

Article

The origin of invasion of an alien frog species in Tibet, China

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Received on 18 July 2016; accepted on 10 December 2016

Abstract

Identifying the origins of alien species has important implications for effectively controlling the spread of alien species. The black-spotted frog *Pelophylax nigromaculatus*, originally from East Asia, has become an alien species on the Tibetan Plateau (TP). In this study, we collected 300 individuals of *P. nigromaculatus* from 13 native regions and 2 invasive regions (including Nyingchi and Lhasa) on the TP. To identify the source region of the TP introductions, we sequenced portions of the mitochondrial *cyt b* gene. We sequenced a ~600-bp portion of the mitochondrial *cyt b* gene to identify 69 haplotypes (124 polymorphic sites) in all sampled populations. According to the network results, we suggest that the *P. nigromaculatus* found on the TP was most likely originated from Chongqing by human introduction. Furthermore, we found that the genetic diversity was significantly lower for invasive than for native sites due to founder effects. Our study provides genetic evidence that this alien species invaded the cold environment of high elevations and expanded the distribution of *P. nigromaculatus* in China.

Key words: alien species, amphibians, chytridiomycosis, cold environment, invasion genetics, invasion route, Tibetan Plateau.

Invasive species are responsible for changes to native biological diversity, the extinction of many native species around the globe, and the disruption of ecosystem functions (Lockwood et al. 2013). Their presence can inflict huge economic costs (Mack et al. 2000). Several methods for measuring how species invade, establish, and spread have been proposed to provide information to prevent or manage invasive species (Hulme et al. 2008). Molecular approaches are among the most important methods and have become widely used to better understand the invasion process and the relationship between invasive and source populations (Bai et al. 2012; Liebl et al. 2015; Moule et al. 2015; Rius et al. 2015). Exploring invasion pathways and sources can contribute to identifying the ecological characteristics and physiological tolerances of source populations (Ficetola

et al. 2008). Invasion pathways and source populations can be used to simulate potential distributions or predict future expansion (Liebl et al. 2015).

Previous studies have suggested that regions of high elevation are viewed as resistant to biological invasions because of an extreme climate and limited accessibility (Bennett et al. 2015; Pauchard et al. 2016). However, the risk of biological invasions is increasing due to land-use change, climate warming, and increasing globalization in these regions (Li et al. 2013). Non-native species move into regions of high elevation and may change the composition of the community (Bennett et al. 2015; Pauchard et al. 2016). These changes can be viewed as with both positive (increasing biodiversity) and negative (decreasing biodiversity) consequences. In contrast to the large

number of studies conducted in low-elevation regions (Rollins et al. 2015; Sherwin et al. 2015; Wang et al. 2016), non-native species invading regions of high elevation represent a problem in invasive biology that remains to be addressed.

The Tibetan Plateau (TP) is the most extensive (covering an area of 2.5 million km²) and highest (approximately 4500 m above sea level on average) plateau in the world (Zhou et al. 2006). The TP is a conservation priority because the plateau and its adjacent areas cross 3 biodiversity hotspots: Indo-Burma, the Himalayas, and the mountains of southwestern China (Mittermeier et al. 2011). The extensive variation in the topography and climate of the TP generates a number of different habitats and supports abundant species diversity (Mittermeier et al. 2011; Li et al. 2016). There are 56 amphibian species on the TP, including 3 caudata species (*Batrachuperus tibetanus*, *Andrias davidianus*, and *Batrachuperus karlschmidti*) and 53 anuran species (Amphibia China 2016). Furthermore, against the background of global climate change, the TP is experiencing faster warming than low-elevation regions at the same latitude (Liu and Chen 2000; Qin et al. 2009; Wei and Fang 2013). This faster warming pattern may increase the risk of biological invasions and facilitate the rapid dispersal of disease vectors on the TP (Di Rosa et al. 2007; Liu et al. 2013).

