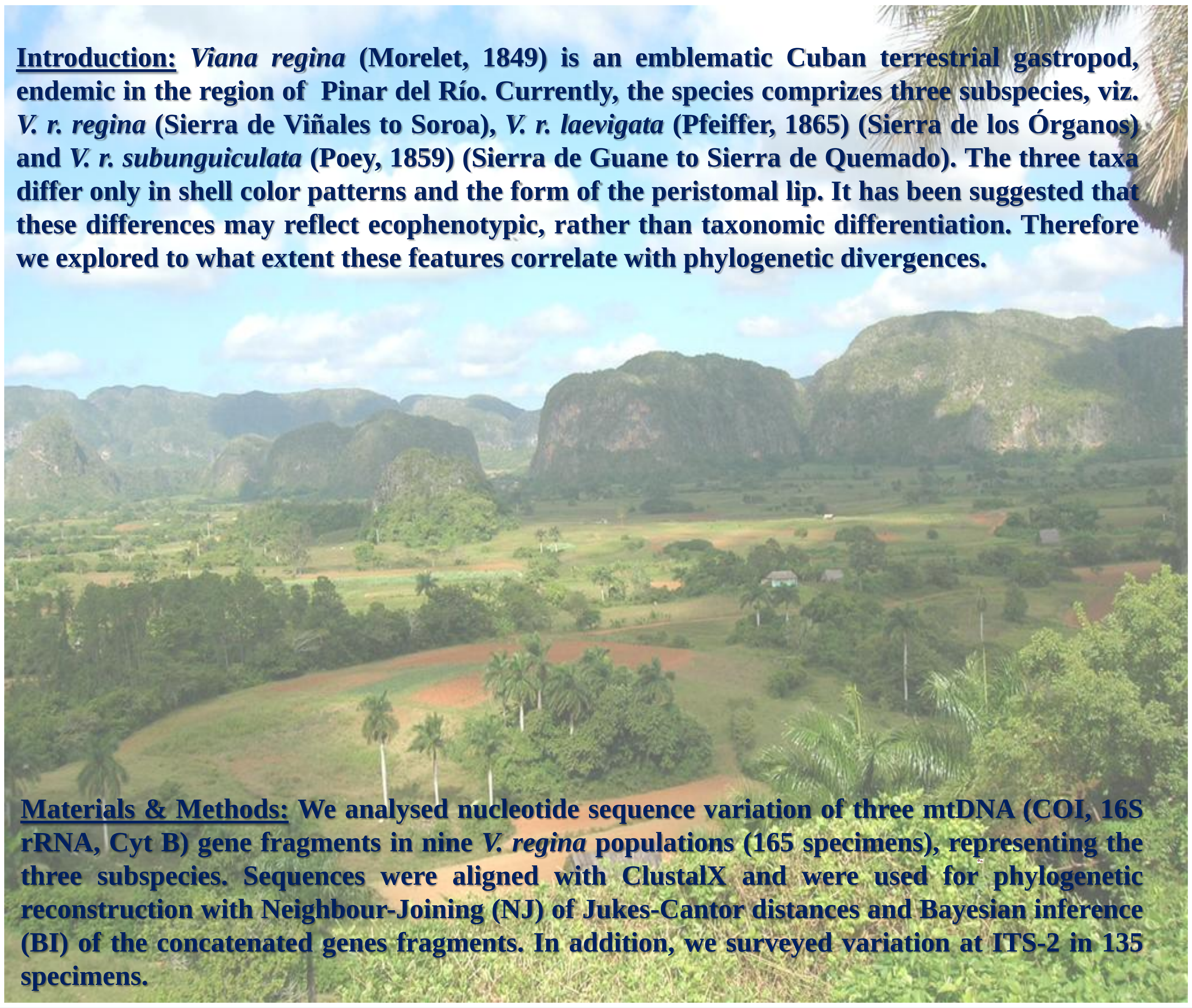
# Molecular taxonomy of *Viana regina* (Morelet, 1849) in Cuba (Gastropoda, Neritimorpha, Helicinidae)

