# Postglacial colonizer or cryptic invader? Case of *Gammarus* roeselii (Crustacea Amphipoda) in Europe

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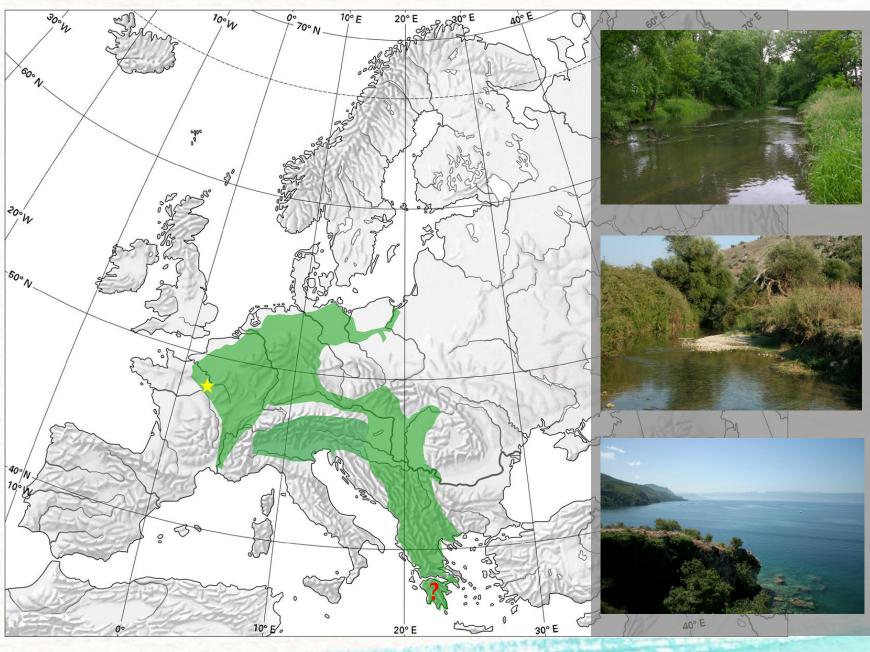








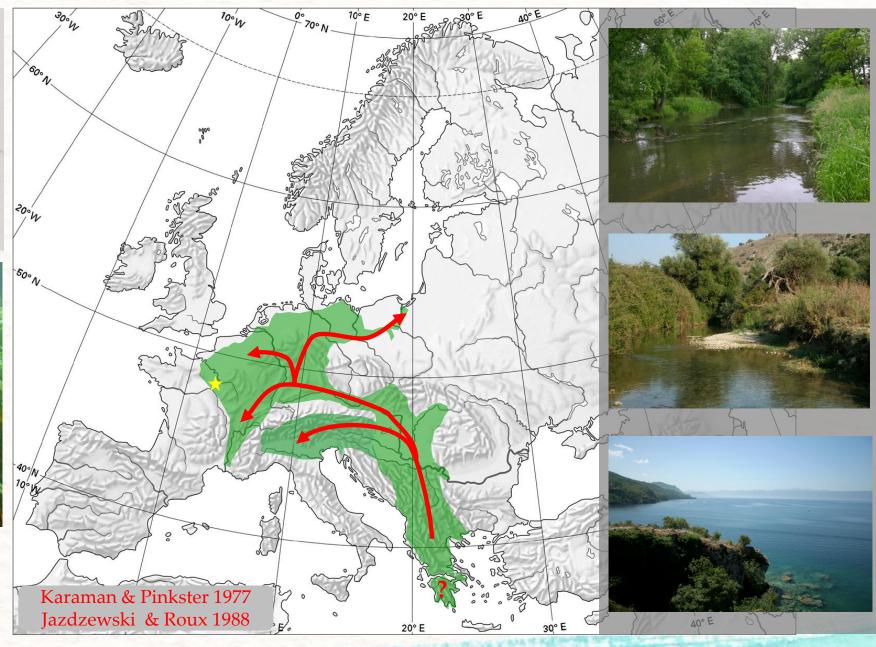
Gammarus roeselii Gervais, 1835 neotype locality: river Yonne, at Coulanges-sur-Yonne, France.







Wide & weird distribution range in Europe suggesting spread from the Balkan region.



Main goal

To reveal whether the current distribution of *Gammarus roeselii* in Europe is a result of population expansion from the diversity hotspot in the Balkans.

