Supplementary Materials

Supplementary Methods

Sample collection

A field investigation of *L. taliangensis* was conducted in the breeding seasons from 2016 to 2019, and 426 tissue samples were collected from 16 sites throughout the southeastern Hengduan Mountains Region (HMR) in China (Figure 1; Supplementary Table S1). Samples were preserved in 95% absolute ethanol and stored at −20 °C. The tissue samples included tail tips of larvae and toes of adults. All individuals were released back to their place of capture after wound disinfection.

DNA extraction, amplification, and sequencing

Three mitochondrial DNA (mtDNA) fragments were extracted from the 426 tissue samples using a TIANGEN Animal Genomic DNA Kit (TIANGEN Biotech Co., Ltd., Beijing, China) following the manufacturer’s protocols. Polymerase chain reaction (PCR) was performed in a 25 µl volume, containing 2 µl of template DNA solution, 12.5 µl of 2×Taq Master Mix (Vazyme Biotech Co., Ltd., Nanjing, China), 1 µl of each primer, and 8.5 µl of ddH2O. The following PCR cycling conditions were applied: initial denaturation at 94 °C for 4 min, 35 cycles at 94 °C for 40 s, annealing (annealing temperature is given in Supplementary Table S2) for 40 s, extension at 72 °C for 70 s, and final extension at 72 °C for 8 min. Identification and visualization of amplification product lengths were performed using 1.2% agarose gel electrophoresis on an ABI 3730xl DNA sequencer (Sangon Biotech Co., Ltd., Shanghai, China).

Microsatellite genotyping

Eleven highly polymorphic microsatellite loci were used as gene markers (Chen et al., 2019; Shu, 2020). The 5’ ends of each forward primer pair were labeled with one of three fluorescent dyes, i.e., FAM, HEX, or TAMRA. The PCR amplification system and conditions followed those of Chen et al. (2019) and Shu (2020). The PCR products with different dye analyses were visualized on an ABI 3730xl DNA sequencer (Sangon Biotech Co., Ltd., Shanghai, China) and genotyped using GeneMarker HID v1.95 (SoftGenetics, LLC, State College, PA, USA).

Divergence date estimation

PartitionFinder v2.1.1 (Lanfear et al., 2017) was run to determine gene partition strategies and the optimal nucleotide substitution before BEAST analysis. Markov chain Monte Carlo (MCMC) analyses were performed assuming a “unlinked uncorrected lognormal relaxed clock” under the Yule speciation model. Bayesian MCMC chains were run for 10 million generations, with sampling every 1 000 generations and the first 10% of generations discarded as burn-in. Effective sampling size convergence and stationarity (ESS) was estimated by checking the logfile in TRACER v1.7 (Rambaut et al., 2018). A maximum clade credibility (MCC) tree was
calculated using TreeAnnotator v1.8.2 (Drummond & Rambaut, 2007).

**Demographic estimation (Bayesian skyline plot construction)**

A strict molecular clock, the mean rate (0.475% site-1 million-1 years-1) of which was evaluated from the second step of divergence date estimation analysis, and the piecewise-constant model were chosen as the tree prior skyline model. Runs of 10 million generations were performed, with samples taken every 1 000 iterations and the first 10% discarded as burn-in.

**Migration pattern analysis**

Three demographic models were estimated: (1) only from the West cluster (XXL-GG) to the East cluster (LS); (2) only from the East cluster (LS) to the West cluster (XXL-GG); and (3) two-way migration between the West cluster (XXL-GG) and East cluster (LS). These analyses were based on the grouping of microsatellite genotypes from all samples into two clusters (results of population structure in Figure 1). For analysis, 20 independent replicates with four heated chains under the following temperatures were applied: 1.0, 1.5, 3.0, and 100 000; each replicate had 8 000 000 MCMC steps, with a burn-in of 80 000 and sampling every 100 iterations. To identify the optimal model, the ln Bayes factors (BF) were calculated based on the differences between log marginal likelihood values (Beerli & Palczewski, 2010).

**Ecological niche modeling**

Variables included the Last Interglacial (LIG, 120 ka) and Last Glacial Maximum (LGM, 21 ka) with three general circulation models (GCMs) (CCSM4, MIROC-ESM, and MPI-ESM-P), mid-Holocene (MH, 6 ka) with four GCMs (CCSM4, MIROC-ESM, MPI-ESM-P, and BCC-CSM1-1), and the present. To maintain consistent climate raster resolution, the resolution of the LGM rasters was increased from 2.5 min to 30 arc-seconds by the “resample” method in ArcGIS v10.3.

Before constructing the ENM, bioclimatic rasters were clipped into the study area from 25–31°N to 100–105°E, and rasters were converted to the ASCII format for MaxEnt analysis. To prevent over-fitting, “band collection statistic” of the spatial analysis tool was used to calculate the correlation coefficients between different bioclimatic rasters in ArcGIS v10.3. Variables included in the ENM were not highly correlated with each other (correlation coefficient<0.8). The following five bioclimatic predictors were retained: isothermality (Bio03), minimum temperature of coldest month (Bio06), annual temperature range (Bio07), annual precipitation (Bio12), and precipitation of driest month (Bio14).

The predictive effectiveness of MaxEnt can be affected by both “feature types” and “regularization constants”, especially for small sample sizes. The following different parameters were set: “L, LQ, H, LQH, LQP, and LQPH” for “feature types” and 0.5–4 for “regularization constants”; then, the optimal parameters were selected based on the minimum value of the corrected Akaike information criterion (AICc) calculated by ENMTOOLS v1.4.3 (Warren et al., 2010).

