Does the Dzungarian racerunner (*Eremias dzungarica* Orlova, Poyarkov, Chirikova, Nazarov, Munkhbaatar, Munkhbayar & Terbish, 2017) occur in China? Species delimitation and identification with DNA barcoding and morphometric analyses

Jin-Long Liu[1], Tatjana N. Dujsebayeva[2], Marina A. Chirikova[2], Xiong Gong[1], Da-Jiang Li[1], Xian-Guang Guo[1,*]

[1] Chengdu Institute of Biology, Chinese Academy of Sciences, Chengdu 610041, China *[2] Institute of Zoology of Republic of Kazakhstan, Almaty 050060, Kazakhstan*

Background

- The taxonomy of The *Eremias multiocellata-przewalskii* species complex has been historically confusing.
- Orlova et al. (2017) for the first time utilized the DNA barcoding sequences (COI) to infer phylogenetic relationships and propose putative species in the *E. multiocellata-przewalskii* species.
- Within this complex, a new species – *E. dzungarica* (Orlova et al. 2017) – has been recently described from western Mongolia and eastern Kazakhstan, but with an apparent distribution gap in northwestern China.

Aim

- Utilizing more rigorous barcoding techniques to deeply explore the distribution pattern of genetic distance and to test species boundaries in this species complex.
- Employing molecular and morphological analyses to determine whether *E. dzungarica* occurs in northwestern China.

Material & Methods

- During 2014 and 2017, we conducted a Sino-Kazh joint field investigation on herpetofauna in eastern Kazakhstan and in the adjacent Junggar Depression in China (Figure 1).
- Thirty specimens from seven sites were collected from eastern Kazakhstan and northwestern Altay region (Figure 2, 3), and initially identified as so-called *E. multiocellata*.
- DNA barcoding diversity analysis (Distance Summary and Barcoding Gap Analysis)
- Phylogenetic analysis (Neighbor-Joining, Maximum Likelihood and Bayesian inference)
- Species delimitation (BIN, GMYC, ABGD, mPTP and BPP)
- Morphological analyses (ANOVA and two independent samples t-test)