Grabowski M, Mamos T, Bącela-Spychalska K, Rewicz T, Wattier RA. 2017. Neogene paleogeography provides context for understanding the origin and spatial distribution of cryptic diversity in a widespread Balkan freshwater amphipod. PeerJ 5:e3016

Krzywozniak P. 2016. Phylogeography of *Gammarus roeselii* in Western and Central Europe based on fragment of cytochrome oxidase I (COI) polymorphism. MSc thesis. Supervised by Michal Grabowski, Tomasz Rewicz.

# Hypothesis I

The species will be characterised by high levels of cryptic diversity in the Balkans.

## Hypothesis II

Most of the diversification and speciation events in the Balkans precede the Pleistocene Ice Ages.

# Hypothesis III

Evolutionary history may be linked to presence and deterioration of the Balkan Neogene paleolake system.

# Hypothesis IV

One of the Balkan populations has been the source for colonisation of the Western and Central Europe.

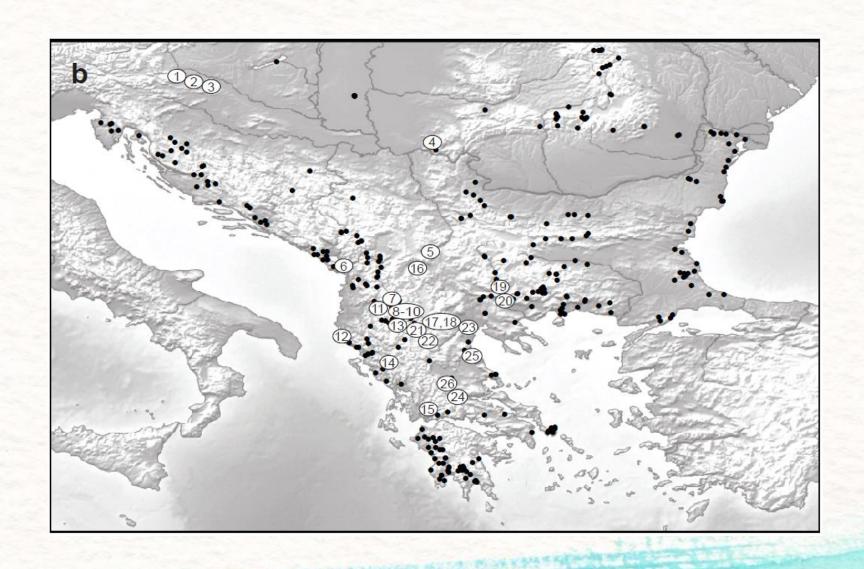
# Hypothesis V

The colonisation of the Western & Central Europe has been due to some anthropogenic factors.

