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Robert I Graham (robert.graham@sydney.edu.au)
Kenneth Wilson (ken.wilson@lancaster.ac.uk)

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Correction: Male-killing *Wolbachia* and mitochondrial selective sweep in a migratory African insect

Robert I Graham[1,2,*]
Email: robert.graham@sydney.edu.au

Kenneth Wilson[1]
Email: ken.wilson@lancaster.ac.uk

[1] Lancaster Environment Centre, Lancaster University, Lancaster LA1 4YQ, UK

[2] School of Biological Sciences, Heydon-Laurence Building A08, University of Sydney, Sydney NSW 2006, Australia

[*] Corresponding author. School of Biological Sciences, Heydon-Laurence Building A08, University of Sydney, Sydney NSW 2006, Australia

Following publication of this work [1], it was brought to our attention that seven of the mitochondrial COI haplotypes described in this manuscript as *Spodoptera exempta* haplotypes were in fact other species. These have been identified as *Amyna punctum* complex (*haplo2*), *Chrysodeixis acuta* (*haplo4*), *Spodoptera triturata* (*haplo5*), *Vittaplusia vittata* (*haplo13*), *Condica* sp. (*haplo14*) and *Mesogenea varians* (*haplo15* and *haplo16*). As a result, we cannot now support one of our original conclusions suggesting that the *Spodoptera* genus does not appear to be monophyletic. The text describing and discussing this claim in the original manuscript [1] should be disregarded.

However, it should be clearly stated that the main findings of the article, namely that the presence of *Wolbachia* appears to be driving a mitochondrial selective sweep within *S. exempta*, still holds true. Indeed, new analysis strengthens the extent of the skew. Here we present the results of the re-analysis with the corrected data sets along with revisions of the relevant figures.

COI sequences were obtained from 157 *S. exempta* specimens and ten haplotypes identified [Genbank: JQ315120, JQ315122, JQ315125 – JQ315131, JQ315136; Figure 1]; 148 (94.3%) of the haplotypes belonged to *haplo1*. Significantly, all the *Wolbachia* infections detected in *S. exempta* were found associated with mtDNA *haplo1*, suggesting that recent selective sweeps associated with the invasion of *Wolbachia* may have affected mtDNA diversity in the armyworm population. The host COI haplotype diversity estimate was found to be very low (haplotype diversity, Hd: 0.112; nucleotide diversity, π: 0.0002). Estimates of D, D^* and F^* statistics were all negative for the COI gene (Tajima's D: -2.157, $p < 0.01$; Fu & Li's D^*: -5.121, $p < 0.02$; Fu & Li's F^*:-4.85017, $p < 0.02$). Apart from *haplo1*, all of the other haplotypes were very rare, each only detected in a single individual, making any inference on distribution-structuring or migratory behaviour difficult (Figure 2).

Figure 1 a: Maximum-Likelihood (GTR+I model) phylogenetic tree of the mtDNA COI gene. *Haplo1*, the most common of the *S. exempta* haplotypes, is indicated by the solid diamond. The scale bar represents a 1% estimated difference in nucleotide sequence. Numbers given at each node correspond to the percentage bootstrap values (for 1000 repetitions). Replicate numbers of <60% were not included in the figure. The nymphalid *Hypolimnas bolina* is used as an outgroup. **b:** A network analysis displaying the skew and selection for mtDNA haplotype *haplo1* (H1) within the *S. exempta* populations. The filled grey segment in the H1 pie-chart indicates the total percentage of *Wolbachia* infections in the samples, all found within *haplo1* haplotypes. The most divergent haplotypes are found furthest from the centre, and brackets indicate the difference in nucleotide substitutions with *haplo1*.

Figure 2 The spatial prevalence of *COI* hapolotypes within armyworm larval populations sampled throughout Tanzania over the course of two field seasons. The numbers correspond to the field sites in Table S1, numbered sequentially through the season. A, B and C refer to the moth trap catches from those districts.

We wish to thank Dr. Scott Miller for bringing this matter to our attention.

References

1. Graham RI, Wilson K: **Male-killing *Wolbachia* and mitochondrial selective sweep in a migratory African insect.** *BMC Evol Biol* 2012, **12**:204.

