An AT Mutational Bias in the Tiny GC-Rich Endosymbiont Genome of Hodgkinia

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Accepted: 18 November 2011
Data deposition: The cicada mitochondrial COI sequences have been deposited in Genbank under the accession numbers JN679206 and JN679207.

Abstract

The fractional guanine + cytosine (GC) contents of sequenced bacterial genomes range from 13% to 75%. Despite several decades of research aimed at understanding this wide variation, the forces controlling GC content are not well understood. Recent work has suggested that a universal adenine + thymine (AT) mutational bias exists in all bacteria and that the elevated GC contents found in some bacterial genomes is due to genome-wide selection for increased GC content. These results are generally consistent with the low GC contents observed in most strict endosymbiotic bacterial genomes, where the loss of DNA repair mechanisms combined with the population genetic effects of small effective population sizes and decreased recombination should lower the efficacy of selection and shift the equilibrium GC content in the mutationally favored AT direction. Surprisingly, the two smallest bacterial genomes, Candidatus Hodgkinia cicadicola (144 kb) and Candidatus Tremblaya princeps (139 kb), have the unusual combination of highly reduced genomes and elevated GC contents, raising the possibility that these bacteria may be exceptions to the otherwise apparent universal bacterial AT mutational bias. Here, using population genomic data generated from the Hodgkinia genome project, we show that Hodgkinia has a clear AT mutational bias. These results provide further evidence that an AT mutational bias is universal in bacteria, even in strict endosymbionts with elevated genomic GC contents.

Keywords: GC content, endosymbiont, mutational bias.

The Smallest Bacterial Genomes Tend to Be Strongly AT Biased, with the Exception of Hodgkinia and Tremblaya

Genome reduction in bacteria is usually associated with a genome-wide shift toward increased AT content (Moran 2002; Bentley and Parkhill 2004; McCutcheon et al. 2009). This pattern is especially pronounced in bacteria that live exclusively in the cytoplasm of host cells; for example, the two most extremely AT-biased bacterial genomes yet reported are from the insect nutritional endosymbionts Candidatus Zinderia insecticola (13.5% GC) (McCutcheon and Moran 2010) and Candidatus Carsonella ruddii (16.5% GC) (Nakabachi et al. 2006). Two mechanisms are thought to explain the reduced GC content of endosymbiont genomes. First, endosymbionts tend to lose genes involved in DNA repair and recombination during genome reduction (Dale et al. 2003; Moran et al. 2008), which increases the load of unrepaired DNA damage. Second, endosymbionts have small effective population sizes and decreased rates of recombination, which reduces the efficacy of selection and allows more slightly deleterious mutations to be fixed by random genetic drift (Moran 1996; Woolfit and Bromham 2003). Combined with what seems to be an AT mutational bias in bacteria lacking DNA repair enzymes (Lind and Andersson 2008), these forces are thought to shift the GC–AT equilibrium toward AT in endosymbiont genomes. Until recently, empirical data from complete bacterial genomes universally supported this hypothesis. Remarkably, the only known exceptions to this trend are from the two bacteria with the smallest reported genomes: Candidatus Hodgkinia cicadicola (hereby referred to as Hodgkinia for simplicity, 144 kb, 58.4% GC; McCutcheon et al. 2009) and Candidatus Tremblaya princeps (Tremblaya, 138 kb, 58.8% GC; McCutcheon and von Dohlen 2011; López-Madrigal et al. 2011). Hodgkinia is a member of the Alphaproteobacteria, a group in which most free-living members have GC-rich genomes and most obligate intracellular members have...
reduced genomes that show the expected decrease in GC content (McCutcheon et al. 2009). These observations led to the hypothesis that the high GC content of Hodgkinia resulted from the retention of a GC mutational bias that was present in its free-living alphaproteobacterial ancestor (McCutcheon et al. 2009). That the GC content at third positions of 4-fold degenerate codons (GC4) in Hodgkinia is higher than the overall GC content in the genome (62.5% vs. 58.4%) seemed to support this hypothesis, as these positions are expected to be under little or no selection for protein-coding sequence and were therefore thought to more clearly reflect the mutational biases inherent in Hodgkinia's replication machinery (McCutcheon et al. 2009).

Recent Work Suggests that all Bacteria Have an Inherent AT Mutational Bias

Two recent reports provide evidence that an AT mutational bias exists in all bacteria (Hershberg and Petrov 2010; Hildebrand et al. 2010). The authors of both papers conclude that selection for increased GC content, or a selection-like process such as biased gene conversion, is the most likely explanation for the diverging patterns of AT-biased mutation and GC-biased substitution observed in most bacterial genomes (Hershberg and Petrov 2010; Hildebrand et al. 2010). Both papers also single out Hodgkinia as an outlier and a possible exception to this rule (Hershberg and Petrov 2010; Hildebrand et al. 2010). To help clarify the roles of mutational biases and selection on the GC content of the Hodgkinia genome, we sought to determine the direction of Hodgkinia's mutational bias (if any) from existing population data generated during genome sequencing.

