

Phylogeography of the tiger-fly, *Coenosia attenuata* (Diptera: Muscidae)

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Introduction:

Coenosia attenuata Stein is a polyphagous predator that has been recognized as a potential biological control agent, especially in greenhouse crops (Mateus, 2012). Adults are the only known predators of adult stage of important pests such as whiteflies and leafminers (Prieto *et al.*, 2005). Despite the importance of *C. attenuata* as part of a crop protection strategy towards sustainability, some aspects of its bioecology are not yet clarified, which denotes the necessity for more studies. With this investigation we intend to study the patterns of genetic variation and differentiation across the distribution range of the species, in order to characterize the existing genetic diversity and to understand its evolutionary history. Here we present the preliminary results obtained through the analysis of a so far limited number of samples.

Methods:

Individuals were collected in Europe, North and South America and Western Asia. They were captured directly into boxes and plastic bags or by using sticky traps and they were preserved in ethanol. A fragment of cytochrome oxidase I (COI) mitochondrial gene (647 bp) was amplified by PCR and sequenced using the BigDye v.3.1 Cycle Sequencing kit (Applied Biosystems) on an ABI PRISM 310 (Applied Biosystems). Sequences were edited in Sequencher v. 4.0.5 (Gene Codes Corporation) and aligned in Clustal X v. 2.0.12 (Thompson *et al.*, 1997). Haplotype and nucleotide diversity were computed using DnaSp v.5 (Librado & Rozas, 2009) and a median-joining haplotype network was constructed using Network v. 4.6.1.0 (Fluxus Technology Ltd. 2004).

