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SPACELAB J AIR FILTER DEBRIS ANALYSIS STS-49 - SLJ

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Filter debris from the Spacelab module SLJ of STS–49 was analyzed for microbial contamination. Debris for cabin and avionics filters was collected by Kennedy Space Center personnel on October 1, 1992, approximately 5 days postflight. The concentration of microorganisms found was similar to previous Spacelab missions averaging 7.4E+4 CFU/mL for the avionics filter debris and 4.5E+6 CFU/mL for the cabin filter debris. A similar diversity of bacterial types was found in the two filters. Of the 13 different bacterial types identified from the cabin and avionics samples, 6 were common to both filters. The overall analysis of these samples as compared to those of previous missions shows no significant differences.

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INTRODUCTION

Filter debris from the avionics and cabin air filters of the space lab module was analyzed for microbial contamination. This analysis was part of an ongoing project to study the potential for the spread of microorganisms aboard the space craft during each mission.

Debris from cabin and avionics filters was collected by Kennedy Space Center personnel on October 1, 1992, approximately 5 days post-flight. Collection procedures were followed as previously described (1). All samples were delivered to the microbial ecology facility in the Analytical and Physical Chemistry Branch of Marshall Space Flight Center on October 3, 1992 for analysis.

METHODS

Processing of debris began within 4 hours of receipt. The procedure used was a modification of previous methods (2). The debris from avionics and cabin air filters was weighed aseptically in sterile 1 L flasks, suspended in 200 ml sterile water per gram debris and sonicated for 15 minutes. After settling for 10 minutes, the liquid was removed from each slurry. Remaining debris was filtered using a Whatman 541 filter paper disc. The filter containing the debris was then placed in plastic holders and dried at 28C for 3 days in preparation for chemical analysis.

Microbial analysis was done by spread plating duplicate 0.1 ml volumes of the liquid from each sample and a 1:100 dilution of the liquid from each sample onto 2 types of microbial growth medium, R2A and BHI (Brain Heart Infusion). The R2A plates were incubated at 28C for 7 days while the BHI plates were incubated at 35C for 3 days. Isolated colonies which grew on each type of medium were streaked onto BUGM (Biolog Universal Growth Medium) for further isolation and identification. Morphologically distinct bacterial colony types were identified using the Biolog Identification System.

RESULTS

Total debris weights and volumes of water added to each sample can be found in Table 1. Microbial total counts from initial isolation plates are found in Table 2. The microorganisms isolated from samples are listed in Table 3.

A total of 10 isolates were recovered from the avionics air filter debris and a total of 12 isolates were recovered cabin air filter debris.

Staphylococcus sp. was the predominant bacterium isolated from the samples. This organism is commonly found on the surface of human skin.

TABLE 1

SLJ AIR FILTER DEBRIS WEIGHT AND VOLUME

	Avionics	Cabin
Final(g)	298.13	300.77
Tare(g)	293.44	297.16
Difference(g)	4.69	3.61
Sterile water added (ml - 200ml/g)	938	722

TABLE 2

SLJ MICROBIAL COUNTS

Medium	Avionics (CFU/g Debris)	Cabin (CFU/g Debris)
BHI 35C	7.6E+4	1.56E+6
	6.5E+4	1.25E+6
R2A 28C	7.4E+4	8.04E+6
	7.9E+4	7.42E+6

