

Camouflage in Conservation:

Background Color-Matching in the Texas Horned Lizard

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Introduction

The Texas Horned Lizard is threatened in the State of Texas and has been declining over its range for the last half century.

Most of the literature on the basic ecology of Texas Horned Lizards cites "cryptic color pattern" as the first line of defense against predation in this taxon, and yet the degree to which horned lizards actually color-match their backgrounds has never been quantified. Texas zoos and state wildlife agencies are releasing captive-bred hatchlings and translocated adults to parts of their former range; however, the new populations are not self-sustaining, with the majority of releases lost to predation. Background color-matching has not been quantified for these reintroduction efforts but may be important to take into account when moving lizards into a new habitat where predation may be higher if they are not closely color-matched to the local soils.

Methods

- I quantify background color-matching in this taxon across its known range in the United States and in Mexico from in situ photos taken, as found, in the wild. I also present background color-matching variation and trends both within and between phenotypically and genetically diverse populations and ask whether lizards more closely match their local soil colors than soils from other areas. Finally, I suggest a method for zoos and wildlife agencies to score coloration in their captive populations of lizards, thus possibly enabling these institutions to objectively take into account color-matching a priori as an applied conservation strategy to potentially increase the survival of reintroduced Texas Horned Lizards.



Results

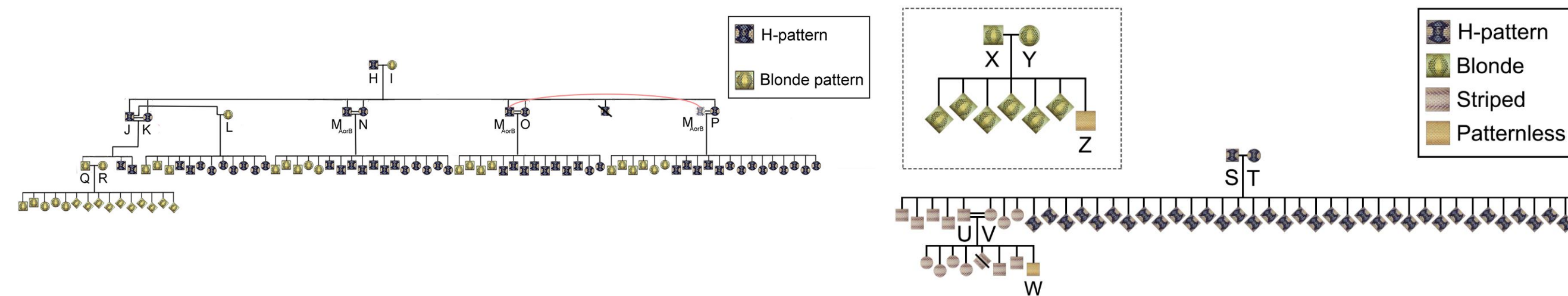


Fig 1. Examples of resultant pedigree charts. Color pattern frequencies among 161 offspring were consistent with inheritance of the Blonde pattern as a Mendelian recessive trait. Likewise, color pattern frequencies among 59 offspring involving Striped and Patternless phenotypes showed a similar mode of inheritance, with Patternless possibly being the double-recessive homozygous result of a combination of Striped × Blonde.

