

## GENOME WATCH

# Natural transformers

Claire Chewapreecha

This month's Genome Watch highlights *in natura* cases showing the role of recombination in bacterial evolution, and *in vitro* studies that focus on the mechanisms of recombination.

More than 60 bacterial species have been shown to be naturally transformable — that is, they can take up, incorporate and express exogenous DNA. The uptake of DNA from the environment allows the exchange of alleles and loci, thus generating diversity and facilitating bacterial survival in selective environments. It is only recently, using second-generation sequencing technology, that recombination in nature has been captured precisely. This, together with *in vitro* studies, has furthered our understanding of the mechanisms of recombination in bacteria.

*Vibrio* is a genus of naturally transformable Gram-negative bacteria that grow and persist in coastal aquatic environments. To investigate environmental differentiation and capture transformation *in natura*, a recent study examined the genomes of 20 *Vibrio cyclitrophicus* isolates from two populations that have recently diverged and live in different marine habitats<sup>1</sup>. In the core genomes, 99% showed no pattern of ecological partitioning (polymorphic sites were stochastically detected in both populations). This suggests that the signal of common evolutionary

ancestry has been blurred by frequent homologous recombination events, in agreement with a previous study in *Vibrio cholerae*<sup>2</sup>. Moreover, recombination affected genes

of all functions equally, indicating that it is not driven by selection.

However, using pairwise genome analysis, the authors observed that for recent recombination events there was a trend towards gene exchange within, rather than between, habitats. This could facilitate differentiation between isolates from different environments. In this case, selection does seem to act on a few discrete genomic regions that harbour potential habitat-specific genes; these regions were detected exclusively in one population. Therefore, here adaptation seems to be driven by gene-specific rather than genome-wide selective sweeps.

It is thus clear that recombination events play a key part in bacterial evolution, allowing the differentiation of species that reside in different environments. To better understand the mechanism of recombination, two recent studies looked at *in vitro* genome-wide transformation of the naturally transformable bacteria *Streptococcus pneumoniae*<sup>3</sup> (a Gram-positive species) and *Haemophilus influenzae*<sup>4</sup> (a Gram-negative species). Using Illumina sequencing technology, the authors generated high-resolution snapshots of individual transformation events against known genomic backgrounds. They were thus able to identify the positions and sizes of inserted fragments, along with physical properties of the DNA that affected the recombination process.

The studies illustrated several features of recombination that seem to be shared between the two species. Although it had previously been assumed that DNA exchange requires flanking regions of high sequence similarity, both studies concluded that regions which had undergone recombination did not have noticeably high sequence identity between donors and recipients. For example, repetitive elements within the genomes (RUP, BOX and SPRITE elements in *S. pneumoniae*, and USS elements in *H. influenzae*) did not

seem to be involved in recombination, as they were not found to be preferentially imported or enriched in the genomes resulting from the recombination events. Croucher *et al.*<sup>3</sup> showed that, instead, the availability of DNA is a key factor regulating transformation, as increasing the concentration of donor DNA by 100-fold caused a 38-fold increase in the number of transformants. Moreover, the presence of insertions or deletions seemed to block strand exchange and limit recombination at those sites in both studies. Finally, Croucher *et al.*<sup>3</sup> found that DNA mismatch repair (MMR), which is required for repairing mismatches formed between recombining sequences and is thought to be a barrier to DNA transfer, had no effect on transformation when recombining fragments showed low sequence similarity.

Recombination is one of the main players in bacterial evolution. Information gathered from these and other *in vitro* studies has helped to capture the mechanistic details of the recombination process at a finer level. Moreover, the *in natura* example reflects the roles of recombination in maintaining genetic flow as well as introducing new advantageous alleles to bacterial populations.

Claire Chewapreecha is at the Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK.  
e-mail: [microbes@sanger.ac.uk](mailto:microbes@sanger.ac.uk)  
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### Competing interests statement

The author declares no competing financial interests.

