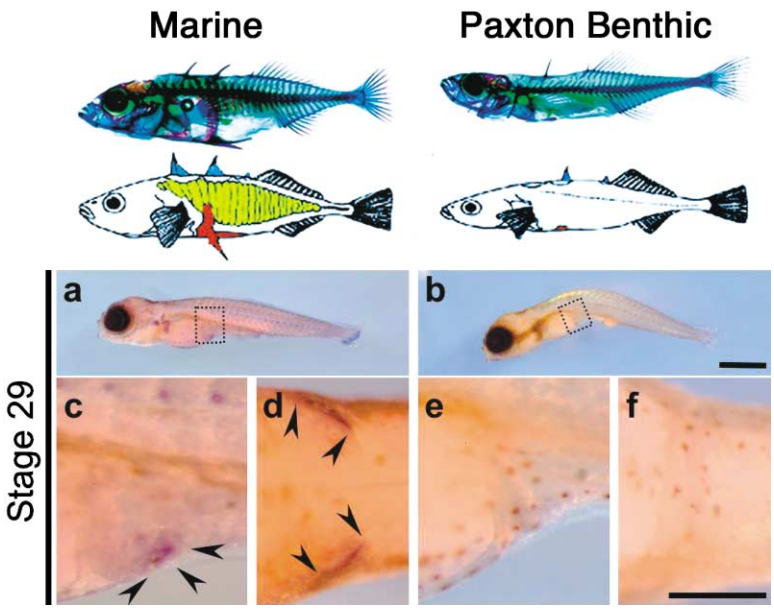

Figure 1. Pitx1 Expression Differences between the Marine and Benthic Forms Correlates with the Level of Pelvic Reduction

The marine species has a more developed pelvic region than the benthic species (drawing from Cole et al., 2003). *Pitx1* is expressed in the pelvic region of the st. 29 marine species (A, C, D). (C) and (D) are enlarged lateral and ventral views, respectively, with the arrows showing *Pitx1* expression. *Pitx1* expression is absent in the st. 29 Paxton benthic individual (B, E, F). (E) and (F) are enlarged lateral and ventral views showing absence of *Pitx1* expression (reprinted by permission from Nature, Shapiro et al., 2004, copyright 2004 Macmillan Publishers Ltd. [http://www.nature.com]).

This study brings us closer to answering many questions about evolution of the pelvic reduction in the Paxton benthic population. A second interesting question is whether pelvic reduction evolved in the same way or different ways in other populations. Fortunately, because of the wealth of isolated populations of sticklebacks, Shapiro et al. were able to examine an Icelandic population with the reduced pelvic phenotype. When an Icelandic individual was crossed to a Paxton individual, the pelvic reduced phenotype was not complemented. Therefore, it is possible that mutations in the same gene are responsible for the pelvic reduction in both populations. This phenomenon of parallel evolution may even translate to the past; amazingly, a fossil stickleback with a reduced pelvis shows the *Pitx1* knockout's characteristic asymmetry.

This study shows the beauty of the stickleback system and its potential for answering many interesting questions in evolutionary biology. The developmental and genetic tools are quickly expanding for this system; it might soon be possible to find the mutations responsible for different phenotypes and to functionally test them by overexpression or transgenic analyses. Furthermore, by examining similar phenotypes in multiple populations, it will be possible to see what range of genetic changes cause the same phenotypic changes. The establishment of evolutionary model systems is allowing us to address questions about the evolution of body form that naturalists would never have thought possible and that dieters can only fantasize about.

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Reduction and Compaction in the Genome of the Apicomplexan Parasite *Cryptosporidium parvum*

The complete genome of the apicomplexan parasite *Cryptosporidium parvum* reveals many new insights into apicomplexan biology and evolution, as well as the general process of genome reduction in parasites. The genome is globally compacted, but gene loss seems to be focused, in particular in relation to organelles. Massive losses of mitochondrial genes have taken place and there is no evidence of any plastid-related genes, providing a useful tool for examining putative plastid proteins in *Plasmodium* and other apicomplexans.

Parasites genomes are often considered to be "reduced" or "degenerate," but exactly what do these terms mean? How various are the forces that affect genome size and density, and how do their effects differ in different parasites? While it has been clear for some time that parasite genomes are often small, these questions have persisted. Now, however, genomic data are emerging from a number of parasites that will allow us to begin to examine how parasite genomes react to growing specialization and loss of self-sufficiency. One of the first lessons is the distinction between what we could call "elimination" and "compaction." To understand the difference, consider a bus (the genome) filled with travelers (the genes). If the bus pulls over and half the travelers get off, that is elimination. If, however, the bus pulls over and the travelers are transferred to a small van, that is compaction. Putting yourself in the traveler's shoes, the difference is clear. The newly completed genome of *Cryptosporidium parvum* reported by Abrahamsen et al. (2004) represents a major advance in our understanding of both these processes in parasite genomes.

