World Journal of Biology Pharmacy and Health Sciences
eISSN: 2582-5542
Cross Ref DOI: 10.30574/wjbphs
Journal homepage: https://wjbphs.com/

(RESEARCH ARTICLE)

Check for updates

Microorganisms across the intrinsic Gravito–thermal continuum from cosmos to deep earth

Iresh Ranjan Bhattacharjee *

Independent Researcher (Institute for Intrinsic Gravitation Biology) Assam, India.

World Journal of Biology Pharmacy and Health Sciences, 2026, 26(02), 259-284

Publication history: Received on 12 April 2026; revised on 18 May 2026; accepted on 20 May 2026

Article DOI: https://doi.org/10.30574/wjbphs.2026.26.2.0266

Abstract

Microorganisms inhabit nearly every known ecological niche, extending from atmospheric aerosols and extraterrestrial microgravity systems to hydrothermal vents, polar cryospheres, terrestrial soils, host-associated ecosystems, and deep lithospheric biospheres. Although microbial adaptation has traditionally been interpreted through genetics, metabolism, and ecological selection, microbial systems simultaneously exist as physicochemical architectures governed by mass distribution, thermal gradients, hydrostatic pressure, diffusion dynamics, osmotic regulation, and environmental confinement. The present article advances an integrative gravito–thermal framework in which active poroelastic mass of microbial organization (analogous to fluid filled sponge) is interpreted as emerging through dynamic equilibrium between inward intrinsic gravito-compressive stabilization and outward thermo-fluidic redistribution. Within this framework, intrinsic gravitation is conservatively interpreted not as a dominant direct force at microbial scales, but as a collective background structural parameter associated with density stabilization, sedimentation, hydrostatic organization, and environmental compression operating alongside prevailing biochemical and physicochemical processes. Counteractive thermal and fluid-mediated processes including convection, buoyancy, diffusion, osmotic expansion, and entropy-driven redistribution are examined as dispersive tendencies balancing compressive organization. Representative microorganisms inhabiting atmospheric, aquatic, cryospheric, hydrothermal, terrestrial, host-associated, and deep subsurface environments are analysed to explore both conformity and deviation from common gravito–thermal organizational principles. Biofilms, density-dependent sedimentation systems, hydrothermal vent communities, and microgravity-associated microbial architectures are discussed as particularly informative models of coupled physicochemical organization. The article proposes a “Grand Microbial Continuum” extending from cosmic microgravity environments to compression-dominated deep Earth biospheres, integrating microbiology, hydrostatics, thermodynamics, fluid mechanics, environmental physics, and systems ecology within a unified conceptual framework. The proposed interpretation is intended to stimulate interdisciplinary discussion regarding the role of physical constraint regimes in microbial organization across environmental scales rather than replace established microbiological theory.

Keywords: Intrinsic Gravitation; Microorganisms; granular; poroelasticity; Gravito–Thermal Architecture; Microbial Ecology; Biofilms; Deep Biosphere; Microgravity; Hydrostatic Pressure; Thermodynamics; Environmental Microbiology

1. Introduction

Microorganisms constitute the most widely distributed biological entities known, inhabiting environments that range from atmospheric aerosols and glacial ice to hydrothermal vents, host tissues, saline lakes, radioactive environments, and deep subsurface rocks. Classical microbiology explains microbial adaptation primarily through genetics, metabolism, environmental selection, and biochemical evolution. However, microbial systems are simultaneously physical entities possessing mass, density gradients, thermal exchange mechanisms, osmotic architectures, fluid interactions, and spatial organization.

* Corresponding author: Iresh Ranjan Bhattacharjee.

Gravity has traditionally been considered negligible at microbial scales because viscous and Brownian forces dominate many cellular processes (Purcell, 1977). Nevertheless, microorganisms continuously experience gravity indirectly through sedimentation, hydrostatic pressure, fluid stratification, nutrient layering, buoyancy, convection, diffusion constraints, biofilm orientation, colony morphology, and environmental compression.

Simultaneously, thermal processes generate counteractive tendencies through convection, thermal expansion, molecular agitation, fluid redistribution, osmotic transport, and entropy-driven dispersion.

The present work proposes that microbial organization may be interpreted within a broader gravito–thermal continuum, wherein intrinsic gravitation contributes toward compressive stabilization and structural coherence, while thermo-fluidic processes promote outward redistribution and dynamic expansion. Rather than proposing intrinsic gravity as a dominant deterministic force at microbial scale, the present framework interprets it as a persistent structural constraint operating through environmental mediation.

