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RESEARCH

Bacterial Growth Responses to Simulated Microgravity: Implications for Space Biotechnology and Sustainable Development

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ABSTRACT

PURPOSE: The current study investigates the adaptive responses of four bacterial strains in terms of physiology, morphology, and genetic behaviour under simulated microgravity (SMG) compared to their real exposure to the outer space stratosphere.

DESIGN/METHODOLOGY/APPROACH: Four nonpathogenic bacterial strains: Escherichia coli, Bacillus subtilis, Salmonella typhimurium, and Staphylococcus aureus, were cultured under SMG using a 3D clinostat and their growth, viability, morphology, antibiotic susceptibility, and gene stability were tested.

FINDINGS: The bacterial strains under study survived SMG, with certain species showing phenotypic changes, shifts in antibiotic susceptibility, and a few genetic variations.

ORIGINALITY/VALUE: The study showed gravitational effects and shed light about the importance for control of space contamination and microbial risk, which contribute to SDG 3, SDG 9, and SDG 13.

RESEARCH LIMITATIONS: Longer- duration exposure, and multi omics analyses are recommended.

PRACTICAL IMPLICATIONS: The findings point to health management of space missions and the design of space relevant microbial bioprocesses.

KEYWORDS: *Simulated Microgravity; Bacterial Adaptation; Clinostat; Antibiotic Sensitivity; Genomics; Sustainable Development*

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INTRODUCTION

Microorganisms exhibit unique adaptability for survival among diverse terrestrial and extraterrestrial environments. In space, microbes are subjected to certain stressors, including microgravity, radiation, vacuum, and nutrient limitation, which affect their physiology, gene regulation, and ecological interactions (Milojevic and Weckwerth, 2020). Microgravity is one of the main factors to affect microbial growth rates, stress tolerance, virulence, biofilm formation, and antimicrobial resistance (Rosenzweig *et al.*, 2010; Vukanti *et al.*, 2008; Zhang *et al.*, 2025).

A recent study (Wilson *et al.*, 2008) demonstrates that bacteria rapidly adjust to reduced gravity conditions. Escherichia coli, for instance, exhibits physiological shifts within 12–48 hours of SMG exposure (Chavez *et al.*, 2024). Likewise, Salmonella typhimurium demonstrates altered virulence under microgravity, with its response affected by growth media composition. Genomic, transcriptomic, and proteomic analyses have revealed that microgravity influences certain cellular pathways, including Deoxyribonucleic acid (DNA) repair, protein folding, and stress regulation (Arunasri *et al.*, 2013; Ott *et al.*, 2019; Lozzi *et al.*, 2025).

While real microgravity experiments conducted aboard low Earth orbit platforms such as the International Space Station (ISS) provide realistic conditions, they remain constrained by cost, limited access, and logistics (Klomchitcharoen *et al.*, 2024). Ground-based simulators such as the Random Positioning Machine (RPM) and three-dimensional (3D) clinostat offer practical, reproducible, and cost-effective models for studying microbial responses by continuously reorienting samples with a constant gravity (Sharma and Curtis, 2022). These devices provide an average gravity of approximately 10^{-3} g, allowing researchers to study microbial adaptation under controlled laboratory conditions.

Previous studies have reported that microorganisms exposed to SMG or spaceflight may develop changes in colony morphology, biofilm formation, different secondary metabolite production, and variations in antibiotic sensitivity (Zea *et al.*, 2017; Tirumalai *et al.*, 2017). These phenotypic changes indicate implications for long-term human spaceflight, as more virulent microbes could affect crew health, damage life support systems, or reduce bioreactor stability.

Understanding how microorganisms adapt to microgravity has practical implications for space missions. Microbial behaviour in space can affect crew health, risks of biocontamination, and the performance of bioprocesses intended for life-support. Considering these challenges, our previous CubeSat work demonstrated that bacterial strains transported to outer space conditions, at 33 km altitude adapted and survived even when exposed to microgravity and stratospheric stressors (Malkawi *et al.*, 2025). While this showed microbial viability under true outer space microgravity, it also raised vital questions about the actual mechanisms underlying such adaptation.

