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Shozo Yokoyama, Emory University
Ahmet Altun, Faith University
Huiyong Jia, Emory University
Hui Yang, Emory University
Takashi Koyama, Emory University
Davide Faggionato, Emory University
Yang Liu, Emory University
William T. Starmer, Syracuse University

Journal Title: Science Advances
Volume: Volume 1, Number 8
Publisher: American Association for the Advancement of Science: Science Advances | 2015-09-01, Pages e1500162-e1500162
Type of Work: Article | Final Publisher PDF
Publisher DOI: 10.1126/sciadv.1500162
Permanent URL: https://pid.emory.edu/ark:/25593/rg43j

Final published version: http://dx.doi.org/10.1126/sciadv.1500162

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Accessed June 16, 2018 10:19 PM EDT
Adaptive evolutionary paths from UV reception to sensing violet light by epistatic interactions

Shozo Yokoyama,1* Ahmet Altun,2 Huiyong Jia,1 Hui Yang,1 Takashi Koyama,1 Davide Faggionato,1 Yang Liu,1 William T. Starmer3

Ultraviolet (UV) reception is useful for such basic behaviors as mate choice, foraging, predator avoidance, communication, and navigation, whereas violet reception improves visual resolution and subtle contrast detection. UV and violet reception are mediated by the short wavelength–sensitive (SWS1) pigments that absorb light maximally ($\lambda_{\text{max}}$) at ~360 nm and ~395 to 440 nm, respectively. Because of strong nonadditive (epistatic) interactions among amino acid changes in the pigments, the adaptive evolutionary mechanisms of these phenotypes are not well understood. Evolution of the violet pigment of the African clawed frog (Xenopus laevis, $\lambda_{\text{max}}$ = 423 nm) from the UV pigment in the amphibian ancestor ($\lambda_{\text{max}}$ = 359 nm) can be fully explained by eight mutations in transmembrane (TM) I–III segments. We show that epistatic interactions involving the remaining TM IV–VII segments provided evolutionary potential for the frog pigment to gradually achieve its violet-light reception by tuning its color sensitivity in small steps. Mutants in these segments also impair pigments that would cause drastic spectral shifts and thus eliminate them from viable evolutionary pathways. The overall effects of epistatic interactions involving TM IV–VII segments have disappeared at the last evolutionary step and thus are not detectable by studying present-day pigments. Therefore, characterizing the genotype-phenotype relationship during each evolutionary step is the key to uncover the true nature of epistasis.

INTRODUCTION

In 1918, Ronald Aylmer Fisher introduced the notion of “dual epistacy” to explain the deviations from linearity due to interactions between different genes involved in producing quantitative characters. He concluded that because of their second-order contribution, nonadditive (epistatic) interactions only provided small changes in phenotypes, and thus, epistasis could be ignored (1). On the other hand, Sewall Wright argued that epistatic effects were common and that most complex characters are expected to have netlike relationships among genes, and thus, epistasis is of central importance to the evolutionary process (2). This difference in viewpoint remains a primary question in evolutionary biology (3).

In laboratories, epistatic interactions in microorganism systems can be controlled and analyzed using short- and long-term experimental evolution (4–9). In contrast, using vertebrate systems, it is extremely difficult to perform such experimental evolution of phenotypic adaptation. However, light-sensitive visual pigments provide a useful model system to investigate the adaptive evolutionary steps and their functional changes that have occurred over long time periods (10–13). One possible evolutionary trajectory might reveal a stepwise series of single amino acid replacements that additively accumulate changes in the capacity to detect specific wavelengths of light (14, 15); alternatively, the stepwise changes could involve one or more interactions with previous changes that produce epistatic effects (16).

By the early 1930s, it was already known that the behavior of many insects was strongly affected by their ability to detect and see ultraviolet (UV) light (17). It took about 60 additional years, but it became clear that a wide range of vertebrates also use UV reception for such basic behaviors as mate choice, foraging, predator avoidance, communication, and navigation (18–21); however, human and many other species have replaced the ancestral UV reception by violet (or blue) reception even when they receive abundant UV light in their environment (22). Newly evolved eye structures of the latter animals prevent their retinas from receiving UV light, protecting them from UV damage, whereas the more recently evolved violet reception have improved their visual resolution and subtle contrast detection (23). In the avian ancestor, UV reception was lost, but more recently, certain present-day species have switched back to UV reception, which, in turn, became critical in orienting themselves using the sun compass during migration (19, 24).

