

## **Molecular Identification and Evolutionary Status of *Lucilia bufonivora*: An Obligate Parasite of Amphibians in Europe**

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**Abstract :** *Lucilia bufonivora* Moniez, is an obligate parasite of toads and frogs widely distributed in Europe. Its sister taxon *Lucilia silvarum* Meigen behaves mainly as a carrion breeder in Europe, however it has been reported as a facultative parasite of amphibians. These two closely related species are morphologically almost identical, which has led to misidentification, and in fact, it has been suggested that the amphibian myiasis cases by *L. silvarum* reported in Europe should be attributed to *L. bufonivora*. Both species remain poorly studied and their taxonomic relationships are still unclear. The identification of the larval specimens involved in amphibian myiasis with molecular tools and phylogenetic analysis of these two closely related species may resolve this problem. In this work seventeen unidentified larval specimens extracted from toad myiasis cases of the UK, the Netherlands and Switzerland were obtained, their COX1 (mtDNA) and EF1- $\alpha$  (Nuclear DNA) gene regions were amplified and then sequenced. The 17 larval samples were identified with both molecular markers as *L. bufonivora*. Phylogenetic analysis was carried out with 10 other blowfly species, including *L. silvarum* samples from the UK and USA. Bayesian Inference trees of COX1 and a combined-gene dataset suggested that *L. silvarum* and *L. bufonivora* are separate sister species. However, the nuclear gene EF1- $\alpha$  does not appear to resolve their relationships, suggesting that the rates of evolution of the mtDNA are much faster than those of the nuclear DNA. This work provides the molecular evidence for successful identification of *L. bufonivora* and a molecular analysis of the populations of this obligate parasite from different locations across Europe. The relationships with *L. silvarum* are discussed.

**Keywords :** calliphoridae, molecular evolution, myiasis, obligate parasitism

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