

# Adaptive evolution of color vision of the Comoran coelacanth (*Latimeria chalumnae*)

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**ABSTRACT** The coelacanth, a “living fossil,” lives near the coast of the Comoros archipelago in the Indian Ocean. Living at a depth of about 200 m, the Comoran coelacanth receives only a narrow range of light, at about 480 nm. To detect the entire range of “color” at this depth, the coelacanth appears to use only two closely related paralogous RH1 and RH2 visual pigments with the optimum light sensitivities ( $\lambda_{\max}$ ) at 478 nm and 485 nm, respectively. The  $\lambda_{\max}$  values are shifted about 20 nm toward blue compared with those of the corresponding orthologous pigments. Mutagenesis experiments show that each of these coadapted changes is fully explained by two amino acid replacements.

The coelacanth, *Latimeria chalumnae*, is the sole surviving species of the old lineage of crossopterygian fishes that were abundant during the Devonian period. The morphology of the coelacanth has changed very little over 400 million years (1–3). This “living fossil” lives at a depth of about 200 m near the Comoros archipelago in the western Indian Ocean (4, 5). Living at a depth of 200 m, the Comoran coelacanths receive only a narrow range of color, at about 480 nm (6). To see in this photic environment, the retina of the coelacanth consists mostly of rods, with a much smaller number of cones (7, 8). The molecular genetic basis of coelacanth vision is unknown, although one visual pigment from the Comoran coelacanth has been identified (9). Here we report the structure and function of the opsin genes of the coelacanth and elucidate how the coelacanth has modified its visual pigments to adapt to its natural habitat.

Visual pigments consist of a chromophore, 11-*cis* retinal, and a transmembrane protein, an opsin (10). Vertebrate retinal opsins (or pigments) are classified into five evolutionarily distinct groups: (i) rhodopsin (RH1), (ii) RH1-like (RH2), (iii) short wavelength-sensitive (SWS1), (iv) SWS1-like (SWS2), and (v) long wavelength-sensitive (LWS) or middle wavelength-sensitive (MWS) (LWS/MWS) opsin clusters (11–13). RH1 pigments are usually expressed in rods and the four other classes of pigments in cones. All five classes of pigments appear to have coexisted in the common ancestor of vertebrates (11–13). A central unanswered question in phototransduction is how these visual pigments achieve the wavelength of maximal absorption ( $\lambda_{\max}$ ) ranging from 360 nm (ultraviolet) to 700 nm (infrared). Recent molecular genetic analyses show that the difference in the  $\lambda_{\max}$  values of LWS/MWS pigments in mammals is primarily controlled by amino acids at five critical sites (14). Receiving a restricted range of light, the Comoran coelacanth provides an excellent opportunity to study not only the molecular basis of blue-shifted color vision but also the processes of adaptive evolution to its unique photic environment.

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## MATERIALS AND METHODS

**Genomic DNA Library Cloning and DNA Sequencing.** Genomic DNA was isolated from the Comoran coelacanth, which was obtained from the American Museum of Natural History, NY (tissue loan no. AMNH 59196). A genomic library of this coelacanth was constructed with *Bam*HI-digested  $\lambda$ EMBL3 vector and *Sau*3AI partially digested coelacanth genomic DNA (10–20 kb). By using bovine RH1 and human SWS1 cDNAs as probes, we screened about  $1.4 \times 10^6$  and  $10^7$  recombinant plaques, respectively. From the first screening, we isolated two clones,  $\lambda$ Lc16 and  $\lambda$ Lc58, which represent two distinct functional opsin genes. From the second screening, we isolated two nonoverlapping clones,  $\lambda$ Lc17 and  $\lambda$ Lc01, which represent a pseudogene. These genomic clones were subcloned into pBluescript SK(–), and the nucleotide sequences were determined for both strands by the dideoxy-chain-termination method (15).

