

Obstacles and Opportunities: Comparative Phylogeography of *Hemidactylus* Geckos and insights into Biogeographic Barriers in Eastern Myanmar.

Matthew L. Murdoch, L. Lee Grismer, Todd R. Jackman, Aaron M. Bauer
Villanova University, Villanova, PA



Introduction

Phylogeography

- Phylogeography is different from a typical phylogeny in that rather than simply deducing patterns of relatedness, geographic space and evolutionary timeframes are taken into account. Avise (2000)
- Throughout its evolutionary history a population of organisms may be impacted by geological, climatological, and historical factors that have influenced the distribution of present-day lineages.

Biogeographic Barriers

- Many widespread amphibian and reptile species extend from the east or west into Myanmar but not continue any farther (Theobald 1868; Grismer 2018; Zug 2007)
- One of the primary boundaries is the elevational and climate border between the Central Myanmar Basin in the west, characterized by dry seasonal forests and the Shan Plateau/ Kayah hill complex in the east characterized by subtropical forests in the north and montane rainforests in the south (Fig. 4).

Hemidactylus

- With approximately 1450 species in 118 genera Geckos are among the most species-rich and geographically widespread of terrestrial vertebrate lineages Gamble et al. (2012).
- This study focuses on four species present in Eastern Myanmar that fall within the East Asian *bowringii* complex: *Hemidactylus aquilonius*, *H. thayene*, *H. garnotii*, and *H. karenorum* (Fig 2).

Materials and Methods

- Material collected by the joint La Sierra University and Fauna & Flora International Myanmar Herpetological Survey (Fig 3).
- GPS and natural history observations taken for each specimen
- DNA from the mitochondrial gene ND2 extracted and sequenced from liver tissue using Villanova University Jackman Lab 2019 sequencing protocol
- Sequences aligned using Geneious
- Maximum Likelihood trees constructed using IQ-TREE (Nguyen et al. 2015)
- Nodes having ML bootstrap values of 95 and above considered well supported
- Uncorrected pairwise sequence divergences calculated in MEGA X (Kumar et al. 2018) (Table. 1)
- Identity of potential biogeographic boundaries based on described trends in past literature, elevational gradient, and the WWF Terrestrial Ecoregions of the World (Olson et al. 2012)

Purposes of Study

- Is there phylogenetic substructuring in *Hemidactylus* species found throughout Eastern Myanmar?
- If not what are the possible reasons for ready gene flow?
- If there is does it correspond with the Shan Plateau/ Kayah Hills biogeographic boundary or something else such as niche partitioning?

