Identifying flies used for maggot debridement therapy

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To the Editor: The use of maggots to clean necrotic wounds, known as maggot debridement therapy (MDT), has long been known to the scientific world. Its use has been recorded since the 1500s when soldiers' wounds were often infested with maggots. Napoleon's surgeon, Baron Dominic Larrey, reported that wounds that were infested with maggots appeared to heal faster than those without maggots.[1] William Baer is considered to be the founder of modern MDT. While treating soldiers in World War I, he noted the good condition of wounds that had been infested with maggots, and was the first doctor on record to experiment with the use of maggots in treating infections.[1] MDT even featured in the recent version of the film 'Spartacus'.

Various species of flies have been used for MDT,[1] the most commonly used being *Lucilia sericata*, a greenbottle blowfly (Figs 1 and 2). This fly is closely related to another greenbottle, *L. cuprina*, but *L. cuprina* feeds on live as well as necrotic tissue, which is undesirable in MDT. *L. cuprina* is commonly named the 'sheep blowfly' because it is responsible for fly-strike in sheep, a form of massive, usually rectal myiasis that can kill sheep.

A recent article[2] suggested that *L. cuprina* was being used successfully for MDT at the Eugene Marais Hospital Wound Care Centre (EMHWCC). As this would be inconsistent with international experience in MDT and at odds with the usual biology of *L. cuprina*, it was decided to check the identity of these flies.

Materials, methods and results

Flies were sampled from two different colonies of *Lucilia* held at the EMHWCC. DNA was extracted and polymerase chain reaction (PCR) amplification was performed. PCR products were sequenced for the respective genes using the primers used for their amplification.[3]

A total of 654 base pairs were sequenced for the 28S gene and a total of 601 base pairs were sequenced for the COI gene. The nuclear sequences (28S) of the MDT flies formed a distinct group with the *L. sericata* sequences obtained from Genbank, with a bootstrap support value of 66% and a neighbourhood joining value of 98%, while *L. cuprina* sequences from Genbank formed a separate cluster with a bootstrap support value of 67% and a neighbourhood joining value of 99%. Similarly, the COI sequences separated into two distinct branches with respective bootstrap support values and neighbourhood joining values of 74% and 53% and 72% and 71%, respectively. Bootstrap values about 80% are considered to indicate very reliable groups. The *L. sericata* group included all of the EMHWCC MDT flies.

Fig. 1. Sterile larvae in biobag.

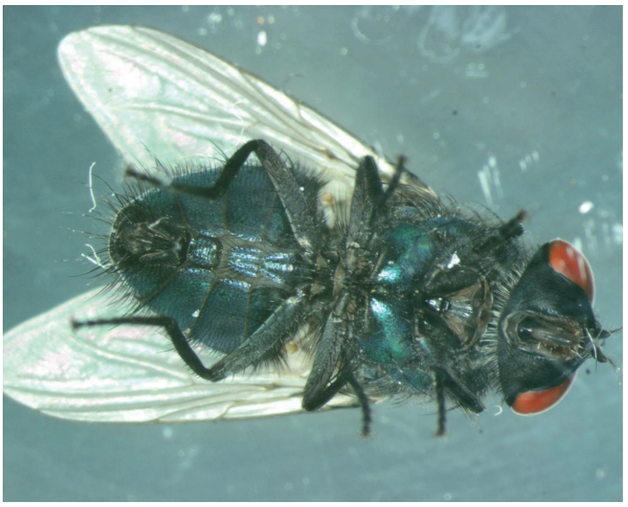

Fig. 2. Lucilia cuprina.

Discussion

L. sericata and *L. cuprina* are similar in morphology and it is extremely difficult to correctly identify them using the literature as many characters in these works are subtle and subjective, e.g. colour being bright green or metallic green.[4-6] This also makes it difficult for non-entomologists to identify these flies correctly.

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Our study shows that the flies from the EMHWCC MDT colony are in fact *L. sericata* and not *L. cuprina*. This is what would be expected, as *L. sericata* is widely used in Europe and the USA for MDT.[1]

The issue of correct identification of these blowflies becomes a medical issue when they are used for MDT, and it is advisable to have adequate quality assurance criteria and protocols in place. The most reliable protocol is to sequence the DNA of these flies for a diagnostic gene.

This study highlights the need for quality assurance protocols for identifying flies for MDT. It demonstrates that the nuclear 28S rRNA gene would be a good choice for this task, and suggests that qualified entomologists who specialise in DNA sequencing of flies assist in this matter.

References

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