Evolution and the origin of the visual retinoid cycle in vertebrates

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Absorption of a photon by visual pigments induces isomerization of 11-cis-retinaldehyde (RAL) chromophore to all-trans-RAL. Since the opsins lacking 11-cis-RAL lose light sensitivity, sustained vision requires continuous regeneration of 11-cis-RAL via the process called ‘visual cycle’. Protostomes and vertebrates use essentially different machinery of visual pigment regeneration, and the origin and early evolution of the vertebrate visual cycle is an unsolved mystery. Here we compare visual retinoid cycles between different photoreceptors of vertebrates, including rods, cones and non-visual photoreceptors, as well as between vertebrates and invertebrates. The visual cycle systems in ascidians, the closest living relatives of vertebrates, show an intermediate state between vertebrates and non-chordate invertebrates. The ascidian larva may use retinochrome-like opsin as the major isomerase. The entire process of the visual cycle can occur inside the photoreceptor cells with distinct subcellular compartmentalization, although the visual cycle components are also present in surrounding non-photoreceptor cells. The adult ascidian probably uses RPE65 isomerase, and trans-to-cis isomerization may occur in distinct cellular compartments, which is similar to the vertebrate situation. The complete transition to the sophisticated retinoid cycle of vertebrates may have required acquisition of new genes, such as interphotoreceptor retinoid-binding protein, and functional evolution of the visual cycle genes.

Keywords: visual cycle; opsin; chromophore regeneration; RPE65; photoisomerase; ascidian

1. INTRODUCTION

In the eyes of animals, including both vertebrates and invertebrates, the visual pigments responsible for sensing light in the photoreceptor cells consist of an 11-cis-retinaldehyde (11-cis-RAL) chromophore and a G-protein-coupled receptor, opsin. Absorption of a photon by the visual pigments induces isomerization of 11-cis-RAL to all-trans-RAL. This photoisomerization is the initial and only light-dependent reaction in the phototransduction cascade that converts light signal into electrical signal in the photoreceptors. Since the opsins lacking 11-cis-RAL chromophore lose light sensitivity, sustained vision requires continuous regeneration of 11-cis-RAL via the process called ‘visual cycle’ (Wald 1935). In this process, all-trans retinoids are isomerized to 11-cis retinoids and visual pigments are reconstituted.

In photoreceptor cells of the vertebrate retina, all-trans-RAL produced by the photoisomerization dissociates from opsin and enters into an enzymatic reaction pathway that regenerates 11-cis-RAL chromophore (Saari 2000; Rando 2001; Lamb & Pugh 2004; Travis et al. 2007). The retinal pigment epithelium (RPE) plays an essential role in the visual cycle. The isomerized chromophore (all-trans-RAL) released from opsin is reduced to all-trans-retinol (all-trans-ROL) and sent to adjacent RPE, where the trans-to-cis reisomerization reaction occurs. The regenerated chromophore re-enters the photoreceptor cells.

Protein components and their roles in a visual cycle pathway were first established in cephalopods by pioneer works by Hara and Hara. They found two RAL-bearing proteins, retinochrome and RAL-binding protein (RALBP) in addition to rhodopsin (Hara & Hara 1968, 1973, 1991). Retinochrome binds and allows light to photoisomerize all-trans-RAL to 11-cis-RAL. RALBP serves to send the 11-cis-RAL into the rhodopsin system and to carry away all-trans-RAL. Consequently, rhodopsin and retinochrome can interchange their chromophores through the mediation of
RALBP to reform their original pigments, rhodopsin and retinochrome, in photoreceptor cells (Terakita et al. 1989). However, another chromophore regeneration system has also been evolved. In invertebrates, photosomizerized all-trans-RAL chromophore remains bound through its Schiff base to rhodopsin, forming a thermally stable metarhodopsin. Reisomerization of chromophore occurs through the absorption of a second photon by metarhodopsin, resulting in the regeneration of the original rhodopsin. This mode of chromophore regeneration can occur in rhodopsin in insects (Hardie 1986) and octopus (Tsuda 1987; Ashida et al. 2004). Thus, unlike the visual cycle in vertebrate eyes, the entire process of the visual cycle, including trans-to-cis reisomerization of chromophore, could occur in the photoreceptor cell of protostome eyes.

Protostomes and vertebrates use essentially different machinery of visual pigment regeneration, and the origin and early evolution of the vertebrate visual cycle is an unsolved mystery. Comparison of visual cycle systems between different vertebrate systems as well as between vertebrates and their close relatives would give us insights into the origin and evolution of the vertebrate visual cycle. Tunicates, including ascidians, are the closest living relatives of vertebrates (Delsuc et al. 2001; Putnam et al. 2008). Although the adult ascidian is a sessile organism with little resemblance to the vertebrate, the ascidian larva is similar to a frog tadpole and shares basic body structures with vertebrates. The photoreceptive system of the ascidian larva has recently been extensively investigated (Kusakabe & Tsuda 2007; Takimoto et al. 2007). In this article, we review our current understanding of the diversity of visual cycle systems in vertebrates and ascidians. We also present some original data on the visual cycle in the ascidians as well as phylogenetic analysis of protein families involved in the retinoid cycle with new sequence data obtained from the cephalochordate amphioxus genome. Taken together with the information obtained from these analyses, we discuss evolution and the origin of the retinoid cycle in vertebrates.

