

CORRECTION

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

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Correction

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 triturrata* (*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.

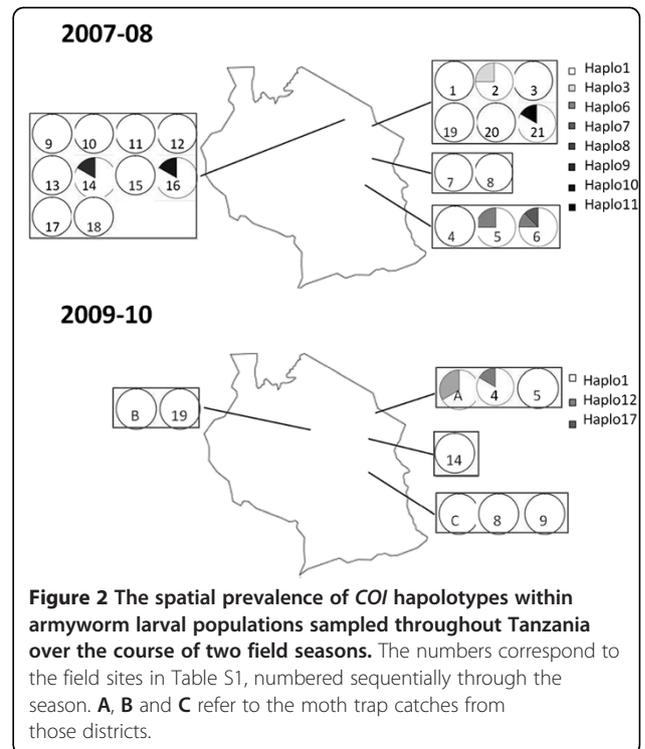
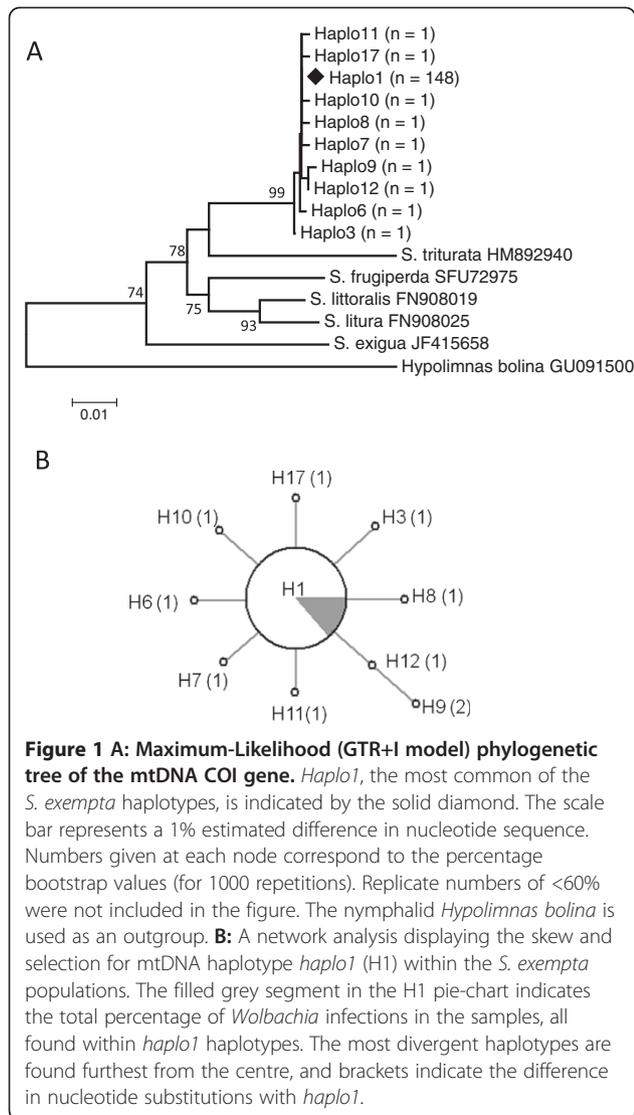
COI sequences were obtained from 157 *S. exempta* specimens and ten haplotypes identified [Genbank: JQ315120, JQ315122, JQ315125 – JQ315131, JQ315136; Figure 1]; 148 (94.3%) of the haplotypes belonged to *haplo1*. Significantly, all the *Wolbachia* infections detected in *S. exempta* were found associated 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).

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

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Received: 19 December 2012 Accepted: 8 January 2013
 Published: 10 January 2013

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

doi:10.1186/1471-2148-13-6

Cite this article as: Graham and Wilson: Correction: male-killing *Wolbachia* and mitochondrial selective sweep in a migratory African insect. *BMC Evolutionary Biology* 2013 **13**:6.

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