Figure 1

Figure 2

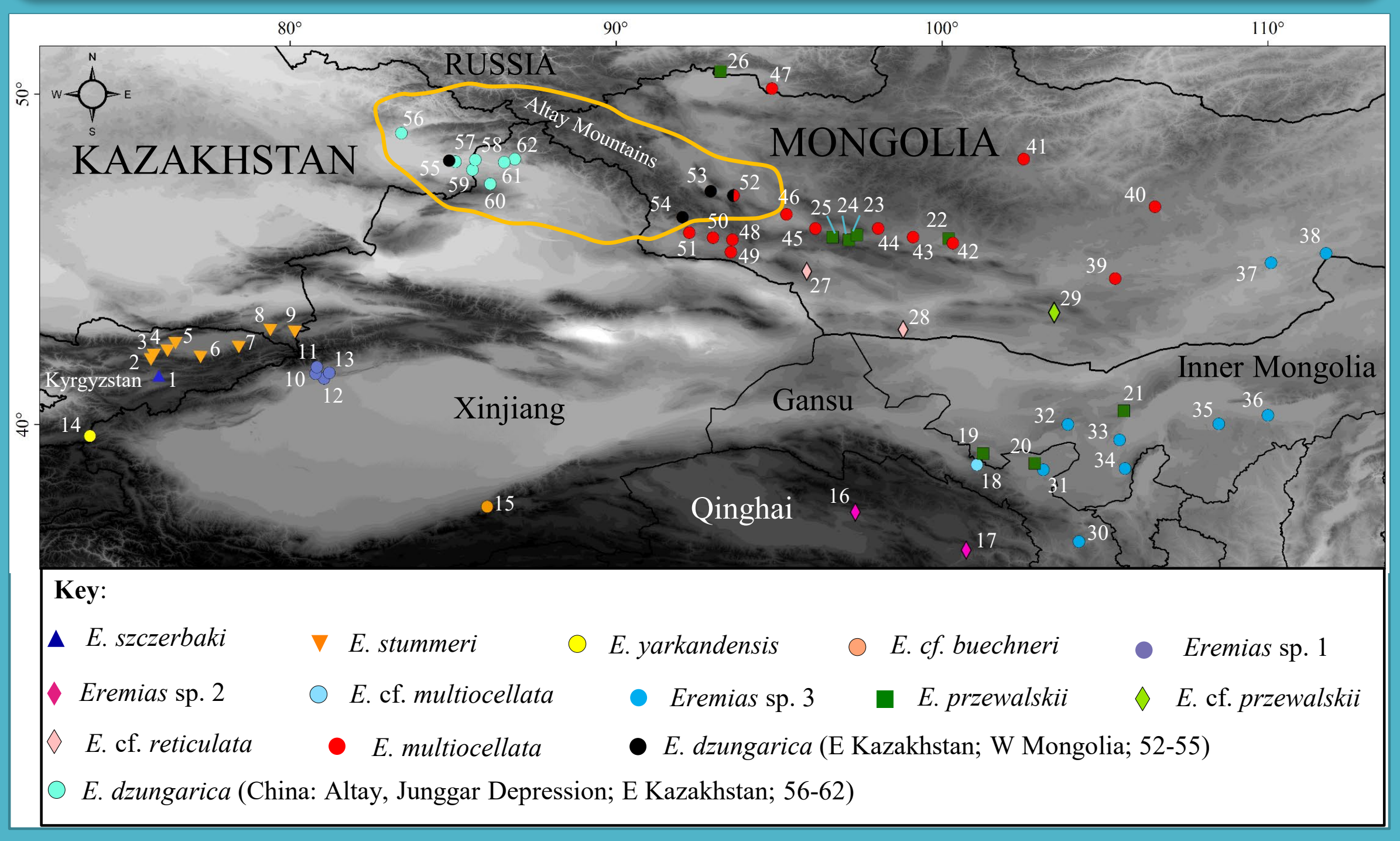
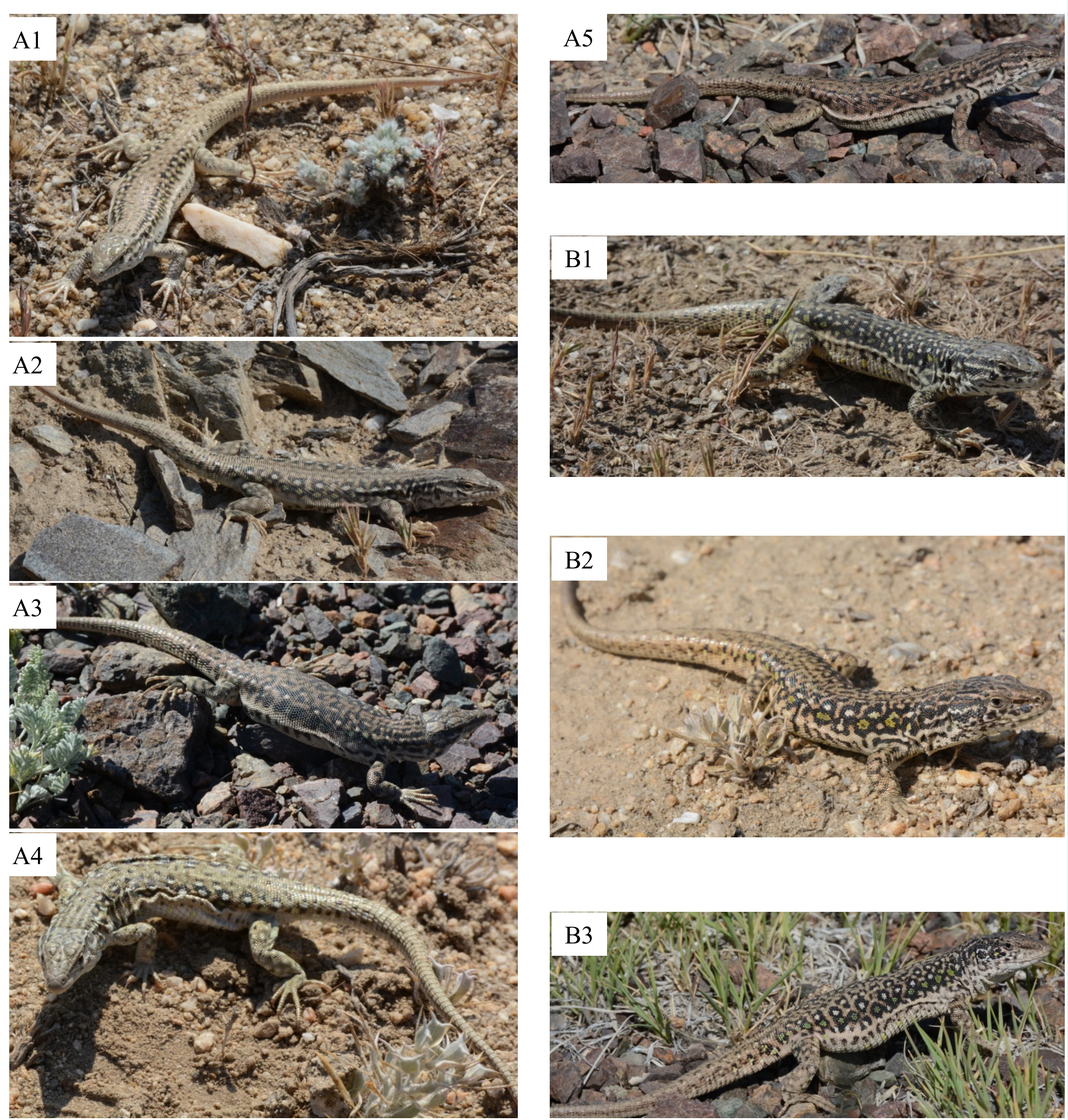


