

Daily activity patterns influence retinal morphology, signatures of selection, and spectral tuning of opsin genes in colubrid snakes.

Hauzman E, Bonci DMO, Suárez-Villota EY; Neitz M, Ventura DF

Additional file 1 with Tables S1-S7 and Figures S1-S2.

Table S1. Primers designed and used in this study, to amplify the opsin genes *LWS*, *RH1* and *SWS1*, expressed in retinas of Colubridae snakes.

Primer	Opsin	Annealing Temperature	Nucleotide Sequence
<i>SquaLWSFw</i>	LWS	59.5	5' ATGACAGAGGCCTGGAATGT 3'
<i>SquaLWSRv</i>	LWS	60.0	5' CCTTGCTGGCATTCTTTCT 3'
<i>LWS DipsFw</i>	LWS	62.0	5' CTCGTACCCATCAAGTACAAGAAGT 3'
<i>LWS DipsRv</i>	LWS	62.0	5' GTCTTCTGAGAGCTCAGGTCAGACT 3'
<i>LWS DegFw</i>	LWS	62.4	5' GRYCCTTTTGAAGGYCCAAAYTAYC 3'
<i>LWS DegRv</i>	LWS	62.8	5' GTTGAAATGGTKGCGCTTTTTG 3'
<i>LWS TdorFw</i>	LWS	61.6	5' TTTACTTACACCAACAGCAACAATACC 3'
<i>LWS TdorRv</i>	LWS	61.5	5' TTCATGAAGACATAGATAAATTGGGTTG 3'
<i>LWS LpoeFw</i>	LWS	62.5	5' GTGTATTTGCTTACACCAATAGCAACA 3'
<i>LWS LpoeRv</i>	LWS	63.4	5' AAAATGTATATGGTCCCCAGCAGAC 3'
<i>SquaRH1Fw</i>	RH1	59.9	5' GCATTGTTCCGAGTCCATTT 3'
<i>SquaRH1Rv</i>	RH1	62.5	5' TTCTGCTGGCACCAAGACAG 3'
<i>RH1SmikFw</i>	RH1	65.8	5' TATTTGGCAGATCCATGGAAATATTCTG 3'
<i>RH1SmikRv</i>	RH1	66.1	5' GGGGAAACCTTACTTGTGGAGACTGTAG 3'
<i>RH1OxyFw</i>	RH1	64.5	5' GTCACCATCCAACACAAGAACTCA 3'
<i>RH1OxyRv</i>	RH1	64.0	5' AAATCACTGGGTTGTAGATTGAAGAGC 3'
<i>RH1Tdor1Fw</i>	RH1	60.0	5' CACCACTACCATGTACACTTCCAT 3'
<i>RH1Tdor1Rv</i>	RH1	60.0	5' GTCATAAAGACAGGGCCAAAGT 3'
<i>RH1Tdor2Fw</i>	RH1	60.0	5' CAAGAACTCAGAACACCTCTGAA 3'
<i>RH1Tdor2Rv</i>	RH1	60.0	5' CGGAACTGTTTGTTTATTACGATA 3'
<i>SquaSWS1Fw</i>	SWS1	55.6	5' CCTCTTTGAAAACATCTCCTC 3'
<i>SquaSWS1Rv</i>	SWS1	59.8	5' GTCCTCCTGTCAAGTCAGCC 3'
<i>SWS1ArtfFw</i>	SWS1	64.0	5' GACGGTCCCCAGTATCACATTG 3'
<i>SWS1ArtfRv</i>	SWS1	64.7	5' CTTGACAGGAGGACACTGAGGAAAC 3'
<i>SWS1 TdorFw</i>	SWS1	63.7	5' CTTTCCACTTCAAACCATCTTCAT 3'
<i>SWS1 TdorRv</i>	SWS1	63.4	5' TTCTGAGAAGTCACATCAGAGTCGT 3'
<i>SWS1 Tdor2Fw</i>	SWS1	64.8	5' ATCCTCTTCGTCACCATCAAGTACAAG 3'
<i>SWS1 Tdor2Rv</i>	SWS1	64.1	5' ATGAAGCAGTAGATGATGGGGTTGT 3'
<i>SWS1 DipsFw</i>	SWS1	62.0	5' TACCACCAGGAGAGTGTATTTGTGTA 3'
<i>SWS1 DipsRv</i>	SWS1	62.0	5' ACTTTCTTGCCAAAGAGCTGCATTAT 3'

Table S2. Species used as outgroups for phylogenetic analysis and respective GenBank accession numbers.

