
与菌共舞在浩瀚宇宙 BMC Microbiology

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论文标题：Multi-drug resistant Enterobacter bugandensis species isolated from the International Space Station and comparative genomic analyses with human pathogenic strains

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与菌共舞在浩瀚宇宙 BMC Microbiology。最近发表在BMC Microbiology上的一项研究显示，科学家们在国际空间站内发现了一些肠杆菌(Enterobacter)的菌株，这些细菌与最近在一些医院中发现的机会性传染性病菌相似。太空中发现的这些菌株对人类而言并非致病菌，但研究者们认为应该研究它们对未来的航天任务可能造成的健康影响。



美国加州理工学院喷气推进实验室的研究人员研究了2015年3月从国际空间站的马桶和运动台上收集分离的5个肠杆菌菌株，此举是为了更好地鉴定空间站内各种表面上存在的细菌群落。为了确认空间站内肠杆菌的品种、详细展示每一品种的基因组成，研究人员将国际空间站内的菌株与地球上收集到的所有1291种肠杆菌的公开基因组信息进行了对比。

喷气推进实验室生物技术和行星保护小组的高级研究科学家Kasthuri Venkateswaran博士说：为了鉴别出国际空间站上的细菌是哪些品种，我们使用了多种办法来详细鉴定它们的基因组。我们发现5种国际空间内的肠杆菌菌株与新近在地球上发现的3种菌株在基因组成上最为相似。这3种菌株均属同一品种的细菌*Enterobacter bugandensis*，这种细菌会导致新生儿和缺乏抵抗力的病人患病，病例曾出现在3个不同的医院(分别位于东非、华盛顿州和科罗拉多州)。

将5种国际空间站菌株的基因组和3种临床发现的地球菌株进行比较，可以让作者们更好地了解国际空间站菌株的耐药特性——它们是否与已知的多药耐药性细菌拥有相似的基因特征，并找出与它们的致病潜力相关的基因。

研究的第一作者Nitin Singh博士说：鉴于这些空间站的*E. bugandensis*细菌的基因组中发现的多药耐药性结果和我们已经确认的致病性升高的概率，这些细菌可能对未来的任务有重要的健康影响。不过很重要的一点是，在国际空间站上发现的细菌菌株都是无毒的，这意味着它们不会给人类健康带来主动威胁，但应该被监测起来。

作者们发现国际空间站中分离出的菌株与地球上医院中的3个细菌菌株有相似的耐药性模式，他们研究了112个参与决定毒性、疾病和防御的基因。虽然国际空间站上的*E. bugandensis*对人类不具有致病性，但作者们通过电脑分析预测它们致病的潜在可能性为79%。不过还需要以生物体为

对象进行分析来进一步确认这一点。

Venkateswaran博士说：像*E. bugandensis*这样的机会性病原体是否会导致疾病以及它能造成多大的威胁，与很多因素有关，其中也包括环境因素。我们还需要进一步的体内研究来鉴别空间站上的条件——如微重力、外太空和飞船相关的因素——可能会给致病性和毒性带来怎样的影响。

摘要：

Background

The antimicrobial resistance (AMR) phenotypic properties, multiple drug resistance (MDR) gene profiles, and genes related to potential virulence and pathogenic properties of five *Enterobacter bugandensis* strains isolated from the International Space Station (ISS) were carried out and compared with genomes of three clinical strains. Whole genome sequences of ISS strains were characterized using the hybrid de novo assembly of Nanopore and Illumina reads. In addition to traditional microbial taxonomic approaches, multilocus sequence typing (MLST) analysis was performed to classify the phylogenetic lineage. Agar diffusion discs assay was performed to test antibiotics susceptibility. The draft genomes after assembly and scaffolding were annotated with the Rapid Annotations using Subsystems Technology and RNAMmer servers for downstream analysis.

Results

Molecular phylogeny and whole genome analysis of the ISS strains with all publicly available *Enterobacter* genomes revealed that ISS strains were *E. bugandensis* and similar to the type strain EB-247T and two clinical isolates (153_ECLO and MBRL 1077). Comparative genomic analyses of all eight *E. bugandensis* strains showed, a total of 4733 genes were associated with carbohydrate metabolism (635 genes), amino acid and derivatives (496 genes), protein metabolism (291 genes), cofactors, vitamins, prosthetic groups, pigments (275 genes), membrane transport (247 genes), and RNA metabolism (239 genes). In addition, 112 genes identified in the ISS strains were involved in virulence, disease, and defense. Genes associated with resistance to antibiotics and toxic compounds, including the MDR tripartite system were also identified in the ISS strains. A multiple antibiotic resistance (MAR) locus or MAR operon encoding MarA, MarB, MarC, and MarR, which regulate more than 60 genes, including upregulation of drug efflux systems that have been reported in *Escherichia coli* K12, was also observed in the ISS strains.

Conclusion

Given the MDR results for these ISS *Enterobacter* genomes and increased chance of pathogenicity (PathogenFinder algorithm with > 79% probability), these species pose important health considerations for future missions. Thorough genomic characterization of the strains isolated from ISS can help to understand the pathogenic potential, and inform future missions, but analyzing them in in-vivo systems is required to discern the influence of microgravity on their pathogenicity.

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