

Online Supplementary File 5

Fluctuating fire regimes and their historical effects on genetic variation in an endangered savanna specialist

Supplementary Table 1. Sample information, localities, and Genbank accession numbers

Supplementary Table 2. Primers used in loci amplification

Supplementary Figure 1. Bayesian phylogeny of selected *Vireo* lineages

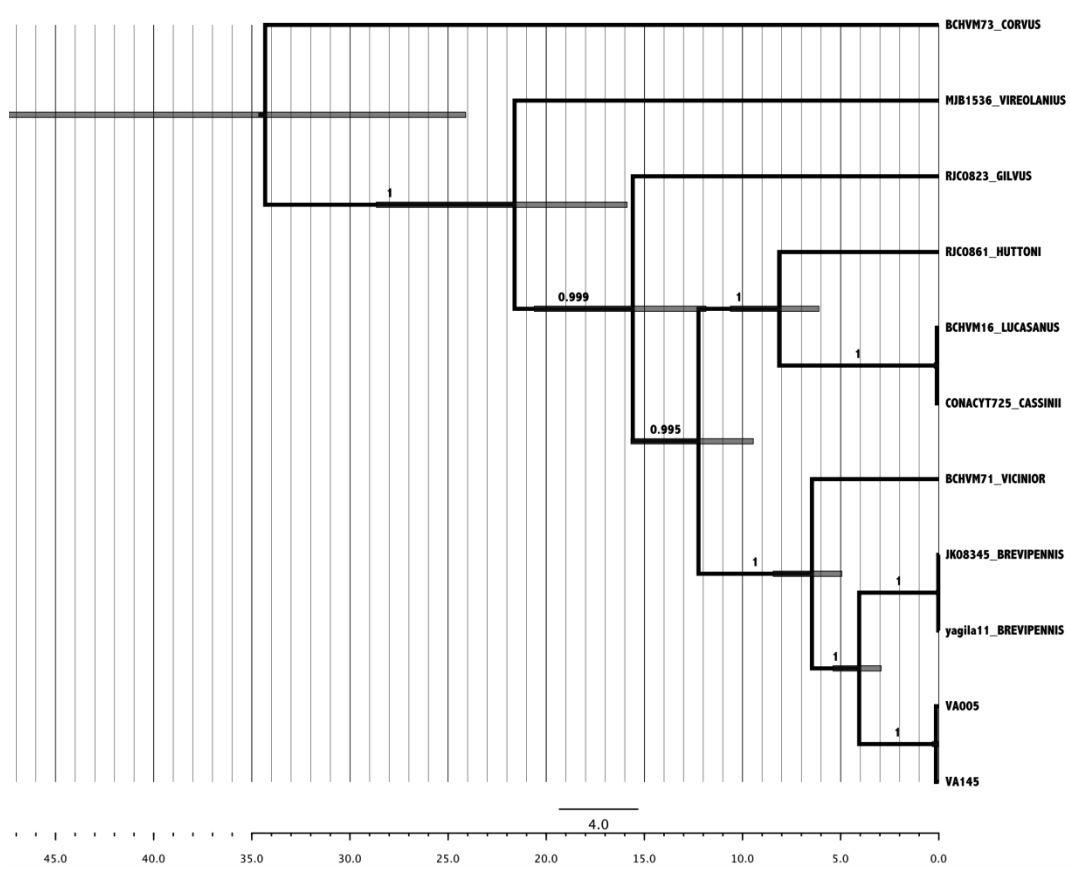
Supplementary Table 2. Primers used for DNA amplification and sequencing. Part (A) includes all the new primers designed for this study to target fragmented DNA from feathers. Sequences are given in a 5' – 3' direction. Melting temperature (T_m) is given in degrees Celsius. (See Materials and Methods for PCR conditions.) Product length is given in base-pairs. Part (B) includes primers from the literature used on samples with high quality DNA from tissues.

(A)

Forward	Sequence	T _m (basic)	Reverse	Sequence	T _m (basic)	Product Length
MC1R_Vaf	CGTGTCTTCCTCTCCTTCCT	56.3	MC1R_VAr2	TTCTGCTGGCTGGAGATGCTGT	56.7	294
ADAMS6_VAf3	GGTCAGTTGTTAAGCCTTCTGA	53	ADAMS6_VAr4	GGAATATTCCTCATGTATCATCTC	52.3	291
AETC-F	TGGACTTCAAATCCCCGATGATCCAGC	64.3	AETC_R2	GAGTGGTACCAAAGTGTGCAGACAAGTCC	64.4	278
FIB5_Vaf	GCATATTAATTTATCGATGCTACCAA	51.7	FIB5_VAr2	AAATGAGTCAGGCTGTCCTTAT	51.1	256
GAPDH-F	ACCTTTCATGCGGGTGCTGGCATTGC	62.7	GAPDH_Var	CCTCTGAGGGGAAAGGAGGCAGC	62.4	236
TGFB2_Vaf	GGGARGTGTTCATGCAGTTGTT	52.4-54.4	TGFB2.I5_VAr2	GTGAAGGTGATAATTTGGCTCTAAC	54.4	235
TROP.6_Vaf	ACCTCCTGTGCAGCCAAAAGA	54.4	TROP.6_VAr	GAAAGGGGCGGATGGAAGATT	54.4	280
IQGAP2_VAF	GTGCTGAGCTAGGACTCTC	53.2	IQGAP2_VAR	TGCCACTCCCTTGAAACTC	53.8	249
LAMA2_F	CCAAGAAGCAGCTGCAGGATGAGATGC	53.2	LAMA2_R	CTGCCGCCCGTTGTCGATCTCCACCAG	53.8	295

(B)

Locus	Primer pairs	Reference
ND2	L5215 and H1064	Zink et al. (2010) <i>Auk</i> 127: 797-806
MC1R	MSH8 and MSH9	MacDougall-Shackleton et al. (2003) <i>Mol. Biol. Evol.</i> 20: 1675-1681
ADAMS6	ADAMS6-F and ADAMS6-R	Backström et al. (2006) <i>Genetics</i> 174: 377-386
AETC	AETC-F and AETC-R	Primmer et al. (2002) <i>Mol. Ecol.</i> 11: 603-612
FIB5	Fib5 and Fib6	Kimball et al. (2008) <i>Mol. Phylogen. Evol.</i> 50: 654-660
GAPDH	GAPDH-F and GAPDH-R	Borge et al. (2005) <i>Genetics</i> 171: 1861-1873
TGFB2I5	TGFB2-F and TGFB2-R	Borge et al. (2005) <i>Genetics</i> 171: 1861-1873
TROP6	Trop.6F and Trop.6R	Kimball et al. (2008) <i>Mol. Phylogen. Evol.</i> 50: 654-660
IQGAP2	IQGAP2-F and IQGAP2-F	Backström et al. (2006) <i>Genetics</i> 174: 377-386
LAMA2	Same as above	Borge et al. (2005) <i>Genetics</i> 171: 1861-1873



Supplemental Figure 1. Bayesian phylogeny of selected lineages of Vireonidae from 10 concatenated loci. The tree is rooted with a common raven (*Corvus corax*). The X-axis is in millions of years. Horizontal bars represent the 95% high posterior density (HPD) of divergence times. The value on each branch is the posterior probability of the clade.