UV and violet reception are regulated by the short wavelength–sensitive (SWS1) pigments that absorb light maximally ($\lambda_{\text{max}}$) at ~360 nm and 390 to 440 nm, respectively (22). Because of strong nonadditive (epistatic) interactions among adaptive mutations within each SWS1 pigment (10, 11), the potential of new mutations for changes in color vision can be significantly modified or constrained during evolution by existing and subsequent mutations (16, 25–29). It is widely accepted that the variable $\lambda_{\text{max}}$s of SWS1 pigments are generated by mutations in the transmembrane helices (TM) I–III of SWS1 pigments (30–34), which can be divided into six segments, roughly containing TM I, II, III, IV, V, and VI–VII (Fig. 1 and fig. S1). Indeed, the evolution of the violet-sensitive pigment in the African clawed frog (frog-423, $\lambda_{\text{max}}$ = 423 nm) from its UV-sensitive ancestral amphibian pigment (AncAmphibian-359, $\lambda_{\text{max}}$ = 359 nm) can be fully explained by eight mutations in TM I–III, each with only small or no individual effect, but TM IV–VII were also suspected to have been involved during frog-423 evolution (34). Therefore, frog-423 offers a rare opportunity to test the commonly held view that only TM I–III are involved in the spectral tuning of SWS1 pigments and also to learn the true nature of epistatic interactions in evolution.

To interpret the subsequent sections, the following explanation of nomenclature with examples may be helpful (Table 1).
RESULTS

New adaptive mutations
To find the amino acid changes in TM IV–VII that have contributed to the $\lambda_{\text{max}}$ shift during frog-423 evolution, we have constructed various chimeric pigments between AncAmphibian-359 and frog-423 and introduced mutations into them. The results show that A2F has a $\lambda_{\text{max}}$ of 383 nm and series of chimeric pigments A24F, A25F, A26F, and A2456F increase the $\lambda_{\text{max}}$ of A2F by 8, 3, 7, and 21 nm, respectively; hence, TM IV–VII are also involved in the spectral tuning in frog-423 (Fig. 2). When we introduce II79M (in TM IV), L207I (TM V), and V256F and N277T (or V256F/N277T) (both in TM VI) into A2F, the mutant pigments achieve new $\lambda_{\text{max}}$ of 394, 386, and 387 nm, respectively, and the four mutations in A2F together increase the $\lambda_{\text{max}}$ to 403 nm, which is virtually identical to the $\lambda_{\text{max}}$ of A2456F (Fig. 2). Hence, the actual number of adaptive mutations that contributed to the frog-423 evolution is 12, which is distributed throughout TM I–VI (Fig. 1, black and blue circles). As described below, the six amino acid sites in black play critical roles in causing $\lambda_{\text{max}}$ shift and are distinguished from the other sites in blue. Consequently, the commonly used tenet on the spectral tuning in SWS1 pigments is rejected.

Ancestral amino acids
We inferred the 12 amino acids present at the nodes of a phylogenetic tree during the frog-423 evolution by using 14 representative pigments (fig. S2) and the maximum likelihood–based Bayesian method [phylogenetic analysis by maximum likelihood (PAML) (35) with Jones-Taylor-Thornton (JTT) and Whelan and Goldman (WAG) substitution models]. In particular, we inferred the amino acids at the 12 sites of three ancestral pigments in a composite tree of 14 representative SWS1 pigments: (i) AncAmphibian-359; (ii) the common ancestor of African clawed frog, Western clawed frog, and bullfrog pigments (AncFrog); and (iii) the common ancestor of the two clawed frog pigments (AncClawed-frog) (fig. S2). The 12 amino acids predicted using the two models have very similar PPs and are highly consistent (table S1). With the exception of site 109, the amino acids of AncAmphibian-359 have a PP of >0.95 and are highly reliable. For AncClawed-frog, all 12 amino acids have a PP of >0.90. For AncFrog, the amino acids (sites 113 to 277) in TM III–VI are