Results

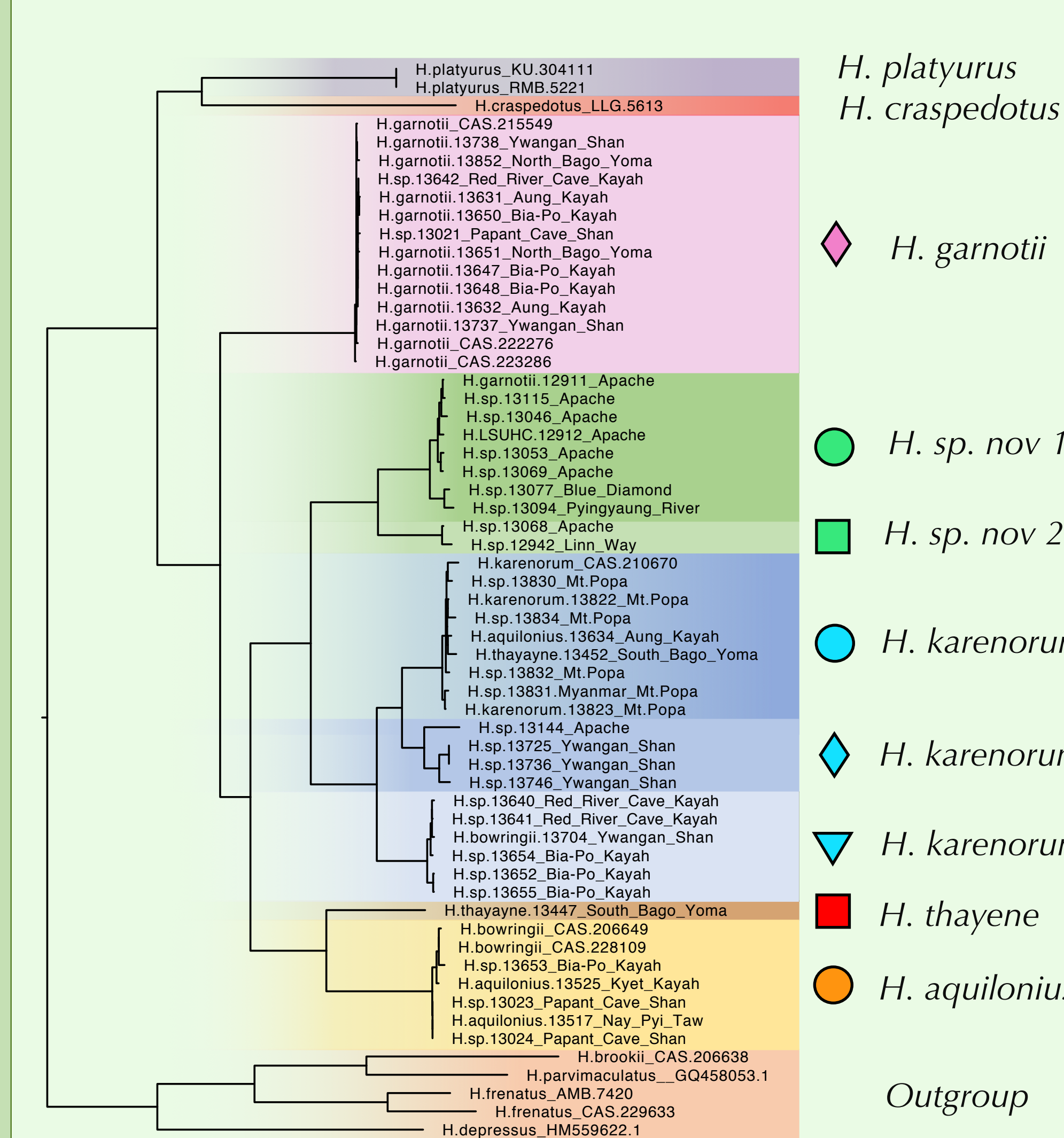


Figure 1. Maximum likelihood tree illustrating the relationships of the *bowringii* group of the genus *Hemidactylus*

	1	2	3	4	5	6	7	8	9	10
1. <i>aethiops</i>										
2. <i>thayene</i>	0.1665									
3. <i>sp. nov 1</i>	0.1670	0.1671								
4. <i>sp. nov 2</i>	0.1669	0.1672	0.0983							
5. <i>karenorum 1</i>	0.1660	0.1669	0.1719	0.1655						
6. <i>karenorum 2</i>	0.1616	0.1635	0.1461	0.1462	0.0916					
7. <i>karenorum 3</i>	0.1628	0.1604	0.1659	0.1622	0.1004	0.0807				
8. <i>garnotii</i>	0.1660	0.1672	0.1673	0.1661	0.1663	0.1664	0.1969			
9. <i>platyurus</i>	0.2484	0.2434	0.2395	0.2405	0.2424	0.2326	0.2437	0.2485		
10. <i>craspedotus</i>	0.2661	0.2648	0.2571	0.2588	0.2597	0.2496	0.2639	0.2587		
11. <i>subgroup</i>	0.1642	0.1787	0.1718	0.1773	0.1665	0.1751	0.1811	0.1887	0.1839	

Table 1. Uncorrected pairwise sequence divergence for the clades of the *Hemidactylus bowringii* group

