Functional Comparison of Rod and Cone G α **^t on the Regulation of Light Sensitivity***

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Background: A similar phototransduction cascade confers different light sensitivity in rods and cones. **Results:** Rod and cone Ga_t are similar with respect to coupling to visual pigments and light-induced translocation. **Conclusion:** Rod and cone Ga_t are equivalent functionally.

Significance: Reduced sensitivity in cones does not result from reduced coupling efficiency between the GPCR and G protein or a lower concentration of G protein in cones.

The signaling cascades mediated by G protein-coupled receptors (GPCRs) exhibit a wide spectrum of spatial and temporal response properties to fulfill diverse physiological demands. However, the mechanisms that shape the signaling response of the GPCR are not well understood. In this study, we replaced cone transducin α (cT α) for rod transducin α (rT α) in rod pho**toreceptors of transgenic mice, which also express S opsin, to** evaluate the role of $G\alpha$ subtype on signal amplification from **different GPCRs in the same cell; such analysis may explain functional differences between retinal rod and cone photore**ceptors. We showed that ectopically expressed $cT\alpha$ 1) forms a heterotrimeric complex with rod $G\beta_1\gamma_1$, 2) substitutes equally for $rT\alpha$ in generating photoresponses initiated by either rho**dopsin or S-cone opsin, and 3) exhibited similar light-activated translocation as endogenous rT** α **in rods and endogenous cT** α in cones. Thus, $rT\alpha$ and $cT\alpha$ appear functionally interchange**able. Interestingly, light sensitivity appeared to correlate with the concentration of cT when expression is reduced below 35% of normal. However, quantification of endogenous cT concen**tration in cones showed a higher level to $rT\alpha$ in rods. Thus, **reduced sensitivity in cones cannot be explained by reduced coupling efficiency between the GPCR and G protein or a lower concentration of G protein in cones** *versus* **rods.**

Two photoreceptor cell types, rods and cones, and the retinal circuitry that carries their signals to higher visual centers collectively allow our vision to report luminance information over the course of night and day. Rods are exquisitely sensitive and can detect single photons $(1, 2)$, whereas cones are \sim 100-fold less sensitive and do not saturate under bright light (3, 4). Furthermore, the kinetics of the photoresponse in cones is 5-fold faster than rods, allowing increased temporal resolution (5).

These two types of photoreceptors utilize a similar G protein signaling cascade for phototransduction, but the differences in the cascades that produce these functional distinctions are just beginning to be understood. Some components of the cascades are identical in both cell types, whereas others, including the visual pigments and G proteins, have distinct rod and cone isoforms. Thus, functional differences between rods and cones may arise from 1) different levels of expression of transduction components or 2) different functional properties of their respective transduction proteins. For example, a higher expression level of rhodopsin kinase (6, 7), or RGS9-1 (8), has been proposed to allow for faster recovery of the photoresponse in cones. Higher guanylyl cyclase activity and a faster cGMP turnover in cones may also contribute to speeded responses in cones compared with rods (9). Differences in rod/cone sensitivity likely arise from multiple mechanisms, and a full understanding of what sets the differences requires approaches to quantify the contribution of individual phototransduction components.

Previous biochemical (7, 10) and physiological (11–13) evidence suggest that a lower amplification gain in cones may be a primary contributor to lower sensitivity. To test whether this alteration arises from cell-type specific transducin α (T α),² we expressed mouse $cT\alpha$ (GNAT2) in rT α (GNAT1) knock-out mice. By crossing these mice with those whose rods also express the S-cone pigment (14), we also compared the coupling efficiencies between rod and cone visual pigments with $cT\alpha$ and evaluated the influence of $T\alpha$ concentration on visual sensitivity. We obtained two lines of mice that expressed $cT\alpha$ at 15 and 35% of endogenous rT α in rods. Suction electrode recordings showed that these rods were less sensitive to light. However, the decreased sensitivity correlated with the reduced Ta concentration. Normalized photoresponses from $cT\alpha$ rods displayed similar rising and recovery phases. Because lowered $T\alpha$ concentration leads to lowered sensitivity, we investigated whether endogenous cones express a lower concentration of $cT\alpha$. To the contrary, we found that the $cT\alpha$ concentration in cones is higher than rT α concentration in rods. We also provide evi-

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² The abbreviations used are: T α , transducin α ; GPCR, G protein-coupled receptor; rT α , rod transducin α ; cT α , cone transducin α ; GAP, GTPase accelerating protein; RGS, regulator of G protein signaling; ROS, rod outer segment; FWHM, full width half maximum.

dence that $rT\alpha$ and $cT\alpha$ are indistinguishable biochemically, as evidenced by their similar activation by both rod and S-cone pigments. Lastly, we observed that endogenous $cT\alpha$ in cones translocated away from the outer segment in response to light, a property that was recapitulated by ectopically expressed $cT\alpha$ in rods.

EXPERIMENTAL PROCEDURES

All experimental procedures involving the use of mice were performed in compliance with regulations set forth by the ARVO Statement for the Use of Animals in Ophthalmic and Visual Research, with protocols approved by the University of Southern California's Institutional Animal Care and Use Committee.

Generation of cTα Transgenic Mice—The pBKS-cTα transgenic construct contained the \sim 1.3-kb mouse cone transducin α subunit cDNA flanked by the 4.4-kb fragment of mouse rod opsin promoter (15) at the 5' end and a 0.6-kb polyadenylation signal from the mouse protamine gene at the 3' end that also provided a splice site (see Fig. 1A). The 1.3-kb $cT\alpha$ cDNA coding sequence was synthesized by reverse transcription-PCR with primers cTa_F (CCGCTCGAGTCTCAAGGCAAGG-TAGGC) and cTa_R (GAAGATCTCTATCACCAACAG-GATGGG) using mRNA prepared from mouse retinas. The $pBKS-cT\alpha$ plasmid was purified by CsCl gradient and digested with XhoI and XbaI to yield the 6.3-kb insert fragment, which was then purified by QIAEXII gel extraction kit (Qiagen, Hilden, Germany) and Elutip-d column (Schleicher and Schuell Bioscience, Keene, NH). The DNA fragment was microinjected into fertilized eggs from C57BI/6J and DBA/2J F1 strains according to standard procedures. The $cT\alpha$ transgenic mice were identified by PCR of DNA obtained from tail biopsies. Transgenic mice that expressed $cT\alpha$ were generated by G. Shi and the Norris Transgenic Core Facility. To increase $cT\alpha$ dosage, the cT α transgene was bred to homozygosity (cT α ++). Both cT α + and cT α + transgenic mice were subsequently crossed with rT α knock-out mice (GNAT1-/-) (16) to produce $cT\alpha + rT^{\alpha-/-}$ and $cT\alpha + rT^{\alpha-/-}$ mice, respectively. Rod transducin α knock-out mice were provided by J. Lem. Hereafter, these lines are referred to as $cT\alpha$ + and $cT\alpha$ ++ mice to simplify the nomenclature. In addition, the $cT\alpha$ + transgenic mice were crossed with S-opsin $r^{\text{ho}-/-}$ mice, which expresses cone short wave S-opsin in mouse rods in the rod opsin knockout background (14) to obtain $cT\alpha$ +/S-opsin+^{rho+/-} mice.