Comon name	Species	GenBank acesion number				
		RH1	RH2	SWS1	SWS2	LWS/MWS
Salamander	<i>Ambystoma tigrinum</i>	Q90245	-	-	AF038946	-
Worm lizard	<i>Amphisbaena alba</i>	KR336729	-	KR336720	-	KR336705
Worm lizard	<i>Amphisbaena infraorbitale</i>	KR336730	-	KR336719	-	KR336704
Lizard	<i>Anolis carolinensis</i>	NM001291387	AF134189	AH007736	-	P41592
Lizard	<i>Bachia flavescens</i>	KR336731	-	KR336715	-	KR336703
Cow	<i>Bos taurus</i>	NM001014890	-	NP776992	-	AAG49893
Goldfish	<i>Carassius auratus</i>	L11863	-	Q90309	-	L11867
Pigeon	<i>Columba livia</i>	-	AH007731	AH007798	-	-
Zebrafish	<i>Danio rerio</i>	NP571287	Q9W6A6	Q9W6A9	BAC24133	NM001002443
Chicken	<i>Gallus gallus</i>	P22328	P28683	P28684	P28682	P22329
Lizard	<i>Gekko gekko</i>	-	-	P35357	-	P35358
Lamprey	<i>Geotria australis</i>	AAR14682	AAR14683	AY366495	AAR14681	AY366491
Gorilla	<i>Gorilla gorilla</i>	XM004036292	-	XM004046176	-	-
Human	<i>Homo sapien</i>	NP00530	-	P03999	-	NM020061.5
Coelacanth	<i>Latimeria chalumnae</i>	-	AF131258	-	-	-
Lizard	<i>Melanoseps occidentalis</i>	KR336743	-	KR336718	-	KR336713
Mouse	<i>Mus musculus</i>	NP663358	-	P51491	-	O35599
Lungfish	<i>Neoceratodus forsteri</i>	EF526295	EF526296	EF526298	-	EF526297
Platypus	<i>Ornithorhynchus anatinus</i>	-	-	-	ABN43075	-
Day Gecko	<i>Phelsuma madagascariensis</i>	-	AF074044	AAD45183	-	AAD25917
Rat	<i>Rattus norvegicus</i>	NM033441	-	NM031015	-	NM053548
Fish	<i>Scleropages formosus</i>	XM018762271	-	XM018755948	-	XM018725556
Canary	<i>Serinus canaria</i>	XM009099359	-	AY227178	-	XM009100678
Boar	<i>Sus scrofa</i>	NM214221	-	NM214090	-	NM001011506
Zebra finch	<i>Taeniopygia guttata</i>	AF222329	NM00107669	AF222331	NM001076697	AF222333
Lizard	<i>Takydromus sexlineatus</i>	KR336727	-	KR336722	-	KR336707
Lizard	<i>Uta stansburiana</i>	DQ100323	DQ100324	DQ100325	DQ100326	DQ129869
Frog	<i>Xenopus laevis</i>	AAC42232	-	P51473	AAO38746	U90895
Frog	<i>Xenopus tropicalis</i>	NM00109733	-	NM001126076	-	NM001102861

Table S3. Colubridae species used for phylogenetic and evolutionary analysis and respective GenBank accession numbers. In bold, species sequenced in this study.

