UMR 5244 Université de Montpellier-CNRS-IFREMER- Université de Perpignan via Domitia
Interactions Hôtes-Pathogènes-Environnements (IHPE)
Université de Montpellier
Place Eugène Bataillon, Bât 24, CC 80, F-34095 Montpellier Cedex 5, France
Tel : 33 (0)4 67 14 47 09
https://ihpe.fr

Titre du stage: Unveiling the history and the patterns of invasion of the North American freshwater snail *Pseudosuccinea columella* in Southern France

Niveau : M2
Encadrant(s) : Annia ALBA & Antonio A. VAZQUEZ
Laboratoire : IHPE, CNRS, UM, UPVD & MIVEGEC, IRD
Candidature avant le 31/10/25 à : annia.alba-menendez@umontpellier.fr; antonio.vazquez@ird.fr
Site web : https://ihpe.fr/ & https://mivegec.fr/fr

Problématique générale :
Biological invasions—including those by pathogens, vectors, and hosts—pose serious threats to ecosystem functioning. Their impacts are especially severe in fragile freshwater habitats, where invasions can lead to local biodiversity loss, species extinctions, and broader risks to food security, livelihoods, and human well-being (1). In particular, invasions involving hosts, vectors, or parasites can disrupt disease ecology and co-evolutionary dynamics, with potential consequences for biodiversity and public and veterinary health (2). Europe currently hosts over 10 000 alien species, with introductions rising in recent decades—an upward trend continuing across most taxa except mammals (3). This pattern is largely driven by human-induced changes such as climate change, globalization, habitat alteration, and international trade that have facilitated the arrival and spread of invasive species, with the Mediterranean basin among the most vulnerable regions (4). A key unresolved question in invasion biology is why some species become successful invaders while others do not. Species-level traits (e.g., dispersal ability, competitiveness) may influence invasiveness (5), but intraspecific variation plays a significant role too as often, only a small subset of populations becomes invasive (6). Region-specific and population-level studies providing detailed descriptions of invasion history, geography, demography, and genetics are essential first steps toward identifying the drivers of invasion success (7,8).

Sujet et objectifs du stage :
The freshwater snail *Pseudosuccinea columella*, a known vector of parasitic diseases, has been introduced to France and poses a significant risk of spreading throughout the Mediterranean basin. Its presence may trigger spillback events involving local snail-borne parasites and disrupt established transmission dynamics. This species is particularly concerning due to its rapid, global "flash invasion"—with established populations on all inhabited continents except Asia. Its spread is largely driven by a single mitochondrial haplotype and a few microsatellite multilocus genotypes (9). In addition, invasive populations of *P. columella* have demonstrated high susceptibility to *Fasciola* parasites, acting as effective vectors of fasciolosis, a reemerging zoonotic disease (e.g., 10,11). In France, the species was first detected along the Lot River and shown to be fully compatible (100%) with local isolates of *F. hepatica* under laboratory conditions (12). Its spread across Mediterranean France is becoming increasingly evident, with new populations recently recorded in the metropolitan region (unpublished data) and in Corsica (13). The current M2 project, part of the InvaSnail project (ExposUM Fellowship, Université de Montpellier), aims to reconstruct the history and patterns of invasion of *P. columella* in southern France. This will be achieved by integrating phylogeography, population genetics, and field ecology.

Rapide description des méthodes utilisées :
This master stage proposes the genotyping of 18 newly-recorded populations using polymorphic microsatellites markers previously used in a global-scale study (9) to locate the possible origin(s) of the introduction event(s) and to reconstruct the invasion pattern of this species in France. The newly originated genetic dataset will be complemented with geospatial datasets to determine landscape connectivity. In addition, population genetics using the same markers will be applied to a one-year temporal survey of this species in three different sites to study temporal dynamics in relation with demographic and ecological data recorded throughout the same period.

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