2. DIVERSITY OF THE VISUAL RETINOID CYCLE IN VERTEBRATES

(a) Rod photoreceptor cells

The vertebrate retinas contain two types of photoreceptors: the rods and cones. Rods are highly sensitive to light and mediate black-and-white vision in dim light, whereas cones are less sensitive to light and provide high-resolution colour vision during daylight. Ever since the early discoveries by Wald (Wald 1935), the biochemistry of the rod visual cycle has been well explored.

The entire reaction of the rod visual cycle takes place in the photoreceptors and RPE (Zimmerman 1974). The first enzymatic reaction of the visual cycle is the reduction of all-trans-RAL to all-trans-ROL by an NADPH-dependent retinol dehydrogenase (RDH) (Rattner et al. 2000). This photoreceptor-specific RDH (prRDH) is localized to the outer segments of rods and cones via its C-terminal 16 amino acids sequence (Luo et al. 2004). Disruption of prRDH in mouse did not affect the rate of 11-cis-RAL regeneration after short light exposure (Maeda et al. 2005). However, it caused significant accumulation of all-trans-ROL following exposure to bright lights and delayed recovery of rod function (Maeda et al. 2005).

All-trans-ROL is then released from photoreceptors to interphotoreceptor space, where it binds the interphotoreceptor retinoid-binding protein (IRBP), an abundant 140 kDa glycoprotein secreted by photoreceptors (Liu et al. 1982; Redmond et al. 1985). The endogenous retinoid ligands of IRBP include all-trans-ROL and 11-cis-RAL (Chen & Noy 1994). The binding of retinoids by IRBP protects them from oxidation and isomerization (Crouch et al. 1992). In vitro studies showed that IRBP promotes the release of all-trans-ROL from photoreceptors following the photobleach of the visual pigments (Qtaishat et al. 2005) and release of 11-cis-RAL from RPE cells (Carlson & Bok 1992), suggesting that IRBP functions as a transporter protein for all-trans-ROL and 11-cis-RAL during translocation between photoreceptors and RPE cells. However, the irbp−/− mice exhibited a very mild visual cycle phenotype (Palczewski et al. 1999; Ripps et al. 2000).

In the RPE, lecithin:retinol acyltransferase (LRAT) is the dominant ester synthase responsible for esterification of all-trans-ROL (Ruiz et al. 1999). Ocular tissues of brat−/− mice contain a trace amount of all-trans retinyl esters (all-trans-REs) and 11-cis-RAL (Batten et al. 2004). A second ester synthase called acyl CoA:retinol acyltransferase may complement LRAT to provide additional RE synthase activity under high concentration of all-trans-ROL (Kaschula et al. 2006). This condition occurs in the RPE, following exposure to bright light.

All-trans-RE was shown to be the substrate for retinoid isomerase (or isomerohydrolase) in the RPE (Deigner et al. 1989). Phenotypes of rpe65−/− mice suggested that RPE65 is involved in the all-trans to 11-cis isomerization. Photoreceptors in the rpe65−/− retina contain only apo-opsin, but not 11-cis-RAL (Redmond et al. 1998). In contrast, all-trans-RE was accumulated in the RPE cells. These observations suggested that RPE65 may be the isomerase. Against this hypothesis are the reports that partially purified RPE65 possessed no isomerase activity (Znoiko et al. 2002). Moreover, depletion of RPE65 from RPE membranes has no effect on the isomerase activity in the membranes (Choo et al. 1998). Instead, it was suggested that RPE65 binds insoluble all-trans-REs and presents them to the isomerase (Mata et al. 2004). Recently, three groups (Jin et al. 2005; Moiseyev et al. 2005; Redmond et al. 2005) demonstrated that RPE65 itself is the retinoid isomerase in the visual cycle.

Oxidation of 11-cis-ROL to 11-cis-RAL in the RPE is catalysed by RDH5 (Driessen et al. 1995). RDH5 and prRDH (RDH8) are members of the RDH family, which belongs to the short-chain dehydrogenase/reductase superfamily. Disruption of the rdh5 gene in mouse leads to the accumulation of cis-ROL and cis-REs (Driessen et al. 2000). However, the rdh5−/− and the rdh5−/rdh11 double knockout mice...
are still able to produce 11-cis-RAL efficiently, suggesting that the oxidation of 11-cis-ROL to 11-cis-RAL may involve additional, yet unidentified, RDH(s) (Kim et al. 2005).

RPE cells express two retinoid-binding proteins involved in the visual cycle. One is the cellular retinol-binding protein that binds all-trans-RL, and the other is cellular retinaldehyde-binding protein (CRALBP) that binds 11-cis-ROL and 11-cis-RAL (Bunt-Milam & Saari 1983; Bok et al. 1984; Saari et al. 2001). Mutations in the human gene encoding CRALBP (RLBP) cause autosomal-recessive retinitis pigmentosa: a condition characterized by progressive photoreceptor degeneration and night blindness (delayed dark adaptation) (Maw et al. 1997; Burstedt et al. 1999; Morimura et al. 1999). In CRALBP knockout mice, isomerization of all-trans- to 11-cis-ROL in the visual cycle was substantially impaired and delayed dark adaptation was observed (Saari et al. 2001).

β-Carotene 15,15′-monooxygenase (BCO) in RPE supplies all-trans-RL to the visual cycle via central cleavage of β-carotene (Redmond et al. 2001; Lampert et al. 2003; Chichili et al. 2005). Mammalian BCO is expressed in RPE (Hamel et al. 1993; Redmond et al. 2001; Yan et al. 2001). It is generally accepted that central cleavage of β-carotene by BCO gives rise to two molecules of all-trans-RL (Redmond et al. 2001). Because animals cannot synthesize vitamin A (retinol) de novo from endogenous isoprenoid precursors, BCO is a crucial enzyme in development and metabolism that governs the de novo entry of vitamin A from plant-derivative precursors. BCO was formerly known as β-carotene 15,15′-dioxygenase. Recently, it was demonstrated that the reaction mechanism of enzymatic cleavage of the central carbon 15,15′-double bond in β-carotene involves a monooxygenase-type mechanism (Leuenberger et al. 2001; Lindqvist & Andersson 2002). In Drosophila, mutations in the BCO gene are responsible for the ninaB photoreceptor degeneration (von Lentig & Vogt 2000).

Retinal G-protein-coupled receptor (RGR) is a non-visual opsin expressed in RPE. RGR bound to all-trans-RL is capable of operating as a photoisomerase that generates 11-cis-RL in the light-dependent manner (Hao & Fong 1996; Chen et al. 2001a). This has a similar amino acid sequence to retinochrome that isomerizes all-trans-RL to 11-cis-RL in cephalopods. The photoisomerase activity of RGR was demonstrated only in vitro (Maeda et al. 2003; Wenzel et al. 2005). RGR has been shown to interact with proteins involved in the retinoid cycle (Chen et al. 2001b), and it has been suggested that RGR facilitates the mobilization of all-trans-REs from storage causing following enhancement of isomerizing activity (Wenzel et al. 2005). Thus, it is currently believed that RGR does not act as an isomerohydrolase, rather it behaves as a cofactor in the retinoid cycle that modulates isomerohydrolase activity (Wenzel et al. 2005).

**Figure 1.** Photoreceptor systems in the ascidian *C. intestinalis* larva. (a) Photoreceptor cells visualized by immunofluorescence staining using antibody against photoreceptor-specific protein, Ci-Arr. (b) Immunofluorescence staining of the visual pigment Ci-opsin1 visualizing outer segments of the photoreceptor cells. The *Ciona* brain contains three distinct groups of photoreceptor outer segments: groups I, II and III (Horie et al. 2008). (c) Immunofluorescence staining using antibody against the *C. intestinalis* orthologue of RPE65. Specific localization of Ci-RPE65 is not observed in the larva. oc, ocellus; ot, otolith.

**The more important photoreceptors because they serve daylight vision.** In order to investigate the visual cycle for cone visual pigment regeneration, Mata et al. (2002) analysed retinoid metabolism in the eyes of chickens and ground squirrels, in which cones constitute 60 and 96 per cent of total photoreceptors, respectively. Based on the biochemical data, the authors proposed a novel visual cycle for cone visual pigment regeneration. The cone visual cycle takes place in cones and Müller cells and involves four new enzymes: (i) an all-trans-ROL isomerase, (ii) an 11-cis-RE synthase, (iii) an 11-cis-RE hydrolase, and (iv) an 11-cis-ROL dehydrogenase (Mata et al. 2002).

Using cultured chicken Müller cells, Das et al. (1992) observed the formation of all-trans-retinyl palmitate (all-trans-RP), 11-cis-ROL and 11-cis-RP from all-trans-ROL, which was added into the culture medium after labelling with radioisotope. This observation suggests that Müller cells may express all-trans-ROL isomerase and 11-cis-RE synthase. Until now, there is no direct in vivo evidence that Müller cells provide visual retinoid for cone vision. The all-trans-ROL isomerase expressed in Müller cells is distinct from RPE65 isomerase, because the former converts all-trans-ROL to 11-cis-ROL (Mata et al. 2002, 2005; Muniz et al. 2007), whereas the latter uses all-trans-RP as its substrate. In another study, it was shown that only all-trans-RP is the direct precursor of 11-cis-ROL in chicken RPE/retina mixture membranes, suggesting that RPE65 may be involved in the synthesis of 11-cis-ROL in the chicken retina (Gollapalli & Rando 2003). Consistent with this suggestion, Znoiko et al. (2002) found that RPE65 is expressed in cone photoreceptors. Neural retina leucine zipper (NRL)-deficient mice, a mouse model

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for cone-dominant retina (Mears et al. 2001), contained elevated levels of RPE65 (Wenzel et al. 2007). Similar to the phenotype of the rpe65<sup>−/−</sup> mouse, ablation of RPE65 in <i>nr1a1</i> mice led to the absence of 11-cis-RAL, but increased all-trans-REs, suggesting that RPE65 is indispensable for the production of 11-cis-RAL in the cone-dominant mice (Wenzel et al. 2007; Feathers et al. 2008).

Although the 11-cis-RE synthase has not been identified, several early studies also suggested the existence of the enzyme in the cone-dominant retinas. Bridges et al. (1987a) found that 11-cis-RE was predominantly contained in the chicken retina. In contrast, rod-dominated frog and cow eyes had mainly all-trans RP in the RPE.

The 11-cis RDH involved in the cone visual cycle was also different from the 11-cis-specific RDH5 expressed in the RPE. In the cone-dominant retina, the oxidation of 11-cis-ROL to 11-cis-RAL is NADP dependent and takes places in cones (Mata et al. 2002), whereas in rod-dominant eyes, this oxidation reaction is NAD dependent. In an early study using isolated rods and cones from salamander, it was shown that 11-cis-ROL added to the medium could confer light sensitivity to photobleached cones, but not to rods (Jones et al. 1989), suggesting that cones contain RDH(s) that catalyses oxidation of 11-cis-ROL to 11-cis-RAL. Haeseleer et al. (2002) showed that RDH12 expressed in the photoreceptors could be involved in the production of 11-cis-RAL from 11-cis-ROL during regeneration of the cone visual pigments. Very recently, Miyazono et al. (2008) reported that the reduction of all-trans-RAL and the production of 11-cis-RAL are much more efficient in cones than in rods. The reducing activity in the outer segment of cones is 30 times higher than that of rods. The high activity of RDHs is attributed to the high content of RDH8 in cones (Miyazono et al. 2008). They further found a novel and effective pathway to convert 11-cis-ROL to 11-cis-RAL in cones; this oxidative conversion does not require NADP<sup>+</sup> and instead is coupled with the reduction of all-trans-RAL to all-trans-ROL. The activity is 50 times more effective than the oxidizing activity of NADP-dependent RDHs. Miyazono et al. (2008) proposed that these highly efficient reactions of removal of all-trans-RAL by RDH8 and production of 11-cis-RAL by the coupling reaction are probably the underlying mechanisms that ensure effective visual pigment regeneration in cones that function under much brighter light conditions than rods.

Recently, Schonthaler et al. (2007) analysed the role of RPE65 in zebrafish, a species with a cone-dominant retina. The zebrafish genome contains two RPE65 genes: <i>RPE65a</i> and <i>RPE65b</i>. Only the <i>RPE65a</i> transcript was expressed in RPE cells. <i>RPE65a</i> mRNA was detectable in early larval stages, but faded out at later larval stages. Targeted knockdown of <i>RPE65</i> by antisense morpholinos resulted in morphologically altered rod outer segments and overall reduced 11-cis-RAL levels. However, cone vision of RPE65-knockdown larvae remained functional as demonstrated by behavioural tests and by metabolite profiling for retinoids (Schonthaler et al. 2007). The zebrafish genome also contains two CRALBP orthologues: <i>rhlbp1a</i> and <i>rhlbp1b</i> (Collery et al. 2008; Fleisch et al. 2008). CRALBP-a is exclusively expressed in the RPE, whereas CRALBP-b is localized to Müller cells. Knockdown of CRALBP in the RPE or Müller cells with antisense morpholinos results in the diminution of 11-cis RAL under both conditions. Light sensitivity in both CRALBP-a- and CRALBP-b-knockdown larvae was reduced, but it was more pronounced in CRALBP-b-knockdown larvae (Collery et al. 2008; Fleisch et al. 2008). Together, these studies suggest that zebrafish may possess an RPE65-independent pathway for the regeneration of 11-cis-RAL for cone vision.

(c) Retinoid cycles in non-visual photoreceptors

Vertebrates have several non-visual photoreceptive systems that use opsins as the photoreceptor molecule (Foster & Hankins 2002; Vigh et al. 2002; Mano & Fukada 2007). The most well-known non-visual photoreceptor organ is the pineal complex in non-mammalian vertebrates. In chick, the gene encoding RGR is expressed in the pineal organ (Bailey & Cassone 2004). The expression of <i>Rgr</i> mRNA was observed primarily in parafollicular cells broadly interspersed among pinealocytes. The distribution of <i>Rgr</i> mRNA is different from that of pinealocyte markers, arylalkylamine-N-acetyltransferase and pinopsin, suggesting that <i>Rgr</i> is not expressed in the photoreceptive pinealocytes (Bailey & Cassone 2004). The gene encoding another photoisomerase, peropsin, is also expressed in the chick pineal organ with expression patterns similar to those of <i>Rgr</i> (Bailey & Cassone 2004). The chick pineal organ expresses various visual cycle genes, including those encoding IRBP, RPE65, RGR, CRALBP and all-trans-ROL dehydrogenase (Bailey & Cassone 2004; Bailey et al. 2004). In zebrafish, the pineal organ expresses genes encoding orthologues of RPE65 and CRALBP (Schonthaler et al. 2007; Collery et al. 2008). Thus, the photoreceptive pineal organ in non-mammalian vertebrates may possess a visual cycle system similar to that of rod photoreceptors in the retina. Interestingly, however, IRBP and CRALBP are also present in the mammalian pineal gland, which is thought to be a non-photoreceptive organ (Rodrigues et al. 1986; van Veen et al. 1986; Bridges et al. 1987b). In bovine pineal, CRALBP-positive cells are glia-like and seem not to be pinealocytes (Saari et al. 1997).

Another mode of visual cycle in the pineal organ is the photoregeneration of parapinopsin in lamprey (Koyanagi et al. 2004). The lamprey parapinopsin is the bistable UV pigment that exhibits an absorption maximum at 370 nm. UV light causes <i>cis</i>–<i>trans</i> isomerization of its chromophore, forming a stable photoproduc that having an absorption maximum at 515 nm, in the green region. The photoproduction reverts to the original pigment upon visible light absorption, showing photoregeneration of the pigment. The bistable nature of the parapinopsin can account for the photorecovery of the pineal UV sensitivity by background green light in the lamprey (Koyanagi et al. 2004).
Opsins and phototransduction cascade proteins have been demonstrated in neurons in the brain of various vertebrates. These photoreceptive systems, mainly comprising telencephalic and hypothalamic groups of cerebrospinal fluid-contacting neurons, are called ‘deep brain photoreceptors’ (Vigh et al. 2002). Although physiological roles and photoreceptive abilities of the encephalic photoreceptors have not been elucidated, visual cycle proteins have been reported in the brain of various vertebrates. For example, in the mammalian brain, CRALBP is expressed in oligodendrocytes (Saari et al. 1997). In chicke, expression of Rgr and peropin was observed throughout the brain (Bailey & Cassone 2004). In zebrafish, one of the two RPE65 orthologue genes, RPE65b, is expressed in the ventricular zone of the brain of early larvae (Schonthaler et al. 2007). At present, however, physiological and/or developmental relevance of visual cycle proteins in the vertebrate brain is totally unknown.

In the past decade, non-visual opsins have been identified and characterized in the inner retina (Provencio et al. 1998; Soni et al. 1998; Kojima et al. 2000). In zebrafish, one of the two duplicated IRBP genes is expressed in the inner nuclear layer and in the ganglion cell layer (Nickerson et al. 2006). Most fully characterized among inner retinal opsins is melanosin. Vertebrate melanopsins are structurally similar to the cephalopod opsins (Provencio et al. 1998; Koyanagi et al. 2005); mouse melanopsin has been reported from knockout studies to be involved in the response of the pupil to light (Lucas et al. 2003) and in the entrainment of circadian rhythm by light (Hattar et al. 2003). Like invertebrate rhodopsin, visual pigments, melanopsin acts as a bistable photopigment and dark melanopsin can be regenerated by light (Koyanagi et al. 2005; Walker et al. 2008). However, the analysis of chromophore isoforms in melanopsin suggests that melanopsin must use light-independent mechanism to regenerate the photopigment (Walker et al. 2008). Thus the regeneration of melanopsin remains an important unresolved question.

3. PHOTORECEPTORS AND RETINOID CYCLES IN THE ASCIDIAN LARVA

The ascidian tadpole larva has a central nervous system derived from the dorsal neural tube, consisting of approximately 330 cells. The brain of the ascidian larva contains an eyespot (ocellus), which consists of three lens cells, one pigment cup cell and a group of photoreceptor cells (Kusakabe & Tsuda 2007; Horie et al. 2008) (figure 1). Larvae of the ascidian Ciona intestinalis start to show photo response behaviour at around 4 h after hatching (Nakagawa et al. 1999). The larvae start swimming when light intensity decreases and stop swimming when light intensity increases (Tsuda et al. 2003a).

Vertebrate retinal photoreceptors are ciliary photoreceptors and they hyperpolarize in response to light, whereas most photoreceptors of invertebrate eyes are rhodopinic and depolarize in response to light. Ciliary photoreceptors and rhodopinic photoreceptors use different types of opsins, which are clearly distinguished by their primary structures. The ciliary photoreceptor cells of the ocellus of the C. intestinalis larva use a vertebrate-type ciliary opsin, Ci-opsin1, as the visual pigment (Kusakabe et al. 2001; Inada et al. 2003; Horie et al. 2008). Four genes encoding putative visual cycle proteins, orthologues of RGR (Ci-opsin3), CRALBP (Ci-CRALBP), RPE65 (Ci-RPE65) and BCO (Ci-BCO), have been identified in C. intestinalis (Nakahama et al. 2003; Tsuda et al. 2003b; Takimoto et al. 2006). Ci-opsin3 and Ci-CRALBP are localized in both ocellus photoreceptor cells and surrounding non-photoreceptor cells in the brain vesicle of the larva (Tsuda et al. 2003b). In contrast to Ci-BCO, which is predominantly localized in the ocellus photoreceptor cells of the larva, the Ci-RPE65 gene is not significantly expressed in the ocellus and brain vesicle of the larva, as shown by in situ hybridization and expressed sequence tag (EST) profiles (Takimoto et al. 2006). We further examined localization of Ci-RPE65 in the larva by immunohistochemical analysis using anti-Ci-RPE65 antibody (see electronic supplementary material for experimental details). The result consistently suggests that Ci-RPE65 is not significantly present in the ocellus and brain vesicle of the larva (figure 1c).

4. PHOTORECEPTORS AND RETINOID CYCLES IN THE ASCIDIAN ADULT

At least three types of light-responsive behaviours have been described in the adult ascidians: siphon
Figure 2. Localization of visual cycle proteins in the brain vesicle of *C. intestinalis* larvae. Localization of Ci-Arr (green) and visual cycle proteins (magenta) are visualized by double immunofluorescence staining. White colour indicates co-localization of Ci-Arr and a visual cycle protein in photoreceptor cells. Visual cycle proteins were visualized with antibodies against Ci-opsin3 (a–d), Ci-CRALBP (e–h) and Ci-BCO (i–l). Photographs shown in (a), (e) and (i) are confocal composite images generated from a series of optical sections. Photographs shown in (b–d), (f–h) and (j–l) are optical sections taken at different depths: (b), (f) and (j) position near the basal surface of the photoreceptor cell bodies; (c), (g) and (k) medial position of the cell bodies with respect to the apico-basal polarity of photoreceptor cells; (d), (h) and (l) inner (apical) position of the photoreceptor cells where outer segments are observed. OS, outer segments. Scale bar, 20 μm.

contraction, phototropism and gamete release (Kusakabe & Tsuda 2007). The cerebral ganglion has been suggested to be a candidate photoreceptor organ underlying these behaviours (Kajiwara et al. 1990; Ohkuma & Tsuda 2000; Ohkuma et al. 2000; Tsutsui & Oka 2000). In a previous study, expression of visual cycle protein genes was examined in adult tissues of *C. intestinalis* by RT–PCR (Takimoto et al. 2006). Ci-RPE65 is expressed in the neural complex, a photoreceptor organ of an adult ascidian, at a level comparable to that of Ci-opsin3 and Ci-CRALBP. These results suggest that the visual cycle of the adult photoreceptors is RPE65 dependent. Ci-RPE65 is also expressed in various adult tissues, including the gill, body wall and intestine, suggesting that Ci-RPE65 plays an unrecognized role in addition to that in the visual cycle (Takimoto et al. 2006).

The neural complex is roughly explained to consist of three components: neural grand, ciliated funnel and cerebral ganglion. The cerebral ganglion and neural gland do not have direct connection. Ciliated duct connects neural gland and ciliated funnel, which opens into the pharynx, constituting the neural gland complex (Deyts et al. 2006). To elucidate localization of the visual cycle system in the neural complex, spatial expression patterns of Ci-opsin3, Ci-CRALBP, Ci-BCO and Ci-RPE65 were analysed by *in situ* hybridization (figure 3; see electronic supplementary material for experimental details). All of these genes are expressed in the neural complex. Ci-opsin3 expression was detected specifically in the ciliated duct (figure 3a–c). Similarly, Ci-CRALBP is specifically expressed in the ciliated duct (figure 3d–f). Ci-BCO was expressed widely in the neural gland and duct-like structure circumscribing the ciliated funnel (figure 3g–i), and Ci-RPE65 was broadly expressed in the neural gland, including the ciliated duct (figure 3j–l). Thus, in contrast to the larval brain, where Ci-RPE65 is not expressed, the adult neural complex expresses Ci-RPE65 in a specific manner. These results suggest that Ci-RPE65 may be involved in the visual cycle of the adult ascidians. The results also suggest that the trans-to-cis isomerization reaction occurs in the neural complex and ciliated duct in adult ascidians. Since the existence of photoreceptor cells has been suggested in the cerebral ganglion (Kajiwara et al. 1990; Ohkuma & Tsuda 2000; Ohkuma et al. 2000; Tsutsui & Oka 2000), the visual cycle of the adult ascidian may occur in two distinct cellular compartments: the 11-cis to all-trans isomerization of the visual pigment chromophore in the cerebral ganglion and trans-to-cis regeneration in the neural gland/ciliated duct. This presumed compartmentalization of the adult ascidian, together with the possible involvement of RPE65, is reminiscent of the visual cycle in the vertebrate retina. Thus, the visual cycle in the adult ascidian might be more similar to the visual cycle in the vertebrate retina than the larval visual cycle.

5. MOLECULAR AND FUNCTIONAL EVOLUTION OF RETINOID CYCLE PROTEINS
(a) Molecular phylogeny of retinoid cycle protein families
(i) RPE65/BCO/BCO2 family
RPE65 and BCO are similar in amino acid sequences, evolved from a common ancestor (Wyss 2004). Both
mammalian RPE65 and BCO are expressed in RPE
(Hamel et al. 1993; Redmond et al. 2001; Yan et al.
2001). RPE65 and BCO constitute a protein family
with β-carotene 9',15'-dioxygenase (BCO2), another
enzyme involved in carotenoid metabolism (Kiefer
et al. 2001; Wyss 2004). The molecular phylogenetic
analysis performed using amino acid sequences of
vertebrate and ascidian RPE65/BCO/BCO2 family
proteins suggested that the ascidian C. intestinalis has
distinct orthologues of RPE65 (Ci-RPE65) and BCO.

Figure 3. Spatial localization of mRNAs for visual cycle proteins in the neural complex of the adult C. intestinalis. Spatial localizations of transcripts of Ci-opsin3 (a–c), Ci-CRALBP (d–f), Ci-BCO (g–i) and Ci-RPE65 (j–l) were visualized by whole-mount in situ hybridization (ISH). In (a), (d), (g) and (j), anterior is up and dorsal is to the left (right lateral view). In (b), (e), (h) and (k), anterior is up (dorsal view). After ISH, the neural complexes were embedded in paraffin and sectioned for further observation ((c), (f), (i) and (l)). In these sagittal sections, anterior is up and dorsal is to the left. Arrowheads indicate specific expression of Ci-opsin3 and Ci-CRALBP in the ciliated duct. cg, cerebral ganglion; ng, neural gland. Scale bar, 200 μm.

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they show only moderate amino acid sequence similarity to each other (Nakashima et al. 2003). Peropsins have been identified in various vertebrates and amphioxus and form another subfamily of photoisomerase opsin that can photoisomerize between 11-cis-RAL and all-trans-RAL (Sun et al. 1997; Koyanagi et al. 2002). The widespread distribution of photoisomerase opsins among different animal groups suggest an ancient origin of the light-dependent trans-to-cis isomerization system in metazoans.

(iv) IRBP family

IRBP has been reported only in vertebrates. It is not found in the Drosophila genome (Gonzalez-Fernandez 2002). We have not been able to identify IRBP homologues in the amphioxus and Ciona genomes. IRBP consists of four consecutive modules, each approximately 300 amino acid residues in size (Gonzalez-Fernandez 2002). The gene appears to have arisen from the quadruplication of an ancestral gene present in an early common ancestor of vertebrates (Nickerson et al. 2006). In teleosts, the IRBP gene has been further duplicated into two genes, each of which shows distinct structural features and expression patterns (Nickerson et al. 2006). The three-dimensional structure of an individual module of IRBP suggested a probable homology between IRBP and two diverse protein families, the C-terminal transferase (CPTase) and the crotenase families (Gonzalez-Fernandez 2002). The early vertebrate ancestor might have recruited a CPTase/crotenase family protein for a new purpose, retinoid transport between photoreceptor cells and their neighbour cells, having facilitated the establishment of the vertebrate-type visual cycle.