# **Balkan Region**

26 sites 177 individuals

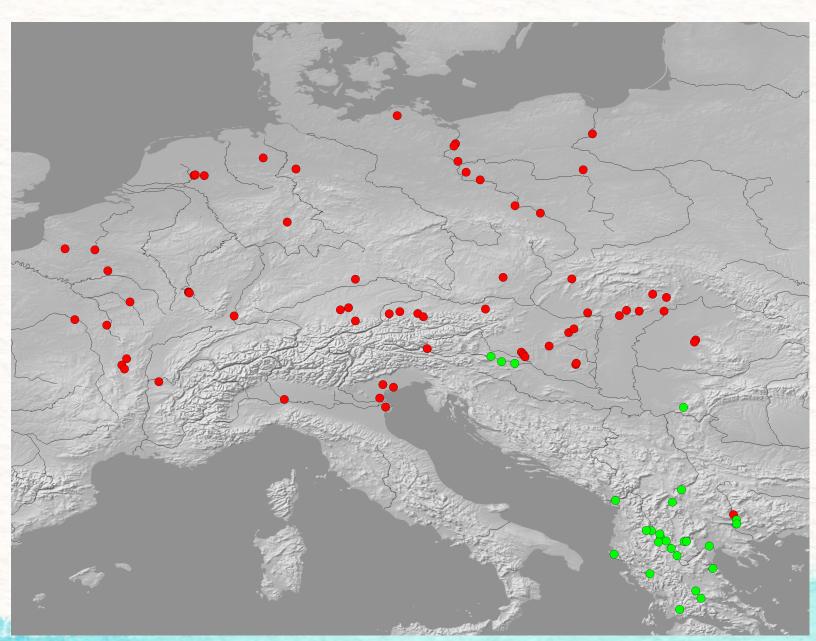




# Western & Central Europe

66 sites 651 individuals

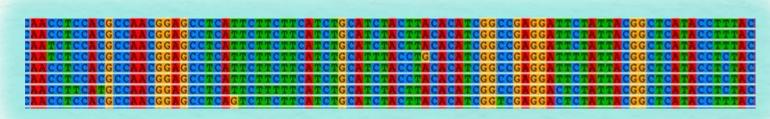




mitochondrial DNA: cytochrome oxidase I – 650/533 bp 828 individuals sequenced

nuclear DNA: 28S rDNA – 900 bp

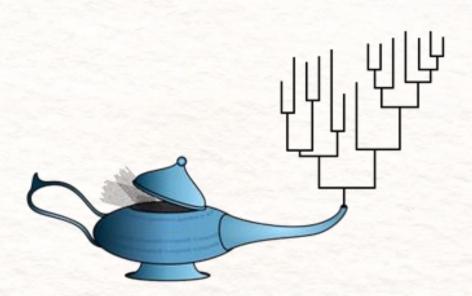
50 individuals sequenced

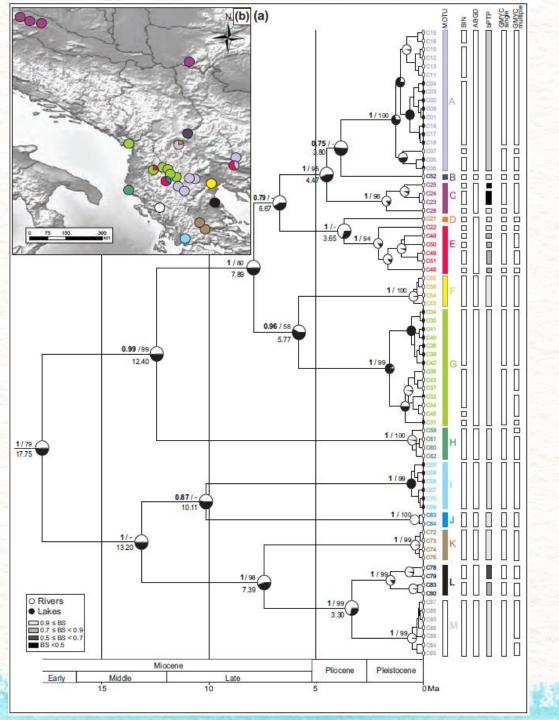




- DNA barcoding
- Bayesian chronogram
- Neighbor-Joining tree
- Haplotype Minimum Spanning Network
- Ancestral state reconstructions
  - habitat
  - divergence area
- MOTU delimitation
  - distance-based
  - phylogeny-based
- Demographic analyses
  - mismatch distribution
  - neutrality tests
  - Bayesian skyline plots







#### Results

High cryptic diversity at least 13 MOTUs in the Balkans

High level of endemism localised distribution of most MOTUs

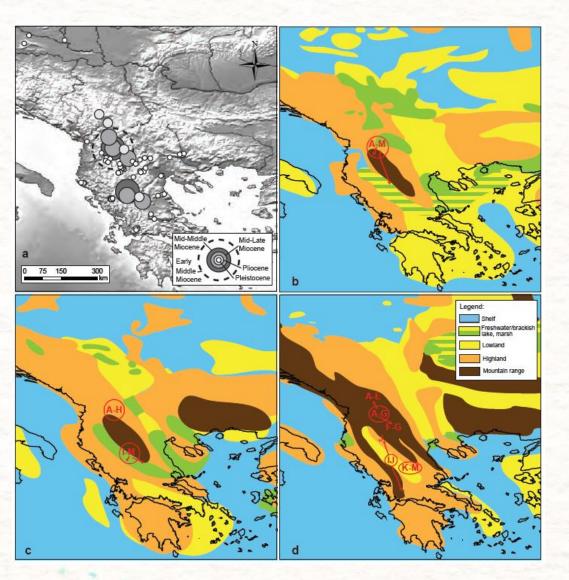
#### Old divergence

lineage diversification from early Miocene till Pleistocene

#### Evidence of habitat shifts

during Pleistocene, lakes could serve as microrefugia for riverine populations

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# **High cryptic diversity** at least 13 MOTUs in the Balkans

