SAPIENZA
UNIVERSITÀ DI ROMA

Biosecurity in Space

Simposio ASI Biomedicina Spaziale

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The ISS microbiota is dominated by human-associated microorganisms

The ISS crew in 2009, 13 astronauts.

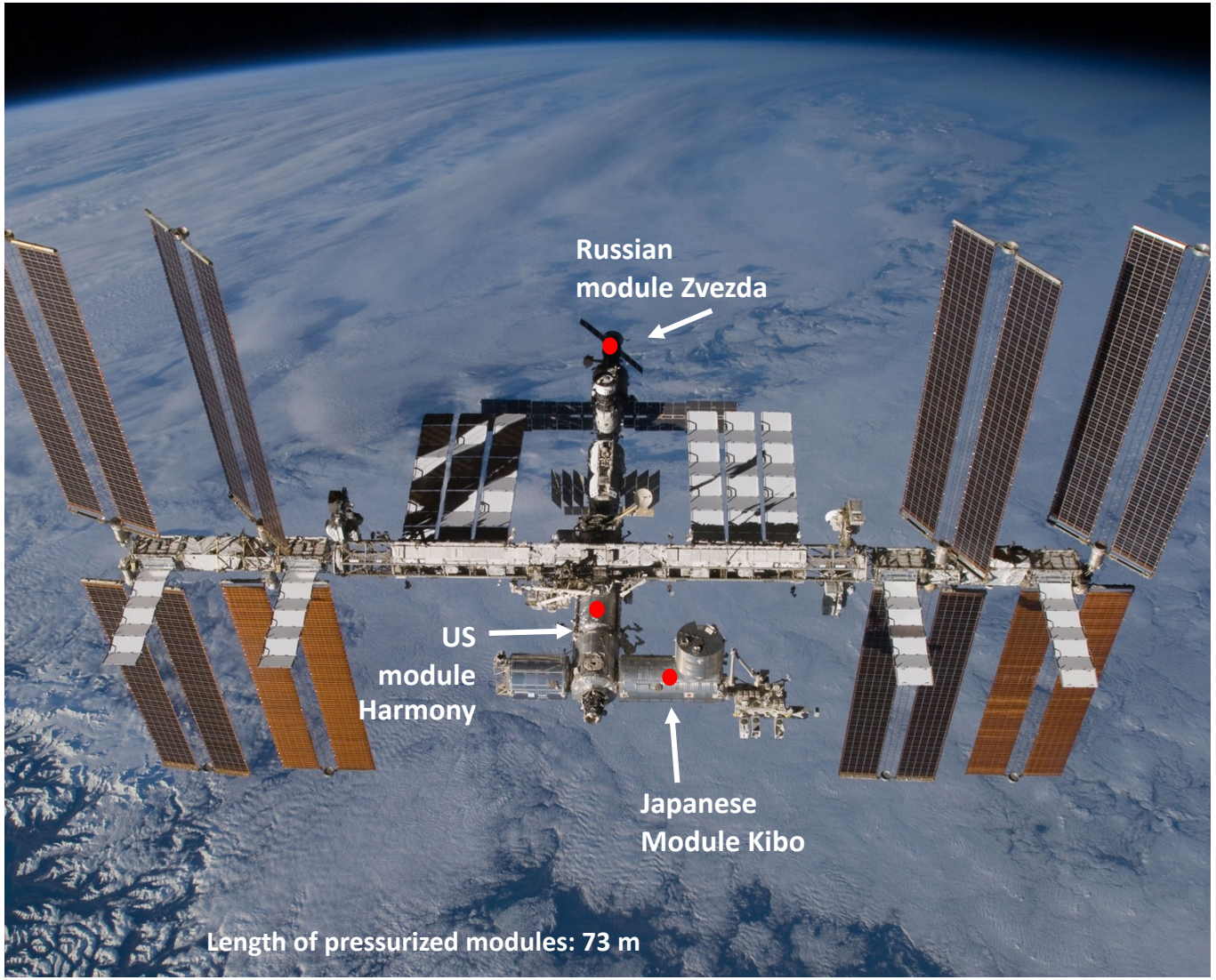
The ISS is an extremely isolated environment with a low influx of new microbes. Most microbes detected on surfaces within the ISS are transient, and that shortly after one crew departs and a new crew arrives, the distribution of microbes on the ISS changes to reflect its new crew's skin microbiome.
Still, it was found that a small proportion of the environmental bacteria were ubiquitously present in the ISS.

Scientific Reports (2019) 9:9911. 10.1038/s41598-019-46303-8

11 peculiar *Bacillus* strains were recovered during microbiological surveys in the ISS

The red dots in the picture indicate the Russian, Japanese and US modules of the ISS.
The mentioned 11 *Bacillus* species were isolated from:

- the Russian segment Zvezda Service Module (DOS-8), from surface samples collected with a Swab Rinse Kit tube (ESA Delta mission expedition 8, 2004 and expedition 11, 2005);
- the Kibo Japanese experimental module, from air diffuser samples collected with a surface sample kit (Expedition 19, 2009);
- the US segment Harmony Node 2, from air HEPA filters used 40 months (returned with flight STS-134/ULF6, 2011).



