

# Multiple cryptic species in *Heterocypris incongruens* (Ramdohr, 1808) (Ostracoda)

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## INTRODUCTION

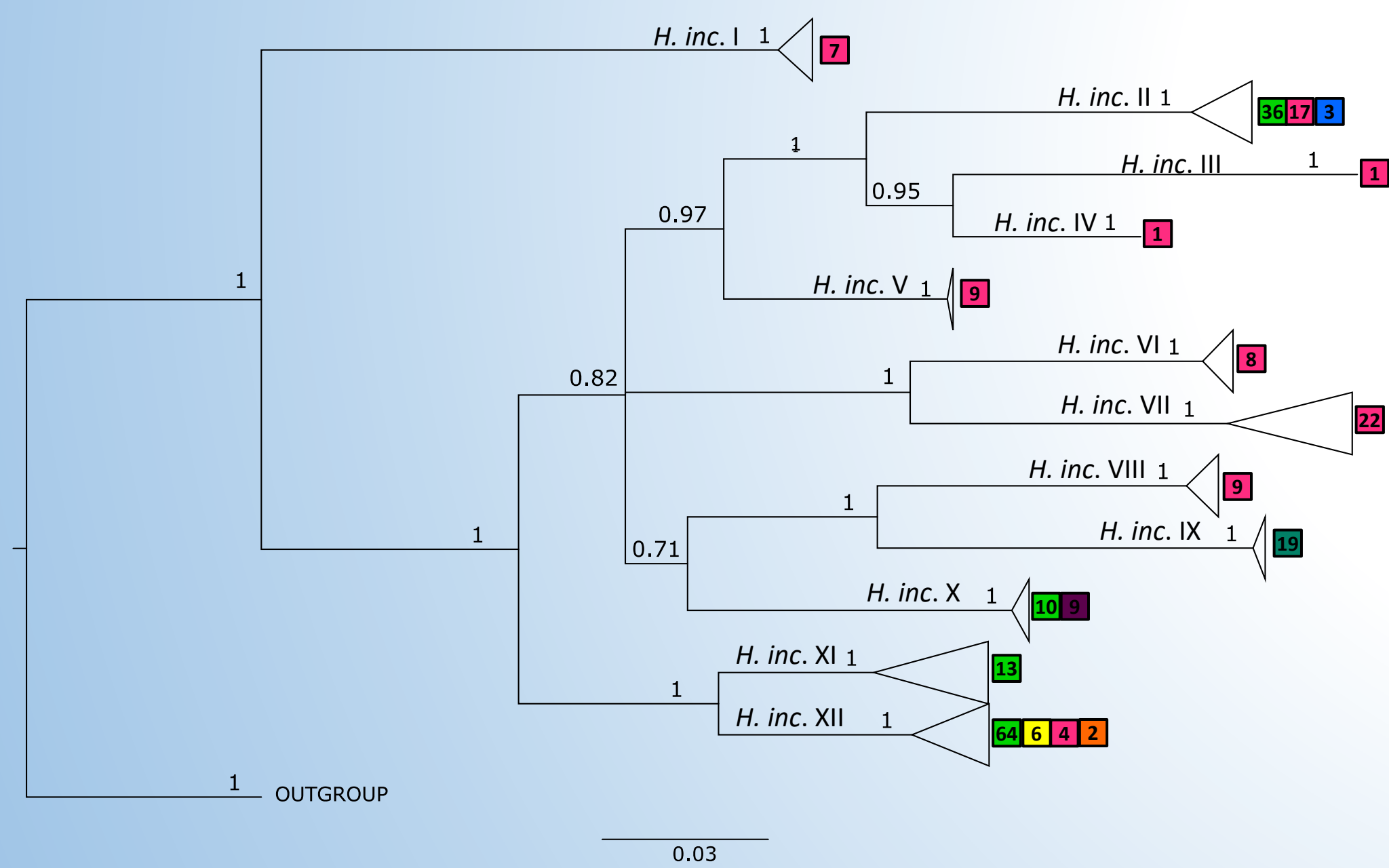
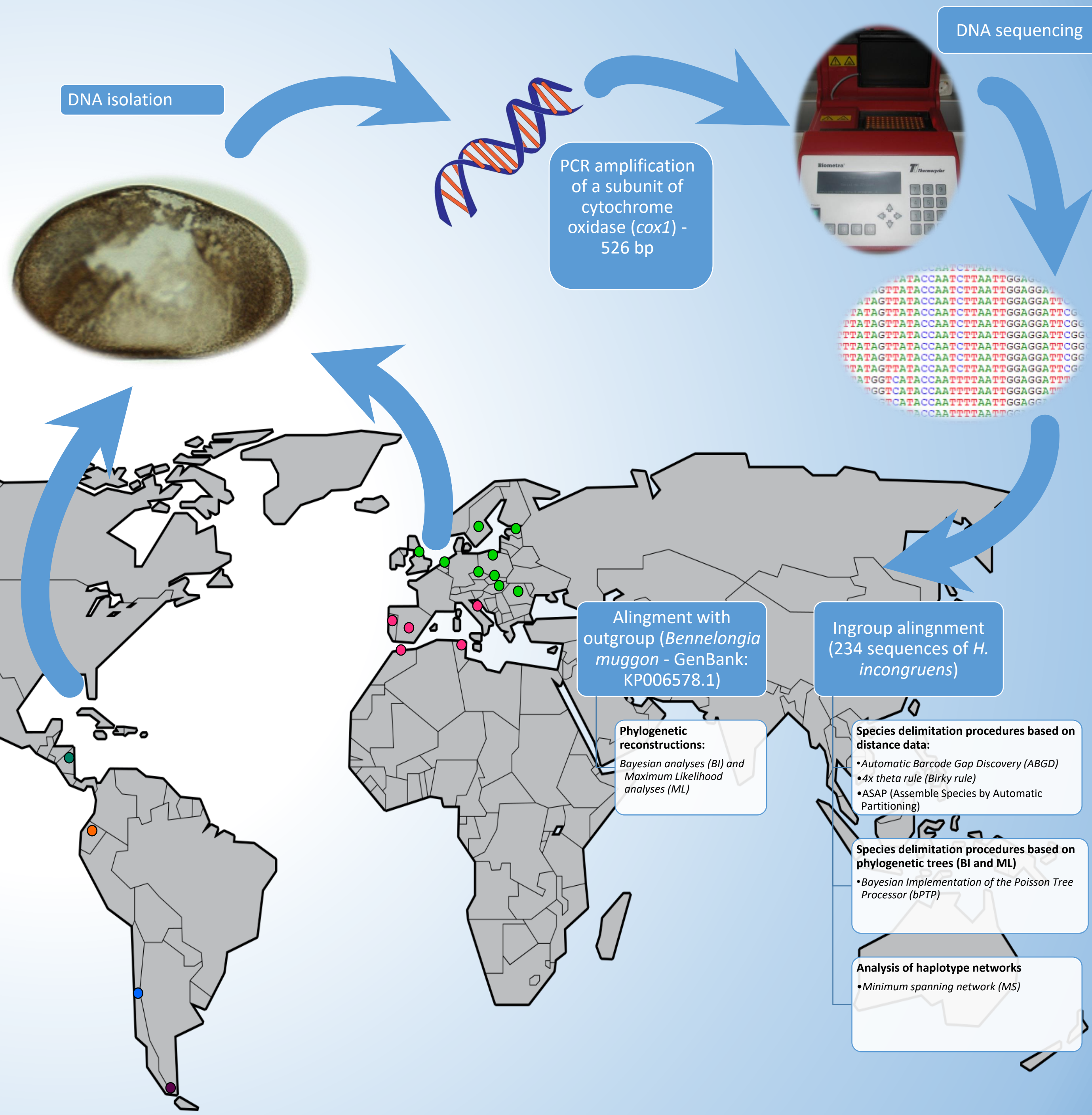
The problem of species identity still remains one of the most controversial issues in biology. Hidden genetic diversity and incompatibility of the rate of morphological and molecular evolution often results in overestimation or underestimation of species boundaries. Particularly problematic in this respect seem to be asexually reproducing species, or species with mixed reproduction, such as some freshwater ostracods.