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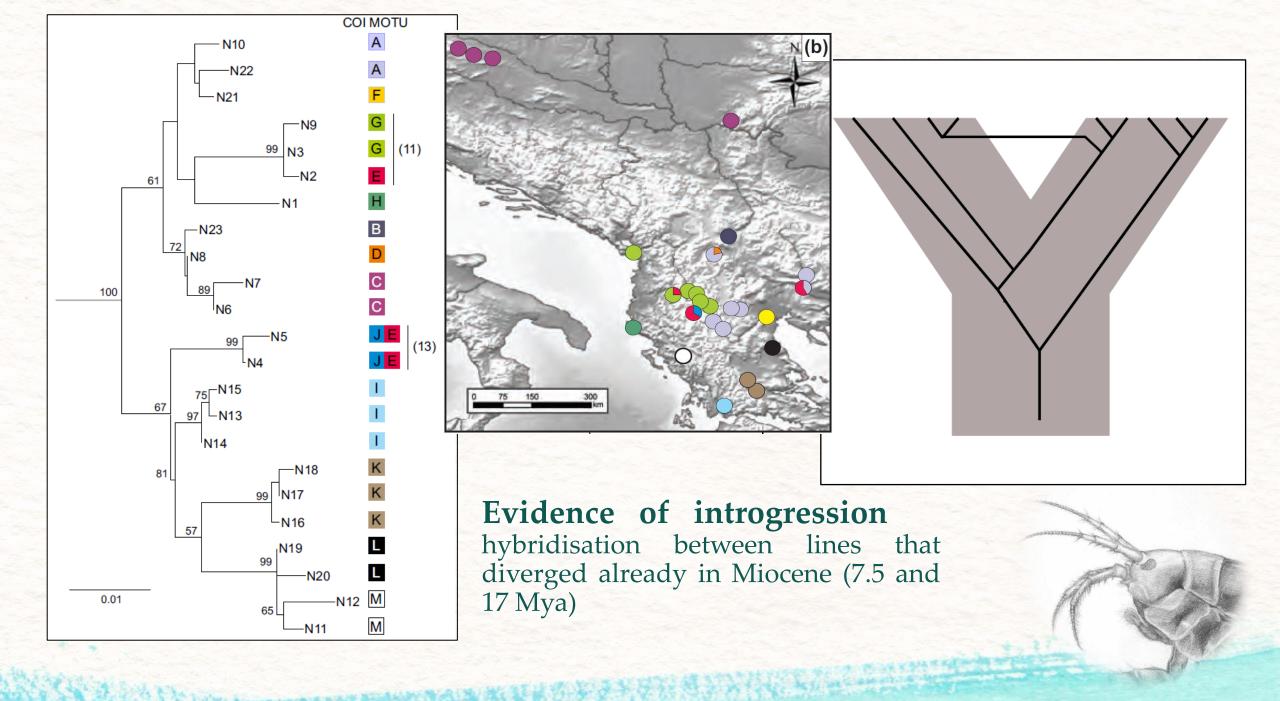
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#### **Evidence of habitat shifts**

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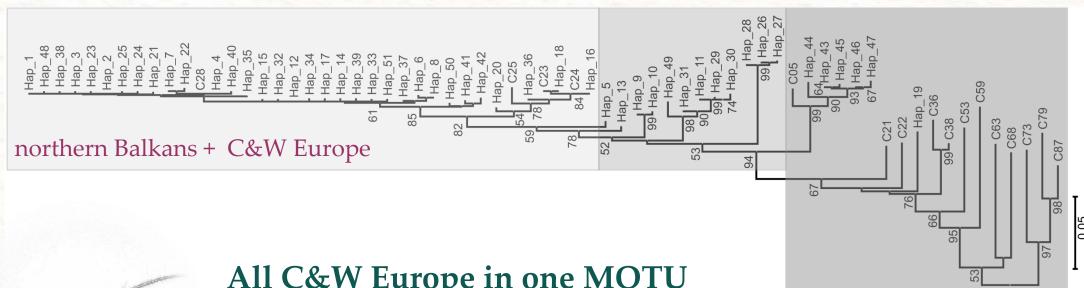
lineage divergence could be associated with Neogene lacustrine systems



