

Used genome sequencing to solve the origins of the fungus *Batrachochytrium dendrobatidis*, a driver of global amphibian declines. The study traced *B. dendrobatidis* to one lineage from the Korean peninsula that looks like the origin of the epidemic. It dates the emergence of this pathogen to the early 20th century, coinciding with the global expansion of commercial trade in amphibians, and shows that intercontinental transmission is ongoing.

Suitable Maybe

Organism Batrachochytrium

dendrobatidis

Substrate DNA

Full Genome Yes

Genome size 24 Mb

Reference available Yes



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