**Creation of Minigenes and Site-Directed Mutagenesis.** The five exon regions of each of the two functional opsin genes were PCR-amplified by using five sets of oligonucleotides. For  $\lambda$ Lc16, we used 5'-CCAAGGGAATTCCACCATGAATGGAACAGAGGGTCC-3' (forward) and 5'-TTACCTCCTAGGGTAGCGAAAAATCCCTCAAT-3' (reverse) for exon 1, 5'-CCTTCCCCTAGGAGGTCAAGTTGCTCTGTGG-3' (forward) and 5'-GAGCTATCTAGACCATCCGAAAAGAGGAGGAAC-3' (reverse) for exon 2, 5'-CTGAATTCTAGATATATCCAGAGGGTATGCA-3' (forward) and 5'-ACAAAGCTGCAGCATCCTTGACAGTGCAGAC-3' (reverse) for exon 3, 5'-TTAGGCTGCAGCAGCAGCAGGAGTCTGCC-3' (forward) and 5'-TTTG-CATCCGGA~~ACTGTTT~~GTTTCAGGAGAATGTAG-3' (reverse) for exon 4, and 5'-TACAGTCCGGA~~ACTGCATGATCACCACCCTC-3'~~ (forward) and 5'-CCGAGGTCGACGCGGGTGAGACACTGCTGGA-3' (reverse) for exon 5. The underlined sequences indicate restriction enzyme site for cloning purposes. The extra 5–6 nt at the 5' end are to facilitate restriction enzyme digestion. For  $\lambda$ Lc58, we used 5'-CAAACAGAATTCACCATGAACGGCAGCGAA-3' (forward) and 5'-CTACCTCCTAGGGTGGCAAAGAAACCTCCAT-3' (reverse) for exon 1, 5'-TTCCTCCTAGGAGGTCAGGTAGCTCTCTGG-3' (forward) and 5'-ACCAA TCTAGACCAGCCAACGAGTGGCGGTGC-3' (reverse) for exon 2, 5'-CCTTTTCTAGATATATC-CCCAGGGACTGCAG-3' (forward) and 5'-AAACAACCTCGAGCCTCTTGACTTTGCAGAT-3' (reverse) for exon 3, 5'-CCAGGCTGCAGCACAAACAGCAGGAATCTGCA-3'

Abbreviations: RH1<sub>Lc</sub>, rhodopsin (or pigment) of coelacanth; RH2<sub>Lc</sub>, RH1-like opsin (or pigment) of coelacanth; SWS, short wavelength-sensitive; MWS, middle wavelength-sensitive; LWS, long wavelength-sensitive.

Data deposition: The sequences reported in this paper have been deposited in the GenBank database (accession nos. AF131253–AF131257 for *rh1*<sub>Lc</sub> and AF131258–AF131262 for *rh2*<sub>Lc</sub>).

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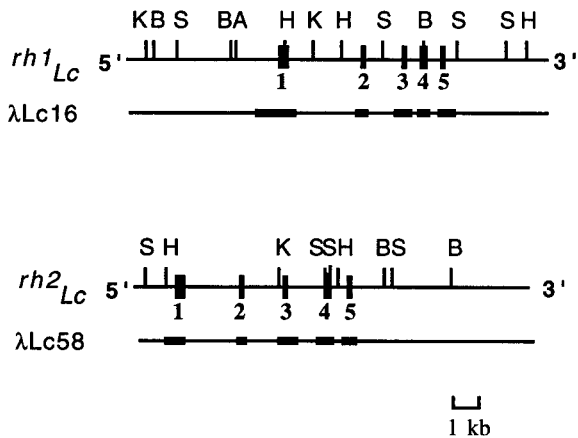


FIG. 1.  $\lambda$ clones and sequencing strategies of *rh1<sub>Lc</sub>* and *rh2<sub>Lc</sub>*. The five exons are indicated by black boxes in the restriction maps. DNA segments subcloned and sequenced are represented as thick bars in  $\lambda$  clones. A, *Sall*; B, *Bam*HI; H, *Hind*III; K, *Kpn*I; S, *Sst*I.

