

Clam (*Corbicula*) Lineages

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Introduction

Corbicula, commonly known as Asian clams, represent a group of highly adaptable mollusks with diverse reproductive strategies, which have successfully dispersed globally through rapid radiation and ecological plasticity. Given the prevalence of gene flow and incomplete lineage sorting (ILS), simple bifurcating tree models and allopatric speciation scenarios cannot fully capture the complexity of *Corbicula* evolution.

Aim

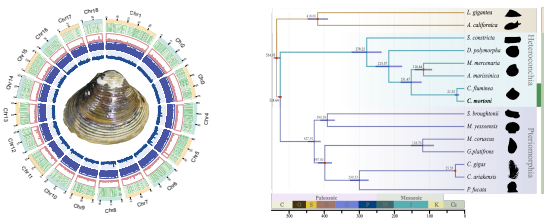
- Constructing the phylogenetic relationships within *Corbicula*
- Reveal the complex evolutionary history of *Corbicula*
- Providing molecular resources for the breeding and conservation of *Corbicula* species

Methods and Materials

We produced reference genome of *C. mortoni* and whole-genome sequencing data for *Corbicula* samples from China. We first used whole-genome SNPs, non-coding region SNPs, and mitochondrial protein-coding genes to infer the phylogeny of *Corbicula* clams using both coalescent and concatenated methods. We then assessed introgressive hybridization and identified signatures of ILS within *Corbicula*.

Results

1. The reference genome of *C. mortoni* was sequenced and assembled.
2. Phylogenetic analysis based on orthologous genes of mollusc revealed the taxonomic classification of *Corbicula*.

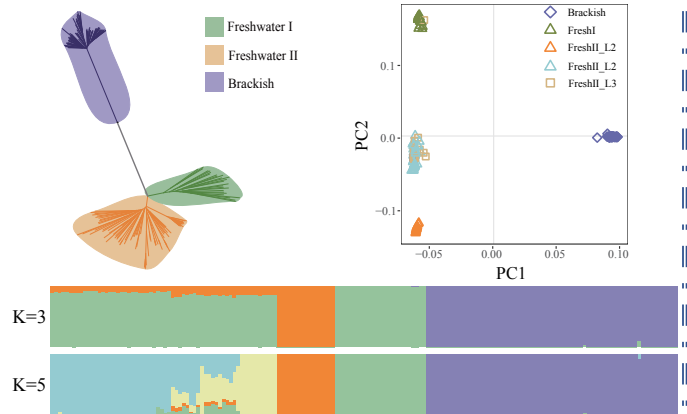


Conclusion

We found support for the division of *Corbicula* into five lineages despite the existence of extensive gene flow between different lineages.

We also conclude that both introgression and ILS are crucial factors resulting in phylogenetic discordances in *Corbicula*.

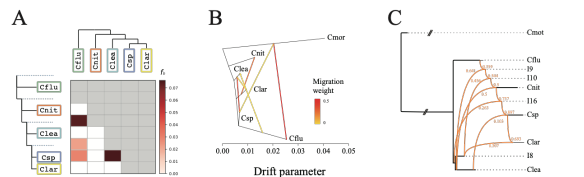
3. A maximum-likelihood tree, PCA, and genetic structure analysis were conducted based on SNPs from the whole-genome dataset of *Corbicula*.



4. We observed conflicting maximum-likelihood gene tree topologies for *Corbicula*.



5. Testing for introgression between different lineages.



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