2. Fundamentals of Microbial Organization Under Physical Constraint Regimes

2.1. Microorganisms as Physicochemically Constrained Systems

Microorganisms may be interpreted as physicochemically constrained biological systems in which mass distribution, thermal exchange, osmotic gradients, hydration, and structural boundaries collectively regulate organization and function. Microbial mass occupies an intermediate physical regime between solids, fluids, and granular matter. Most stimulating fact is that these exhibit viscoelasticity, poroelasticity, mechanical anisotropy, pressure redistribution, and active force generation, analogous to a piece of wet, fluid-saturated sponge, where on application of external load, the volume of the pores decreases, increasing the fluid pressure and causing the water to flow out (Fig 2b). Rather than existing as purely biochemical entities, microbial systems continuously interact with physical forces operating through fluids, density gradients, diffusion fields, mechanical confinement, and environmental interfaces. Within the present framework, intrinsic gravitation is interpreted conservatively not as an isolated dominant force at microbial scales, but as a background parameter associated with mass distribution and environmental compression interacting continuously with prevailing physicochemical processes.

2.2. Physical constraint regimes in microbial organization across molecular, cellular, microenvironmental, and colony scales

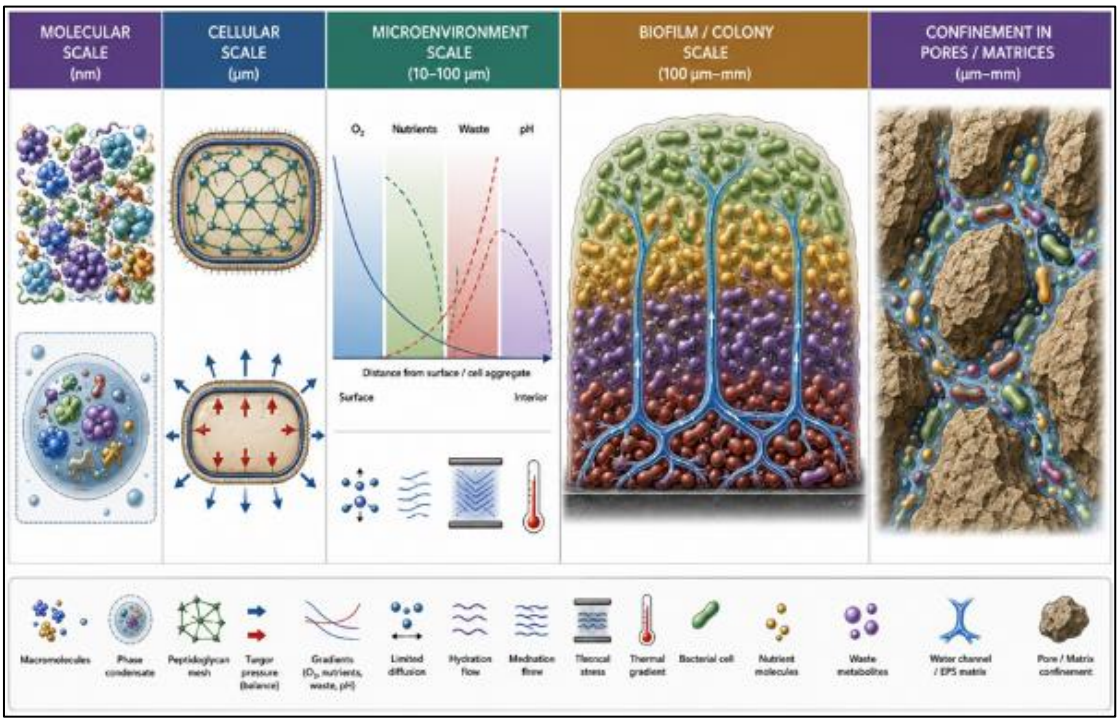

Figure 1 Conceptual schematic illustrating major physicochemical constraints governing microbial organization from molecular to biofilm and environmental scales. The figure integrates macromolecular crowding, phase-separated condensates, peptidoglycan mesh architecture, turgor pressure balance, diffusion gradients, biofilm layering, and confinement within pores or matrices. Molecular-scale organization is represented through crowded intracellular environments and condensate formation, while cellular-scale organization highlights peptidoglycan-mediated mechanical stability and osmotic balance. Microenvironmental gradients of oxygen, nutrients, waste products, hydration, and temperature regulate diffusion-driven spatial heterogeneity. At colony scales, biofilms exhibit layered metabolic organization, interconnected extracellular polymeric substance (EPS) networks, and emergent multicellular-like coordination. Confinement within pores, sediments, and matrices further imposes structural and diffusion-related constraints on microbial architecture. Collectively, the schematic illustrates how microbial systems emerge through coupled interactions among mechanical stabilization, diffusion limitation, thermo-fluidic redistribution, osmotic balance, and mass-associated structural organization across hierarchical biological scales

