(fMRI) were shown to correlate with attentional demands during a visuospatial attention task [9]. These systematic changes in the fMRI signal occurred in spatially selective regions of human parietal cortex. A component of the BOLD signal was low when the task was either too easy or too hard, and high when attentional demands were intermediate. This human neuroimaging work is an example of additive activity of both the focus of spatial attention and attentional load. In light of the new macaque LIP study [8], perhaps changes within the BOLD signal represent not only the attentional focus, but also the value placed on responses at varying levels of difficulty. Further electrophysiological recordings in the macaque will be required both within and outside of the spatial receptive fields of LIP to address the issue of coding within parietal cortex.

Thus, it remains to be clarified whether, or how, multiple levels of information are encoded by cells in LIP. Indeed, this topic has already been the focus of much attention; the novel approach taken in the study by Klein *et al.* [8] is to incorporate more naturalistic motivations for allocation of attention and choices, to shed light on the neural activity used for choice behavior in real social settings. While this goal is commendable, and proved fruitful, on this point the authors leave room for further advances.

The testing paradigm described by Klein *et al.* [8] was many steps removed from 'naturalistic'. Static images of monkeys were presented on a computer monitor, in the laboratory setting removed from the monkey colony. These images were artificially associated with juice rewards, and repeated hundreds upon hundreds of times over the course of many daily recording sessions. Despite these unnatural conditions, the images were given a value that was consistent with their importance in the monkeys' actual social settings. This suggests an almost compulsory importance placed on social dominance and reproductive salience, and may indicate neural specializations that are associated with parietal cortex to extract this 'valued' information.

Visual social cues independently modulated LIP activity, but only in the context of *choice* behavior. Other brain areas are apparently responsible for attaching attentional salience or reward value to visual social cues, implying a complex link between perceptions of — and behaviors towards — social cues (Figure 1). Brain regions important for processing visual social cues [10] also show modulation associated with eye movements [11] or show altered eye movements when lesioned [12]. Yet, to date, the connection between the perception of — and orienting towards — social cues remains to be tested in these areas. Other brain regions that might link the processing and valuation of social cues to behavioral responses include the orbitofrontal cortex, the inferior prefrontal convexity, the auditory cortex, and the hippocampus, all of which contain neurons that respond differentially to stimuli such as faces, body parts, and/or expressions and gestures (Figure 1; see [13] for review).

The data of Klein *et al.* [8] do not address the neural substrates for *perceiving* social cues; nevertheless, it is one of the first studies to show a neural link between evaluations of and actions towards social signals, as part of a broader network of regions concerned with processing social signals. Moreover, the addition of social cues as reward-associated modulators of LIP 'choice' activity may provide another framework from which to view the growing number of attention- and intention-based studies of parietal cortex function in human and non-human primates alike.

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Organelle Evolution: What's in a Name?

Plastids are organelles derived from cyanobacterial endosymbionts and the evolutionary process that gave rise to them is well understood. Or is it? The complete genome sequence of a recently evolved photosynthetic body in *Paulinella chromatophora* is cause for reflection on the distinction between 'endosymbiont' and 'organelle', and how the boundaries between these terms can blur.

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On Christmas Eve 1894 the German biologist Robert Lauterborn discovered a strange new eukaryotic microbe, which he called *Paulinella chromatophora* [1,2]. The organism had blue–green photosynthetic bodies — 'chromatophores' — reminiscent of