The present study uses a 3D clinostat to investigate the behavioural responses of the bacterial strains: E. coli, Bacillus subtilis, S. typhimurium, and Staphylococcus aureus under SMG. Growth dynamics, viability, colony morphology, antibiotic susceptibility, and genetic stability based on the 16S rRNA, recA and dnaK genes, were assessed and compared to our prior stratosphere outer space results. Understanding microbial adaptation to microgravity is important not only for ensuring astronaut health and maintaining spacecraft biocontamination control, but also for advancing space biotechnology and supporting sustainable space exploration. By comparing SMG experiments with previous outer space results, this study aims to unravel the molecular and phenotypic mechanisms of bacterial adaptation, which will help to mitigate microbial risks in spaceflight missions and to harness microbial systems for space biotechnology. In addition, our study aligns with the United Nations Sustainable Development Goals (SDGs), mainly SDG 3 (Good Health and Well-Being), SDG 9 (Industry, Innovation, and Infrastructure), and SDG 12 (Responsible Consumption and Production), by enabling safe, efficient, innovative, sustainable use of astrobiology for future human missions.

MATERIALS AND METHODS

Using a 3D Clinostat to generate SMG conditions

A 3D clinostat, also called a Random Positioning Machine (RPM) (see figure 1), is available at the American University of Madaba, Jordan, and is used to generate SMG conditions for bacterial culture strains. The clinostat achieves SMG by continuously rotating the bacterial samples along multiple randomly oriented axes with a speed of 4 revolutions per minute (rpm), optimised to prevent gravitational sedimentation of cells while ensuring homogeneous distribution and adequate nutrient mixing within the growth medium under simulated microgravity conditions (Arunasri *et al.*, 2013). Parallel control samples were maintained under normal gravity (1 incubated without rotation to serve as baseline comparison. All experiments were performed under controlled and identical conditions with respect to temperature, nutrient composition and aeration, thereby isolating microgravity as the sole experimental variable. The use of a 3D clinostat is a well-established ground-based analog that reduces sedimentation and mimics microgravity effects (Mondal *et al.*, 2025).

Bacterial Strains

Four non-pathogenic bacterial strains were selected to represent both Gram-negative and Gram-positive groups, providing a wide-ranging model for comparative analysis under SMG. The Gram-negative strains included Escherichia coli ATCC 25922 and Salmonella enterica serovar Typhimurium ATCC 14028, while the Gram-positive group consisted of Staphylococcus aureus ATCC 29213 and Bacillus subtilis ATCC 6051. All bacterial strains were purchased from the American Type Culture Collection (ATCC; Manassas, VA, USA). They were preserved as stock cultures on nutrient agar slants and agar plates and stored at 4 °C. Prior to each experiment, working cultures were generated by transferring a loopful of cells from the stock slants into fresh nutrient broth culture medium and incubating them under standard growth conditions to obtain actively growing inocula.

Bacterial Culture Preparation

Each bacterial strain was cultivated in Luria–Bertani (LB) broth under aerobic conditions. Cultures were incubated at strain-specific optimal growth temperatures, ranging between 30 °C and 37 °C, with continuous agitation at 200–225 rpm using an orbital shaker to ensure adequate aeration and homogenous nutrient distribution. Growth was monitored at 600 nm (OD_{600}) using a spectrophotometer, and cultures were harvested during mid-logarithmic growth phase.

For Bacillus subtilis, cultures with a predominance of vegetative cells were used. Following SMG exposure, aliquots of B. subtilis cultures were subjected to controlled heat treatment (80 °C for 10 min) to selectively inactivate vegetative cells. This allowed subsequent colony-forming unit (CFU) enumeration to distinguish between heat-resistant spores and heat-sensitive vegetative cells, enabling assessment of survival and sporulation dynamics under SMG conditions.

Sample Preparation for Clinostat Exposure

Overnight cultures of each bacterial strain were sub-cultured by diluting 1:100 into fresh, LB broth and incubated under standard growth conditions until reaching an optical density at 600 nm (OD_{600}) of approximately 0.1–0.2, corresponding to early- to mid-logarithmic phase. This ensured that cells were metabolically active and physiologically comparable at the start of the SMG exposure.

For clinostat experiments, two-milliliter aliquots of each culture were transferred into sterile, culture tubes, ensuring the absence of air bubbles to minimise shear stress and turbulence during rotation, as recommended by Topolski *et al.* (2022). Both liquid cultures and solid cultures grown on LB agar plates were prepared for exposure (see figure 1), allowing parallel assessment of planktonic and surface-associated growth behaviour under SMG conditions.

