GENOME EVOLUTION

Embracing change the microbial way

Evolutionary geneticists and business strategists alike realize the importance of dealing with change. An important question that both of these groups must address is how strategies to adapt to change are implemented on a global scale. Aras and colleagues now answer this question for *Helicobacter pylori*, which is highly adapted to live in the stomach of its human host. They show that in the absence of co-colonizing microbes, *H. pylori* retains its ability to adapt to the environmental changes in its niche, thanks to extensive repetitive DNA stretches that facilitate intragenomic recombination. This strategy allows new genetic variation to be generated that ultimately provides the phenotypic options that are required to adapt to new environments. The density and distribution of repetitive DNA sequences in *H. pylori* are representative of bacteria with smaller (<2 Mb) genomes, which indicates that the proposed mechanism might be conserved among prokaryotes to increase genome plasticity.

Bacteria, such as *Escherichia coli*, which share their niche with other bacterial species might diversify and evolve through interspecies horizontal DNA transfer. This option is not open to *H. pylori*, which is essentially alone in colonizing the stomach. Aras *et al.* proposed that the numerous direct DNA repeats that are present in the *H. pylori* genome might contribute to its diversity by promoting the duplication or deletion of intervening sequences. They first characterized direct repeats in 51 prokaryotic genomes and found species-specific variation in repeat size, density and distribution. Repeat distribution was not random — paired repeats <5 kb apart were clustered, perhaps serving as potential hotspots of recombination.

The authors found that these potential hotspots lie in hypervariable chromosome sequences and that variation in these regions affects the host–microbe relationship.

Using a genetically-engineered deletion cassette flanked by direct repeats of different sizes, Aras *et al.* then showed that repeat length affects recombination frequency — the longer the repeats, the more frequent the rearrangement — and that intragenomic deletion frequencies were similar to mutation or natural DNA-uptake frequencies.

So, the authors have proposed a new way in which organisms such as *H. pylori* that do not share their niche with other species can generate genomic diversity; among other medically important examples in this class is *Mycobacterium tuberculosis*. They argue that this mechanism might be as important in generating diversity as mutation or transformation. *H. pylori* might be limited in its ability to exchange genetic material with other species, but because it can naturally uptake DNA from the environment it can regain deleted DNA from fellow *H. pylori* that occupy the same host.

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References and links

ORIGINAL RESEARCH PAPER Aras, R. A. *et al.* Extensive repetitive DNA facilitates prokaryotic genome plasticity. *Proc. Natl Acad. Sci. USA* 30 October 2003 (doi:10.1073/pnas.1735481100)