Speciation process in *Callosciurus* squirrels in the Indochina Peninsula: Does the 'riverine barrier hypothesis' explain their evolutionary history?

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To test the riverine barrier hypothesis in Callosciurus squirrels, I examined the phylogenetic relationships between C. caniceps and C. inornatus geographically isolated in the northern part of the Indochina Peninsula and between C. finlaysonii and C. erythraeus griseimanus parapatrically occurring in the southern part of the Indochina Peninsula. This study compared complete mitochondrial DNA cytochrome b gene sequences of these four squirrels and three other *Callosciurus* species: C. nigrovittatus, C. notatus, and C. prevostii. Phylogenetic trees showed three main lineages: 1) a lineage containing C. caniceps, C. erythraeus, C. finlaysonii, and C. inornatus; 2) a C. notatus lineage; and 3) a lineage containing C. nigrovitattus and C. prevostii. Callosciurus caniceps was most closely related to C. inornatus; their ancestors may have diverged by a drastic eastward shift of the Mekong River. Callosciurus erythraeus griseimanus was more closely related to C. finlaysonii rather than to the other C. erythraeus the classification of C. showing that population, C. finlaysonii ervtheaeus and remains unclear. Callosciurus erythraeus griseimanus and C. finlaysonii

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may have been geographically separated from each other by formation of the Mekong River. Based on these two phylogeographical results, I show how the riverine barrier hypothesis explains speciation in *Callosciurus* squirrels in the Indochina Peninsula.