Whole genome sequence characterizations showed that ISS strains had the plcR non-B. anthracis ancestral allele and lacked anthrax toxin-encoding plasmids pXO1 and pXO2, excluding their identification as B. anthracis. Nevertheless, these isolates are in a clade that is distinct from previously described members of the B. cereus, closely related to B. anthracis.

Biological experiments with BSL-3 and BSL-4 agents are not allowed in the ISS.

mSystems 2:e00021-17. 2017. https://doi org/10.1128/mSystems.00021-17

The ISS *Bacillus* strains are closely related to the pathogenic Ames *B. anthracis*

Genomes

B. anthracis str. Ames aligned with ISS *Bacillus* strains

Number of genetic variants detected

40902

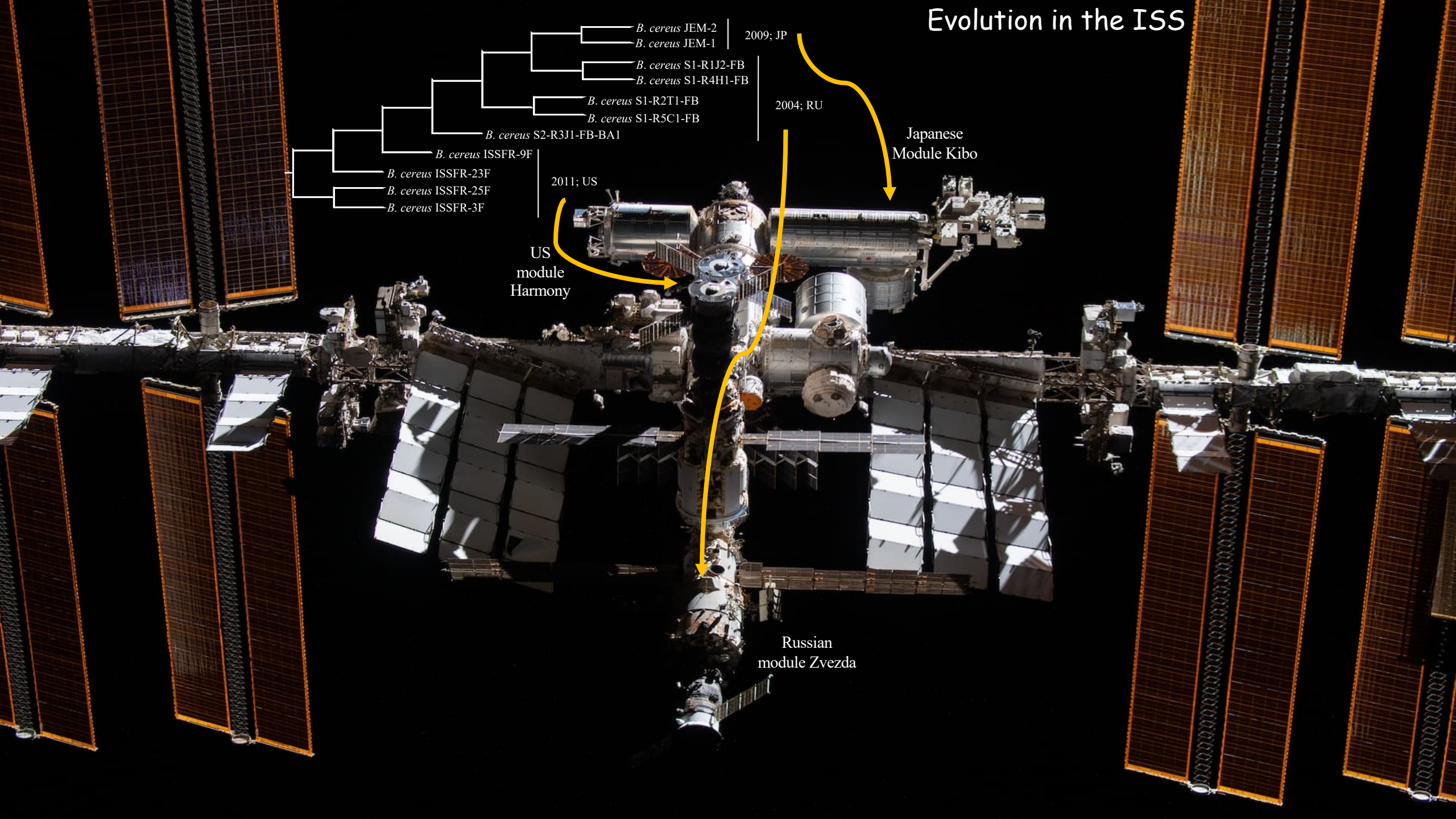
Distribution of differences amongst the ISS strains