Immunoblot Analysis and Quantification of Transgene $\emph{Expression}$ —Each isolated retina was homogenized in 200 μ l of buffer (80 mm Tris, pH 8.0, 4 mm $MgCl₂$ and protease inhibitor mixture (Roche Diagnostics, Indianapolis, IN). The samples were incubated with the addition of 30 units of DNase I (Roche Diagnostics) at room temperature for 30 min. After adding the SDS-loading buffer, the indicated amount of proteins were loaded onto a 12% Bis-Tris SDS-PAGE gel (Invitrogen), transferred onto nitrocellulose membranes (Schleicher and Schuell Bioscience), and probed with the following primary antibodies: anti-c $T\alpha$ (SC390) (Santa Cruz Biotechnology, Santa Cruz, CA), anti-rT α (T α 1A, obtained from M. Simon, Caltech), anti-T α common region, KENLKDCGLF (Meridian Life Science, Inc.) anti-G β 5 (17), anti-RGS9–1 (18), and anti- β actin (Millipore).

The secondary antibodies of IRDye 680 goat anti-rabbit and IRDye 800 goat anti-mouse (LI-COR Biosciences, Lincoln, NE) were applied accordingly. The proteins were visualized and quantified using Odyssey Infrared Imaging System (LI-COR Biosciences).

For quantitation of endogenous rT α , each C57BL/7 retina was homogenized in 120 μ l buffer (50 mm Tris, pH 8.0, 1 mm EDTA, 0.1% dodecyl maltoside and protease inhibitor mix), from this 2 μ l was further diluted to 80 μ l containing the indicated amount of chi8 and either 10 μ l or 15 μ l of the samples were loaded on SDS-PAGE, blotted and probed with an anti- GTa common region antibody (KENLKDCGLF, Meridian Life Science, Inc.) as described above. To quantify endogenous $cT\alpha$, two retinas from $GNAT1-/-$ mouse were combined and homogenized in 120 μ l buffer. Indicated amount of chi8 was added to 5 μ l of this homogenate and separated by SDS-PAGE. The gels were blotted and probed with an antibody that targets a highly divergent sequence in $cT\alpha$ (sc-390, Santa Cruz Biotechnology). Signals were visualized and quantified as described in the previous section. The values were plotted and fitted using Excel software.

Biochemical Analysis of ADP-ribosylation in Mouse ROS Membranes—Mice were dark-adapted overnight and rod outer segment (ROS) membranes were isolated under dim red light as described previously (19). Rhodopsin (Rho) concentrations were determined using the difference in absorbance at 500 nm before and after photobleaching. The procedures of pertussis toxin catalyzed ADP-ribosylation was similar to the method described by Kerov *et al*. (20). ROS membranes containing 1 μ м Rho per sample were used. Pertussis toxin was preactivated by 15 min incubation at 30 °C with 100 mM dithiothreitol and 0.2% SDS. ROS samples were then incubated with 3 μ g/ml of pertussis toxin and $\frac{1}{2}$ μ M $\left[\frac{32P}{P}\right]$ nicotinamide adenine dinucleotide $([{}^{32}P]NAD)$ for 1 h at 25 °C in the darkness or under light exposure. Meanwhile, 30 μ m AlCl₃ and 10 mm NaF were added to half of the samples of each condition. The reactions were stopped by SDS-loading buffer and analyzed by 12% SDS-PAGE gels followed by autoradiography of dried gels.

Light-dependent Translocation and Light Calibration—Mice were dark-adapted for at least 12 h before light exposure. For the dark condition, mice were euthanized, and the eyes were enucleated and fixed with 4% paraformaldehyde under infrared illumination. To see light-dependent translocation of $T\alpha$ in wild-type, rT α -/-, and cT α ++ mice, their eyes were treated with 0.5% tropicamide and 2.5% phenylephrine hydrochloride to dilate the pupils prior to exposure to diffuse white light (2000 lux) for 1 h. For calibrated light exposure, mice were anesthetized and immobilized, and one of the eyes was dilated and exposed to light for 30 min. The light source was a 100-watt quartz tungsten halogen lamp connected to a fiber optic guide (Oriel Instruments, Stratford, CT) and a narrow bandwidth interference filter (10 nm FWHM, Oriel Instruments) with peak center wavelength at 500 nm; light intensity was adjusted using neutral density filters and measured with a calibrated photodiode (United Detector Technology Sensors, Inc., Hawthorne, CA). The delivered photon flux was calculated using the following equation,

TABLE 1 **Rate of R*/rods determined for neutral density filters**

Current	R^* /rod·s
μA	
2.26	3.3×10^{4}
1.18	1.7×10^{4}
0.67	9.7×10^3
0.417	6.1×10^3
0.214	3.1×10^3

$$
\theta/s = \frac{1 \times \frac{1W}{0.18}}{4 \times 10^{-19} J/\theta} \times \frac{\pi r_{\text{pupil}}^2}{4 \pi r_d^2}
$$
 (Eq. 1)

where θ is the number of photons, the current (*I*) was measured from the calibrated photodiode (Table 1), r_{punil} is the radius of the pupil of the mouse, which is \sim 1 mm, and r_d is the distance from the light source to the mouse pupil (5 mm). The bleached rhodopsin (*R**) can be further estimated by the following equation,

$$
R^*/\text{rod·s} = \begin{pmatrix} \theta/\text{s} \\ \hline 6.4 \times 10^6 \text{ rod/retina} \end{pmatrix} \times \text{efficiency} \quad \text{(Eq. 2)}
$$

where one mouse retina is estimated to contain ${\sim}6.4 \times 10^6 \, \mathrm{rod}$ cells (21), and the quantum efficiency, or the probability that the adsorption of a photon initiates rhodopsin activation, is 0.67 (22). In this manner, the rate of R^* /rod·s was determined for the different neutral density filters, as shown in Table 1.

