

Frog Study Points to New “Out of Asia” Hypothesis

The true frogs of genus *Rana*, which include over 100 species, are mainly found in the northern hemisphere: Asia, Europe, North America and north of South America. They have received extensive attention as model animals widely used in behavior, genetics, physiology, ecology and evolution studies, and their various habitats have provided optimistic materials for large-scale investigations on their biogeography and diversifications. However, difficulties in understanding their intercontinental dispersal as well as conservation concerns have hindered the progress of these studies, and some earlier results were even misinterpreted due to inaccurate phylogeny of these groups. It is critical to build the evolutionary relationships of genus *Rana* in a systematic way.

Recently, an “Out of Asia” theory regarding the origination and diversification of *Rana* was proposed as the result of a joint study conducted by researchers from the US, Europe and Asia. It was described that genus *Rana* originated in the East Asia region, perhaps in southwest of China, and this “Out of Asia” pattern involved two independent dispersals of *Rana* from East

Asia to North America via Beringian land bridge and a third one into Europe and Central Asia.

The study included 91 species of the 101 currently recognized *Rana*. By analyzing three fragments of mitochondrial DNA (mtDNA) and six nuclear DNA (nuDNA) loci of the samples, the scientists yielded a comprehensive and well-resolved phylogeny for the genus *Rana*. The results indicated significant differences in the diversification among the species of the New World and Old World. For example, the more species-rich lineage of New World *Rana* appears to have experienced a rapid radiation following its colonization of the New World, especially with its expansion into montane and tropical areas of Mexico, Central America, and South America, whereas, Old World *Rana* exhibited very slow diversification and later underwent a distinct increase in speciation rate.

Their work rebuilt our understanding of the evolution and diversification patterns of the well studied genus *Rana*, and the comprehensive and time-calibrated phylogeny constructed in this study will surely benefit related studies in the future.

