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**Leptospira Genomes Are Modified at 5'-GTAC**

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Genomic DNAs of 14 strains from seven species of the spirochete Leptospira were resistant to cleavage by the restriction endonuclease RsaI (5'-GTAC). A modified base co-migrating with m^5C was detected by chromatography. Genomic DNAs from other spirochetes, Borrelia group VS461, and Serpulina strains were not resistant to RsaI digestion. Modification at 5'-GTAm^5C may occur in most or all strains of all species of Leptospira but not in all genera of spirochetes. Genus-wide DNA modification has rarely been observed in bacteria.

Genomic DNAs of 14 strains from seven species in the spirochete genus *Leptospira* were cleaved with the restriction enzymes AflII (5'-GGWCC), HindIII (5'-AACTT), and EcoRI (5'-GAATTC), but not with RsaI (5'-GTAC) (for example, see Fig. 1). When bacteriophage λ DNA was mixed with *Leptospira* genomic DNAs and RsaI, only the λ DNA was cleaved. Thus, *Leptospira* genomic DNA is modified against restriction at the sequence 5'-GTAC or at a shorter sequence that encompasses 5'-GTAC. Previous publications indicate that Leptospira DNAs are cleaved by *AciI*, BamHI, BgiII, CiaI, EcoRI, EcoRV, HindIII, HpaI, NarI, NdrI, NruI, PstI, PvuII, SacI, SgrAI, SmaI, SseI, SrfI, Stul, XbaI, XhoI, and XmnI digestion (4, 10, 12, 18, 20, 21, 27, 30-32), indicating that most DNA sequences in *Leptospira* genomes are not modified.

Genomic DNAs of the type strain of *Borrelia* group VS461 (2, 28) and six *Serpulina* strains (T. B. Stanton, U.S. Department of Agriculture, Ames, Iowa) were susceptible to RsaI cleavage (data not shown). Thus, the modification of RsaI sites occurs in at least one genus but not in all genera of spirochetes.

DNA modification by bacterium-encoded enzymes has been reported at 6N-methyladenine (m^6A), SC-methylcytosine (m^5C), and 4N-methylcytosine (m^4C) (29). In addition, more exotic modifications have occasionally been observed in bacteriophage DNAs (e.g., glucosylated 5-hydroxymethylcytosine in *Escherichia coli* phage T4 [13, 24]). The ability of RsaI to cleave some DNA modifications has been tested (reviewed in reference 17). These data indicate that RsaI cleaves DNA modified at G*TA*m^5C but not G*TA*m^4C. The effect of G*TA*m^5C on RsaI activity is unknown. In addition, it is possible that a previously unknown modification is responsible for preventing cleavage. Of the known modifications, only 5'-G*TA*m^4C was excluded by the observation that *Leptospira* genomic DNA was resistant to cleavage by RsaI.

Genomic DNAs from three species of *Leptospira* were enzymatically hydrolyzed to nucleosides (11). The nucleosides were chromatographed on a reverse-phase RP-8 column (Brownlee Labs Inc., Santa Clara, Calif.) with the buffer systems of Gehrke et al. (11). Deoxynucleoside standards A, C, G, T, m^6A, and m^4C were purchased from Sigma (St. Louis, Mo.). m^6A was obtained from hydrolysates of BamHI polylinker after methylation with BamHI methyltransferase (New England Biolabs, Beverly, Mass.). All three strains contained no detectable m^6A or m^4C but did contain a small amount of a nucleoside that coeluted with m^5C. The levels of this base (expressed as a percentage of cytosines) were estimated to be 0.6% in *L. santarosai* shermani 1342 K (type strain), 1% in *L. borgpetersenii* ballum Mus 127, and 1.2% in *L. noguchii* Louisiana LSU 1945. The error associated with these measures is at least 50%.

Statistical calculations were performed to estimate the number of RsaI sites in *Leptospira* genomic DNA and thus the level of DNA modification necessary to block all RsaI sites. RsaI sites would occur once every 256 bp [(1/4)^4] in a completely random DNA sequence with all 4 bases represented equally. However, *Leptospira* genomes are actually A+T-rich and vary in G+C content from about 35 to 40% (6). In a genome of 40% G+C, the sequence 5'-GTAC should occur about once every 278 bp [1/(0.2)*(0.3)] if the bases are distributed randomly. Such a frequency of RsaI sites would require that 1.8% of cytosines be modified. The observed level of m^5C would therefore seem barely sufficient or insufficient to block all RsaI sites. An alternative and potentially more accurate strategy to estimate the frequency of RsaI sites was to observe the number of sites in sequences from various *Leptospira* genes available in the GenBank v70 data base plus more recently available sequences from Ralph et al. (23). The sample contained 19,227 bp after removal of closely homologous genes. This sample had a G+C content of 41.8%, slightly high because of the rRNA genes. RsaI sites were present in this sample only 33 times, an average of once every 582 bp (Table 1), which was significantly less than the once every 278 bp predicted from the base composition of the sample. Thus, on the basis of the observed frequency of 5'-GTAC sequences in *Leptospira* DNA, modification at all RsaI sites might require that only 0.86% of the cytosines (1/0.2 x 1/582) be modified. The level of modification detected by high-performance liquid chromatography could then more easily explain the resistance of the genomes to RsaI. These calculations also make it unlikely that the modification involves a much shorter sequence, such as 5'-TAC, because one would then expect a higher percentage of cytosines to be modified.