The black-spotted frog *Pelophylax nigromaculatus*—native to East Asia, including low-elevation regions of northern, eastern, central, and southwestern mainland China; the Korean Peninsula; Japan; and far-eastern Russia—has become an invasive species in areas of western China, such as the Xinjiang Uyghur Autonomous Region (Wang et al. 2016). Wang et al. (2016) showed that the invasion of the alien *P. nigromaculatus* population in Yining originated from the Beijing and Chongqing area based on an mtDNA analysis. Prior to the present study, the black-spotted frog was never recorded in the TP (Li et al. 2010). The TP is at a higher elevation than Yining (average elevation 620 m); for example, the elevations of the Chabalong Wetland and Nyingchi City are, respectively, 3,600 m and 3,000 m. Such different environments may be the cause of different invasion processes.

In this study, we used an mtDNA marker to investigate the genetic patterns underlying the expansion of *P. nigromaculatus* population on the TP. We 1) compared the genetic diversity and examined the genetic structure of *P. nigromaculatus* in its 13 native ranges in China and in the 2 invaded territories of the TP, 2) identified the source region(s) of the TP introductions, 3) discuss possible potential damage caused by the invasion of *P. nigromaculatus* on the TP, and 4) discuss the application of our results to the planning of suitable control measures.

Materials and Methods

Surveying and sampling of *P. Nigromaculatus*

We estimated the introduction range of *P. nigromaculatus* by line transect methods in the TP (Heyer et al. 1994; Li et al. 2011). We suggested that *P. nigromaculatus* breeding populations had been established in this site when both adult and sub-adult *P. nigromaculatus* (and tadpoles) were found at survey sites (Li et al. 2011). We obtained information on the introduction history of *P. nigromaculatus* in the TP using a questionnaire survey (Li et al. 2006, 2011). We usually interviewed 2 or 3 residents living near the sampled water bodies. The residence time was based on the time the first sighting by the resident of tadpoles, eggs, or juvenile or adults of *P. nigromaculatus* or heard calls. If the interviewees gave different answers on the residence time of *P. nigromaculatus* invasion for a water body,

we used the average value (year) of these answers. The longest value for all surveyed sites in a region was defined as the residence time.

We collected 260 adult individuals from different locations (20 samples per locality) in 13 native ranges (Figure 1) in 2012. These locations encompassed most of the distribution of this species in northeastern, northern, central, northwestern, southeastern, and southwestern China. We collected 40 frogs from the 2 different regions of introduction (Nyingchi and Lhasa) on the TP (Figure 1) between 2014 and 2015. To determine whether a site has been invaded successfully by *P. nigromaculatus*, we searched for tadpoles of *P. nigromaculatus* using line transects that surveyed all accessible water bodies at each site for 3 consecutive nights. The third toes of individuals of *P. nigromaculatus* were collected, and then the tissue samples were preserved separately in 95% ethanol and stored at −20°C in the laboratory.

DNA extraction and amplification

Total genomic DNA was extracted from the toe tissue following the standard method published previously (Wang et al. 2014; Shine et al. 2016). A 695-bp segment of the mitochondrial cytochrome *b* (*cyt b*) gene from all specimens was amplified using the primers RanaLeuF5d (5'-AA T MCC GWA AA T CTC ACCCCC T-3') and RanacytbB1 (5'-GCT GGT GTAAA T TGT CTG GGT C-3') (Yang et al. 2003). The PCR protocol was initiated with an initial step of denaturing of 95°C for 5 min, followed by 35 cycles of 94°C for 30 s, annealing of 56°C for 30 s, extension of 72°C for 30 s, and a final extension step of 72°C for 10 min. The PCR products were subjected to electrophoresis on 2% agarose gels and directly sequenced using the same forward and reverse primers used for amplification (Beijing Genomics Institute, Beijing, China).

