ENBE 2025

XXI International Meeting of the Portuguese Association for Evolutionary Biology

BOOK OF ABSTRACTS

18th-19th December 2025

Bragança

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M. Alice Pinto
Dora Henriques
Ana Rita Lopes

Instituto Politécnico de Bragança, Portugal
December, 2025

Welcome message

It is our great pleasure to welcome you to **ENBE 2025 – XXI International Meeting of the Portuguese Association for Evolutionary Biology,** held in Bragança from **18 to 19 December 2025**. This XXI edition is jointly organised by *Associação Portuguesa de Biologia Evolutiva* (APBE), *Centro de Investigação de Montanha* (CIMO), and *Instituto Politécnico de Bragança* (IPB). ENBE is a unique event where young and senior scientists share and celebrate their research achievements in Evolutionary Biology, strengthening collaborations and fostering new connections.

ENBE 2025 will bring together more than 100 participants who will contribute to a diverse scientific programme featuring 31 oral communications and 38 posters across five thematic areas: (i) genome architecture, structural evolution and biogeography; (ii) domestication, population genomics and conservation; (iii) experimental evolution and adaptation; (iv) co-evolution, host–pathogen and parasite evolution; and (v) hybridisation, introgression and phenotypic diversity. The programme will also include exciting keynote lectures from three renowned scientists: Margarida Matos (University of Lisbon, Portugal), Matthew Webster (Uppsala University, Sweden), and Ricardo Pereira (Stuttgart State Museum of Natural History, Germany).

In addition, this XXI edition will, for the first time, host a roundtable focusing on improving engagement between evolutionary biologists, science communicators, educators, and journalists. This topic will be debated by a panel of eminent contributors from the science communication, media, and education sectors.

I am confident that this will be a successful event, and this success is the result of the commitment of our keynote speakers and roundtable participants, who readily accepted our invitation, as well as our session chairs and all participants, whose dedication and enthusiasm make this meeting possible. Last but not least, I would like to express my deepest gratitude to all supporting institutions and sponsors, and especially to the organising committee, the scientific committee, and student volunteers, whose hard work and dedication were essential in bringing this event to life.

Bragança welcomes you with its beautiful historic centre, including a remarkably well-preserved castle, and a rich cultural heritage. The region is also renowned for its exceptional gastronomy. We invite you to take the opportunity to discover the flavours and traditions of the *Nordeste Transmontano*.

I wish you all an inspiring and productive conference and a Merry Christmas.

M. Alice Pinto, Chair of ENBE 2025

Organisation

Instituto Politécnico de Bragança (IPB)

Centro de Investigação de Montanha (CIMO)

Laboratório Associado para a Sustentabilidade e Tecnologia nas Regiões de Montanha (SUSTEC)

Associação Portuguesa de Biologia Evolutiva (APBE)

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POSTER 26| EVOLUTION OF AMITRAZ RESISTANCE IN *VARROA DESTRUCTOR*: HISTORICAL ASSESSMENT OF THE F290L MUTATION IN IBERIAN POPULATIONS

Costa, M (1); Pérez-Pérez, A (2); Santos, AC (1); Prado, R (1); Lopes, D (1); Lopes, AR (1); Yadró, CA (1); Martín-Hernández, R (2); Higes, M (2); Pinto, MA (1); Henriques, D (1)

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Keywords: *Varroa destructor*; historical; amitraz; resistance; mutation

Abstract

Varroa destructor is one of the main parasites of the honey bee (*Apis mellifera*), causing significant colony losses worldwide. The control of this mite often relies on acaricides, with amitraz being among the most widely used products in Portugal and Spain over the last decade. However, the continuous and persistent use of the same active substance exerts strong selective pressure on parasite populations, potentially favouring alleles associated with treatment resistance. Recently, a point mutation resulting in a phenylalanine-to-leucine substitution at position 290 (F290L) was identified in *V. destructor* populations from Spain, putatively associated with amitraz resistance. This mutation has been detected at high frequency in recent samples, suggesting resistance may have evolved due to sustained amitraz use. To assess whether the F290L mutation was already present before the widespread amitraz adoption, DNA extraction and sequencing analysis will be performed on mites collected since 2006, prior to the massive use of this treatment in Iberian beekeeping. This approach will clarify whether the allele frequency of F290L increased because of the selective pressure exerted by amitraz or if it already existed in high frequencies in earlier populations. This study will contribute to a better understanding of the evolution of resistance and to the development of more effective monitoring and management strategies to combat *V. destructor*.

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