2.3. Macromolecular Crowding, Phase Separation, and Structural Organization

At molecular and subcellular scales, biological organization emerges through competing interactions including hydrophobic effects, electrostatic attraction and repulsion, entropy-driven redistribution, steric exclusion, and macromolecular crowding (Ellis, 2001). Dense intracellular environments are highly structured rather than homogeneous solutions, and local density gradients strongly influence molecular mobility, self-assembly, phase behaviour, and diffusion dynamics. Biomolecular condensates and phase-separated intracellular domains demonstrate that stable organization can arise through localized variations in concentration and mass distribution without membrane boundaries (Hyman et al., 2014). Such systems resemble active granular–poroelastic matter analogous to a piece of wet, fluid-saturated sponge having coupled deformation of microbial–EPS networks and pore-fluid redistribution under compressive hydrostatic stress and equilibrium emerges from competing cohesive and dispersive interactions. Within this broader physicochemical context, intrinsic gravitation may be interpreted as a non-local background parameter associated with mass distribution and equilibrium stabilization in dense biological assemblies rather than as a direct deterministic force.

2.4. Prions and Minimal Structural Biology

Prions provide an important conceptual example of minimal biological organization arising primarily through structural architecture. These proteinaceous infectious entities propagate without nucleic acids and transmit biological information through conformational templating and aggregation dynamics (Prusiner, 1998). Their propagation depends upon structural compatibility, energetic stability, aggregation kinetics, and molecular packing. Consequently, prions illustrate that biological information may be encoded structurally and that organization can emerge from energy minimization under physicochemical constraint. Stability in such systems depends strongly upon conformational geometry, intermolecular interactions, and spatial packing density, suggesting that biological organization may arise fundamentally from physical architecture itself even in the absence of conventional genetic systems.

2.5. Spatial Confinement and Environmental Constraint

Microorganisms rarely exist in complete isolation in natural environments. Instead, they occupy physically constrained niches including biofilms, rhizospheric matrices, mucus layers, sediment interfaces, hydrothermal mineral surfaces, ice microchannels, soil pores, and host-associated tissues. Within these confined environments, microbial organization is influenced not only by biochemical signalling but also by geometry, hydration, diffusion limitation, pressure distribution, and mechanical interaction with surrounding structures. Spatial confinement restricts cellular movement, modifies local physicochemical gradients, and alters microbial morphology, metabolic coordination, colony architecture, and stress adaptation. Experimental evidence demonstrates that environmental confinement itself can influence bacterial growth organization independently of classical biochemical differentiation pathways (Sreepadmanabh et al., 2024).

2.6. Mechanical Stress, Peptidoglycan Architecture, and Structural Stability

Mechanical stress represents another major determinant of microbial structural organization. Microbial systems continuously experience compression, osmotic pressure, hydrostatic loading, shear stress, viscoelastic resistance, and surface tension within both natural and laboratory environments. In bacteria, the peptidoglycan sacculus forms a mechanically resistant mesh-like structure surrounding the cytoplasmic membrane and counterbalancing internal turgor pressure while preserving morphology and integrity (Vollmer et al., 2008). This lattice-like organization resembles soft matter networks in which cohesive interactions and structural constraints generate stable geometries. Extracellular polymeric substance (EPS)-rich biofilms similarly redistribute stress through interconnected hydrated matrices exhibiting viscoelastic and diffusion-regulated behaviour. Mechanical constraints influence microbial adhesion, orientation, growth direction, colony geometry, and structural adaptation, while densely packed colonies frequently display alignment and emergent pattern formation associated with local stress fields and physical boundary conditions.

