

Ratio of different bacterial genera in oral biofilm in polar researchers during an Antarctic summer-season expedition 2026 to James Ross Island

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Abstract

Short- and long-term stays in Antarctica may induce microbiome changes in oral cavity. In our study, pre- and post-Antarctic expedition oral microbiome were analysed in the participants of Czech Antarctic expedition 2026. Saliva samples were taken from the expedition members before (Day 0, January 16th, 2026), during, and after (Day 62, March 20th, 2026) the Czech Antarctic Expedition to Mendel station, James Ross, Island. Within the expedition time, the samples were taken on Day 34 (February 19th, 2026) and Day 47 (March 5th, 2026). The objective of this study was to investigate whether inducing stress conditions occurring during the Antarctic mission would affect oral microbiome composition. The results suggest that the ratio of common bacteria of oral microbiome, namely share of *Streptococcus* genus to other genera, decreased during the expedition time. After the return of the expedition staff to the Czech Republic, the composition of the oral microbiome shifted back to pre-expedition status. The ratio of *Streptococcus* genus to other bacterial strains increased again.

Key words: Antarctica, James Ross Island, oral microbiome, isolated crews, confined and extreme environments, space mission analog

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Introduction

Antarctica is considered isolated, confined, and extreme (ICE) environment with many effects on humans during short- or long-term stays, typically Antarctic expe-

ditions organized by countries with established national polar programmes. The ICE effects on human health may vary depending on the operational context, such

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as research stations, camps, or ships (Srivastava *et al.* 2024), each characterized by distinct structural, social, and environmental features. Typically, health issues, diseases and injuries differ between seasonal (austral summer) and overwintering (a year-round) crews. The latter ones have a higher share of the cases related to environmental factors (63 cases, *i.e.* 32%), indoor and outdoor work (55 cases, *i.e.* 28%), than those related to daily life other than tasks (34 cases, *i.e.* 17%) – Ohno *et al.* (2018).

Stay at Antarctic research stations and field activities represents a unique co-action of extreme environmental conditions, restricted diets, and cold temperature, affecting human microbiota, an important factor in host health. However, knowledge of the effects of Antarctic expeditions on human microbiome is still fragmentary due to small cohort sizes and short study durations in austral summer expeditions. However, some aspects of human microbiome in Antarctica have been targeted in the studies published within the last decade that focused salivary microflora (Bhushan *et al.* 2019, Cameron *et al.* 2023), intestinal (Jin *et al.* 2014), and gut microbiota dynamics (Wang *et al.* 2024, Lee *et al.* 2025). Recent study of Rumão *et al.* (2026) focuses on the changes of human microbiome composition and the ways by which environmental or behavioural factors modulate these changes. Apart from metadata analysis aimed to evaluate the effects of participant demographics, type of microbiome sample collected (gut, skin, oral), ICE environment (station, shipboard, or camp), study design and timeline, sequencing methods, the study addresses oral cavity microbiome. It concluded that oral microbiota exhibited lower stability when compared to gut microbiota. Study of Lee *et al.* (2025) reports that gut microbiota is significantly influenced during a long-term residence in Antarctic stations. Dominant taxa remains relatively stable, whereas minor taxa exhib-

it greater variability. The gut microbiota change depends on the intrinsic microbiota prior to staying in the stations. The study also pointed out some important aspects driving the microbiota change such as co-habitation effects among genetically unrelated individuals.

Oral microbiota, however, showed high diversity and marked sensitivity to environmental factors similarly to the study of Gao *et al.* (2018). These findings align with evidence from other confined environments, including the MARS500 mission (Turroni *et al.* 2017). Similarly, an increase in saliva microbiome has been reported by Urbaniak *et al.* (2020) after a short-term space flight, as well as by Hao *et al.* (2022) for a long-term on-Earth test of crew within the Lunar Palace project. The oral cavity contains the second – largest microbiota in the human body. Recent review by Tian *et al.* (2024) characterizes assemblage of microorganisms in the oral cavity and their changes under external influences. The study reports planktonic bacteria in saliva are more likely to be affected by the chemical composition of saliva, whereas biofilms are more likely to be affected by physical forces. Among a great variety of factors affecting oral cavity microbiome, oral hygiene habits may affect the oral microbiota, with scraping having the most significant effect on the microbiota (Sedghi *et al.* 2021). Different oral hygiene habits of the studied Antarctic crew may have effect on the oral microbiome.

