Supporting Information

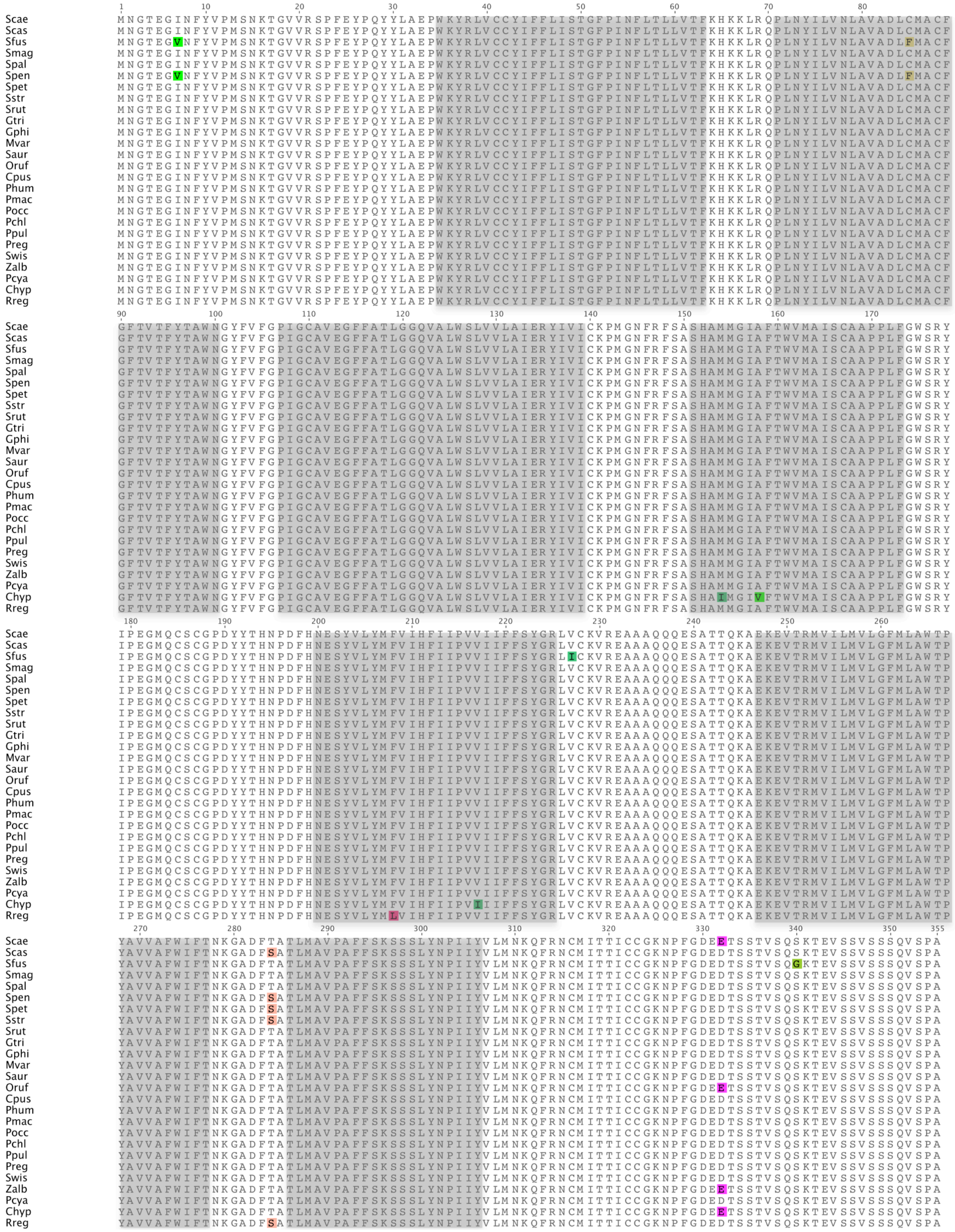
Evolutionary dynamics of Rh2 opsins in birds demonstrate an episode of accelerated evolution in the New World warblers *(Setophaga)*