(forward) and 5'-AAGAGCATCCGGAAGCTTGT-TCAACAACAC-3' (reverse) for exon 4, and 5'-TCTAGT-TCCGGAAGCTTATGATCACCACGTTG-3' (forward) and 5'-GAAGTGGTCGACGCGGGCGAAACCTGACTGGA-3' (reverse) for exon 5. PCR was performed by using 30 cycles at 92°C for 45 sec, 55°C for 60 sec, and 72°C for 90 sec. At each cycle, the duration of the extension reaction was progressively extended by 3 sec. The PCR products were digested by appropriate restriction enzymes and ligated into pBluescript SK (-). Nucleotide sequences of the entire regions of the minigenes were determined. We selected clones that

encode identical amino acid sequences to those of the corresponding sequences deduced from the genomic sequences.

Mutants were generated by using QuikChange site-directed mutagenesis kit from Stratagene. All DNA fragments that were subjected to mutagenesis were sequenced to rule out spurious mutations.

**Absorption Spectra.** The two coelacanth minigenes were ligated into an expression vector pMT, expressed in cultured COS1 cells, and regenerated with 11-*cis* retinal, and the resulting visual pigments were purified as described (16, 17). UV-visible spectra were recorded at 20°C by using a Hitachi U-3000 dual beam spectrophotometer. Visual pigments were bleached for 3 min by using a 60 W standard light bulb equipped with a Kodak Wratten no. 3 filter at a distance of 20 cm. Data were analyzed with SIGMAPLOT software (Jandel, San Rafael, CA).

**Sequence Data Analyses.** The amino acid sequences of the coelacanth visual pigments were compared with those of other vertebrate pigments. The root of the phylogenetic tree of these pigments was determined by using goldfish LWS (GenBank accession no. L11867), African clawed frog LWS (U90895), chicken LWS (M62903), and human MWS (K03490-K03497) pigments as the outgroup. The number (K) of amino acid replacements per site for a pair of sequences was estimated by  $K = -\ln(1 - p)$ , where p is the proportion of different amino acids per site. Topology and branch lengths of the phylogenetic tree were evaluated by using the neighbor-joining method (18). The reliability of the neighbor-joining tree topology was evaluated by the bootstrap analysis with 1,000 replications (19).

The amino acid sequences of ancestral pigments were inferred by using likelihood-based Bayesian method (20) with a modified version of the Jones, Taylor, and Thornton (JTT; ref.

		I	
Coelacanth RH1	MNGTEGPNFYVPM SNK TGVVRNPF GYPQYYLADPWKYSALAA YMF FL ILVGFPI N FL TLFVTTIQHKKLRTP LNYILL		77
Coelacanth RH2	MNGTEGMNFYVPLSNRTGLVRS PF EY TQYYLAE PWKFSVLCAYMFL LI ILGFP IN FL TLLVTFKHKKLRQPLNYILV		77
Coelacanth $\psi$ B	M. .LRGEDFYL. FSKISSV. .GLWDGLQYHIAP I WAFY LQAVFMGF MFFVGTLLNAIVLIVTLKY NKL *QPLNYILL		72
		tga	
	II	III	IV
RH1	DLAVADLCMVFGGFFVTMYSSMNGYFVLGPTGCNIEGFFATLGGQVALWALVVLAIERYVVVCKPMSNFRFGENHAIMGVIFTWIMAL		165
RH2	NLAVASLFMVVFGFTVTFYSSLNGYFVLGPMGCAMEGFFATLGGQVALWLSLVLA IERYIVVCKPMGNFRFASSHAIMGIAFTWIMAL		165
$\psi$ B	NISLAGFIVCLF. IFTVF ISSR GYFIFGRAVCAIESFLGSM TGLITG. . . TLAFERDIVICKPFSNFCFGSKQSLLAVGATWVIGL		160
	c	a	
		V	
RH1	SCAVPPLFGWSRYIPEGMQSSCGVDYITLKPE INNESFVIYMFVVHFTIPLIVIFFCYGRVCTVKD. .AAAQQQESATTQKAKEKVT		251
RH2	ACAAPPLVGWSRYIPEGLQCSCGPDYITLNPDFHNESYVMYFLVHFLLPITTIFFTYGR LICKVKE. .AAAQQQESASTQKAKEKVT		251
$\psi$ B	GAALPPVFGWSQYIPEGLQCSCGPEWYTVNNKWNNESYVIFLFSFCFGLPLSIIIFSYTKLLM TLHT. *VAKQQEQSASAQKAEREVT		248
		a	taa
	VI	VII	
RH1	RMVIVMVISFLVCWVPYASVAGYIFFNQSEFGPVFMTAPSF FAKSASFYNPVIYFLLNKQFRNCMITTLCCGKNPFGDE DATSSAGS		339
RH2	RMVILMVIGFLTAWVPYASAAFWIFCNRGEEFATLMTVPAFFSKSSCLFNPIIYVLLNKQFRNCMITRLCCGENPLGDDDTSSAVSQ		339
$\psi$ B	KMVIVMVLGFLMCWLPYASFALWVITHRGEFFDLR MASIPSVFSKASTVYNPIIYIFM NKQ. . . . .		310
RH1	SKTEASSVSSSSVSPA		355
RH2	RKTDVSSVSSQLSPA		355
$\psi$ B	.....		

