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Short Communication

## Occurrence of Bondar's Nesting Whitefly, *Paraleyrodes bondari* (Hemiptera: Aleyrodidae), on cassava in Uganda

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### ABSTRACT

Cassava is a valued calorific source to millions of Africans who eat it daily and a vital staple for their food security. One of the key constraints to this crop is whiteflies which are both a vector of viral diseases and a direct pest. Although the African cassava whitefly is known to cause physical damage on cassava with considerable tuberous yield loss, a recent whitefly outbreak caused unusually severe damage, which prompted the current reported investigation. Molecular identification of whitefly adults sampled from the affected cassava field revealed the presence of a new whitefly species, *Paraleyrodes bondari*. This communication is the first report of the occurrence of *P. bondari* on cassava in Uganda.

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Whiteflies (Hemiptera: Aleyrodidae) are amongst the major insect pests causing direct damage to cassava in Africa. Although more than 1500 whitefly species have been described globally (Ouvrard and Martin, 2018), few are known to colonize *Manihot esculenta* Crantz (cassava, mandioca, manioc, yucca). Only eight whitefly species have been identified colonizing cassava in east Africa with *Bemisia tabaci* (Gennadius), *Aleurodicus dispersus* (Russell), and *Bemisia afer* (Priesner and Hosny) the most common in studies in Tanzania (Guastella et al., 2015) and Kenya (Kamau et al., 2005; Mware et al., 2010). Interestingly, only *B. tabaci* is reported as predominant on cassava in Uganda (Kamau et al., 2005; Legg, 1995; Mugerwa et al., 2018; Omongo, 2003).

Despite previous studies reporting limited diversity, we recently observed heavy infestation of whitefly on cassava in fields in the central region of Uganda. Infested cassava plants showed severe feeding damage such as wilting and leaf-fouling by sooty-

molds, and inspection of the leaves revealed masses of white wax on the lower surface of the leaves (Figs. 1, 2). Numerous adults, each having two oblique gray bands on the forewings, were present on the ventral surface of the leaves (Fig. 3). Conspicuous gray bands on the wing of adults and prolific white wax are not features of cassava whitefly, *B. tabaci*, which suggested that a previously undocumented whitefly species was attacking cassava in Uganda. This motivated us, as a first step, to characterize samples of the apparent “new” whitefly using molecular methods.

Adult specimens collected from cassava plants by aspiration were preserved in 90% ethanol and submitted to the Natural Resources Institute (NRI), UK for molecular characterization and to the Natural History Museum (NHM) for morphological identification and preservation. Genomic DNA was extracted from two specimens using a modified Chelex extraction method (White et al., 2009). The barcoding region located in the 5' end of the mitochondrial cytochrome oxidase I gene (mtCOI) was amplified using standard methods (Folmer et al., 1994), purified and sent to Eurofins GATC Biotech (Germany) for Sanger sequencing in both directions.

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**Fig. 1.** Severe wilting and sooty mold mass on cassava caused by heavy infestation and feeding by *P. bondari*.