Regarding oral cavity microbiome in Antarctic crews, earlier study of the Brazilian team (Moraes *et al.* 2023) revealed that staying in a long-term Antarctic camp resulted in microbiome fluctuations with a reduction in Pseudomonadota – a “microbial signature” of disease. However, the pro-inflammatory marker leptin and IL-8 tended to increase suggesting that suggest that distinct Antarctic natural environments and behavioural factors modulate oral microbiome and inflammation of Ant-

arctic crews. Our study focused the crew of the Czech Antarctic expedition (Jan–March 2026) to James Ross Island and the changes in oral microbiota induced by Antarctic environmental conditions and expeditional life. Expedition crew members were sampled by before, during and after the expedition in order to detect even short-term changes. Unlike some previous studies on oral biofilm (for review, *see* Lv et al. 2025), our study has been targeted on

detection of the part of the biofilm that can be cultivated. Therefore, our study was not able to detect anaerobic bacteria, spirochetes that cannot be cultured, and many other bacteria. On the other hand, it was possible to identify the bacteria to genus and species level and also the fact that the bacteria have been cultured makes a proof that the bacteria represent viable cells and not just some parts of microbial genome.

Material and Methods

Activities performed during expedition by the probands

Travelling to/from Antarctica, and the activities performed during the expedition at James Ross Island, both at the Mendel station and in the field, are important factors that may affect oral microbiome. Within the Czech Antarctic expedition 2026, crew members spent 10 days at King George Island (Escudero station) after the flight from Punta Arenas (Southern Chile) followed by a 3-d ship trip to the James Ross Island on board of a Chilean ice-breaker. Journey back was 5 d travel by a small-size vessel, across the Drake Passage to Punta Arenas where the staff spent 3 days before the flight to Europe.

The crew members (16 probands) were 12 men and 4 women, within an age range of 25–59 years. The crew members involved into the study were scientists of several professional specializations: 2 climatologists, 1 algologist, 5 geoscience specialists (2 glaciologists, 3 permafrost people), 4 plant physiologists, 2 microbiologists, 1 ecologist, 1 medical doctor. They spent 35 days at James Ross Island and performed the following activities: (1) laboratory-based research, (2) permanent research sites visits and management of automated data records, (3) field sampling activities, typically long-distance walking

in stony areas, (4) glaciological research including a-day-long glacier walks, (5) permafrost research, (6) climate and microclimate monitoring by a net of weather station distributed over a deglaciated area, (7) AUV-based monitoring of deglaciated areas including several localities, (8) field camps related mainly to the (3) and (4) activities. Some of the field works represented physically-demanding activities and the impact of increased workload during active research periods combined with environmental stressors on the crew members.

All participants of the study met the following criteria: (1) They were medically and psychologically qualified for Antarctic expedition; (2) They had no active thyroid, adrenal, or infectious disease, and (3) They did not take any medication that might potentially affect the oral microbiome study. The diets and lifestyles of all the expedition crew members included into the study in Antarctica were similar. Their diet differed slightly between those performing their field activities at the station or in close neighbourhood (1–7 km away of the station) and those taking a part in field camp outside the station (3 days off).

Medical research

Apart from two sampling of oral microbiota that was done on day 34, and 47 (February 19th, and March 5th) at the James Ross Island, there were an array of medical research performed during the expedition. First, several new medical devices were delivered to and installed at the Mendel station to increase a standard of medical care. They were an automated external defibrillator BeneHeart C1A, Mindray[®], vital signs monitor uMec10, Mindray[®] with accessories, an ultrasound machine Compact Ultrasound System MX3, Mindray[®] with a convex and Phased array probes, minor medical supplies, medical cabinet and medications and other medical equipment. The new equipment allowed to perform higher-quality basic diagnostics, treat inju-

ries, monitor vital signs/functions, and conduct ultrasound examinations. Medical research conducted during the expedition focused monitoring of blood pressure and heart activity of the crew members. The research examined the changes in the adaptability of the cardiovascular system, as well as changes in the regulation of the autonomic nervous system and the composition of body tissues. Furthermore, microbiological research was conducted focusing on the occurrence of fungi at the polar station and among the expedition members, and finally, pharmaceutical research was conducted, which monitored the effect of year-round storage of selected oral and injectable medications on their stability, release, and effectiveness.