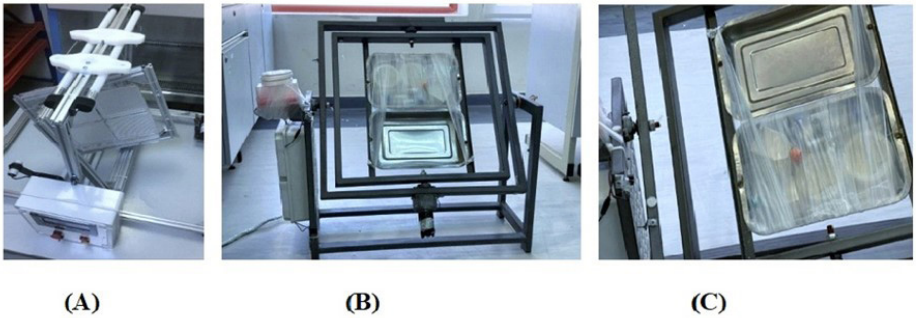

Figure 1 Three-dimensional clinostat. (A) Device without cultures; (B, C) clinostat with bacterial culture plates mounted for SMG exposure.

Source: Original results of this work

Prepared samples were positioned on the 3D clinostat and subjected to continuous multi-axis rotation to SMG. Control samples (1 g) were maintained under identical temperature, nutrient and incubation conditions but were kept without rotation, serving as gravitationally normal reference groups.

Assessment of Bacterial Growth under SMG

The impact of SMG compared to control conditions on bacterial growth and survival was evaluated by measuring the optical density at 600 nm (OD_{600}). Bacterial survivability was quantified using a standard CFU assay, which provides a direct measure of viable, culturable cells. Following incubation under the respective conditions, bacterial suspensions were serially diluted in sterile LB broth to obtain dilutions within a countable range. Aliquots (100 µL) from each dilution were spread evenly onto nutrient agar plates using sterile spreaders. The inoculated plates were incubated at (30–37 °C) for 24–48 hours until bacterial colonies became visible.

After incubation, the number of colonies was recorded and used to calculate the concentration of viable bacteria in the original sample, expressed as CFU per milliliter (CFU/mL). The combined approach of OD_{600} measurements for real-time growth tracking and CFU enumeration for viability, enabled an evaluation of how SMG affected bacterial growth and survival.

Morphological Analysis

The morphological characteristics of the bacterial cells were examined using both microscopic observation and Gram straining. For cellular morphology, smears were prepared from bacterial cultures and subjected to Gram straining to visualise cellular arrangements, shape, and structural integrity under both SMG and control conditions. Microscopic examination was conducted to assess potential alterations in cell size, shape, and clustering patterns, which may reflect adaptive response behaviour to the growth environment.

In addition, colony morphology and pigmentation were observed. Bacterial colonies obtained from nutrient agar plates were visually inspected for pigmentation intensity, distribution, and any changes in coloration associated with SMG exposure compared to the control group. Colony size, margin characteristics, surface texture, and overall structural appearance were also recorded.

Antibiotic Susceptibility Testing

The antimicrobial susceptibility of the bacterial strains was evaluated using the Kirby–Bauer disk diffusion method performed on Mueller–Hinton agar, in accordance with the procedures of the Clinical and Laboratory Standards Institute (CLSI) (Tirumalai *et al.*, 2017). Briefly, freshly grown bacterial cultures were adjusted to the appropriate turbidity standard to ensure uniform inoculum density and then evenly spread across the Mueller–Hinton agar plates to create a confluent lawn of growth. Sterile antibiotic-impregnated disks were aseptically placed on the agar plates.

The antibiotics used for testing included azithromycin (15 µg), tetracycline (30 µg), gentamicin (10 µg), and oxytetracycline (30 µg), representing agents with different mechanisms of action. Following antibiotic-disk placement, the plates were incubated under 30-370C for a period of 24 to 48 hours, depending on the growth rate of the test bacterial strain. After incubation, the diameter of the inhibition zones surrounding each disk was measured in millimeters using a ruler. These values provided a quantitative assessment of the bacterial sensitivity or resistance to each antibiotic, allowing for direct comparison.