Immunocytochemistry—The superior pole of the mouse eye was marked by cauterization before enucleation. Cornea and lens were removed, and the remaining eyecups were fixed in 4% paraformaldehyde, infiltrated with 30% sucrose overnight, and embedded in O.C.T. (Tissue-Tek, Sakura Finetech, Torrance, CA) as described previously (23) . Ten- μ m-thick frozen retinal sections were obtained using a cryostat (Leica, Nussloch, Germany) at -20 °C. Sections were air-dried and treated with 0.1 mg/ml proteinase K (Roche Applied Science). After blocking with PBS containing 1% BSA, 5% normal goat serum, and 0.3% Triton X-100, the sections were incubated with 1:200 dilution of TF15 recognizing a common peptide on both rT α and cT α (Cytosignal, San Diego, CA). Rhodopsin 1D4 antibody (gift from Robert Molday) was biotinylated following manufacturer's protocols (Pierce Biotechnology). Proteins were visualized with FITC or Texas Red-conjugated secondary antibodies at 1:400 dilutions, or Texas Red Avidin D (Vector Laboratories, Burlingame, CA). Images were acquired on an Axioplan2 microscope (Zeiss, Oberkochen, Germany). All images for each section were taken at the same detection gain unless indicated.

Expression and Purification of Recombinant Rod Tro—His₆tagged $\text{G}\alpha_\text{t}/\text{G}\alpha_\text{i1}$ chimeric construct previously characterized for functional activity and solubility in *Escherichia coli* expression system (24) (chi8, obtained from N. Artemyev) was transformed into $E.$ $coll$ $BL21(DE3)$ and grown in $2\times$ YT media containing $100\ \mathrm{\mu g/mol}$ ampicillin at room temperature up to A_{600} of 0.5, and induced with 30 μ M isopropyl 1-thio- β -D-galactopyranoside for 18 h at 18 °C. The cell pellet was resuspended in 1:20 of the original cell culture volume with a buffer containing 50 mm Tris-HCl, pH 8.0, 50 mm NaCl, 5 mm MgCl $_2$, 50 μ m GDP, 0.1 mm phenylmethylsulfonylfluoride (PMSF), and 5 mm

Concentration Dependence of G^t on Rod Sensitivity

 β -mercaptoethanol, and then disrupted by sonication. The cell homogenate was centrifuged at $45,000 \times g$ for 1 h at $4 °C$. Solid ammonium sulfate was slowly added to the supernatant to a final concentration of 30% with continued stirring at 4 °C for 30 min. After centrifugation at 10,000 $\times g$ for 20 min, the pellet was resuspended in 20 mm Tris-HCl, pH 8.0, 450 mm NaCl, 6 m urea, 0.1% Triton X-100, 1 mm β -mercaptoethanol, and 10 mm imidazole. This crude sample was loaded onto a nickel-nitrilotriacetic acid-agarose resin (Invitrogen) column, washed, and eluted with loading buffer containing 100 mm imidazole. The elution fraction was dialyzed against 20 mm Tris-HCl, pH 8.0, 50 mM NaCl, and 0.1 mM PMSF, concentrated using Aquacide II (Calbiochem), and dialyzed again against the same buffer. The sample was then subjected to preparative Tris-glycine SDS-PAGE, and the gels were subsequently stained with SYPRO[®] Ruby (Invitrogen) in 250 mm KCl, 1 mm DTT. The recombinant chi8 was excised from the gel. The gel slices were minced and homogenized using a Kontes pestle in passive elution buffer (50 mm Tris, pH 7.9, 150 mm NaCl, 0.1% SDS, 1 mm DTT, 0.5 mm EDTA). The sample was dialyzed extensively against 25 mm ammonium bicarbonate and lyophilized. To quantify the amount of chi8, an aliquot was subjected to amino acid analysis in triplicates by the Biopolymer Laboratory at the University of California, Los Angeles.

Electroretinography—The protocol used for electroretinography measurements was similar to those described previously (25). Briefly, 6-week-old mice were dark-adapted overnight. The procedures were carried out under dim red light the following day. Mice were anesthetized with an intraperitoneal injection of 100 mg of ketamine and 10 mg of xylazine per kg of body weight. Pupils were dilated with 0.5% tropicamide (Tropicacyl®, Akorn Co., Buffalo Grove, IL) and 2.5% phenylephrine hydrochloride (Akorn Co.). A drop of GonakTM (2.5% hypromellose ophthalmic solution, Akorn) placed on the cornea facilitated electrical contact with the corneal electrode and kept the eye moist during the recording session. A steel needle placed subcutaneously near the eye served as the reference electrode. The light source was a xenon arc lamp, and 10-ms flashes of light at 500 nm were presented to the eye. A series of neutral density filters were used to control light intensity. Electroretinography signals were amplified by an AC/DC differential amplifier (A-M Systems, Inc., Carlsborg, WA), band pass-filtered at 0.1–1000 Hz, sampled at 2000 Hz, and digitized with a Digidata 1322A using pClamp software (Axon Instruments, Union City, CA).