ENM was conducted in MaxEnt v3.4.1. Here, 10 000 background points were set,
and the logistic output format and each model were run with 10 cross-validation replicates. The averages of projections of 10 iterations were used as the prediction results of each time period. Projections were then averaged across the three GCMs for LGM and four GCMs for MH to arrive at the final distribution prediction for these two periods.

**Isolation-by-resistance (IBR) as an alternative to IBD**

Euclidean geographical distance was once commonly used as a geographic factor to explain population differentiation (IBD; Wright, 1943); however, interpopulation migration is not straightforward, and Euclidean geographical distance cannot completely reflect the impact of landscape heterogeneity. Resistance distance, a geographic distance metric based on circuit theory, is a reliable and stable predictor of genetic divergence compared to traditional distance measures (e.g., Euclidean geographical distance) (Emel et al., 2021; McRae, 2006; McRae et al., 2008; Myers et al., 2019; Vasconcellos et al., 2019; Wang, 2013). Here, instead of Euclidean geographical distances, resistance distances can reflect topographic complexity and population connectivity as a new geographic distance metric.

**Resistance surface construction**

Twenty-three environmental rasters (including 19 bioclimatic variables, altitude, normalized difference vegetation index (NDVI) (1998–2018 average), Global Human Influence Index (HII), and river) were used to develop an ENM for the 26–31°N to 101–105°E region.

Bioclimatic variables and altitudinal data were downloaded from the WorldClim website (https://www.worldclim.org); NDVI (1998–2018) and river (.shp format) data were obtained from the Resource and Environment Science and Data Center (http://www.resdc.cn). Distance analysis (Euclidean distance) of river layers was conducted in ArcGIS v10.3 to construct a new river raster for MaxEnt analysis; HII was derived from EARTHDATA (https://sedac.ciesin.columbia.edu). All variable rasters had a resolution of 30 s.

Before construction of the ENM, the correlation coefficients between different rasters were calculated in ArcGIS v10.3, and variables with high correlation (correlation coefficient $\geq 0.8$) were removed. Finally, the following nine environmental predictors were selected: temperature seasonality (Bio04), temperature annual range (Bio07), annual precipitation (Bio12), precipitation of driest month (Bio14), precipitation seasonality (Bio15), altitude, NDVI, HII, and river. Furthermore, model parameter filtering was performed using ENMTOOLS v1.4.3 (Warren et al., 2010).

A grid cell of an ENM raster with a higher suitability score means a lower friction value; therefore, here, the ENM grids were inverted to create a resistance surface to calculate the resistance distance in Circuitscape v4.0 (McRae, 2006; McRae et al., 2016).

**Environmental dissimilarity matrix calculation**

Nineteen bioclimate variables (https://www.worldclim.org) and NDVI
with 30 arc-second resolutions were extracted from each site in ArcGIS, and two principal components (PCs) were obtained (PC1: 58.98% and PC2: 29.23%). The two sets of environmental dissimilarity matrices, used for isolation-by-environment (IBE) analysis (Wang & Bradburd, 2014), were calculated separately by the two PCs using the “dist” function in R v3.6.1.
### Supplementary Table S1 Sampling information of *L. taliangensis* in southeastern Hengduan Mountains Region

| Mountains                      | Location                | Population code | Sample size (N) | Altitude (m) | Longitude (°E) | Latitude (°N) |
|-------------------------------|-------------------------|-----------------|-----------------|--------------|----------------|---------------|
| Xiaoxiangling (XXL)           | Pusagang, Mianning      | PSG             | 28              | 2518         | 102.3081       | 28.8991       |
|                               | Zhuma, Shimian          | ZUM             | 24              | 1688         | 102.4308       | 29.1356       |
|                               | Zima, Shimian           | ZM              | 20              | 1984         | 102.2736       | 28.9809       |
|                               | Yeniuhe, Shimian        | YNH             | 16              | 2201         | 102.2809       | 29.0147       |
|                               | Jinghuahu, Shimian      | JHH             | 22              | 2607         | 102.2858       | 28.9738       |
|                               | Gongyi hai, Shimian     | GYH             | 46              | 2019         | 102.3932       | 29.0205       |
|                               |                         |                 |                 |              |                |               |
| Gonggar (GG)                  | Ximmin, Shimian         | XM              | 36              | 2410         | 102.1889       | 29.3715       |
|                               | Ganluo                  | GL              | 23              | 3022         | 102.8545       | 28.9663       |
|                               | Chuhongjue, Meigu       | CHJ             | 29              | 2837         | 103.1300       | 28.6448       |
|                               | Longwo, Meigu           | LW              | 39              | 2172         | 103.2017       | 28.7188       |
|                               | Bingtu, Meigu           | BT              | 27              | 2319         | 103.0488       | 28.5686       |
|                               | Shengliping, E’bian     | SLP             | 22              | 2279         | 103.0502       | 28.7367       |
|                               | Sanhekou, Mabian         | SHK             | 35              | 1700         | 103.3246       | 28.8811       |
|                               |                         |                 |                 |              |                |               |
| Daliangshan (DLS)             | Qiliba, Zhaojue         | QLB             | 22              | 3140         | 102.5240       | 27.8734       |
|                               | Wuke, Butuo             | WK              | 12              | 3214         | 102.7444       | 27.5974       |
|                               | Yuexi                    | YX              | 6               | 2206         | 102.5774       | 28.4582       |
**Supplementary Table S2** Amplification primer pairs for three mitochondrial gene markers