Characteristics of oral microbiome sampling

We performed a study of 16 polar researchers. An oral swab had been taken from all of them in the moment when they left to the James Ross Island, then twice during their expeditional stay at the island, and after they came back to Czech Republic (*see* Table 1). In all of them a swab

from buccal mucosa has been taken using Amies (MTS-002) swab with charcoal. The medium (pH 7.3 ± 0.2) reduces overgrowth of coliform organisms. The presence of activated carbon neutralizes toxic metabolic byproducts produced by microbial growth.

Day 0 (before)	Day 34	Day 47	Day 62 (after arrival)
Brno (CZ)	Mendel station	Mendel station	Brno
January 16 th , 2026	February 19 th , 2026	March 5 th 2026	March 20 th , 2026

Table 1. Overview of the sampling days.

Microbiome Analysis

After the expedition member's arrival, the collected samples collected at the James Ross Island together with those taken before and after expedition were transferred to the microbiology laboratory (Institute of Microbiology, Medical Faculty of Masaryk University and St. Ann's Faculty hospital). The swab had been

stored in refrigerator temperature (5°C). After that, all these swabs had been cultivated in 37°C on a blood agar for 24 hours. Then, 20 well isolated colonies were identified using MALDI-TOF MS (Bruker). The result comes from these twenty best isolated colonies from each of the researchers.

No.	Day 0 (before) Brno (CZ) January 16 th , 2026 1 st replicate	Day 34 Mendel station February 19 th , 2026 1 st replicate	Day 47 Mendel station March 5 th , 2026 1 st replicate	Day 62 (after arrival) Brno (CZ) March 20 th , 2026 1 st replicate	No.
1	<i>S. gordonii</i> 20	<i>Ps. plecoglossicida</i> 20	<i>Chryobacterium shangdonense</i> 4	<i>S. salivarius</i> 3	17
2	<i>S. mitis</i> 17	<i>C. dubliniensis</i> 17	<i>S. oralis</i> 2	<i>S. salivarius</i> 2	18
3	<i>S. parosanguinis</i> 18	<i>S. mitis</i> 20	<i>S. oralis</i> 20	<i>S. salivarius</i> 12	8
4	<i>S. oralis</i> 14	<i>Se. marcescens</i> 20	<i>Sm. maltophilia</i> 20	<i>Rothia mucilag.</i> 5	15
5	<i>S. mitis</i> 20	<i>S. salivarius</i> 20	<i>K. pneumoniae</i> 20	<i>S. parosanguinis</i> 2	18
6	<i>S. parosanguinis</i> 14	<i>Ps. putida</i> 2	<i>S. salivarius</i> 3	<i>S. mitis</i> 20	
7	<i>N. subflava</i> 17	<i>Gr. adiacens</i> 16	<i>St. warneri</i> 15	<i>S. mitis</i> 20	
8	<i>S. mitis</i> 20	<i>S. oralis</i> 20	<i>Chryobacterium indologenes</i> 20	<i>S. cristatus</i> 5	
9	<i>S. mitis</i> 20	<i>C. albicans</i> 20	<i>S. mitis</i> 20	NT	
10	<i>S. mitis</i> 15	NT	<i>K. varicola</i> 20	<i>S. oralis</i> 20	
11	<i>S. oralis</i> 16	NT	<i>S. aureus</i> 12	<i>S. mitis</i> 20	
12	<i>S. vestibularis</i> 20	<i>K. pneumoniae</i> 18	<i>S. salivarius</i> 4	<i>Rothia mucilaginosa</i> 2	18
13	<i>S. salivarius</i> 20	<i>Acidovorax temperans</i> 20	<i>S. mitis</i> 20	<i>Rothia mucilaginosa</i> 20	
14	<i>S. parosanguinis</i> 15	<i>E. faecalis</i> 5	<i>C. albicans</i> 20	<i>Shewanella algae</i> 6	14
15	<i>S. oralis</i> 20	<i>C. dubliniensis</i> 20	<i>St. hominis</i> 10	<i>S. mitis</i> 20	
16	NT	<i>St. epidermidis</i> 5	<i>S. salivarius</i> 3	NT	
21	<i>S. mitis</i> 20	NT	NT	NT	
22	<i>S. mitis</i> 17	NT	-	<i>S. mitis</i> 20	
23	<i>S. vestibularis</i> 18	NT	NT	NT	
24	<i>N. macacae</i> 15	NT	NT	NT	
25	<i>S. mitis</i> 20	NT	NT	NT	
	Σ 356	Σ 223	Σ 213	Σ 192	108
	Sum of all colonies, genera	Sum of all colonies, genera	Sum of all colonies, genera	Sum of all colonies, genera	
	<i>S. gordonii</i> 20	<i>Ps. plecoglossicida</i> 20	<i>S. oralis</i> 22	<i>S. salivarius</i> 5	
	<i>S. mitis</i> 151	<i>C. dubliniensis</i> 37	<i>S. mitis</i> 91	<i>S. mitis</i> 177	
	<i>S. salivarius</i> 37	<i>S. oralis</i> 23	<i>Sm. maltophilia</i> 20	<i>R. mucilaginosa</i> 39	
	<i>S. oralis</i> 72	<i>S. mitis</i> 39	<i>K. pneumoniae</i> 20	<i>S. sanguinis</i> 15	
	<i>S. vestibularis</i> 47	<i>Se. marcescens</i> 20	<i>S. salivarius</i> 10	<i>S. parosanguinis</i> 2	
	<i>S. parosanguinis</i> 47	<i>S. salivarius</i> 20	<i>St. warneri</i> 15	<i>S. oralis</i> 56	
	<i>N. macacae</i> 15	<i>Ps. putida</i> 2	<i>S. cristatus</i> 5	<i>S. oralis</i> 6	
	<i>N. lactamica</i> 5	<i>Sm. maltophilia</i> 18	<i>C. albicans</i> 28	<i>Shewanella algae</i> 2	
	<i>N. subflava</i> 6	<i>Gr. adiacens</i> 16	<i>St. hominis</i> 10		
		<i>C. albicans</i> 20	<i>S. vestibularis</i> 4		
		<i>K. pneumoniae</i> 18	<i>Chryobacterium shangdonense</i> 4		
		<i>S. infantis</i> 2	<i>Chryobacterium indologenes</i> 20		
		<i>Ac. temperans</i> 20	<i>K. varicola</i> 20		
		<i>E. faecalis</i> 5	<i>S. parosanguinis</i> 17		
		<i>S. vestibularis</i> 15	<i>Sp. paucimobilis</i> 16		
		<i>St. epidermidis</i> 5	<i>St. aureus</i> 12		
	Σ 400	Σ 280	Σ 320	Σ 300	