**Jane Herrera[1], Karin Breugelmans[2] & Thierry Backeljau[2,3]**

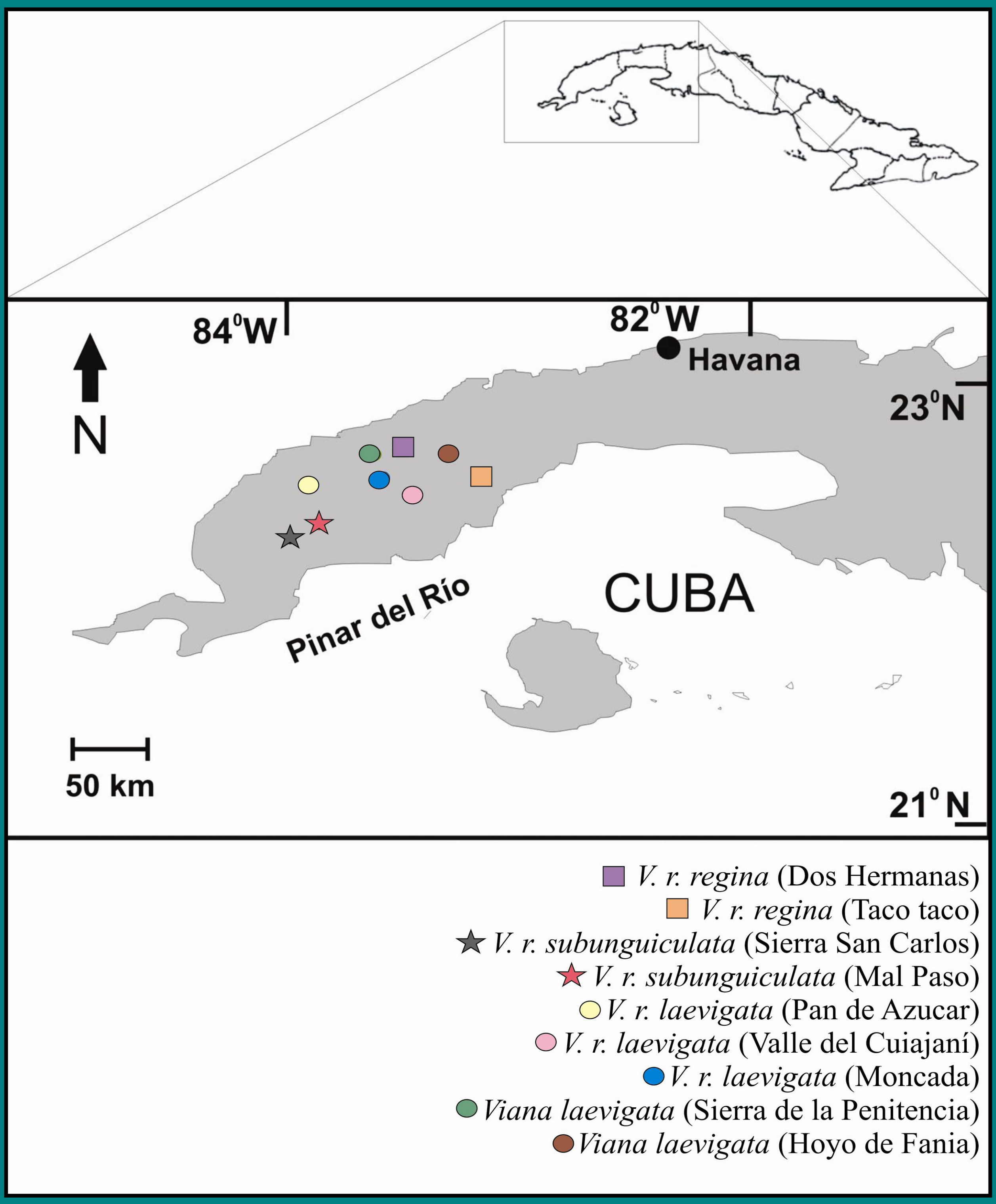
[1]Museo Nacional de Historia Natural de Cuba, Obispo 61, CP-10100, Habana Vieja, Cuba janehu@mnhnc.inf.cu
[2]Royal Belgian Institute of Natural Sciences, Vautierstraat 29, B-1000 Brussels, Belgium Karin.Breugelmans@naturalsciences.be
[3]Evolutionary Ecology Group, University of Antwerp, Groenenborgerlaan 171, B-2020 Antwerp, Belgium Thierry.Backeljau@naturalsciences.be



