Molecular mechanisms responsible for stress hyper resistance of Bacilli strains isolated from the International Space Station

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Microbes accompany humans everywhere, including orbiting space stations. The rather harsh living conditions inside the International Space Station (ISS) facilitate the emergence of bacterial strains that are hyper resistant to the action of various stress factors, including antibiotics, DNA damaging factors, and oxidative stress. The pathogenic microorganisms and biodestructors are found among these strains and represent a potential biological threat to long-term space missions. To date, the mechanisms of hyper resistance of ISS strains to the action of various stress factors are unknown. Strains Bacillus subtilis-20 and Bacillus licheniformis-24 were isolated from the Russian segment of the ISS's interior volumes. The isolated strains are highly resistant to stress factors that cause DNA damage and oxidative stress, such as 4-nitroquinoline 1-oxide (4-NQO), methyl methanesulfonate, and ultraviolet radiation. Compared with terrestrial strains, the ISS strains display overexpression of genes encoding components of DNA damage repair systems by homologous recombination (HR) and non-homologous end-joining (NHEJ). Overexpression of DNA repair genes is associated with overexpression of the corresponding transcriptional regulators. Using the CRISPR /dCas9 repressor system, we showed that both HR and NHEJ systems are required for the terrestrial B. licheniformis strain resistance to 4-NQO and zeocin. In contrast, in B. licheniformis-24 an essential role in resistance to these stress agents is played only by the NHEJ system. The data obtained indicate the greater significance of the NHEJ repair system in the hyper resistance of Bacilli strains to stress factors.

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