Table 2. Appearance of bacterial strains in particular sampling dates. *Note:* Additionally, 5 probands were sampled just only before the expedition. They were individuals taking a part in a short-term expedition to the Nelson Island (numbered 21-25 in Table 2).

Results

The first results of this pilot study show important difference between oral swabs taken before the stay, during the stay and after coming back. The first set contained just two microbial genera: *Streptococcus* and *Neisseria*. *Streptococcus* participated by 93.5%, *Neisseria* by 6.5%. The species of *Streptococcus* included various oral streptococci, mainly *S. mitis*, *S. parasan- guinis* and *S. oralis*. In both sets taken dur- ing the stay the ratio had been completely different. The first set (samples from Feb- ruary 19th, 2026) included only 35.3% of genus *Streptococcus*, but 20.4% of *Candi- da*. Other genera included *Pseudomonas*,

Serratia, *Stenotrophomonas*, *Klebsiella*, *Acidovorax*, *Granulicatella* (all having ra- tio between 5 and 8%) and also *Entero- coccus* and *Staphylococcus* (both around 2%). The second set (samples taken on March, 3rd, 2026) taken during the stay at the Mendel station included *Streptococcus* in 48.4%, followed by *Klebsiella* (12.5%), *Staphylococcus* (11.6%), *Stenotrophomo- nas*, *Candida* and *Chryseobacterium* (5–9% for all of them). In the set taken after coming back, only three genera had been included: *Streptococcus* in 85% (mostly *S. mitis* and *S. oralis*), *Rothia* (13%) and *Shewanella* (2%).