Natasha I. Bloch, Trevor D. Price and Belinda S.W. Chang

TABLE OF CONTENTS

1. Supplementary figures

Figure S1: Amino acid sequence alignment of Rh2 opsins of New World and Old World warblers.



```
     1        10        20        30        40        50        60        70        80
Scae MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
Scas MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
Sfus MNGTEGVNFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLFMACF
Smag MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
Spal MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
Spen MNGTEGVNFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLFMACF
Spet MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
Sstr MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
Srut MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
Gtri MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
Gphi MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
Mvar MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
Saur MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
Oruf MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
Cpus MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
Phum MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
Pmac MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
Pocc MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
Pchl MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
Ppul MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
Preg MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
Swis MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
Zalb MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
Pcya MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
Chyp MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
Rreg MNGTEGINFYVPMSNKTGVVRSPFEYPQYYLAEPWKYRLVCCYIFFLISTGFPINFLTLLVTFKHKKLRQPLNYILVNLAVADLCMACF
     90        100       110       120       130       140       150       160       170
Scae GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Scas GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Sfus GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Smag GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Spal GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Spen GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Spet GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Sstr GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Srut GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Gtri GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Gphi GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Mvar GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Saur GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Oruf GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Cpus GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Phum GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Pmac GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Pocc GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Pchl GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Ppul GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Preg GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Swis GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Zalb GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Pcya GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
Chyp GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAIMGIVFTWVMAISCAAPPLFGWSRY
Rreg GFTVTFYTAWNGYFVFGPIGCAVEGFFATLGGQVALWSLVVLAIERYIVICKPMGNFRFSASHAMMGIAFTWVMAISCAAPPLFGWSRY
     180       190       200       210       220       230       240       250       260
Scae IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Scas IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Sfus IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLICKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Smag IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Spal IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Spen IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Spet IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Sstr IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Srut IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Gtri IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Gphi IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Mvar IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Saur IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Oruf IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Cpus IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Phum IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Pmac IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Pocc IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Pchl IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Ppul IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Preg IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Swis IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Zalb IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Pcya IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Chyp IPEGMQCSCGPDYYTHNPDFHNESYVLYMFVIHFIIPVIIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
Rreg IPEGMQCSCGPDYYTHNPDFHNESYVLYMLVIHFIIPVVIIFFSYGRLVCKVREAAAQQQESATTQKAEKEVTRMVILMVLGFMLAWTP
     270       280       290       300       310       320       330       340       350  355
Scae YAVVAFWIFTNKGADFTATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEETSSTVSQSKTEVSSVSSSQVSPA
Scas YAVVAFWIFTNKGADFSATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEDTSSTVSQSKTEVSSVSSSQVSPA
Sfus YAVVAFWIFTNKGADFTATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEDTSSTVSQGKTEVSSVSSSQVSPA
Smag YAVVAFWIFTNKGADFTATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEDTSSTVSQSKTEVSSVSSSQVSPA
Spal YAVVAFWIFTNKGADFTATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEDTSSTVSQSKTEVSSVSSSQVSPA
Spen YAVVAFWIFTNKGADFSATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEDTSSTVSQSKTEVSSVSSSQVSPA
Spet YAVVAFWIFTNKGADFSATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEDTSSTVSQSKTEVSSVSSSQVSPA
Sstr YAVVAFWIFTNKGADFSATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEDTSSTVSQSKTEVSSVSSSQVSPA
Srut YAVVAFWIFTNKGADFTATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEDTSSTVSQSKTEVSSVSSSQVSPA
Gtri YAVVAFWIFTNKGADFTATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEDTSSTVSQSKTEVSSVSSSQVSPA
Gphi YAVVAFWIFTNKGADFTATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEDTSSTVSQSKTEVSSVSSSQVSPA
Mvar YAVVAFWIFTNKGADFTATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEDTSSTVSQSKTEVSSVSSSQVSPA
Saur YAVVAFWIFTNKGADFTATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEDTSSTVSQSKTEVSSVSSSQVSPA
Oruf YAVVAFWIFTNKGADFTATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEETSSTVSQSKTEVSSVSSSQVSPA
Cpus YAVVAFWIFTNKGADFTATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEDTSSTVSQSKTEVSSVSSSQVSPA
Phum YAVVAFWIFTNKGADFTATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEDTSSTVSQSKTEVSSVSSSQVSPA
Pmac YAVVAFWIFTNKGADFTATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEDTSSTVSQSKTEVSSVSSSQVSPA
Pocc YAVVAFWIFTNKGADFTATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEDTSSTVSQSKTEVSSVSSSQVSPA
Pchl YAVVAFWIFTNKGADFTATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEDTSSTVSQSKTEVSSVSSSQVSPA
Ppul YAVVAFWIFTNKGADFTATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEDTSSTVSQSKTEVSSVSSSQVSPA
Preg YAVVAFWIFTNKGADFTATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEDTSSTVSQSKTEVSSVSSSQVSPA
Swis YAVVAFWIFTNKGADFTATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEDTSSTVSQSKTEVSSVSSSQVSPA
Zalb YAVVAFWIFTNKGADFTATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEETSSTVSQSKTEVSSVSSSQVSPA
Pcya YAVVAFWIFTNKGADFTATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEDTSSTVSQSKTEVSSVSSSQVSPA
Chyp YAVVAFWIFTNKGADFTATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEETSSTVSQSKTEVSSVSSSQVSPA
Rreg YAVVAFWIFTNKGADFSATLMAVPAFFSKSSSLYNPIIYVLMNKQFRNCMITTICCGKNPFGDEDTSSTVSQSKTEVSSVSSSQVSPA
```

