



NOTE

New records and a DNA barcode for the brood parasitic bee *Lasioglossum ascheri* (Hymenoptera: Halictidae)

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The sweat bee genus *Lasioglossum* Curtis 1833 (Hymenoptera: Halictidae) is notable for its extreme diversity, with over 1800 described species (Ascher and Pickering 2024). Social variation is well-documented, with solitary and varying levels of social nesting observed in the genus (Michener 1974; Schwarz et al. 2007). Brood parasitism has arisen multiple times in *Lasioglossum*, in at least four locations—North America, central Africa, Samoa, and New Caledonia (Michener 2007; Pauly et al. 2013). Two separate brood-parasitic lineages occur in North America, the *L. cephalotes* (Dalla Torre 1896) and the *L. platyparius* (Robertson 1895) groups (Gibbs et al. 2012a, 2012b). The two species in the *L. cephalotes* group, *L. cephalotes* and *L. lionotus* (Sandhouse 1923), attack the closely related species *L. zephyrus* (Smith 1853) and *L. imitatum* (Smith 1853), respectively. Host records of the seven species in the *L. platyparius* group, including *L. ascheri*, are lacking, with only *L. simplex* (Robertson, 1901) associated with *L. trigeminum* Gibbs 2011 and/or *L. versatum* (Robertson 1902) (Michener 1966, 1978; Gibbs 2011). Both lineages seem to follow the loose form of Emery's rule, which states that social parasites are closely related to their hosts (Emery 1909; Bourke and Franks 1991). All known hosts belong to closely related clades (Gibbs et al. 2012a). However, it remains unclear what the hosts are for the remaining species in the *platyparius* group and whether these also follow Emery's rule.

The brood parasite *Lasioglossum ascheri* Gibbs 2011 was described from two female specimens from Westchester and Suffolk Counties in New York. Two additional females from Maryland and West Virginia, were described separately under the name *L. curculum* Gibbs 2011. The names were applied to individuals without a preapical tooth and with a distinct preapical tooth, respectively (Gibbs 2011). The names were later synonymized based on four additional females from Algonquin Provincial Park, Ontario, Canada at the J.B. Wallis / R.E. Roughley Museum of Entomology (WRME), which had the preapical tooth present or absent (Gardner and Gibbs 2021). The synonymy was based on the assumption that two rare species in close proximity was less likely than variability in the mandibular character. Gibbs (2011) also suggested a minor difference in the inner metatibial spur, but this alone were not deemed sufficient given the new records and limited sampling.

Lasioglossum ascheri can be recognized as a brood parasite by its enormous head, carinate pronotum, and reduced pollen-collecting and nest-building structures (Figures 1 & 2). Specimens may have a distinct preapical tooth absent or present. In two specimens, not part of the type series, there is a tooth on one mandible but not the other (Figure 1). The mesepisternum has obscure punctation, which differs from typical members of the *L. platyparius* group, which lack any visible punctures (Gibbs 2011). The broad flat labrum distinguishes it from the similar species *L. michiganense* (Mitchell 1960), which also has a preapical tooth (Figure 3), but whose labrum has a distinct apicomedial carinate projection, which is a remnant of the dorsal labral keel of nest-building halictines (Michener 2007). Furthermore, *L. michiganense* has the gena less broad (Figure 4) and the pronotal carina less strong. *Lasioglossum platyparius* has a similar gena and pronotal carina (Figure 4), but the distinct preapical tooth is not evident (Figure 3; a very small tooth may occur), the labrum has a distinct basomedial tubercle, and tergum 3 has a row of short setae overhanging the margin, particularly evident laterally (Figure 5). These setae are absent in *L. ascheri*. *Lasioglossum rozeni* Gibbs 2011 is also similar but the hypostomal carinae are widely divergent and it also has apical setae on tergum 3 forming a weak fimbria (Figure 5).

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Figure 1. Female *Lasioglossum ascheri*. A) Head, frontal view. B) Head and mesosoma, dorsal view. C) Mandibles, showing presence (left mandible) and absence of preapical tooth (right mandible). D) Head, lateral view. Scale bar = 1 mm.

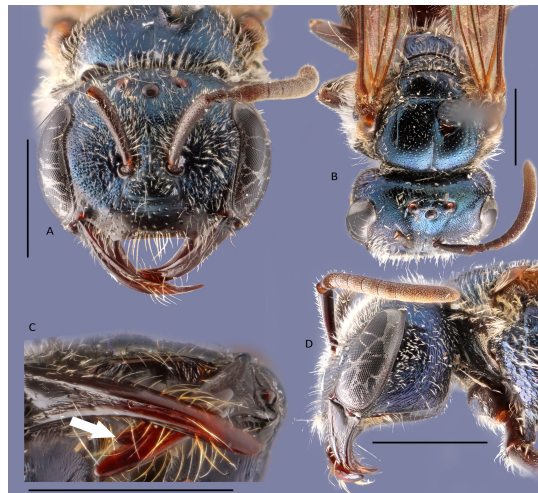
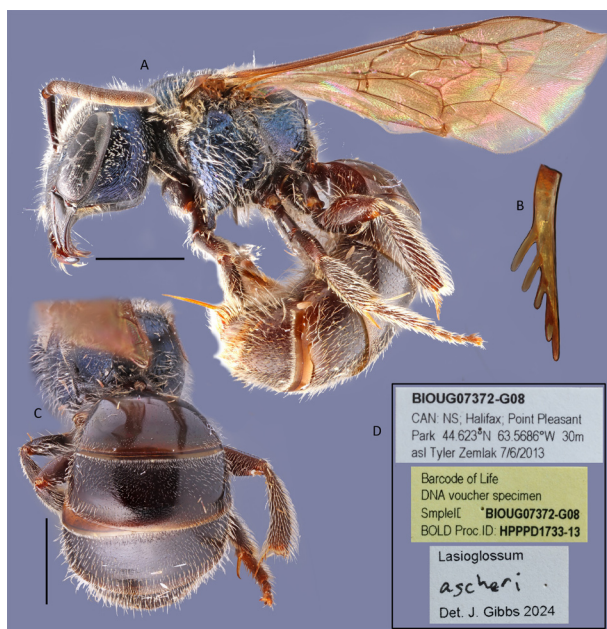


Figure 2. New Nova Scotian record of *L. ascheri*. A) Lateral habitus. B) Inner metatibial spur. C) Metasoma, dorsal view. D) Labels. Scale bar = 1 mm.



During examination of material from various sources, two new distribution records of *L. ascheri* were found: Michigan (state record; first record from the Midwestern USA), and Nova Scotia (provincial record; first record from the Maritime Provinces) (Figure 2).

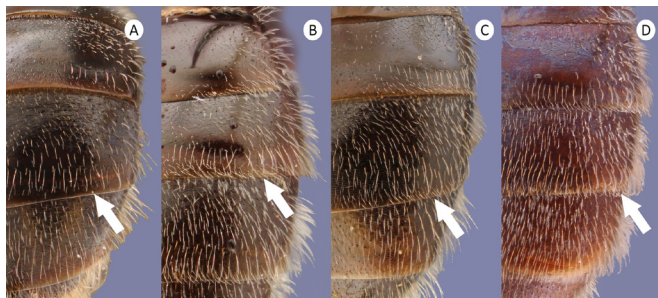
Figure 3. Female mandibles, frontal view. A) *Lasioglossum ascheri*. B) *L. platyparius*. C) *L. michiganense*. D) *L. rozeni*.



Figure 4. Female heads, lateral view. A) *Lasioglossum ascheri*. B) *L. platyparius*. C) *L. michiganense*. D) *L. rozeni*.



Figure 5. Female metasomal terga 2–4, dorsal view. A) *Lasioglossum ascheri*. B) *L. platyparius*. C) *L. michiganense*. D) *L. rozeni*.