Molecular PCR Analysis

Genomic DNA was extracted from bacterial cultures using the Wizard Genomic DNA Purification Kit (Promega, USA), following the manufacturer's protocol. The integrity and concentration of the extracted DNA were confirmed by spectrophotometric analysis and agarose gel electrophoresis.

Polymerase chain reaction (PCR) was employed to amplify both 16S rRNA and specific gene sequences. Target genes included the 16S rRNA gene, which serves as a universal taxonomic marker, as well as the housekeeping genes recA and dnaK, which provide additional discriminatory tools at the species and strain levels. Amplification was performed using gene-specific primers listed in Table 1, under optimised thermal cycling conditions designed to maximise yield and specificity.

The PCR amplification products were analysed on 1% agarose gel electrophoresis. PCR products were subsequently purified and sent for sequencing (Princess Haya Biotechnology Centre, Irbid-Jordan). The obtained sequences were compared against available databases using the National Centre for Biotechnology Information (NCBI) and the Basic Local Alignment Search (BLASTn) tool to determine taxonomic identity and to detect potential genetic variations among SMG exposed bacterial strains compared to the control ones.

Table 1 Primers and their DNA sequences used for PCR amplification of specific genes

Gene name	Primer's sequence	Annealing temp ^{0}C	Reference
16S rRNA gene	V3 F: 5' CCAgACTCCTACGGGAGGCAG 3' V3 R: 5' CGTATTACCGCGGCTGCTG 3'	64	(Chakravorty *et al.*, 2007)
16S rRNA gene	V6F: 5' TCGAtGCAACGCGAAGAA 3' V6R: 5' ACATtTCACaACACGAGCTGACGA 3`	60	(Chakravorty *et al.*, 2007)
RecA gene	*RecA*-F: 5' CCTGAATCTTCYGGTAAAAC 3` *RecA*-R: 5' GTTTCTGGGCTGCCAAACATTAC 3	55	(Diancourt *et al.*, 2010)
DnaK gene	*DnaK* F: 5' TCTGGTTGGTCAGCCGGCTAA 3` *DnaK* R: 5'CGTCGCCGTTATCAGCAGCAA3`	62	(Seyer *et al.*, 2003)

Source: (Malkawi *et al.*, 2025)

RESULTS

Bacterial Survival and Growth under SMG

The effects of SMG on the growth and survival of E. coli, S. aureus, B. subtilis and S. typhimurium were investigated, versus control cultures. Phenotypic changes under SMG are shown in Figure 2, and bacterial CFU are summarised in Table 2.

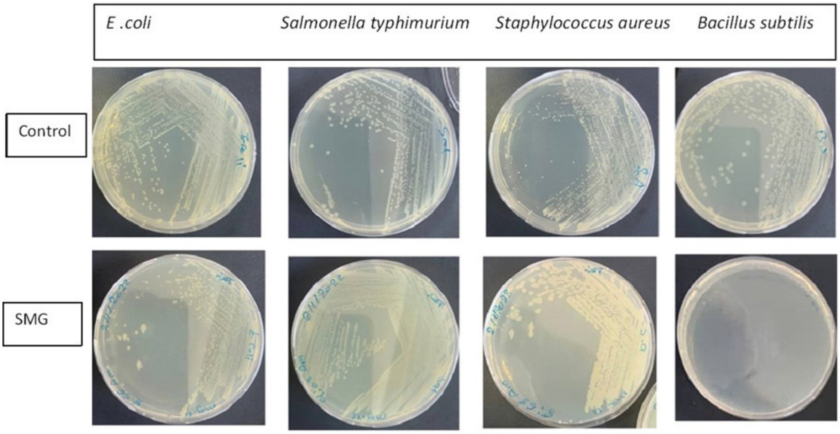

Figure 2 Phenotypic and pigmentation changes of bacterial colonies under control (upper panels) and simulated microgravity (lower panels), showing noticeable differences in pigmentation intensity and colony morphology.

Source: Original results of this work

All bacterial strains remained viable after 24–48 hours in incubation at 30–37 °C, indicating that SMG did not eliminate bacterial survival. However, distinct phenotypic adaptations were observed, S. aureus colonies displayed lighter pigmentation under SMG, consistent with previous studies linking gravitational stress to altered pigment biosynthesis (Antonic *et al.*, 2013; Azzam *et al.*, 2012).