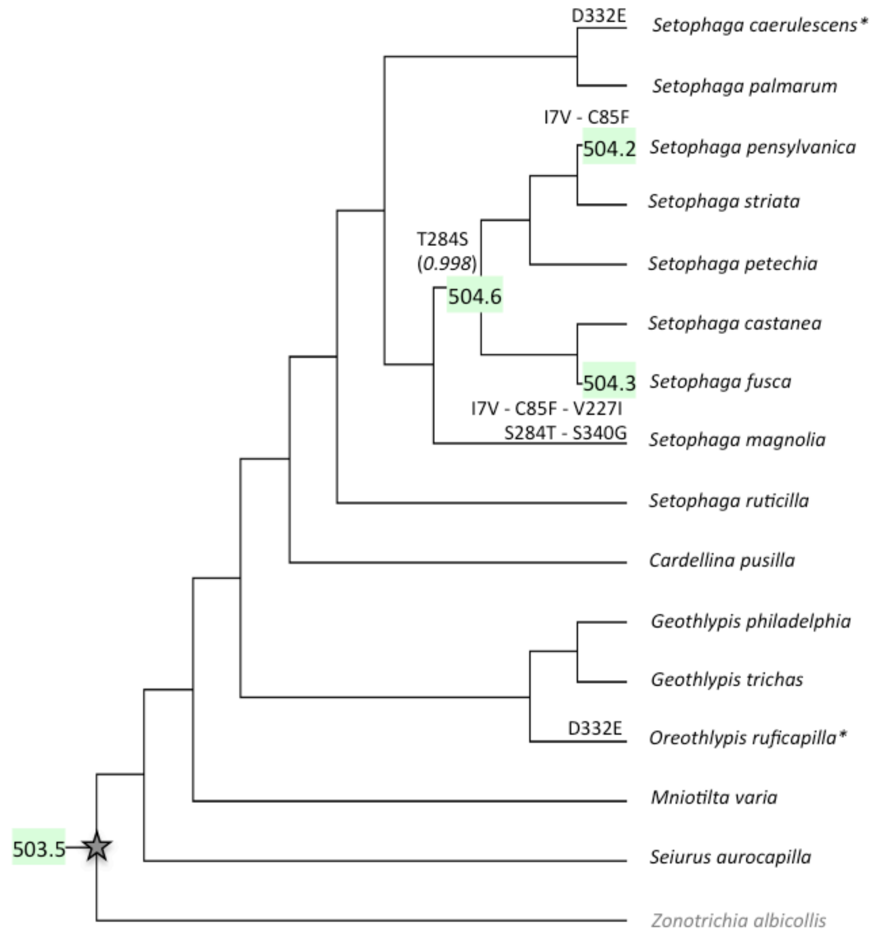
Numbering corresponds to Bovine rhodopsin (GenBank M21606). Grey boxes indicate the seven transmembrane helices (H-I through H-VII) (Palczewski et al. 2000). The variables sites across warbler clades are highlighted indicating their position relative to the transmembrane domains and colored according to amino acid identity. Species names are abbreviated as the first letter of the genus and the three first letters of the species. Full names can be found in Figs. 1 & 2.

Figure S2: Rh2 variable site summary based on consensus of all clades.

```
                                *
          111111111122222222222333333
      3558003555567901112334488033344
     79265489014859882787130849423607
New World warblers
Scae ...........................E....
Scas ........................S.......
Sfus V...F..............I..........G.
Smag ................................
Spal ................................
Spen V...F...................S.......
Spet ........................S.......
Sstr ........................S.......
Gtri ................................
Gphi ................................
Mvar ................................
Saur ................................
Srut ................................
Oruf ...........................E....
Cpus ................................

Zalb ...........................E....
Pcya ................................
Scan .....V..........S...P......E....
Tgut .........L.................E....
Gfor .....................CA.........
Falb .............................S..

Old World warblers
Phum ................................
Pmac ................................
Pocc ................................
Pchl ................................
Ppul ................................
Preg ................................
Swis ................................

Chyp ..........IV.....I.........E....
Rreg ...............L........S.......
Pshu .............................A..

Bowerbirds
Aino ---..MV....V.....I.........-----
Amac ---...V....V.....I.........-----
Cnuc ---........V.....I.........-----
Pvio ---........V.....I.........-----
Cgut ---........V.....I.........-----
Cmac ---........V.....I.........-----
Apap ---........V.....I.........-----
Acra ---...V....VV....I.........-----
Asub ---...V....V.....I.........-----
Pnew ---...V....V.....I.........-----

Mund VVLLF..VS...FMY...VI...RSSV..A.I
Ggal ..LLF.VV.T..FMY...VI........V...
CONS ILFFCVIIASMAIIFFFVIVRASKTAIDTTSV
```

Numbers correspond to amino acid positions standardized by the bovine Rhodopsin (GenBank M21606). Here complete amino acid sequences were used. The last line (CONS) corresponds to the consensus sequence. Dots indicate the identity of the amino acids with the consensus sequences at each site, thus species that only have dots match the consensus amino acid sequence at all sites. Dashes (-) indicate positions for which we do not have sequence information in bowerbirds (Sites missing in the limited sequence dataset because Bowerbird sequences from Coyle et al. (2012) cover amino acids residues 55 to 314). *Indicates the site that was inferred to be evolving under positive selection in models using the limited sequence dataset. Species names are abbreviated as the first letter of the genus and the three first letters of the species see Fig. 1 & 2 for full species names). Abbreviations of bowerbird species correspond to *Ailuroedus crassirostris, Archboldia papuensis, Amblyornis macgregoriae, Amblyornis subalaris, Amblyornis inornatus, Chlamydera nuchalis, Chlamydera maculata, Chlamydera guttata, Prionodura newtoniana, Ptilonorhynchus violaceus*.