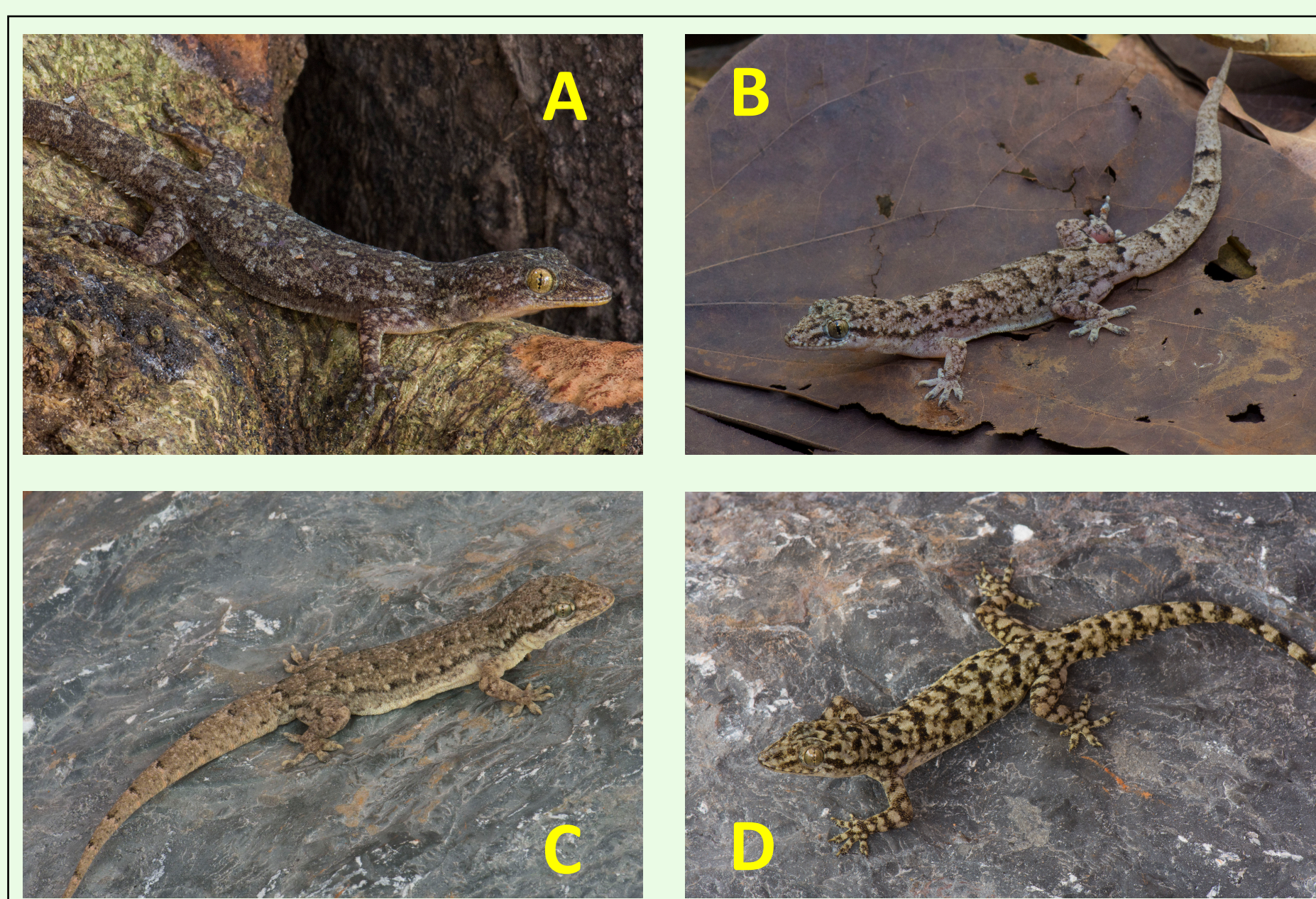


Figure 2. The four known species of the *Hemidactylus bowringii* group included in this study. (A) *H. garnotii* (B) *H. thayene* (C) *H. aquilonius* (D) *H. karenorum*

