



# New record of the cotton aphid, *Aphis gossypii* (Hemiptera: Aphididae) on soybean in Zambia

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## Abstract

The cotton aphid, *Aphis gossypii* (Glover), is a highly polyphagous and is distributed worldwide. It is an important agricultural pest that causes direct damage to plants and transmits many plant viruses. *Aphis gossypii* taxonomy is challenging due to similar morphology to other *Aphis* species and polymorphic variation (body size and color). It has been recorded in most African countries on cotton (*Gossypium* spp.), cowpea (*Vigna unguiculata* (L.) Walp.), cucurbits (*Cucurbita* spp.) and pepper (*Capsicum* spp.), but not on soybean (*Glycine max* (L.) Merr). In March of 2019, apterous viviparae (immature and adults, dwarfs) were found on soybean in Mpongwe, Zambia. The range of pair-wise distances of its mitochondrial cytochrome oxidase 1 (*Cox1*) sequences (MN083247 and MN083248) and *A. gossypii*'s GenBank retrieved sequences was 0.0–0.1%. Morphological observations such as the ratios of antenna processus terminalis and base (2.2–2.6, n = 5), and siphunculi and cauda (1.1–1.3, n = 5) confirmed the identity of this species.

**Keywords** Cotton aphid · Soybean · *Aphis* · Morphology · Sequences

## Introduction

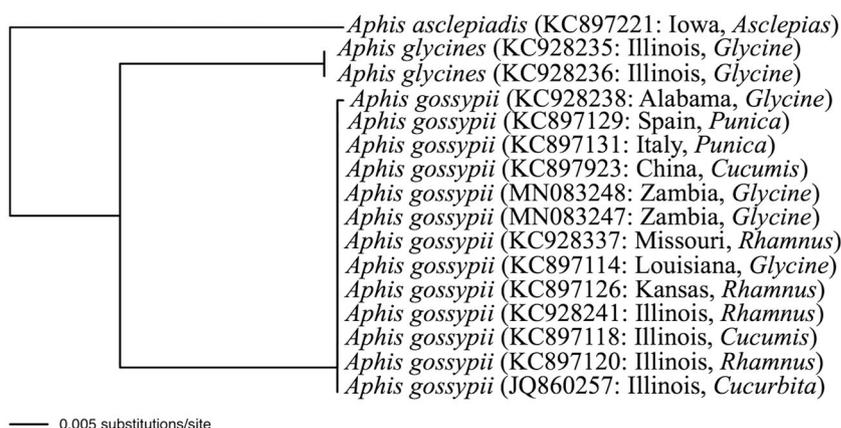
The cotton aphid, *Aphis gossypii* Glover, is an important agricultural pest because it causes direct damage even at low densities to many plant species including those belonging to the Asteraceae, Cucurbitaceae, Malvaceae, Rutaceae, and Solanaceae families (Ebert and Cartwright 1997; Blackman and Eastop 2006). *Aphis gossypii* is known to transmit many plant viruses (CABI 2019). The biology of *A. gossypii* is complex and its morphological identification is challenging (Blackman and Eastop 2006). It has many primary and secondary host plants and exhibits both holocyclic and anholocyclic life cycles (Blackman and Eastop 2006; Margaritopoulos et al. 2006). Its taxonomic complexity is attested to by its 42 available synonyms (Remaudière and Remaudière 1997). *Aphis gossypii* also has host specialized biotypes described in China (Wang et al. 2016). In North America, morphological studies show that 48 species of the

*A. gossypii* group were misidentified (Voegtlin et al. 2004), but several studies using mitochondrial, nuclear, and intron length polymorphism in the sodium channel para-type genes have achieved some resolution discriminating *A. gossypii* and other *Aphis* species (Carletto et al. 2009; Kim et al. 2010; Lagos-Kutz et al. 2014). The discrimination of species closely related to *A. gossypii* was of particular importance when the soybean aphid, *A. glycines* Matsumura, was reported in the USA (Hartman et al. 2001) since *A. gossypii* has been found on soybean, *Glycine max* (L.) Merr., as well (Blackman and Eastop 2006; Lagos-Kutz et al. 2014). *Aphis glycines* is obligately holocyclic and heteroecious, feeding on soybean as a secondary host, and on buckthorn, *Rhamnus* spp., as a primary host. *Aphis gossypii* also has been reported to colonize soybean and buckthorn in North America, and while its colonization on soybean is uncommon in the north central United States, a few specimens have been collected in Alabama and Louisiana (Lagos-Kutz et al. 2014) and Florida (S. Halbert, personal communication). These collections suggest that *A. gossypii* may infest soybean but it seems to be a non-preferred host plant in the southern part of the USA. This aphid has been recorded in most Africa countries on cotton (*Gossypium* spp.), cowpea (*Vigna unguiculata* (L.) Walp.), cucurbits (*Cucurbita* spp.), and pepper (*Capsicum* spp.), but not on soybean (CABI 2019).