Microbial architecture also emerges through the equilibrium between outward osmotic expansion and inward structural resistance. In bacteria, internal turgor pressure exerts continuous outward force against the cell envelope, whereas the peptidoglycan wall provides stabilizing inward resistance. This establishes a mechanically stabilized system in which stress distribution contributes directly to cellular integrity and morphology. Rod-shaped bacteria exhibit beach-ball pattern directional growth, whereas cocci approach isotropic geometry under relatively symmetrical mechanical constraints. Spherical morphology may therefore approximate a minimum-energy configuration under isotropic physicochemical conditions, consistent with broader physical principles governing surface energy minimization and structural symmetry.

2.1 Compressional and tensional stress fields on Earth's crust compared to poroelasticity in microbial mass

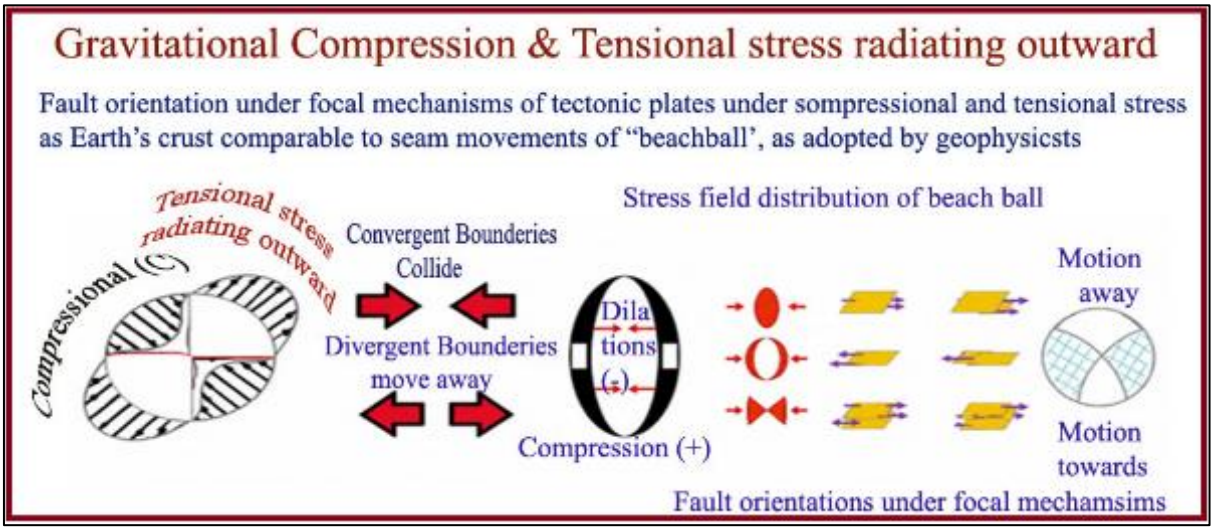

Figure 2 (a) Conceptual illustration of compressional and tensional stress fields, showing fault orientation and motion patterns in geophysical tectonic systems analogous to stress-mediated structural organization under gravito-compressive forces

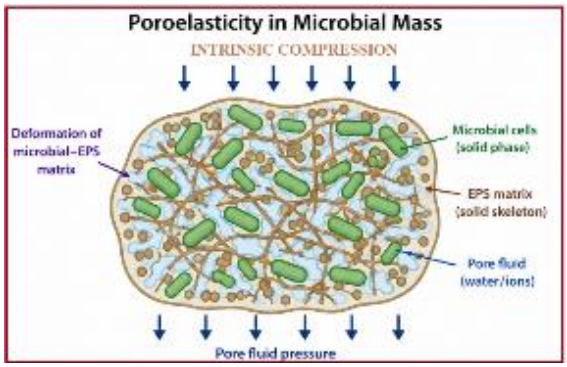

Figure 2 (b): Active granular–poroelastic behavior in microbial mass illustrating coupled deformation of microbial–EPS networks and pore-fluid redistribution under compressive hydrostatic stress

Mechanical stress fields, compression–tension equilibria, and deformation patterns are fundamental organizing principles across physical systems ranging from tectonic structures to biological materials. In geophysics, compressional and tensional stress regimes generate predictable structural orientations and fault geometries within deformable media (Anderson, 1905; Jaeger et al., 2007). Analogously, bacterial morphology and colony organization may emerge through mechanically constrained growth, peptidoglycan-directed stress distribution, hydrostatic turgor balance, and environmental confinement (Koch, 1983; Huang et al., 2008). Rod-shaped bacterial cells, filamentous growth forms, and biofilm architectures therefore may be interpreted as biologically regulated structures developing under localized mechanical and physicochemical stress fields.

