

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.

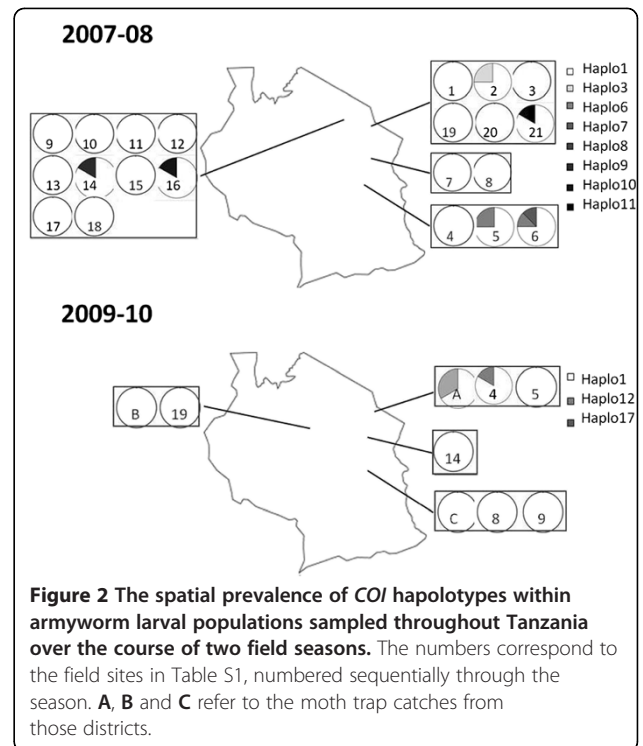
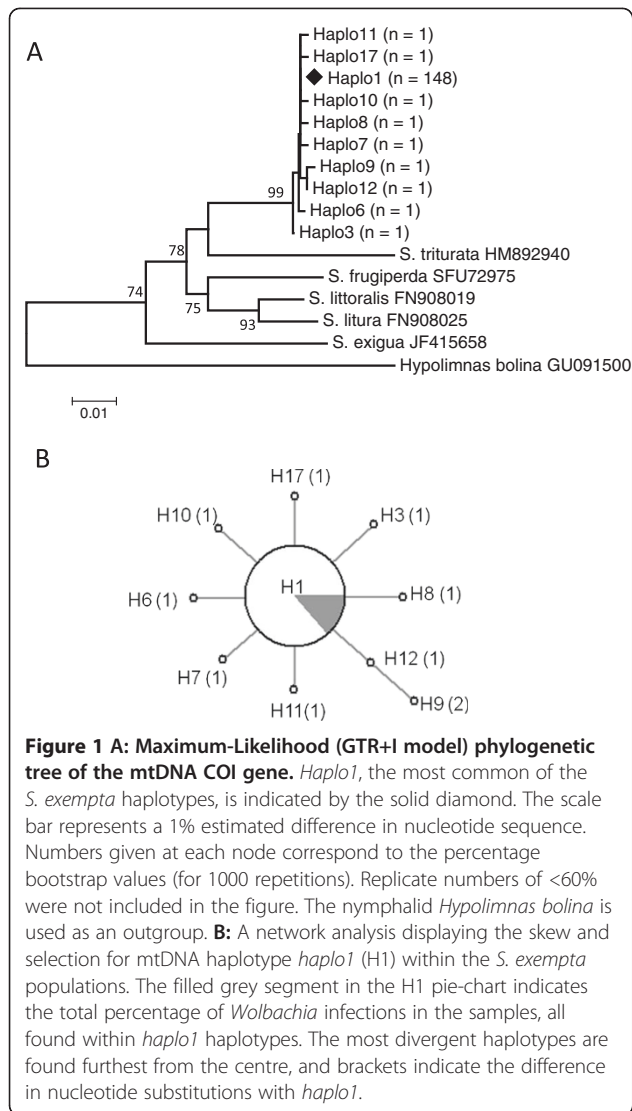
COI sequences were obtained from 157 *S. exempta* specimens and ten haplotypes identified [Genbank: JQ315120, JQ315122, JQ315125 – JQ315131, JQ315136; Figure 1]; 148 (94.3%) of the haplotypes belonged to *haplo1*. Significantly, all the *Wolbachia* infections detected in *S. exempta* were found associated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

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