**Fig. 2.** Waxy mass on the undersurface of cassava leaf due to *P. bondari* infestation.

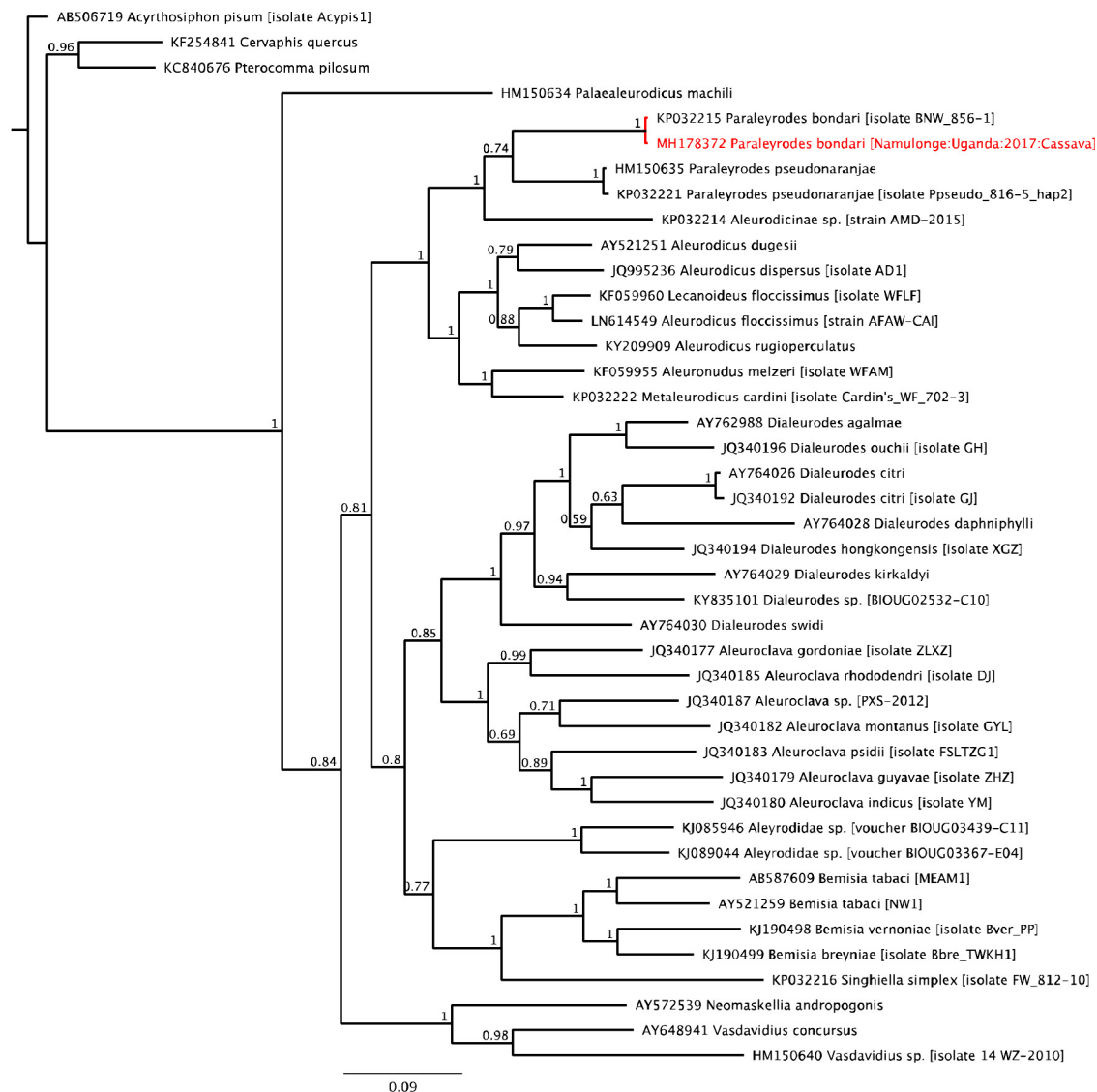


**Fig. 3.** *P. bondari* adults underneath waxy mass on cassava leaf.

Sequence analysis was performed using Geneious version 9.1.8 (Kearse et al., 2012). Contiguous mtCOI sequences were assembled, trimmed and aligned using MAFFT (Katoh and Standley, 2013). The best-fit model of evolution (Jukes-Cantor) was determined from likelihood ratio tests performed using jModeltest (Posada and Crandall, 1998). Phylogenetic relationships were reconstructed via Bayesian analyses using MRBAYES v3.1.2 (Ronquist and Huelsenbeck, 2003). Four Markov chains were run for a total of 2,000,000 generations, with chains sampled every 200 generations (the first 10% of trees were discarded as burn-in). TRACER 1.5 (Rambaut and Huelsenbeck, 2003) was used to select appropriate burn-in cycles and confirm that the effective sample size was sufficient. Aphid species (Aphididae, Hemiptera: Sternorrhyncha) were included as outgroups (Fig. 4).

Partial mtCOI sequences (632 nt) from the two adults shared 100% nt identity (haplotype GenBank accession MH178372) and 100% nt identity with Bondar's nesting whitefly *Paraleyrodes bondari* Peracchi (GenBank accession KP032215), reported as a new invasive species in Florida USA in 2011 (Dickey et al., 2015). Haplotype sequence of the Uganda specimens also grouped with sequences of the congeneric species *Paraleyrodes pseudonaranjajae* Martin, a nesting whitefly that invaded China in 2010, and form a moderately-supported clade within the phylogeny (Fig. 4). Individuals that were slide-mounted by Gillian Watson (NHM) were authoritatively identified by D. Ouvrard based on the following diagnostic characters: shape of male aedeagus; structure of cephalic and abdominal compound pores of puparium. Unpublished data from NHM collections also show that *P. bondari* was present in Uganda on cassava as early as 2006 (10 puparia on 2 slides, collected by D. Gerling on 17 March 2006 in Kampala). Taken together, these results confirm the presence and establishment of *P. bondari* in Uganda on cassava, and this plant species represent a new host for this whitefly.

Documenting the presence of this new pest in Uganda and its association with cassava provides great impetus for a Uganda-wide survey to establish the host range, distribution and pest status of this species, and is critical to understanding the threat to cassava posed by this pest and designing a suitable management strategy.



**Fig. 4.** Bayesian consensus phylogeny based on partial mitochondrial cytochrome oxidase 1 gene sequences. Haplotype sequence of *Paraleyrodes bondari* recovered in this study is shown in red. Posterior probabilities are noted above each node.

## Conflicts of interest

The authors declare no conflicts of interest.

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