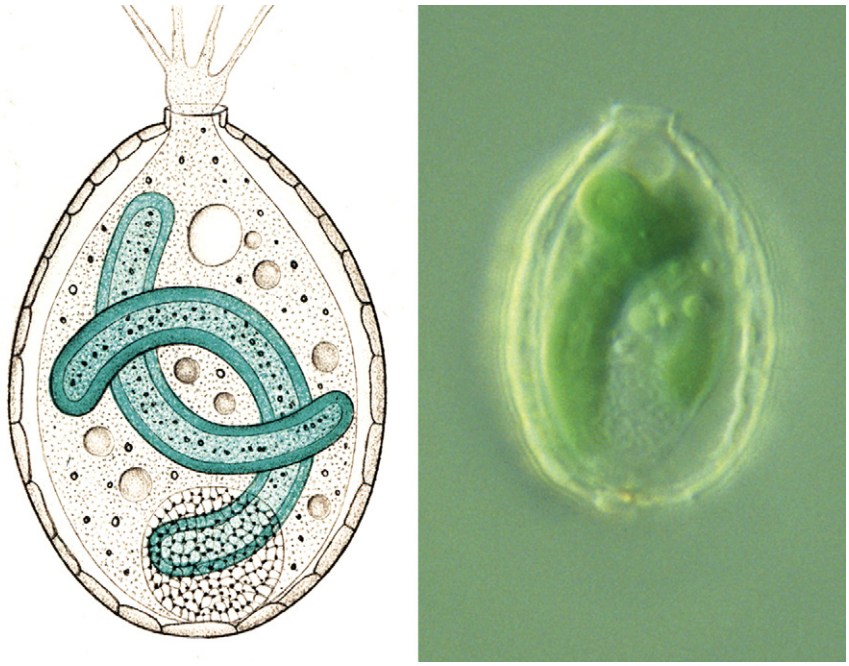

Figure 1. *Paulinella* then and now.

On the left is a line drawing from the original description of *Paulinella* in 1895 by Lauderborn [1] as reproduced on the cover of *Protist* (Vol. 156 issue 2). On the right, a light micrograph of *Paulinella* in culture today (image courtesy of Michael Melkonian). In both, the distinctive pair of green, sausage-shaped chromatophores are readily visible.

plastids, though clearly much more cyanobacterial in essence than the well-known photosynthetic organelles of plants and algae (Figure 1). With the benefit of hindsight, it would seem that Lauterborn recognized the general significance of his discovery [2], though at the time our understanding of the relationship between endosymbiosis and organelles was still in its infancy. More recent speculation has centered on the extent to which the chromatophore might represent a second origin of plastids [3–9]. If so, comparison with other plastids could illuminate basic principles of endosymbiotic integration by showing how the transformation from endosymbiont to organelle unfolded twice independently. Now, more than 100 years after Lauterborn's exciting find, Nowack *et al.* [10], in a recent issue of *Current Biology*, make a major leap forward in settling, or perhaps reframing, this question by presenting the complete sequence of the chromatophore genome. The genome is significantly reduced compared with that of its closest free-living cyanobacterial relatives and its gene complement provides fascinating insight into the potential metabolic connections it has forged with its host.

Until recently, unlocking the secrets of *P. chromatophora* has progressed slowly, as the organism is rare in nature and not easily tamed in the lab. Decades of painstaking work have nevertheless shown that *P. chromatophora* is indeed phototrophic, unlike its close relative *P. ovalis* (which feeds on cyanobacteria [11]), and that its chromatophores cannot be cultured in the absence of their host [12]. Furthermore, the chromatophores are reminiscent of plastids in that their division is tightly linked to that of the cell in which they reside, and that they transfer photosynthate to the host cytoplasm [13]. Recent molecular data [7,9] have confirmed original speculations that the chromatophores are similar to cyanobacteria of the genus *Synechococcus*, but tantalizingly little has been discovered about how the host and chromatophore have integrated.

Nowack and colleagues [10] now show that the chromatophore genome is a miniature among cyanobacteria. It is ~1 megabase pairs (Mbp) in size and contains a mere 867 protein-coding genes, in stark contrast to the ~3 Mbp genome of its close relatives in the genus *Synechococcus*, which have ~3,300 genes. Finding a reduced gene set in an endosymbiont genome comes as no surprise, but the pattern of missing genes in the chromatophore is important. In particular, the types of gene that are retained or missing are decidedly non-random. In general, whole metabolic pathways are either present or absent. For example, all genes related to the synthesis of several amino acids and other small molecules are completely absent from the genome (which is not unusual for a symbiont dependent on its host). However, the remaining pathways are, for the most part, both essential and represented in their entirety. Most importantly, nearly every gene encoding a protein involved in light harvesting and photosynthesis is retained in the genome. Both of these characteristics stand in contrast to the gene content of what are considered *bona fide* organellar genomes, such as those of mitochondria, plastids, and nucleomorphs [14,15]. In all these genomes, genes for many essential cellular processes (e.g. DNA replication and translation initiation) are completely missing, and other processes are only partially represented — some genes remain and others are absent. This is because the 'missing' genes have been moved to the host genome and their protein products are targeted back to the compartment in which they originally functioned [16,17]. On the whole, the *Paulinella* chromatophore genome sequence suggests that this cellular entity is dependent on its host for consumables, but perhaps not for organelle-specific information, in contrast to mitochondria and plastids.