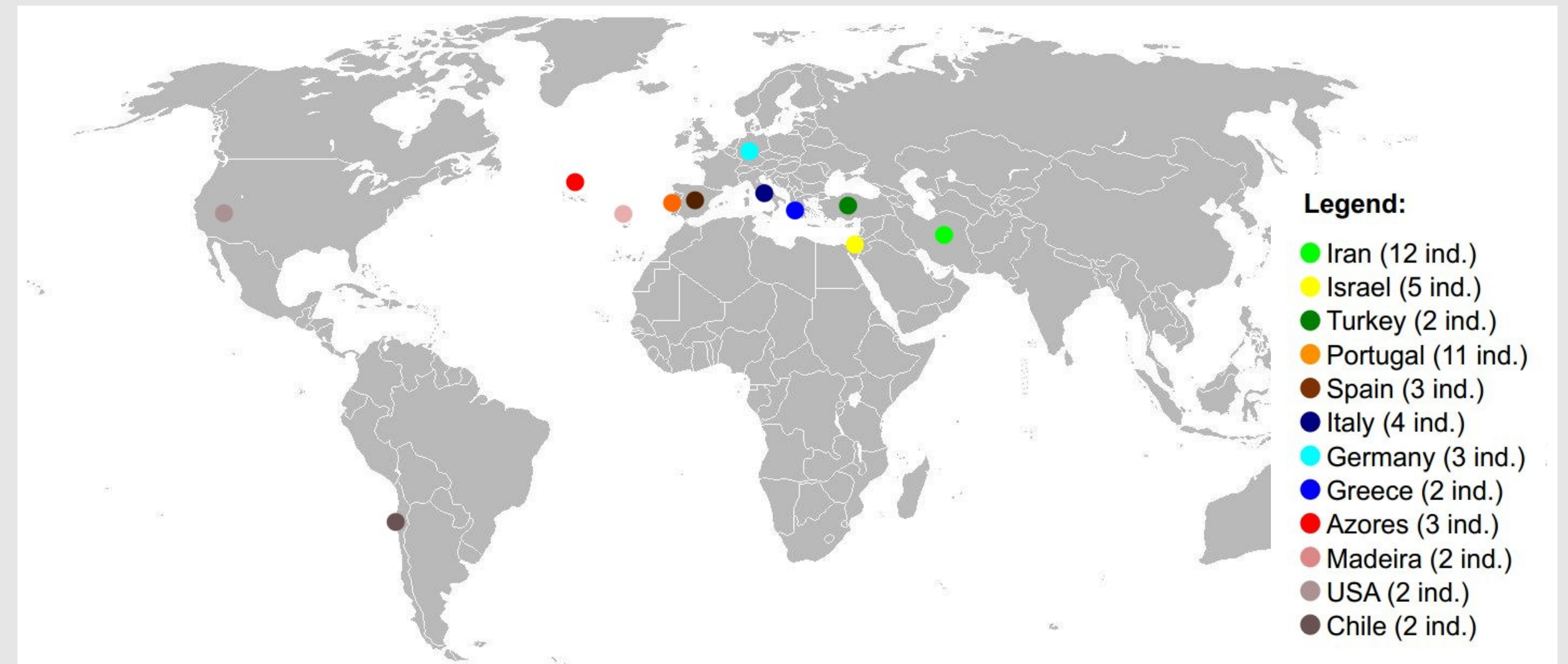


Fig. 1- Location of the sampled populations of *Coenosia attenuata*.

