[BIOLOGICAL DATA] (INVITED)

Bee Mite ID - an online resource on identification of mites associated with bees of the World*

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(Received 8 February 2017; Accepted 10 March 2017)

A number of bee pollinators and their ecological services are facing sharp declines due to habitat destruction, pesticide use, pathogen spillover from commercial colonies, and other causes (Buchmann and Ascher, 2005; Colla and Packer, 2008; Gallai et al., 2009; Mazer, 2007; Potts et al., 2010). In particular, significant losses of European honey bee (*Apis mellifera*) populations due to diseases and attacks by parasitic mites could result in failure of crops requiring pollination - an estimated 35% of the human diet. Currently, the development of alternative, non-*Apis* pollinators is underway. Of these, mason bees (*Osmia* spp.) and bumblebees (*Bombus* spp.) are the most important. As the pollinator trade increases worldwide, the opportunity for introductions of new harmful mites and/or host switching also substantially increases (Goka, 2010; Goka et al., 2001, 2006). In addition to the direct threat posed by parasitic mites, mites colonizing new hosts may spread harmful pathogens, such as viruses, bacteria, and fungi (Cornman et al., 2010). Only quarantine measures can prevent this situation. Unfortunately, implementing these measures is difficult because bee-associated mites are understudied, the taxonomic information is scattered, incomplete and difficult to access by the non-specialist, and few revisionary works are available. As an example, our survey of published literature records yielded 715 species, 219 genera, and 89 families of known bee-associated mites, most of which are known from honey bees (294 species) or bumblebees (91 species). For many of these mites, the geographical distributions, host ranges, and their basic biology (e.g., mites' roles in bee-mite associations: harmful, nearly neutral, or mutualistic) are unknown. As a result of this impediment, the likelihood of potential cross-border travel of harmful bee mites greatly increases. This is a critical flaw that needs to be remedied by developing a computer-assisted identification system accessible on a worldwide

* A Japanese translation has been published on the website of the Acarological Society of Japan (<http://www.acarology-japan.org/>).

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DOI: 10.2300/acari.26.25

basis. The urgent need for such a system can be illustrated by one example, the case of *Tropilaelaps* mites. This genus includes harmful mite species attacking honeybees in Asia. These are not yet established in the USA, and quarantine measures should be taken to prevent these harmful pests from entering the USA. Unfortunately, currently at the US ports of entry it is impossible to distinguish these pests from nearly 300 species of mites that have been found in association with honeybees. Many of these species are harmless neutral scavengers or beneficial predators of other pests living in honeybees nests. An electronic identification system, thus, can be instrumental in this situation to quickly detect such pests.

To address this situation and overcome the current impediment in bee mite systematics we have collaborated with the U.S. Department of Agriculture to create an online Tool, *Bee Mite ID: Bee-associated Mite Genera of the World*, <http://idtools.org/id/mites/beemites/> (Klimov et al., 2016). In this Tool, the existing mite taxonomy and basic biology is organized for convenient retrieval, synthesis, and analysis for users who have no prior knowledge of mites (Fig. 1). The tool uses modern technological and cyber-infrastructure developments.

For identification of mite genera, the Tool uses a Lucid-based electronic identification system (Fig. 1D), supplemented with relational databases containing images and data on geographical distribution, host range, biology, control, and other properties of pest or quarantine species (ID Tools, <http://idtools.org/id/mites/beemites/key.php>) (Fig. 1B). Electronic identification is a very powerful tool, especially for large datasets. In contrast to conventional dichotomous keys relying on a predefined path for identification, electronic keys use dynamic optimization at each step of identification. For example, an identification strategy can be optimized to prioritize multistate characters dividing the remaining taxon sets in equal parts. With this strategy, 256 taxa can be identified in as little as 4 steps. If 4-state characters are used ($4^4=256$); 8 steps for binary characters ($2^8=256$); or even 1 step if the identification strategy emphasizes unique characters. In addition, to computer algorithms dynamically optimizing identification, electronic keys are generally easier to use because each character state is linked to an image or a series of images, thus, making the identification more comprehensive. These properties of electronic keys make them extremely useful for inexperienced people, who are not familiar with the particular terminology necessary for identification of unknown species. As such, biosecurity agencies around the world can greatly benefit from using these electronic identification systems given the current lack of personnel trained in acarology.

In addition to the Lucid, character-based interactive identification system, our Tool extensively relies on image-based identification. There are nearly 1000 diagnostic images for different stages and sexes of mites organized by mite taxonomy as part of our Fact Sheets (http://idtools.org/id/mites/beemites/factsheet_index.php) (Fig. 2). The images are annotated and diagnostic characters are highlighted and described directly on the image (Fig. 1B, 2C,D). This provides a convenient way for the user to match the unknown mite specimen with the diagnostic image(s) and complete identification quickly.

The Tool also offers seven quick reference guides (http://idtools.org/id/mites/beemites/quick_reference.php) organized to show mites associated with specific bee groups (Fig. 1C). These seven bee groups include the most abundant and most commonly used bees for pollination worldwide, such as, honey bees, bumble bees, and stingless bees. For quick comparison, the

Fig. 2. Examples of *Fact Sheets* diagnostic images. A - Females of *Imparipes* phoretic on bee *Halictus farinosus*; photo by Lindsey Seastone & Laura Hartmann, ITP; http://idtools.org/uploads/idtools/37/223/Imparipes_on_Halictus-farinosus_BMOC_15-0606-034.jpg; B - *Horstia* (*Amhorstia*) *virginica* phoretic deutonymph, ventral view; bright field. http://idtools.org/uploads/idtools/37/223/3-Horstia_virginica_hdn_vent_BF40_HK_85-0108-004.jpg; C - *Imparipes* sp. (ex *Nomia nortoni*) female, dorsal view http://idtools.org/uploads/idtools/37/223/1-Imparipes_female_dors_BF40_BMOC_96-0916-062.jpg; D - Phoretic deutonymphs of *Horstia trifilis* on bee *Xylocopa coronata combinata* http://idtools.org/uploads/idtools/37/223/Sennertia_bifilis_Horstia_trifilis_on_Xylocopa_combinata_BMOC-05-0420-115.jpg.

seven guides show high-resolution images of each of the mite genera associated with each bee. This strategy allows, in many cases, to complete identification simply by mite overall shape, without using any detailed characters (Fig. 1C).

In conclusion, we believe that with this Tool, researchers can make valuable observations and associations about bee mites, identifying potential problem mite species and introductions, which

can support future risk assessments and detection and eradication efforts. This is especially important for citizen naturalists, beekeepers (managing either honeybees or replacement pollinators), sustainable crop growers, and backyard farming or bee garden enthusiasts, who readily use bee pollinators for their purposes. Our Tool aims to provide an understanding of the diversity and the role played by the various mite associates of native bees in their natural situations, which is necessary in order to monitor host shifts into economically important species of introduced bee pollinators (e.g., *Bombus* spp. and *Osmia* spp.) from different parts of the world). As an easy-to-use, web-based resource, this Tool will potentially allow for the dissemination of critical information pertaining to the classification and nomenclatural issues within the group. This will allow for ease of collaborative research efforts within the broader entomological and acarological communities.

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