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Mitogenome Announcement

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

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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 (Nieto-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

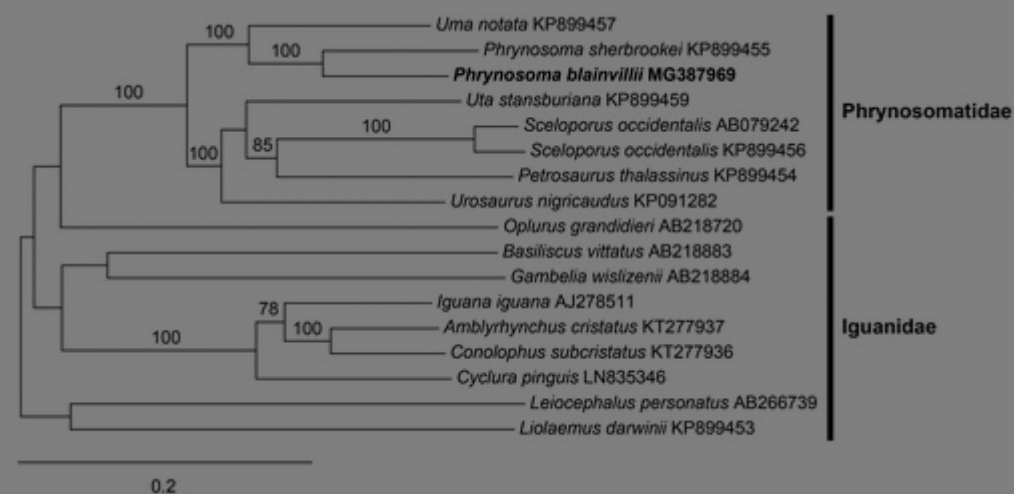
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The base cod (trnL and oxidative codon, h but nad2 The nad6 gene and eight tRNAs encode on the light strand, while the others encode on the



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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Additional information

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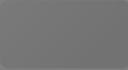
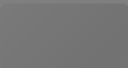
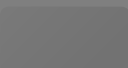
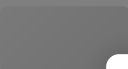
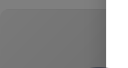
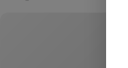
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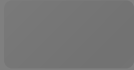


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