

The origin of Parnassiinae has been previously estimated ca. 38 Mya in Central Asia (Condamine et al. 2018)

Reconstructing time-calibrated phylogenies, including both extant and fossil taxa as lineages (**total-evidence dating**) under fossilized birthdeath process, can provide new information on the age and historical biogeography inferred.

Dated to the late Oligocene (*Thaites ruminiana*) and late Miocene (*Doritites bosniackii*) in the **western Palearctic**, the two fossil taxa belonging to the Parnassiinae challenge the Central Asian origin.

What impact does the inclusion of fossils have on what we know about the

origin of the Parnassiinae?

DATED PHYLOGENY MrBayes

Fossil placement tests

- Phylogeny vs. Dated phylogeny
- Changes in outgroups
- Number of morphological characters

4 mitonchondrial and 1 nuclear genes 180 morphological characters

Partition tests

From 1 partition to 9 partitions (one by codon position)

Clock model tests

Combinations of strict, autocorrelated and uncorrelated clocks

Doritites bosniackii sister to genus Archon (PP=0.99)

Thaites ruminiana sister to tribe Parnassiini (PP=0.58)

Best model using 3 uncorrelated clocks (mitochondrial, nuclear, morphology).

Older age than previously inferred with an origin recovered *ca*. 57 Mya





Origin in Central Asia and Himalaya, followed by colonization of western Palearctic and Irano-Turanian region



Origin in western Palearctic and Irano-Turanian region, followed by colonization of Central Asia and Himalaya

Origin of *Parnassius* coincides with the intensification of the Himalaya and Tibetan Plateau orogeny (early Miocene)

Older origin of the Parnassiinae *ca*. 57 Mya in western Palearctic and Irano-Turanian region, instead of *ca*. 38 Mya in Central Asia.

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Institut des Sciences de l'Evolution-Montpellier drivers of the macroevolution of Apollo butterflies. *Syst. Biol.* 67:940–964.