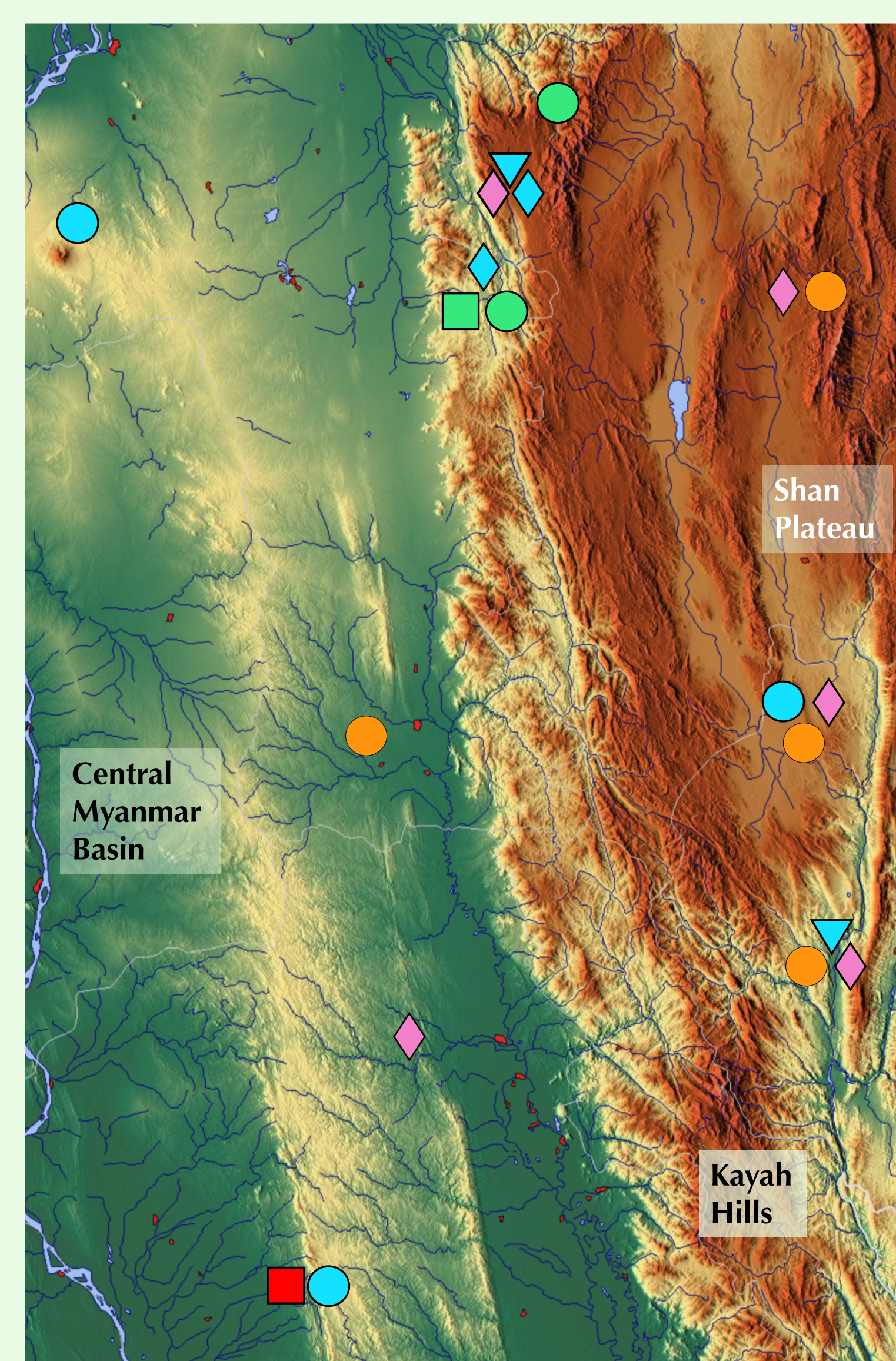


Figure 3. Elevation map of La Sierra University/ FFI survey area with symbols corresponding to the locality of members of clades uncovered in phylogeny.