Single-cell Recordings and Analysis—Light-evoked currents from mouse rod photoreceptors were measured with suction electrodes from finely chopped pieces of retinal tissue under recording conditions that have been described previously (26). Briefly, clusters of cells with the outer segments protruding were targeted and an individual outer segment was drawn gently into a suction electrode containing Ames' media (Sigma-Aldrich) buffered with 10 mm HEPES to pH 7.4. The tissue was bathed with 35–37 °C bicarbonate-buffered Ames' media that was equilibrated with 5% $CO₂$, 95% $O₂$. Families of light-evoked currents were measured following 10 ms flashes from an LED $(\lambda_{\text{max}} \sim 470 \text{ nm}, \text{FWHM} \sim 30 \text{ nm}; \lambda_{\text{max}} \sim 571 \text{ nm}, \text{FWHM} \sim 1$ 10 nm; $\lambda_{\text{max}} \sim 367$ nm, FWHM \sim 10 nm; Optodiode Corp.,

FIGURE 1.**Characterization of cTtransgene expression.** *A*, transgene construct to express $cT\alpha$ in rods. *B*, Western blot analysis of serial dilutions of retinal homogenates. Cone T α and rT α were recognized by SC390 and T α 1A antibodies, respectively. Actin was used as loading control. *C*, relative quantities of both cT α and rT α from Western blots ($n = 7$) utilizing TF15 antibody, which recognizes a conserved epitope on $cT\alpha$ and rT α . The relative expression levels from different genotypes were normalized to retinal extracts from C57 mice (WT). *D*, Western analyses of $G\beta_1$, $G\beta_5$, and RGS9-1 from WT, rT α –/–, and cT α retinas. The G β_5 antibody recognized both the long and the short isoform of the protein. No changes in these transduction proteins were detected as a consequence of cT α expression. *E*, cone T α associates with rod $G\beta_1\gamma_1$. Pertussis toxin catalyzed heterotrimeric G-protein dependent ADPribosylation of wild-type rT α and transgenic cT α . ADP-ribosylation was inhibited by light or in the presence of AlF⁻² ions for both WT and cT α samples.

Newbury Park, CA) or 30-ms flashes from a tungsten-halogen source passed through an interference filter ($\lambda_{\text{max}} \sim 500$ nm, FWHM \sim 15 nm). In experiments where UV light (*i.e.* λ_{max} \sim 367 nm) was used to stimulate the preparation, light was delivered to the recording chamber through a quartz fiber optic (Newport Corp., Irvine, CA). Families of responses to flashes of increasing intensity were collected from rods for each of the lines of mice described above. The elementary response of the rod, or the response to a single absorbed photon, was estimated from linear range responses by scaling the average response by a factor proportional to the ratio between the time-dependent variance and the mean (1). Currents were low-pass filtered at 20 Hz with an 8-pole Bessel filter and digitized at 1 kHz.

RESULTS

Expression of cT in Rod Photoreceptors of Transgenic Mice— Cone transducin α (GNAT2; here referred to as $cT\alpha$) cDNA was reverse-transcribed from retinal RNA extracted from C57/B6 mice and cloned downstream of the mouse rod opsin promoter (Fig. 1*A*). Two independent lines were obtained; both showed similar expression level and pattern, and both lines

were used interchangeably in this study. The $cT\alpha$ mice were crossed with the rod transducin α (GNAT1; here referred to as rT α) knock-out mice (16) to replace cT α for rT α (Fig. 1*B*). Western blot of retinal extracts showed a noticeable over-expression of cT α in the cT α + line when compared with the endogenous level of cT expressed in cones (Fig. 1*B*, *upper panel*). For some experiments, the $cT\alpha$ + transgene was also bred to homozygosity to increase expression level ($cT\alpha$ ++). Relative expression levels of rT α and cT α was quantified using an antibody that recognized a common epitope on both isoforms (KENLKDCGLF, Meridian Life Science, Inc.), as shown in Fig. 1*C*. The relative level of ectopically expressed $cT\alpha + t\alpha$ endogenous rT α in rods was 15 \pm 1.2%. Doubling the gene dosage increased the level to 35 \pm 2.0%. Swapping cT α for rT α appeared to have no discernible effect on the expression level of other transduction proteins that interact with $T\alpha$ (Fig. 1*D*) nor on retinal morphology (data not shown).

The subunit composition for T α in rods is rT $\alpha\beta_1\gamma_1$, whereas for cones the subunit composition is $cT\alpha\beta_3\gamma_8$ (27). The $\beta\gamma$ subunit plays an important role in presenting the α subunit to the GPCR and enhances the coupling efficiency (28–30). To determine whether cT α forms a heterotrimeric unit with $\beta_1 \gamma_1$ in these rods, we used the pertussis toxin assay in which the toxin catalyzes ADP-ribosylation of the α -subunit when it is complexed with $\beta\gamma$. Control experiments show rT α labeled strongly in the dark-adapted sample, and this labeling was reduced by light exposure (Fig. 1*E*). Application of AlF_{4}^{-} , which activates T α -GDP by mimicking the γ -phosphate of GTP, dissociates the subunits, effectively reducing ADP-ribosylation in both dark and light-exposed samples (Fig. 1*E*). Reduced ADPribosylation was also observed in the $cT\alpha$ samples following light exposure and AlF_{4}^{-} application, albeit the signal was weaker due to the low expression level of $cT\alpha$ (Fig. 1*E*). These results indicate that $cT\alpha$ forms a heterotrimeric unit with rod $\beta_1\gamma_1$.

Rhodopsin and S-opsin Activate cT with Similar Efficiency— Having discerned that $cT\alpha$ forms a heterotrimeric complex with G $\beta_1\gamma_1$, we sought to determine whether cT α can substitute for rT α to drive rod photoresponses. Furthermore, we sought to compare the efficiencies by which rhodopsin and a cone pigment (S-opsin) activate $cT\alpha$. Previously, Shi *et al.* (14) showed that S-opsin and rhodopsin, when co-expressed in the same rod, generated single-photon responses through $rT\alpha$ with similar amplitudes and kinetics. In other words, S-opsin and rhodopsin activated endogenous $rT\alpha$ with similar efficiency. We generated $Sop + Rh+/-$,cT α + mice that coexpressed cone S-opsin (\sim 12%) and rhodopsin (\sim 88%) in the rod outer segment, as well as the substitution of $cT\alpha$ for rT α , to compare the activation of $cT\alpha$ by the two visual pigments in the same rod cell. The spectral sensitivities of S-opsin and rhodopsin peak near 360 and 500 nm, respectively (31). Using this spectral separation, we compared the light-evoked responses produced mostly by S-opsin activation at 367 nm and almost completely by rhodopsin activation at 571 nm. For 367 nm stimuli, the absorption of S-opsin was near its maximum and rhodopsin absorption was less than one-fifth of its peak value, whereas the response for 571 nm stimuli was generated almost completely by rhodopsin (14). The photoresponses and derived single pho-