Single Nucleotide Polymorphisms in the Hodgkinia Genome Reveal an AT Mutational Bias

The published Hodgkinia genome was generated by combining samples from 10 wild-caught individuals of the cicada Diceroprocta semicincta (McCutcheon et al. 2009). We reasoned that it might be possible to calculate mutational patterns from these population genomic data. We first reconfirmed that the pooled sample was from a single species of cicada by verifying a low level of sequence polymorphism in its mitochondrial cytochrome c oxidase I (COI) gene (about 0.6% of 815 sites were polymorphic, well within the 1–2% divergence levels typically seen in conspecific pairs of animal COI sequences; Hebert et al. 2003). We then calculated the number of single nucleotide polymorphisms (SNPs) in the Hodgkinia genome falling into all possible nucleotide change categories and found that the majority of the mutations (115 of 179 or 64%) were in the GC to AT direction. (The Tremblaya genome was generated from only three lab-reared insects, and no high-quality SNPs were observed in these data.)

To unambiguously assign a mutational direction to these SNPs, we used a draft Hodgkinia genome assembly from a closely related but undescribed cicada species (referred to here as the cryptic species) as an outgroup to verify the ancestral state of each position where a SNP was identified (for a complete description of the methods, see Supplementary Materials online). The pairwise nucleotide divergence between partial mitochondrial COI sequences from Diceroprocta semicincta and the cryptic species was 3.5%. Of the 179 SNPs initially identified, 12 were not covered by contigs from the cryptic species. These 12 were removed from the data set, resulting in 167 SNPs in which the direction of mutation could be confidently determined (fig. 1 and table 1; table S1, Supplementary Materials online). The expected equilibrium GC content (GCeq) given the mutational patterns observed in the polarized data is 42%, significantly lower than the observed genomic value of 58% (table 1).

To estimate the strength of selection acting on these SNPs, we calculated the ratio of nonsynonymous and synonymous polymorphisms per nonsynonymous and synonymous site (dN/dS) and found evidence for weak purifying selection (dN/dS = 0.37). This value is slightly lower but consistent with values reported previously for populations of clonal bacterial pathogens, which range from 0.45 to 0.64 (Hershberg and Petrov 2010). Differences in the magnitude of dN/dS need to be interpreted with caution in this situation, as this measure assumes that sequence polymorphisms are fixed substitutions between species and not intraspecific mutations segregating in a population (Kryazhimskiy and Plotkin 2008). Some SNPs in the pooled data set include those at high frequencies, and we assume that these SNPs have been segregating in the population for some time and may have been exposed to significant levels of purifying selection. To assess whether we could...
measure differences in 1) the levels of purifying selection and 2) the magnitude of the AT mutational bias for SNPs partitioned into different frequency bins, we calculated \(dN/dS\) and \(GC_{eq}\) values for SNPs binned at 0.1 frequency intervals (fig. 2). As 10 individuals were pooled for sequencing, an ideal experiment would reveal SNPs clustering at frequencies of 0.1, 0.2, 0.3, and so on up to 0.9. We did not observe an increased number of SNPs near these expected frequencies, and attribute this nonideal behavior to numerous potential experimental and computational artifacts (for a full discussion, see the Supplementary Materials online). Nevertheless, these results confirm that the SNPs present in the population at lower frequencies have been exposed to less purifying selection (indicated by a higher \(dN/dS\) value) and are more strongly AT biased than SNPs present at higher frequencies (fig. 2). For example, the \(GC_{eq}\) content of the \textit{Hodgkinia} genome is calculated to be 37% using only SNPs called at a frequency of 0.1 or less, lower than the 42% calculated when all SNPs are included. The true \textit{Hodgkinia} \(GC_{eq}\) is therefore probably closer to 37%, or perhaps even lower. From these data, we conclude that \textit{Hodgkinia} has an AT mutational bias.

Why Does \textit{Hodgkinia} Have an Elevated Genomic GC Content?