| Table 1. Abbreviations and explanation of key terms with examples. |
|-----------------|-------------------------------------------------|
| SWS1 pigment | The short wavelength-sensitive type 1 visual pigment |
| $\lambda_{\text{max}}$ | The wavelength of maximal absorption |
| $\Delta\lambda_{\text{max}}$ | The magnitude of $\lambda_{\text{max}}$ shift |
| TM | Transmembrane helix of a visual pigment |
| PP | Posterior probability of an amino acid inferred |
| SBN | Schiff base nitrogen—when it is unprotonated, a pigment is UV-sensitive; otherwise, it is violet-sensitive |
| A2F | The chimeric pigment, in which the TM II of AncAmphibian-359 was replaced by the corresponding segment of frog-423 |
| A24F | The chimeric pigment, in which the TM II and IV of AncAmphibian-359 were replaced by the corresponding segments of frog-423 |
| E113 | Amino acid glutamic acid (E) at site 113 |
| E113D | Amino acid change from glutamic acid (E) to aspartic acid (D) at site 113 |
| F1.086I0.52 | Phenylalanine (F) is replaced by isoleucine (I) at site 86, where F and I have PP of 1.0 and 0.52, respectively. |
| $\zeta_{86}$ | The $\Delta\lambda_{\text{max}}$ of AncAmphibian-359 caused by an amino acid change, F86M |
| $\zeta_{86\times93}$ | The $\Delta\lambda_{\text{max}}$ of AncAmphibian-359 caused by the epistatic interaction between F86M and T93P |
| $\theta_2$ | The $\lambda_{\text{max}}$ shift of AncAmphibian-359 caused by replacing its TM II by the corresponding segment of frog-423 |
| $\theta_{23}$ | The $\lambda_{\text{max}}$ shift of AncAmphibian-359 caused by the epistatic interaction between the TM II and III of frog-423 |

Fig. 1. Two-dimensional model of AncAmphibian-359. Twelve amino acid changes that shifted the $\lambda_{\text{max}}$ are shown in black (highly critical) and blue (less so). Seven arrowheads indicate restriction recognition sites (fig. S1). The model is after Palczewski (46).
more reliable than those (sites 49 to 93) in TM I-II. When the frog-evolution is divided into three stages, that is, from AncAmphibian to AncFrog (stage 1), from AncFrog to AncClawed-frog (stage 2), and from AncClawed-frog to frog (stage 3), most of the adaptive changes occurred in stages 1 and 2 (Fig. 3), in which the levels of reliabilities of the 12 inferred amino acids using the JTT model are also indicated using the logos.

At amino acid site 86, the JTT model of AncAmphibian predicts phenylalanine (F) with a PP of 1.0, whereas that of AncFrog can be I86 or M86 with PPs of 0.52, 0.41, and 0.05, respectively (table S1). Therefore, at this position, the most probable occurrence of F1.086I0.52 was during stage 1 of the frog-evolution, whereas the frog-evolution was completed by I0.5286M1.0 at stage 2. Alternatively, F1.086M0.41 could have occurred during stage 1 of the frog-evolution. Extending the same argument to other sites (table S1), it is likely that V0.9691I0.81 and T0.5393P1.0 occurred at stages 1 and 2, respectively. Hence, considering the entire TM II segment, V91I, and possibly F86M, preceded T93P. Similarly, the most probable amino acid replacements in TM III are V0.45109A0.99 (stage 2) (or V0.61109A0.25 in stage 1), E0.94113D0.98 (stage 2), L0.99116V0.94 (stage 1), and S0.99118T0.99 (stage 1); therefore, L116V and S118T, and possibly V109A, preceded E113D. The most probable occurrence of I0.99179M0.99 was during stage 3 in TM IV and L1.0207I0.99 at stage 1 in TM V. In TM VI–VII, N0.98277T0.99 (stage 1) occurred much earlier than V1.0256T1.0 (stage 3).

A more specific order of the six critical mutation accumulations can be predicted by considering their roles in gradual phenotypic adaptation by recapitulating evolutionary trajectories (see below).