FIGURE 2. Rod and cone Ta couple to rhodopsin and cone S-opsin with similar efficiency. A, averaged response families for Rh+/-, cTa+ rods for 10 ms flashes of green light ($\lambda_{\rm max}$ = 571 nm) with flash strengths of 46, 90, 180, 360, 700, and 1400 photons μ m $^{-2}$, or UV light ($\lambda_{\rm max}$ = 367 nm) with flash strengths of 85, 170, 330, 660, 1300, 2600, and 5300 photons μ m⁻². *B*, for Rh+/-,cT $\alpha+$ mice, the single photon response was determined as the ratio of the time-dependent variance of all dim flash responses (< 25% R_{max}) to the mean amplitude for flashes of light from a green LED (λ_{max} = 571 nm; mean \pm S.E., *n* = 5 rods) or a UV LED ($\lambda_{\text{max}} = 367$ nm; mean \pm S.E., $n = 6$). The mean single-photon response amplitude was 0.32 \pm 0.10 pA for the 571-nm stimulus, compared with 0.36 ± 0.09 pA for the 367-nm stimulus. C, averaged response families for Sop+Rh+/− cTα+ rods for 10-ms flashes of green light (λ_{max} = 571 nm; *n* = 17 rods)
with flash strengths of 45, 89, 180, 350, 700, 1400, 2800, an and kinetics independent of the wavelength of stimulation. The mean single-photon response amplitude was 0.27 \pm 0.07 pA for the 571-nm stimulus, compared with 0.21 + 0.04 pA for the 367-nm stimulus. *E*, the normalized mean single photon response for Rh+/-,cT α + (black trace; *n* = 11 rods) and Sop+,Rh+/-,cT α + (red trace; $n = 28$ rods). The normalized single photon responses demonstrate similar kinetics for both Rh+/-,cT α + and Sop+,Rh+/-, $cT\alpha$ + in both the rising phase (activation of the cascade) and in the decay (inactivation).

ton response from rhodopsin coupled to $cT\alpha$ elicited by 571 nm (green trace) or 367 nm (blue trace) is shown in Fig. 2, *A* and *B*, respectively ($Rh+/-$, $cT\alpha+$). These results were similar to that obtained from $Sop + Rh+/-$,cT α + rods (Fig. 2, *C* and *D*). Furthermore, the results showed that the amplitude of the elementary responses of for 367- and 571-nm stimuli was indistinguishable in these rods (Fig. 2D). Thus, we find that $cT\alpha$ is activated by S-opsin and rhodopsin similarly well, and the inactivation of cT α expressed in rods is similar to rT α inactivation in rods.

T Concentration Affects Sensitivity—Suction electrode recordings form ROS showed that photoresponses from single allele $cT\alpha$ + mice displayed similar single photon response amplitude and time course to WT rods (Fig. 3, *A* and *B*), indicating that cT α is capable of functionally replacing rT α in the rod phototransduction cascade. However, these rods were 10-fold less sensitive than WT rods (Fig. 3*C*). The half-maximal flash strength was ${\sim}27$ photons/ ${\mu}{\rm m}^2$ in WT rods but was ~330 photons/ μ m² in cTa+ rods. This decrease in flash sensitivity was also observed in electroretinography recordings where the light sensitivity of $cT\alpha$ mice was in between that of wild-type and $rT\alpha$ – mice, whose responses arise exclusively

from cones (Fig. 3*D*). A similar dependence was also observed in mice expressing half of the native rhodopsin $(Rh+/-; Fig.$ $3E$). Rh + / - rods displayed a half-maximal flash strength of ~66 photons/ μ m², whereas on the same Rh+/- background, the half-maximal was \sim 490 photons/ μ m² in cT α + rods and ~140 photons/ μ m² in cTa++ rods. Thus, the light sensitivity appears to correlate with the expression level of $T\alpha$ within this concentration range. Along with the similar activation and deactivation phase of responses in rods expressing either $cT\alpha$ or $rT\alpha$ (Fig. 4*A*), these results indicate that the difference in light sensitivity between rods and cones are not likely due to a cell-specific $T\alpha$.

The Concentration of Endogenous rT and cT in Rods and Cones—The dependence of sensitivity on $T\alpha$ concentration prompted us to compare the concentration of endogenous rT α in rods and $cT\alpha$ in cones. To quantify accurately the concentration of endogenous T α , we obtained a $\text{G}\alpha_\text{t}/\text{G}\alpha_\text{i1}$ chimeric construct (chi8), which has been used for functional (24) and crystallographic studies (32), and substituted $cT\alpha$ sequences in the chimeric construct so the recombinantly expressed protein can serve as standards. Chi8 was expressed and purified to apparent homogeneity as visualized by $\text{SYPRO}^{\circledast}\text{-}\text{Ruby stained}$

FIGURE 3. **Sensitivity of rods expressing cTis correlated with expression level.** A, representative flash response families from WT and $cT\alpha$ + rods. 10-ms flashes were delivered at the time indicated by the *arrow*. *B*, population mean single-photon responses from WT (*black trace*) and $cT\alpha + mice$ (*red trace*). The responses have been normalized to compare the kinetics. *C*, normalized flash response amplitude is plotted against flash strength for WT and $cT\alpha$ + rods. *Smooth curves* are fitted according to the exponential saturation equation: $y = 1 - e^{-kt}$. Half-maximal flash strengths for these populations were 27 \pm 1.8 photons/ μ m² in WT rods (mean \pm S.E.; *n* = 14) and 330 \pm 36 photons/ μ m² in cT α + rods (mean \pm S.E.; *n* = 12). The ~10-fold shift in this value is similar to the 10-fold reduction in Ta in these rods. *D*, ERG recorded from 6-week-old WT, $cT\alpha +$. Responses from rT α –/– were shown to illustrate the cone threshold. Sensitivity was presented as normalized b-wave *versus* light intensity (photons/ μ m² at the cornea). *E*, normalized flash response amplitude is plotted against flash strength for rods expressing a single $(+)$ or double dose $(++)$ of cT α in mice expressing half of the normal rhodopsin (Rh+/-). The half-maximal flash strengths were 66 \pm 8.0 photons/ μ m² in $Rh+/-$ rods (mean \pm S.E.; *n* = 7), 490 photons/ μ m² in Rh+/-,cT α + rods (mean \pm S.E.; *n* = 18), and 140 photons/ μ m² in Rh+/-,cT α ++ rods (mean \pm S.E.; $n = 14$). Thus, in the Rh $+/-$ background, a dependence of half-maximal flash strength on $T\alpha$ concentration remains.

