

# Comparative phylogeography of two commensal rat species (*Rattus tanezumi* and *R. norvegicus*) in China: insights from mitochondrial DNA, microsatellite and RADseq

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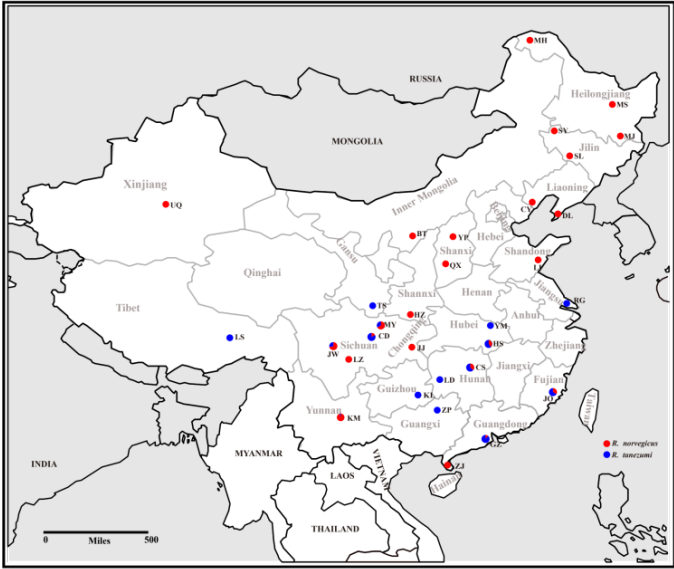
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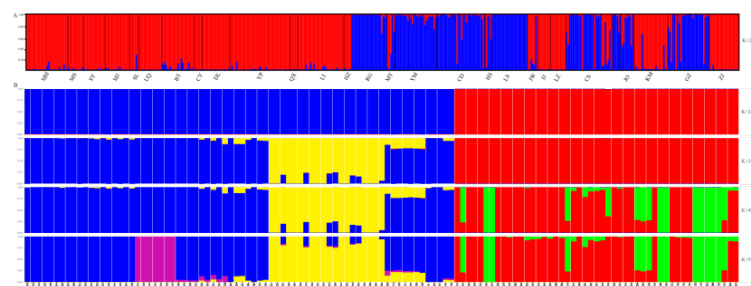
## Abstract

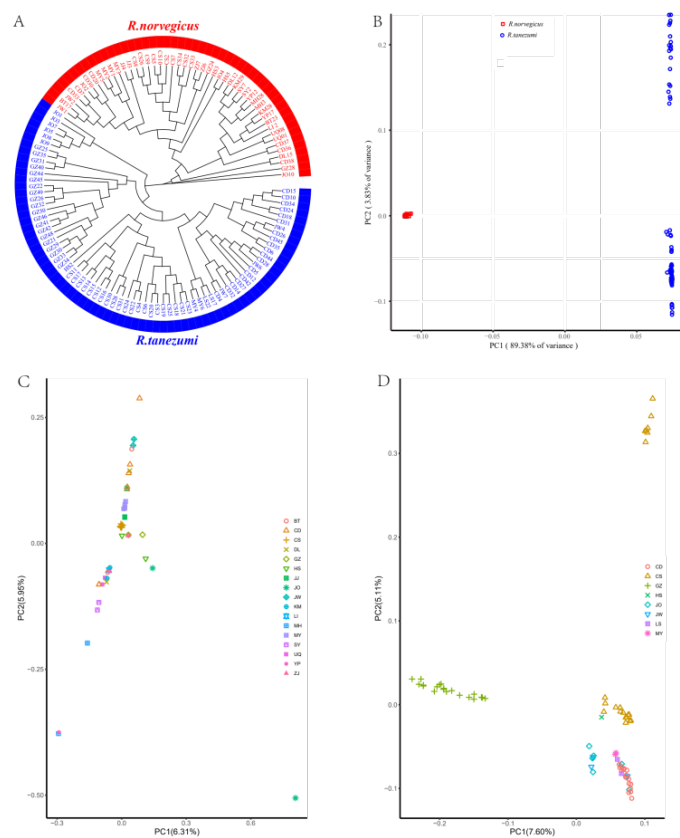
To explore the phylogeography of *Rattus tanezumi* and *Rattus norvegicus* in China, 486 individuals collected from 31 localities were initially analyzed with mitochondrial DNA and 10 microsatellite loci. Then, 123 individuals from 18 localities were subjected to 2b-RAD analyses. There were several major findings. Although *R. norvegicus* is widely distributed in China, *R. tanezumi* is mainly distributed in southern China, but is currently invading northward and has occupied many regions of northern China. Development of shipping transportation in ancient China had an important role in expansion of these two species; except for westward and southward colonization by land, some individuals of *R. norvegicus* reached the southeast coast of China by shipping transportation and subsequently expanded to central China; *R. tanezumi* immigrated to the southeast coast of China from Southeast Asia, and then expanded to central and western China. Before large-scale expansion associated with human transportation, changes in  $N_e$  of these species were closely related to climate changes. However, after immigration of *R. tanezumi* into China, interspecies' competition may have had a great role in their population sizes, as the *R. norvegicus* population declined rapidly with the increase of  $N_e$  for *R. tanezumi*. Analyses with 2b-RAD sequences did not support interspecies hybridization, although microsatellite data indicated potential gene introgression. Our study provided a valuable framework for further investigations on the expansion of the two dominant rat species in China. Finally, results also indicated that previous investigations on hybridization based solely on microsatellite data should be verified with genomic SNP data.

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