Family	Subfamily	Species	GenBank Accession Number		
			LWS	RH1	SWS1
Colubridae	Colubrinae	<i>Ahaetulla nasuta</i>	KX237798	KX237852	KX237906
		<i>Arizona elegans</i>	KU323986	KU324006	KU323997
		<i>Bogertophis subocularis</i>	KX237822	KX237844	KX237920
		<i>Boiga ceylonensis</i>	KX237819	-	-
		<i>Boiga forsteni</i>	KX237818	KX237867	-
		<i>Chironius carinatus</i>	KX237795	KX237846	KX237914
		<i>Chironius bicarinatus</i>	MG544928	MG544945	MG544962
		<i>Chironius fuscus</i>	KX237794	KX237845	KX237913
		<i>Chrysopelea ornata</i>	KX237799	KX237851	KX237907
		<i>Dasypeltis scabra</i>	KX237821	KX237856	KX237908
		<i>Elaphe climacophora</i>	KX237817	KX237845	KX237917
		<i>Hemorrhois hippocrepis</i>	KX237911	KX237835	KX237911
		<i>Lampropeltis californiae</i>	KX237825	KX237858	KX237921
		<i>Lampropeltis floridana</i>	KX237826	KX237857	KX237922
		<i>Lycodon aulicus</i>	KX237820	KX237875	KX237915
		<i>Macroprotodon brevis</i>	KX237815	-	KX237909
		<i>Opheodrys aestivus</i>	KX237797	KX237839	KX237912
		<i>Orthriophis taeniurus</i>	KX237816	KX237862	KX237916
		<i>Pantherophis guttatus</i>	KX237824	KX237863	KX237918
		<i>Phyllorhynchus decurtatus</i>	KU323985	-	KU323996
		<i>Pituophis catenifer</i>	KX237823	KX237854	KX237919
		<i>Pseustes poecilonotus</i>	KR336711	KR336741	KR336725
		<i>Spalerosophis diadema</i>	KX237814	KX237853	KX237910
		<i>Spilotes pullatus</i>	MG544940	MG544957	MG544974
		<i>Telescopus fallax</i>	KU323984	KU324005	KU323995
		<i>Atractus flammigerus</i>	KR336712	KR336740	KR336726
		<i>Atractus badius</i>	KX237809	KX237842	KX237902
	<i>Atractus reticulatus</i>	MG544927	MG544944	MG544961	
	<i>Dipsas indica</i>	KX237813	KX237849	KX237904	
	<i>Dipsas catesbyi</i>	KX237812	KX237848	KX237905	
	<i>Dipsas petersi</i>	MG544929	MG544946	MG544963	
	<i>Echinanthera cephalostriata</i>	MG544930	MG544947	MG544964	
	<i>Echinanthera undulata</i>	MG544931	MG544948	MG544965	
	<i>Erythrolamprus aesculapii</i>	MG544932	MG544949	MG544966	
	<i>Erythrolamprus miliaris</i>	MG544933	MG544950	MG544967	
	<i>Erythrolamprus poecilogyrus</i>	MG544934	MG544951	MG544968	
	<i>Erythrolamprus reginae</i>	KX237800	KX237855	KX237894	
	<i>Helicops angulatus</i>	KX237806	KX237836	KX237895	
	<i>Helicops modestus</i>	MG544935	MG544952	MG544969	
	Dipsadinae	<i>Heterodon nasicus</i>	KX237793	KX237850	KX237893
		<i>Hypsiglena jani</i>	KU323988	KU324007	KU323998
		<i>Imantodes lentiferus</i>	KX237807	KX237841	KX237900
		<i>Leptodeira annulata</i>	KX237808	KX237840	KX237901
		<i>Oxyrhopus guibei</i>	MG544936	MG544953	MG544970
		<i>Oxyrhopus melanogenys</i>	KX237804	KX237838	KX237899
		<i>Philodryas patagoniensis</i>	MG544937	MG544954	MG544971
		<i>Pseudoboa coronata</i>	KX237803	KX237837	KX237898
<i>Sibon nebulatus</i>		KX237811	KX237843	KX237902	
<i>Sibynomorphus mikanii</i>		MG544938	MG544955	MG544972	
<i>Sibynomorphus neuwiedi</i>		MG544939	MG544956	MG544973	
<i>Taeniophallus persimilis</i>		MG544941	MG544958	MG544975	
<i>Thamnodynastes hypoconia</i>		MG544942	MG544959	MG544976	
<i>Tomodon dorsatus</i>		MG544943	MG544960	MG544977	
<i>Xenopholis scalaris</i>		KX237810	KX237834	KX237897	
Xenopeltidae		<i>Xenopeltis unicolor</i>	FJ497235	FJ49723	FJ497234
Pythonidae		<i>Python regius</i>	FJ497238	FJ497236	FJ497237

Table S4. Summary of phylogenetic evolutionary branch-site and site models parameters for *LWS*, *RH1* and *SWS1* opsin genes.

