rather than an extrinsic contamination during the preparation and infusion in hospital. The batch number of the Hôpital Erasme strain was not recorded. However, our observation of identical genomic profiles, together with the fact that this particular patient received RATG provided by the same distributor at the same time as the outbreak in our institution, makes a common source of contamination very likely. The bacteraemia in that hospital could not have been prevented by an interhospital alert policy, however, because it occurred at the time as we started our investigation.

All patients in this study recovered from the *Ochrobactrum anthropi* bacteraemia, some even without antimicrobial therapy. This is in agreement with the previously reported low pathogenicity of this organism (1). This outbreak reminds us that despite stringent manufacturing procedures currently in practice, a certain risk of contamination of nonterminally sterilized injectable drugs persists. Since this contamination does not always cause turbidity, prevention is possible only by the early detection of outbreaks and the investigation of the source. Interhospital communication is advisable because these drugs are often distributed to different centres. This report points out the need for a permanent contact between infection control teams.

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Evaluation of the Automicrobic System for the Identification of *Streptococcus mutans*

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The performance of the Automicrobic System with the Vitek gram-positive identification card (bioMérieux, France) in identifying strains of *Streptococcus mutans* was studied. Of 160 strains assayed, 72.5 % were confirmed to be *Streptococcus mutans*; the remainder were identified as other species of streptococci (*Streptococcus bovis*, *Streptococcus uberis*, *Streptococcus anginosus*, *Streptococcus sanguis* I and II, *Streptococcus intermedius*, and *Streptococcus constellatus*).

Viridans streptococci comprise a large group of microorganisms, some of which form part of the normal flora of the oral cavity and have no known pathogenicity. Others, however, behave as pathogens, and cause a variety of infections in humans and animals. Among the diseases associated with *Streptococcus mutans* are local infections such as dental caries and, less frequently, periodontal diseases (1–3), bacteremia, endocarditis, and abscesses (4–6). The clinical consequences of these microorganisms make it necessary to develop appropriate, rapid, and reliable systems to identify them.

Because most strains cannot be grouped according to serological category on the basis of the Lancefield classification and capsular antigens,

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and because cross-reactions are frequent, rapid latex-based tests are unsuitable. In addition, the wide battery of manual biochemical tests required are not routinely available in many laboratories. In response to these problems, several automatic systems have been developed (e.g., MicroScan, Baxter USA, and ATB and Automicrobic System, bioMérieux, France), which claim to facilitate the identification of streptococci. We investigated the performance of the Automicrobic System (AMS) in identifying *Streptococcus mutans*.

Material and Methods. A total of 160 strains of *Streptococcus mutans* was obtained from clinical oral isolates and identified using conventional methods. In addition, three reference strains of *Streptococcus mutans* (NCT 10832, ATCC 25175, and NCTC 10449) were used.

Cultured microorganisms were Gram stained and subjected to the following tests: arginine hydrolysis; esculin hydrolysis in the presence and in the absence of bile; mannitol, raffinose, and inulin fermentation; and resistance to 2 U bacitracin. The culture media, techniques, and interpretation of results were in accordance with the methods of Cowan and Steel (7). The identification criteria were those of Maiden et al. (8) (arginine hydrolysis negative, esculin hydrolysis in the presence of bile negative and in its absence positive, mannitol, raffinose, and inulin fermentation positive, and resistance to 2 U bacitracin positive).

All strains of *Streptococcus mutans* identified by conventional means were reidentified with the AMS. This system repeats these conventional assays in an automated fashion. We used a Vitek GPI card (V.1305, version 4.2), and followed the manufacturer's recommendations for inoculation and reading. All assays were repeated three times to verify the results.

Results and Discussion. The AMS correctly identified 116 of the 160 (72.5 %) strains as *Streptococcus mutans*. Of the remaining 44 (27.5 %) strains misidentified by the AMS, 45.5 % were identified as *Streptococcus bovis*, 9.1 % as *Streptococcus intermedius*, 9.1 % as *Streptococcus anginosus*, 4.5 % as *Streptococcus sanguis* I, 9.1 % as *Streptococcus sanguis* II, 13.6 % as *Streptococcus uberis*, and 9.1 % as *Streptococcus constellatus*. Of the reference strains, NCTC 10832 and ATCC 25175 were identified by the AMS as *Streptococcus mutans*, while NCTC 10449 was identified as *Streptococcus bovis*. The reproducibility of the tests was 100 % – that is, the same results were obtained in each of the three assays.

The AMS uses the same biochemical assays as are used in conventional analyses. Tables 1 and 2 summarize the results of these tests, which did not match the conventionally obtained results both for strains identified as *Streptococcus mutans* and for other strains.

The accurate identification of *viridans* streptococci continues to be an obstacle in studies of this group. The classification of these microorganisms has been modified many times (9–11). Changes in the taxonomic classification of these microorganisms have been frequent and have led to the development of new techniques for their identification. Of these methods, studies of the homology between nucleic acids, genetic fingerprinting (12, 13), and examination of characteristics such as antigenic structure and physiological properties have helped clarify the classification of these microorganisms.

Table 1: Results of conventional biochemical assays of strains identified by conventional methods and the Antimicrobic System as *Streptococcus mutans*.

No. of strains	BAC	ESC	ARG	MAN	RAF	INU
6	+	–	–	+	+	–
2	+	–	–	+	+	+
2	+	+	+	+	+	–
2	+	+	+	+	–	+
28	+	+	–	+	+	+
76	+	+	–	+	+	–

BAC, bacitracin resistance; ESC, esculin hydrolysis; ARG, arginine hydrolysis; MAN, mannitol fermentation; RAF, raffinose fermentation; INU, inulin fermentation; +, positive; –, negative.

