nova Scotia (Canada), and West Virginia (United States of America). The specimens in the small cluster derive from Ontario,

New Brunswick (Canada), and Nova Scotia (Canada) and associate with a *H. mystacinus* sequence from the United Kingdom. The Canadian *H. mystacinus* specimens run to this species in van Achterberg's (1992) key, and examination revealed no noticeable morphological differences when compared with European material.

The broad distribution of *H. mystacinus* in Canada, ranging between 43°N and 46°N and

60°W to 80°W, suggests that it has been there for a considerable period and is not a recent introduction. This conclusion is reinforced by fact that they differ from the United Kingdom *H. mystacinus* sequence at 14 of 652 base pairs that overlap (2.15%), a divergence value compatible with their isolation from the western Palaearctic population for at least several hundred thousand years (see *e.g.*, Brower 1994; Farrell 2001; Quek *et al.* 2004; Papadopoulou *et al.* 2010). The known Old World distribution of *H. mystacinus* is more extensive in both latitude and longitude (Belokobylskij *et al.* 2013). Longitudinally its distribution extends from Ireland in the west through to western Russia, Georgia and northern Iran in the east; and latitudinally between Campania, Italy (40.8°N) to southern Sweden and Latvia in the north (~56°N). It remains to be determined whether its North American distribution is markedly larger than what is already known.

The extensive barcoding of Canadian insects has also revealed the occurrence of several taxa that had previously only been known from the Palaearctic Region in the Canadian far north (*e.g.*, Blagoev *et al.* 2013; Landry *et al.* 2013; Fernandez-Triana *et al.* 2014). In the case of spiders (Araneae), half the species found at Churchill, Manitoba, Canada have Holarctic distributions. As more, especially taxonomically poorly known, groups such as parasitic hymenopterans are investigated, the number of known circumpolar species will almost certainly increase yet further.

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