Opsins	Model	Ln L	P	Parameter Estimates
LWS	Branch-Site Models			
	Null Model	-11,370.8	150	$\omega = 1.00$
	Model A (diurnal)	-11,347.9	152	$\omega_0 = 0.05$ ($p_0 = 0.798$), $\omega_1 = 1.0$ ($p_1 = 0.18$); $\omega_2 = 34.3$ ($p_2 + p_3 = 0.03$)
	Model A (nocturnal)	-11,320.3	152	$\omega_0 = 0.05$ ($p_0 = 0.77$), $\omega_1 = 1.0$ ($p_1 = 0.17$); $\omega_2 = 14.8$ ($p_2 + p_3 = 0.06$)
	Site Models			
	Model 0	-4,598.5	101	$\omega_0 = 0.49$
	Model 3	-4,235.5	105	$\omega_0 = 0.03$ ($p_0 = 0.82$), $\omega_1 = 1.8$ ($p_1 = 0.14$); $\omega_2 = 6.08$ ($p_2 = 0.04$)
	Model 1a	-4,316.4	102	$\omega_0 = 0.014$ ($p_0 = 0.798$), $\omega_1 = 1.0$ ($p_1 = 0.202$)
	Model 2a	-4,238.3	104	$\omega_0 = 0.017$ ($p_0 = 0.78$), $\omega_1 = 1.0$ ($p_1 = 0.13$); $\omega_2 = 4.19$ ($p_2 + p_3 = 0.08$)
	Model 7	-4,324.8	102	$p = 0.0158$, $q = 0.0987$
Model 8	-4,238.7	104	$p_0 = 0.9095$, $p = 0.038$, $q = 0.24$ ($p_1 = 0.090$, $\omega = 3.989$)	
RH1	Branch-Site Models			
	Null Model	-10,943.6	146	$\omega = 1.00$
	Model A (diurnal)	-10,939.4	148	$\omega_0 = 0.055$ ($p_0 = 0.86$), $\omega_1 = 1.0$ ($p_1 = 0.14$); $\omega_2 = 4.36$ ($p_2 + p_3 = 0.007$)
	Model A (nocturnal)	-10,918.9	148	$\omega_0 = 0.057$ ($p_0 = 0.86$), $\omega_1 = 1.0$ ($p_1 = 0.12$); $\omega_2 = 11.4$ ($p_2 + p_3 = 0.02$)
	Site Models			
	Model 0	-4,692.8	97	$\omega_0 = 0.288$
	Model 3	-4,479.1	101	$\omega_0 = 0.002$ ($p_0 = 0.67$), $\omega_1 = 0.43$ ($p_1 = 0.23$); $\omega_2 = 2.02$ ($p_2 = 0.10$)
	Model 1a	-4,497.7	98	$\omega_0 = 0.022$ ($p_0 = 0.77$), $\omega_1 = 1.0$ ($p_1 = 0.23$)
	Model 2a	-4,483.4	100	$\omega_0 = 0.024$ ($p_0 = 0.77$), $\omega_1 = 1.0$ ($p_1 = 0.18$); $\omega_2 = 2.7$ ($p_2 + p_3 = 0.048$)
	Model 7	-4,496.8	98	$p = 0.018$, $q = 0.059$
Model 8	-4,479.5	100	$p_0 = 0.926$, $p = 0.098$, $q = 0.555$ ($p_1 = 0.074$, $\omega = 2.26$)	
SWS1	Branch-Site Models			
	Null Model	-14,248.6	154	$\omega = 1.00$
	Model A (diurnal)	-14,225.3	156	$\omega_0 = 0.05$ ($p_0 = 0.84$), $\omega_1 = 1.0$ ($p_1 = 0.077$); $\omega_2 = 1.23$ ($p_2 + p_3 = 0.078$)
	Model A (nocturnal)	-14,237.9	156	$\omega_0 = 0.05$ ($p_0 = 0.87$), $\omega_1 = 1.0$ ($p_1 = 0.08$); $\omega_2 = 1.7$ ($p_2 + p_3 = 0.046$)
	Site Models			
	Model 0	-5,784.0	99	$\omega_0 = 0.1$
	Model 3	-5,565.2	103	$\omega_0 = 0.00$ ($p_0 = 0.64$), $\omega_1 = 0.17$ ($p_1 = 0.25$); $\omega_2 = 0.73$ ($p_2 = 0.11$)
	Model 1a	-5,618.6	100	$\omega_0 = 0.039$ ($p_0 = 0.86$), $\omega_1 = 1.0$ ($p_1 = 0.14$)
	Model 2a	-5,618.6	102	$\omega_0 = 0.039$ ($p_0 = 0.86$), $\omega_1 = 1.0$ ($p_1 = 0.1$); $\omega_2 = 1.0$ ($p_2 + p_3 = 0.039$)
	Model 7	-5,568.3	100	$p = 0.13$, $q = 0.899$
Model 8	-5,568.3	102	$p_0 = 0.998$, $p = 0.13$, $q = 0.92$ ($p_1 = 0.002$, $\omega = 1.04$)	

