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Mitogenome Announcement

The complete mitochondrial genome of the horned lizard *Phrynosoma blainvillii* (Squamata: Phrynosomatidae) from California, USA

Laura Ayala, Ga Hun Boo, Sung Min Boo, Brandon Cluff, Gage H. Dayton, Leah Edwards, ... show all

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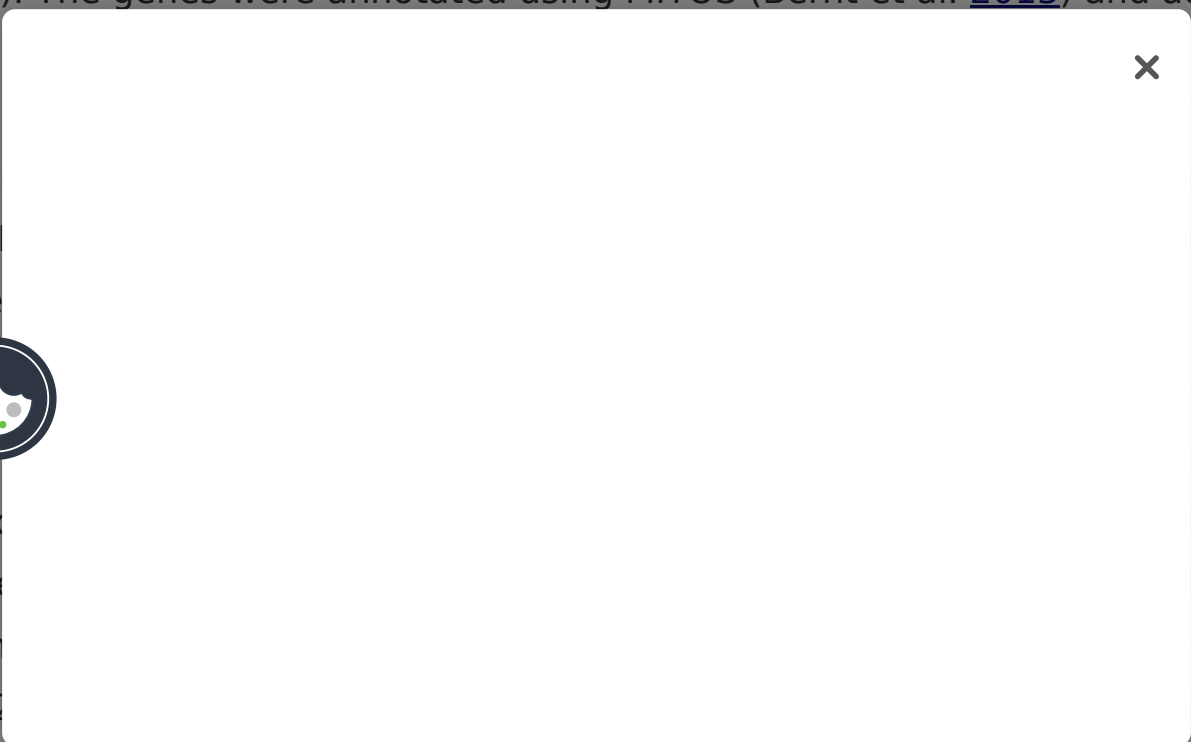


The family Phrynosomatidae consists of North American spiny lizards classified into nine genera and 148 species (Leaché et al. [2015a](#)). Three complete mitogenomes have been published for the family: *Uta stansburiana* Baird & Girard (Leaché et al. [2015b](#)), *Sceloporus occidentalis* Baird & Girard (Kumazawa [2004](#)), and *Urosaurus nigricaudus* Cope (Bernardo et al. [2016](#)). One of the 9 genera, *Phrynosoma* Wiegmann, includes 17 species of horned lizards (Niето-Montes de Oca et al. [2014](#)). Here, we describe the complete mitogenome of *Phrynosoma blainvillii*, a California Department of Fish and Wildlife 'Species of Special Concern', distributed from Northern California to Northern Baja California, Mexico (Leaché et al. [2009](#)).

DNA was extracted from *P. blainvillii* (specimen voucher deposited in the Herpetological Collection - Museum of Vertebrate Zoology at UC Berkeley: MVZ:Herp:283805) collected from the UCSC Fort Ord Natural Reserve, Marina, California using the DNeasy Blood and Tissue Kit (Qiagen, Valencia, CA). The 150 bp paired-end library construction and sequencing was performed by myGenomics, LLC (Alpharetta, GA), yielding 4,978,820 reads. The mitogenome was assembled de novo using MEGAHIT (Li et al. [2015](#)) and by mapping the reads against *U. stansburiana* (GenBank NC_027261) with the Medium-Low Sensitivity/Fast setting in Geneious R11 (Biomatters Limited, Auckland, New Zealand). The genes were annotated using MITOS (Bernt et al. [2013](#)) and adjusted in