| Gene marker | Primer Pairs | Primer sequence | Annealing temperature (°C) | Amplified fragment length (bp) | References                  |
|-------------|--------------|-----------------|----------------------------|--------------------------------|----------------------------|
| cyt b       | MVZ-F 5'-GAACTAATGGCCCACAC(AA/TT)TACGNAAT-3' | 49              | 823                        | Moritz et al., 1992          |
|             | MVZ-R 5'-AAATAGGAA(A/G)TATCA(T/C)TCTGGATT(A/G)AT-3' |                |                            |                                |
|             | 2 cyt b-F 5'-ACCAAGACCTCTGACCTG-3' | 50              | 980                        | This study                    |
|             | 2 cyt b-R 5'-GTATGTAATAATGGGAAG-3' |                |                            |                                |
|             | 3 cyt b-F 5'-AACCCACCCACTAATAAA-3' | 52              | 832                        | This study                    |
|             | 3 cyt b-R 5'-ATAAGCGAAGGATGCTAAGC-3' |                |                            |                                |
| ND2         | Pmet 5'-AAGCTTTGGGGCCCATACC-3' | 53              | 1100                       | Wang et al., 2009             |
|             | Ptrp 5'-TRCTTBGCTTTGAAGG-3' |                |                            |                                |
|             | ND2-F 5'-TACTAATGCAACCCACACG-3' | 50              | 1054                       | This study                    |
|             | ND2-R 5'-AGTCTTTAGTTAGTATT-3' |                |                            |                                |
| COI         | COI-F 5'-TATATGCTAGACATACAGG-3' | 60              | 1716                       | This study                    |
|             | COI-R 5'-TTGAAGAAGGTTGATGATTG-3' |                |                            |                                |
|             | 3COI-F 5'-CACAGGGCTTGGTAA-3' | 54              | 1800                       | This study                    |
|             | 3COI-R 5'-GATGCAGCGCTTGGAAACC-3' |                |                            |                                |
### Supplementary Table S3 GenBank number of outgroup species

| Outgroup species name         | GenBank number |
|-------------------------------|----------------|
| Tylotriton kweichowensis      | NC_029231      |
| Tylotriton shanorum           | KU255459       |
| Tylotriton verrucosus         | AB689009       |
| Tylotriton yangi               | KU297946       |
| Tylotriton shanjing            | KR154461       |
| Tylotriton ziegleri           | KY398015       |
| Tylotriton asperrimus         | EU880340       |
| Tylotriton wenxianensis       | NC_027507      |

### Supplementary Table S4 GenBank numbers of four calibration points (C1–C4) and of other Salamandridae species used in first step of molecular dating analysis