p , number of parameters; p_0 , p_1 , p_2 , proportion of sites in different omega classes; l , likelihood.

Table S5. Known amino acid spectral tuning sites of the *LWS* opsin gene and predicted peak absorbance (λ_{\max}) [1]. Sites numbered based on the bovine rhodopsin sequence. All λ_{\max} values are estimates predicted based on amino acid sequences. Predominant daily activity patterns established based on [2, 3].

Species	164	181	261	269	292	λ_{\max}
Primarily Nocturnal						
<i>Atractus reticulatus</i>	A	H	Y	A	A	~537
<i>Dipsas petersi</i>	A	H	Y	A	A	~537
<i>Sibynomorphus mikanii</i>	A	H	Y	A	A	~537
<i>Sibynomorphus neuwiedi</i>	A	H	Y	A	A	~537
<i>Oxyrhopus guibei</i>	A	H	Y	T	A	~553
Primarily Diurnal						
<i>Chironius bicarinatus</i>	S	H	Y	T	A	~560
<i>Echianthera cephalostriata</i>	S	H	Y	T	A	~560
<i>Echianthera undulata</i>	S	H	Y	T	A	~560
<i>Erythrolamprus aesculapii</i>	S	H	Y	T	A	~560
<i>Erythrolamprus miliaris</i>	S	H	Y	T	A	~560
<i>Erythrolamprus poecilogyrus</i>	A	H	Y	T	A	~553
<i>Helicops modestus</i>	S	H	Y	T	A	~560
<i>Philodryas patagoniensis</i>	S	H	Y	T	A	~560
<i>Spilotes pullatus</i>	S	H	Y	T	A	~560
<i>Taeniophallus persimilis</i>	S	H	Y	T	A	~560
<i>Thamnodynastes hypoconia</i>	A	H	F	T	A	~543
<i>Tomodon dorsatus</i>	A	H	F	T	A	~545

Table S6. Known amino acid spectral tuning sites of the RH1 rhodopsin gene and predicted peak absorbance (λ_{\max}) [4, 5, 6]. Sites numbered based on the bovine rhodopsin sequence. All λ_{\max} values are estimates predicted based on amino acid sequences. Predominant daily activity patterns established based on [2, 3].

