

# *Comprehensive FT-IR reference data bases for microbial species identification and strain typing*

Mareike Wenning and Siegfried Scherer

Abteilung Mikrobiologie, Zentralinstitut für Ernährungs- und Lebensmittelforschung  
(Z I E L) Weihenstephan, Technische Universität München, Weihenstephaner Berg 3,  
85350 Freising, Germany

Over the past years, FT-IR spectroscopy has gained more and more interest as a valuable technique for microbial identification in different fields of microbiology. Well composed data bases combined with appropriate statistical analysis for spectra identification ensure high reliability and the high sensitivity of the technique enables typing of isolates even down to the strain level. However, for reasonably applying this technology in routine diagnostic processes, extensive reference data bases are needed comprising high numbers of species represented by strains from different sources and habitats.

Over the past 13 years, comprehensive reference data bases covering almost 1000 species belonging to yeasts, Gram-positive spore-formers, staphylococci, actinobacteria, lactic acid bacteria, and Gram-negative bacteria have been established at the Department of Microbiology at the Z I E L Research Center for Nutrition and Food Sciences following the latest findings of taxonomic research. Originating from dairy microbiology, many data bases have later been extended with isolates from diverse food and environmental samples in order to adapt them to other fields of food and feed microbiology as well as environmental monitoring processes in the pharmaceutical industry.

Beside species identification, typing of organisms below the species level is another task FT-IR spectroscopy is applied to successfully. Particularly for the quality assessment of animal feed, cell counts are not an objective measure as many feed products are supplemented with probiotic yeast or bacteria. Therefore, a species identification of the microorganisms detected is necessary and, in addition, for all cases where species have been identified that are also used as probiotics the distinction of environmental contaminations and probiotic feed additive strains is required to elucidate the origin of those isolates and to obtain a realistic picture of microbial feed quality. As convenient and cost-effective tools for such analyses are still lacking, FT-IR data bases have been extended with official feed additive strains of yeasts, bacilli, and lactic acid bacteria and artificial neural networks (ANN) have been trained for the differentiation of probiotic and environmental yeast and lactic acid bacteria. The ANNs obtained not only enable a reliable differentiation of probiotic and environmental strains but also distinguish between different probiotics of the same species [1].

## **References:**

- [1] N. R. Büchl, M. Wenning, M. Hutzler, H. Mietke-Hofmann and S. Scherer, Differentiation of probiotic and environmental *Saccharomyces cerevisiae* strains in animal feed, *Appl. Microbiol.*, submitted.