mesylate is now recognized as the gold standard for treatment of chronic myeloid leukemia (CML). Imatinib mesylate inhibits the bcr-abl tyrosine kinase, which is the constitutive abnormal tyrosine kinase created by the Philadelphia chromosome abnormality [1]. Treatment with this drug has caused an increase the number of patients who experience a cytogenetic and molecular response, and it has improved the quality of life for a large number of CML patients.

The majority of patients treated with imatinib experience an adverse event at some point. Most events are of a mild-to-moderate grade. In 1 study, treatment was discontinued because of drug-related adverse events in only 3.1% of patients in whom CML was newly diagnosed, in 4% of patients with chronic CML who were receiving imatinib after they experienced IFN-α therapy failure, in 4% in the accelerated phase, and in 5% experiencing blast crisis. No relevant opportunistic infections were described during treatment with imatinib mesylate, except in the case of a patient who developed pulmonary tuberculosis during treatment for a malignant gastrointestinal stromal tumor [2]. Here, we report a case of CML complicated by tuberculosis reactivation during treatment with imatinib and the management of appropriate therapy.

**Case report.** A 59-year-old woman received a diagnosis of CML in first chronic phase (Sokal risk score, 0.86) in November 1997. She initially experienced a complete cytogenetic response to IFN-α. In July 2001, cytogenetic bone marrow analysis revealed a Philadelphia chromosome abnormality in 3 of 9 specimens obtained during metaphases of mitosis. No hematological relapse was registered. A few months later, the patient presented with persistent and productive cough without fever or dyspnea. A CT scan of the lungs showed an infiltrate of the right upper lobe, and Mycobacterium tuberculosis was detected in sputum samples by PCR. The patient was given isoniazid, rifampicin, and pyrazinamide, and our infectious disease consultant performed follow-up. The patient’s symptoms promptly resolved. In January 2002, IFN-α therapy was discontinued, because of a lack of cytogenetic response and intolerance to the therapy. The patient began therapy with imatinib (400 mg daily). She experienced complete cytogenetic and molecular response after 12 months of therapy. In March 2006, while receiving imatinib, she experienced reactivation of pulmonary Mycobacterium tuberculosis infection, identified in sputum samples by PCR. The patient then once again began therapy with isoniazid, rifampicin, and pyrazinamide. Imatinib was not discontinued, and its dosage was increased to 600 mg daily (a 50% increase), as recommended for patients receiving imatinib who are being treated with a potent CYP3A4 inducer, such as rifampicin or phenytoin [3, 4]. In fact, studies of healthy volunteers have shown that, during concomitant treatment with rifampicin, there is an imatinib dosage range that may be subtherapeutic. No hematological toxicity developed in our patient: she is alive and well and is receiving imatinib and antituberculosis therapy. This represents, to our knowledge, the first reported case of concomitant imatinib and antituberculosis therapy including rifampicin in which the current recommendations were adopted [3, 4]. The 50% increase in the imatinib dosage was feasible and did not result in significant hematological or extrahematological toxicity. We stress the need for feedback from different specialists caring for patients who are receiving new-generation drugs, such as imatinib, for the treatment of CML who required significant dosage adjustment for the treatment of concomitant serious illness.

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**Potential conflicts of interest.** All authors: no conflicts.

**References**


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**Colonization or Infection with Multidrug-Resistant Acinetobacter baumannii May Be an Independent Risk Factor for Increased Mortality**

We read with great interest the article by Fourrier and Richet [1], and we noted the correspondence by Falagas et al. [2]. During an epidemic of multidrug-resistant (MDR) Acinetobacter baumannii colonization and infection in a Chicago teaching hospital (University of Illinois at Chicago Medical Center) [3], we conducted a retrospective case-control study comparing all patients who were colonized or infected with MDR A. baumannii with all patients who were colonized or infected with MDR Pseudomonas aeruginosa from the same year; 78 MDR A. baumannii and 112 MDR P. aeruginosa isolates were included. Be-
between these 2 groups, statistically different parameters from the univariate analysis included the number of days that a urinary catheter was in place, the number of days that an intravascular catheter was in place, the number of mechanical ventilation days, length of stay in an intensive care unit, transplantation status, and use of third-generation cephalosporins, trimethoprim, vancomycin, or fluoroquinolones during the 14 days before a clinical specimen culture was positive. Kaplan-Meier analysis showed a significantly increased mortality in the A. baumannii group, even after adjusting for stay in an intensive care unit (P = .0002).