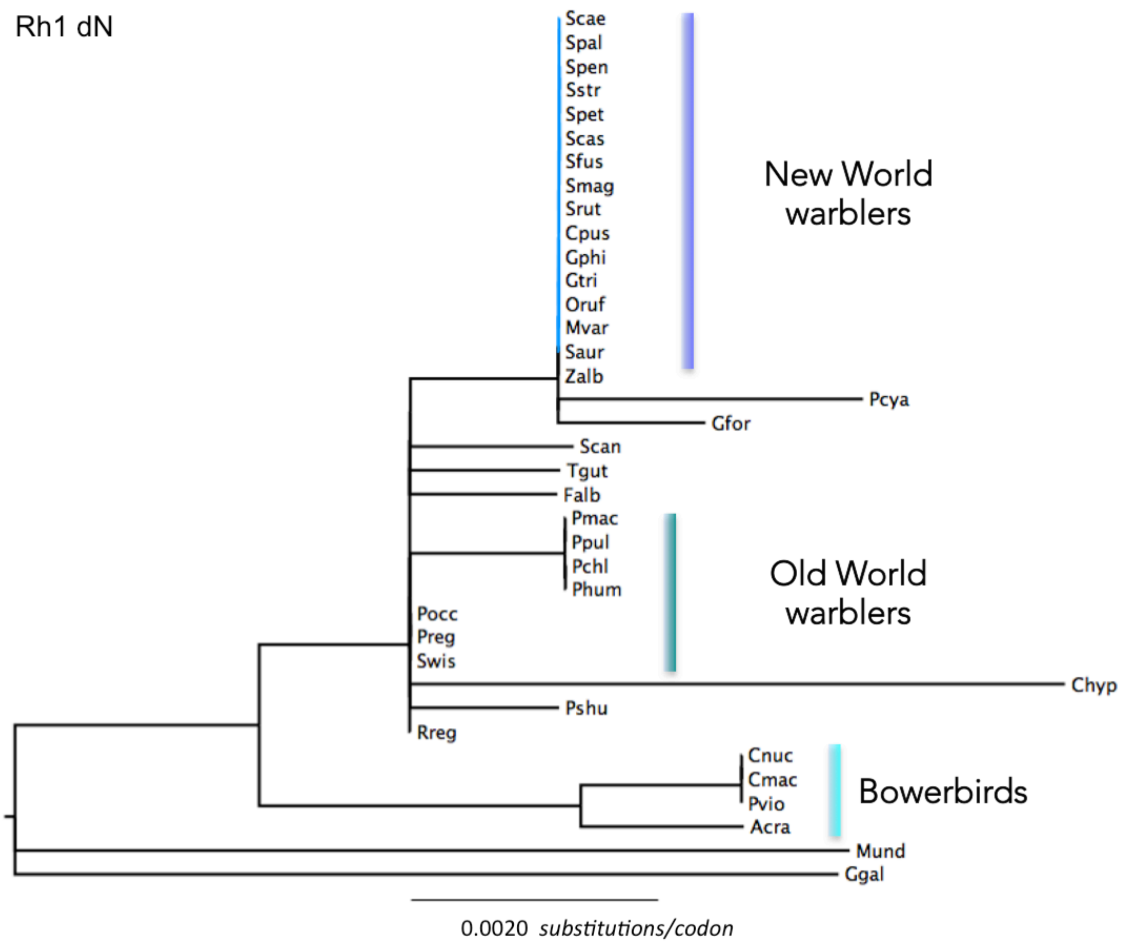
Figure S3: Cladogram of the New World warbler species tracing the accumulation of Rh2 substitutions across New World warblers.



★ 7I(*0.969*) - 85C(*0.991*) - 227V(*0.998*) - 284T(*1.00*) - 332D(*1.00*) - 340S(*0.998*)

Substitutions are shown next to the branch where they occur. The phylogeny for New World warblers and *Z. albicollis* is based on Lovette et al. (2010). Posterior probabilities for variable amino acid sites at every node from Empirical Bayes ancestral reconstructions are shown in parentheses. All ancestral reconstruction models agreed on the identity of amino acids at all nodes. We show posterior probabilities for nucleotide EB models, which were the most conservative compared to codon and amino acid models. Values in green boxes indicate the λ_{max} values of the RH2 pigment for the ancestor of New World warblers and each species or node where a substitution occurred. Unless otherwise indicated the RH2 of all species following a node have the same λ_{max}.

Figure S4: Variation in Rh1 non-synonymous rates of evolution (dN) across Passerines.



Branch lengths are scaled by d_N rates. Branch lengths were estimated using a free ratio model as implemented in PAML, that estimates independent d_N rates for each branch in the tree. Branches in blue highlight New World warblers. Scale bar indicates value of d_N as in the Rh2 trees in Fig. 4.

2. Supplementary tables

Table S1: Species with available Rh2 and Rh1 sequences used in evolutionary analyses

Order	Family	Species	Common name	Rh2 Accession #	Rh1 Accession #	Reference
Passeriformes	Estrildidae	*Taeniopygia guttata*	Zebrafinch	AF222332	AF222329	(Yokoyama *et al.* 2000)
Passeriformes	Thraupidae	*Geospiza fortis*	Medium ground-finch	XM_005428907	NA	Derived from genome by computational analysis
Passeriformes	Muscicapidae	*Ficedula albicollis*	Collared flycatcher	XM_005059479	NA	Derived from genome by computational analysis
Passeriformes	Fringillidae	*Serinus canaria*	Canary	AJ277923	AJ277926	(Das *et al.* 1999)
Passeriformes	Paridae	*Pseudopodoces humilis*	Hume's ground-tit	XM_005529357	NA	Derived from genome by computational analysis
Psittaciformes	Psittacidae	*Melopsittacus undulatus*	Budgerigar	AF021241	AJ277926	(Heath *et al.* 1997)
Galliformes	Phasianidae	*Gallus gallus*	Chicken	NM205517	NM_001030606	(Okano *et al.* 1992)
Passeriformes	Ptilonorhynchidae	*Ailuroedus crassirostris*	Green catbird	JQ034374	JQ034381	(Coyle *et al.* 2012)
Passeriformes	Ptilonorhynchidae	*Archboldia papuensis*	Archbold bowerbird	JQ034403	NA	(Coyle *et al.* 2012)
Passeriformes	Ptilonorhynchidae	*Amblyornis macgregoriae*	Macgregor bowerbird	JQ034402	NA	(Coyle *et al.* 2012)
Passeriformes	Ptilonorhynchidae	*Amblyornis subalaris*	Streaked bowerbird	JQ034400	NA	(Coyle *et al.* 2012)
Passeriformes	Ptilonorhynchidae	*Amblyornis inornatus*	Vogelkop bowerbird	JQ034401	NA	(Coyle *et al.* 2012)
Passeriformes	Ptilonorhynchidae	*Chlamydera nuchalis*	Great bowerbird	JQ034395	JQ034384	(Coyle *et al.* 2012)
Passeriformes	Ptilonorhynchidae	*Chlamydera maculata*	Spotted bowerbird	JQ034394	JQ034385	(Coyle *et al.* 2012)
Passeriformes	Ptilonorhynchidae	*Chlamydera guttata*	Western bowerbird	JQ034393	NA	(Coyle *et al.* 2012)
Passeriformes	Ptilonorhynchidae	*Chlamydera cerviniventris*	Fawn-breasted bowerbird	JQ034396	NA	(Coyle *et al.* 2012)
Passeriformes	Ptilonorhynchidae	*Prionodura newtoniana*	Golden bowerbird	JQ034399	NA	(Coyle *et al.* 2012)
Passeriformes	Ptilonorhynchidae	*Ptilonorhynchus violaceus*	Satin bowerbird	JQ034392	JQ034383	(Coyle *et al.* 2012)