Bacterial CFU analysis revealed strain-specific growth responses. E. coli showed a little decrease in viable counts (8.2×10^7 CFU/mL to 7.8×10^7 CFU/mL), whereas B. subtilis exhibited a more reduction (7.3×10^7 CFU/mL to 3.4×10^7 CFU/mL), suggesting elevated sensitivity to microgravity-associated stress. Microscopy examination further revealed morphological changes: E. coli cells became elongated, while B. subtilis aggregated into dense clusters like biofilms. Such adaptations are like previous findings that microgravity can alter cell shape, extracellular matrix production, and spatial organisation (Tirumalai *et al.*, 2017; Zea *et al.*, 2017).

The results of this study demonstrate that while survival is maintained under SMG, bacterial strains exhibit some morphological and physiological responses, reflecting adaptive mechanisms to altered physical forces.

Table 2 CFU/mL of bacterial strains under SMG versus control conditions

Bacterial Strain	Control (CFU/mL)	SMG (CFU/mL)
E. coli	8.2×10^7	7.8×10^7
S. typhimurium	7.0×10^7	5.6×10^7
S. aureus	9.2×10^7	8.0×10^7
B. subtilis	7.3×10^7	3.4×10^7

Source: Original results of this work

Bacterial Sensitivity to antibiotics under SMG

Antibiotic sensitivity profiles were observed and compared between SMG-exposed and control cultures for all four bacterial strains. Zones of inhibition were measured and presented in Table 3. SMG exposure induced strain-specific changes in antimicrobial sensitivity. In S. typhimurium, susceptibility to azithromycin and gentamicin slightly increased (33 mm to 35 mm and 27 mm to 28 mm, respectively), whereas tetracycline and oxytetracycline resistance remained, indicating no impact on resistance mechanisms.

S. aureus exhibited reduced susceptibility to gentamicin (35 mm to 26 mm; sensitive to intermediate), but showed a minor increase in tetracycline sensitivity (27 mm to 28 mm). Azithromycin inhibition zones were slightly reduced (34 mm to 32 mm) but remained in the sensitive range. Reduced pigmentation in SMG-grown colonies may reflect altered cell wall or metabolic processes influencing antibiotic interaction.

B. subtilis maintained intermediate resistance to azithromycin and full resistance to oxytetracycline under normal gravity, but no SMG inhibition data was obtained due to low post-exposure growth.

The most observed effects were seen in E. coli, where tetracycline susceptibility changed from intermediate to sensitive (19.5 mm to 22 mm), and oxytetracycline resistance shifted to intermediate (17 mm to 20 mm). Gentamicin sensitivity increased slightly (28 mm to 29 mm), while azithromycin inhibition zones decreased slightly but remained in the sensitive range (33 mm to 31 mm). These changes indicated the potential of microgravity to induce modifications in membrane permeability, stress-response signaling, efflux activity and improving antibiotic uptake.

Results showed that SMG modulated antibiotic susceptibility in a strain-dependent way, which is consistent with some studies revealing that microgravity can influence gene expression, membrane composition, and biofilm dynamics (Tirumalai *et al.*, 2017; Zea *et al.*, 2017).

Findings extend the previous observations (Malkawi *et al.*, 2025) by demonstrating that altered gravitational conditions not only affect growth but also antimicrobial susceptibility, which has implications for infection control during space missions and mild-shear bioprocessing environments.

Table 3 Antibiotic susceptibility of bacterial strains under control and SMG conditions

Bacterial Strain	Condition	Azithromycin	Gentamicin	Tetracycline	Oxytetracycline
S. typhimurium	Control	S (33)	S (27)	R (0)	R (1)
	SMG	S (35)	S (28)	R (0)	R (1)
S. aureus	*Control*	S (34)	S (35)	S (27)	I (24)
	SMG	S (32)	I (26)	S (28)	I (24)
B. subtilis	Control	I (27)	S (35)	S (21)	R (17)
	SMG	–	–	–	–
E. coli	Control	S (33)	S (28)	I (19.5)	R (17)
	SMG	S (31)	S (29)	S (22)	I (20)

Source: Original results of this work

(S: Sensitive, I: Intermediate, R: Resistant). The concentration of each antibiotic is 30 µg/mL. Inhibition zone diameter measured in (mm).