polyacrylamide gel (Fig. 4*A*). The trace amount of higher molecular weight bands appears to be higher order aggregates, whereas the lower molecular weight bands are likely degradation products because these bands also appeared in the West-

FIGURE 4. Quantification of endogenous rT α and cT α proteins using **recombinant protein chi8.** *A*, purified chi8 was visualized by SYPRO-Ruby stained polyacrylamide gel. At 0.1 μ g, chi8 appeared as a single band, whereas bands of higher and lower molecular weights were detected when 1 -g was loaded (*arrow*). *B*, Western blot of purified chi8 protein probed with a Gt α antibody, which recognizes a common epitope in rT α and cT α (Meridian Life Science). Aside from the band corresponding to the full-length protein (*arrow*), similar bands of higher and lower molecular weights as in *A* were also present, indicating higher aggregates of chi8 as well as its degradation products. The concentrations of endogenous rT α (*C*) and cT α (*D*) proteins were measured by Western blots of retinal homogenates from C57BL/6 mice containing known quantities of chi8. Serial dilutions were loaded onto each gel and proteins were detected using a Gt α antibody (Meridian Life Science) for rT α and sc390 (Santa Cruz Biotechnology) for cT α . The fluorescence signals from chi8 was quantified, plotted, and fitted with the best polynomial curve and served as the standard to calculate the quantity of $T\alpha$ in each lane.

ern blot (Fig. 4*B*). The concentration and purity of chi8 was determined by amino acid analysis. T α in rods (rT α) was quantified using an antibody that recognizes the carboxyl-terminal sequence, KENLKDCGLF (Meridian Life Science, Inc.) which is conserved between rT α and cT α . However, this antibody showed cross-reactivity with Gi that co-migrated with $cT\alpha$ (but not $rT\alpha$); therefore, a different antibody that recognized a highly divergent epitope on $cT\alpha$ (I-20, Santa Cruz Biotechnology) was used to quantify cT α . Because in the retina rT α is expressed only in rods and $cT\alpha$ is expressed only in cones, we can use the value obtained from whole retinal homogenates to quantify the amount of each $T\alpha$ in these cells. It is known that detection efficiency inWestern blots can be strongly influenced by protein complexity of the sample. To circumvent this issue, known quantities of chi8 were mixed with whole retinal homogenates prepared from C57/B6 mice or rT α -/- mice as an internal standard. The His-tagged recombinant protein migrated slower on SDS-PAGE, allowing it to be distinguished

from the endogenous proteins (Fig. 4, *C* and *D*). The fluorescence signal from chi8 was plotted as a standard curve, and the best polynomial fit was applied, from which the quantity of endogenous rT α and cT α was calculated to be 59 \pm 6 pmol (*n* = 11) and 2.6 \pm 0.4 ($n = 5$; mean \pm S.D.), respectively, per retina. As a point of comparison, we measured rhodopsin concentration by differential absorption at 500 nm in the dark and after bleaching and obtained 500 \pm 30 pmol per retina ($n = 9$), a value that is \sim 9-fold higher than the concentration of rT α determined here. This ratio of rhodopin: $rT\alpha$ as well as their absolute levels agree well with previous reports (19, 33–36). Because the proportion of rods:cones in the mouse retina is 33:1, and the cone outer segment is approximately half of the length and volume of rod outer segment (37), the normalized ratio of rT α :cT α concentration per cell is ~1:3. These measurements show that cones appear to express a higher level of T α . Therefore, the reduced sensitivity of the cone to light cannot be explained by a lower concentration of Ta .

Transgenic cT Expressed in Rods Show Similar Translocation Pattern as Endogenous cT in Cones—The heterotrimeric transducin is localized to the membranous ROS in the darkadapted rods due to the synergistic effect of the lipid modifications on the α and γ subunit (38, 39). Consistent with this idea, $G\beta_1\gamma_1$ localization is no longer restricted to ROS and instead is evenly dispersed in the rT α -/- rods (40). Light activation of transducin dissociates the GTP-loaded α subunit from the $\beta\gamma$ subunits, weakening their membrane association, and causes a massive translocation from the ROS to the inner segment (41, 42). This translocation decreases the gain of phototransduction and has been suggested to be an adaptation mechanism for long term light exposure (35). As another functional comparison, we studied light-dependent T α translocation in WT, $cT\alpha$ ++, and rT α -/- mice in response to 2,000 lux diffuse white light. As shown in Fig. 5, WT retina displayed the classically robust translocation of rT α to inner segments in response to light (Fig. 5, *upper panels*). In $cT\alpha$ + + retinas, $cT\alpha$ is concentrated to the ROS in darkness (Fig. 5, *middle panels*), consistent with results obtained from the pertussis toxin assay, indicating that $cT\alpha$ forms a heterotrimeric complex with $G\beta_1\gamma_1$. These data also provide independent support of the association between $cT\alpha$ and $G\beta_1\gamma_1$ based on what we know about the mechanism of transducin localization to ROS in the dark-adapted state (43, 44). Light exposure similarly triggered translocation of $cT\alpha$ in $cT\alpha$ ++ transgenic rods. To determine whether endogenous $cT\alpha$ also translocates in cones, we studied rT α –/– mice where only cT α is expressed (Fig. 5, rT α – / – panels). Their identity as cones was verified using rhodamine-conjugated peanut agglutinin (Fig. 5, *bottom panels*), a known cone marker (45). Upon light exposure, we found that $cT\alpha$ moved to the cone inner segment compartments in a pattern that is qualitatively similar to endogenous rT α in WT and transgenic cT α in rods. These results show that ectopically expressed $cT\alpha$ is functionally similar to endogenous rod and cone $T\alpha$ with respect to its ability to move between photoreceptor outer and inner segments following light exposure.