FIG. 2. The deduced amino acid sequences of coelacanth RH1 (RH1<sub>Lc</sub>), coelacanth RH2 (RH2<sub>Lc</sub>), and coelacanth  $\psi$ B ( $\psi$ B<sub>Lc</sub>). Gaps, denoted by dots, were inserted in the sequences for the optimal alignment. Deletion, insertion, and nonsense nucleotide mutations in  $\psi$ sws1<sub>Lc</sub> are noted by lower case letters. \* indicates a stop codon. Exon 5 of  $\psi$ sws1<sub>Lc</sub> is missing. Putative transmembrane domains I-VII are indicated by horizontal lines.

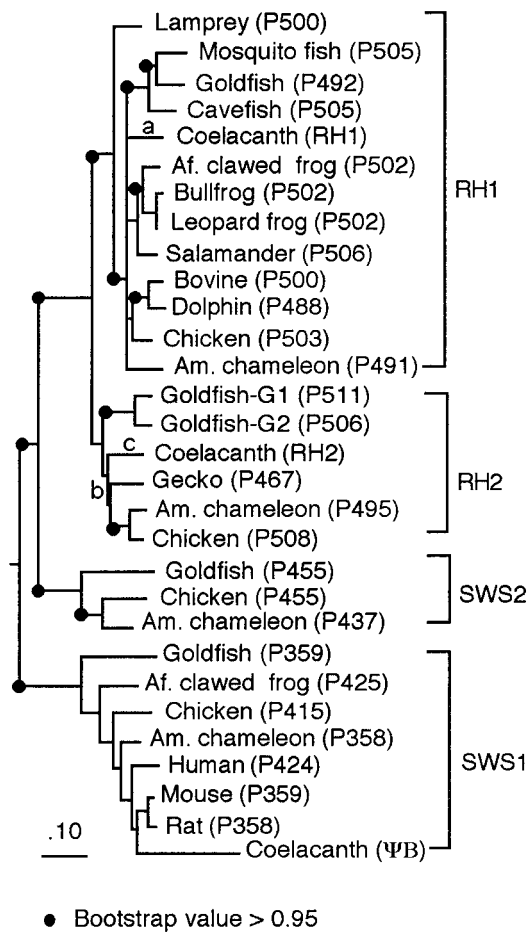


FIG. 3. Phylogenetic tree of vertebrate visual pigments whose  $\lambda_{max}$  values (given after P) have been evaluated. Opsin (or visual pigment) names and their references (accession numbers) are: lamprey, *Lamptera japonica* (M63632); mosquito fish, *Gambusia affinis* (Y11146); goldfish, *Carassius auratus* (L11863); cavefish, *Astyanax fasciatus* (U12328); African clawed frog, *Xenopus laevis* (L07770); bullfrog, *Rana catesbeiana* (S79840); leopard frog, *Rana pipiens* (S49004); salamander, *Ambystoma tigrinum* (U36574); American chameleon, *Anolis calominensis* (L31503); chicken, *Gallus gallus* (D00702); bovine, *Bos taurus* (M21606); and dolphin, *Tursiops truncatus* (AF055456) for RH1 cluster; goldfish-G1 (L11865) and -G2 (L11866); chicken (M92038); American chameleon (31); and gecko, *Gekko gekko* (M92035) for RH2 cluster; goldfish (D85863); African clawed frog (U23463); American chameleon (32); chicken (M92039); human, *Homo sapiens* (M13295); mouse, *Mus musculus* (U49720); and rat, *Rattus norvegicus* (U63972) for SWS1 cluster; and goldfish (L11864); American chameleon (32); and chicken (M92037) for SWS2 cluster.