Day 0 (before) Brno (CZ) January 16 th , 2026 Σ (Sum of all colonies, genera)	Day 34 Mendel station February 19 th , 2026 Σ (Sum of all colonies, genera)	Day 47 Mendel station March 5 th 2026 Σ (Sum of all colonies, genera)	Day 62 (after arrival) Brno (CZ) March 20 th , 2026 Σ (Sum of all colonies, genera)
<i>Streptococcus</i> 374 93.5% <i>Neisseria</i> 26 6.5%	<i>Streptococcus</i> 99 35.3% <i>Serratia</i> 20 7.1% <i>Stenotrophomonas</i> 18 6.4% <i>Klebsiella</i> 18 6.4% <i>Granulicatella</i> 16 5.7% <i>Staphylococcus</i> 5 1.8% <i>Candida</i> 57 20.4% <i>Acidovorax</i> 20 7.1% <i>Enterococcus</i> 5 1.8% <i>Pseudomonas</i> 22 7.9%	<i>Streptococcus</i> 155 48.4% <i>Stenotrophomonas</i> 20 6.2% <i>Klebsiella</i> 40 12.5% <i>Staphylococcus</i> 37 11.6% <i>Candida</i> 28 8.8% <i>Chrysobacterium</i> 24 7.5% <i>Sphingomonas</i> 16 5.0%	<i>Streptococcus</i> 255 85% <i>Rothia</i> 39 13% <i>Shewanella</i> 6 2%
Σ 400 100%	Σ 280 100%	Σ 320 100%	Σ 300 100%

Table 3. Summary of appearance of bacterial strains in particular sampling dates.

Discussion

During polar expeditions, the unique combination of limited space, extreme cold, and disrupted circadian rhythms has a direct impact on the host’s physiology. It is well-established that identifying the characteristic functional changes in polar expeditioners can help preserve health, enhance work capacity, and improve adap- tive potential in specific and the ICE en- vironments. Recent studies from Antarcti- ca focus the impact of a short-term expe- dition on selected physiological param-

eters among expedition participants (Alexan- drova *et al.* 2026), including oral micro- biome changes. The oral cavity is highly sensitive to external stressors. Since saliva serves as a non-invasive diagnostic tool, researchers can closely monitor how oral homeostasis responds to the conditions during Antarctic expeditions. Recent study (Araujo-Muro *et al.* 2026) from a two- month expedition stay at the Machu Pic- chu Antarctic Research Station reports a significant worsening of periodontal health

and salivary flow, likely due to environmental factors and diet. The changes included a significant increase in papillary bleeding on probing and a decrease in normal salivary flow.

When exposed to extreme environmental stress (such as high altitudes, extreme cold environment), oral bacterial networks become much tighter, compact, and highly reactive. The gut microbiome, in contrast, acts as a thoroughly isolated metabolic unit that maintains the balance of the internal environment during temperature and altitude stress. In long-term confined environments, however, gut microbial communities may change as reported by Wang et al. (2026) for eight crew members of the ground-based space simulation (Lunar Palace). Our data support the above-mentioned responsivity of oral microbiome to the factors acting during an Antarctic expedition. The results presented in Table 2 and 3 show that the ratio of common bacteria of oral microbiome, namely *Streptococcus* genus, dramatically decreases during the stay of the researchers in Antarctica. The results are, however, going to be further examined. Nevertheless, already now we can conclude that the microbiome in the oral cavity is dramatically influenced by stay of the researchers on Antarctica. The shift from oral staphylococci to Gram-negative bacteria (Enterobacteriales and Gram-negative non-fermenters) is evident. After coming back, the composition of the oral microbiome (or at least its culturable part) shifted back – ratio of *Streptococcus* increased again; the role of *Rothia* and *Shewanella* is unclear and maybe accidental.

Our data showing the change in oral microbiota in time during the Czech expedition 2026 are similar to those reported for Indian Antarctic expedition, *i.e.* sea voyage and stay at the Indian Antarctic station Maitri. Bhushan et al. (2019) reported that the oral microbial diversity of the expedition members was significantly changed between three sampling dates.