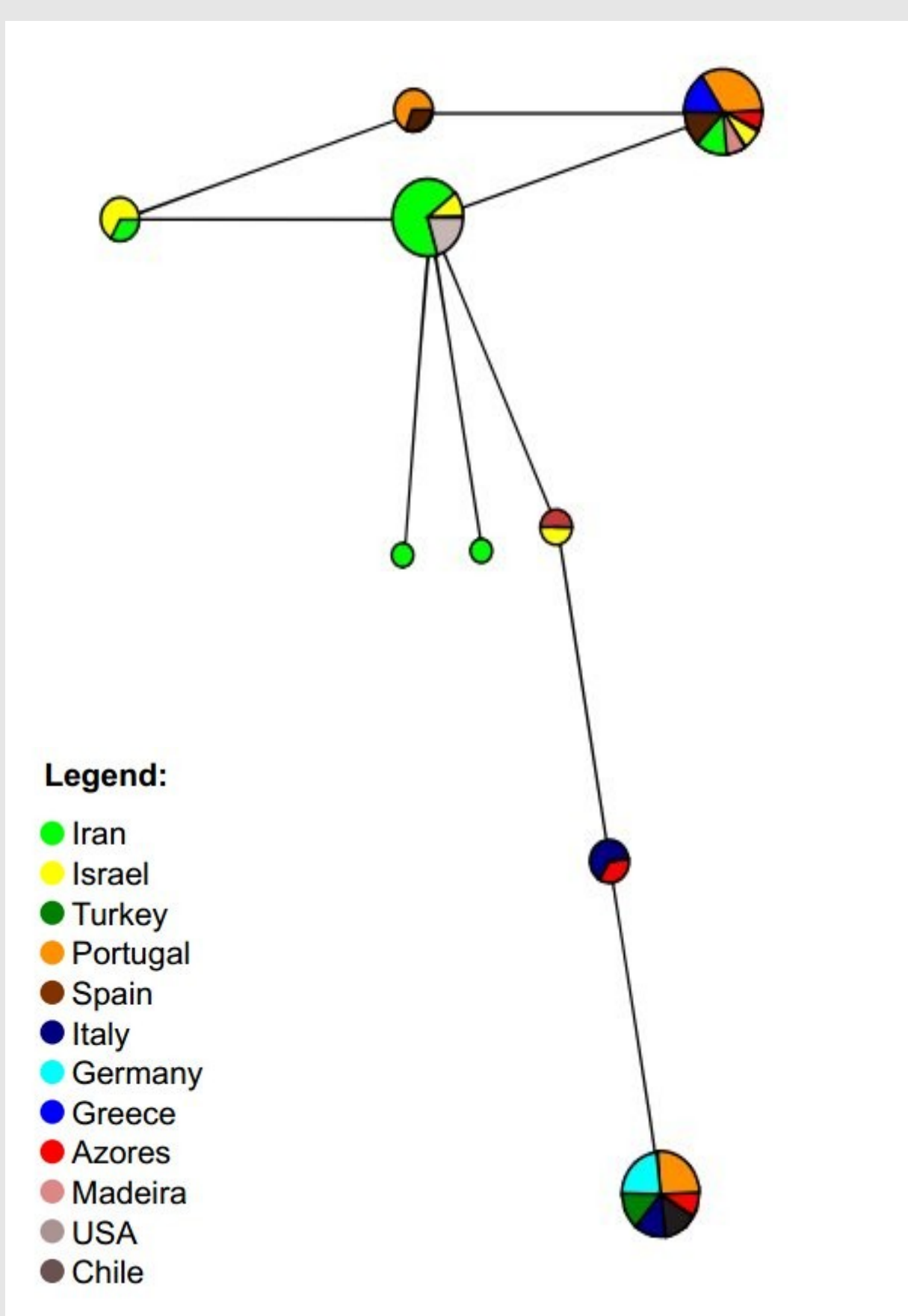


Fig. 2 — Haplotype network of COI sequences (647 bp) from *Coenosia attenuata* (51 individuals). Size of the circles are in proportion with the number of individuals.

Results and Discussion:

Despite the reduced number of samples and the difference in number of individuals analyzed per population so far, some patterns are revealed:

- The haplotype diversity (Hd) found was 0.814 and the nucleotide diversity (Pi) was 0.00321. This pattern of high haplotype diversity and low nucleotide diversity may be an indication of recent expansion.
- Both samples of Chile (South America) have the same haplotype as one of the haplotypes present in Europe, and both samples of California, USA (North America), have the same haplotype as one of the haplotypes present in Iran and Israel. This may support the hypothesis of recent colonization of North and South America from the Palearctic.
- Although Iran has the highest number of haplotypes, it has also the highest sample size. In proportional terms we have more haplotypes in Azores (3 haplotypes in 3 individuals) and Madeira (2 haplotypes in 2 individuals), followed by Israel (4 haplotypes in 5 individuals).

We are proceeding with the analysis of more samples for each population and of more populations across the distribution range of the species, and using nuclear genes (elongation factor-1 α and white gene), in order to do a detailed phylogeographic study with the aim of: characterizing the worldwide genetic diversity in this species; finding the probable origin of the species within Palearctic region (Henning, 1964), where it is referred specifically the Mediterranean region (Martinez & Cocquempot, 2000; Couri & Salas, 2010); describing the dispersal patterns of the species; and dating the divergence of populations.

References:

- Couri, M. S. & Salas, C., 2010. First record of *Coenosia attenuata* Stein (Diptera, Muscidae) from Chile, with biological notes. *Revista Brasileira de Entomologia*, 54: 144-145.
- Hennig, W., 1964. Muscidae. In: Lindner, E., Die fliegen der Paläarktischen region. 7(2) E. Schweizerbatsche Verlagsbuchhandlung, Stuttgart.
- Kühne, S., 2000. Predaceous flies of the genus *Coenosia* Meigen, 1826 (Diptera: Muscidae) and their possible use for biological pest control. *Studia dipterologica Supplement*, 9: 1-78.
- Larkin, M. *et al.*, 2007. Clustal W and Clustal X version 2.0. *Bioinformatics*, 23(21): 2947-2948.
- Librado, P. & Rozas, J., 2009. DnaSP v5: A software for comprehensive analysis of DNA polymorphism data. *Bioinformatics*, 25: 1451-1452.
- Mateus, C., 2012. Bioecology and behaviour of *Coenosia attenuata* in greenhouse vegetable crops in the Oeste region, Portugal. *Bulletin of Insectology*, 65 (2): 257-263.
- Martinez, M. & Cocquempot, C., 2000. La mouche *Coenosia attenuata*, nouvel auxiliaire prometteur en culture protégée. *PHM-Revue Horticole*, 414: 50-52.
- Prieto, R., Figueiredo, E., Miranda, C. & Mexia, A., 2005. *Coenosia attenuata* Stein (Diptera: Muscidae): prospecção e actividade em culturas protegidas em Portugal. *Bol. San. Veg. Plagas*, 31: 39-45.
- Thompson, J., Gibson, T., Plewniak, F., Jeanmougin, F. & Higgins, D., 1997. The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Research*, 25, 4876-4882.

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