2.7. Emergent Spatial Organization and Metabolically Interlinked Infrastructures (MII)

Spatial organization constitutes one of the most prominent emergent properties of microbial systems. Biofilms, microbial mats, colonies, and planktonic aggregates often develop highly ordered architectures despite lacking centralized multicellular control. Such organization arises through coupled interactions among nutrient gradients, oxygen availability, waste accumulation, hydration status, cell density, diffusion limitation, and mechanical confinement. Mature biofilms may contain differentiated aerobic surface layers, anaerobic inner regions, nutrient transport channels, and localized metabolic specialization (Flemming et al., 2016). These coordinated microbial systems may therefore be interpreted as metabolically interlinked infrastructures (MII), wherein microbial populations exchange nutrients, metabolites, signalling molecules, electrons, and mechanical support across confined spatial domains.

2.8. Diffusion Dynamics and Microenvironmental Heterogeneity

Diffusion remains one of the dominant organizational mechanisms at microbial scales. Nutrient transport, gas exchange, metabolite redistribution, signalling molecule movement, and thermal equilibration are strongly governed by diffusion dynamics. In physically constrained systems such as biofilms and densely packed colonies, diffusion limitation generates pronounced internal heterogeneity, including oxygen depletion, nutrient starvation, metabolite accumulation, and pH gradients across micrometre-scale distances (Stewart & Franklin, 2008). Consequently, distinct physiological microenvironments may emerge within apparently continuous microbial masses. Diffusion therefore functions simultaneously as a transport process, an organizational regulator, and a limiting physical constraint within microbial systems.

2.9. Culture Media as Engineered Physicochemical Environments

Culture media and transport media used routinely in microbiology laboratories may also be interpreted within this broader gravito–thermal and physicochemical framework. Culture media constitute structured nutrient environments designed to support microbial growth under controlled physicochemical conditions. Basal, enriched, selective, and differential media regulate microbial organization through variations in nutrient density, osmotic balance, pH, oxygen diffusion, hydration, ionic composition, and thermal stability. Selective agents such as salts, antibiotics, and dyes impose physicochemical constraints that favour some microbial populations while suppressing others. Semi-solid and solid media further influence microbial colony morphology, diffusion gradients, hydration distribution, and spatial expansion patterns.

2.10. Transport Media and Viability Preservation Under Constrained Conditions

Transport media, in contrast, are specifically designed not to promote multiplication but to preserve viability through physicochemical stabilization during transit. Media such as Amies, Stuart, Cary–Blair, and Viral Transport Medium maintain equilibrium by minimizing metabolic activity, buffering pH fluctuations, reducing oxidative injury, and suppressing overgrowth of contaminants. Semisolid consistency reduces excessive oxygenation and fluid turbulence, while buffering systems maintain chemical stability. Charcoal-containing transport systems additionally adsorb toxic metabolites and reactive compounds that may otherwise destabilize delicate pathogens. From the perspective of the present framework, transport media may therefore be interpreted as engineered low-metabolic equilibrium systems that preserve microbial structural integrity under constrained thermal, osmotic, and diffusion-regulated conditions.

2.11. Sedimentation, Centrifugation, and Density-Dependent Organization

Similarly, laboratory procedures such as centrifugation, ultracentrifugation, density-gradient separation, and sedimentation analysis directly illustrate the influence of mass distribution and density-dependent organization in microbial and molecular systems. Differential sedimentation depends upon molar mass, density, particle geometry, hydration state, and viscous resistance. During centrifugation, microbial cells, viruses, ribosomes, proteins, and nucleic acids redistribute according to buoyant density and sedimentation coefficients under externally imposed acceleration fields. Such methods operationally demonstrate how mass-dependent spatial organization can emerge under controlled physicochemical constraints. Although these processes are classically interpreted through fluid mechanics and particle dynamics, they remain conceptually compatible with the broader interpretation of intrinsic gravitation as a background parameter associated with mass distribution and equilibrium stabilization within biological systems.

Differential centrifugal force and density gradients separate biological particles according to their sedimentation behaviour, enabling fractionation, purification, and analysis of cells, viruses, ribosomes, proteins, and macromolecules.