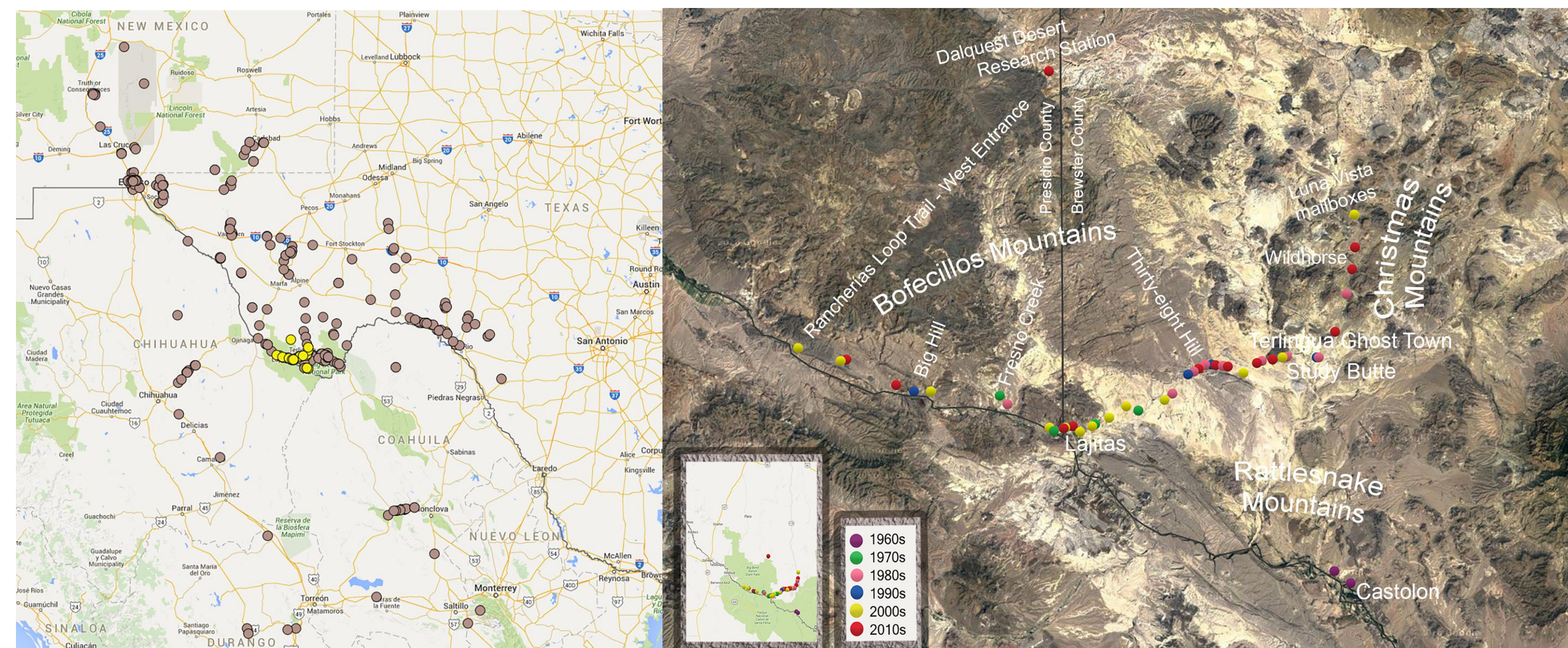


Fig 2. Geographic maps of 58 Blonde phase specimens: with comparison to range of the H-pattern phenotype (left) and zoomed-in satellite image of Blondes alone (right). Blonde individuals on the satellite image are color-coded by decade found.

Dorsal blotches	Blonde (n=10)	H-pattern (n=7)
Range	30 - 36	29 - 36
Mean	32.2 ± 1.93	32.57 ± 2.23

Fig 3. Results of comparative meristic data analysis of wild-caught Blondes and H-patterned ratsnakes across the known geographic range of the Blonde phase.

Frequencies	Blonde	Heterozygote	H-pattern
Morph	4.3 - 20%	33 - 49.4%	30.6 - 62.6%
Allele	20.9 - 44.7%		55.3 - 79.1%

Fig 4. Results and ranges of morph and allele frequency estimates for Blonde and H-patterned ratsnakes, from four datasets of field observations between 1986-2009.

Conclusions

- The Blonde, Striped, and Patternless phenotypes appear to be inherited as discrete Mendelian recessive traits.
- The similarity of ~32 dorsal markings on both Blondes and H-patterned ratsnakes seems to indicate a homologous genetic nature.
- Geographic distribution of the yellowish Blonde phase seems most associated with similarly colored substrate—yellow Upper Cretaceous sedimentary rocks—namely, Santa Elena and Boquillas limestones, highest near the center and lowest along, and adjacent to, the ecotones.
- Early estimates of morph and allele frequencies of the Blonde phase in the wild suggest that it is a polymorphism and not a rare mutation.
- Color pattern inheritance in this taxon indicates that the typical H-pattern is composed of two genes—blotches and stripes.
- Blondes, thus, appear to be essentially *stripeless* and Striped ratsnakes, *blotchless*.

Fig 5. H-patterned (left) and Blonde patterned (right) ratsnakes; apparent substrate matching.

References

HEDRICK, P. W. 2005. Genetics of populations. 3rd ed. Jones & Bartlett Learning, Sudbury. 737 pp.

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