Table 2: Results of conventional biochemical assays of strains identified by the Automicrobic System as species other than *Streptococcus mutans*.

Species	No. of strains	BAC	ESC	ARG	MAN	RAF	INU
S. bovis	20	+	+	–	+	+	–
	2	–	–	–	–	+	+
S. intermedius	2	+	+	+	+	–	–
	2	+	+	–	+	+	–
S. anginosus	2	+	+	+	+	+	–
S. sanguis II	4	–	–	–	–	+	–
S. sanguis I	2	+	+	–	–	–	–
S. uberis	6	+	+	–	+	–	–
S. constellatus	4	+	+	–	–	–	–

BAC, bacitracin resistance; ESC, esculin hydrolysis; ARG, arginine hydrolysis; MAN, mannitol fermentation; RAF, raffinose fermentation; INU, inulin fermentation; +, positive; –, negative.

Streptococcus mutans is currently considered a member of the socalled *mutans* group. Of the seven species in this group (*Streptococcus mutans*, *rattus*, *cricetus*, *sobrinus*, *ferus*, *downei*, and *macacae*), only the first four are human pathogens (9, 14). The AMS with the Vitek GPI card was developed for the identification of the major strains of streptococci involved in human disease and of other gram-positive bacteria. This system includes most of the conventional tests for *mutans* streptococci, and makes it possible to compare the results of the automated system with a battery of conventional tests.

The 72.5 % rate of identification by the AMS of the strains we tested was higher than the figure given in an earlier study (18). Of the 116 strains identified by the Vitek card, the results fully matched those obtained with conventional methods only in 28 cases (24.1 %) (Table 1).

When we compared the results of the conventional tests done manually with those of the same tests done by the AMS, we found that although 100 % of the 116 strains correctly identified as *mutans* streptococci were resistant to bacitracin and mannitol fermentation according to the automated system, agreement between the two series of assays was lower for other tests. The greatest discrepancy was found for the inulin fermentation test, which, according to the AMS, was positive in only 32 of the 116 (27.6 %) strains. Differences between automatic and manual results were also described in an earlier study of other identification systems (19). The possibility that strains not identified by the AMS as *Streptococcus mutans* were, in fact, different species was ruled out by the results of the manually performed conventional tests. This was exemplified by streptococci identified by the AMS as *Streptococcus bovis*, while in the conventional assays, none of the strains grew in bile esculin agar (7, 8, 15). Some authors have reported *Streptococcus intermedius*, *Streptococcus constellatus*, and *Streptococcus anginosus* to be mannitol negative (8, 15), although one study found that some strains were able to ferment this sugar (20). Although strains may differ in their behavior in this assay, a negative result in the arginine hydrolysis test rules out the presence of these three species (7, 8, 15).

Because neither *Streptococcus sanguis* I nor *Streptococcus sanguis* II is able to ferment mannitol (7, 8, 15), these species cannot have been among our sample of 160 strains of *Streptococcus mutans*, all of which are able to metabolize this polyalcohol. Because none of the strains we investigated was able to hydrolyze arginine (7, 8, 15), the presence of *Streptococcus uberis* was likewise ruled out.

In conclusion, identification of strains of *Streptococcus mutans* by the AMS did not entirely match the results of manual identification with conventional assays. The discrepancies we found are common when modifications of conventional methods are used, including micromethods or commercial identification systems (19, 21, 22), and may be caused by the shorter incubation times used by these systems. Although the shorter incubation times are sufficient for other species, they are inadequate for oral streptococci, and particularly *Streptococcus mutans*, given their slow growth rates.

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In Vitro Activity of MDL 62,879 against Gram-Positive Bacteria and *Bacteroides* Species

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The new thiazolyl peptide antibiotic MDL 62,879 (GE2270 A) showed excellent in vitro activity in testing against staphylococci and streptococci, with MIC90s ranging from 0.23 to 0.9 mg/l. It was very active against *Clostridium difficile* and *Propionibacterium acnes* (MIC90 0.06 mg/l in each case) and had variable activity against *Bacteroides* spp. MDL 62,879 had exceptionally good activity against *Enterococcus faecalis*, including against a collection of high-level aminoglycoside-resistant isolates where it had an MIC90 of 0.047. The antibiotic was bacteriostatic for enterococcal isolates but bactericidal for a methicillin-resistant isolate of *Staphylococcus aureus*.

MDL 62,879 (GE2270 A) is a novel thiazolyl peptide antibiotic isolated from *Planobispora rosea* strain ATCC 53773 (1, 2). It inhibits bacterial protein biosynthesis by interacting with elongation factor Tu (EF-Tu) (1, 3, 4). MDL 62,879 has been reported to be active against aerobic and anaerobic gram-positive bacteria and some gram-negative anaerobes (1, 5, 6). In this study we evaluated the in vitro activity of MDL 62,879 in comparison with that of teicoplanin, vancomycin, ramoplanin, ampicillin, and clindamycin, and against aerobic and anaerobic gram-positive bacteria and *Bacteroides* spp., including a large collection of high-level aminoglycoside-resistant enterococci.

Materials and Methods. MDL 62,879, teicoplanin, and ramoplanin were obtained from Lepetit Research Center (Italy). Vancomycin was

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