Molecular Characterisation and Sequencing Analysis of PCR Products

PCR amplification of 16S rRNA, recA, and dnaK genes yielded PCR products from both SMG-exposed and control cultures, which were sequenced and subjected to BLASTn analysis. Such analysis confirmed taxonomic identity, with E. coli and B. subtilis showing 98–100% similarity to reference genomes, and S. aureus and S. typhimurium showing 97–99% identity with more than 98% coverage.

SMG-exposed samples exhibited high sequence conservation relative to controls. Minor nucleotide differences were observed, including four single-nucleotide changes in E. coli recA gene (99% identity) and one substitution in S. aureus dnaK gene, with no predicted effect on protein function. No sequence differences were detected in B. subtilis or S. typhimurium across any of the genes analysed.

Given the roles of recA and dnaK in DNA repair and protein homeostasis, these findings suggest that short-term SMG exposure does not induce major genetic rearrangements but may trigger early adaptive responses. Future large scale genomic, transcriptomic, and proteomic approaches could provide deeper insight into regulatory changes that are responsible for microbial adaptation under microgravity (Zhao *et al.*, 2013).

The results of this study build directly upon our recently published findings on bacterial adaptation to outer space stress conditions (Malkawi *et al.*, 2025), where we reported alterations in growth kinetics, biofilm formation, and stress response pathways when bacterial strains were exposed to stratospheric conditions aboard a CubeSat platform. The present study extends those observations by demonstrating that SMG can induce comparable phenotypic and physiological changes, including altered pigmentation, cell aggregation, and strain-specific changes in antibiotic susceptibility. These findings reinforce the concept that gravitational forces are key regulators of microbial behaviour, and they highlight the importance of taking into consideration microgravity effects when developing microbial risk assessments and biotechnological strategies for space mission exploration.

The demonstrated maintenance of viability and altered antimicrobial susceptibility under SMG highlights critical considerations for infection prevention and control during spaceflight, advancing SDG 3 (Good Health and Well-being). The change in bacterial growth and morphology provides good data for the development of safer, more robust biotechnological processes, contributing to SDG 9 (Industry, Innovation and Infrastructure). Furthermore, understanding microbial adaptation to altered gravity conditions can provide predictive models of microbial behaviour in extreme environments on Earth, improving the resilience to climate-driven disruptions and supporting SDG 13 (Climate Action). This integrated perspective underscores the importance of space microbiology research as a driver of innovation with terrestrial benefits.

DISCUSSION

This study provides evidence that SMG exerts strain-specific but reproducible effects on bacterial physiology, morphology and antibiotic susceptibility, while maintaining viability. Results obtained earlier from the outer space microgravity work (Malkawi *et al.*, 2025), where E. coli, S. aureus, S. typhimurium and B. subtilis survived stratospheric flight exposure, indicating that gravitational stress alone is not lethal. No significant reduction in CFU counts was observed after SMG exposure, and in some cases, slightly higher CFU occurred compared to controls, suggesting that low-shear, vector-averaged environments may enhance metabolic efficiency, which is similar to other studies of stimulated growth in Salmonella and E. coli under microgravity (Nickerson *et al.*, 2004; Topolski *et al.*, 2022).

Phenotypic alterations, including reduced pigmentation in S. aureus, indicating modifications of secondary metabolism, possibly involving staphyloxanthin biosynthesis, aligning with evidence that microgravity can regulate pigment production as a stress-protective mechanism (Arunasri *et al.*, 2013). Similarly, B. subtilis aggregation under SMG resembles biofilm formation and supports studies that microgravity promotes extracellular matrix deposition (Zea *et al.*, 2017), potentially enhancing persistence. E. coli cell elongation under SMG further supports the hypothesis that altered mechanical forces influence cell division, consistent with previous studies (Tirumalai *et al.*, 2017). Results suggest that bacteria adapt to microgravity via regulatory and structural adjustments rather than population decline.