**Amino acid replacements and TM changes**

Given 12 critical amino acid replacements, the total number of possible evolutionary trajectories is 12! (or ~500 million). Because of this prohibitive number, we investigated the possibility of using the TM segments to capture the effects of the amino acid replacements within them. When a TM change is dominated by one amino acid replacement, we consider that a chimeric pigment with the TM change effectively represents the amino acid replacements. Within TM II, F86M and T93P together increase the \( \lambda_{\text{max}} \) of AncAmphibian-359 (\( \zeta_86 + \zeta_93 + \zeta_{8693} \)) by 35 nm, but when V91I precedes one of these mutations, the \( \lambda_{\text{max}} \) only increases by 21 nm (Table 2), where \( \zeta_i \) is the \( \lambda_{\text{max}} \) shift caused by an amino acid change \( i \) (Table 1). Hence, V91I determines the effect of the TM II replacement on the upper limit of \( \lambda_{\text{max}} \) shift. Within TM III, V109A, L116V, and S118T do not shift the \( \lambda_{\text{max}} \) of AncAmphibian-359 at all (\( \zeta_{109} + \zeta_{116} + \zeta_{109116} + \zeta_{109118} + \zeta_{116118} + \zeta_{109116118} = 1 \) nm), whereas E113D in AncAmphibian-359 decreases the \( \lambda_{\text{max}} \) by 4 nm. However, when V109A, L116V, and S118T are followed by E113D, the significant effects of epistatic interactions occur between V109A and E113D (\( \lambda_{\text{max}} \) shift, or \( \Delta \lambda_{\text{max}} = 14 \) nm), and among V109A, E113D, and L116V (\( \Delta \lambda_{\text{max}} = 21 \) nm); V109A, E113D,
and S118T (Δλ_{max} = 20 nm), and V109A, E1113D, L116V and S118T (Δλ_{max} = −6 nm). The four mutations together increase the λ_{max} by 49 nm (Table 2). As described in the next section, the TM III change occurred toward the end of the frog-423 evolution; in that case, the λ_{max} shift caused by the TM III change is only 15 nm. This value is very close to the λ_{max} shift caused by E1113D near the end of the frog-423 evolution, which can be seen from the reverse experiment of D113E in frog-423 (Fig. S3). In A3F, D113 forms an H-bond with S90 rather than SBN; the space between D113 and SBN is filled with a water molecule that is stabilized by epistatic interactions among the seven mutations. Therefore, the significant epistatic interactions among V109A, L116V, and S118T in TM III and the amino acid changes in the other TMs did not occur during the frog-423 evolution. These observations suggest that F49L, V91I, E1113D, I179M, L207I, and N277T roughly correspond to TM I, II, III, IV, V, and VI–VII replacements, respectively (Fig. 1, black circles).

To establish the one-to-one relationship between TM replacement and λ_{max} shift, we constructed all 63 possible (6 single and 57 multiple) chimeric pigments, performed in vitro assays (37), and attempted to evaluate their λ_{max} values. We then found that nine (A34F, A35F, A36F, A134F, A345F, A346F, A356F, A1345F, and A1346F) pigments were nonfunctional. The other chimeric pigments have λ_{max} between 359 and 423 nm (table S2, nonfunctional pigments in bold italics). Because of its involvement in all nine nonfunctional pigments, the TM III change seems to be causing the nonfunctionalization. However, much to our surprise, the real cause is traced to the TM IV–VII changes.

**Chemical impairments**

The function of visual pigments is to convert light waves into an electrical signal. This phototransduction process depends on how the amino acid sequence interacts with 11-cis-retinal and is sensitive to the size and shape of the retinal binding pocket. In UV-sensitive pigments, Schiff base nitrogen (SBN) covalently bound to 11-cis-retinal is unprotonated, whereas its neighboring E113 is protonated (38). In AncAmphibian-359, its SBN and E113 are connected by an H-bond, making the pigment structurally stable and functional (fig. S3). In A3F, D113 forms an H-bond with S90 rather than SBN; the space between D113 and SBN is filled with a water molecule that is stabilized by two H-bonds with SBN and D113 (Fig. 4A). A34F becomes nonfunctional because the M179 side chain cleaves the C110–C118 disulfide bond and places D113 near the protein surface (Fig. 4B). A35F and A36F become nonfunctional because they cannot achieve the distances larger than 2.2 Å between 11-cis-retinal and Y265 (A35F, Fig. 4C) or W191 (A36F, Fig. 4D).