Table S2: Primers used to amplify full opsin coding sequences

A		**Rh2**	
		Outer	**Nested**
Initial Degenerate Primers	for	GGG ACG GAR GGS RTC AAT TTT TA	TTT ACG TGC CTA TGT CCA ACA AGA C
	rev	ACT TGG CTG GAG GAR AYR GA	GAC CTC RGT CTT GCT CTG GGA TA
RACE primers *(used in combination with universal primers (UOP & NUP))*	5’	AAA GCA GGC CAT GCA CA	GCT TCT TGT GCT TGA AGG TG
	3’	TTC GGC TGG TCC AGG TAC	TTC GGC TGG TCC AGG TAC
Primers for coding sequences amplification	for	CAG GGC AGC ATG AAC GGG ACG G	ATG AAC GGG ACG GAG GGG AT
	rev	GCT CGG CAG GTC ACC CCA GTT C	ACC CCA GTT CAA ACT GTC CAT GC

B		**Rh1**	
		Outer	**Nested**
Initial Degenerate Primers	for	ATG AAC GGG ACM GAA GGC CAA	GAC TTC TAY GTG CCC ATG TCC AA
	rev	GAG ACC TGG CTG GTG GAR ACG GA	CTC TGT CTT GCC MGC AGA YGT GT
RACE primers *(used in combination with universal primers (UOP & NUP)*	5’	TGT ACA TGG TGG TTG TGA AGC C	TTG TGC TGG ATG GTG ACG TA
	3’	TGG TTC ACT TCA TGA TCC CGC T	TTC TGC TAT GGG AAC CTG GTC T
Primers for coding sequences amplification	for	TGG GGT GAC AGT GAA GGC TGA	CAT GAA CGG GAC AGA AGG CCA
	rev	TTT CAG CCT TGT TCC CAG GGT	CCT ATG CAG GAG AGA CCT GGC TG

Primers used for amplification of full coding sequences for A) Rh2 and B) Rh1 opsin genes.
UOP: Universal outer primer. NUP: Nested universal primer.
**These primers are the same. “for” stands for forward primer, “rev” stands for reverse primers.

Table S3: Sequences used in the construction of the time-calibrated phylogeny of species used in this study.

	SPECIES	SWS1	RAG1	Myoglobin	ODC	GAPDH	Cytb	ND2
New World warblers	*Mniotilta varia*	KM516261	KC007795.1				AF383006.1	
	Setophaga ruticilla	KM516263	KC007796.1	GU932298.1	EU325831.1		AF383008.1	AF383124.1
	Setophaga palmarum	KM516255					EU815685.1	JN568665.1
	Setophaga fusca	KM516253		GU932300.1			AY340208.1	
	Setophaga castanea	KM516252					EU815675.1	
	Setophaga striata	KM516258		GU932313.1			EU815688.1	EU815772.1
	Setophaga petechia	KM516257		GU932308.1			AF382996.1	JQ218962.1
	Setophaga pensylvanica	KM516256		GU932307.1			AY216828.1	
	Setophaga magnolia	KM516254					EU815682.1	
	Setophaga caerulescens	KM516251		GU932289.1			EU815674.1	JN568626.1
	Oreothlypis ruficapilla	KM516264		GU932348.1			GU932421.1	
	Seiurus aurocapilla	KM516262		GU932257.1			AF383007.1	AF383123.1
	Geothlypis philadelphia	KM516260					GU932399.1	
	Geothlypis trichas	KM516259					AF383003.1	AF383119.1
	Cardellina pusilla	KM516265					GU932416.1	
	Setophaga coronata		KC007793.1	GU932292.1			EU815677.1	AY030146.1
	Cardellina canadensis		KC007805.1	GU932342.1			AF383016.1	
Old World warblers	*Phylloscopus pulcher*	KM516270		KJ454867.1	KJ455871.1	KJ455124.1	KJ456396.1	KJ455565.1
	Phylloscopus maculipennis	KM516267		AY887701.1	KJ455868.1	KJ455121.1	KJ456395.1	KJ455562.1
	Phylloscopus reguloides	KM516271		AY887709.1	KJ455872.1	KJ455125.1	KJ456397.1	KJ455566.1
	Phylloscopus chloronotus	KM516269		DQ008556.1	KJ455864.1		KJ456391.1	KJ455558.1
	Phylloscopus humei	KM516266		KJ454866.1	KJ455867.1	KJ455120.1	KJ456394.1	KJ455561.1
	Phylloscopus occipitalis	KM516268		AY887703.1	KJ455870.1	KJ455123.1	AY635057.1	KJ455564.1
	Seicercus whistleri	KM516272	KJ456144	AY887726.1	KJ455876	KJ455174.1	AY635065.1	KJ455643.1