This leads to a larger question — what differentiates an organelle from an endosymbiont? A common view is that, unlike endosymbionts, organelles have transferred genes to their host and are dependent on a dedicated targeting system to re-import their protein products [18]. This is to say, the endosymbiont-turned-organelle is reliant on its host to maintain its

genetic information. Under this definition, the chromatophore genome cannot explicitly tell us whether it is an organelle or not, since the defining data are in the host nucleus. Nevertheless, the pattern of missing genes certainly suggests that it is not genetically integrated with its host in the same way as mitochondria and plastids.

Tidy though it may be, this conclusion does not do justice to the question of the status of the *Paulinella* chromatophore, because there are other criteria one might use to distinguish organelle from endosymbiont. For example, what about the degree of cellular integration between endosymbiont and host? In *Paulinella,* there are always two chromatophores per cell that are carefully partitioned between dividing daughter amoebae and subsequently divide at a specific and consistent point in the host cell cycle [12]. This process does not necessarily involve genetic integration, but to achieve this level of synchrony the host must exert a significant degree of control over the chromatophore at the level of the cell. One might therefore argue that an endosymbiont becomes an organelle when its host controls its division and segregation, even without genetic integration (a situation that might also be true of some 'tertiary' plastids commonly regarded as organelles, e.g. [19]). Metabolic integration is an even more vague criterion as there is a huge range of such associations known and it is difficult to single out a specific event as the tipping point between endosymbiont and organelle. That said, however, one can imagine equally ambiguous situations with other criteria. Imagine an endosymbiont that has transferred genes to its host and imports their protein products. It is fully genetically integrated, but, if circumstances change such that these genes become disposable while others retained in the endosymbiont remain essential, then the process of genetic integration could be reversed. Admittedly, this is not a likely series of events, but it does illustrate that no criterion is completely immune to ambiguity.

Biological diversity is notoriously difficult to pigeonhole, and defining recurring events is especially hard, as illustrated by the ambiguous nature of parasites, commensals, and symbionts in general [20]. In distinguishing organelles and endosymbionts, the spectrum of symbiotic interactions between cells is vast and non-linear, since there are not only varying degrees of integration between cells, but cells also integrate at different levels (genetic, cellular, metabolic) and for many different reasons. Drawing a line beneath some and calling them organelles and others endosymbionts will never be completely unambiguous. One definition may facilitate discussion on one aspect of a range of possible associations but prove useless in a different context.

Returning to *Paulinella*, the significance of this organism is that it has the potential to reveal how the transformation from endosymbiont to organelle may have unfolded twice independently. If the pattern of gene loss in the *Paulinella* chromatophore genome augurs an absence of gene transfer and protein targeting, then the chromatophore is not an organelle under a strict definition based on genetic integration. So has it failed to deliver on its promise? Not if one looks at it with an open mind. In our view, to seek a parallel case of organellogenesis but at the same time define the outcome so strictly that only one possible chain of events could have led to the outcome is circular and restrictive. Specifically, if we use genetic integration as *the* defining feature of an organelle, we will never be able to compare different routes to organellogenesis because we have artificially predefined a single route. If the chromatophore is not genetically integrated with its host, it might prove to be even more interesting than if it were, but only if we look past definitions and focus on the biology. By focusing on how it *did* integrate, perhaps we will find a truly parallel pathway for the integration of two cells.

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