Material examined. CANADA – Nova Scotia • 1♀; Halifax; Point Pleasant Park; 44.623, -63.5686; 20 m asl; 2013-06-07; Tyler Zemplak leg.; Centre for Biodiversity Genomics – Ontario • 1♀; Algonquin Provincial Park; 45.4487, -78.4939; 2011-06-21/07-06; E. Nardone leg.; WRME • 1♀; Algonquin Provincial Park; 45.451, -78.4704; 2011-06-28/07-11; E. Nardone leg.; WRME • 1♀; Algonquin Provincial Park; 45.451, -78.4704; 2011-06-28/07-11; E. Nardone leg.; WRME • 1♀; Algonquin Provincial Park; 45.4614, -78.423; 2011-07-26/08-10; E. Nardone leg.; WRME – UNITED STATES – Maryland • 1♀ (holotype of *L. curculum*); Laurel; [39.0992, -76.8483]; 1965-05.20; W.R.M. Mason leg.; Canadian National Collection – Michigan • 1♀; Antrim Co.; Eastport; 45.1138, -85.3326; 2015-09-06; Petrice | Haack leg.; WRME – New York • 1♀ (paratype of *L. ascheri*); Suffolk Co.; Kalbfleisch Field Research Station, Huntington; [40.868, -73.4261]; 1962-08-15; P.H. Arnaud leg.; American Museum of Natural History • 1♀ (holotype of *L. ascheri*); Westchester Co.; Pleasantville, Fellows Garden; [41.1476, -73.7768]; 2005-06.27; ex. *Oenothera*; E. Fetridge leg.; American Museum of Natural History – West Virginia • 1♀ (paratype of *L. curculum*); Hardy Co.; [39.0075, -78.8579]; 2007-06-07/27; Cornell University Insect Collection.

These new distributional records extend the range of this species >500 km to the west and approximately 900 km northeast (Figure 6). There have been recent efforts to document bees in New England (e.g., Dibble et al. 2017; Veit et al. 2022), but this species has gone undocumented. Based on the Canadian records it is plausible that *L. ascheri* occurs in all the New England states, and possibly New Brunswick and southern Quebec.

The Nova Scotian specimen has an associated partial DNA barcode (403 bp; GenBank accession: MG339688), which was sequenced at the Centre for Biodiversity

Figure 6. Distribution map of *Lasioglossum ascheri* (circles) and *L. wheeleri* (star). New distributional records are red. Created using simplemapp.net (Shorthouse 2010).

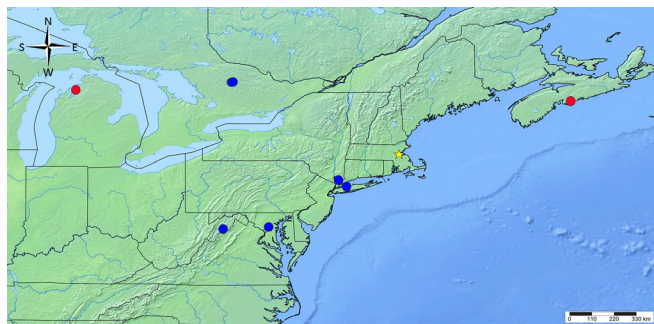
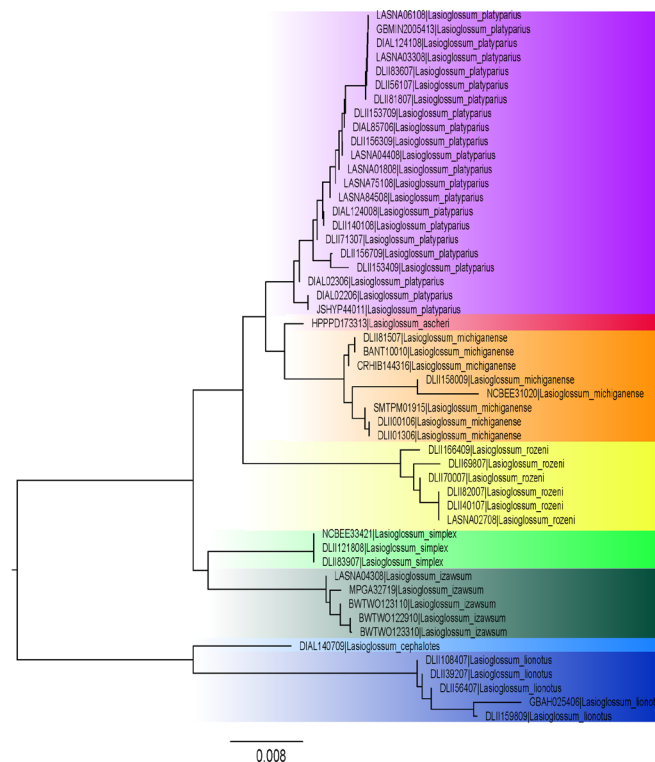