Data analysis

We used Clustal X in MEGA 6 (Tamura et al. 2013) to align and edit the mitochondrial *cyt b* gene sequences. To identify unique haplotypes in all sampling populations, we used DnaSP 5.10 to define these sequences (Rozas et al. 2003). Genetic diversity was assessed by calculating the number of haplotypes (*Hn*), haplotype diversity (*Hd*), and nucleotide diversity (π) within each sampling population using ARLEQUIN ver3.5 (Excoffier and Lischer 2010). A neighbor-joining tree of mtDNA was constructed from the Kimura 2-parameter nucleotide distances using Mega 6 (Tamura et al. 2013). Branch support was calculated by the bootstrap method according to 1,000 replicates. To identify the origin of the TP population, we utilized the software package TCS 1.21 (Clement et al. 2000) to construct cladogram networks of *P. nigromaculatus cyt b* haplotypes by statistical parsimony. We compared differences in the number of haplotypes (*Hn*) between native and invasive populations using the independent samples *t*-test (R Development Core Team 2012).

Results

We identified only 2 invasion sites (Nyingchi and Lhasa) for *P. nigromaculatus* that has established breeding populations in the TP. The residence time for *P. nigromaculatus* invasion is approximately 15 years (since the start of this century) in Nyingchi and 10 years (since 2005) in Lhasa. We determined that alien *P. nigromaculatus* in the TP originated from accidental introduction by fish farming.

In total, 300 individuals of *P. nigromaculatus* were collected from the 2 invasive regions and 13 native regions (Figure 1) and

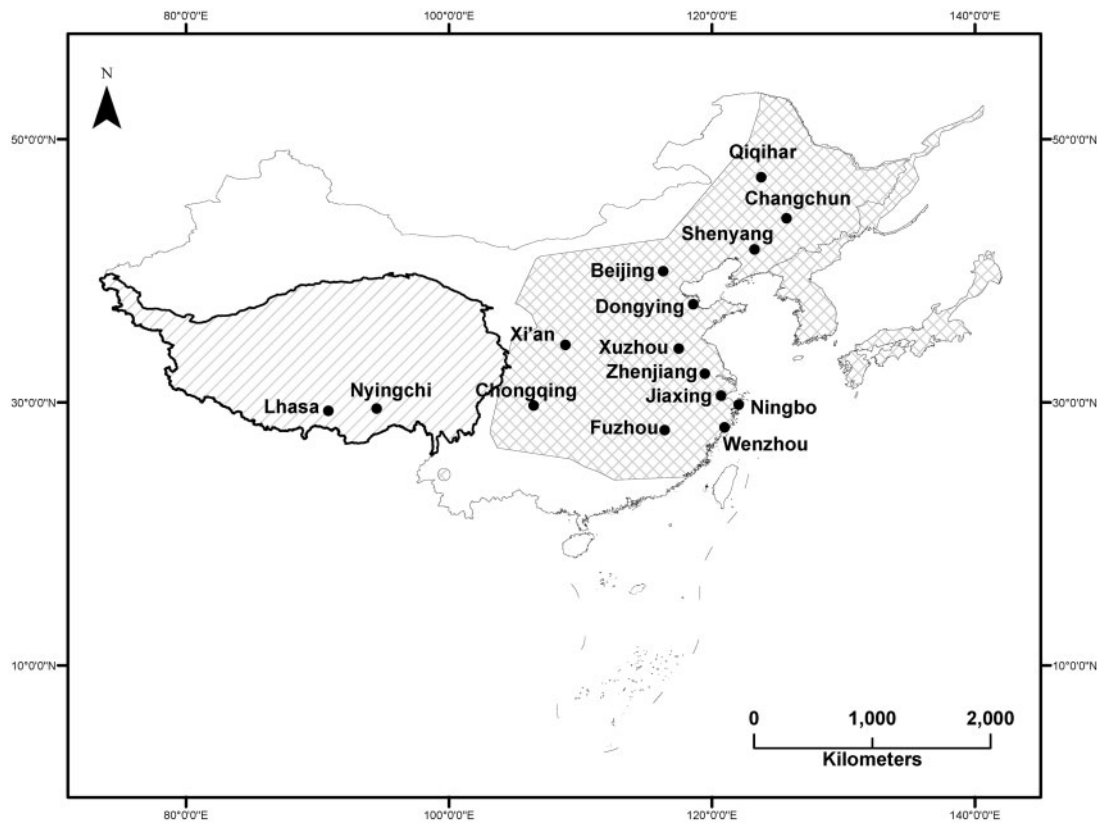


Figure 1. Sampled areas for *P. nigromaculatus* in China. Backward diagonal areas indicate the Tibet Plateau. Diagonal cross areas indicate the distribution area in Asia. Closed circles denote the sampling sites.

