

Early Career Research Grant Reports

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Cryptic and invasive freshwater *Galba* snails

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Morphological discrimination has proved to be difficult between certain species. In some cases, morphological variability can be higher *within* than *between* the species. When these cryptic species easily colonize environments beyond their native distribution, accurately identifying and tracking species becomes challenging. However, crypticity can be disclosed and species boundaries can be delimited by studying the genetic diversity and the phylogeography of the taxon of interest. Knowing the distribution of cryptic non-native species is essential to protect biodiversity, economy, and health⁽¹⁾.

Galba species are a group of small-shelled freshwater snails which distribution remains poorly known mainly due to the difficulty in morphologically differentiating them^(2,3). Most *Galba* species have a similar shell morphology (Fig. 1) and internal anatomy⁽³⁾. This is the reason why *Galba* species have been widely misidentified all over the world. For instance, *G. schirazensis* has often been confused with *G. truncatula* (Fig. 2) in Europe and Asia and with *G. truncatula* or *G. cubensis* in the Americas⁽²⁾. *Galba* species boundaries cannot be established by crossing experiments in the laboratory (as has been done, for instance, for snail species in the genus *Physa*) because *Galba* species reproduce mainly by self-fertilization⁽⁴⁾. Except for *G. cousini* that has a distinct morphology, *Galba* individuals can be accurately ascribed to one species or another only by DNA-based approaches.



Figure 1. Shell morphology of *Galba* species. Pictures taken by Jean-Pierre Pointier.

Galba species can be dispersed for long distances thanks to their mode of reproduction⁽²⁾ and their capacity to withstand drought. One or a few individuals can settle and create a population because individuals are capable of (and mostly prefer) self-fertilization⁽⁴⁾. The great capacity for dispersal of *Galba* snails has facilitated the worldwide expansion of fasciolosis, the disease caused by the liver fluke *Fasciola hepatica* and transmitted by *Galba* snails to livestock and humans⁽⁵⁾. The absence of an accurate species identification and, hence, a lack of a well-known distribution can prevent us from correlating the arrival of an invading species with the (re)emergence of the disease. Despite the epidemiological relevance of *Galba* species, up to now most studies have focussed on one or a few species of *Galba* in specific localities or regions⁽⁴⁾.

I am a member of a group of malacologists and parasitologists⁽⁶⁾ who aimed to study the current distribution and the phylogenetic relationships of *Galba* species. We achieved this goal mainly thanks to a large-scale sampling mostly collected by Dr. Jean-Pierre Pointier in 13 countries (~200 sites) from the whole Americas—the largest and the most-covering geographical scale study done up to now (Fig. 3). We focussed this study in The Americas because it is the region of the world where these snail species originated and diversified and where fasciolosis represents a serious disease.

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Thanks to an Early Career Research Grant from the Malacological Society of London and other grants, we used an integrative approach combining morphological observations with molecular markers (microsatellites and DNA sequences for four genes) to analyze *Galba* samples taken from across the Americas⁽⁶⁾. Our American database was augmented with data retrieved from GenBank (including Old World samples; Fig. 3) and analyzed using species delimitation methods and Bayesian phylogenetic reconstruction. Our analysis suggest that the genus *Galba* evolved ca. 22 myr ago and today comprises six clusters of populations.



Figure 2. *Galba truncatula*.

We recommend redefining species boundaries such that three of these clusters are understood as one species each, and that the other three clusters correspond to two highly diverse species or species complexes⁽⁶⁾. We also conclude that cryptic species in the genus *Galba* may best be explained by a 'shared morphological stasis'. *Galba* populations live in temporary habitats and are more amphibious than other freshwater snails, which may mitigate both predation and interspecific competition. Adaptation to such habitats may impose strong stabilizing selection for a shell morphology able to resist desiccation and concomitant morphological stasis⁽⁶⁾. We emphasize that cryptic *Galba* species must be accurately identified with molecular markers since these species demonstrate different patterns of invasiveness and susceptibility, host-parasite compatibility, and immunological resistance to *Fasciola hepatica*.

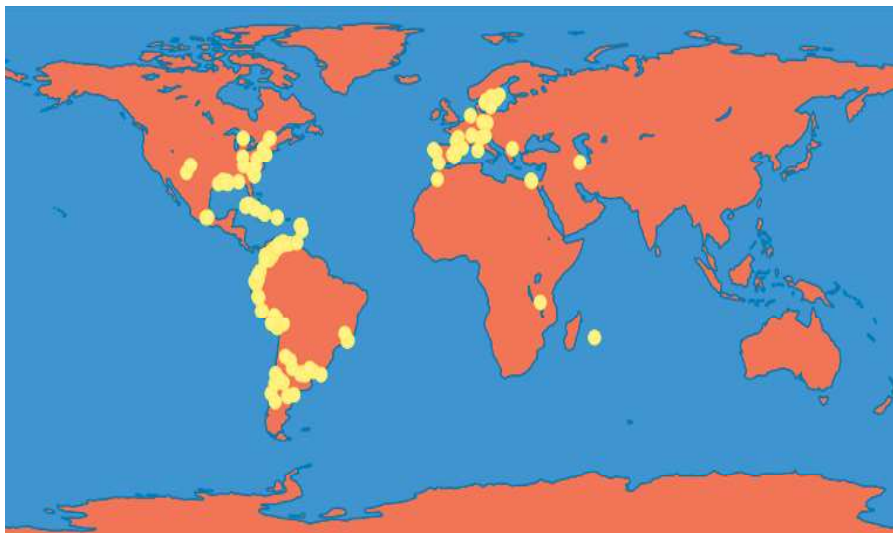


Figure 3. Worldwide records of *Galba* species based on DNA approaches.

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