Regulus regulus	N. Bloch, *unpublished data*	JX236451.1					
Chelidorhynx hypoxantha	N. Bloch, *unpublished data*			GQ369664.1		EF081357.1	GQ145403.1
Zonotrichia albicollis	N. Bloch, *unpublished data*	XM_005480147.1	XM_005488552.1		XM_005486061.1	EF529931.1	FJ547327.1
Passerina cyanea	N. Bloch, *unpublished data*		EU191798.1			AF089047.1	AF447296.1
Serinus canaria	AJ277922.1		JN715301.1	JN715393.1	JN715213.1	AY914116.1	JN715484.1
Taeniopygia guttata	NM_001076704.1	XM_002199682.1	XM_002199380.2		NM_001198610.1	AY491525.1	AY323596.2
Geospiza fortis	XM_005430818.1	XM_005419485.1	XM_005421806.1		XM_005420667.1	AF447369.1	AF447282.1
Ficedula albicollis	XM_005061513.1	XM_005046928.1	XM_005039827.1		XM_005038447.1	DQ674491.1	DQ674464.1
Pseudopodoces humilis	XM_005533413.1	XM_005522398.1	XM_005527553.1	KF183744.1	XM_005523849.1	EU382201.1	KF183833.1
Melopsittacus undulatus	Y11787.1	XM_005150647.1	XM_005150402.1		XM_005146692.1	DQ143295.1	EU327633.1
Gallus gallus	NM_205438.1	NM_001031188.1	NM_001167752.2		NM_204305.1	L08376.1	KF792740.1

Table S4: Time calibrations used for date estimates in the phylogeny construction

CALIBRATION TAXON	SISTER TAXA IN TREE	CALIBRATION SOURCE	DATE RANGE (UPPER TO LOWER)	LOWER BOUND	CALIBRATION TYPE	ORIGINAL REFERENCES
Chlorospingus ophthalmicus	*Chlorospingus pileatus*	Biogeographic (age of Talamanca uplift)	4.5 to 0.0	NA	Uniform	(Gräfe *et al.* 2002; Weir & Schluter 2008)
Tangara dowii	*Tangara nigroviridis*	Biogeographic (formation of isthmus of Panama)	3.5 to 0.0	NA	Uniform	(Coates & Obando 1996; Burns & Naoki 2004; Weir & Schluter 2008)
Sylvia melanothorax	*Sylvia rueppelli*	Biogeographic (reformation of Cyprus)	5.3 to 0.0	NA	Uniform	(Krijgsman *et al.* 1999; Böhning Gaese *et al.* 2006; Weir & Schluter 2008)
Cyanocorax ynca	Old World crows and jays	Fossil *Miocitta galbreathi* (earliest New World jay)	80.0 to 16.3-13.6	14.95	Uniform	(Brodkorb 1972; Becker 1987)
Oreothlypis celata	*Oreothlypis ruficapilla*	Fossil *Oreothlypis celata*	80.0 to 2.0	2.0	Uniform	(Emslie 1998; Lovette & Hochachka 2006; Weir & Schluter 2008)
Psittaculirostris edwardsii	*Melopsittacus undulatus*	Fossil *Melopsittacus*	80.0 to 5.5	5.5	Uniform	(Boles 1998)
Acanthisitta chloris	All Eupasseres	Fossil *Wieslochia weissi* (Oldest Stem Eupasseres)	80.0 to 34.0-30.0	32.0	Uniform	(Mayr & Manegold 2004; 2006)
Passeriformes	Psittaciformes	Fossil *Cyrilavis* (Halcyornithidae) member of Pan-Psittaciformes (oldest stem parrot lineage)	135.0 to 51.81	51.81	Uniform	(Smith 2010; Ksepka *et al.* 2011; Ksepka & Clarke 2012)
Coraciidae	Alcedinidae	Fossil *Primobucco mcgrewi* (oldest stem Coraciidae)	135.0 to 51.81	51.81	Uniform	(Clarke *et al.* 2009; Ksepka & Clarke 2010)
Eudyptula minor	*Puffinus griseus*	Fossil *Waimanu manneringi* (oldest stem penguin)	135.0 to 61.0	61.0	Uniform	(Slack *et al.* 2006)

All time-calibration taxa are a subset of those used in (Price *et al.* 2014).

Table S5: Parameters used to choose the most appropriate models for Empirical Bayes ancestral reconstructions

GENE	TREE	MODEL	lnL	LRT	
Rh2	NEW WORLD WARBLERS	**CODON**		**F61 + Γ**	
		F1/61 + Γ	-1920.22	382.56**(60)	
		F1X4 + Γ	-1891.15	324.45**(57)	
		F3X4 + Γ	-1783.62	109.37**(51)	
		F61	**-1728.94**	NA	
		NUCLEOTIDE		**HKY85 + Γ**	**GRT + Γ**
		HKY85+G	-1889.43	NA	53.44** (4)
		JC69+G	-1946.54	114.20** (4)	
		F81+G	-1916.15	53.44 **(1)	
		K80+G	-1921.22	63.58 **(3)	
		GTR+G	**-1916.15**	-	
		AMINO ACID			
		Poisson + F + Γ	-1150.21		
		Jones + F + Γ	**-1095.48**		
		Dayhoff78 + F + Γ	-1100.69		
		MTMAM + F + Γ	-1097.83		
	PASSERINES	**CODON**		**F61 + Γ**	
		F1/61 + Γ	-3591.51	206.07**(60)	
		F1X4 + Γ	-3558.90	140.85**(57)	
		F3X4 + Γ	**-3494.61**	12.26^{NS}(51)	
		F61	-3488.48	NA	
		NUCLEOTIDE		**HKY85 + Γ**	**GRT + Γ**
		HKY85+G	-3629.34	NA	26.77**(4)
		JC69+G	-3765.51	272.34**(4)	
		F81+G	-3729.57	200.47**(1)	
		K80+G	-3670.89	83.11**(3)	
		GTR+G	**-3615.95**	-	
		AMINO ACID			
		Poisson + F + Γ	-1485.42		
		Jones + F + Γ	-1360.03		
		Dayhoff78 + F + Γ	**-1369.71**		
		MTMAM + F + Γ	-1364.34		
Rh1	PASSERINES	**CODON**		**F61 + Γ**	
		F1/61 + Γ	-3144.81	323.04**(60)	
		F1X4 + Γ	-3132.38	298.18**(57)	
		F3X4 + Γ	-3045.48	124.39**(51)	
		F61	**-2983.29**	NA	