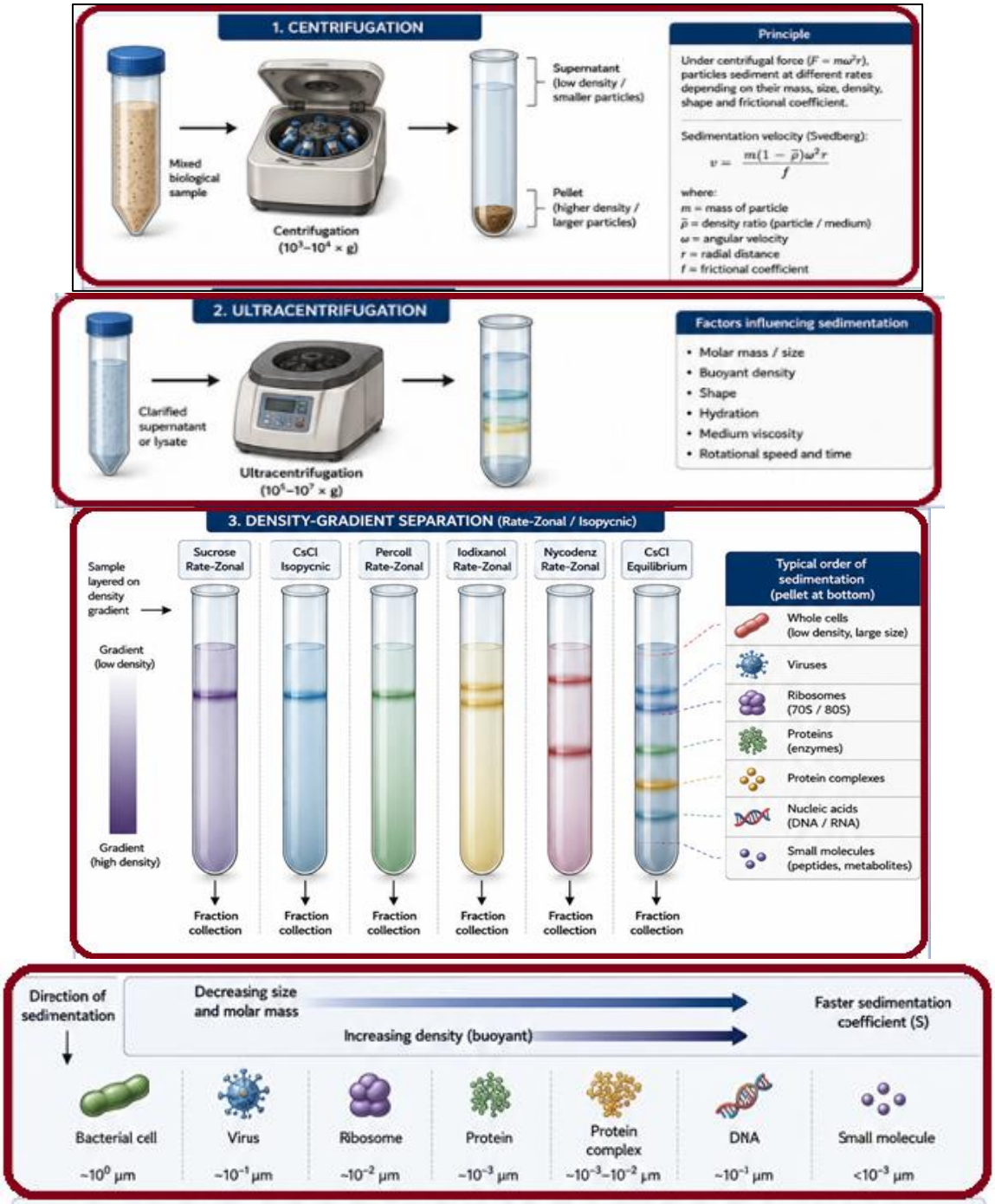

Figure 3 Density-dependent separation and sedimentation in microbiology: Schematic illustration of the principles of centrifugation, ultracentrifugation, and density-gradient separation commonly employed in microbiological and molecular biological laboratories. Biological particles sediment according to differences in molar mass, size, buoyant density, geometry, and hydration state under centrifugal acceleration. Differential centrifugation separates mixed biological samples into supernatant and pellet fractions, whereas ultracentrifugation enables high-resolution separation of viruses, ribosomes, nucleoprotein complexes, proteins, and macromolecular assemblies. Density-gradient systems such as sucrose, cesium chloride (CsCl), Percoll, iodixanol, and Nycodenz gradients facilitate stratified separation based upon sedimentation coefficients and equilibrium buoyant densities. The figure illustrates progressive layered fractionation of whole cells, viruses, ribosomes, proteins, nucleic acids, and smaller macromolecules within gradient media. These laboratory techniques operationally demonstrate density-dependent spatial organization and mass-associated redistribution under externally imposed acceleration fields, thereby providing experimentally observable examples of physicochemical separation and equilibrium behaviour in biological systems

