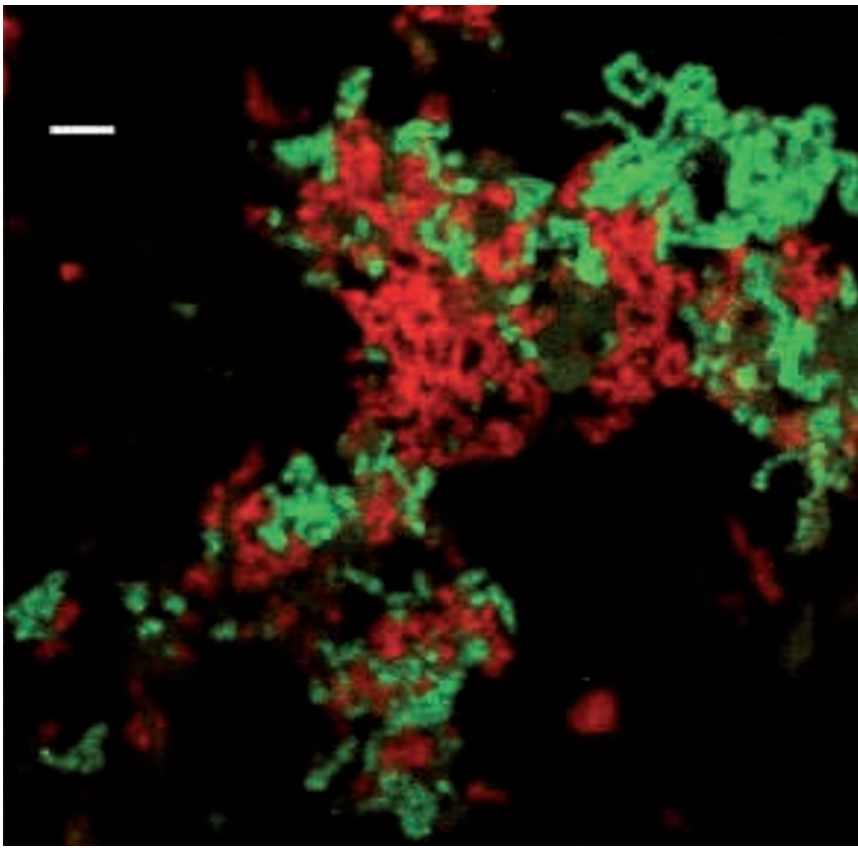
BACTERIAL GENETICS

A tiny alternative

In bacteria, there is a strong correlation between genome size and GC content: the smaller the genome, the lower the GC content. Now, John McCutcheon, Bradon McDonald and Nancy Moran describe a fascinating exception to this rule.

It is estimated that more than 10% of insect species carry bacterial endosymbionts, which supply nutrients that are essential for insect growth. The genomes of the bacterial endosymbionts that have been sequenced so far are much smaller than the genomes of other intracellular or free-living bacteria and all have a low GC content. In this study, the authors analysed the genome of a previously uncharacterized cicada endosymbiont, which they propose should be called *Candidatus* Hodgkinia cicadicola.

At 144 kb, this is the smallest bacterial genome that has been sequenced to date, and the authors identified several unusual genomic features. The most striking of these was the GC content, which, at 58%, is unusually high for such a small genome. Intriguingly, the authors also noticed that *Candidatus* Hodgkinia cicadicola uses an alternative genetic code. In most species the codon UGA is a stop codon, but in a few exceptions, such as the mycoplasma and in some mitochondria, a recoding event has occurred and UGA encodes the amino acid tryptophan. Genetic analysis revealed that in *Candidatus* Hodgkinia cicadicola UGA codes for tryptophan, and this was verified by mass spectrometry-based shotgun protein sequencing.



Micrograph showing *Candidatus* Hodgkinia cicadicola (red) in close association with another endosymbiont, *Candidatus* Sulcia muelleri (green) in the cicada *Diceroprocta semicincta*. The scale bar represents 10 μm. Image reproduced from McCutcheon, J. P., McDonald, B. R. & Moran, N. P. Origin of an alternative genetic code in the extremely small and GC-rich genome of a bacterial symbiont. *PLoS Genet.* **5**, e1000565 (2009).

> “…it is genome reduction not GC content that drives codon reassignment.”

Such recoding events are rare and had previously only been observed in genomes with a low GC content. It had been proposed that recoding occurred as a result of ‘codon capture’: the AT bias of these genomes would allow UGA to be replaced by UAA, and UGA could eventually be reassigned to code for an amino acid. Given the high GC content found in the *Candidatus* Hodgkinia cicadicola genome, McCutcheon *et al.* propose instead that it is genome reduction not GC content that drives codon reassignment. Clearly, endosymbionts have much left to teach us.

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ORIGINAL RESEARCH PAPER McCutcheon, J. P., McDonald, B. R. & Moran, N. P. Origin of an alternative genetic code in the extremely small and GC-rich genome of a bacterial symbiont. *PLoS Genet.* **5**, e1000565 (2009)