

pLDDT parameter value for this control G4 ($90 > \text{pLDDT} > 70$) has the same value or lower than that predicted for the 3D models in the *rpoB* and *rpoC* genes. This indicates that all generated 3D models, including those with the parameter $90 > \text{pLDDT} > 70$, are substantiated.

The generally accepted planar structure of the G-tetrad assumes the presence of a maximum of eight H-bonds through the linking of adjacent guanines by two H-bonds: one classical Watson-Crick (internal) bond and a Hoogsteen (external) bond. All identified G4s have a parallel topology and are characterized by varying numbers of H-bonds in the two quartets (from two to eight) and up to 4 stacking interactions between the corresponding guanines.

Along with the classical (two-center) H-bonds between adjacent guanines, four G4s with bifurcated H-bonds were found including one G4 in the *rpoB* gene, two G4s in the *rpoC* gene.

3D models of G-quadruplexes generated by the AlphaFold 3 AI with atomic resolution may indicate on putative targets for antimycobacterial drugs. Complex formation between determined G4 and a drug specific to the structure of certain G4 should result in its stabilization and subsequent inhibition of RNA polymerase, the subunits of which are encoded by *rpoB* and *rpoC* genes.

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Lysak M., Lysak T., Melnyk O., Lavryk H.

MICROBIAL DIVERSITY AND CATALASE PROFILE OF ORAL MICROORGANISMS IN CHILDREN WITH GASTRITIS AND GASTRODUODENITIS

State Non-Profit Enterprise “Danylo Halytsky Lviv National Medical University”,
69 Pekarska St., Lviv, 79010, Ukraine
e-mail: viruszet8@gmail.com

Abstract. The oral microbiome was compared between 33 children aged 5–18 years with gastritis or gastroduodenitis and multiple dental caries and 20 controls. Culture-based analysis revealed 16 taxa in controls and 20 identified taxa plus unidentified strains in the study group. Shannon diversity was higher in the study group (2.969 vs. 2.614), whereas Simpson dominance was lower (0.055 vs. 0.083). Bray-

Curtis dissimilarity reached 0.685, indicating marked restructuring of the microbial profiles. Catalase-positive phenotypes occurred among *Neisseria spp.*, *Rothia spp.*, *Staphylococcus spp.*, and *Candida albicans*, while isolated streptococci were catalase-negative. These findings demonstrate greater and more even microbial diversity in children with gastroduodenal pathology and multiple caries. The functional contribution of catalase-positive taxa to oxidative-stress tolerance in dental biofilms requires further investigation.

Keywords: oral microbiome, gastritis, gastroduodenitis, dental caries, catalase activity.

Dental plaque is a metabolically integrated microbial biofilm whose composition changes under ecological pressure (Marsh, 2006; Takahashi & Nyvad, 2011). In children, gastroduodenal disease may coincide with alterations in oral microbial homeostasis, while multiple caries is associated with acidogenic biofilm activity and impaired local protective mechanisms. Catalase decomposes hydrogen peroxide and may enhance microbial survival under oxidative stress; therefore, the distribution of catalase-positive and catalase-negative taxa can characterize the functional potential of the oral community.

The aim was to determine the qualitative and quantitative composition, diversity, and catalase profile of oral-fluid microorganisms in children aged 5–18 years with gastritis or gastroduodenitis and multiple caries in comparison with controls.

Materials and Methods. A clinical and microbiological study was conducted involving 33 children aged up to 18 years diagnosed with gastritis or gastroduodenitis and multiple dental caries. Dental examination was performed using generally accepted methods, including assessment of dental hard tissues and determination of caries intensity according to the child's age. Gastritis or gastroduodenitis was diagnosed based on clinical and instrumental examination findings.

The qualitative and quantitative composition of the microbiota was determined using a bacteriological method by inoculating the collected material onto appropriate culture media, followed by incubation. Microbial counts were expressed as colony-forming units per millilitre (CFU/mL).

Catalase activity of the isolated cultures was determined based on their ability to decompose hydrogen peroxide with the release of molecular oxygen. The appearance of gas bubbles after hydrogen peroxide solution was applied to the culture was considered a positive catalase reaction, whereas the absence of gas formation was considered a negative reaction. Based on the results, the ratio of catalase-positive to catalase-negative representatives of the oral microbiome was determined.

