Table. Distribution of the vacA und cagA genes in 91 clinical *H. pylori* isolates.

	cagA +	*cagA* −
vacA +	51.7%	13.2%
vacA −	18.7%	16.5%

The intention of our investigation was to identify the cytotoxin and the cagA gene in well characterized *H. pylori* isolates by means of the polymerase chain reaction (PCR).

The 91 *H. pylori* isolates used in the present study were isolated from human gastric biopsies from 68 patients. We were able to detect the vacA gene in 64.8% and the cagA gene in 70.3% of our *H. pylori* isolates 51.7% harboured both genes, whereas 16.5% lacked both genes. With our selected primer pairs we could detect the cag A gene without concomitant vacA in 18.7% and the vacA gene without concomitant cagA in 13.2% of the tested strains.

In a significant portion of our tested *H. pylori* strains neither the cytotoxin gene nor the cagA gene could be detected, which is in contrast to the results of the above mentioned research groups. One possible explanation for these contradictory results is the chosen primer pairs. Additional specific primers for different parts of the genes may give us comparable results.

To evalute the PCR results further it seems necessary to show the cytopathic effect of *H. pylori* strains with different expression of the vacA or cagA genes in a cell culture system.

1 Leunk, R. D., Johnson, P. T., David, B. C., Draft, W. G., and Morgan, D. R., J. med. Microbiol. *26* (1988) 93.
2 Burroni, D., Dell'Orco, M., Commanducci, M., Bugnoli, M., Rappuoli, R., and Telford, J. L., Acta Gastroenterol. Belg. *56* (1993) 62.
3 Tummuru, M. K. R., Cover, T. L., and Blaser, M. J., Infect. Immun. *61* (1993) 1799.
4 Telford, J. L., Ghiara, P., Dell'Orco, M., Comanducci, M., Burroni, D., Bugnoli, M., Tecce, M. F., Censini, S., Covacci, A., Xiang, Z., Papini, E., Montecucco, C., Parente, L., and Rappuoli, R., J. expl Med. *179* (1994) 1653.

Identification of new oral treponemes by comparative sequence analysis of in vitro amplified 16S rRNA genes

B.-K. Choi[a], C. Wyss[b] and U. B. Göbel[a]

[a]*Institut für Mikrobiologie und Hygiene, Universitätsklinikum Charité, Dorotheenstr. 96, D-10117 Berlin (Germany)*
[b]*Zahnärztliches Institut, Universität Zürich, Plattenstr. 11, CH-8028 Zürich (Switzerland)*

Rapid and unequivocal identification of new bacterial isolates is a prerequisite to determine their aetiological role in inflammatory processes. This is particularly true for oral treponemes associated with periodontal infections. Molecular genetic evidence suggested the presence of a large number of yet uncultured treponemal phylotypes identified by comparative 16S rRNA sequence analysis[1].

To study the phenotypic traits, physiological properties and pathogenicity of these newly identified organisms we have cultured subgingival plaque material on the semi-solid, defined medium OMIZ-W1. Treponemal isolates were subjected to microscopic examination and biochemical analysis, e.g. SDS-PAGE and API-zym enzyme test. Twenty-three isolates could not be identified by phenotypic analysis and were selected for comparative 16S rRNA sequence analysis. Molecular genetic analysis identified six isolates as *T. socranskii*. The remaining 17 isolates were characterized by sequences identical to previously described 'cluster 17' treponemes[1]. They exhibited a marked phenotypic heterogeneity and could not be grown in NOS medium. All attempts failed to identify these very small 'cluster 17' treponemes by in situ hybridization.

In conclusion, we have isolated and characterized a new group of small oral treponemes, which may represent a new species. Due to their marked phenotypic heterogeneity they could only be classified by molecular genetic analysis.

1 Choi, B. K., Paster, B. J., Dewhirst, F. E., and Göbel, U. B., Infect. Immun. *62* (1994) 1889.