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RESEARCH ARTICLE

The damage risk evaluation of *Aphis gossypii* on wheat by host shift and fitness comparison in wheat and cotton

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Abstract

Aphids are considered as one of the key pests for wheat production worldwide. Major aphid species that infest wheat in China include *Sitobion avenae*, *Rhopalosiphum padi*, *Schizaphis graminum* and *Metopolophium dirhodum*. However, during our wheat field survey in Wenshang County of Shangdong Province, China, we observed that *Aphis gossypii* can feed on wheat. The damage risk of *A. gossypii* on wheat was assessed using host shift method. A population of *A. gossypii* collected from a wheat field in 2015 and another population reared on cotton under laboratory conditions for a decade without exposure to insecticides were used in the study. The results of host shift demonstrated that the *A. gossypii* colony from wheat has not yet developed wheat specialization. Moreover, the assessment of *A. gossypii* fitness on wheat and cotton showed that fecundity and net reproductive rate of *A. gossypii* population fed on wheat was significantly higher comparing to the population fed on cotton, whether the initial host of *A. gossypii* population was wheat or cotton. This study raises a warning that the cotton aphid has potential to establish well on wheat and it may cause significant effects under specific circumstances. Therefore, future studies are required to evaluate the effects of *A. gossypii* on wheat production.

Keywords: wheat, *Aphis gossypii*, cotton, intercropping cotton with wheat, fitness

1. Introduction

Aphids (Hemiptera: Aphididae) are considered as one of the most significant problems for wheat production worldwide, including both direct (feeding) and/or indirect (as vectors of plant pathogenic viruses) damage (Migui and Lamb 2003; Xin *et al*. 2014). The grain aphid, *Sitobion avenae* (Fabricius), the bird cherry-oat aphid, *Rhopalosiphum padi* (Linnaeus), the greenbug, *Schizaphis graminum* (Rondani) and the rose-grain aphid, *Metopolophium dirhodum* (Walker), were recorded as the major wheat aphid species in China (Lu

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and Gao 2009; Zhang *et al.* 2009). However, we observed a new aphid species on wheat plants of filling stage, which was different from the species above, during a wheat field experiment in Wenshang County of Shangdong Province, China in 2015. The aphid morphologically looked similar to *Aphis gossypii*. Subsequently, we identified the species as *A. gossypii* based on the barcode region of cytochrome oxidase I (COI) (Lee *et al.* 2015), the gene that encodes ATP6 (Lee *et al.* 2014), and a length polymorphism for an intron in the sodium channel *para*-type (SCP) gene (Carletto *et al.* 2009a). Besides, Fagundes and Arnt (1978) also reported that *A. gossypii* occurred in the wheat from the glasshouses and the wheat field in Brazil, but the damage risk of *A. gossypii* on the wheat was not evaluated.

Host plant shifts are common in herbivorous insects. This allows insects to escape from natural enemies or competition and seek better nutrition (Blair *et al.* 2010; Zvereva *et al.* 2010). In addition, host plant shifts of herbivorous insects may cause sympatric speciation and can create new pests for agricultural crops (Bass *et al.* 2013; Mattsson *et al.* 2015). Life table analysis is able to provide some useful biological and demographic parameters for studying insect populations under specific conditions, and these parameters can be used as indicators for assessing the potential of the growth of a pest population under new conditions (Maia *et al.* 2000; Diaz and Fereres 2005; Obopile and Ositile 2009). Therefore, in our study, the risk of species shift between cotton and wheat was assessed using this life table. These results will be used to monitor the occurrence of wheat aphids and to control aphid damage.

2. Materials and methods

2.1. Aphid collection

Aphids were collected from a wheat field (during wheat filling stage) in Wenshang County (Shangdong Province, China) in May of 2015 and were reared and maintained for four generations on wheat seedlings under controlled laboratory conditions (a climatic chamber with temperature of (22±1)°C, relative humidity (RH) of (70±10)%, and a photoperiod of 18 h L:6 h D). Apteral individuals were used as specimens for molecular identification. In addition, a colony of cotton aphid, which was maintained on cotton seedlings under the same laboratory conditions mentioned above for more than 17 years (since 1999) without exposure to insecticides, was used for host shift assessment.

2.2. Molecular identification

Individual was crushed in a 1.5-mL microcentrifuge tube and genomic DNA was extracted using DNAVzol (Vigorous Biotechnology Beijing Co., Ltd., China), according to the standard protocol recommended by the manufacturer. The primer sequences of LEP-F1 (5′-ATTCAACAATCATAAAGATAT-3′) and LEP-R1 (5′-TAAACTTCTGGATGTCCAAAAA-3′) were used to amplify mitochondrial gene COI (Lee *et al.* 2015). The primer sequences of tRNALysAf2 (5′-GACTGAAAAGC AAAGTAATGATCTCT-3′) and CO3WWRD (5′-TCW CGAATWACATCWCGTCATCA-3′) were used to amplify ATP6 gene (Lee *et al.* 2014). The length polymorphism of an intron in SCP was sequenced using the primers Aph13 (5′-GATTGAATCAATGTGGGACTGCTTAC-3′) and Aph15 (5′-ACTCAGCAACAACGCCAAGAAAAG-3′) (Carletto *et al.* 2009a). All primers were synthesized by Huada Corporation, Beijing, China.

PCR reactions were performed in a 20-μL of reaction volume. Each reaction mixture contained 13 μL of water, 0.5 μL of *Taq* polymerase, 2.5 μL of dNTPs (2.5 mmol L^{-1}), 2.0 μL of 10×buffer (+Mg^{2+}) (TaKaRa Biotechnology Co., Ltd., Dalian, China), 1 μL of 10 μmol L^{-1} of each primer and 1 μL of DNA template (approximately 10 ng). PCR was performed using a GS1 Thermo-Cycler (Gene Technologies Ltd., UK) according to the following procedure: initial denaturation at 94°C for 5 min, followed by 30 cycles at 94°C for 30 s; an annealing temperature of 55°C for 30 s; an extension at 72°C for 40 s and a final extension at 72°C for 10 min. The PCR products were sequenced in both directions by using an ABI 3730xl Sequencer (Applied Biosystems, USA). Raw sequence data were examined and assembled using Sequencher 4.7 (Gene Codes Corporation, USA). Sequences were then aligned with Clustal X.

In order to more accurately identify whether the aphid is *A. gossypii* or not, the PCR primers (forward: 5′-ATTTATAACCTATTATCAGCCATTT-3′ and reverse: 5′-GAAATCTTAGTTTTATTCAAGTTAT-3′) were used to amplify COI of the aphid species, based on the complete mitochondrial gene of *A. gossypii* (KJ669654.1). The annealing temperature was 50°C, and other PCR conditions and methods were the same as above.

2.3. Phylogenetic analysis

In order to identify species, we retrieved 23 COI, 18 ATP6, and 5 SCP sequences (especially those of species closely related to *A. gossypii* and wheat aphids) from the GenBank database. These retrieved sequences and sequences of this species then were aligned with Clustal X (ver. 2.0, 2007). All of the sequences to be analyzed were initially examined to merge forward and reverse strands using SeqMan Pro ver. 7.1.0 (DNASTAR, Inc., Madison, WI). After the