

Taxonomic relationships within Lake Baikal deep-water scavenger amphipods of the genus *Ommatogammarus* revisited with molecular methods

Polina Drozdova*, Ekaterina Telnes, Maxim Timofeyev

Irkutsk State University, Irkutsk, Russia

* drozdovapb@gmail.com



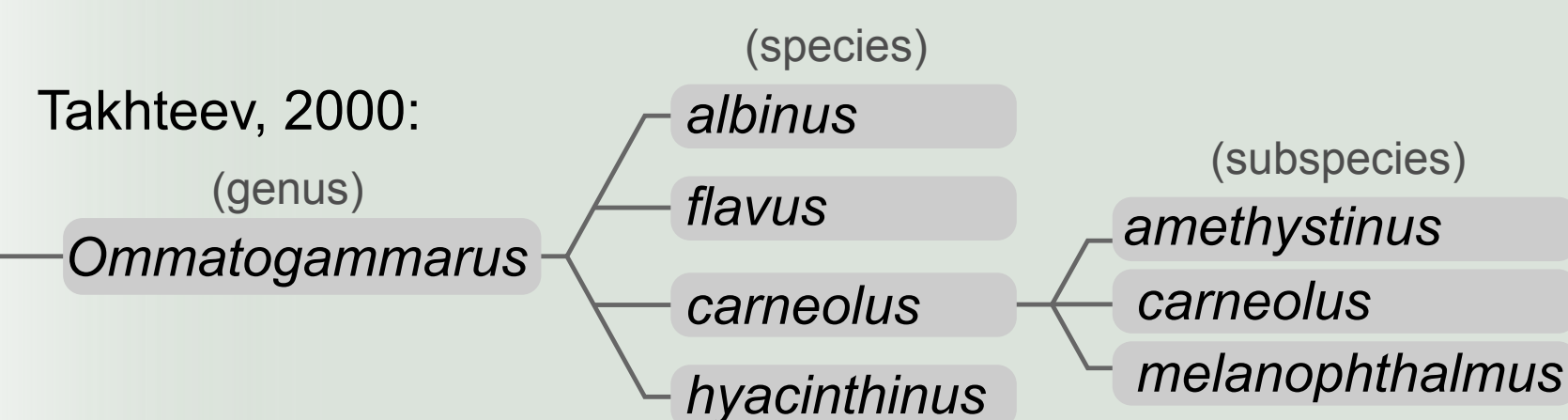
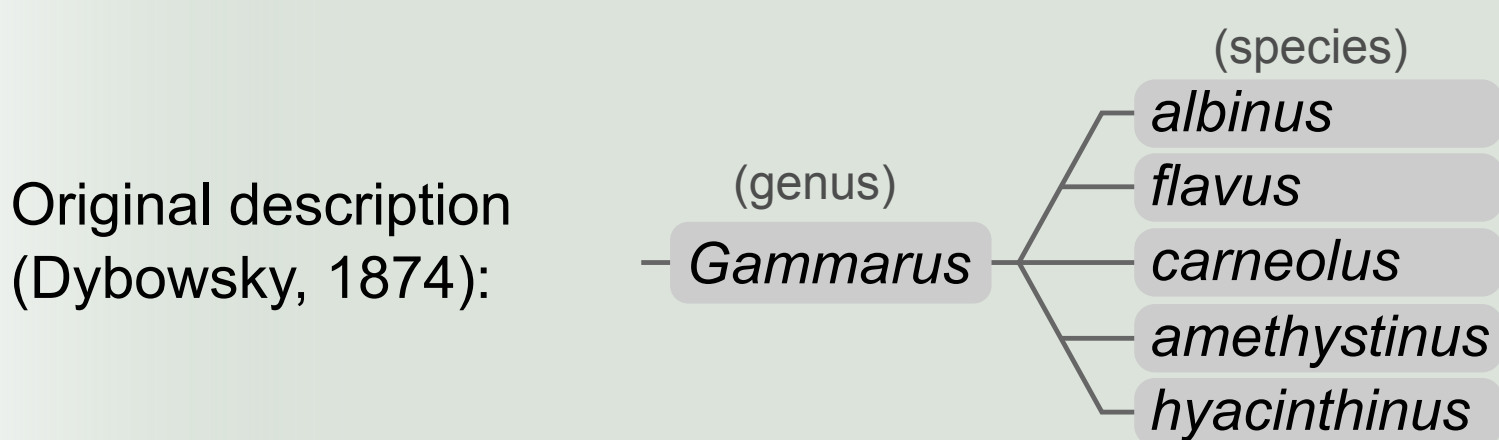
INTRODUCTION