With the above-mentioned limitations in mind, we believe that colonization or infection with MDR A. baumannii may be an independent risk factor for increased mortality.

Acknowledgments


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Variant IS1016 Insertion Elements in Invasive Haemophilus influenzae Type b Isolates Harboring Multiple Copies of the Capsulation b Locus

To the Editor—We read with interest the article by Kapogiannis et al. [1] describing 2 cases of invasive Haemophilus influenzae infection caused by serotype b isolates possessing the putative virulence-enhancing IS1016-bexA partial deletion. Such a deletion is usually observed in invasive H. influenzae type b (Hib) strains, in which the capsulation (cap) locus lies between direct repeats of the IS1016 insertion element and contains a duplication of the genes carrying a 1.2-kb deletion at the 5′ end of the cap gene. We have been hypothesized that the IS1016-bexA deletion stabilizes the gene duplication, resulting in increased capsule production and virulence [4]. It has also been suggested that direct repeats of IS1016 provide a molecular substrate for further cap gene amplification [2, 3]. We are particularly concerned with this issue, because strains harboring >2 copies of the cap b locus (multiple-copy strains) have been recently observed in Italy [6]. No data were available for the IS1016 sequence in amplified cap b loci.

Here, we report the detection of a new Hib clone exhibiting remarkable polymorphism within its IS1016 sequences, with further deletions and point mutations in addition to the usual IS1016-bexA deletion. This clone included 3 Hib isolates (strains 37, 149, and 205) recovered from children aged ≤24 months who had severe invasive disease and who had not received Hib conjugate vaccine. All 3 isolates were found to contain 4 copies of the cap b locus by Southern blotting [6]. In each isolate, the IS1016 element at the 5′ end (IS1016-V5), the “inner” IS1016-V2 elements, and the IS1016-V2 element at the 3′ end were separately amplified by PCR, employing 3 sets of primers complementary to the flanking genes [7] (table 1). Sequencing of the IS1016-V5 PCR products revealed 100% identity in nucleotide sequences among the 3 isolates. In comparison with the reference sequence (GenBank accession number AF549213), the IS1016-V5 sequences herein described (EMBL accession numbers AM268182–AM268184) exhibited 2 new deletions (a 40-bp deletion within a previously described open reading frame [2] plus a single nucleotide deletion within the 19-nucleotide inverted repeat bracketing the

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Table 1. PCR primers and products used in sequence analysis of IS1016 insertion elements from Haemophilus influenzae type b strains 37, 149, and 205, compared with those from the reference sequence AF549213.

<table>
<thead>
<tr>
<th>Primer set</th>
<th>Nucleotide sequence (5′ to 3′)</th>
<th>Position*</th>
<th>Region amplified</th>
<th>Size, bp</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rd sec97/lef bexA</td>
<td>AGGTTCAGGGGTATGATCCTCCGCG</td>
<td>34–57</td>
<td>IS1016-V5</td>
<td>477</td>
</tr>
<tr>
<td></td>
<td>CAATGTTGCGCTGAATATGT</td>
<td>510–489</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Region III Orf3 bexA</td>
<td>TGTTTCCTCGTCGAACCTGG</td>
<td>16884–16903</td>
<td>IS1016-V2, in the bridge region</td>
<td>1724</td>
</tr>
<tr>
<td></td>
<td>CAATGTTGCGCTGAATATGT</td>
<td>18608–18597</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Region III Orf3</td>
<td>TGTTTCCTCGTCGAACCTGG</td>
<td>34981–35000</td>
<td>IS1016-V2, at the 3′ end of cap b locus</td>
<td>931</td>
</tr>
<tr>
<td></td>
<td>AATGTGGGGGAAGTAAAGGA</td>
<td>35912–35893</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

* Position on AF549213.