| Species                                      | GenBank number |
|----------------------------------------------|----------------|
| C1 Pleurodeles poireti (Estes, 1981)          | EU880329       |
| (Estes, 1981) Pleurodeles waltl (Herre, 1935) | EU880330       |
| Milner, 2000) Echinotriton chinhaiensis       | EU880315       |
| C2 Notophthalmus viridescens (Estes, 1981)   | EU880323       |
| (Estes, 1981) Notophthalmus meridionalis      | EU880322       |
| (Böhme, 2003) Taricha rivularis              | EU880334       |
| Taricha granulosa                            | EU880333       |
| C3 Triturus marmoratus (Böhme, 2003)          | EU880337       |
| (Estes, 1981) Triturus cristatus             | EU880336       |
| C4 Cynops orientalis (Estes, 1981)            | EU880311       |
| Cynops pyrrhogaster                          | EU880313       |
| Paramesotriton deloustali                    | EU880327       |
| Laotriton laoensis                           | EU880328       |
| (Paramesotriton laoensis)                     |                |
| Pachytriton labiatus                         | EU880325       |
| Others                                       |                |
| Euproctus platycephalus                      | EU880317       |
| Ichthyosaura alpestris                       | EU880335       |
| (Mesotriton alpestris)                        |                |
| Calotriton asper                             | EU880307       |
| Neurergus kaiseri                            | EU880320       |
| Salamandrina terdigitata                     | EU880332       |
| Chioglossa lusitanica                        | EU880308       |
| Lyciasalamandra atifi                        | AF154053       |
| Salamandra salamandra                        | EU880331       |
| Hap   | Frequency | Sequences name                        |
|-------|-----------|---------------------------------------|
| Hap_1 | 33        | BT01-02,04-28                         |
|       |           | CHJ01,06,08,10,19,22                  |
| Hap_2 | 1         | CHJ02                                 |
| Hap_3 | 9         | CHJ03,07,14-15,25,27,30               |
|       |           | LW04,21                               |
| Hap_4 | 1         | CHJ04                                 |
| Hap_5 | 7         | CHJ05,13,17-18,21,24,28               |
| Hap_6 | 1         | CHJ09                                 |
| Hap_7 | 3         | CHJ11-12,26                           |
| Hap_8 | 1         | CHJ16                                 |
| Hap_9 | 1         | CHJ20                                 |
| Hap_10| 1         | CHJ29                                 |
| Hap_11| 1         | GL01                                  |
| Hap_12| 9         | GL02-04,06,09,12,14,17,23             |
| Hap_13| 1         | GL05                                  |
| Hap_14| 3         | GL07,11,18                            |
| Hap_15| 3         | GL08,10,19                            |
| Hap_16| 4         | GL13,16,20,22                         |
| Hap_17| 1         | GL15                                  |
| Hap_18| 1         | GL21                                  |
| Hap_19| 38        | GYH01-04,07,09-20,23,26-32,34-36,38-46|
|       |           | JHH18                                 |
| Hap_20| 5         | GYH05,08,21,22,24                     |
| Hap_21| 68        | GYH06,33,37                           |
|       |           | JHH02-03,07,09-11,14,19,22            |
|       |           | PSG01-09,11-19,21-25,27,28            |
|       |           | YNH01-04,06-11,13-16                  |
|       |           | ZM01-03,05-09,11-19                   |
| Hap_22| 1         | GYH25                                 |
| Hap_23| 6         | JHH01,12-13,16,20                     |
|       |           | ZM20                                  |
| Hap_24| 10        | JHH04-06,08,15,17,21                  |
|       |           | PSG20                                 |
|       |           | ZM04,10                               |
| Hap_25| 3         | LW01,14,26                            |
| Hap_26| 46        | LW02,06-07,10-11,13,15,17,19-20,23,32-35,37-38|
|       |           | SHK01-07,09,13-15,18-20,22-26,29-30,32-33,35-40|
| Hap_27| 3         | LW03,16,29                            |
| Hap_28| 15        | LW05,08,12,18,22,24-25,27-28,30-31,40  |
|       |           | SLP04,10,20                           |
| Hap_29| 1         | LW36                                  |
| Hap_30 | 1 | LW39 |
| Hap_31 | 1 | PSG10 |
| Hap_32 | 1 | PSG26 |
| Hap_33 | 3 | QLB01,31,33 |
| Hap_34 | 7 | QLB02,06-07,26-27,32,34 |
| Hap_35 | 6 | QLB03,05,09,14,16,29 |
| Hap_36 | 5 | QLB08,23-25,28 |
| Hap_37 | 1 | QLB30 |
| Hap_38 | 3 | SHK08,11,31 |
| Hap_39 | 1 | SHK10 |
| Hap_40 | 1 | SHK17 |
| Hap_41 | 1 | SHK21 |
| Hap_42 | 15 | SLP01-03,09,11-19,21-22 |
| Hap_43 | 2 | SLP05-06 |
| Hap_44 | 2 | SLP07-08 |
| Hap_45 | 6 | WK01,03,06,08-10 |
| Hap_46 | 4 | WK02,04-05,07 |
| Hap_47 | 2 | WK11-12 |
| Hap_48 | 8 | XM02,22,24,27,40,45-47 |
| Hap_49 | 8 | XM03,11-12,18,29,34-35,42 |
| Hap_50 | 13 | XM08-09,20-21,26,30,32,36-39,43-44 |
| Hap_51 | 1 | XM10 |
| Hap_52 | 1 | XM14 |
| Hap_53 | 1 | XM15 |
| Hap_54 | 1 | XM19 |
| Hap_55 | 1 | XM28 |
| Hap_56 | 2 | XM33,41 |
| Hap_57 | 2 | YNH05,12 |
| Hap_58 | 3 | ZUM01,07,22 |
| Hap_59 | 10 | ZUM02-03,06,08,13-14,16-17,21,23 |
| Hap_60 | 5 | ZUM04-05,09-10,24 |
| Hap_61 | 5 | ZUM12,15,18-19,25 |
| Hap_62 | 1 | ZUM20 |
| Hap_63 | 1 | YX01 |
| Hap_64 | 1 | YX02 |
| Hap_65 | 1 | YX03 |
| Hap_66 | 2 | YX04-05 |
| Hap_67 | 1 | YX06 |
Supplementary Table S6 Results of genetic diversity for each population based on mitochondrial genes

| Populations | H   | Hd     | π        |
|-------------|-----|--------|----------|
| PSG         | 4   | 0.206 ± 0.100 | 0.00031 ± 0.00024 |
| JHH         | 4   | 0.710 ± 0.049  | 0.00161 ± 0.00026  |
| XM          | 9   | 0.786 ± 0.042  | 0.00050 ± 0.00011  |
| ZUM         | 5   | 0.754 ± 0.056  | 0.00340 ± 0.00086  |
| GYH         | 4   | 0.344 ± 0.085  | 0.00011 ± 0.00003  |
| ZM          | 3   | 0.279 ± 0.123  | 0.00075 ± 0.00039  |
| YNH         | 2   | 0.233 ± 0.126  | 0.00014 ± 0.00008  |
| LW          | 7   | 0.718 ± 0.051  | 0.00062 ± 0.00009  |
| CHJ         | 10  | 0.852 ± 0.036  | 0.00836 ± 0.00040  |
| BT          | 1   | -      | -        |
| QLB         | 5   | 0.788 ± 0.042  | 0.00109 ± 0.00011  |
| WK          | 3   | 0.667 ± 0.091  | 0.00056 ± 0.00008  |
| SHK         | 5   | 0.313 ± 0.099  | 0.00036 ± 0.00022  |
| SLP         | 4   | 0.524 ± 0.116  | 0.00400 ± 0.00124  |
| GL          | 6   | 0.810 ± 0.062  | 0.00527 ± 0.00031  |
| YX          | 5   | 0.933 ± 0.122  | 0.00051 ± 0.00013  |

Notes: H, number of haplotypes; Hd, haplotype diversity; π, nucleotide diversity
**Supplementary Table S7** Results of genetic diversity, neutrality test, and mismatch distribution analysis for all populations and two main clades of *L. taliangensis*

| Populations     | N  | H   | $\pi$             | Hd     | Tajima’s $D$ ($P$) | Fu’s $F_S$ ($P$) | SSD ($P$)  | Harpending’s $H_{rag}$ ($P$) |
|-----------------|----|-----|-------------------|--------|-------------------|-----------------|-----------|-----------------------------|
| All             | 407| 67  | 0.00860 ± 0.00015 | 0.937 ± 0.006 | 0.54189 (0.769) | 2.69639 (0.732) | 0.01616 (0.000)** | 0.01014 (0.000)** |
| South clade     | 77 | 18  | 0.00153 ± 0.00008 | 0.795 ± 0.043 | -0.17659 (0.470) | -1.67923 (0.300) | 0.03318 (0.070) | 0.04707 (0.160)          |
| North clade     | 330| 49  | 0.00702 ± 0.00016 | 0.915 ± 0.008 | 0.28641 (0.708) | 4.59049 (0.812) | 0.05236 (0.000)** | 0.01630 (0.040)*          |