#### **MOTU C**

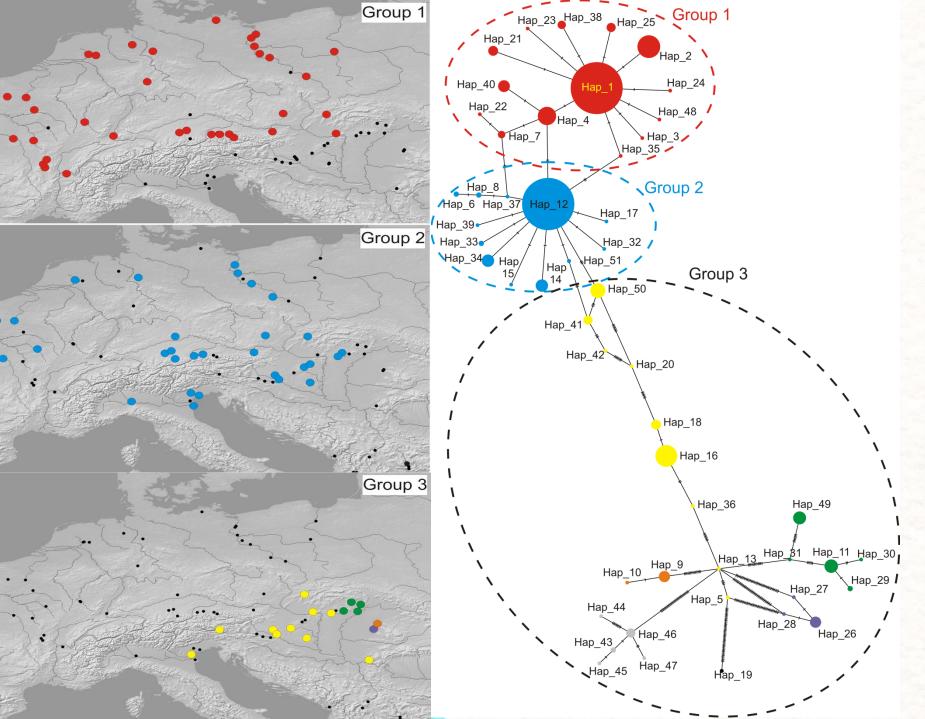
# Pannonian MOTUs

#### **Balkan MOTUs**





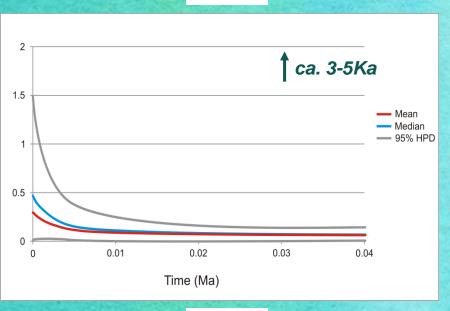
All C&W Europe in one MOTU three new MOTUs in Pannonian Basin



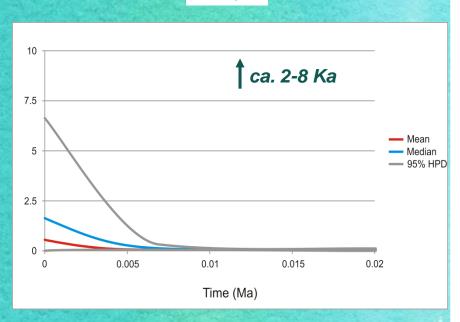
Several group of haplotypes spatial structure starlike/reticulate topology

