

ORAL PROBIOTIC REDUCES PAIN AFTER THIRD MOLAR EXTRACTION PROCEDURE

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Introduction: The oral microbiota contains hundreds of bacterial species [1], which can influence physiological processes of recovery and the risk of complications after tooth extraction procedures.

Objective: To evaluate the impact of an oral probiotic on clinical parameters after tooth extraction.

Methods: Double-blind, randomized, clinical trial, comparing probiotic (AB-Dentalac, AB-Biotics SA) to placebo oral tablets, twice daily for 7 days, in subjects undergoing a third molar extraction. Exclusion criteria included chronic disease, current antibiotic or probiotic use, and toxic habits. Subjects rated each of swelling, eating difficulty and pain in a 0-10 scale, daily. Extraction site infection was assessed by specialists 1 week post-extraction. Normality was assessed by Shapiro-Wilk test. Continuous data was compared using Mann-Whitney's test and proportions using Fisher test.

Results: 20 subjects were randomized to probiotic and 17 to placebo. No differences were observed in drop-out rate (n=3 probiotic, n=4 placebo) or infection rate (n=2 probiotic, n=2 placebo). Subject's diary recovery was low, without differences among groups (n=12 probiotic, n=9 placebo). Per-protocol (n=21), swelling and pain scores were comparable among groups ($p > 0.10$) at baseline (day 1), as were age, gingival index and gender distribution, but eating difficulty score was marginally higher in the probiotic group ($p < 0.05$). Reductions vs. day 1 in pain score and eating difficulty score were larger in probiotic group than placebo on days 5, 6 and 7 ($p < 0.05$). No other significant differences were observed.

Conclusions: After third molar extraction, oral probiotic helped achieve a larger reduction in pain towards the end of the first week.

References: Samaranayake, L., Matsubara, V.H. Normal Oral Flora and the Oral Ecosystem. Dent Clin N Am 61 (2017) 199–215

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Track 3: Microbiology

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MICROBIOME CORE IN PATIENTS WITH RELAPSING-REMITTING MULTIPLE SCLEROSIS

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Introduction: Recent findings indicate the effect of gut microbiome on certain neurological diseases such as multiple sclerosis (AD). In this study we attempt to reveal the microbiome composition in a case series of Caucasian population with relapsing-remitting multiple sclerosis (RRMS).

Objectives: To describe the gut microbiome in a case series of Caucasian population with RRMS, comparing these results with the gut microbiome in healthy people. We also describe bacteria form groups (clusters) according to their similarity amongst individuals.

Methods: Patients with RRMS were included in the study. Massive genome sequencing of stool samples of patients was performed. DNA from stool samples was isolated following the protocols of Yuan and coworkers with minor modifications, with the aid of MagnaPure Compact System (Roche Life Science). The microbiome of a cohort of 16 patients with remittent recurrent active sclerosis multiple was obtained by 16s rRNA massive sequencing with MiSeq platform (Illumina inc, San Diego).

Results: Microbiome in 17 patients with RRMS was obtained. We have a mean of 112 different species of bacteria in each patient. In our series the most prevalent bacteria are Bacteroides. Most