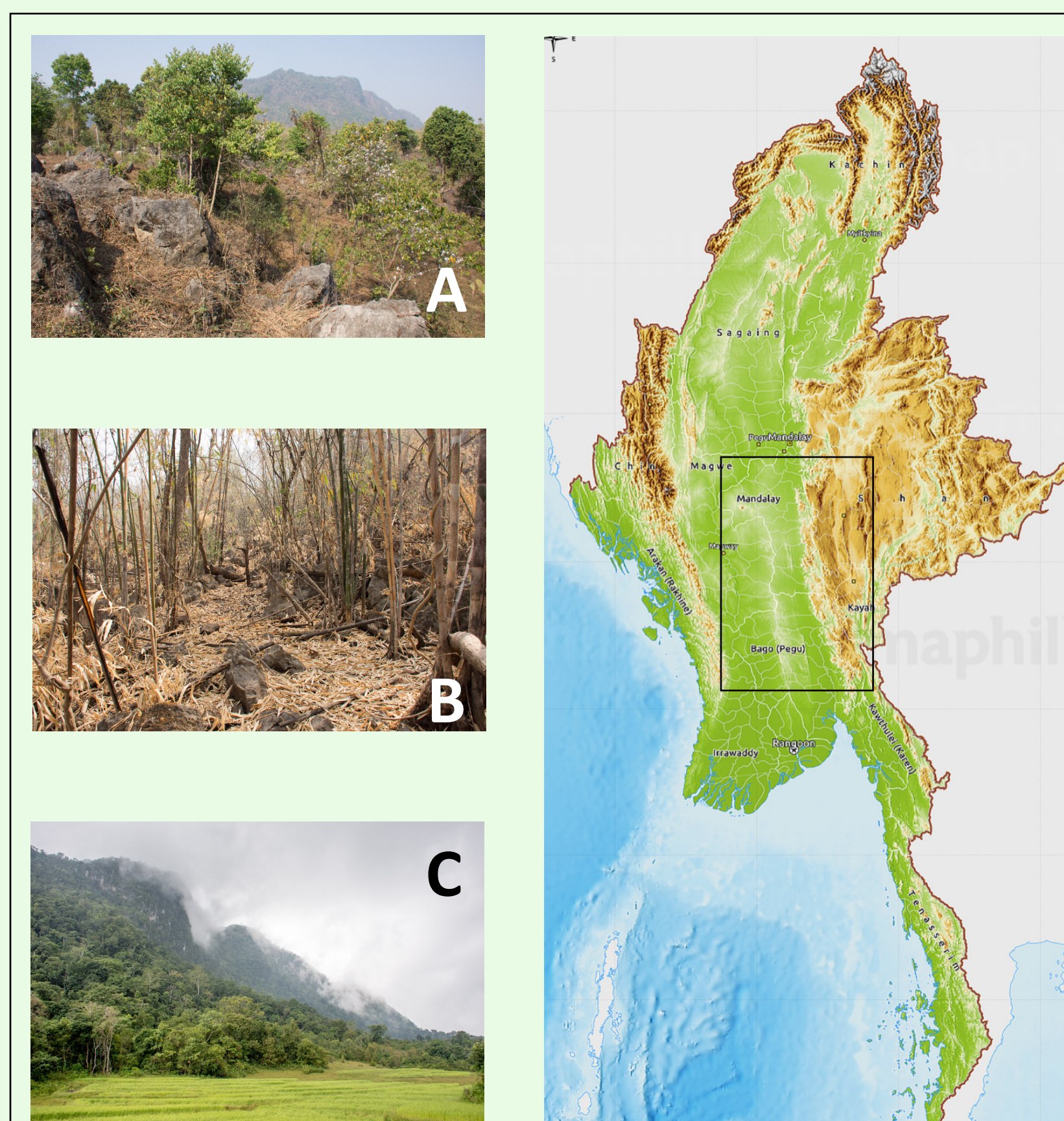


Figure 4. Map of Myanmar with box representing area enlarged in Fig 3. Photos of typical habitats where *Hemidactylus* are found. (A) Subtropical forests of the Shan Plateau (B) Dry scrub forests of the central depression (C) Montane rainforests of the Kayah Hills.

