

GENOME WATCH

Animals learn new tricks from microorganisms

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This month's Genome Watch reviews a series of recent papers that describes horizontal gene transfer from microorganisms to nematodes.

Most — if not all — animals depend on microorganisms for survival. But for some animals, having microorganisms as symbionts is not enough. They have gone a step further and incorporated copies of microbial genes into their own genomes through a process known as lateral or horizontal gene transfer (HGT). Inter-kingdom HGT was initially controversial, as it is hard to prove that a gene has really been transferred from a microorganism, rather than being similar through common ancestry or convergent evolution. However, there is now mounting evidence for inter-kingdom HGT¹, even though a bona fide method of excluding all scenarios other than HGT remains to be established.

Whole-genome sequencing of nematodes has contributed to the identification of many HGT candidates originating from a diverse set of microorganisms. For instance, gamma-proteobacteria have contributed six glycoside hydrolase family 16 (GH16) proteins to the genome of *Bursaphelenchus xylophilus* (the pine wilt nematode). The genome of *B. xylophilus* also contains two hydrolases from the phylum Firmicutes, as well as four aspartic-type endopeptidases and 11 GH45 cellulases thought to originate from the fungal phylum Ascomycota². The genome of *Pristionchus pacificus* (a necromenic nematode with cosmopolitan distribution) contains genes thought to originate from slime moulds and soil bacteria³, and *Meloidogyne incognita* (the root-knot nematode) contains genes similar to those of actinobacteria, proteobacteria and fungi⁴.

These are not a random selection of genes; they have highly specialized functions that are important for the biology of the nematodes². In fact, most of the candidate HGT genes in nematodes encode enzymes that break down the cell walls of plants and fungi^{2,4,5}. It seems that, with the help of HGT, animals can harness the incredible capacity of microorganisms to break down almost any organic substance.

Although whole-genome sequencing has identified several HGT candidates, many questions remain about their functions and evolutionary paths. Are these genes really functional in the nematode? Which evolutionary forces affect the genes after HGT? An attempt at addressing these questions was recently made using 454-sequencing of ten diplogastrid nematode transcriptomes⁵. Transcripts of functioning cellulase genes — thought to have become part of the nematode genome through HGT — were identified, and the phylogenetic relationship between the ten species as inferred from the cellulases was found to be similar to a previously published phylogeny of ribosomal proteins⁵. This indicates that all nematode cellulases were derived from a single HGT event to an ancestral diplogastrid nematode. For three of these HGT genes, DNA sequences were obtained from a further 24 *P. pacificus* specimens of worldwide origin. These data show that after the HGT event

the genes continued to evolve, with several gene duplications or deletions and high DNA substitution rates⁵. Theoretically, HGT between kingdoms should cause a massive change in selection pressures for a gene, as this gene needs to maintain functionality in a novel genomic and epigenetic setting. Apart from

selective amino acid changes, the codon usage bias may also evolve neutrally to match that of the new genome. Both processes should result in an elevated evolutionary rate in the transferred gene just after the HGT event. However, an understanding of the expected patterns of molecular evolution in horizontally transferred genes can only be gained by gathering more observations from a wider range of recent and well-supported HGT events.

Genome studies of microorganisms have important contributions to make to the study of inter-kingdom gene transfers. First, having genomes from a larger diversity of microbial organisms will facilitate pinpointing of the species involved in the exchange and provide stronger evidence for HGT. Second, if gene functions and pathways can be understood in the microorganism and compared to those in the nematode, we can better understand how genes that are transferred between kingdoms can remain functional in their new genomes. This will require collaboration over phylogenetic barriers, and across biological disciplines too.

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Competing interests statement

The author declares no competing financial interests.

1. Richards, T. A. *et al.* Horizontal gene transfer facilitated the evolution of plant parasitic mechanisms in the oomycetes. *Proc. Natl Acad. Sci.* **108**, 15258–15263 (2011).
2. Kikuchi, T. *et al.* Genomic insights into the origin of parasitism in the emerging plant pathogen *Bursaphelenchus xylophilus*. *PLoS Pathog.* **7**, e1002219 (2011).
3. Dieterich, C. *et al.* The *Pristionchus pacificus* genome provides a unique perspective on nematode lifestyle and parasitism. *Nature Genet.* **40**, 1193–1198 (2008).
4. Abad, P. *et al.* Genome sequence of the metazoan plant-parasitic nematode *Meloidogyne incognita*. *Nature Biotech.* **26**, 909–915 (2008).
5. Mayer, W., *et al.* Horizontal gene transfer of microbial cellulases into nematode genomes is associated with functional assimilation and gene turnover. *BMC Evol. Biol.* **11**, 13 (2011).