21), Dayhoff (22), and the equal-input models (20) of amino acid replacements.

**RESULTS AND DISCUSSION**

**Coelacanth Opsin Genes.** To determine what types of opsin genes the Comoran coelacanths possess, we hybridized Southern blots containing the coelacanth genomic DNA, digested with various restriction enzymes, to bovine RH1 (23), human SWS1 (24), and human LWS (24) opsin cDNAs separately. The Southern analysis revealed strongly hybridizing bands to the first two probes, but no band to the third probe (data not shown). Thus, the coelacanth has RH1 and SWS1-like genes but no LWS/MWS genes.

After genomic DNA library screening using bovine RH1 opsin cDNA as a probe, we isolated 12 positive phage clones. Among these,  $\lambda$ Lc16 and  $\lambda$ Lc58 were found to contain the

entire coding regions of functional opsin genes, designated as  $rh1_{Lc}$  and  $rh2_{Lc}$ , respectively (Fig. 1). Similarly, by using human SWS1 opsin cDNA as a probe, we isolated 13 positive clones. Among these, 2 nonoverlapping clones,  $\lambda$ Lc17 containing exons 1 and 2 and  $\lambda$ Lc01 containing exons 3 and 4, were found to represent a pseudogene, designated as  $\psi sws1_{Lc}$ . As previously noted, the coelacanth does not have any LWS/MWS opsin genes. From an extensive screening of genomic DNA library with human SWS1 opsin cDNA as a probe, we could isolate only one SWS1 pseudogene. This strongly suggests that the coelacanth has also lost a functional SWS2 opsin gene.

The RH1<sub>Lc</sub> and RH2<sub>Lc</sub> opsins, deduced from the DNA sequences of  $rh1_{Lc}$  and  $rh2_{Lc}$ , consist of 355 aa (Fig. 2). The pseudogene  $\psi sws1_{Lc}$  contains premature stop codons because of nonsense and frameshift mutations (Fig. 2). When the coding regions of  $rh1_{Lc}$  and  $rh2_{Lc}$  are compared, the proportion of identical nucleotides is 70%. When  $rh1_{Lc}$  and  $rh2_{Lc}$  are compared with bovine  $rh1$ , the sequence similarities are given by 76% and 71%, respectively. Thus,  $rh1_{Lc}$  is more closely related to bovine  $rh1$  gene than to  $rh2_{Lc}$ , suggesting that  $rh1_{Lc}$  and  $rh2_{Lc}$  were duplicated before the vertebrate radiation.

**Evolution of Coelacanth Visual Pigments.** Fig. 3 shows the rooted phylogenetic tree of RH1<sub>Lc</sub>, RH2<sub>Lc</sub>,  $\psi B_{Lc}$ , deduced from  $\psi sws1_{Lc}$ , and RH1, RH2, SWS1, and SWS2 pigments in other vertebrates whose  $\lambda_{max}$  values have been directly determined. The bootstrap values of forming RH1, SWS1, and SWS2 clusters are 99%, 100%, and 100%, respectively, and are highly reliable, but that for RH2 cluster is only 81%. Note that RH1 cluster includes a wide range of vertebrates, from lamprey to mammals, and furthermore, the bootstrap value of forming the cluster of RH1 and RH2 groups is 100%. Thus, RH1 and RH2 clusters consist of two sets of paralogous pigments. These observations show that RH1<sub>Lc</sub>, RH2<sub>Lc</sub>, and  $\psi B_{Lc}$  belong to the RH1, RH2, and SWS1 clusters, respectively.