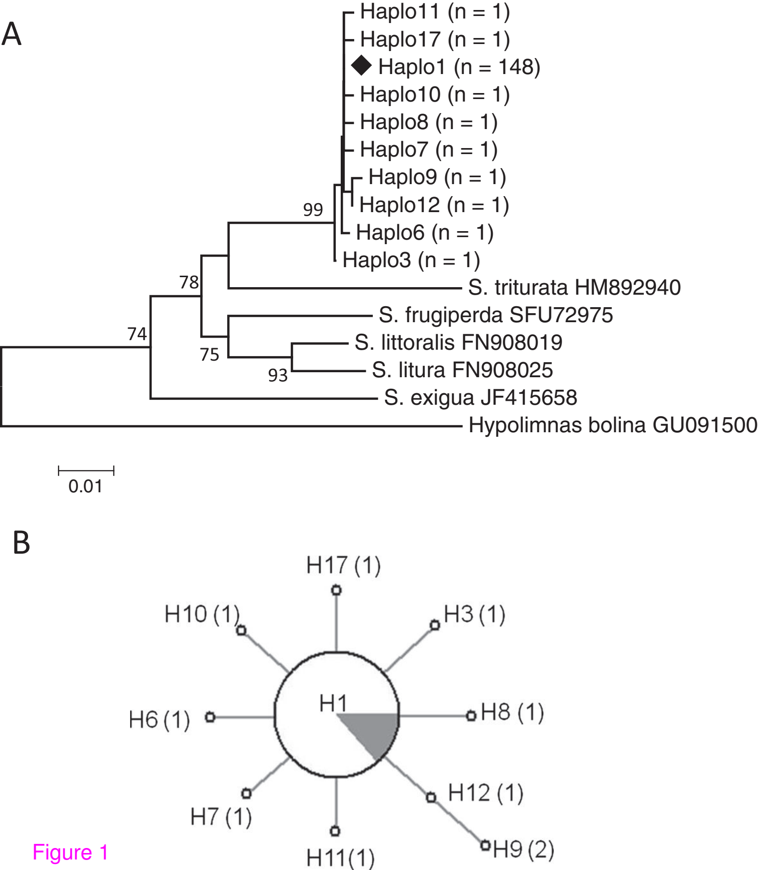
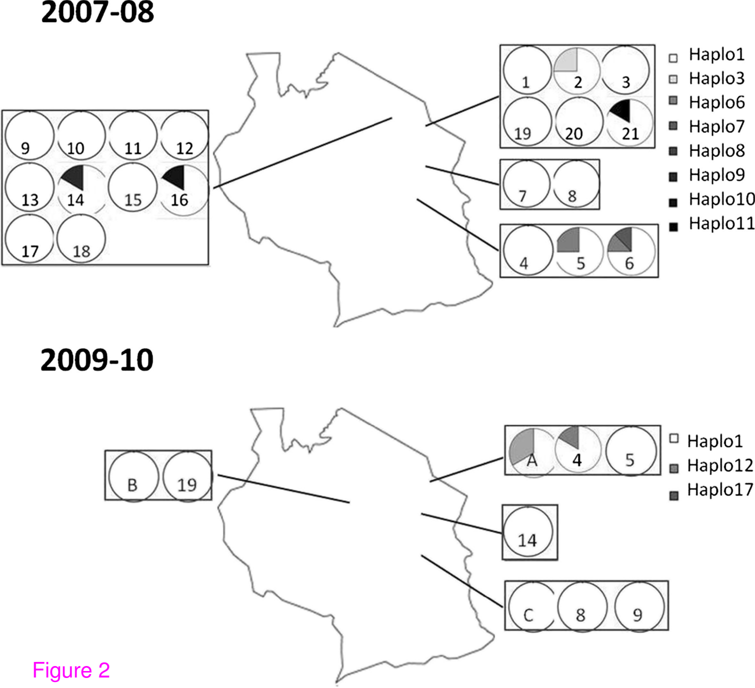

A
Haplo11 (n = 1)
Haplo17 (n = 1)
◆ Haplo1 (n = 148)
Haplo10 (n = 1)
Haplo8 (n = 1)
Haplo7 (n = 1)
Haplo9 (n = 1)
Haplo12 (n = 1)
Haplo6 (n = 1)
Haplo3 (n = 1)
99
S. triturata HM892940
78
S. frugiperda SFU72975
74
S. littoralis FN908019
75
S. litura FN908025
93
S. exigua JF415658
Hypolimnas bolina GU091500
0.01
B
H17 (1)
H10 (1)
H3 (1)
H1
H6 (1)
H8 (1)
H12 (1)
H7 (1)
H11(1)
H9 (2)

Figure 1


2007-08
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6
□ Haplo1
□ Haplo3
■ Haplo6
■ Haplo7
■ Haplo8
■ Haplo9
■ Haplo10
■ Haplo11
2009-10
B
19
A
4
5
14
C
8
9
□ Haplo1
■ Haplo12
■ Haplo17

Figure 2