Discussion

- We uncovered the scenario of no genetic substructuring in *H. garnotii* which can be expected for a parthenogenic species that can readily colonize new locations
- H. aquilonius* as had viturally no variation across the survey range which raises the interesting question as to why it can readily share genes across its range
- H. karenorum* had significant variation with 6%-10% pairwise sequence divergence. However while some clades were grouped within a location clade 1 was found both above and below the elevational barrier leading to the consideration of other factors such as microhabitat type.
- We unexpectedly uncovered a sister lineage to *H. karenorum* which may represent a new species representing hitherto unknown *Hemidactylus* diversity in Southeast Asia similar to the Bauer 2010 assessment of a high degree of endemic diversity of the Indian Subcontinent. Habitat data shows that where this lineage is sympatric with *H. karenorum* the two groups occur on different habitat types.
- Future directions will include detailed morphological analyses to test if genetic variation within groups have morphological plasticity and if the sister lineage to *H. karenorum* has morphological difference corresponding with different habitat types.
- Nuclear loci will be sequenced to test if mitochondrial variation may be due to female territory bias or variation over distance.

Literature Cited

Avise, J.C. (2000) *Phylogeography: the history and formation of species*. Harvard University Press, Cambridge, MA.

Bauer, A.M., Jackman, T.R., Giri, V.B. & de Silva, A. (2010) South Asia supports a major endemic radiation of *Hemidactylus* geckos. *Molecular Phylogenetics and Evolution* 57, 343–352.

Gamble, T., Greenbaum, E., Jackman, T.R., Russell, A.P. & Bauer, A.M. (2012) Repeated Origin and Loss of Adhesive Toe pads in Geckos J. Castresana (Ed). *PLOS ONE* 7, e39429.

Grismer, L.L., Wood, P.L., Thura, M.K., Quah, E.S.H., Grismer, M.S., Murdoch, M.L., Espinoza, R.E. & Lin, A. (2018a) A new *Cyrtodactylus* Gray, 1827 (Squamata, Gekkonidae) from the Shan Hills and the biogeography of Bent-toed Geckos from eastern Myanmar. *Zootaxa* 4446, 477–500.

Nguyen, L.T., Schmidt, H.A., von Haeseler, A. & Minh, B.Q. (2015) IQ-TREE: A fast and effective stochastic algorithm for estimating maximum likelihood phylogenies. *Molecular Biology and Evolution*, 32 (1), 268–274.

Olson, D.M., Dinerstein, E., Wikramanayake, E.D., Burgess, N.D., Powell, G.V.N., Underwood, E.C., D'Amico, J.A., Itoua, I., Strand, H.E., Morrison, J.C., Loucks, C.J., Allnutt, T.F., Ricketts, T.H., Kura, Y., Lamoreux, J.F., Wettengel, W.W., Hedao, P. & Kassem, K.R. (2001) Terrestrial ecoregions of the world: a new map of life on Earth. *Bioscience* 51, 933–938.

Theobald, W. (1868) Catalogue of the reptiles of British Birma, embracing the provinces of Pegu, Martaban, and Tenasserim; with descriptions of new or little-known species. *Journal of the Linnean Society, Zoology* 10, 4–67.

Zug, G.R., Vindum, J.V. & Koo, M.S. (2007) Burmese *Hemidactylus* (Reptilia, Squamata, Gekkonidae): Taxonomic Notes on Tropical Asian *Hemidactylus*. *Proceedings of the California Academy of Sciences* 58, 387–405.

Acknowledgements

- Villanova University Herpetology Lab
- La Sierra University
- Faunal Flora International Myanmar Office