Lake Baikal amphipods:

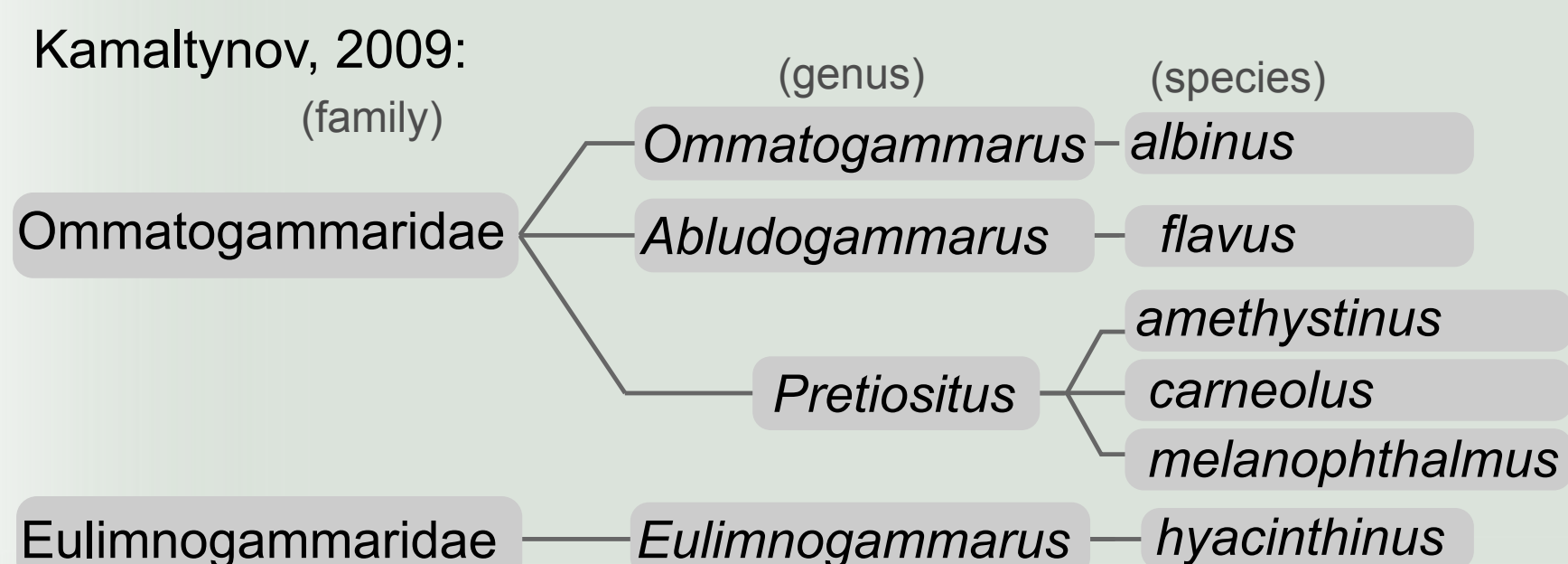
- >350 morphological species and subspecies;
- 2 conflicting taxonomies;
- 0 comprehensive identification keys.

for review see:
Drozdova et al., 2024

Here: deep-water genus *Ommatogammarus* (ὄμμα = eye)