The Light Threshold for cT Translocation Did Not Correspond to To Concentration—The ability of T α to translocate depends on its level of activation; when the concentration of

FIGURE 5. **Rod and cone T** α undergo similar light-induced translocation. A , T α (*green*) is primarily localized to the outer segment (*os*) of WT and cT α + rods in the dark-adapted state. Endogenous $c\bar{r}_{\alpha}$, here visualized in a darkadapted rT α (GNAT1) knock-out retina, is also localized to the outer segment. The bottom rT α -/- panels are also co-labeled with rhodamine-conjugated peanut agglutinin (*red*), a known cone marker. Adjacent panels show the differential interference contrast image of the same field to highlight the boundary of the outer nuclear layer. Exposure to 2,000 lux light causes endogenous $T\alpha$ in both rods and cones to move toward the inner segment compartments (*is*, *onl*). This pattern was also demonstrated by ectopically expressed $cT\alpha$ in transgenic rods. The sections were counterstained with DAPI to visualize cell nuclei (*blue*). *White scale bar*, 25 μm; *black scale bar*, 10 μ m.

 $T\alpha$ -GTP exceeds that of the GTPase complex, it moves to the compartments in the rod inner segment (46, 47). Because $cT\alpha$ + and $cT\alpha$ ++ rods display reduced T α concentration compared with WT rods, a simplistic expectation is that there should be a corresponding increase in the threshold for translocation. Under these circumstances, more R* would be required to activate the same number of $T\alpha$ to reach the threshold level to saturate the GTPase complex. We observed in the WT retina that T α translocation was driven by a light yielding an initial rate of 9.7 \times 10³ *R**/rod·s (2.8 OD, Fig. 6*B*), whereas translocation in the retina of $cT\alpha$ ++ and $cT\alpha$ + mice was driven by a light yielding $1.7 \times 10^4 R^*$ /rod·s (Fig. 6, *F* and *H*, 2.6 OD), a light intensity only 1.7-fold higher than WT mice. In $cT\alpha$ retinas, low level translocation can be observed at similar light threshold asWT retinas (Fig. 6*E*). Therefore, the threshold for translocation does not appear to depend on the relative concentration of T α .

DISCUSSION

In this study, we replaced cT α for rT α in transgenic mouse rods to evaluate how the G α subtype influences signal amplification from different GPCRs and how this might explain functional differences between rods and cones. We showed that ectopically expressed $cT\alpha$ forms a heterotrimeric complex with $G\beta_1\gamma_1$, displays light-triggered translocation, and can substitute equally for $rT\alpha$ in generating photoresponses initiated by

FIGURE 6. Light threshold for cT α translocation does not correlate with T α concentration. Both rT α and cT α were detected using the TF15 antibody (*green*). The *left strip* of each panel shows rhodopsin immunofluorescence (*red*) highlighting the outer and inner segment boundary, whereas the remaining panel is the merged image of rhodopsin (red) and T_{α} (green). The nuclei were stained with DAPI (*blue*). A–C, C57 retinas (WT); *D–F*, CT α ++ retinas; G–I, CT α + retinas. Translocation of rT α in WT retina was detected at 9.7 \times 10³ *R**/rod·s from using a 2.8 OD neutral density filter (*B*). At this light intensity, translocation for $cT\alpha$ + $+$ can be detected (*E*) but was much more robust at 1.7 \times 10⁴ *R**/rods (*F*, 2.6 OD). For $cT\alpha$ +, translocation is evident at 1.7 \times 10⁴ *R**/rods (*H*, 2.6 OD). The g reen arrow marks the light intensities where translocation is evident. *Scale bar*, 25 μ m.

either rhodopsin or S-cone opsin. Thus, from a functional standpoint rT α and cT α appear interchangeable. Below, we discuss this functional interchangeability.

The Role of T in Setting the Properties of the Rod and Cone Photoresponse—A number of studies have investigated whether signal amplification at the first step of visual transduction, between the pigment and G protein, may provide a mechanism that explains the difference in light sensitivity between retinal rod and cones. In support of this notion, *Xenopus* short-wave cone opsin heterologously expressed in COS-1 cells exhibited lower T α activation when compared with rhodopsin (10). In addition, biochemical assays performed on purified rods and cones from carp retina revealed a lower amplification of G protein activity, as well as faster visual pigment phosphorylation in cones (6, 7, 48). We also observed a decrease in sensitivity in mice that expressed $cT\alpha$ in rods. However, this decrease in sensitivity correlated with the level of $cT\alpha$ expression (Fig. 3). A comparison of the normalized single photon response arising from rT α and cT α showed them to be similar in rising phase as well as response recovery, indicating the similar amplification efficiency of rT α and cT α by rhodopsin and similar deactivation by the GAP complex. Deng *et al.* (49), who used AAV to introduce cT α into GNAT1-/- rods, also observed a similar sensitivity and response recovery when compared with $rT\alpha$, a result qualitatively similar to our findings.

The co-expression of S-cone opsin in rods allowed us, for the first time, to determine whether cell-type specific $T\alpha$ interacted preferentially with visual pigment subclasses. We demonstrated that $cT\alpha$ is activated by rhodopsin and S-cone opsin equally when both are expressed in the same cell. These results, together with our previous finding that S-opsin and rhodopsin produced equivalent light responses when coupled to endogenous $rT\alpha$, suggest strongly that the difference in sensitivity between rods and cones does not lie within $rT\alpha$ and $cT\alpha$.

Our findings are also similar to a previous study of rods and cones in the tiger salamander, whose green rods and blue cones contain the same S-cone opsin that is coupled to rT α and cT α , respectively. It was found that these cells display similar light sensitivities and response kinetics, indicating that S-cone opsin activates the native rT α and cT α with the same efficiency regardless of the structural features of the photoreceptor outer segment (50). The interchangeability between rT α and cT α may not be totally surprising. Structural studies of the interaction between rT α -GDP and G $\beta\gamma$ between activated rT α and γ PDE and between activated rT α and the RGS complex found that the interface between these interactions often show complete conservation of the amino acids between rT α and cT α (32, 51). One distinction is at the amino terminus, where $cT\alpha$ contains an insert of four amino acids, ELAR, in a domain determined to participate in G $\beta\gamma$ as well as receptor binding (32, 52,

53). Our data show that this insert does not appear to affect these interactions within the rod cell. Given this apparent interchangeability of $T\alpha$, it is remarkable that rods and cones express different forms of transducin. Although our results show that $T\alpha$ in rods and cones is interchangeable, it remains possible that the cell type-specific $G\beta\gamma$ subunits are functionally specific in the phototransduction cascade or perhaps at the synapse (54).