Species	83	96	102	122	183	194	195	253	261	289	292	299	317	λ_{\max}
Primarily Nocturnal														
<i>Atractus reticulatus</i>	N	Y	Y	E	M	P	T	M	F	T	A	A	M	~493
<i>Dipsas petersi</i>	D	Y	Y	E	M	P	S	M	F	T	A	S	M	~500
<i>Sibynomorphus mikanii</i>	D	Y	Y	E	M	P	S	M	F	T	A	S	M	~500
<i>Sibynomorphus neuwiedi</i>	D	Y	Y	E	M	P	S	M	F	T	A	S	M	~500
<i>Oxyrhopus guibeii</i>	D	Y	Y	E	M	P	S	M	F	T	A	S	M	~500
Primarily Diurnal														
<i>Chironius bicarinatus</i>	N	Y	Y	E	M	P	T	M	F	T	S	A	M	~483
<i>Echinerteron cephalostriata</i>	N	Y	Y	E	M	P	T	M	F	T	S	A	M	~483
<i>Echinerteron undulata</i>	N	Y	Y	E	M	P	T	M	F	T	S	A	M	~483
<i>Erythrolamprus aesculapii</i>	N	Y	Y	E	M	P	T	M	F	T	S	A	M	~483
<i>Erythrolamprus miliaris</i>	N	Y	Y	E	M	P	T	M	F	T	S	A	M	~483
<i>Erythrolamprus poecilogyrus</i>	N	Y	Y	E	M	P	T	M	F	T	S	A	M	~483
<i>Helicops modestus</i>	N	Y	Y	E	M	P	T	M	F	T	S	A	M	~483
<i>Philodryas patagoniensis</i>	N	Y	Y	E	M	P	T	M	F	T	S	A	M	~483
<i>Spilotes pullatus</i>	N	Y	Y	E	M	P	T	M	F	T	S	A	M	~483
<i>Taeniophallus persimilis</i>	N	Y	Y	E	M	P	T	M	F	T	S	A	M	~483
<i>Thamnodynates hypoconia</i>	N	Y	Y	E	M	P	T	M	F	T	S	A	M	~483
<i>Tomodon dorsatus</i>	N	Y	Y	E	M	P	T	M	F	T	S	A	M	~483

Table S7. Known amino acid spectral tuning sites of the SWS1 [7] and predicted peak absorbance (λ_{\max}). Site numbered based on bovine rhodopsin. Asterisk indicates amino acids with stronger effects on spectral tuning [8, 9, 10]. All λ_{\max} values are estimates predicted based on amino acid sequences (for a review see [11]). Predominant daily activity patterns established based on [2, 3].

Species	46	49	52	86*	90	93*	97	113*	114	116	118	265	λ_{\max}
Primarily Nocturnal													
<i>Atractus reticulatus</i>	L	F	T	F	A	T	S	E	A	L	T	Y	UV
<i>Dipsas petersi</i>	L	F	T	F	A	T	S	E	A	L	T	Y	UV
<i>Sibynomorphus mikanii</i>	L	F	T	F	A	T	S	E	A	L	T	Y	UV
<i>Sibynomorphus neuwiedi</i>	L	F	T	F	A	T	S	E	A	L	T	Y	UV
<i>Oxyrhopus guibeii</i>	L	F	T	F	A	V	S	E	A	L	T	Y	UV
Primarily Diurnal													
<i>Chironius bicarinatus</i>	L	F	T	V	A	V	S	E	A	L	T	Y	?
<i>Echiantera cephalostriata</i>	L	F	T	F	A	V	S	E	A	L	T	Y	UV
<i>Echiantera undulata</i>	L	F	T	F	A	V	S	E	A	L	T	Y	UV
<i>Erythrolamprus aesculapii</i>	L	F	T	F	A	T	S	E	A	L	T	Y	UV
<i>Erythrolamprus miliaris</i>	L	F	T	F	A	T	S	E	A	L	T	Y	UV
<i>Erythrolamprus poecilogyrus</i>	L	F	T	F	A	T	S	E	A	L	T	Y	UV
<i>Helicops modestus</i>	L	F	T	F/V	A	T/V	S	E	A	L	T	Y	UV/?
<i>Philodryas patagoniensis</i>	L	F	T	F	A	T	S	E	A	L	T	Y	UV
<i>Spilotes pullatus</i>	L	F	T	F	A	V	S	E	A	L	T	Y	UV
<i>Taeniophallus persimilis</i>	L	F	T	F	A	V	S	E	A	L	T	Y	UV
<i>Thamnodynates hypoconia</i>	L	F	T	F	A	T	S	E	A	L	T	Y	UV
<i>Tomodon dorsatus</i>	L	F	T	F	A	T	S	E	A	L	T	Y	UV