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**Fig. 1** Neighbor-joining tree of K2P distances of mitochondrial gene cytochrome oxidase I of *Aphis gossypii*, *A. glycines* and the outgroup *A. asclepiadis*. Species names are followed by GenBank accession number, locality and genus of host plant



## Materials and methods

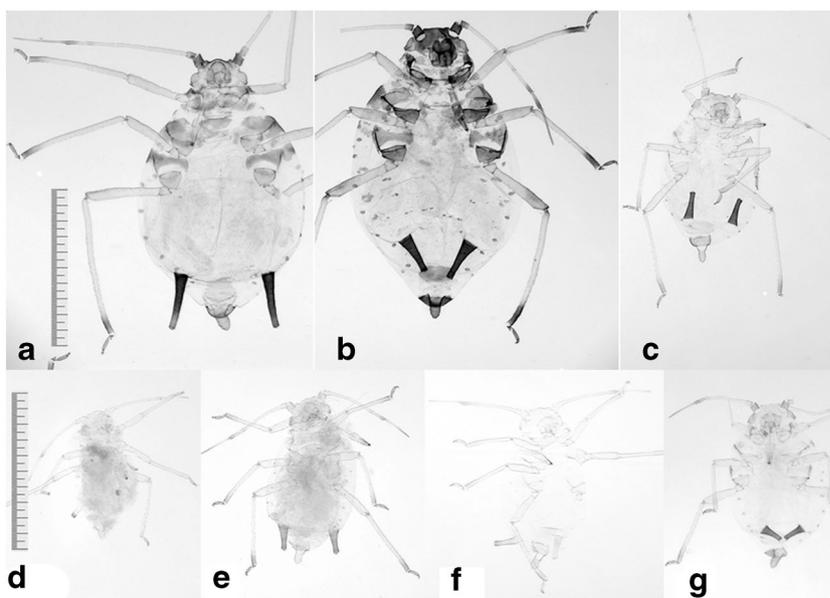
On 9 March 2019, a survey of soybean foliage was performed in research plots in Mpongwe, Zambia (-13.512000, 28.156200). In each of 10 plots representing different soybean genotypes, a soybean leaflet from the mid canopy was collected arbitrarily, and aphids were counted. A few of the aphids were hand-picked from the leaves, stored in 90% ethanol, and shipped to the USDA-ARS Laboratory for Soybean Disease and Pest Research in Urbana, Illinois for identification. Archival slides were deposited in the Illinois Natural History Survey (INHS) Insect Collection (voucher # 819422–819424). Aphids from the sample were sequenced following the mitochondrial cytochrome oxidase I (*CoxI*) (1291 bp) described in Lagos-Kutz et al. (2014). Raw sequence data were analyzed using Sequencher 4.7 (Gene Codes Corporation, Ann Arbor, MI). To calculate the pair-wise distances for *CoxI* sequences Kimura 2-Parameter distance model in PAUP 4.0b10 was used. The following sequences were

retrieved from GenBank: *Aphis asclepiadis* Fitch: KC897221, *A. glycines*: KC928235 and KC928236, and *A. gossypii*: JQ860257, KC897114, KC897118, KC897120, KC897923, KC897126, KC897129, KC897131, KC928237, KC928238 and KC928241 for building a neighbor-joining tree.

## Results and discussion

The average colony counts for 10 leaflets was  $7.3 \pm 1.5$  aphids per leaflet. Two sequences were blasted in GenBank (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>) and matched the identity of *A. gossypii* (MN083247 and MN083248). The pair-wise intraspecific sequence divergence (%) among most of the retrieved sequences, and the ones from Zambia was 0.0 and 0.1 among the comparison of these sequences to KC92823, obtained from an aphid collected on soybean in Alabama (Fig. 1). Morphological observations showed that the apterous vivipara adult specimens were smaller (body length: 0.8–1.0

**Fig. 2** Slide-mounted *Aphis gossypii* collected on different plants. (A) on *Cucumis sativus* in China (INHS: 510350), (B) on *Rhamnus cathartica* in Illinois (INHS:512278), (C) on *Cucurbita pepo* in Illinois (INHS:511639), (D) on *Glycine max* in Zambia (INHS: 819423), (E) same colony from Zambia (INHS: 819422), (F) on *Glycine max* in Alabama (INHS: 510473), (G) on *Glycine max* in Louisiana (INHS:510331). All images were magnified to 51x, and the scales in images A and D correspond to 1 mm



mm, n = 5) than those collected on other host plants (1.1–2.0 mm, n = 27) and have only five antennal segments (summer tropical forms) and not six like others (Fig. 2). Also, the color pattern of alive apterous vivipara adults is white yellowish. The siphunculi, which usually are dark, or dusky, are pale (also characteristic of summer tropical forms). The other characters such as the ratios of processus terminalis and base of antennae (2.2–2.6, n = 5), and siphunculi and cauda (1.1–1.3, n = 5) match the ratios of body size for *A. gossypii*. The cauda usually is spoon-shaped and has 4–6 hairs curved inwards (Blackman and Eastop 2006; Lagos-Kutz et al. 2014). African specimens from soybean are similar to those collected in Alabama and Louisiana (small body length with five antennal segments), based on the INHS insect collection records: 510331 and 510473.

The identification of *A. gossypii* is challenging because of its polymorphic variation (body size and color) and morphological resemblance to other *Aphis* species. Therefore, to rely solely on morphological characters can be insufficient to verify the identification of this highly polyphagous species. Additional molecular data are necessary to verify its identity for establishment of new records. The morphological characters and the color (white yellowish) of alive aphids found on soybean in Zambia matched the ones reported by other researchers (Wall 1933; Setokuchi 1981; Blackman and Eastop 2006; Lagos-Kutz et al. 2014). Wall 1933; Setokuchi 1981 stated that the yellowish aphid morphs are much smaller and occurred during warmer summer conditions. *Aphis gossypii* has been cited as one of the worst crop pests in Zambia (Javaid et al. 1987), and certainty of its identity is necessary for an integrated pest management program. By sequencing the 1291 bp of *Cox1* and finding 100% matching sequences (Fig. 1) with multiple sequences retrieved from GenBank, further molecular markers were not explored.

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## Compliance with ethical standards

**Conflict of interest** The authors declare that they have no conflict of interest.

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