- 37679 genetic variants present in all the ISS strains
- 3223 genetic variants present in one or more ISS strains

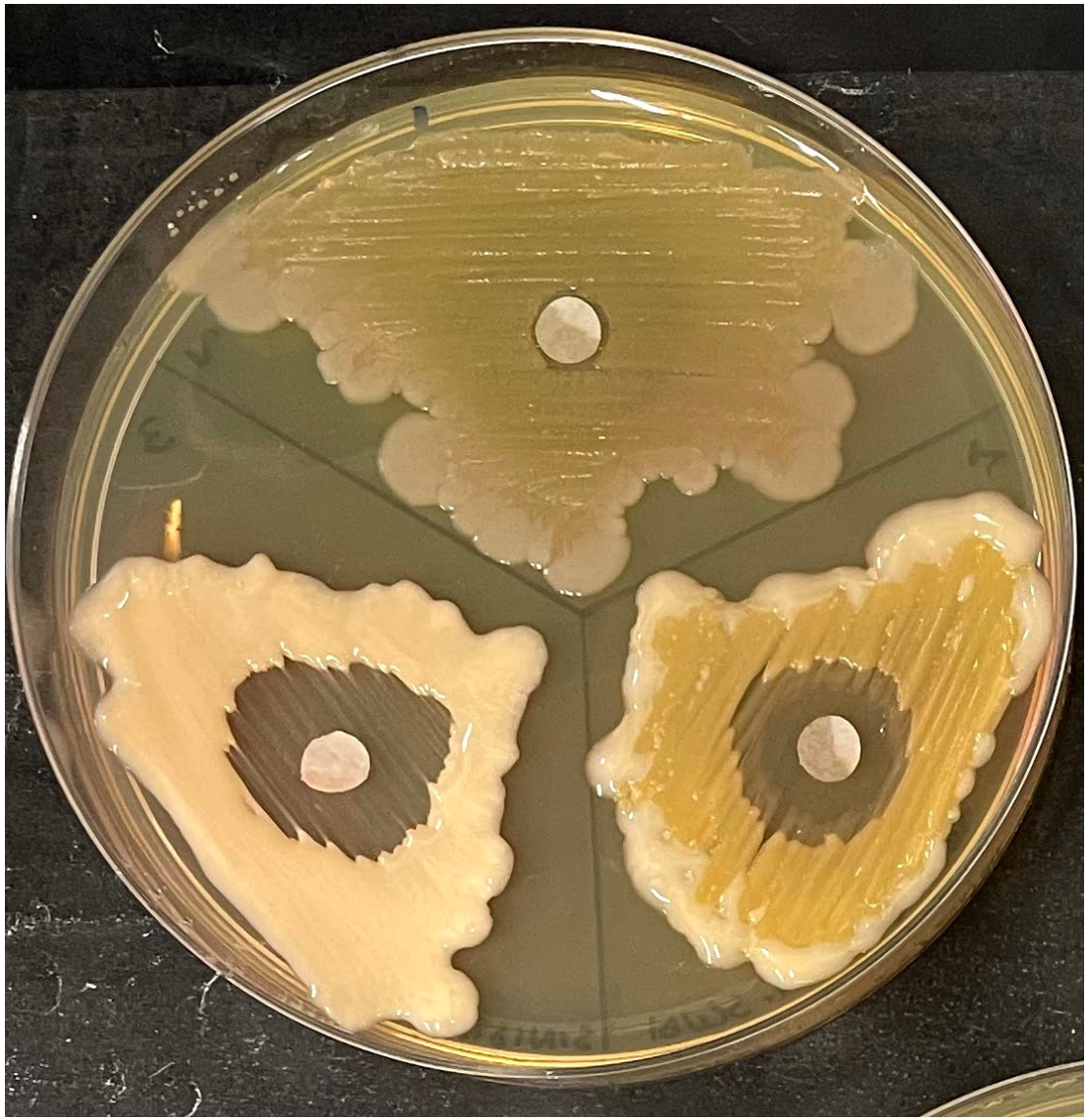
Maximum-likelihood phylogenetic tree was constructed using the PathoSystems Resource Integration Center (PATRIC) using complete genome sequences of 11 ISS *Bacillus* isolates sampled in the ISS between 2005 and 2011 (indicated by orange font) and four terrestrial *Bacillus* isolates for comparison. *B. anthracis* str. Ames and *B. cereus* biovar *anthracis* str. CI are pathogenic strains.

Quagliariello, Cirigliano, Rinaldi Microorganisms dic 2022

Evolution in the ISS



Environmental bacteria sensitivity to Benzalkonium chloride



Benzalconium Cloride, 10% solution

The cleaning reagent used in ISS consists of benzalkonium chloride, the crew use wipes with 0.1% dimethyl ammonium chloride derivatives.