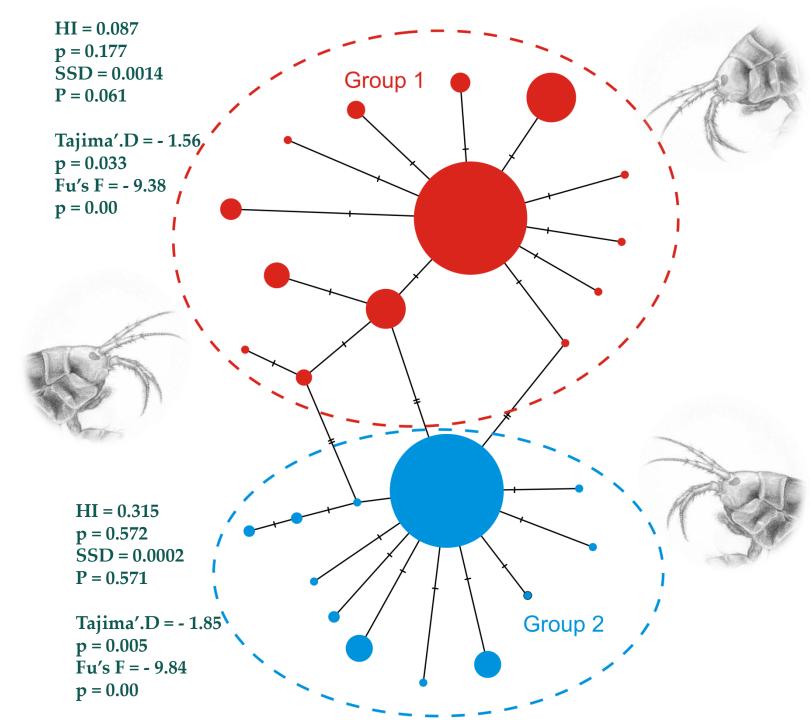


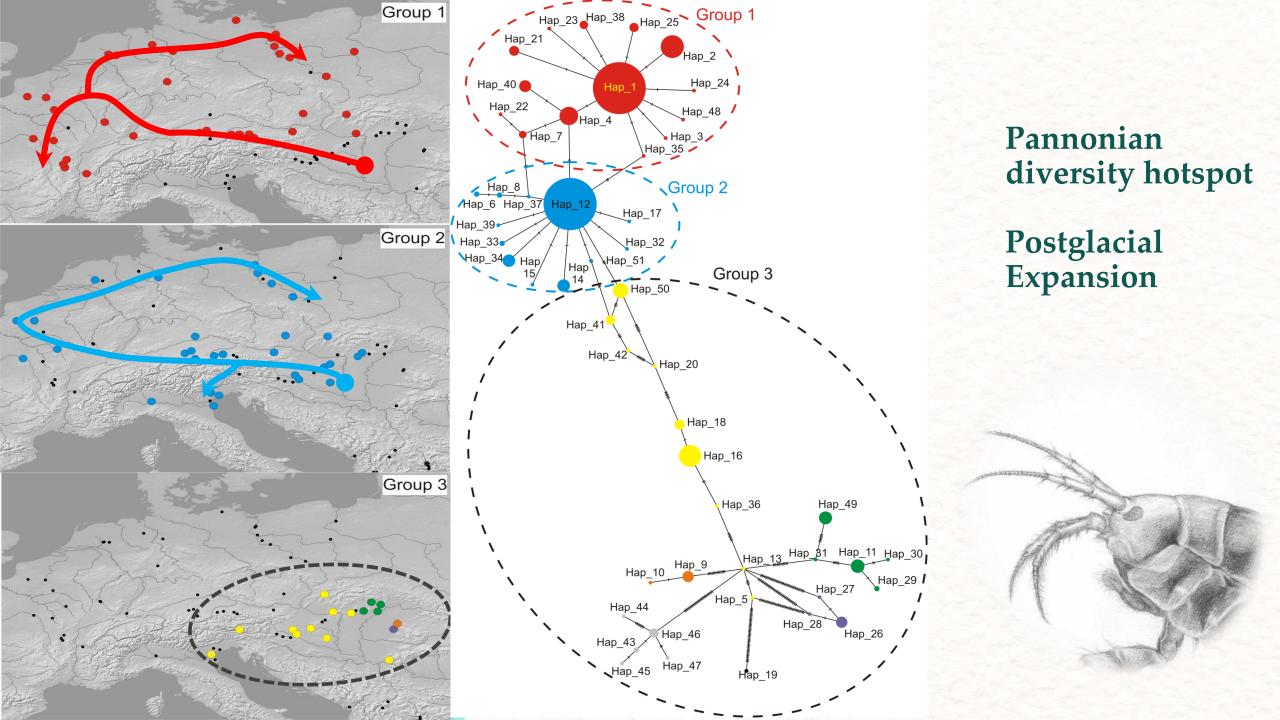




#### Group 2







#### **Conclusions**

- Set of cryptic/pseudocryptic species
- Two diversity hotspots:
  - Balkan Peninsula
  - Pannonian Basin
- Long history of divergence since Early Miocene
- Neogene paleolake systems could promote divergence
- Postglacial expansion of two Pannonian haplotype groups
- Probably partially promoted by canal construction



Gammarus roeselii Gervais, 1835