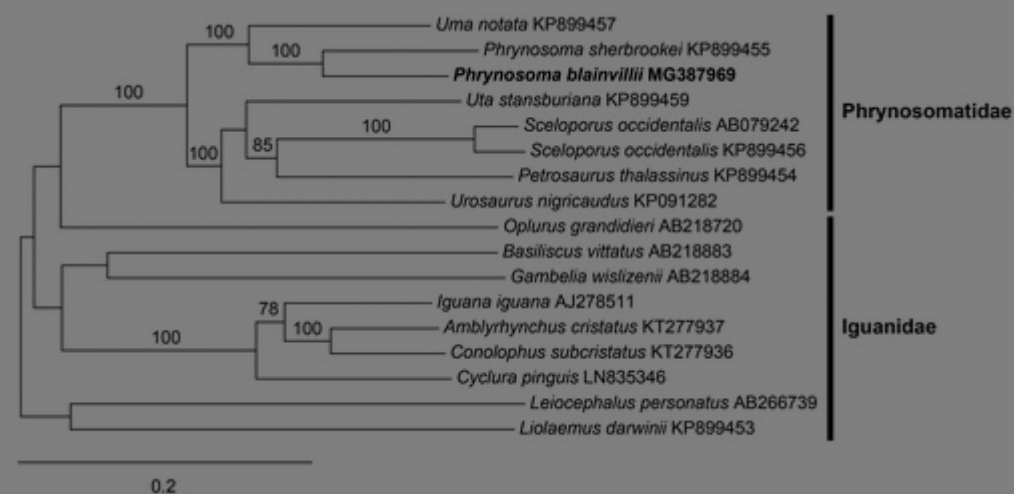
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The base codon (trnL and oxidative codon, but nad6 gene and eight tRNAs encode on the light strand, while the others encode on the



heavy strand. The putative OL is located between *trnN* and *trnC*, and is 30 bp in length, and the control region is 1540 bp. Phylogenetic analysis of *P. blainvillii* resolves it with *P. sherbrookei* in a fully supported clade sister to the genus *Uma* Baird (Figure 1). This relationship is similar to the findings of previous workers (Reeder and Wiens 1996; Wilgenbusch and de Queiroz 2000). Comparison of the complete *P. blainvillii* mitogenome to published *P. blainvillii* sequences (Leaché et al. 2009) found nearly identical sequences of *nad1* and *nad2* from a specimen from the Santa Lucia Mountain Range, but divergent sequences compared to a specimen of *P. blainvillii* from the nearby Gabilan Mountain Range. These data show that the Fort Ord, Marina and Santa Lucia populations of *P. blainvillii* represent a distinct coastal mitochondrial haplogroup.

Figure 1. Maximum-likelihood phylogram of *P. blainvillii* and representative Phrynosomatidae and Iguanidae mitogenomes. Numbers along branches are bootstrap supports based on 1000 nreps (<75% support not shown). The legend below represents the scale for nucleotide substitutions.



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Acknow



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The authors report no conflicts of interest. The authors alone are responsible for the content and writing of this article.

Additional information

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References

1. Bernardo PH, Aguilera-Miller EF, Álvarez-Castañeda ST, Cruz FRMDL, Murphy RW. 2016. The complete mitochondrial genome of the black-tailed brush lizard *Urosaurus nigricaudus* (Reptilia, Squamata, Phrynosomatidae). *Mitochondrial DNA A DNA Mapp Seq Anal.* 27:4023–4025.


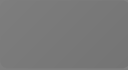



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2. Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsch G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. *Mol Phylogenet Evol.* 69:313–319.

3. Boc A, ... validating ... 573–W579.

4. Derec ... JF, Guindon ... analysis for the non-sp ...



5. Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. *Mol Biol Evol.* 30:772–780.
 | [PubMed](#) | [Web of Science ®](#) | [Google Scholar](#)
6. Kumazawa Y. 2004. Mitochondrial DNA sequences of five squamates: phylogenetic affiliation of snakes. *DNA Res.* 11:137–144.
 | [PubMed](#) | [Web of Science ®](#) | [Google Scholar](#)
7. Leaché AD, Banbury BL, Felsenstein J, Nieto-Montes de Oca A, Stamatakis A. 2015a. Short tree, long tree, right tree, wrong tree: new acquisition bias corrections for inferring SNP phylogenies. *Syst Biol.* 64:1032–1047.
 | [PubMed](#) | [Web of Science ®](#) | [Google Scholar](#)
8. Leaché AD, Chavez AS, Jones LN, Grummer JA, Gottscho AD, Linkem CW. 2015b. Phylogenomics of phrynosomatid lizards: conflicting signals from sequence capture versus restriction site associated DNA sequencing. *Genome Biol Evol.* 7:706–719.
 | [PubMed](#) | [Web of Science ®](#) | [Google Scholar](#)
9. Leaché AD, Koo MS, Spencer CL, Papenfuss TJ, Fisher RN, McGuire JA. 2009. Quantifying ecological, morphological, and genetic variation to delimit species in the coast horned lizard species complex (*Phrynosoma*). *Proc Natl Acad Sci USA.* 106:12418–12423.
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10. Li D, L... angle-node
solutio... ruijn graph.
Bioinfo...
11. Nie... 2014. A
new s... with an
updat...



2. Reeder TW, Wiens JJ. 1996. Evolution of the lizard family phrynosomatidae as inferred from diverse types of data. *Herpetol Mon.* 10:43-84.



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3. Wilgenbusch J, de Queiroz K. 2000. Phylogenetic relationships among the phrynosomatid sand lizards inferred from mitochondrial DNA sequences generated by heterogeneous evolutionary processes. *Syst Biol.* 49:592-612.



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