Notes: N, sample size; H, number of haplotypes; $\pi$, nucleotide diversity; Hd, haplotype diversity; SSD, sum of square differences; $H_{rag}$, Harpending’s raggedness index

Statistical significance ($P$): *0.01 < $P$ < 0.05; **0.001 < $P$ < 0.01; *** $P$ < 0.001
### Supplementary Table S8 Genetic diversity and fixation index for each population and two main genetic clusters of *L. taliangensis* based on microsatellite data

| Populations | N   | TA  | Ar   | pAr  | Ne  | Ho (SE) | uHe (SE) | SE  | F_{IS} |
|-------------|-----|-----|------|------|-----|---------|----------|-----|--------|
| XM          | 42  | 43  | 2.716| 0.591| 2.120| 0.383 (0.071) | 0.436 (0.076) | 0.154 |
| ZUM         | 26  | 49  | 3.464| 0.298| 2.921| 0.531 (0.086) | 0.567 (0.078)  | 0.039 |
| GYH         | 46  | 43  | 2.751| 0.085| 2.196| 0.417 (0.090) | 0.420 (0.085)  | -0.011|
| YNH         | 17  | 30  | 2.387| 0.006| 1.848| 0.348 (0.068) | 0.385 (0.075)  | 0.033 |
| JHH         | 22  | 33  | 2.449| 0.028| 1.856| 0.393 (0.074) | 0.404 (0.069)  | 0.023 |
| ZM          | 20  | 28  | 2.182| 0.037| 1.764| 0.373 (0.074) | 0.386 (0.067)  | 0.026 |
| PSG         | 28  | 32  | 2.316| 0.095| 1.826| 0.370 (0.073) | 0.382 (0.072)  | 0.004 |
| GL          | 23  | 68  | 4.389| 0.573| 3.815| 0.664 (0.055) | 0.695 (0.045)  | 0.032 |
| SHK         | 40  | 48  | 3.370| 0.185| 2.921| 0.559 (0.075) | 0.579 (0.071)  | 0.030 |
| SLP         | 22  | 43  | 3.136| 0.154| 2.700| 0.545 (0.085) | 0.544 (0.072)  | 0.030 |
| LW          | 41  | 52  | 3.320| 0.049| 2.624| 0.608 (0.051) | 0.575 (0.046)  | -0.074|
| CHJ         | 30  | 60  | 3.826| 0.125| 3.159| 0.591 (0.048) | 0.641 (0.046)  | 0.066 |
| BT          | 28  | 32  | 2.193| 0.011| 1.763| 0.360 (0.086) | 0.357 (0.074)  | 0.012 |
| YX          | 6   | 45  | 4.091| 0.547| 3.129| 0.576 (0.088) | 0.640 (0.063)  | 0.058 |
| QLB         | 23  | 55  | 3.908| 0.250| 3.295| 0.644 (0.035) | 0.643 (0.049)  | -0.044|
| WK          | 12  | 36  | 2.754| 0.117| 2.053| 0.447 (0.082) | 0.448 (0.069)  | -0.021|
| West cluster| 201 | 82  | 7.040| 1.944| 2.790| 0.405 (0.058) | 0.567 (0.063)  | 0.310 |
| East cluster| 225 | 119 | 9.917| 4.820| 4.653| 0.560 (0.038) | 0.737 (0.038)  | 0.241 |

Note: N, sample size of each population; TA, total number of alleles; Ar, allele richness; pAr, private allele richness, standardized for sample size; Ne, number of effective alleles; Ho, observed heterozygosity; uHe, unbiased expected heterozygosity; SE, standard error; F_{IS}, fixation index/inbreeding coefficient.
**Supplementary Table S9** Genetic distance ($F_{ST}$) between populations of *L. taliangensis* based on microsatellite data

|       | PSG  | ZUM  | ZM   | YNH  | JHH  | XM   | GYH  | GL   | CHJ  | LW   | BT   | SLP  | SHK  | QLB  | WK   |
|-------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| PSG   |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| ZUM   | 0.236|      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| ZM    | 0.087| 0.257|      |      |      |      |      |      |      |      |      |      |      |      |      |
| YNH   | 0.093| 0.207| 0.100|      |      |      |      |      |      |      |      |      |      |      |      |      |
| JHH   | 0.033| 0.215| 0.089| 0.056|      |      |      |      |      |      |      |      |      |      |      |      |
| XM    | 0.394| 0.364| 0.358| 0.413| 0.357|      |      |      |      |      |      |      |      |      |      |      |
| GYH   | 0.153| 0.190| 0.221| 0.134| 0.152| 0.450|      |      |      |      |      |      |      |      |      |      |
| GL    | 0.380| 0.218| 0.358| 0.339| 0.351| 0.369| 0.358|      |      |      |      |      |      |      |      |      |
| CHJ   | 0.402| 0.275| 0.416| 0.378| 0.373| 0.416| 0.372| 0.212|      |      |      |      |      |      |      |      |
| LW    | 0.380| 0.258| 0.415| 0.375| 0.355| 0.410| 0.356| 0.278| 0.152|      |      |      |      |      |      |      |
| BT    | 0.571| 0.475| 0.598| 0.562| 0.553| 0.577| 0.536| 0.403| 0.265| 0.337|      |      |      |      |      |      |
| SLP   | 0.496| 0.335| 0.506| 0.475| 0.469| 0.458| 0.466| 0.269| 0.183| 0.200| 0.341|      |      |      |      |      |
| SHK   | 0.450| 0.339| 0.472| 0.437| 0.427| 0.465| 0.433| 0.271| 0.131| 0.145| 0.265| 0.194|      |      |      |      |
| QLB   | 0.389| 0.194| 0.396| 0.352| 0.362| 0.394| 0.362| 0.166| 0.177| 0.227| 0.355| 0.231| 0.234|      |      |      |
| WK    | 0.493| 0.336| 0.521| 0.481| 0.477| 0.540| 0.454| 0.270| 0.323| 0.375| 0.511| 0.402| 0.357| 0.210|      |      |
| YX    | 0.487| 0.275| 0.483| 0.465| 0.464| 0.460| 0.460| 0.178| 0.285| 0.355| 0.492| 0.341| 0.326| 0.186| 0.303|      |
**Supplementary Table S10** Analysis of molecular variance (AMOVA) for *L. taliangensis* in all populations and two main genetic clusters