Table 1. Sampling information and genetic diversity indices of *P. Nigromaculatus*

Population	Abbreviation	<i>N</i>	<i>H_n</i>	<i>H_d</i>	π
Nyingchi	LZ	20	2	0.526	0.01692
Lhasa	LS	20	1	0	0
Chongqing	CQ	20	4	0.742	0.01762
Xi'an	XA	20	3	0.195	0.00032
Jiaxing	JX	20	9	0.795	0.00748
Beijing	BJ	20	10	0.863	0.00674
Dongying	DY	20	14	0.963	0.00763
Ningbo	NB	20	5	0.442	0.00127
Zhenjiang	ZJ	20	12	0.926	0.00651
Qiqihar	QQ	20	7	0.732	0.00162
Changchun	CC	20	9	0.832	0.01631
Shenyang	SY	20	6	0.621	0.00987
Xuzhou	XZ	20	13	0.932	0.00721
Wenzhou	WZ	20	6	0.579	0.00542
Fuzhou	FZ	20	2	0.1	0.00016
Total		300	69	0.952	0.02461

Note: *N*, number of samples sequenced; *hn*, number of haplotypes; *hd*, haplotype diversity; π , nucleotide diversity.

yielded a 622-bp DNA sequence for *cyt b* gene. All 69 haplotypes (H1–69) were identified by the 124 polymorphic sites in all sampled populations (Table 1). A list of their distributions is provided in the Appendix, and the phylogenetic relationships are shown in Figure 2. Collectively, 49 unique haplotypes and 20

haplotypes are shared among sampled populations (Appendix). Haplotypes H1 and H2 are not found in locations other than Chongqing and the introduced populations. *H_n*, *H_d*, and π ranged, respectively, from 1 to 14, 0 to 0.963, and 0 to 0.01762 among the sampled populations (Table 1). We found that the H1 and H2 haplotypes occurred in the Tibet (including Nyingchi and Lhasa) and Chongqing populations, suggesting that the *P. nigromaculatus* found in Tibet most likely originated from Chongqing (Figure 3). The number of haplotypes (*H_n*) was significantly higher for native than for invasive sites (native vs introduced populations: $df=13$, $t=2.21$, $P=0.046$).

Discussion

Our results suggest that the alien *P. nigromaculatus* population on the TP originated from a single native-range source region (Chongqing population). Our data provide new evidence that low genetic diversity does not impede successful amphibian invasion on the TP. Our study also provides a new case of a non-native species invading high-elevation environments due to human activities and raises awareness of the growing importance of the expansion of non-native species in high-elevation cold environments. Furthermore, the new record from the TP extends the known distribution range of *P. nigromaculatus* in Asia by approximately 1,000 km from its ancestral area (Fei et al. 1999).

Our study shows that the recently established populations of *P. nigromaculatus* on the TP have reduced genetic variability in

on the TP should be prioritized based on those likely to have the greatest impact. Management should be more directed toward preventing the arrival of this species or catch it in the early stages of invasion. Other types of management could include developing early detection and rapid response programs and increasing educational outreach and public awareness.

Acknowledgments

We thank 3 anonymous referees for many valuable comments on an earlier draft.

Funding

This study was funded by the National Natural Science Foundation of China (31370545), the Beijing Natural Science Foundation (5164036), China Postdoctoral Science Foundation (2016M601132), and Collaborative Innovation Center for Research and Development of Tibetan Agricultural and Animal Husbandry Resources.

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