XII. Summary

Considerable attention has been paid to the existence of *Helicobacter pylori* in the oral cavity recently. The bacterium, or its DNA, have been isolated from dental plaques, periodontal pockets, tooth pulp, saliva, the tongue surface, mucosal ulcerations, and neoplastic lesions. The presence of *H. pylori* in the saliva is considered to be a factor involved in the development of periodontal diseases and dental caries, as well as lesions such as aphthae, leukoplakia, lichen planus, and may even affect inflammatory processes in the palatine tonsils.

This study attempts to answer the following questions: is the oral cavity a reservoir of *Helicobacter pylori*, is the presence of bacteria in the saliva of children associated with dental caries, is the presence of bacteria in the oral cavity correlated with infections of the gastric mucosa, are gastric mucosa infections synonymous with the presence of bacteria in the oral cavity, and is there an association between a specific bacterial genotype and clinical symptoms.

A questionnaire study and a polymerase chain reaction (PCR) test were performed in a selected population of 116 children. The PCR assessed the *s1* and *s2* alleles of the *vacA* genotype of the *H. pylori* genome in saliva samples and gastric mucosa samples. The study group consisted of children with confirmed infections of the gastric mucosa with *H. pylori* by a positive histopathological examination of the gastric mucosa. The control group consisted of children with excluded *H. pylori* infection of the gastric mucosa, in whom the urease test and histopathological examinations were negative.

Based on the data obtained in the questionnaires, no significant differences were found in the incidence of *H. pylori* infection between girls and boys living in rural and urban areas ($p = 0.577$). There were also no significant differences between the study and control groups in terms of parental incidence of *H. pylori* infection ($p = 0.654$). Children from the study group had more siblings than children from the control group. The number of siblings did not influence the acquisition of *H. pylori* infection ($p = 0.358$) but in families where the number of children was 4 and more the tendency to *H. pylori* infection was noticeable ($p = 0.057$).

Abdominal pain was the dominant symptom of an *H. pylori* infection in the study group with a reported prevalence of 84.1%. In the group of children without infection, the percentage of abdominal pain was 97.2%. Loss of appetite was found in 54.5% of infected

children and in 55.6% of children without *H. pylori* infection. Symptoms of gastroesophageal reflux disease were found in 36.4% of the infected and 45.8% of the non-infected children.

The PCR test in the saliva showed the presence of *H. pylori* genetic material in 81.6% of patients in the study group, including the *s1* allele in 71.1% of saliva samples and the *s2* allele in 42.1% of the patients. Both alleles were present in 31.6% of patients. The *s1* allele was found more frequently than the *s2* allele ($p = 0.011$).

The PCR test in the gastric mucosa was performed only in the study group and genetic material was detected in 65.9% of patients. None of the alleles were detected in 34.1%. The *s1* allele was detected in 61.0% of cases, the *s2* allele in 26.8% of cases. Both alleles of the *H. pylori vacA* gene were present in 22% of patients. The *s1* allele was found significantly more often in the gastric mucosa ($p = 0.002$).

The children's dentition was assessed using the DMF index. There were no significant differences in the occurrence of DMF changes between the study and the control group ($p = 0.561$). No statistically significant correlation was found in the number of DMF and the presence of one of the alleles of the *H. pylori vacA* gene ($p = 0.746$). The correlation between the presence of *H. pylori* in the gastric mucosa and the presence of caries was also analyzed. There were no statistically significant differences in the number of alleles of the *H. pylori vacA* gene (0 vs 1 vs 2) in the gastric mucosa biopsy in relation to the DMF index ($p = 0.441$).

It was possible to obtain genetic determination of the *s1* and *s2* alleles in the saliva and in the gastric mucosa in a group of 37 patients. A significantly more frequent occurrence of the *s1* allele in the saliva and the gastric mucosa simultaneously was found compared to the frequency of occurrence of the *s2* allele ($chi2 = 12.9$; $p = 0.002$).

Based on this research, the following conclusions were drawn:

1. PCR analyses of saliva of children infected with *H. pylori* revealed the presence of genetic material of *H. pylori* bacteria in 81.6% of examined children. The *s1* allele was present in 71.1% of tested saliva samples, and the *s2* allele was found in 42.1% of the examined children, which indicates more frequent occurrence of the *s1* allele in the saliva of the tested children.
2. Simultaneous evaluation of the *s1* and *s2* alleles in the saliva and gastric mucosa of children infected with *H. pylori* showed more frequent occurrence of the *s1* allele in saliva and stomach compared to the *s2* allele.
3. No relationship was found between clinical symptoms and the presence of the vacA genotype of the *H. pylori* genome in the gastric mucosa.

4. The presence of the *vacA* genotype of the *H. pylori* genome both in the gastric mucosa and in the saliva of the examined children did not show a statistically significant relationship with the occurrence of caries.