Within the SWS1 cluster,  $\psi B_{Lc}$  is most closely related to mammalian opsins, but this "misclassification" is probably caused by the much faster evolutionary rate of  $\psi sws1_{Lc}$ , a characteristic of pseudogenes. Fig. 3 suggests that, in the RH1 cluster, American chameleon (P491) pigment is not closely related to chicken (P503) pigment. This unexpected tree topology arises because of an accelerated rate of amino acid replacements in the former pigment in the rodless American chameleon (13). In the RH2 cluster, the American chameleon (P495) pigment is more closely related to the chicken pigment than to the gecko pigment. This may be explained not only by the accelerated evolutionary rate of the gecko pigment but also by the decelerated rate of the chicken pigment. This can be seen by making pairwise comparisons of chicken (P508), gecko (P467), and American chameleon (P495) pigments with an appropriate outgroup. For example, although they are not statistically significant, chicken (P508) pigment has shorter branch lengths than gecko (P467) and American chameleon (P495) pigments (Table 1). The branch length, 0.149, for gecko (P467) pigment is significantly longer than 0.003 for American chameleon (P495) pigment (Table 1).

It is widely accepted that tetrapods originated from lobe-finned fish, which include the coelacanth (25). According to

Table 1. The numbers of amino acid replacements per site ( $K \times 100$ ) in the RH2 cluster

Branch (pigment)			
Chicken (P508)	Gecko (P467)	American chameleon (P495)	Outgroup (pigment)
3.1 ± 0.95	—	4.9 ± 1.21	Goldfish (P511)
7.8 ± 1.52	12.2 ± 1.93	—	Goldfish (P511)
—	14.9 ± 2.15*	3.0 ± 0.93*	Chicken (P508)

\*, Significantly different at 1% level.



to us, the 5'- and 3'-flanking regions and the four intron segments of *rh1<sub>Lc</sub>* and *rh2<sub>Lc</sub>* were deleted by using recombinant DNA techniques (see *Materials And Methods*). The resulting minigenes containing only the five exon sequences were ligated into an expression vector pMT, expressed in COS1 cells, and reconstituted with 11-*cis* retinal. The RH1<sub>Lc</sub> and RH2<sub>Lc</sub> pigments constructed in this way were shown to have  $\lambda_{\max}$  values of  $485 \pm 3$  nm and  $478 \pm 1$  nm, respectively (Fig. 5). The latter  $\lambda_{\max}$  of the cone-specific pigment corresponds to the previously described pigment with a  $\lambda_{\max}$  of 473 nm (9), suggesting that the coelacanth pigment described by Dartnall (9) might have been sampled from a rare cone photoreceptor cell.

With the exception of gecko (P467) pigment, most RH1 and RH2 pigments have  $\lambda_{\max}$  values of about 500 nm (Fig. 3). Compared with them, the  $\lambda_{\max}$  values of RH1<sub>Lc</sub> and RH2<sub>Lc</sub> pigments are about 20 nm blue-shifted. The fascinating part of the two  $\lambda_{\max}$  values (478 nm and 485 nm) is that they correspond to the narrow range of light around 480 nm in the Comoran coelacanth's natural photic environment (6). Thus, the RH1<sub>Lc</sub> and RH2<sub>Lc</sub> pigments have coevolved to detect two edges of the available light spectra so that the coelacanths can distinguish the entire range of "colors" available to them. Because the coelacanth retina has both rods and cones (7, 8), the finding of a rod-specific RH1<sub>Lc</sub> pigment and at least one cone-specific pigment is expected. However, it was unexpected to find that the coelacanth uses RH2 pigment instead of SWS1 or SWS2 pigments for its blue vision. It has been demonstrated that color vision is possible with only rods and a single class of cones in cats. By using rods and blue-sensitive cones simultaneously, cats can distinguish wavelengths in the range 440–500 nm at twilight (27). Evidently, the coelacanths use rod-specific RH1<sub>Lc</sub> pigments and cone-specific RH2<sub>Lc</sub> pigments to visualize the entire, albeit limited, range of color available to them.

