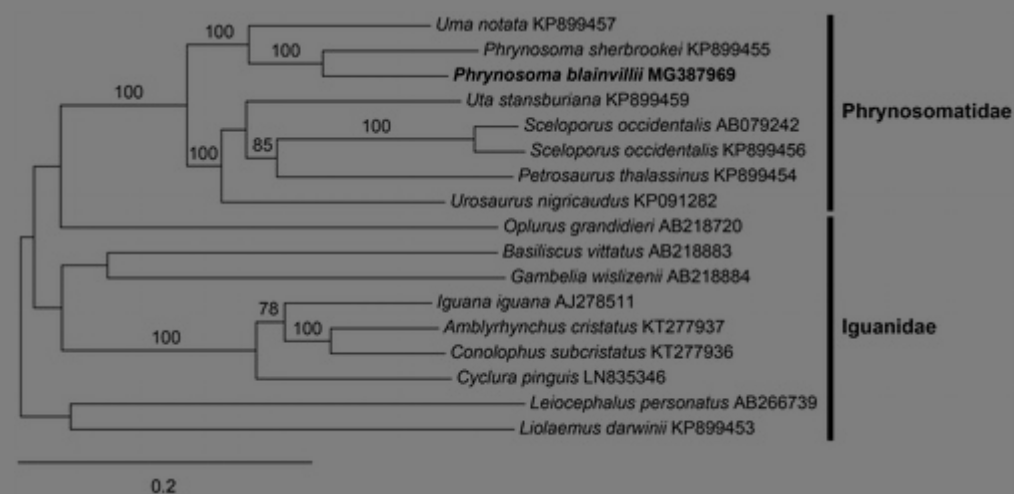


heavy strand. The putative OL is located between trnN and trnC, and is 30 bp in length, and the control region is 1540 bp. Phylogenetic analysis of *P. blainvillii* resolves it with *P. sherbrookei* in a fully supported clade sister to the genus *Uma* Baird (Figure 1). This relationship is similar to 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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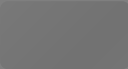
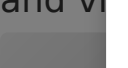

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Additional information

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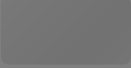



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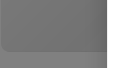
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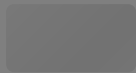
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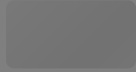


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