The oral microbiota comprised mainly of the phyla *Firmicutes* (46%, 29% & 36%); *Proteobacteria* (40%, 48% & 44%), *Bacteroidetes* (10%, 22% & 14%), *Fusobacterium* and *Actinobacteria* (5% – 1%), and unclassified phyla (17%, 25% & 23%). A complex study of Cameron et al. (2023) focused on saliva and stool microbiota changes during a Transarctic Winter Traverse expedition and reported significant activity-associated changes in terms of both bacterial diversity and load in saliva. The study introduced a new aspect into Antarctic science related to human microbiome, *i.e.* combination of the microbiota assessment and metabolomic markers. Salivary microbiome was tested in twelve expeditioners overwintering at the Chinese Antarctic station (Great Wall, King George Island, Antarctica) by Wang et al. (2024). The study reported the following dominant bacteria in saliva and throat swab samples: *Streptococcus*, *Prevotella*, *Veillonella*, *Neisseria* and *Porphyromonas*.

The changes in oral microbiome during Antarctic mission are comparable data gained for astronauts during and after spaceflight. Morrison et al. (2021) reports that the relative abundance of *Prevotella* in saliva samples increased during two astronauts' time onboard the ISS while the relative abundance of other commensal taxa such as *Neisseria*, *Rothia*, and *Haemophilus* decreased. Apart of the mission way of life, microgravity effect might be pointed out as a cause of oral microbiome changes, specifically an increase in anaerobic bacteria in dental plaque as well as the increase of *Mycoplasma* in saliva (Lloro et al. 2020). The study also reported an increase in cortisol, and salivary immunoglobulin A, G (IgA, IgG). These findings might be supported by salivary IgG levels and increased *Streptococcus mutans* activity in the staff simulated Mars mission at the Mars Desert Research Station, Utah, USA (Rai and Kaur 2013). The study reports stress-induced significant difference in clinical periodontal parameters (probing

depth, bleeding on probing, and clinical loss of attachment) even after 1 week of the mission.

Similar changes were found for people taking a part in the Skylab missions. (Brown *et al.* 1974) reported secretory IgA increased persistently during chamber confinement and reached a maximum level by day 55 of sampling. In the Skylab missions, the anaerobic *Bacteriodes* sp., *Veillonella* sp., *Fusobacterium* sp., *Neisseria* sp., and *S. mutans* are reported. They are considered the main causes of dental caries (Costalonga and Herzberg 2014). More recent data from ISS (Agha *et al.* 2020) confirmed increased salivary secretory IgA, together with lysozyme, and antimicrobial peptide LL-37. The same study refers to an increase in the cortisol-to-dehydroepiandrosterone ratio. The recent evidence gained for astronauts, commercial divers, and elite expedition crews suggests that extreme physical and psychological stress may cause the oral microbiome changes and significant restructuring, often leading to the overgrowth of plaque-associated pathobionts and elevated viral shedding.

Apart of geographical aspects of oral cavity microbiome, the distribution of oral microbiota may differ across different oral sites. Mark Welch *et al.* (2019, 2020) classified nine distinct areas: the specialized epithelium (tonsils and back of the tongue), throat and attached gum, hard palate and buccal mucosa, tooth surface (supragingival and subgingival), and saliva. However, the biofilms and bacteria are not static. The

top of the attached bacteria can detach, enter the saliva, and be transported to new colonization sites.

The current trend is to mitigate fluctuations in the microbiome during Antarctic expeditions. To counteract the effects of isolation and extreme conditions, expedition protocols often include measures to support homeostasis in the oral cavity and gut (Huo *et al.* 2026). They include probiotic supplementation, and dietary adjustment. First, clinical studies conducted during expeditions have shown that supplementation with multi-strain probiotics can stabilize the microbial ecosystem and thus help counteract travel-related stress. Secondly, maintaining microbiome diversity depends largely on consuming nutrient-rich foods and, when available, fermented foods, which help maintain beneficial bacteria in the oral cavity. Finally, majority of disruptions to the microbiome and immune system observed during expeditions typically return to baseline levels after the expedition ends and participants return to their normal environment. To further explore the underlying mechanisms of oral microbiome changes in Antarctic crews, the Czech Antarctic Program will focus, apart of dental check before and after the expedition (Peřina *et al.* 2023), on detailed oral microbiome analysis and measurement of systemic stress biomarkers, such as *e.g.* salivary cortisol, as reported by Kuzmenko *et al.* (2026) for Antarctic and Arctic expedition crews.

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