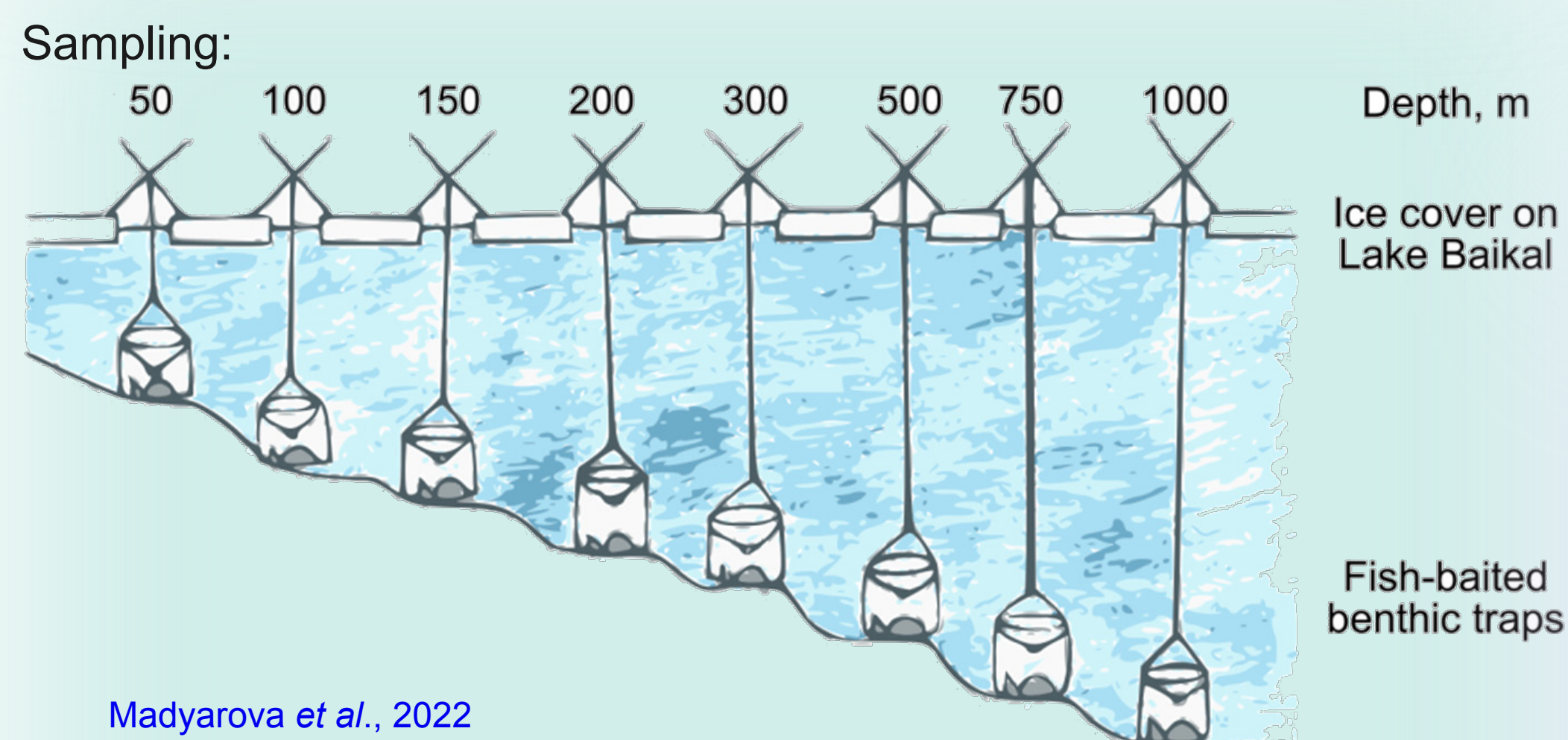


The only
existing key



Aim: can we resolve the conflict with molecular data?

METHODOLOGY



Madyarova et al., 2022

Sequencing:

- cytochrome oxidase subunit one gene (5' fragment);
- 18S rRNA gene (5' fragment);
- low-coverage whole-genome sequencing

mitochondrial genomes

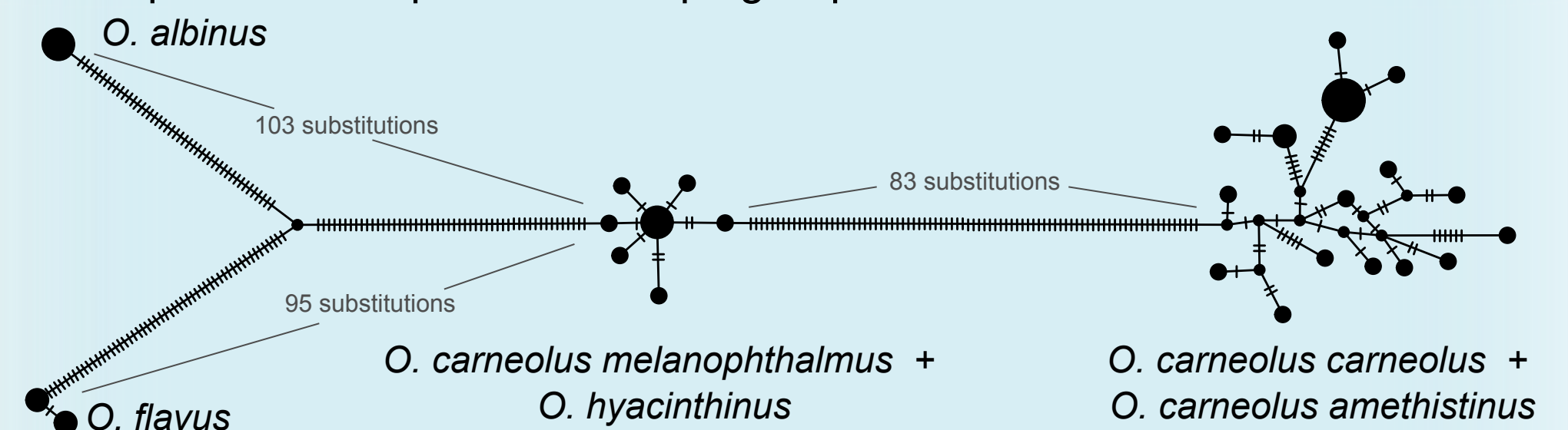
time-calibrated phylogeny

haplotype networks

RESULTS

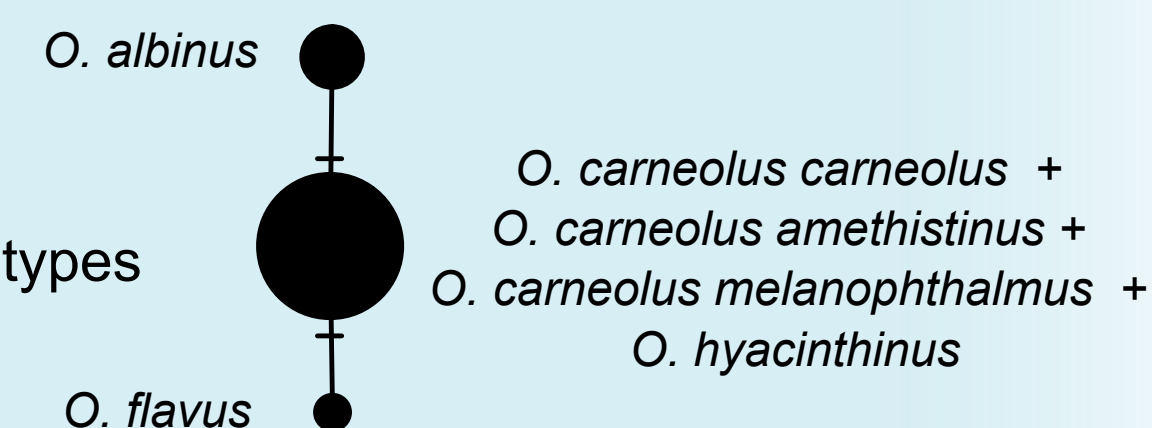
COI haplotype network:

6 species / subspecies = 4 haplogroups



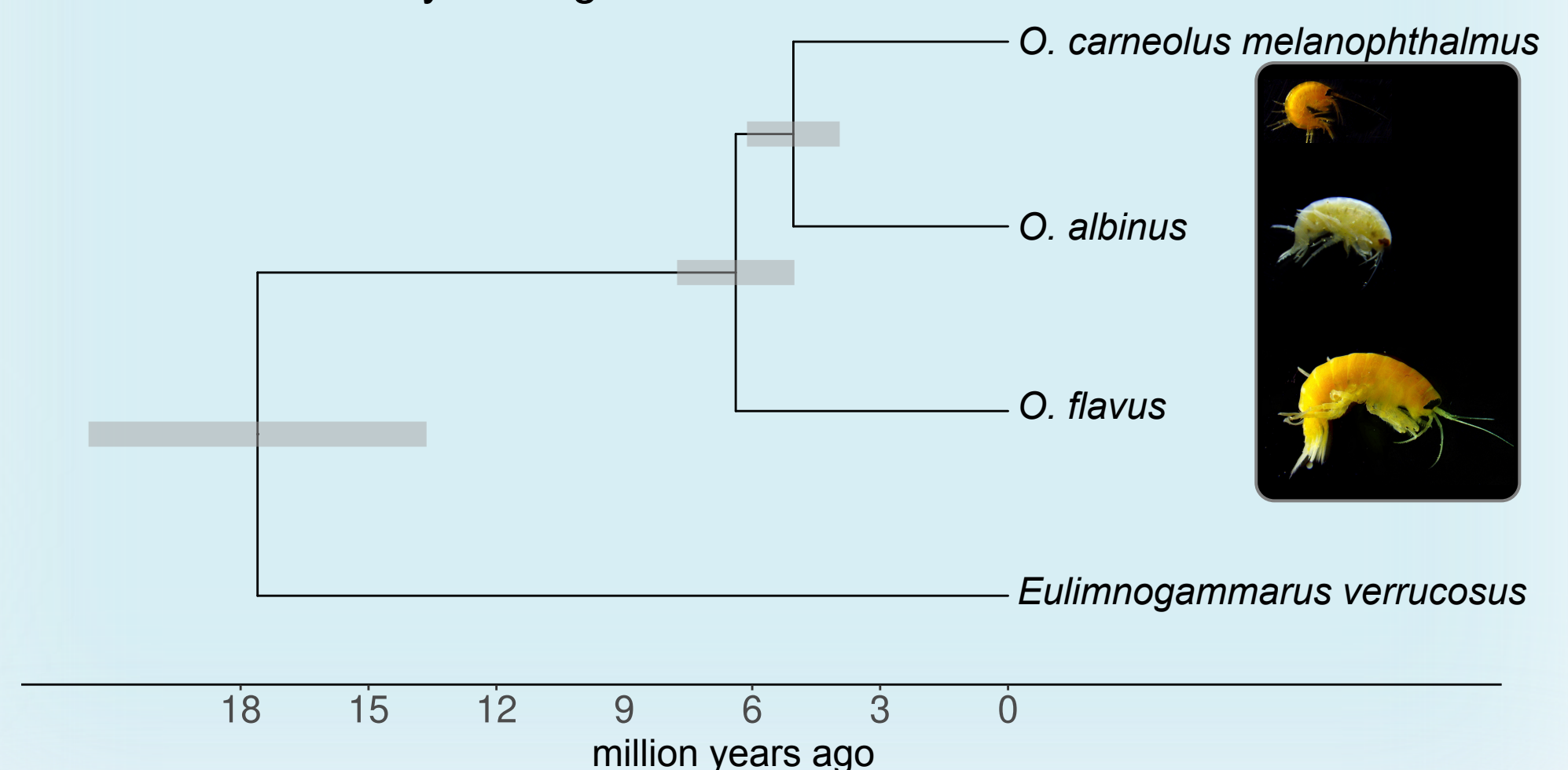
18S haplotype network:

6 species / subspecies = 3 haplotypes



Time-calibrated tree of 15 mitochondrial genes:

The last common ancestor of all *Ommatogammarus* s.l. existed ~6 million years ago.



CONCLUSIONS

- *Ommatogammarus sensu* Tachteew = 3 or 4 separated species:
 - *O. flavus* (= *A. flavus*)
 - *O. albinus*
 - two more diverged genetic lineages might require further direct checks for reproductive isolation
- *hyacinthinus* is *Ommatogammarus* / *Pretiositus*, not *Eulimnogammarus*.

Suggested taxonomy:

