

wall. We propose that the high speed of discharge is due to the release of energy stored in the stretched configuration of the collagen polymer of the capsule wall. How the ejection of the stylets is initiated during exocytosis and after fusion pore formation remains to be shown.

Acknowledgements

This work was supported by the DFG and Hamamatsu Photonics Germany. We thank Uwe Denzer for his generous help.

Supplemental data

Supplemental data including Experimental Procedures are available at <http://www.current-biology.com/cgi/content/full/16/9/R316/DC1/>

References

- Holstein, T., and Tardent, P. (1984). An ultrahigh-speed analysis of exocytosis: nematocyst discharge. *Science* 223, 830–833.
- Kurz, E.M., Holstein, T.W., Petri, B.M., Engel, J., and David, C.N. (1991). Mini-collagens in hydra nematocytes. *J. Cell Biol.* 115, 1159–1169.
- Engel, U., Pertz, O., Fauser, C., Engel, J., David, C.N., and Holstein, T.W. (2001). A switch in disulfide linkage during minicollagen assembly in Hydra nematocysts. *EMBO J.* 20, 3063–3073.
- Holstein, T.W., Benoit, M., Herder, G.V., Wanner, G., David, C.N., and Gaub, H.E. (1994). Fibrous mini-collagens in Hydra nematocysts. *Science* 265, 402–404.
- Weber, J. (1989). Nematocysts (stinging capsules of Cnidaria) as Donnan-potential dominated osmotic systems. *J. Biol. Chem.* 265, 9664–9669.
- Brinkmann, M., Oliver, D., and Thurm, U. (1996). Mechanoelectric transduction in nematocytes of a hydrozoan (Corynidae). *J. Comp. Physiol.* 178A, 125–138.
- Weber, J., Klug, M., and Tardent, P. (1987). Some physical and chemical properties of purified nematocysts of *Hydra attenuata* Pall. (Hydrozoa, Cnidaria). *Comp. Biochem. Physiol.* 88B, 855–862.
- Fix, M., Melia, T.J., Jaiswal, J.K., Rappoport, J.Z., You, D., Sollner, T.H., Rothman, J.E., and Simon, S.M. (2004). Imaging single membrane fusion events mediated by SNARE proteins. *Proc. Natl. Acad. Sci. USA* 101, 7311–7316.
- Fernandez, J.M., Villalon, M., and Verdugo, P. (1991). Reversible condensation of mast cell secretory products in vitro. *Biophys. J.* 59, 1022–1027.
- Szczepanek, S., Cikala, M., and David, C.N. (2002). Poly-gamma-glutamate synthesis during formation of nematocyst capsules in *Hydra*. *J. Cell Sci.* 115, 745–751.

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Molecular evidence for dim-light vision in the last common ancestor of the vertebrates

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Animal vision is mediated through pigments belonging exclusively to the opsin family. These are members of the G-protein-coupled receptor family that bind retinal [1]. Based on function and phylogenetic relationship, vertebrate visual opsins can be clustered in five groups: Rhod photoreceptors (Rh1), Rh1-like (Rh2), Short Wave Sensitive (SWS1), SWS1-like (SWS2), and Long (LWS) or Medium (MWS) Wave Length Sensitive (LWS/MWS). Rh1 is used for seeing under dim light conditions (scotopic vision), while the others permit full colour (photopic) vision in bright light [2–5]. Opsins have diversified by a series of gene duplications, and the inferred

order of these duplications indicates that photopic vision predated scotopic vision in vertebrates [2–5].

Assuming that the jawless vertebrates (Agnatha) are monophyletic [6], the broad distribution of opsins associated with photopic vision indicates that these – and thus the capacity for photopic vision – were present in the last common ancestor of all living vertebrates [2–5]. However, it is still unclear whether ‘true’ (i.e., Rh1-mediated [3]) dim-light vision predated the split between Agnatha and the jawed vertebrates (Gnathostomata), or whether it is an apomorphy of the Gnathostomata [2–5,7]. Solving this question has important palaeoecological implications and, assuming that orthologous opsins have inherited a common ancestral function, it depends on the correct classification (phylogeny based orthologous clustering) of the few agnathan Rh sequences available to date.

Based on a Neighbour Joining (NJ) analysis, Yokoyama [2] suggested that the two agnathan Rh sequences available at that time represented Rh1 opsins. This would imply that the vertebrate ancestor was potentially capable of

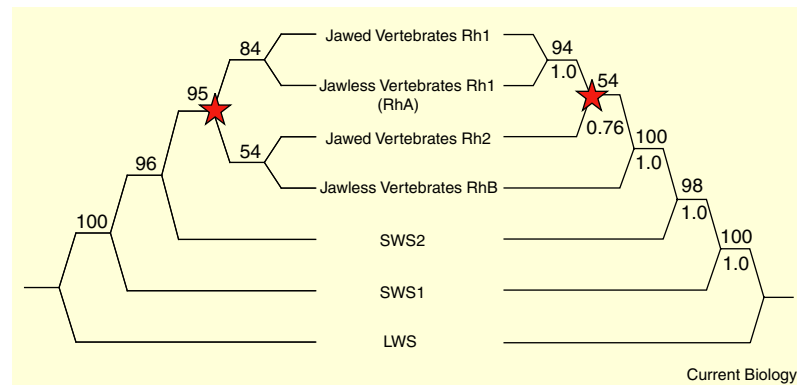


Figure 1. Phylogenetic relationships among vertebrate visual opsins.

The left tree shows a summary of the relationships obtained from the quartet puzzling and the minimum evolution analyses (Supplemental data). Numbers at the nodes represent quartet-puzzling support values. The right tree shows a summary of the relationships obtained in the ML analyses (PHYML, SPR-PHYML and SPR), in the Bayesian analysis, and in the equally and differentially weighted parsimony analyses (Supplemental data). Numbers at the nodes represent the bootstrap support values obtained in the PHYML analysis (above) and posterior probabilities (below). The red star represents the gene duplication resulting in the origin of Rh1.

true dim-light vision. Alternatively, Collin and co-workers [3–5,7] suggested that the vertebrate cenacestor did not possess an Rh1 gene and could not have been capable of true dim-light vision. This conclusion was based on the isolation and NJ analysis of LWS/MWS, SWS1, SWS2, and two Rh sequences from the southern lamprey *Geotria australis*. Collin *et al.* [3] included also the other available agnathan Rh sequences (i.e., a putative *Lampetra* and *Petromyzon* Rh1 sequences) in their analysis and recovered all four agnathan Rh sequences as the monophyletic sister group of the gnathostomatan Rh1 and Rh2. This implies that agnathan Rh opsins originated from a gene duplication predating that giving rise to Rh1 and Rh2, such that agnathans have neither an Rh1 nor an Rh2 gene [3–5,7]. They named the new agnathan-specific opsins they isolated in *G. australis* RhA and RhB, and reassigned the *Lampetra* and the *Petromyzon* Rh1 to RhA [3], thus concluding that the cenacestor did not possess the Rh1 gene and thus no true scotopic vision.

Here, we analyse the amino acid sequences of 47 representative vertebrate visual opsins (LWS, SWS1, SWS2, Rh1, Rh2, RhA, and RhB) using a variety of phylogenetic methods to test the alternative hypotheses that true dim-light vision evolved in the stem vertebrate lineage, or within the Gnathostomata. We analysed the data with minimum evolution, equally and differentially weighted maximum parsimony, Bayesian analysis and Maximum Likelihood while testing for long branch attraction artefacts using the method of Pisani [8] (see Supplemental Data available with this article online). Our analyses show that a clade containing RhA plus RhB is never recovered (Figure 1). Rather, quartet-puzzling Maximum Likelihood strongly supports the agnathan RhA being orthologous with the gnathostome Rh1 and, albeit less strongly, identifies the agnathan RhB as an Rh2 (Figure 1A). Standard Maximum

Likelihood analyses and the Bayesian analysis provide very high support for the orthology of RhA and Rh1 (Figure 1B), but not for the orthology of RhB and Rh2. Minimum evolution supports the tree shown in Figure 1A, while the maximum parsimony analyses support that in Figure 1B. Pisani's method [8] for countering long branch attraction does not change the inferred relationships of RhA or RhB. Although the data do not allow us to choose between the alternative trees in Figure 1, the approximately unbiased test [9] unequivocally shows that these trees explain the data significantly better than the tree of Collin *et al.* [3] ($p = 0.0002$).

Based on these results, we can confidently conclude in accordance with [2] that the last common ancestor of the vertebrates possessed an Rh1 gene, which is thus much older than suggested in many recent studies and reviews [3–5,7]. The function of Rh1 in agnathans is not yet known, but assuming its function in the vertebrate cenacestor was not dramatically different from its scotopic function in most vertebrates, this implies that both photopic and scotopic vision evolved in the stem vertebrate lineage and must have been in place in the Cambrian by about 522–518 Ma [10,11].

Early vertebrate evolution probably took place in a brightly lit environment and thus the earliest stem vertebrates were probably diurnal and inhabited shallow waters. However, at some stage after photopic vision was already in place, scotopic vision also evolved in the stem vertebrate lineage, which implies that a behavioural or ecological shift — perhaps a move into deeper water or to nocturnality — occurred in an ancestral vertebrate. What drove this shift can only be conjectured, such as the emergence of large macrophagous predators [12], and is certainly a topic for further palaeobiological investigations.

Acknowledgements

This work was supported by an MRF grant to MW, a Marie Curie Intra European Fellowship (contract Number MEIF-CT-2005-01002) to DP and a BBSRC studentship (BBS/S/K/2003/10085) to SMM. We thank David Hunt, Philip Donoghue, Thomas Keane, Jennifer Commins and four referees for advice and comments on earlier drafts.

Supplemental data

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References

1. Nilsson, D.-E. (2004). Eye evolution: a question of genetic promiscuity. *Curr. Opin. in Neurobiology* 14, 407–414.
2. Yokoyama, S. (2000). Molecular evolution of vertebrate visual pigments. *Prog. Retin. Eye Res.* 19, 385–419.
3. Collin, S.P., Knight, M.A., Davies, W.L., Potter, I.C., Hunt, D.M., and Trezise, A.E.O. (2003). Ancient colour vision: multiple opsin genes in the ancestral vertebrates. *Curr. Biol.* 13, R864–865.
4. Collin, S.P., and Trezise, A.E.O. (2004). The origin of colour vision in vertebrates. *Clin. Exp. Optom.* 87, 217–223.
5. Trezise, A.E.O., and Collin, S.P. (2005). Opsins: Evolution in waiting. *Curr. Biol.* 15, R749–796.
6. Takezaki, N., Figueroa, F., Zaleska-Rutczynska, Z., and Klein, J. (2003). Molecular phylogeny of early vertebrates: Monophyly of the agnathans as revealed by sequences of 35 genes. *Mol. Biol. Evol.* 20, 287–292.
7. Schwab, I.R., and Collin, S.P. (2005). Are you calling me primitive? *Br. J. Ophthalmol.* 89, 1553.
8. Pisani, D. (2004). Identifying and removing fast evolving sites using compatibility analysis: An example from the Arthropoda. *Syst. Biol.* 53, 978–989.
9. Shimodaira, H. (2002). An approximately unbiased test of phylogenetic tree selection. *Syst. Biol.* 51, 492–508.
10. Shu, D.-G., Conway Morris, S., Han, J., Zhang, Z.-F., Yasui, K., Janvier, P., Chen, L., Zhang, X.-L., Liu, J.-N., Li, Y., *et al.* (2003). Head and backbone of the early Cambrian vertebrate *Haikouichthys*. *Nature* 421, 526–529.
11. Gradstein, F.M., Ogg, J.G., and Smith, A.G. (2005). *A geologic timescale 2004*, Cambridge University Press, Cambridge, UK.
12. Bengtson, S. (2002). Origins and early evolution of predation. In *The fossil record of predation*, M. Kowalewski and P. H. Kelley, eds. (The Paleontological Society Papers 8), pp. 289–317.

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