(b) Functional evolution of the RPE65/BCO1/BCO2 family

RPE65 was first described as an abundant protein of the RPE (Bavik et al. 1992; Hamel et al. 1993). In S9 cells and bovine RPE, RPE65 is expressed in two forms (Ma et al. 2001): one is a cytosolic form (sRPE65), and the other is a membrane-associated form (mRPE65). The sRPE65 has a molecular mass of 61,161, which is close to the calculated value (60,944), whereas the molecular mass of mRPE65 was 61,961, suggesting that RPE65 contained post-translational modification. Jahng et al. (2003) showed that RPE65 binds all-trans-RP. Later, it was shown that RPE65 is S-palmitoylated by LRAT on three cysteine (Cys) residues (Cys231, Cys329 and Cys330) and that this palmitoylation is required for isomerase activity and the association of RPE65 with membranes (Xue et al. 2004). The authors proposed a novel ‘palmitoylation switch model’: the palmitoylation of RPE65 serves to switch off the visual cycle in darkness and to switch it on in the daylight (Xue et al. 2004). However, substitution of Cys231, Cys329 and Cys330 with Ala or Ser in all combinations did not significantly change enzyme activity and/or association of RPE65 with membrane (Redmond et al. 2005; Takahashi et al. 2006; Jin et al. 2007).
RPE65 belongs to the evolutionarily diverse carotenoid oxygenase family. This family also contains BCO and BCO2, as mentioned earlier. The entire Drosophila genome contains only one bco gene of the family. Invertebrates, however, encode RPE65, BCO and BCO2 proteins, respectively. Mammalian genomes contain a single copy of the RPE65 gene, whereas the zebrafish genome has RPE65a and RPE65b genes, a consequence of the genome duplication in the teleost ancestry. RPE65, BCO and BCO2 share approximately 40 per cent overall sequence identity (Kiefer et al. 2001). The basic function of the family is to catalyse the oxidative cleavage of carbon–carbon double bonds in the polyene backbone of RE and carotenoid. BCO cleaves β-carotene into all-trans-RAL, the first step of vitamin A metabolism in animals.

X-ray diffraction analysis of the crystallized apo-carotenoid oxygenase, a member of the family, suggests that the proteins share a common seven-bladed β-propeller structure containing a non-haeme ferrous iron coordinated by four histidine residues (Kloer et al. 2005). These four histidines are strictly conserved among the members of the family. On binding of iron, the apo-carotenoid oxygenase converted all-trans-carotenoid to cis–trans–cis conformation. This observation suggests that the apo-carotenoid oxygenase of cyanobacterial Synechocystis may have potential isomerase activity. However, we observed that Ci-RPE65 and Ci-BCO could not synthesize 11-cis-ROL from all-trans-RP, whereas bovine RPE65 converted all-trans-RP to 11-cis-ROL in the same condition (M. Jin, N. Takimoto, T. G. Kusakabe & M. Tusada 2007, unpublished data). The individual family members may differ in their substrate preference and the position of the cleaved double bond. Interestingly, the bovine and mouse RPE65 expressed in a β-carotene accumulating Escherichia coli strain did not synthesize apo-carotenoid cleavage products, suggesting that vertebrate RPE65 dose not have β-carotene cleaving activity (von Lintig & Vogt 2000).

Figure 4. Molecular phylogenetic trees of the RPE65/BCO/BCO2 family (a) and the CRALBP family (b). Phylogenetic trees were inferred from amino acid sequences using the neighbour-joining method using CLUSTALX. Numbers at nodes are bootstrap values based on 1000 replicates. Scale bar, 0.1 amino acid replacements per site. See electronic supplementary material for amino acid sequences used to reconstruct the phylogenetic trees.

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6. EVOLUTIONARY PERSPECTIVES

The genome-wide survey and molecular phylogeny of gene families involved in the visual cycle across the chordate subphyla suggested that basic components used in the visual cycle of the vertebrate eye had been already established in the last common ancestor of tunicates and vertebrates. The visual cycle systems in tunicates, namely ascidians, show a kind of an intermediate state between vertebrates and non-chordate animals such as cephalopods. Similar to the cephalopod visual cycle, the ascidian larva uses retinochrome-like opsin (Ci-opsin3), but not RPE65, as the major isomerase; the entire process of the visual cycle can occur inside the photoreceptor cells with distinct subcellular compartmentalization. On the other hand, the ascidian larva also shows a vertebrate-like character: the visual cycle components are also present in non-photoreceptor cells surrounding the ocellus. The visual cycle system of the adult ascidian may be more similar to that of the vertebrates: it probably uses RPE65, and trans-to-cis isomerization may occur in distinct cellular compartments. The current data together with previous findings enabled us to deduce possible scenarios for the chordate visual cycle evolution (figure 5). A visual cycle system using photoisomerase opsin was probably present in photoreceptor cells of the last common ancestor of bilaterian animals. The vertebrate/tunicate common ancestor had acquired visual cycle in adjacent non-photoreceptor cells. RPE65 was also recruited to the system as another isomerase in a chordate ancestor. In the lineage towards vertebrates, photoreceptor cells lost trans-to-cis isomerization machinery. The complete transition to the vertebrate-type system may have required the acquisition of some genes with new function, such as IRBP, which is absent in the genomes of ascidians and amphioxus. Thus, recruitment of new genes and functional evolution within the gene families might have facilitated the evolution of the sophisticated retinoid cycle system for the vertebrate photoreceptors.

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