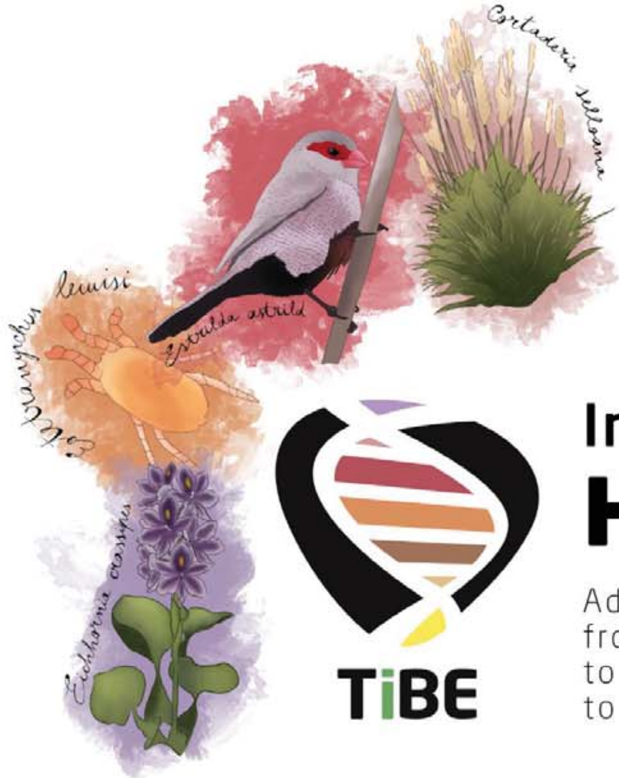

TiBE

Invaders on the HORIZON!

Advancing Invasion Science
from Genes
to Ecosystems
to Society

28 - 30 November 2023
VILA DO CONDE, PORTUGAL

Book of Abstracts

The Conference

TiBE - **Trends in Biodiversity and Evolution -** Conference, is an annual meeting organized by CIBIO – Research Centre in Biodiversity and Genetic Resources – InBIO Associate Laboratory, that aims to bring together researchers, post-graduate and graduate students working on the field of biodiversity and evolutionary biology to present and discuss cutting-edge findings in relevant topics related with speciation, behaviour, molecular evolution, comparative genomics, ecology, population and conservation genetics research, among others.

Since the creation of the TEAMING project **BIOPOLIS**, with a strong link with the University of Montpellier, TiBE is part of the strategy for communication and dissemination of BIOPOLIS/CIBIO-InBIO into the future.

This year's edition - 2023

Invaders on the Horizon! Advancing Invasion Science from Genes to Ecosystems and Society aims to foster interdisciplinary collaboration and explore the multifaceted challenges posed by ***invasive alien species***, a major driver of global change. With a strong focus on the genetic, ecological, and societal aspects of biological invasions, this conference provides a unique platform to exchange knowledge and insights.

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Vespa velutina: using microsatellites to compare the genetic diversity of founding nests in the leading-edge populations in Portugal

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The invasive yellow-legged hornet (*Vespa velutina nigrithorax*) is a voracious predator of honeybees and other pollinators, its diffusion generates relevant environmental and socio-economic impacts. Native from China, it rapidly started spreading throughout Europe, after its first sight in France in 2004. *V. v. nigrithorax* was first reported in Portugal, in the region of Viana do Castelo, in 2011 and since then it has been spreading through the country, with Bragança representing the Northeastern edge of its distribution in Portugal. The aim of this study was to compare the genetic diversity between nests collected in Viana do Castelo and Bragança. Four nests were analysed, two from Viana do Castelo and two from Bragança. Each sample nest is represented by 30 workers making up a total of 120 individuals analysed for this study. Total DNA was extracted from the thorax of each individual using the Nucleospin® Tissue (Macherey-Nagel). The individuals were genotyped using 16 microsatellite loci divided into three multiplex combinations. The lengths of the fragments were determined using GeneMapper 3.7 (Applied Biosystems). Genetic diversity statistics, which included observed number of alleles (Na), effective number of alleles (Ne), observed heterozygosity (Ho), expected heterozygosity (He), and unbiased expected heterozygosity (uHe) were estimated using GENALEX 6.5. This software was also implemented to assess genetic structure using a Principal Coordinate Analyses (PCoA). Our results show that both nests from both origins have low genetic diversity, with Bragança showing higher genetic diversity (Na=2; Ne= 1.600; Ho=0.427; He=0.330; uHe=0.333) than Viana do Castelo (Na=1.750; Ne=1.482; Ho=0.363; He=0.258; uHe=0.260). The genetic structure show that distinct groups might be in the origin of both nests' location. These results suggest that the population of *Vespa velutina* from the region of Bragança may be an expansion from multiple source populations.

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