**Evolutionary trajectories**

The pattern of mutation accumulation, epistatic interactions among mutations, and premature termination of evolutionary trajectories with drastic λ_{max} shifts all point to one thing: frog-423 gradually achieved its λ_{max}. To recapitulate the processes of frog-423 evolution, we constructed all 6! (or 720) possible evolutionary trajectories from AncAmphibian-359 to frog-423. The results show that 244 trajectories are prematurely terminated because of the nine nonfunctional pigments (fig. S4A) and the A1F, A2F, A3F, A4F, A5F, or A6F pigments generate 92, 120, 38, 70, 78, and 78 evolutionarily acceptable trajectories, respectively (fig. S4B). To extract biological significance of these data, it is useful to consider the orthologous pigment in humans (human-414, λ_{max} = 414 nm), which also attained its violet sensitivity by multiple adaptive mutations (F46T, F49L, T52F, F86L, T93P, A114G, and S118T) in TM I–III (16). Human-414 gradually achieved its current λ_{max} (Δλ_{max} < 25 nm) at every evolutionary step almost exclusively by epistatic interactions among the seven mutations.

By recapitulating the evolutionarily acceptable trajectories from AncAmphibian-359 to frog-423, we can see that the magnitudes of λ_{max} shifts caused by specific TM replacements significantly vary depending on which TM replacement(s) they follow (table S3). For example, the most prominent individual effects on the λ_{max} shift come from TM II change (Δλ_{max} = 24 nm) and III change (Δλ_{max} = 51 nm). However, if the TM II change occurs in A456F, then the Δλ_{max} increases to 44 nm. On the other hand, as we saw earlier, if the TM III change occurs at the last evolutionary step, the Δλ_{max} is only 15 nm. Moreover, TM I, IV, V, and VI changes cause no λ_{max} shift individually, but when TM I change occurs in A245F, it causes a [Δλ_{max}] of 11 nm, whereas when TM IV, V, and VI changes occur in A1356F, A136F, and A135F, respectively, they cause a [Δλ_{max}] of 16 to 22 nm.

These evolutionary trajectories can be classified into two groups depending on whether or not the evolutionary paths that contain at least one Δλ_{max} burst during evolution. All evolutionary trajectories
started with A1F, A3F, A4F, A5F, and A6F have a burst of the $\Delta \lambda_{\text{max}} > 25$ nm (shown in red paths, fig. S4B), whereas 54 of 120 evolutionarily acceptable trajectories started with A2F are characterized by $\Delta \lambda_{\text{max}} < 25$ nm at every evolutionary step (black paths, fig. S4B). Moreover, 25 of these 54 trajectories are characterized by the more restricted condition of $\Delta \lambda_{\text{max}} < 20$ nm at every mutational step after TM II replacement and are closely clustered along the diagonal paths (black paths, Fig. 5).

These 25 trajectories are best represented by A251643F that is consistent with the results based on PAML using the JTT and WAG models. That is, the amino acid changes in the ancestral pigments suggest that TM I, II, V, and VI changes and TM III and IV changes occurred in stages 1 and 2 of frog-423 evolution, respectively (Fig. 3).

At stage 1, the TM II change has the smallest $\Delta \lambda_{\text{max}}$ shift; after that, the two evolutionary sequences could have increased the $\Delta \lambda_{\text{max}}$ equally smoothly: 1) TM V change ($\Delta \lambda_{\text{max}} = 3$ nm) followed by TM I change ($\Delta \lambda_{\text{max}} = 6$ nm) and TM VI change ($\Delta \lambda_{\text{max}} = 5$ nm), in that order, or 2 TM I change ($\Delta \lambda_{\text{max}} = 6$ nm) followed by TM V change ($\Delta \lambda_{\text{max}} = 3$ nm) and TM VI change ($\Delta \lambda_{\text{max}} = 5$ nm), in that order (table S3). Because the TM V change will stop the early establishment of the TM III change with a burst of $\Delta \lambda_{\text{max}}$ shift, A2516F is the most likely sequence among the 25 trajectories. At stage 2, the evolutionary sequence of the TM IV change ($\Delta \lambda_{\text{max}} = 11$ nm) followed by the TM III change ($\Delta \lambda_{\text{max}} = 15$ nm) is more gradual than that of the TM III change ($\Delta \lambda_{\text{max}} = 24$ nm) followed by the TM IV change ($\Delta \lambda_{\text{max}} = 2$ nm) (table S3). Hence, A251643F has one of the smoothest $\Delta \lambda_{\text{max}}$ shifts (Fig. 5, black path with open circles; table S3, bold italics). In turn, this implies that the amino acid replacements V91I, L207I, F49L, N277T, I179M, and E113D occurred in that order (Fig. 3).

