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SHARED AND CANCER-SPECIFIC ORAL BACTERIAL TAXA IN SOLID TUMOR PATIENTS VERSUS HEALTHY RELATIVES

Background. Oral microbiota influence immunity, inflammation, and carcinogenesis and may serve as non-invasive cancer biomarkers. Because most studies use unrelated controls, we compared solid tumor patients with healthy relatives to distinguish cancer-related shifts from shared genetics and lifestyle. **Methods.** DNA from 31 saliva samples (11 solid tumor patients, 20 healthy relatives) was amplified with the Ion AmpliSeq Pan-Bacterial Research Panel, and libraries were sequenced on an Ion S5 Plus system, with bioinformatic processing performed in Torrent Suite Software. The patients had heterogeneous tumors, including breast, colorectal, gastric, ovarian, prostate, thyroid, and skin cancers. **Results.** Both cohorts shared a core of 115 bacterial species (cumulative relative abundance >32.06%), dominated by the Bacillota phylum (>63%). Distinct shifts appeared in the unique fractions: 33 species were detected only in healthy relatives (Bacteroidota dominating, 37.5%), whereas 29 species were captured solely in tumor patients, led by Bacillota and Actinomycetota. *Streptococcus pneumoniae* was the top taxon in both groups, but its median abundance fell from ~23.6% in relatives to 14.4% in patients. The tumor top-10 included the tumor-associated pathogen *Fusobacterium nucleatum*, along with *Veillonella* and *Actinomyces*, whereas relatives showed a more balanced profile (*Granulicatella adiacens*, *G. elegans*, *Neisseria* sp., *Haemophilus haemolyticus*). Biomarkers detected exclusively in patients – *Leptotrichia wadei*, *Streptococcus equinus*, *S. gallolyticus*, and *Parvimonas micra* – are of particular clinical interest given their established roles in oncogenesis, from immune downregulation and pro-inflammatory epithelial signaling to biofilm-driven mucosal disruption. *Streptococcus mutans* was markedly more prevalent in patients (54.5% vs 10%; $p = 0.02$), and *S. gallolyticus* matched the cohort's burden of colorectal cancer and Lynch syndrome, consistent with its known link to gastrointestinal malignancies. **Conclusions.** These pilot findings reveal reproducible compositional differences between the oral microbiomes of patients with solid tumors and their healthy relatives. Several patient-specific taxa emerge as candidate markers or modulators of tumor presence. Further prospective, well-designed studies are needed to confirm their diagnostic value.

Keywords: oral microbiome, solid tumors, non-invasive biomarkers.

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