Letters to the Editor

A $\text{bla}_{\text{TEM-1b}}$-Derived TEM-6 β-Lactamase: a Case of Convergent Evolution

Since the first communication describing an organism that produces an enzyme capable of hydrolyzing extended-spectrum cephalosporins (5, 6), several outbreaks of Enterobacteriaceae resistant to oxyimino-β-lactams have been reported. In these cases, the adopted survival strategy of bacteria challenged by the introduction of aztreonam, cefotaxime, ceftazidime, and other oxyimino-β-lactams was to expand the β-lactamase spectrum of activity by the mutational alteration of $\text{bla}$-lactams. This allowed discrimination of $\text{bla}_{\text{TEM-1b}}$ from the previously described DNA sequence encoding TEM-6 (3), the gene encoding ceftazidimase activity was found to carry four silent mutations at nucleotides 175, 226, 436, and 604, locations which correspond to the $\text{bla}_{\text{TEM-1a}}$ (Tn2) gene and are known to allow discrimination of $\text{bla}_{\text{TEM-1a}}$ (Tn3) (2, 8). In contrast with the previously described DNA sequence encoding TEM-6 (3), the gene encoding ceftazidimase activity in our strain was more closely related to $\text{bla}_{\text{TEM-1b}}$ than to $\text{bla}_{\text{TEM-1a}}$, and its designations as $\text{bla}_{\text{TEM-6b}}$ are here proposed. These results strongly suggest that the enzyme reported in this work has evolved from a genetic lineage different from that of the previously described TEM-6 (3). The association of $\text{bla}_{\text{TEM-1a}}$ and $\text{bla}_{\text{TEM-1b}}$ with the transposons Tn1, Tn2, respectively, supports this view.

TABLE 1. Sequence differences between $\text{bla}_{\text{TEM-1a}}$, $\text{bla}_{\text{TEM-1b}}$, $\text{bla}_{\text{TEM-6a}}$, and $\text{bla}_{\text{TEM-6b}}$ genes

<table>
<thead>
<tr>
<th>Nucleotide no.</th>
<th>Nucleotide (amino acid) in: $\text{bla}_{\text{TEM-1a}}$ (from Tn2)</th>
<th>$\text{bla}_{\text{TEM-1b}}$ (from Tn2)</th>
<th>$\text{ bla}_{\text{TEM-6a}}$</th>
<th>$\text{bla}_{\text{TEM-6b}}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>175</td>
<td>A</td>
<td>G</td>
<td>A</td>
<td>G</td>
</tr>
<tr>
<td>226</td>
<td>C</td>
<td>T</td>
<td>G</td>
<td>A</td>
</tr>
<tr>
<td>436</td>
<td>C</td>
<td>T</td>
<td>C</td>
<td>T</td>
</tr>
<tr>
<td>512</td>
<td>G (Glu-104)</td>
<td>T</td>
<td>G</td>
<td>A (Lys-104)</td>
</tr>
<tr>
<td>604</td>
<td>G</td>
<td>T</td>
<td>G</td>
<td>T</td>
</tr>
<tr>
<td>693</td>
<td>G (Arg-164)</td>
<td>G</td>
<td>A (His-164)</td>
<td>A</td>
</tr>
</tbody>
</table>

* Nucleotide numbering is according to the method of Sutcliffe (8).

The sequence reported in this paper is shown as $\text{bla}_{\text{TEM-6b}}$. Other data are taken from the works of Sutcliffe (8) for $\text{bla}_{\text{TEM-1a}}$, Goussard and Courvalin (2) for $\text{bla}_{\text{TEM-1b}}$, and Goussard et al. (3) for $\text{bla}_{\text{TEM-6}}$.

The amino acid is indicated for cases in which a point mutation leads to an amino acid substitution compared with the sequence of TEM-1. Numbering is according to the method of Ambler et al. (1).

REFERENCES


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