| Source of variation            | df | Sum of squares | Variance components | Percentage variation | Fixation indexes |
|--------------------------------|----|----------------|---------------------|----------------------|------------------|
| **K = 2 (All)**                |    |                |                     |                      |                  |
| Among groups                   | 1  | 478.219        | 0.974               | 20.594               | \(F_{CT} = 0.206^{***}\) |
| Among populations within groups| 14 | 762.095        | 0.992               | 20.986               | \(F_{SC} = 0.264^{***}\) |
| Among individuals within       | 410| 1167.275       | 0.084               | 1.783                | \(F_{IS} = 0.031^{***}\) |
| populations                    |    |                | 2.678               | 56.637               |                  |
| **Total**                      | 851| 3548.588       | 4.729               |                      |                  |
| **K = 2 (East cluster)**       |    |                |                     |                      |                  |
| Among groups                   | 1  | 132.834        | 0.494               | 11.085               | \(F_{CT} = 0.111^{***}\) |
| Among populations within groups| 7  | 308.907        | 0.834               | 18.719               | \(F_{SC} = 0.211^{***}\) |
| Among individuals within       | 216| 686.198        | 0.048               | 1.086                | \(F_{IS} = 0.015\) |
| populations                    |    |                | 3.080               | 69.109               | \(F_{IT} = 0.309^{***}\) |
| **Total**                      | 449| 1820.938       | 4.457               |                      |                  |
| **K = 4 (West cluster)**       |    |                |                     |                      |                  |
| Among groups                   | 3  | 291.423        | 0.900               | 26.378               | \(F_{CT} = 0.264^{***}\) |
| Among populations within groups| 3  | 26.591         | 0.148               | 4.241                | \(F_{SC} = 0.059^{***}\) |
| Among individuals within       | 194| 484.391        | 0.134               | 3.929                | \(F_{IS} = 0.057^{***}\) |
| populations                    |    |                | 2.229               | 65.352               | \(F_{IT} = 0.346^{***}\) |
| **Total**                      | 401| 1250.405       | 3.411               |                      |                  |

Note: *df*, degrees of freedom; *F_{CT}*; fixation index among groups; *F_{SC}*; fixation index among populations within groups; *F_{IS}*; fixation index among individuals within populations; *F_{IT}*; fixation index within individuals

Statistical significance (*P*): *0.01 < *P* < 0.05; **0.001 < *P* < 0.01; ****P* < 0.001
Supplementary Table S11 Results of bottleneck effect analysis for *L. taliangensis*

| Populations | TPM | SMM |
|-------------|-----|-----|
|             | Hd/He | Sign-test (P) | Wilcoxon-test (P) | Hd/He | Sign-test (P) | Wilcoxon-test (P) |
| XM          | 6/4  | 0.213 | 0.375 | 7/3  | 0.083 | 0.275 |
| ZUM         | 5/5  | 0.410 | 0.625 | 5/5  | 0.414 | 0.922 |
| GYH         | 6/3  | 0.152 | 0.129 | 7/2  | 0.039** | 0.020* |
| YNH         | 5/4  | 0.355 | 1.000 | 5/4  | 0.330 | 0.910 |
| JHH         | 6/3  | 0.133 | 0.910 | 6/3  | 0.125 | 0.570 |
| ZM          | 4/5  | 0.602 | 0.734 | 4/5  | 0.574 | 0.734 |
| PSG         | 4/5  | 0.591 | 0.570 | 4/5  | 0.612 | 0.652 |
| GL          | 5/6  | 0.483 | 0.638 | 5/6  | 0.476 | 0.465 |
| SHK         | 3/7  | 0.332 | 0.131 | 5/5  | 0.412 | 0.432 |
| SLP         | 2/9  | 0.062 | 0.206 | 2/9  | 0.076 | 0.206 |
| LW          | 4/7  | 0.469 | 0.765 | 5/6  | 0.524 | 0.577 |
| CHJ         | 4/7  | 0.512 | 0.765 | 5/6  | 0.483 | 0.898 |
| BT          | 5/5  | 0.476 | 0.770 | 5/5  | 0.456 | 0.695 |
| YX          | 4/7  | 0.576 | 0.765 | 5/6  | 0.444 | 0.831 |
| QLB         | 4/7  | 0.493 | 0.413 | 5/6  | 0.529 | 0.700 |
| WK          | 7/3  | 0.095 | 0.322 | 7/3  | 0.085 | 0.232 |
| ALL         | 8/3  | 0.037* | 0.016* | 10/1 | 0.001*** | 0.003** |
| West cluster | 8/3  | 0.035* | 0.009** | 8/3  | 0.033* | 0.007** |
| East cluster | 7/4  | 0.115 | 0.067 | 9/2  | 0.007** | 0.005** |