Antibiotic susceptibility results revealed species and antibiotic-dependent effects. E. coli exhibited increased sensitivity to tetracycline and oxytetracycline, possibly through enhanced membrane permeability, reduced efflux or altered target expression. In contrast, S. aureus showed reduced susceptibility to gentamicin, which may reflect altered membrane composition or ribosomal target accessibility, which is similar to the results of previous studies, that indicated microgravity-induced changes in cell envelope and antibiotic transport systems (Wilson *et al.*, 2007; Sharma and Curtis, 2022). In addition, another study (Nickerson *et al.*, 2004) showed both increased and decreased resistance under microgravity, highlighting the influence of microbial genetics, growth conditions, and exposure time.

Molecular analysis of this study indicated 97–99% sequence identity between SMG-exposed and control strains across 16S rRNA, recA, and dnaK genes, indicating minimal genomic change. However, few nucleotide mismatches in E. coli recA gene and a corresponding substitution in S. aureus dnaK gene may carry functional significance. recA protein regulates homologous recombination and DNA repair (Johnston *et al.*, 2023; Jones and Baxter, 2017), which may be modified under altered gravity to preserve genome integrity. dnaK encodes a chaperone for proteostasis (Schonfeld *et al.*, 1995; Dahl *et al.*, 2015). In addition, silent polymorphisms could affect regulation, as indicated by a previous study (Ott *et al.*, 2019), that indicated altered dnaK abundance under microgravity, and that SMG primarily triggers subtle regulatory responses rather than major mutational events.

Compared with our outer space work (Malkawi *et al.*, 2025), the current findings show that bacterial survival is maintained, though phenotypic and antibiotic effects were milder here. This supports the notion that combined stressors amplify microbial responses, as proposed by multifactorial models of microbial behaviour in space (Ott *et al.*, 2013; Zea *et al.*, 2017).

These findings have important implications for sustainability and several UN SDGs. By clarifying how microgravity influences growth, morphology, and drug susceptibility. This work advances SDG 3 (Good Health and Well-being) through improved infection risk assessment and antimicrobial management. It supports SDG 9 (Industry, Innovation, and Infrastructure) by informing design of microbial bioprocesses for space-based applications, including life support and pharmaceutical production. Also, by improving models of microbial adaptation to physical stress, it contributes to SDG 13 (Climate Action) and global biosecurity preparedness.

Future research should employ whole-genome sequencing, transcriptomics, metabolomics, and proteomics to map regulatory networks and evaluate long-term evolutionary routes under SMG. Such integrative approaches will enhance understanding of microbial resilience and inform sustainable countermeasures for infection control, biosecurity, and microbial risk management in spaceflight and terrestrial settings.

CONCLUSIONS

This study demonstrates that SMG can maintain microbial viability while causing physiological, phenotypic, antimicrobial susceptibility and genetic modifications. These findings highlight the importance of microgravity as a key environmental factor influencing microbial behaviour, with implications for infection risk management, microbial biotechnology, and planetary protection.

Research in this field advances the understanding of microbial adaptation in spaceflight-like conditions and provides a terrestrial model to provide space exploration strategies, bioprocess design, and environmental monitoring. By supporting better health risk assessment (SDG 3), fostering innovation in sustainable biotechnologies (SDG 9), and improving preparedness for environmental challenges (SDG 13), this work contributes to global efforts in science, health, innovation, and climate resilience. Future studies should focus on long-term exposure and integrative multi-omics approaches to uncover deeper insights into microbial adaptation and its applications in astrobiology and sustainable development.

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Prof. Hanan I. Malkawi earned her BSc at Yarmouk University (YU), followed by MSc in Bacteriology and Public Health and PhD in Microbiology and Molecular Biology, both from Washington State University, USA. She leads research in biotechnology and nanotechnology with applications in healthcare, agriculture, food security, and industry, authoring over 75 publications and holding multiple patents. She has held senior administrative roles, including Vice President for Research and International Relations at YU, Dean of Research and Graduate Studies at YU, Dean of Research and Doctoral Studies at Hamdan Bin Mohammed Smart University-UAE, Vice President at the Royal Scientific Society, and Vice President at Arab Science and Technology Foundation. She has received multiple awards, including the **King Abdullah II ibn Al-Hussein Medal for Excellence** (Second Degree) in May **2022**. Most recently, in November 2025, she was awarded as the **Best Arab Scientist in Biotechnology** for her contributions to microbial biotechnology..