However, analysis of the *Leptospira* genomic DNA sample raised another question. Why was 5'-GTAC underrepresented in the sample of *Leptospira* genomic DNAs? Statistical analysis was performed with the Markov chain (15) and improvements (8) in an attempt to understand this observation. The methods take into account the frequency of shorter oligonucleotide sequences when calculating the expected
frequency of a sequence and should eliminate most of the effects on expected frequency caused by codon usage or other constraints acting at the di- or trinucleotide level. This analysis predicted 45 5'-GTAC sites in the sample, whereas only 33 such sequences were observed. Furthermore, the 23S rRNA gene is different from all of the other Leptospira sequences in the data base in that it has 14 5'-GTAC sites in otherwise be expected (data not shown). We speculate that the underrepresentation of 5'-GTAC in the Leptospira sample is related to the fact that this sequence is modified, as has been found for modifications in certain other species (e.g., references 5 and 9 and the references therein). For unknown reasons, 5'-CTAG is also exceptionally rare in the Leptospira DNA sample (Table 1) and in many other bacterial genomes (8, 16) but not in the Borrelia DNA sample. In contrast, CATG may be exceptionally rare in Borrelia sequences but not rare in the Leptospira DNA sample (Table 1) and is not rare in most other bacterial sequences (data not shown and reference 22). These observations indicate that there may be other unknown selective pressures that are working against these sequences in certain species.

Genomic DNA modifications that protect against restriction enzymes have been found several times in eubacterial genomes. So far, such sequence-specific modification systems are usually present in some, but not all, strains in any species. Such DNA modifications are usually part of sequence-specific restriction modification systems (e.g., see references 7 and 29). The possibility of a restriction endonuclease with a 5'-GTAC specificity present in all Leptospira genomes examined has not been excluded, although we failed to detect a 5'-GTAC-specific system (data not shown). If such a restriction system exists in all strains of all species in a genus, this distribution would be unprecedented.

DNA modifications not associated with a restriction endonuclease have been observed in bacteria, including the adenine-specific methylation (at 5'-GATC or a subset of such sites) which occurs in 3 of 22 strains of the spirochete Borrelia burgdorferi and in the 1 strain examined from five of six other species of Borrelia (19). However, such sequence-specific modification systems are similar to restriction modification that they are usually present in some, but not all, strains in any species.

**TABLE 1. Observed and expected occurrences for some tetranucleotides in a sample of Leptospira and Borrelia genes**

<table>
<thead>
<tr>
<th>Tetranucleotide</th>
<th>Occurrence of tetranucleotide in:</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Leptospira genome</td>
</tr>
<tr>
<td></td>
<td>Observed</td>
</tr>
<tr>
<td>GATC</td>
<td>81</td>
</tr>
<tr>
<td>TCGA</td>
<td>66</td>
</tr>
<tr>
<td>TATC</td>
<td>55</td>
</tr>
<tr>
<td>ACGT</td>
<td>44</td>
</tr>
<tr>
<td>AGCT</td>
<td>40</td>
</tr>
<tr>
<td>CAGT</td>
<td>33</td>
</tr>
<tr>
<td>GTAC</td>
<td>19</td>
</tr>
<tr>
<td>TAGC</td>
<td>18</td>
</tr>
</tbody>
</table>

* A total of 16,140 bases of Leptospira gene sequences and 16,853 bases of Borrelia gene sequences available in the GenBank v70 data base (excluding the 23S rRNA genes) were examined with MacVector software (IBI-Kodak, New Haven, Conn.) run on a Quadra 700.

* Predicted frequencies for tetranucleotide XYZW are calculated from the mono-, di-, tri-, and dinucleotide frequencies by the following equation (8):

\[
\frac{\left[XZW\right] \times \left[XY\right] \times \left[XNW\right] \times \left[YZ\right] \times \left[YNW\right] \times \left[ZW\right] \\
\left[XYZ\right] \times \left[XNYW\right] \times \left[XNWZ\right] \times \left[YZW\right] \times \left[X\right] \times \left[Y\right] \times \left[Z\right] \times \left[W\right]}
\]

* Significant at \( P < 0.1 \) (\( \chi^2 \) test).
One exception to the rule that sequence-specific modification systems are present in some, but not all, strains in any species is the dam methylation system (5'-Gm^6ATC), which occurs in all strains of several species in the family Enterobacteriaceae and related genera (3). Rather than being part of a restriction modification system, dam methylation is part of a daughter strand repair system (1, 14) and also regulates replication (25, 26). It is presumably because of a role in maintaining all cells that the dam modification is found throughout the genome in which it occurs. In contrast, a restriction system in all cells of a species would be obsolete when the first resistant bacteriophage carrying the appropriate modification were propagated, which is presumably why strains within species vary in their restriction systems. The distribution of the DNA modification at 5'-GTAC in Leptospira genomes is more reminiscent of dam methylation than restriction modification. Although this distribution of modification at 5'-GTAC does not necessarily imply a role in functions identical to those of dam, it implies a similar species-wide role in fitness.

In summary, Leptospira genomes carry a sequence-specific DNA modification at 5'-GTAC that is probably mC specific. The distribution of this modification is not typical of a conventional restriction-modification system.

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