Although our data clearly show an AT mutational bias in \textit{Hodgkinia}, they do not directly implicate the force(s) responsible for the disparity between the observed patterns of mutation and substitution. Hershberg and Petrov (2010) and Hildebrand et al. (2010) suggest selection, or a selection-like process such as biased gene conversion, as the force driving the difference in bacteria. In bacteria, biased gene conversion involves horizontal gene transfer, recombination, and DNA repair-based mechanisms (Rocha and Feil 2010). As \textit{Hodgkinia} encodes no gene homologs capable of these processes (McCutcheon et al. 2009), biased gene conversion seems unlikely to be responsible for \textit{Hodgkinia}'s elevated GC content. Therefore, it appears that an unidentified selective force (or forces) is the most likely explanation for the GC compositional bias in the \textit{Hodgkinia} genome, although other explanations cannot be ruled out given the present data. For example, it is possible that the GC content in \textit{Hodgkinia} is mostly driven by mutational patterns, and that it recently underwent a shift from a GC to an AT mutation bias. Were this true, we would have had to have measured the mutational pattern soon after the change from a GC to an AT bias, but before this shift would have had the chance to alter the genome-wide nucleotide composition. This seems unlikely based simply on parsimony. Rather, given the results of Hershberg, Hildebrand, and coworkers, we favor the explanation that \textit{Hodgkinia} has, and has always had, an inherent AT mutational bias (Hershberg and Petrov 2010; Hildebrand et al. 2010).

Our results seem to present a paradox in the way that the population genetics of endosymbionts are normally considered. The prevailing view that endosymbionts have less efficacious selection, resulting from reduced effective population sizes (Moran 1996; Andersson and Kurland 1998; Woolfit and Bromham 2003; Fares et al. 2004), fits well with some features of \textit{Hodgkinia} genome, in particular with its tiny size and overall rapid rate of sequence evolution. The disparity between the \textit{Hodgkinia}'s AT-biased mutational pattern and GC-biased genome does not fit easily into this framework because these results seem to require either an atypically large effective population size for

\[\begin{array}{cccc}
\text{Counts} & \text{Number of GC} & \text{Number of AT} & \text{Rates} \\
& \rightarrow \text{AT} & \rightarrow \text{GC} & \text{GC}_{\text{eq}} \\
S & 54 (43–67) & 31 (22–40) & 1.9 \times 10^{-3} & 1.9 \times 10^{-3} & 63 & 50 (40–58) \\
NS & 40 (29–51) & 19 (12–26) & 8.0 \times 10^{-4} & 4.9 \times 10^{-4} & 56 & 38 (27–50) \\
IG & 12 (7–19) & 6 (2–10) & 2.6 \times 10^{-3} & 1.7 \times 10^{-3} & 56 & 39 (17–56) \\
All & 106 (89–122) & 56 (44–68) & 1.3 \times 10^{-3} & 9.5 \times 10^{-4} & 58 & 42 (36–49) \\
\end{array}\]
Hodgkinia or an unusually large selection coefficient for each individual AT–GC polymorphism in the population, or some combination of the two. It is possible that the population size of the host cicada is large and thus inflates the effective population size of Hodgkinia; theoretical work has shown that host population size can have large effects on mutation accumulation in Buchnera aphidicola in the context of its symbiosis with aphids (Rispe and Moran 2000). Why G or C nucleotides would be globally favored over A or T nucleotides is unclear and is an interesting area of future study.

Hodgkinia is found as a symbiont throughout the cicada lineage (data not shown), and it will be of interest to examine the GC contents and mutational biases of Hodgkinia across the diversity of cicadas. If GC-poor lineages of Hodgkinia are found, then it may be possible to narrow the list of possible selective forces responsible for the elevated GC levels in Hodgkinia from D. semicincta, by considering factors such as the environmental conditions and population structures of the insect hosts. The mutational results reported here would predict that a lineage of Hodgkinia in which the selective restraints on elevated GC content were severely reduced or eliminated would have a genomic GC content as low as, or possibly lower than, 37%.

Materials and Methods
SNPs were identified using both Roche 454 GSmapper and SWAP454 (Brockman et al. 2008) software. Genome-wide dN/dS and GCeq calculations were performed as described (Hershberg and Petrov 2010). The confidence intervals in table 1 were estimated using the rpois and quantile functions of R (2.13.0) by generating 1,000 value Poisson distributions with means equal to the mutation counts; rate, equilibrium, and 95% confidence interval calculations were performed with means equal to the mutation counts; rate, equilibrium, and 95% confidence interval calculations were performed on these distributions. Full Materials and Methods, including a detailed description of how the SNPs were polarized, are included in the Supplementary Materials online.

Supplementary Materials
Supplementary Materials, figure S1, and table S1 are available at Genome Biology and Evolution online (http://www.gbe.oxfordjournals.org/).

Acknowledgments
The Hodgkinia genome sequencing project was supported by the National Science Foundation Microbial Genome Sequencing award 0626716 to Nancy A. Moran. The reanalysis of these data presented in this paper was supported by the National Science Foundation Montana EPSCoR grant EPS-0701906.

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Associate editor: John Archibald