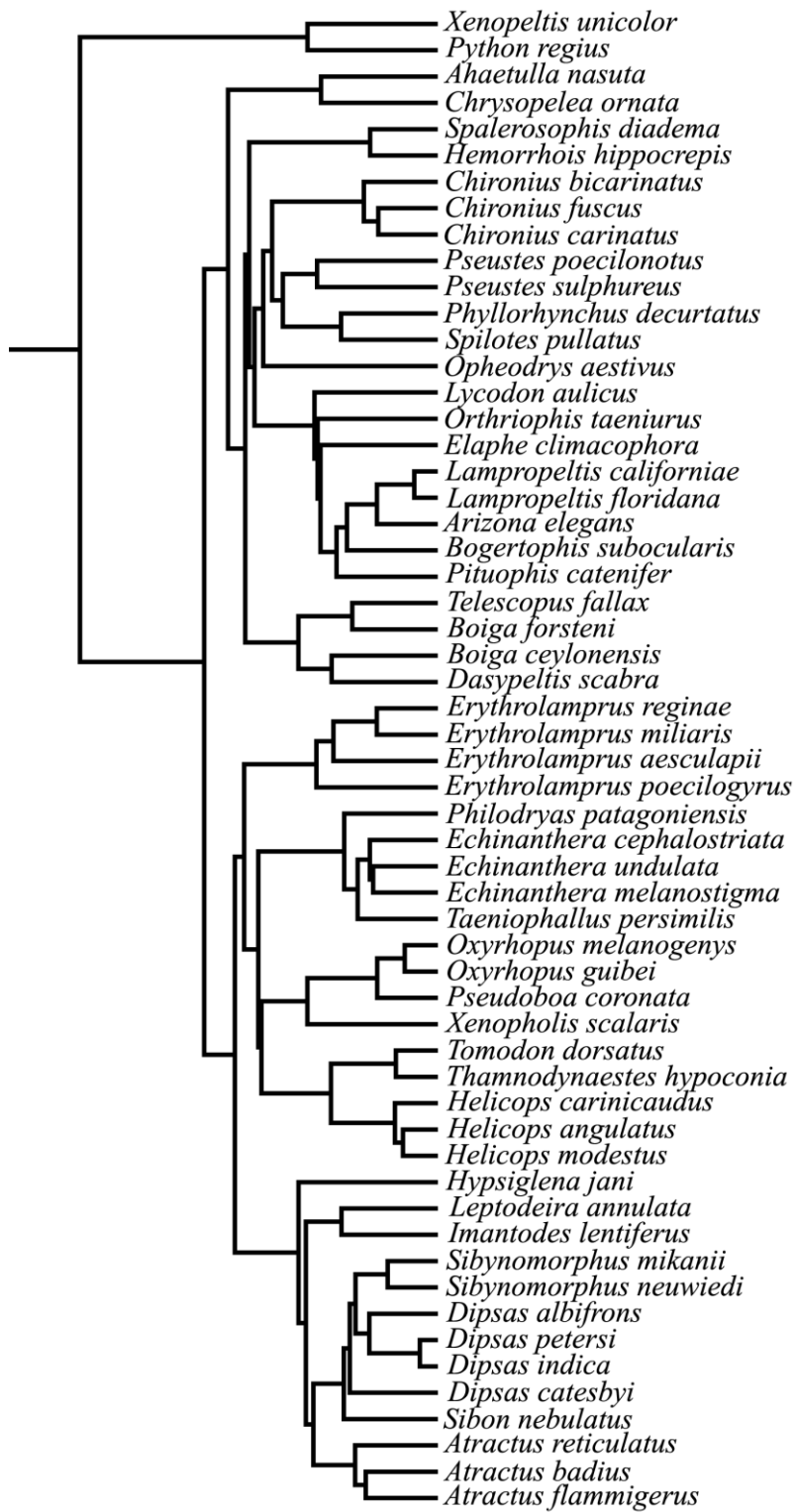


Figure S1. Species phylogenetic tree used for Codeml analysis.