Statistical significance (P): *0.01 < P < 0.05; **0.001 < P < 0.01; ***P < 0.001

Note: TPM, two-phase model; SMM, stepwise mutation model; Hd, heterozygosity deficiency; He, heterozygosity excess

Supplementary Table S12 Results of optimal migration direction between XXL-GG and LS based on microsatellite data

| Model        | Bezier IML | Ln Bayes factor | Model probability |
|--------------|------------|-----------------|-------------------|
| LS to XXL-GG | -74032.29  | -2809.26        | 0                 |
| XXL-GG to LS | -71223.03  | 0               | 1                 |
| Bi-direction | -137254.53 | -66031.50       | 0                 |

Note: Bezier IML, Bezier log marginal likelihood
Supplementary Table S13 Percentage contribution and permutation importance of bioclimatic variables included in ecological niche model (ENM) used for historical distribution analysis

| Variable | Description                          | Percent contribution | Permutation importance |
|----------|--------------------------------------|----------------------|------------------------|
| Bio06    | Minimum temperature of the coldest month | 36.93                | 17.34                  |
| Bio14    | Precipitation of the driest month    | 24.57                | 34.69                  |
| Bio12    | Annual precipitation                  | 18.54                | 20.87                  |
| Bio03    | Isothermality                         | 17.55                | 25.34                  |
| Bio07    | Temperature annual range              | 2.42                 | 1.75                   |
Supplementary Table S14 Results of multiple matrix regression with randomization (MMRR) analysis for relationship between pairwise genetic distances ($F_{ST}$) and landscape distances, including geographical resistance distances (IBR) and environmental dissimilarity (IBE)

| Model                  | $R^2$ | Variable | $P$-value | Coefficient $\beta$ | t     | F      | $P$-value (model) |
|------------------------|-------|----------|-----------|---------------------|-------|--------|------------------|
| ALL                    |       |          |           |                     |       |        |                  |
| RD+PC1+PC2             | 0.163 | RD       | 0.011**   | 0.405               | 3.681 |        | 0.011**          |
|                        |       | PC1      | 0.133     | 0.143               | 1.557 | 7.552  | 0.011**          |
|                        |       | PC2      | 0.215     | -1.679              | -1.557|        |                  |
|                        |       | RD       | 0.032**   | 0.300               | 3.429 | 9.994  | 0.011**          |
| RD+PC1                 | 0.146 | RD       | 0.013**   | 0.339               | 3.912 | 15.306 | 0.013**          |
|                        |       | PC1      | 0.062     | 0.181               | 2.064 |        |                  |
|                          |       | PC1      | 0.155     | 0.252               | 2.808 | 4.110  | 0.068            |
|                        |       | PC2      | 0.075     |                     |       |        |                  |
|                          |       | PC1      | 0.195     | 0.245               | 2.746 | 7.540  | 0.019**          |
|                        |       | PC1      | 0.019**   |                     |       |        |                  |
| West cluster           |       |          |           |                     |       |        |                  |
| (XXL-GG)               |       |          |           |                     |       |        |                  |
| wRD+wPC1+wPC2          | 0.942 | wRD      | 0.002**   | 0.982               | 0.163 |        |                  |
|                        |       | wPC1     | 0.604     | 0.037               | 0.606 | 91.350 | 0.002**          |
|                        |       | wPC2     | 0.627     | -0.040              | -0.666|        |                  |
|                        |       | wRD      | 0.002**   | 0.977               | 16.590| 141.165| 0.002**          |
|                        |       | wPC1     | 0.521     | 0.043               | 0.733 |        |                  |
|                        |       | wRD      | 0.001**   | 0.969               | 16.995| 288.832| 0.001**          |
|                        |       |          |           |                     |       |        |                  |
| Rejected term          |       |          |           |                     |       |        |                  |

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Note: $R^2$, coefficient of determination; AICc, Akaike's information criterion and finite corrections; $\beta$, regression coefficients; $F$, F-statistics; RD, resistance distance based on the current distribution range prediction raster of *L. taliangensis*; PC1 and PC2, two principal components of environmental variables. Alphabet in front of variables represents two genetic clusters respectively.

Statistical significance (*P*): *0.01 < *P* < 0.05; **0.001 < *P* < 0.01; ****P* < 0.001

|                      | PC1   | PC2   | PC1   | PC2   | PC1   | PC2   |
|----------------------|-------|-------|-------|-------|-------|-------|
| wPC1+ wPC2           | 0.029 |       |       |       |       |       |
| wPC1                 |       | 0.024 |       |       |       |       |
| eRD                  |       |       | 0.512 | 0.250 | 1.182 |       |
| East cluster (LS)    |       |       |       |       |       |       |
| eRD+ ePC1+ ePC2      | 0.068 |       |       |       |       |       |
| ePC1                 | 0.843 |       | 0.054 |       | 0.315 | 0.784 |
| ePC2                 | 0.984 |       | 0.005 |       | 0.025 |       |
| eRD                  | 0.408 |       | 0.253 |       | 1.507 | 1.212 |
| ePC1                 | 0.834 |       | 0.054 |       | 0.319 |       |
| ePC2                 |       |       |       |       |       |       |
| eRD                  | 0.390 | 0.256 | 1.544 | 2.385 | 0.390 |
Supplementary Table S15 Principal component loading of environmental parameters used for IBE analysis