A recent study by Chen *et al.* (55) used a similar strategy as ours to replace endogenous rT α with cT α (termed GNAT2C) in transgenic mice and reported a lower amplification of GNAT2C by rhodopsin that resulted in a decrease in light sensitivity and faster response recovery. The level of GNAT2C used in their study was similar to that of endogenous $rT\alpha$, whereas $cT\alpha$ expression used in this study were two different lower doses: 15 and 35% of the endogenous rT α expression. In light of a recent study that showed monomeric rT α expressed in $rT\gamma$ knock-out mice displayed reduced receptor coupling and accelerated response recovery (28), one possibility is that GNAT2C did not associate well with $G\beta_1\gamma_1$. The reason for the discrepancy in the ectopically expressed $cT\alpha$ in our study and that of Chen *et al.* (55) is not clear. One possible explanation is the strain difference of the mice used; transgenic lines with the same gene addition or deletion sometimes display different phenotypes (28, 56–58).

Concentration Dependence of T on Rod Sensitivity—Heck and Hofmann (59), who derived a K_m value for the rate of T α activation by *R** *in vitro*, predicted that the physiological concentration of T α at the ROS discs, being less than K_{m} , would rate limit this reaction. Such a relationship was noted in the phosducin $-$ / $-$ (60) and G γ_1 +/ $-$ rods, where T α expressed at 60–70% of the endogenous level led to a 1.4-fold reduction in sensitivity (61). The remarkable linear correspondence is extended by our studies on Ta expressed at 15 and 35% leading to a \sim 10- and \sim 5-fold decrease in sensitivity, respectively. Altogether, these studies provide support for the hypothesis that the rate of T α activation by R^* is proportional to T α concentration in intact rods in this concentration range. They also underscore the importance of quantitative measurements of protein concentrations for the evaluation of the functional difference between rods and cones.

The correlation between decreased light sensitivity and $cT\alpha$ expression in transgenic rods prompted us to quantify the level of endogenous rT α and cT α relative to the visual pigment. In particular, we asked whether the lower sensitivity of cones could be explained by lower concentrations of endogenous $cT\alpha$. To measure $cT\alpha$ concentration, we expressed a chimeric $G\alpha_t/G\alpha_{i1}$, which was determined to be functionally indistinguishable from $\mathsf{G}\alpha_\mathrm{t}$, and used it as an internal standard followed by quantitative Western blots. Using this approach, we calculated the absolute quantity of rT α to be 58 \pm 6 pmol per retina, which is approximately one-tenth of rhodopsin, a value in good agreement with previous reports (19, 33-36). The value of $cT\alpha$ was ascertained to be 2.6 ± 0.4 pmol, which when normalized to the number of cones and their smaller outer segment volume, is higher than the concentration of $rT\alpha$ in rods. Therefore, the lower sensitivity of cones cannot be explained simply by a lower T α concentration. Considering that G $\beta\gamma$ increases the

Concentration Dependence of G^t on Rod Sensitivity

coupling efficiency between \mathbb{R}^* and $\mathrm{T}\alpha$ (28), the level of endogenous $\mathsf{G}\beta_3\gamma_8$ in cones and their association with $\mathsf{cT}\alpha$ may be important determinants for setting sensitivity in cones. Additional factors that are likely to play a role include a faster rate of cone pigment phosphorylation (6, 7), regeneration (62), and their faster turnover rate of cGMP (9).

Ectopically Expressed cT Translocates Normally—Light-induced $T\alpha$ translocation from the outer segment to the inner compartments decreases the gain of phototransduction and has been proposed to be an adaptation mechanism (35). How translocation is regulated has been a topic of intense investigation, particularly because this process has been reported to be nonlinearly related to light exposure (43). Studies have shown that translocation threshold in rods can be shifted to dimmer or brighter light exposures in the GAP defective mice, or those overexpressing RGS9, respectively, giving rise to the model that T α translocation ensues only when the concentration of T α -GTP exceeds that of the GTPase-activating complex (46, 47). The same rule was proposed for mouse cones as well, where the failure to observe $cT\alpha$ translocation was attributed to the higher expression level of the GAP complex in cones (63). However, in this study, we observed that endogenous $cT\alpha$ in cones readily translocated with moderate light exposure (2,000 lux). A similar observation of $cT\alpha$ translocation was also reported by Chen *et al.* (64). The discrepancy in the observation of $cT\alpha$ translocation by different groups could be due to differences in the tissue preparations, epitope unmasking, and the sensitivity of the antibodies used. The translocation pattern of $cT\alpha$ is consistent with the functional interchangeability of $rT\alpha$ and $cT\alpha$ in rods and cones and suggests that translocation of endogenous $cT\alpha$ in cones may contribute to light adaptation under prolonged light exposure.

We took advantage of mice expressing different $T\alpha$ levels to investigate the relationship between $T\alpha$ concentration and the light threshold that triggers translocation. Because $cT\alpha +$ and $cT\alpha$ ++ rods contain 15 and 35% of T α concentration compared with WT rods, a simple expectation is to see a corresponding increase in light threshold to reach the concentration of $Ta-GTP$ necessary to saturate the GAP complex for translocation to ensue. Instead, we observed only a slight increase in light thresholds (Fig. 6). Although the almost 2-fold difference in the light threshold did correlate with their relative difference in sensitivity, the relation between translocation threshold and absolute sensitivity is non-linear. The non-linearity observed for light threshold for translocation likely reflects a non-linear relationship between the number of activated transducin generated per *R** at bright light levels, which are beyond the functional range of rods. Additional candidates that may affect this non-linearity include lipid modifications on $T\alpha$ (44, 47, 65, 66), lipid microdomains on ROS discs, and protein-protein interactions that restrict their lateral and longitudinal diffusion (67, 68).

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