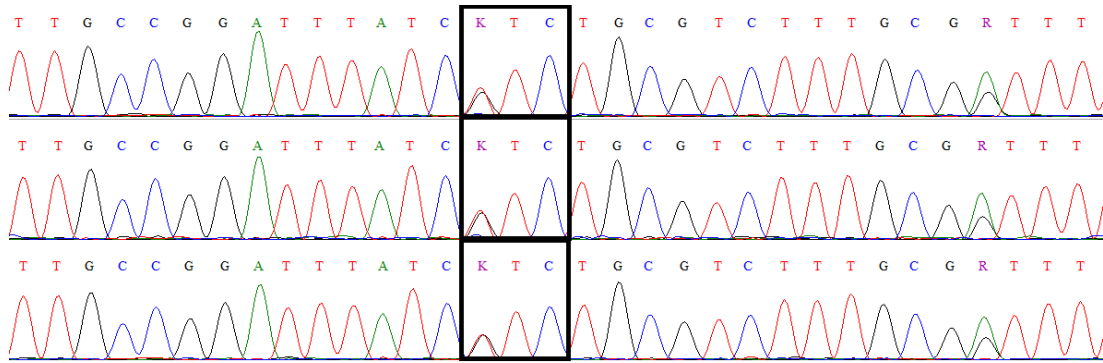


Figure S2. Chromatograms of the same region of the *SWS1* opsin gene of *Helicops modestus*, amplified with different primer pairs. The black boxes indicate the heterozygous site, with codons TTC and GTC, responsible for the transduction of the amino acids phenylalanine and valine at residue 86.

REFERENCES

1. Yokoyama S, Radlwimmer FB. The molecular genetics of red and green color vision in vertebrates. *Genetics*. 2001;158:1697–1710.
2. Torello-Viera NF, Marques OAV. Daily Activity of Neotropical Dipsadids Snakes. *S Am J Herpetol*. 2017;12(2):128-135.
3. Marques OAV, Eterovic A, Sazima I. *Serpentes da Mata Atlântica: guia ilustrado para a Serra do Mar*. Holos. 2001.
4. Hunt DM, Dulai KS, Partridge JC, Cottrill P, Bowmaker JK. The molecular basis for spectral tuning of rod visual pigments in deep-sea fish. *J Exp Biol*. 2001;204:3333–44.
5. Levenson DH, Ponganis PJ, Crognale MA, Deegan JF, Dizon A, Jacobs GH. Visual pigments of marine carnivores: pinnipeds, polar bear, and sea otter. *J Comp Physiol A*. 2006;192:833–43.
6. Yokoyama S, Tada T, Zhang H, Britt L. Elucidation of phenotypic adaptations: Molecular analyses of dim-light vision proteins in vertebrates. *P Natl Acad Sci USA*. 2008;105:13480–85.
7. Yokoyama S, Starmer WT, Takahashi Y, Tada T. Tertiary structure and spectral tuning of UV and violet pigments in vertebrates. *Gene*. 2006;365:95–103.
8. Babu KR, Dukkipati A, Birge RR, Knox BE. Regulation of phototransduction in short-wavelength cone visual pigments via the retinylidene schiff base counterion. *Biochemistry*. 2001;40:13760–66.
9. Cowing JA, Poopalasundaram S, Wilkie SE, Robinson PR, Bowmaker JK, Hunt DM. The molecular mechanism for the spectral shifts between vertebrate ultraviolet- and violet-sensitive cone visual pigments. *Biochem J*. 2002;367:129–35.
10. Fasick JI, Applebury ML, Oprian DD. Spectral tuning in the mammalian short-wavelength sensitive cone pigments. *Biochemistry*. 2002;41:6860–965.
11. Yokoyama S. Evolution of dim-light and color vision pigments. *Annu Rev Genom Hum Genetics*. 2008;9:259–82.