Despite being considered as a model group for studying the evolution of sexuality, there is still a lack of analyses of genetic diversity of these crustaceans. That their taxonomy is based mainly on morphological traits also remains controversial in some cases. Estimating molecular diversity seems to be especially important, since our preliminary study results on *H. Incongruens* confirmed the published data on other Cyprididae and indicated that the occurrence of hidden diversity within this family may be much higher than was previously thought.

The aim of the present study was to determine the cryptic diversity within the morphospecies *Heterocypris incongruens* - a geographic parthenogen, in which sexual females and males co-exist with asexual females in the circum-Mediterranean area only, whereas asexual females occur in its entire range.

## MATERIALS AND METHODS

234 individuals of *H. incongruens* from 15 countries (50 localities), 7 geographical regions: Central Northern Europe, Mediterranean, Central America, Northern South America, Central South America, Southern South America, Polynesia – Easter Island



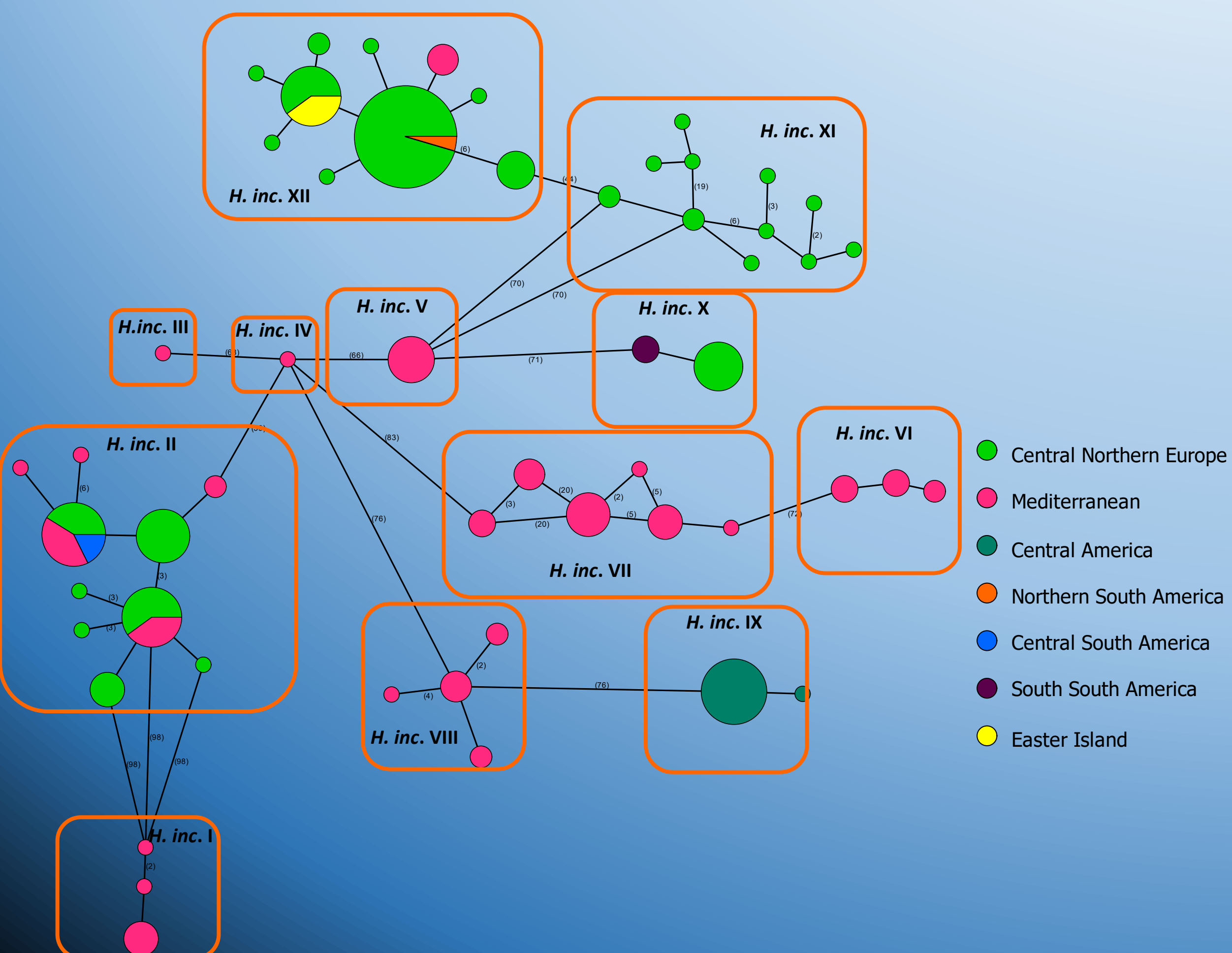
Bayesian Inference tree obtained for mtDNA of all *H. incongruens* *cox1* sequences. The tree is rooted by the species *Bennelongia muggon*. Clades which are identified as genuine genetic species are indicated by Roman numbers. The Arabic numbers indicate the Posterior Probabilities values. On the right side of collapsed branches, the geographical regions of sampling are shown. The colours correspond to different regions and the numbers inside the square indicate the numbers of individuals from a particular region.

## RESULTS AND DISCUSSION

Within 234 individuals from 50 sites representing a significant part of the range of this species, 54 haplotypes were recorded. Some mtDNA haplotypes showed a genetic divergence of more than 20%, which surpasses values of genetic variability commonly accepted for a single species. Analyses of the phylogeny and of genetic species delimitations using various methods reveal the existence of a species complex with at least 12 genetic species. It should also be noted that populations from distinct geographical localities can share the same mtDNA haplotype.

## CONCLUSIONS

Genetic data strongly support the existence of distinct genetic lineages within *Heterocypris incongruens*, suggesting that this morphospecies indeed represents a complex of highly differentiated species. These results indicate that the occurrence of hidden diversity within the family Cyprididae may be more common than previously thought. In order to support this hypothesis, it seems relevant to get insight into the genetic diversity of *H. incongruens* from other localities as well as other representatives of the family Cyprididae.



Minimum Spanning network of *cox1* (526 bp) mtDNA haplotypes of *H. incongruens*. The recognised genetic species are indicated by Roman numbers. The Arabic numbers indicate mutational steps (only values >1 were marked). The colours correspond to different geographical regions.