Summary of likelihood ratio test performed to chose best Codon, Nucleotide and Amino Acid models for ancestral reconstruction and positive selection tests (codon models). LRT = 2(lnL1-lnL2) and its significance is approximated to the χ^2 distribution with degrees of freedom indicated in parentheses. ** LRT p-values <0.05. Best fitting models are highlighted in bold. (for the explanation of the notation see (Yang 2007))

Table S6: Parameter estimates for passerine Rh2 clade model D

RH2			**Purifying selection site class**		**Neutral site class**		**Divergent selection site class**					
Model: Foreground clade	**Tree length**	κ	ω_0	p_0	ω_1	p_1	ω_2 ω_3 ω_4	p_2	***ln*L**	**np**	***p-value* LRT vs M3 (k=2) (df)**	***p-value* LRT vs M3 (k=3) (df)**
CmD: Setophaga warblers	1.73	6.02	0.000	0.754	0.031	0.225	0.28 2.26	0.021	-2716.29	90	0.029 (3)	**0.009** (1)
CmD: New World warblers	1.73	6.01	0.000	0.758	0.314	0.221	**0.303** **1.265**	0.021	-2718.09	90	0.15 (3)	0.07 (1)
CmD: Old World warblers	1.72	6.00	0.000	0.804	0.529	0.014	0.051 0.000	0.182	-2716.83	90	0.048 (3)	**0.016** (1)
CmD: Bowerbirds*	1.71	5.98	0.003	0.906	0.080	0.080	0.443 0.753	0.014	-2719.63	90	0.51 (3)	0.64 (1)
CmD: Setophaga* + Old World warblers	1.74	6.01	0.000	0.747	0.029	0.231	0.354 2.170 0.000	0.022	-2714.24	91	0.011(4)	**0.004** (2)
M3 (k=3)	1.72	6.00	0.000	0.782	0.037	0.199	0.441	0.019	-2719.74	89	0.35 (2)	-
M3 (k=2)	1.70	5.98	0.004	0.951	0.213	0.049			-2720.79	87	-	-

CmD: Clade model D with *k* = 3, a model that allows for different ω between a clade set as foreground and the rest of the tree. The framework is similar to Clade model C (CmC), but CmD places no constraint on the estimates of ω for any of the site classes. In each case the clade associated with each test was set as foreground clade. ω_3 , ω_4 are the ratios for the "foreground" clades. *Based on "limited sequence dataset". Tree length is defined as the sum of the branch lengths along the tree in substitutions per codon.

κ (kappa) transition/transversion rate

p_i refers to the proportion of sites inferred to be in each selection category.

Table S7: Parameter estimates for passerines Rh1 clade models (CmC)

RH1			**PURIFYING SELECTION SITE CLASS**		**NEUTRAL SITE CLASS**		**DIVERGENT SELECTION SITE CLASS**				
Model: Foreground clade	Tree length	κ	ω_0	p_0	ω_1	p_1	ω_2 ω_3	p_2	***ln*L**	**np**	***p-value*** **LRT vs M2a_rel (df)**
CmC: Setophaga warblers	1.52	3.56	0.000	0.605	1.0	0.003	**0.032** **0.000**	0.391	-3437.96	78	**0.009** (1)
CmC: New World warblers	1.54	3.62	0.011	0.997	1.0	0.00	0.031 **0.000**	0.387	-3438.38	78	**0.014** (1)
CmC: Old World warblers	1.52	3.57	0.055	0.000	1.0	0.003	**0.115** **0.000**	0.997	-3440.29	78	0.14
CmC: Bowerbirds	1.52	3.58	0.004	0.807	1.0	0.003	**0.031** **0.151**	0.190	-3440.06	78	0.1
M2a_rel	1.52	3.57	0.000	0.600	1.0	0.003	0.263	0.396	-3441.4	77	-

CmC: Clade model C, a model that allows for different ω between a clade set as foreground and the rest of the tree. In each case the clade associated with each test was set as foreground clade. ω_3 is the ratio for the "foreground" clade. M2a_rel is the improved test for use as a null model in the LRT by (Weadick & Chang 2012a).

Tree length is defined as the sum of the branch lengths along the tree in substitutions per codon.

κ (kappa) transition/transversion rate

p_i refers to the proportion of sites inferred to be in each selection category.

Table S8: Synonymous and non-synonymous rates of evolution estimated for Rh2 and Rh1

Rh2							
Tree/species considered	model	dN Tree length	dS Tree length	κ	*l*	*np*	*ω*
Main dataset	Free ratio	0.062	3.668	4.711	-3420.87	131	Variable
Limited sequence including bowerbirds	Free ratio	0.057	4.985	5.517	-2713.76	167	Variable
Rh1							
Tree/species considered	model	dN Tree length	dS Tree length	κ	*l*	*np*	*ω*
Main dataset	Free ratio	0.039	2.390	3.584	-3454.60	143	Variable

Estimates obtained from a free-ratio model in PAML. Graphical summaries of each branch dN rates can be found in Fig. 4 & S4.