Figure 7. Neighbour-joining optimal tree of DNA barcodes available for North American brood parasitic *Lasioglossum* using Tamura 3-parameter substitution model and gamma distribution for rate variation. Analysis conducted in MEGA 11, edited in FigTree 1.4.4 and Adobe Illustrator (Adobe Inc.). The tree was rooted between the *L. cephalotes* and *L. platyparius* groups based on previous phylogenetic analyses.



Genomics. Tree-based comparison to related members of the *L. platyparius* group (Figure 7), shows closest similarity to *L. michiganense* and *L. platyparius*. Available public and private records of *L. ascheri*, *L. michiganense*, and *L.*

platyparius were downloaded from the Barcode of Life Data Systems (Ratnasingham and Hebert 2007). A minimum sequence length of 400 bp was used to match the *L. ascheri* sequence. Sequences were aligned in MEGA 11 (Tamura et al. 2021) using Muscle (Edgar 2004). The best substitution model based on the Bayesian Information Criterion was the Tamura 3-parameter model with rate variation among sites based on a Gamma distribution. Pairwise distances were calculated in MEGA using the preferred model. The minimum distance of *L. ascheri* from *L. michiganense* was 0.76% and from *L. platyparius* was 1%, which is well within expected ranges for intraspecific variation. Maximum intraspecific variation for *L. michiganense* was 2.2% and for *L. platyparius* was 1.1%. There are three apparent fixed nucleotide substitutions between *L. ascheri* and both *L. michiganense* and *L. platyparius*. Tree-based approaches consistently place *L. ascheri* outside of both other species (Figure 7). DNA barcoded vouchers of both *L. michiganense* and *L. platyparius* were examined to verify identifications.

The male of *L. ascheri* is currently unknown, but a strong candidate is the earlier described species *L. wheeleri* (Mitchell 1960), known from a single specimen collected in Forest Hills, Massachusetts in 1922. *Lasioglossum wheeleri* is likely a brood parasite based on its carinate pronotum, a feature rarely seen in male North American *L. (Dialictus)* outside of brood parasites (Gibbs 2011). *Lasioglossum wheeleri* also has a punctate mesepisternum, which is shared with the female of *L. ascheri*. A synonymy is considered premature until additional males are found, ideally sequenced, and compared directly to the *L. wheeleri* holotype.

This research highlights how much remains to be discovered relating to bee species in northeastern North America, and how little we know about some aspects of their taxonomy and biology. Our Michigan record came from by-catch during emerald ash borer surveys, which also indicates how useful sharing of unwanted specimens can be. The Nova Scotian record and its associated DNA barcode resulted from a campaign to DNA barcode Malaise trap samples led by Centre for Biodiversity Genomics. In this case, this approach was instrumental in documenting this species, however, due to the highly similar DNA barcodes in *L. (Dialictus)* (Gibbs 2018), it was crucial that this was paired with traditional morphological study. There is a great deal of additional material from these surveys that would be valuable for traditional taxonomists to incorporate into their studies.

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