prevalence group not only for HBV but even more so for HCV.

Conclusion. On the basis of the high prevalence of circulating HCV found with both HCV PCRs, one might speculate that chances for transmission of HCV among IVDU occur more frequently than for transmission of HBV via similar routes. Conversely, instead of transmission through needle sharing or sexual contact, community acquisition of HCV infections might be of particular importance in IVDU.

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Identification of mycobacteria species by 23S ribosomal RNA targeted gene probes

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Conserved molecules like the rRNAs are suitable markers for identification of microorganisms. The most common molecule among the rRNAs is the 16S rRNA, which is used for rapid diagnosis of mycobacteria by direct DNA sequencing techniques[2]. The 23S rRNA is double the size of the 16S rRNA and consists of more high variable regions. The 23S rRNA of the genus *Mycobacterium*, members of the phylogenetic group of Gram-positive bacteria with a high DNA G + C content, contains a characteristic insert of about 100 bases in length. Its primary structure is highly variable. We developed specific oligonucleotide probes, which can rapidly identify and differentiate mycobacteria.

Methods and results. Isolation and purification of genomic mycobacterial DNA was done according to a modified standard procedure[1]. PCR reactions were performed on a Cetus 9600 thermocycler (Perkin-Elmer Cetus Corp., Norwalk, Conn.). For direct sequencing amplicons were purified by spin columns (Pharmacia Biotech, Germany). Sequencing reactions were loaded on a direct blotting electrophoresis (DBE) system GATC 1500 (MWG-Biotech GmbH, Germany) and automatically blotted on a noncharged nylon membrane (direct blotting membrane, GATC GmbH, Germany)[4]. Hybridization with the oligonucleotide probes was performed using a dot format and a modified protocol with tetramethylammonium chloride for washing at a specific temperature[5].

For *M. avium*, *M. nonchromogenicum*, *M. phlei*, *M. bovis*, *M. scrofulaceum*, *M. celatum*, *M. terrae*, *M. flavescens*, *M. xenopi*, *M. fortuitum*, *M. tuberculosis*, *M. gastri*, *M. gordonae*, *M. kansasii*, and *M. malmoense*, the 23S rRNA insert of helix 54 was amplified and the primary structure determined by direct sequencing. The primary structures were aligned and completed using published results[3]. Probes were designed for specific detection of *M gastri*, *M. fortuitum*, *M. nonchromogenicum*, *M. phlei*, *M. celatum*, *M. malmoense*, *M. scrofulaceum*, *M. kansasii*, *M. terrae* and *M. xenopi*. Only *M. gastri* and *M. kansasii* could not be distinguished on the level of the helix 54 insert.

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Use of 16S rDNA targeted oligonucleotide probe to detect phenotypic heterogeneity of *Bacillus mycoides*

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Many *Bacillus* species exhibit a high degree of similarity both in phenotye and 16S rDNA sequence, making their identification somewhat difficult. Examples of such species are those of the *B. cereus* group composed of *B. cereus*, *B. mycoides*, *B. thuringiensis* and *B. anthracis* which demonstrate only small differences in phenotype and high 16S rDNA sequence similarity (>99.4%)[1].

Thirty-four *Bacillus* species isolated from a peat bog sample were identified on the basis of fatty acid analysis as strains of the species *Bacillus mycoides*. The degree of similarity to the fatty acid profile of the *B. mycoides* strain in the fatty acid profile database was in the range 20–80% and *B. mycoides* was considered the best match. In some cases these results were in conflict with the phenotypic data, which showed many of these strains to be motile and all to have a non-rhizoid colony morphology, characteristics different to those described for the species *B. mycoides*[2].

Full 16S rDNA sequence was determined for five repre-