**Epistatic interactions**

To determine the individual effects and the effects of all combinations of 12 amino acid replacements on the $\lambda_{\text{max}}$ shift, we traced A251643F as a representative trajectory of frog-423 evolution. Solving linear equations of the $\lambda_{\text{max}}$s of the 63 chimeric pigments, in which the highest level of $\lambda_{\text{max}}$ shifts caused by the nonfunctional pigments is zero (16), we evaluated six individual $\Delta \lambda_{\text{max}}$s ($\theta_i$, $i = 1, 2, \ldots, 6$) and 57 other $\theta$s with multiple interactions. These $\theta$s and the corresponding pure epistatic interactions among TM I–VII (16) without any individual amino acid effects are very similar (table S2). The $\lambda_{\text{max}}$ shifts can be explained by the individual and pure epistatic interactions among TM I–VII.
Fig. 4. The tertiary structures of SWS1 pigments. (A) A3F. (B) A34F. (C) A35F. (D) A36F. Black, blue, red, and white molecules represent carbon, nitrogen, oxygen, and hydrogen atoms, respectively.
Epistasis (TM I–VII)

seen that the violet sensitivity of frog-423 evolved by 12 mutations that
A251643F. That is, the
which, in turn, requires the trajectory A251643F to achieve a prohib-
A25164F are underestimated by 0, 6, 6, 11, and 22 nm, respectively,
ary pathway.

To date, all mutations that have caused the variable $\lambda_{\text{max}}$ of SWS1 pig-
ments have been localized in the TM I–III (30–34). However, we have
seen that the violet sensitivity of frog-423 evolved by 12 mutations that
are distributed in TM I–VI. The evolution of frog-423 is characterized
by the gradual $\lambda_{\text{max}}$ shift caused by strong epistatic interactions among
these mutations. In particular, the epistatic interactions of the amino
acids in TM IV–VII with the other adaptive mutations in TM I–III
prematurely terminated evolutionary trajectories whenever ancestral
pigments could have caused extreme shifts in $\lambda_{\text{max}}$. In human-414,
T52F in TM I played a similar function; if T52F occurred first or in
the early evolutionary stages of human-414, then these mutants became
structurally unstable (16). The latter cases effectively required a future
evolutionary step to incorporate a prohibitive burst of $\Delta\lambda_{\text{max}} > 25$ nm.

The origin of visual pigments may go back to well before 800 million
years ago (39), and the vertebrate ancestor already had five different
types of visual pigments (12, 40, 41). During this long history, most
vertebrates have retained E113 in their visual pigments. The clawed
frogs are unique among them, having incorporated E113D into their
SWS1 pigments (Fig. 3). E113 is structurally critical, serving as the
SBN counterion and regulating the $\lambda_{\text{max}}$ of visual pigments (42–46).
However, in laboratories, visual pigments with mutations such as
E113D, E113N, E113Q, and E113A were found to be functional (45),
suggesting that various mutations occurred at position 113 of visual
pigments in the past. The evolutionary novelty of the clawed frog SWS1
pigments probably took place because E113D occurred at the right time
and in the right molecular environment. Our results suggest that this
mutation occurred toward the end of frog-423 evolution. This timing
and the specific epistatic interactions with other mutations V109A, L116V,
and S118T were the key factors in determining the specific magnitude
of $\lambda_{\text{max}}$ shift needed for the clawed frogs to adapt to their specific
ecological environment.