Detection frequency was expressed as an absolute count and percentage with its standard error. Community structure was assessed using the Shannon index, Simpson dominance and diversity indices, and Bray-Curtis dissimilarity after normalization of taxon detection frequencies.

Results and discussion. The microbial load ranged from 10^3 to 10^8 CFU/mL in both groups. Sixteen species were recovered from controls, whereas the study group yielded 20 identified species and a group of unidentified strains. In controls, the most frequent taxa were *Streptococcus mitis* (25.00 ± 9.68 %), *Streptococcus parasanguinis*, *Streptococcus mutans*, and *Veillonella parvula* (20.00 ± 8.94 % each). In children with gastroduodenal pathology, *Neisseria sicca* and unidentified strains were detected most often (21.21 ± 7.12 % each), followed by *Streptococcus mitis* and *Rothia mucilaginosa* (18.18 ± 6.71 % each) and *Lactobacillus fuchuensis* and *Candida albicans* (15.15 ± 6.24 % each). The study group also included *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Acinetobacter johnsonii*, and *Klebsiella oxytoca*.

Only seven species were shared by both groups: *Streptococcus mitis*, *Streptococcus parasanguinis*, *Neisseria flavescens*, *Veillonella parvula*, *Lactobacillus plantarum*,

Actinomyces oris, and *Candida albicans*. The Shannon index was 2.614 in controls and 2.969 in the study group. Simpson dominance was 0.083 and 0.055, while Simpson diversity was 0.917 and 0.945, respectively. These values indicate a larger number of detected taxa, a more even frequency distribution, and weaker dominance in children with gastritis or gastro-duodenitis. Bray-Curtis dissimilarity was 0.685; thus, the microbial profiles differed by 68.5 %, with a similarity of 31.5 %. These comparisons are descriptive because the statistical significance of between-group differences in diversity indices was not tested.

Catalase-positive phenotypes were recorded among *Neisseria spp.*, *Rothia spp.*, *Staphylococcus spp.*, and *Candida albicans*, whereas the isolated streptococci were catalase-negative. Catalase-positive members of a mixed biofilm may contribute to hydrogen peroxide decomposition and collective protection against oxidative stress, potentially supporting persistence of the microbial community. This functional interpretation should be confirmed in further studies.

In conclusion, children with gastritis or gastroduodenitis and multiple caries displayed a richer, more even, and compositionally distinct oral-fluid microbiome than controls. The presence of additional opportunistic taxa and catalase-positive microorganisms may reflect restructuring of oral microbial interactions. Larger studies controlling for age, oral hygiene, diet, dental status, and treatment are required to establish statistical and causal relationships.

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Melnyk O., Verhun A., Pavliy S., Verhun O., Kovalenko I.

THE ROLE OF *ARCANOBACTERIUM HAEMOLYTICUM* IN THE DEVELOPMENT OF A PURULENT-NECROTIC LESION: A CLINICAL AND MICROBIOLOGICAL CASE REPORT

State Non-Profit Enterprise "Danylo Halytsky Lviv National Medical University",
69 Pekarska St., Lviv, 79010, Ukraine
e-mail: viruszet8@gmail.com

Abstract. *Arcanobacterium haemolyticum* is an under-recognised opportunistic pathogen that may contribute to skin and soft-tissue infections, particularly in patients with malignancy, tissue necrosis, impaired local blood supply, and immune dysfunction. This clinical and microbiological case report aimed to determine the significance of *A. haemolyticum* isolated from a purulent-necrotic lesion in a patient with recurrent basal cell carcinoma of the anterior chest wall. A male patient born in 1948 presented with an extensive malignant wound following repeated surgical interventions and radiotherapy, accompanied by sternal osteomyelitis, a pathological fracture, cachexia, and severe functional impairment. Bacteriological examination of an intraoperatively collected specimen from the deep area of the lesion yielded *A. haemolyticum* at a concentration of 10^5 CFU/mL, and species identification was confirmed by MALDI-TOF mass spectrometry. The clinically significant microbial load and pronounced local signs of infection suggest that the isolate was not merely a surface coloniser but a potential aetiological agent contributing to the persistence