| Environmental parameters | PC1  | PC2  |
|--------------------------|------|------|
| Bio01                    | **0.940** | 0.189 |
| Bio02                    | 0.054 | -0.904 |
| Bio03                    | -0.061 | **-0.961** |
| Bio04                    | 0.134 | **0.979** |
| Bio05                    | 0.902 | 0.38 |
| Bio06                    | 0.901 | 0.205 |
| Bio07                    | 0.39  | 0.674 |
| Bio08                    | 0.877 | 0.413 |
| Bio09                    | **0.945** | -0.09 |
| Bio10                    | 0.877 | 0.413 |
| Bio11                    | **0.945** | -0.09 |
| Bio12                    | 0.543 | 0.428 |
| Bio13                    | 0.573 | -0.164 |
| Bio14                    | 0.34  | 0.907 |
| Bio15                    | 0.333 | -0.902 |
| Bio16                    | 0.665 | 0.022 |
| Bio17                    | 0.345 | **0.912** |
| Bio18                    | 0.665 | 0.022 |
| Bio19                    | 0.345 | **0.912** |
| NDVI                     | 0.537 | 0.521 |

Note: Data presented in boldface indicates the main environmental variables represented by the principal components
**Supplementary Table S16** Percentage contribution and permutation importance of environmental variables included in ENM used for IBR analysis

| Variable | Description                        | Percent contribution | Permutation importance |
|----------|------------------------------------|----------------------|------------------------|
| NDVI     | Normalized difference vegetation index | 34.33                | 1.94                   |
| Bio14    | Precipitation of the driest month   | 22.81                | 17.66                  |
| Alt      | Altitude                           | 20.92                | 35.14                  |
| Bio12    | Annual precipitation               | 9.49                 | 24.44                  |
| Bio07    | Temperature annual range           | 3.88                 | 0.53                   |
| River    | Distance to rivers                 | 3.60                 | 2.53                   |
| HII      | Human disturbance                  | 2.64                 | 1.72                   |
| Bio15    | Precipitation seasonality          | 1.41                 | 3.72                   |
| Bio04    | Temperature seasonality            | 0.92                 | 12.31                  |
Supplementary Figures
Supplementary Figure S1 Results of the network analysis of the mitochondrial concatenated genes (cyt b+ND2+COI) across *L. taliangensis* distribution range.
(A) Geographic distribution of clades of *L. taliangensis*. Black dashed line represents four main distribution mountains of *L. taliangensis* (i.e., Gonggar (GG), Xiaoxiangling (XXL), Xiaoliangshan (XLS), and Daliangshan mountains (DLS)); (B) Geographic distribution of subclades of *L. taliangensis*. Population codes and number of analyzed sequences are shown in Supplementary Table S1; (C) Maximum-likelihood tree (ML) and Bayesian phylogenetic tree (BI), constructed based on mitochondrial concatenated genes. Numbers on branches indicate Bayesian posterior probabilities/ML bootstrap values; (D) TCS-derived haplotype network of 67 concatenated gene haplotype sequences. Each colored circle represents clade and subclade. Size of circles indicates frequency of each haplotype. Black solid dots represent not detected or extinct ancestral haplotypes. Numbers in boxes represent mutation steps.
**Supplementary Figure S2** Divergence date of most recent common ancestor (MRCA) of *L. taliangensis* and *T. pseudoverrucosus* based on four salamandrid fossil records.

Blue solid circles represent minimum age of first calibration point C1, estimated to be ~44 Ma between *Tylototriton* s.l. and *Pleurodeles*. Pink solid circle represents minimum age of second calibration point C2, estimated to be ~22 Ma between *Taricha* and *Notophthalmus* based on a fossil of *Taricha oligocenica*. Yellow solid circle represents third calibration point C3, which was the common ancestor of *Triturus* and minimum age was ~24 Ma. Orange solid circle represents minimum divergence time of fourth calibration point C4, which was ~15 Ma between *Cynops* and *Paramesotriton*. GenBank numbers and references of all above calibration points are in Supplementary Table S4. Red stars represent date of MRCA (mean and range) of *L. taliangensis* and *T. pseudoverrucosus*. Green box represents analysis range of second step of divergence date, which was used to estimate clade divergence time of *L. taliangensis*. 
**Supplementary Figure S3** Mismatch distribution plot of *L. taliangensis*.

(A) All populations; (B) South clade; (C) North clade.
Supplementary Figure S4 Principal coordinate analysis (PCoA) plot of *L. taliangensis* based on microsatellite loci. West cluster includes populations of XXL-GG mountains, East cluster includes populations of LS mountains (i.e., DLS and XLS).
Supplementary Figure S5 Distribution range prediction (averaged from 10 runs) for *L. taliangensis* during LGM based on three different general circulation models (CCSM4, MIROC-ESM, and MPI-ESM-P).

MTSS: maximum training sensitivity plus specificity threshold.
Supplementary Figure S6 Distribution range prediction (averaged from 10 runs) for *L. taliangensis* during MH based on four different general circulation models (CCSM4, MIROC-ESM, MPI-ESM-P, and BCC-CSM1-1). MTSS: maximum training sensitivity plus specificity threshold.
Supplementary Figure S7 Current distribution range prediction raster used for IBR analysis (averaged from 10 runs) of *L. taliangensis* based on bioclimatic, terrain, and human variables.

MTSS: maximum training sensitivity plus specificity threshold.
Supplementary Figure S8 Correlations between genetic distance ($F_{ST}$) and resistance distance (IBR) of West cluster (XXL-GG).
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