Cryptosporidium is an apicomplexan, related to the malaria parasite *Plasmodium*, *Toxoplasma*, and other important parasites. At 9.1 Mbp, the *Cryptosporidium* genome is 2.5 times smaller than the *Plasmodium* genome, but its gene density is 1.8 times greater, resulting in about three-quarters as many genes as *Plasmodium* (Abrahamsen et al., 2004). In *Cryptosporidium*, genome reduction has occurred predominantly through the shortening of intergenic regions, the loss and shortening of introns, and a reduction in the mean length of the genes themselves. In other words, *Cryptosporidium* has eliminated genome content to some extent, but has compacted it a good deal more. Contrast this with the other well-studied intracellular parasite genomes, those of microsporidia (Katinka et al., 2001; Slamovits et al., 2004). Microsporidian genomes are much smaller (the smallest being a mere 2.3 Mbp), and have suffered both severe elimination (the complete genome of *Encephalitozoon* encodes about 2000 genes) and compaction (the *Encephalitozoon* gene density is over twice that of *Cryptosporidium*). Indeed, these two forces do tend to work together in reduced genomes such as those of the organelles and bacteria where they are best studied. The relative gene-richness of *Cryptosporidium* is, therefore, not only somewhat surprising, but also presents an excellent opportunity to study a genome that has apparently not been affected by the two processes equally.

Not to say that the *Cryptosporidium* genome is completely unaffected by elimination: it is glaringly evident in relation to organelles. *Cryptosporidium*'s mitochondrion has long been a source of interest for its unusual anaerobic metabolism and cryptic nature (Slapeta and Keithly, 2004; Williams and Keeling, 2003), and indeed the complement of mitochondrion-targeted enzymes found in the genome is severely reduced, indicating that the organelle has adopted a restricted set of duties. More drastic yet, there was reason to suspect *Cryptosporidium* would contain a plastid, but no molecular trace of this organelle was found in the genome. Plastids are the photosynthetic organelles of plants and algae, and the recent discovery of a cryptic, nonphotosynthetic plastid in other apicomplexan parasites has sparked interest from cell and evolutionary biologists, in part as a potential target for drugs (Foth and McFadden, 2003). Evidence for a plastid in *Cryptosporidium* has always been lacking (Zhu et al., 2000), and the genome sequence now confirms the absence of any plastid-targeted proteins or a plastid genome. This could mean one of two things: the plastid has been lost completely, or it originated in other apicomplexa only after *Cryptosporidium* diverged. To completely lose a plastid, *Cryptosporidium* would have to have significantly retooled its biochemistry to make all plastid-associated proteins unnecessary or redundant, allowing the elimination of the genes that encode them and the organelle itself. While plastid reduction is common in eukaryotes, outright loss has never been unambiguously documented. Given the unusual and reduced nature of *Cryptosporidium*, however, perhaps it is a likely candidate for such a remarkable transformation. If, alternatively, *Cryptosporidium* never had a plastid, there are profound implications for the evolution of apicomplexan plastids, which are amplified by the pivotal position of *Cryptosporidium* in the evolutionary tree of apicomplexa. *Cryptosporidium* was once believed to be related to coccidian apicomplexa; however, molecular data have now shown it to be a relative of the diverse (but little-studied) gregarine apicomplexa, which fall at the base of the apicomplexan tree (Leander and Keeling, 2003). Such a deep position is consistent with a relatively recent origin of plastids in other apicomplexa, but there is also a growing body of molecular evidence to suggest that the ancestors of all apicomplexa and their relatives (the dinoflagellates) already had a plastid (Fast et al., 2001). Distinguishing between these two possibilities is an important step in understanding both the biology of *Cryptosporidium*, and the plastid of all apicomplexa. The solution will likely come from improving our presently poor understanding of the gregarines, since these relatives of *Cryptosporidium* are far less reduced and are, therefore, more likely to retain a cryptic plastid if their ancestors possessed one.

In either case, the absence of a plastid in *Cryptosporidium* can already tell us a great deal about plastids in apicomplexa. For instance, the *Plasmodium* genome has been estimated to encode about 550 genes for plastid-targeted proteins (Ralph et al., 2004). If *Cryptosporidium* never had a plastid or completely lost one, then the validity of these predictions can be tested because most or all *Plasmodium* proteins that are truly associated with the plastid should be absent from *Cryptosporidium*. If this estimate is correct, and *Cryptosporidium* lost its organelle, then plastid proteins alone could represent more than one-third of the genes eliminated from the *Cryptosporidium* genome.

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