Current mutagenesis results suggest that violet pigments of scab-
bardfish (Lepidopus fitchi), bovine (Bos taurus), wallaby (Macropus
eugenii), and elephant (Loxodonta africana) largely evolved by the
deletion of F86 (47), F86Y (32), F86Y (11), and F86S (48), respectively,
and that the reversion of a recent ancestral avian pigment largely oc-
curred by S90C (49, 50). These mutations seem to have caused $\lambda_{\text{max}}$
shifts of 35 to 70 nm in one evolutionary step. However, the [$\Delta\lambda_{\text{max}}$
values caused by S90C in various pigments vary between 0 and 45 nm
(10, 11). Moreover, the F86 deletion in the SWS1 pigment of the ver-
tebrate ancestor only increases the $\lambda_{\text{max}}$ by 19 nm, which is still 43 nm
smaller than the $\lambda_{\text{max}}$ of the scabbardfish pigment. These observations
imply that additional critical mutations are involved and epistatic in-
teractions are operating in most of the SWS1 pigments as well. Know-
ing that identical mutations can have markedly different effects on the
$\lambda_{\text{max}}$ shift during evolution (for example, TM II and TM III changes,
table S3), in future studies, it would not be surprising to find that
seemingly large changes in $\lambda_{\text{max}}$ in a single evolutionary step are ac-
tually the accumulation of gradual changes.

As noted in the beginning, it is difficult to perform experimental
evolution of phenotypic adaptation for vertebrates. However, as exem-
plified by our evolutionary analyses of frog-423, we can obtain similar
information by (i) engineering and manipulating the phenotypes of
ancestral molecules (14, 22, 29, 51), (ii) examining the adaptive signif-
icance by comparing the phenotypic changes to their new molecular
and ecological environments (22, 29), (iii) determining the order of adapt-
ive mutations by locating them in various branches in a phylogenet-
tree (40, 52, 53), and (iv) experimentally recapitulating all possible evolu-
tionary trajectories (16). Chemical structural analyses added a new
dimension to our understanding of hidden epistatic interactions, which
show that structurally stable protein structures lay the foundation for
the evolutionary potential of adaptive mutations. Manipulating ancestral molecules alleviates the potentially confusing mutagenesis results caused by analyzing present-day molecules with variable molecular environments (10, 11). Establishing the one-to-one relationship between an SWS1 pigment and UV/violet reception by manipulating ancestral molecules and their phenotypes is a significant development in that direction.

MATERIALS AND METHODS

Phylogenetic analyses
To study the order of amino acid replacements in the frog-423 lineage, we considered the composite tree of SWS1 pigments sampled from 14 species: the lamprey (Geotria australis, GenBank accession no. AY366495), medaka (Oryzias latipes, AB223058), African clawed frog (Xenopus laevis, U23463), Western clawed frog (Xenopus tropicalis, NM_001126076), bullfrog (Rana catesbeiana, AB001983), salamander (Ambystoma tigrinum, AF038948), chameleon (Anolis carolinensis, AF134192), gcko (Gekko gecko, AY024356), sunbeam (Xenopeltis unicolor, FJ497234), chicken (Gallus gallus, M92039), zebra finch (Taeniopygia guttata, AF222331), human (Homo sapiens, M13295), mouse (Mus musculus, U49720), and wallaby (M. eugenii, YA86017). The divergence times at all nodes of the evolutionary tree have been obtained from the TimeTree of Life web server (www.timetree.org). The ancestral amino acids at all nodes of the composite phylogenetic tree (fig. S2) have been inferred using PAML (35) with JTT and WAG models.

Mutagenesis
AncAmphibian-359 and frog-423 were previously constructed, so their opsins complementary DNAs were inserted into the Eco RI and Sal I restriction sites of the expression vector pMT5 (22, 34). In these pigments, the N and C termini have been replaced by those of the ancestral amino acids at all nodes of the composite phylogenetic tree (fig. S2) have been inferred using PAML (35) with JTT and WAG models.