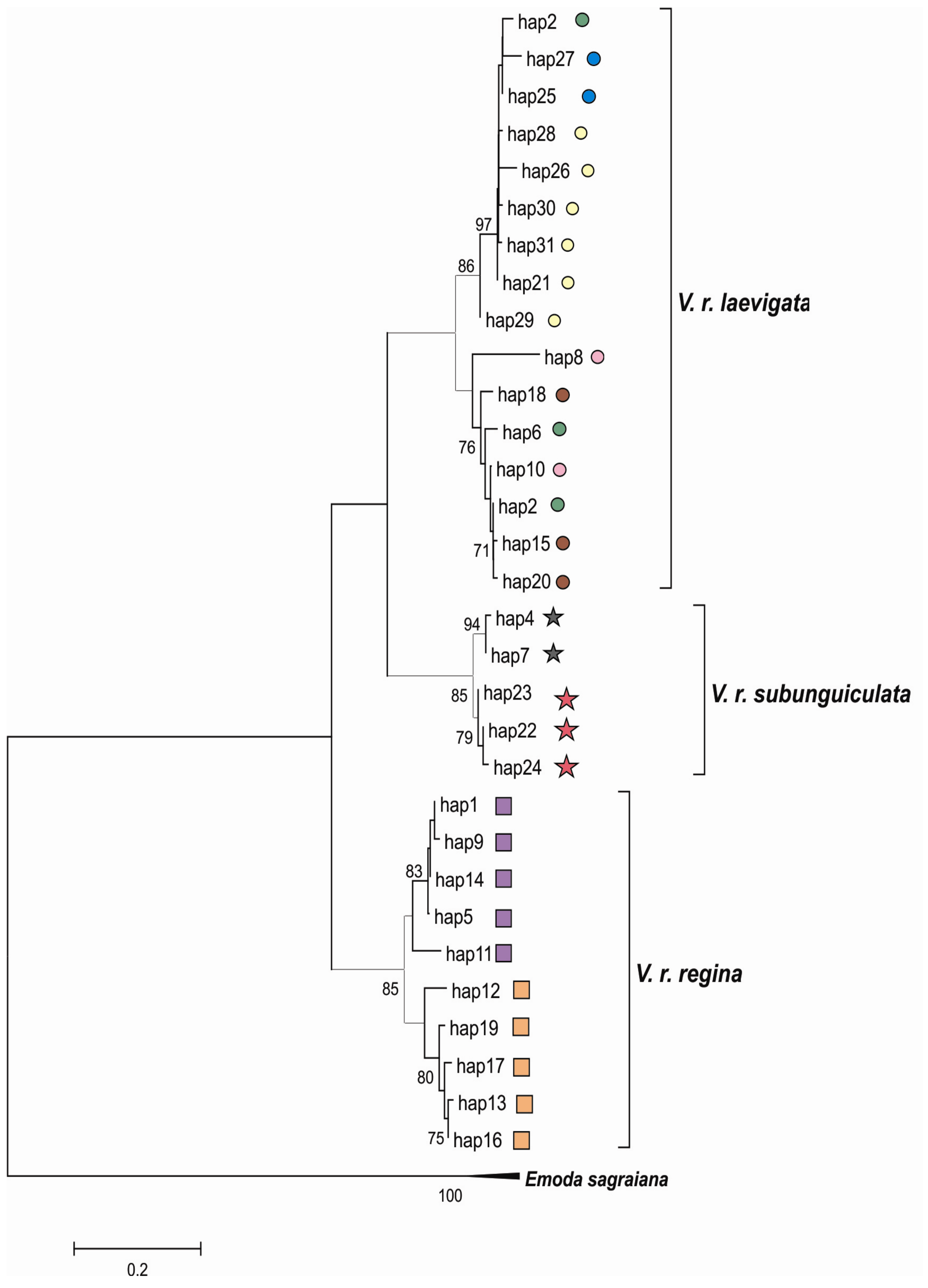
**Introduction:** ***Viana regina*** **(Morelet, 1849) is an emblematic Cuban terrestrial gastropod, endemic in the region of Pinar del Río. Currently, the species comprizes three subspecies, viz.** ***V. r. regina*** **(Sierra de Viñales to Soroa),** ***V. r. laevigata*** **(Pfeiffer, 1865) (Sierra de los Órganos) and** ***V. r. subunguiculata*** **(Poey, 1859) (Sierra de Guane to Sierra de Quemado). The three taxa differ only in shell color patterns and the form of the peristomal lip. It has been suggested that these differences may reflect ecophenotypic, rather than taxonomic differentiation. Therefore we explored to what extent these features correlate with phylogenetic divergences.**

**Materials & Methods: We analysed nucleotide sequence variation of three mtDNA (COI, 16S rRNA, Cyt B) gene fragments in nine** ***V. regina*** **populations (165 specimens), representing the three subspecies. Sequences were aligned with ClustalX and were used for phylogenetic reconstruction with Neighbour-Joining (NJ) of Jukes-Cantor distances and Bayesian inference (BI) of the concatenated genes fragments. In addition, we surveyed variation at ITS-2 in 135 specimens.**

**Map of Pinar del Río in Cuba with indication of the sampling localities. Colours refer to the different populations.**



A: *V. r. laevigata*
B: *V. r. subunguiculata*
C: *V. r. regina*



NJ tree of 16S-CO1-CytB (JC-dist, 1000 bs, complete deletion).

## Preliminary Results & Conclusions:

The concatenated mtDNA alignment comprized 1476 bp, of which 125 were polymorphic (PI = 109), yielding 31 haplotypes. ITS-2 comprized 639 bp, of which 6 were polymorphic (PI = 4), yielding 8 haplotypes. (All data without outgroup)

**mtDNA**:

*V. r. subunguiculata* is well-supported; *V. r. regina* is only supported by NJ; *V. r. laevigata* is neither supported, nor rejected (« paraphyletic » with BI).

Within *V. r. subunguiculata* and *V. r. regina*, there seems to exist more or less well-supported geographic substructuring, even if the position of some haplotypes is unsupported (e.g. hap11, hap12).

**ITS-2**:

Provides no additional resolution and suggests but haplotypes are specific per subspecies.

**Overall**:

The conchological differentiation in Viana reflects phylogenetic, rather than ecophenotypic background.

Yet, the subspecific differentation may need to be reconsidered in relation to the observed more complex geographic substructuring.

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