**Adaptive Mechanisms of RH1<sub>Lc</sub> and RH2<sub>Lc</sub> Pigments.** How did RH1<sub>Lc</sub> and RH2<sub>Lc</sub> pigments achieve the blue shifts? It is known that amino acid changes E122Q and A292S in the bovine (P500) pigment shift the  $\lambda_{\max}$  value 20 nm (28) and 10 nm (29) toward blue, respectively. Within the RH1 cluster, these two amino acid replacements E122Q and A292S occurred in the coelacanth after its divergence from other organisms (Fig. 3, branch a). Our mutagenesis analysis shows that single mutants Q122E and S292A and a double mutant Q122E/S292A of RH1<sub>Lc</sub> pigment have  $\lambda_{\max}$  values of  $495 \pm 2$  nm,  $493 \pm 1$  nm, and  $511 \pm 2$  nm, respectively (Fig. 5). Thus, E122Q and A292S together can cause a 25 nm blue-shift in the  $\lambda_{\max}$  and fully explain the observed  $\lambda_{\max}$  of RH1<sub>Lc</sub> pigment.

The blue-shifted  $\lambda_{\max}$  of RH2<sub>Lc</sub> pigment also is explained by two amino acid replacements, E122Q and M207L. Q122 is shared by the RH2 pigments of coelacanth, gecko, chicken, and American chameleon, and the E122Q replacement occurred before the divergence of coelacanth and tetrapods (Fig. 3, branch b). Figs. 3 and 4 clearly show that amino acid replacements E122Q in RH1<sub>Lc</sub> and in RH2<sub>Lc</sub> occurred independently from each other. With the exception of RH2<sub>Lc</sub> pigment, all RH1 and RH2 pigments have M207, whereas virtually all SWS1 and SWS2 pigments have L207. Thus, L207 is associated with the pigments with blue-shifted  $\lambda_{\max}$  values and M207L is suspected to cause a blue-shift in the  $\lambda_{\max}$  of RH2<sub>Lc</sub> pigment. M207L occurred in RH2<sub>Lc</sub> pigment after its divergence from the rest of RH2 pigments (Fig. 3, branch c). The inferred amino acids of the ancestral pigments support these amino acid replacements at branches b and c in Fig. 3. Mutants Q122E, L207M, and Q122E/L207M of RH2<sub>Lc</sub> pigment have  $\lambda_{\max}$  values of  $491 \pm 1$  nm,  $484 \pm 1$  nm, and  $499 \pm 1$  nm, respectively (Fig. 5). Thus, E122Q and M207L can cause a 21 nm blue-shift in the  $\lambda_{\max}$  and fully explain the adaptation of RH2<sub>Lc</sub> pigment.

As already noted, the gecko RH2 pigment has a  $\lambda_{\max}$  value of 467 nm (Fig. 3). By constructing chimeric pigments, the cause of this blue-shift in the  $\lambda_{\max}$  was previously localized somewhere between transmembrane domains I and III (30).

The present analysis strongly suggests that E122Q in transmembrane domain III (Fig. 2) is a major cause of the blue shift in the  $\lambda_{\max}$  of the gecko RH2 pigment.

## CONCLUSIONS

The molecular mechanisms of color vision in vertebrates may be elucidated in three steps: (i) cloning and characterization of the opsin genes; (ii) identification of amino acid changes that are potentially important in shifting the  $\lambda_{\max}$  of the pigments by using phylogenetic inferences; and (iii) determination of the actual effects of these mutations identified in the second step on the shifts in the  $\lambda_{\max}$  of visual pigments by using the *in vitro* assays (12–14). By so doing, we identified the potentially important amino acid replacements and tested specific hypotheses on the molecular mechanisms of adaptive evolution in the Comoran coelacanth.

The Comoran coelacanth evolved rod-rich retinas to adapt to a depth of about 200 m, where only a narrow range of colors at around 480 nm reaches from the surface. To visualize the entire range of available colors, coelacanths appear to have lost SWS1, SWS2, and LWS/MWS pigments and modified RH1<sub>Lc</sub> and RH2<sub>Lc</sub> pigments so that they can detect the two edges of the available light spectra, 478 nm and 485 nm. Our mutagenesis analyses based on this evolutionary hypothesis demonstrate that the coelacanth accomplished the coadaptations of RH1<sub>Lc</sub> and RH2<sub>Lc</sub> pigments to its unique habitat by two independent sets of amino acid replacements E122Q/A292S and E122Q/M207L, respectively.

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