CFU - colony forming unit

TABLE 3

SLJ ISOLATE IDENTIFICATION

Gram Positive Isolates

Avionics Air Filter Debris	Similarity Index
BACILLUS INSOLITUS	0.510
BACILLUS INSOLITUS	0.632
BACILLUS INSOLITUS	0.728
CORYNEBACTERIUM MINUTISSIMUM	0.586
STAPHYLOCOCCUS AUREUS	0.554
STAPHYLOCOCCUS AUREUS	0.629
STAPHYLOCOCCUS EPIDERMIDIS	0.580
Cabin Air Filter Debris	
BACILLUS INSOLITUS	0.558
BACILLUS INSOLITUS	0.670
BACILLUS INSOLITUS	0.746
CLAVIBACTER MICHIGANENSIS SS SEPEDONICUM	0.485
ENTEROCOCCUS FAECALIS	0.801
MICROCOCCUS NAUCINUS	0.717
STAPHYLOCOCCUS AUREUS	0.634
STAPHYLOCOCCUS AUREUS	0.682
STAPHYLOCOCCUS AUREUS	0.762
STAPHYLOCOCCUS AUREUS	0.785
STAPHYLOCOCCUS AUREUS	0.794
STAPHYLOCOCCUS AUREUS	0.817
STAPHYLOCOCCUS AUREUS	0.821
STAPHYLOCOCCUS HOMINIS	0.580

Gram Negative Isolates

Avionics Air Filter Debris	
HAEMOPHILUS APHROPHILUS	0.613
KLEBSIELLA PNEUMONIAE A	0.565
KLEBSIELLA PNEUMONIAE A	0.728
METHYLOBACTERIUM EXTORQUENS	0.620
PSEUDOMONAS FLUORESCENS B	0.871
XANTHOMONAS CAMPESTRIS PV XANTHOSOMA	0.549
Cabin Air Filter Debris	
ACTINOBACILLUS SEMINIS	0.498
BRUCELLA ABORTUS BIOVAR 2	0.543
BRUCELLA ABORTUS BIOVAR 2	0.599

TABLE 3, continued

ENTEROBACTER ASBURIAE	0.792
ESCHERICHIA HERMANII	0.929
KLEBSIELLA PNEUMONIAE A	0.957
KLEBSIELLA PNEUMONIAE A	0.957
KLEBSIELLA TERRIGENA	0.831
PSEUDOMONAS FLUORESCENS B	0.719

Similarity Index - Goodness of identification relative to the best match for the Biolog data base. One is a perfect match; 0.5 is the minimum match for perfect identification.

DISCUSSION

Filter debris weight is within the same order of magnitude as seen in previous missions (Table 4).

TABLE 4

COMPARATIVE DEBRIS WEIGHTS (g) BY MISSION

	SLS-1	IML-1SLJ	
Cabin filter debris	1.47	8.51	3.61
Avionics filter debris	0.37	2.30	4.69

The concentration of microorganisms was similar to previous findings with much higher concentration found in the cabin filter debris. This is most likely a result of human contamination.

A similar diversity of bacterial types was found in the two filters. Of the 13 different bacterial types identified from the cabin and avionics samples, 6 were common to both filters indicating potenial for the exchange of debris between ventilation systems. This commonality may also be a result of previous filter handling. Many of the isolates are considered normal flora and may even represent a common microbial environment rather than a cross-contamination of air supplies.

The most frequently isolated bacterial genus from either filter type in this analysis was Staphylococcus. The isolation of this bacterium was expected since it is a common contaminant of humans. The organism poses no serious health threat if continuous accumulation is minimized.

Analysis for potentially pathogenic organisms, including coliform bacteria, was negative. No species of the pathogenic genera Salmonella or Shigella were isolated.

In summary, the overall analysis of these samples as compared to those of previous missions shows no significant differences. Even though there were differences in period of time between shuttle landing and analysis, methods, and culture media employed, no unexplained differences were encountered. Future sampling will provide further information toward the establishment of baseline conditions and mcirobial growth trends for long duration human spaceflight. This will be necessary for a better understanding of the accumulation of microbial contamination as

missions are extended in duration. Changes in the amount of microbial contamination should be tracked so that any further problem which could develop can be forseen and prevented.

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APPROVAL

SPACELAB J AIR FILTER DEBRIS ANALYSIS
STS-49 - SLJ

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The information in this report has been reviewed for technical content. Review of any information concerning Department of Defense or nuclear energy activities or programs has been made by the MSFC Security Classification Officer. This report, in its entirety, has been determined to be unclassified.

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