Figure 3



Results and Conclusions

- We detected an absence of a barcoding gap in this complex (Figure 4), which may indicate cryptic species in *Eremias* sp. 3 with high intraspecific diversity and multiple recently evolved species in Clade A (Figure 5).
- Based on evidence from molecular and morphological data, all 30 individuals collected in this study are reliably identified as *E. dzungarica* and confirmed the occurrence of this species in the Altay region, Xinjiang, China.
- Morphological examination revealed many inconsistencies with the original descriptions of *E. dzungarica* that are mainly associated with sexual dimorphism or a broader range of values in various traits (Figure 3).

Figure 5

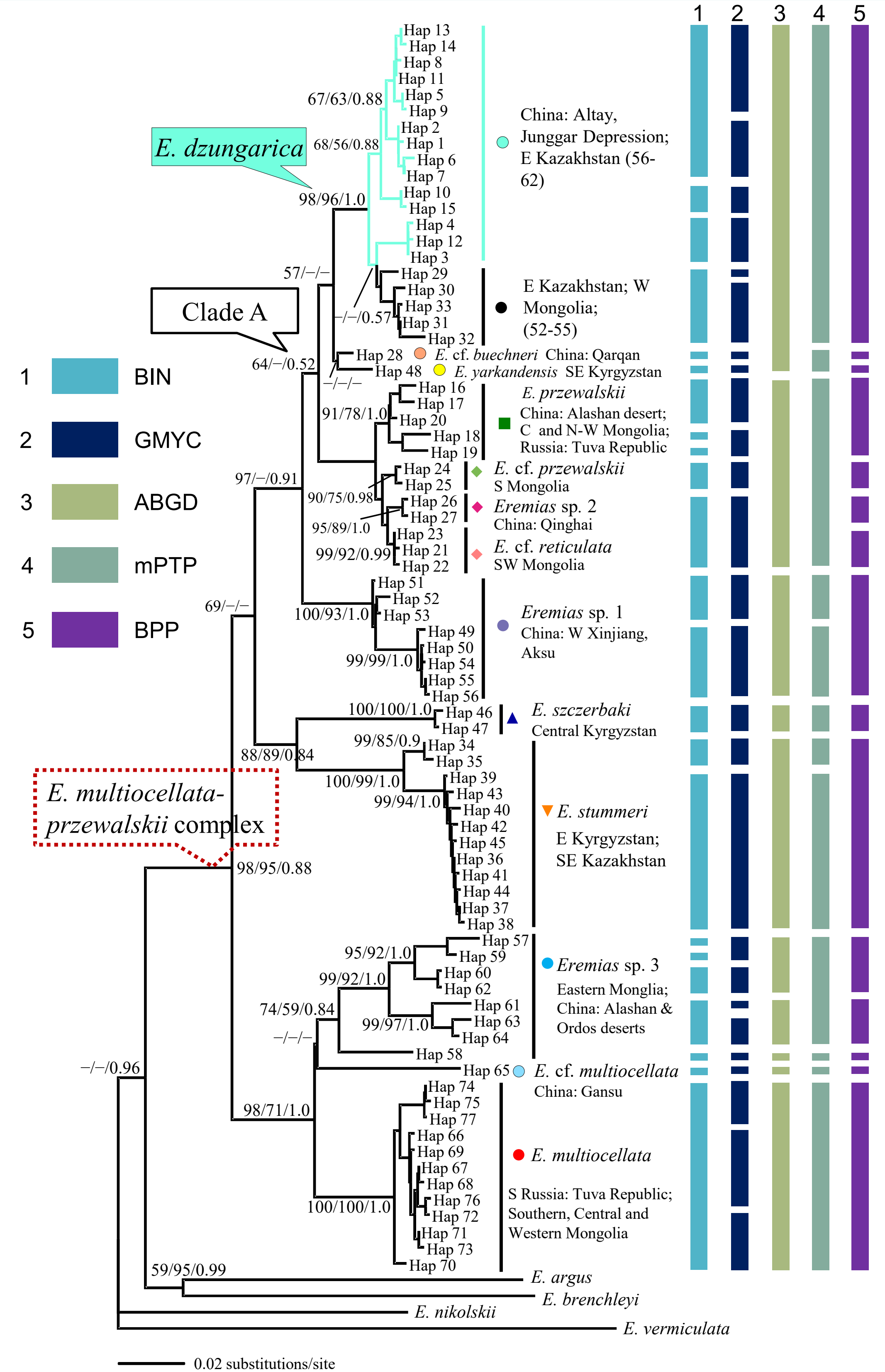
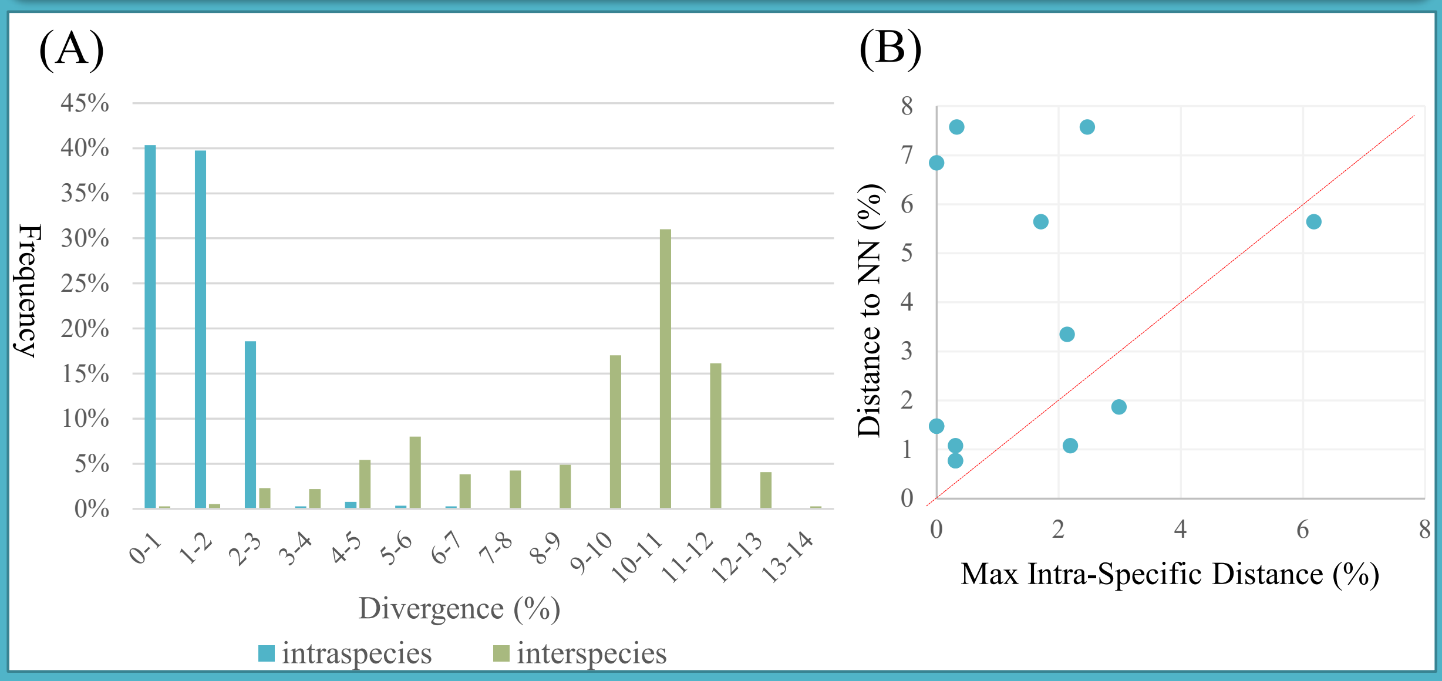


Figure 4



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Contact information:

Address: No.9 Section 4,Renmin Nan Road, Chengdu, Sichuan, P.R. China

E-mail: guoxg@cib.ac.cn