Measure epistasis
To evaluate all 63 θ values associated with the chimeric pigments, it becomes necessary to infer the λmax values of the nine structurally unstable mutant pigments. Take AncAmphibian-359 with two TM replacements (A34F) as an example. Because A34F is nonfunctional, the TM III and IV of frog-423 together “cannot” shift the λmax of AncAmphibian-359 and 359 = 0 nm. Using θ1 = 51 nm and θ2 = 1 nm, λ34 = λ + θ1 + θ2 + θ34 = 359 +51 + 1 + 0 = 411 nm; similarly, for A134F, λ134 = λ + θ1 + θ4 + θ134 + θ134 + θ34 + 0 + 0 = 418 nm, where λ is the λmax of AncAmphibian-359 (table S2). Hence, either when a new TM change prevents the formation of a structurally stable pigment or when it actually does not shift the λmax, the highest level of the synergistic effect is zero. In this way, we evaluated the λmax values of all 9 unstable and 54 stable pigments, and 63 θ values were determined using 63 simultaneous linear equations (table S2, unstable in bold italics).

The estimation of effects and interactions of amino acid changes (ΔS) and TM changes (ΔS) on the λmax values were conducted using matrix algebra and linear statistical models (54). The rows of the coefficient matrix C represent the sequences, and the columns represent the effects and interaction to be estimated. The coefficients in the first column of C contain 1s indicating that the ancestral sequence is included in all derived sequences. The elements of the remaining columns have the coefficients (0 or 1) for the individual effects and interactions present in the sequence designated by the row.

The parameters are designated in the column vector X, whereas column vector Y contains the observed λmax values corresponding to the pigments. The simultaneous equations for the observed λmax values are expressed in matrix algebra as:

$$Y = CX,$$

and the estimates of the effects and interactions are obtained by solving the equation for X, that is:

$$X = (C^T C)^{-1}(C^T Y).$$

Because the estimates are linear functions of the observed λmax values, the variance of each estimate is a function of the variances of the λmax values and the coefficient associated with each parameter. For this analysis, the variances for λmax are assumed to be 1 and the covariance 0. Given the variance-covariance matrix for Y is V, the SEs of the estimates are on the diagonal of Se:

$$Se = [(C^T V^{-1} C)^{-1}]^{1/2}.$$

Structural analysis
The structures of AncAmphibian S1 and chimeric pigments were obtained by (i) applying homology modeling (Modeller 9v7, www.salilab.org/modeller) to bovine rhodopsin (Protein Data Bank code: 1U19); (ii) adding the missing hydrogen atoms, water molecules, and 11-cis-retinal; and (iii) optimizing them first at pure AMBER96 force field level (http://ambermd.org) and then using hybrid quantum mechanical/molecular mechanical (QM/MM) calculations in the ONIOM (our own n-layered integrated molecular orbital and molecular mechanics) electronic embedding scheme (QM = B3LYP/6–31G**, MM = AMBER). It is known that SBV covalently bound to 11-cis-retinal is unprotonated.
whereas its neighboring E113/D113 is protonated in UV-sensitive pigments. The QM portion of the calculations includes 11-cis-retinal with the covalently bound SBN and a hydrogen link atom that saturates the bond cut at the QM and MM boundary.

SUPPLEMENTARY MATERIALS

Supplementary material for this article is available at http://advances.sciencemag.org/cgi/content/full/1/8/e1500162/DC1

REFERENCES AND NOTES

Acknowledgments: We thank R. Yokoyama, J. Belote, H. Y. Yan, and anonymous reviewers for their comments and R. K. Crouch (Storm Eye Institute, Medical University of South Carolina) and the National Eye Institute for supplying 11-cis-retinal. Funding: This research was supported by NIH (EY016400 to S.Y.) and Emory University (S.Y.). Author contributions: S.Y. designed the study. S.Y. and W.T.S. performed data analyses, and H.J., H.Y., T.K., D.F., and Y.L. constructed chimeric pigments and performed mutagenesis experiments. A.A. performed the QM/MM-based molecular analyses. S.Y., A.A., and W.T.S. wrote the manuscript, with contributions from the other authors. Competing interests: The authors declare that they have no competing interests. Data and materials availability: The authors confirm that all data underlying the findings and materials are fully available without restriction.
Adaptive evolutionary paths from UV reception to sensing violet light by epistatic interactions
Shozo Yokoyama, Ahmet Altun, Huiyong Jia, Hui Yang, Takashi Koyama, Davide Faggionato, Yang Liu and William T. Starmer
(September 18, 2015)
Sci Adv 2015, 1:
doi: 10.1126/sciadv.1500162

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