3. Supplementary references

Becker JJ (1987) *Neogene avian localities of North America*. Smithsonian Institution Press, Washington, DC.

Boles WE (1998) A budgerigar *Melopsittacus undulatus* from the Pliocene of Riversleigh, North-western Queensland. *Emu*, **98**, 32–35.

Böhning Gaese K, Caprano T, van Ewijk K, Veith M (2006) Range size: disentangling current traits and phylogenetic and biogeographic factors. *The American Naturalist*, **167**, 555–567.

Brodkorb P (1972) Neogene Fossil Jays from the Great Plains. *The Condor*, **74**, 347–349.

Burns KJ, Naoki K (2004) Molecular phylogenetics and biogeography of Neotropical tanagers in the genus *Tangara*. *Molecular Phylogenetics and Evolution*, **32**, 838–854.

Clarke JA, Ksepka DT, Smith NA, Norell MA (2009) Combined phylogenetic analysis of a new North American fossil species confirms widespread Eocene distribution for stem rollers (Aves, Coracii). *Zoological Journal of the Linnean Society*, **157**, 586–611.

Coates AG, Obando JA (1996) The geological evolution of the Central American Isthmus. In: *Evolution and Environment in Tropical America* (eds JBC J, AF B, Coates AG), pp. 21–56.

Coyle BJ, Hart NS, Carleton KL, Borgia G (2012) Limited variation in visual sensitivity among bowerbird species suggests that there is no link between spectral tuning and variation in display colouration. *Journal of Experimental Biology*, **215**, 1090–1105.

Das D, Wilkie S, Hunt D, Bowmaker JK (1999) Visual pigments and oil droplets in the retina of a passerine bird, the canary *Serinus canaria*: microspectrophotometry and opsin sequences. *Vision Research*, **39**, 2801–2815.

Emslie SD (1998) *Avian community, climate, and sea-level changes in the Plio-Pleistocene of the Florida peninsula*. American Ornithologists' Union, Washington, DC.

Gräfe K, Frisch W, Villa IM, Meschede M (2002) Geodynamic evolution of southern Costa Rica related to low-angle subduction of the Cocos Ridge: constraints from thermochronology. *Tectonophysics*, **348**, 187–204.

Heath LA, Wilkie SE, Bowmaker JK, Hunt DM (1997) The rod and green cone opsins of two avian species, the budgerigar, Melopsittacus undulatus, and the mallard duck, Anas platyrhynchus. *Gene*, **204**, 121–126.

Krijgsman W, Hilgen FJ, Raffi I, Sierro FJ, Wilson DS (1999) Chronology, causes and progression of the Messinian salinity crisis. *Nature*, **400**, 652–655.

Ksepka DT, Clarke JA (2010) *Primobucco mcgrewi* (Aves: Coracii) from the Eocene Green River Formation: new anatomical data from the earliest constrained record of stem rollers. *Journal of Vertebrate Paleontology*, **30**, 215–225.

Ksepka DT, Clarke JA (2012) A new stem parrot from the Green River Formation and the complex evolution of the grasping foot in Pan-Psittaciformes. *Journal of Vertebrate Paleontology*, **32**, 395–406.

Ksepka DT, Clarke JA, Grande L (2011) Stem parrots (Aves, Halcyornithidae) from the Green River Formation and a combined phylogeny of Pan-Psittaciformes. *Journal of Paleontology*, **85**, 835–852.

Lovette I, Hochachka W (2006) Simultaneous effects of phylogenetic niche conservatism and competition on avian community structure. *Ecology*, **87**, S14–S28.

Mayr G, Manegold A (2004) The oldest European fossil songbird from the early Oligocene of Germany. *Naturwissenschaften*, **91**, 173–177.

Mayr G, Manegold A (2006) New specimens of the earliest European passeriform bird. *Acta Palaeontologica Polonica*, **51**, 315–323.

Okano T, Kojima D, Fukada Y, Shichida Y, Yoshizawa T (1992) Primary structures of chicken cone visual pigments: vertebrate rhodopsins have evolved out of cone visual pigments. *Proceedings of the National Academy of Sciences USA*, **89**, 5932–5936.

Palczewski K, Kumasaka T, Hori T, Behnke CA (2000) Crystal structure of rhodopsin: a G protein-coupled receptor. *Science*, **289**, 739–745.

Price TD, Hooper DM, Buchanan CD *et al.* (2014) Niche filling slows the diversification of Himalayan songbirds. *Nature*, **509**, 222–225.

Slack KE, Jones CM, Ando T *et al.* (2006) Early penguin fossils, plus mitochondrial genomes, calibrate avian evolution. *Molecular Biology and Evolution*, **23**, 1144–1155.

Smith ND (2010) Phylogenetic Analysis of Pelecaniformes (Aves) Based on Osteological Data: Implications for Waterbird Phylogeny and Fossil Calibration Studies (R DeSalle, Ed,). *PLoS ONE*, **5**, e13354.

Weir JT, Schluter D (2008) Calibrating the avian molecular clock. *Molecular Ecology*, **17**, 2321–2328.

Yang Z (2007) PAML 4: Phylogenetic analysis by maximum likelihood. *Molecular Biology and Evolution*, **24**, 1586–1591.

Yokoyama S, Blow NS, Radlwimmer FB (2000) Molecular evolution of color vision of zebra finch. *Gene*, **259**, 17–24.