2.12. Gravito–Thermal Interpretation of Microbial Organization

Within the present intrinsic gravito–thermal framework, microbial organization may therefore be interpreted as arising through dynamic equilibrium among confinement, mechanical stress, diffusion, osmotic regulation, hydrostatic gradients, thermal redistribution, and mass-associated structural stabilization. Intrinsic gravitation is not proposed here as a dominant direct microbial force, but rather as a persistent background parameter operating alongside prevailing physicochemical interactions across molecular, cellular, colony-level, ecological, and environmental scales.

3. Theoretical Foundation of Intrinsic Gravito–Thermal Microbial Architecture

3.1. Intrinsic Gravitation as Structural Constraint

The interpretation of gravito–thermal of microbial organization extends conceptually from earlier propositions (Bhattacharjee, 1988; 2013a, 2013b), Bhattacharjee,2025, Bhattacharjee, 2026a, 2026b, 2026(c). Within this framework, intrinsic gravitation here is interpreted conservatively not as an isolated dominant force acting directly at microbial scales, but as a background parameter associated with mass distribution, density stabilization, structural cohesion, and environmental compression operating alongside prevailing physicochemical processes.

At planetary and stellar scales, intrinsic gravity contributes fundamentally to compression, hydrostatic equilibrium, sedimentation, density stratification, and structural cohesion. Hydrostatic equilibrium in self-gravitating systems is classically represented as:

$$\frac{dP}{dr} = -\rho g$$

where pressure gradients balance gravitational loading within organized mass-bearing systems. In stars and planets, such equilibrium governs internal stratification, structural stability, thermal gradients, and material redistribution. Analogically, the present framework proposes that microbial systems inhabit self-gravitationally organized environments in which indirect manifestations of gravitational organization emerge through hydrostatic pressure, suspension dynamics, sedimentation, colony stratification, nutrient layering, fluid-mediated orientation, and density-dependent redistribution.

Intrinsic gravity, often perceived as a long-range force. But due to gravity's non-cancelling nature, it may operate effectively at short-range scales within biological systems (Rothleitner, C. 2021). However individual microorganisms are not expected to generate measurable intrinsic or self-gravity comparable to planetary systems, they continuously interact with media already organized under gravitational constraint. Consequently, microbial architecture may be interpreted within nested gravito–thermal fields extending from molecular and cellular scales to planetary ecological systems. This interpretation aligns conceptually with the broader "Grand Evolutionary Continuum" hypothesis proposed previously, wherein mass organization, thermodynamic gradients, and structural stabilization operate across cosmic, geological, biological, and ecological domains (Bhattacharjee, 2025).

At microbial scales, the influence of gravitation is generally indirect and mediated primarily through fluids, hydrostatic gradients, sedimentation behaviour, diffusion limitation, and environmental confinement rather than through direct organismal self-gravity. Nevertheless, such indirect organization may contribute significantly to spatial orientation, biofilm layering, ecological stratification, and density-dependent microbial distribution patterns.

3.2. Thermodynamic Counteractive Processes

Thermal processes frequently oppose compressive organization by promoting expansion, convection, buoyancy, diffusion, molecular agitation, and entropy-driven redistribution.

Heat transport in physicochemical systems follows:

$$q = -k\nabla T$$

where, heat flows along temperature gradients through conductive, convective, or diffusion-mediated processes. In biological and microbial systems, thermal redistribution contributes to fluid circulation, metabolic heat dissipation, convection currents, buoyancy-associated transport, and dynamic environmental mixing.

Within aqueous systems, hydrothermal environments, atmospheric aerosols, and microbial cultures, thermo-fluidic processes often counterbalance sedimentation and compressive stabilization through outward redistributive tendencies. For example, planktonic microorganisms evolve buoyancy-regulating mechanisms, convection redistributes nutrients and metabolites, and thermal gradients influence microbial stratification and diffusion fields.

Conceptual analogy between intrinsic gravitation in planetary–stellar systems and gravito–thermal organization in microbial systems

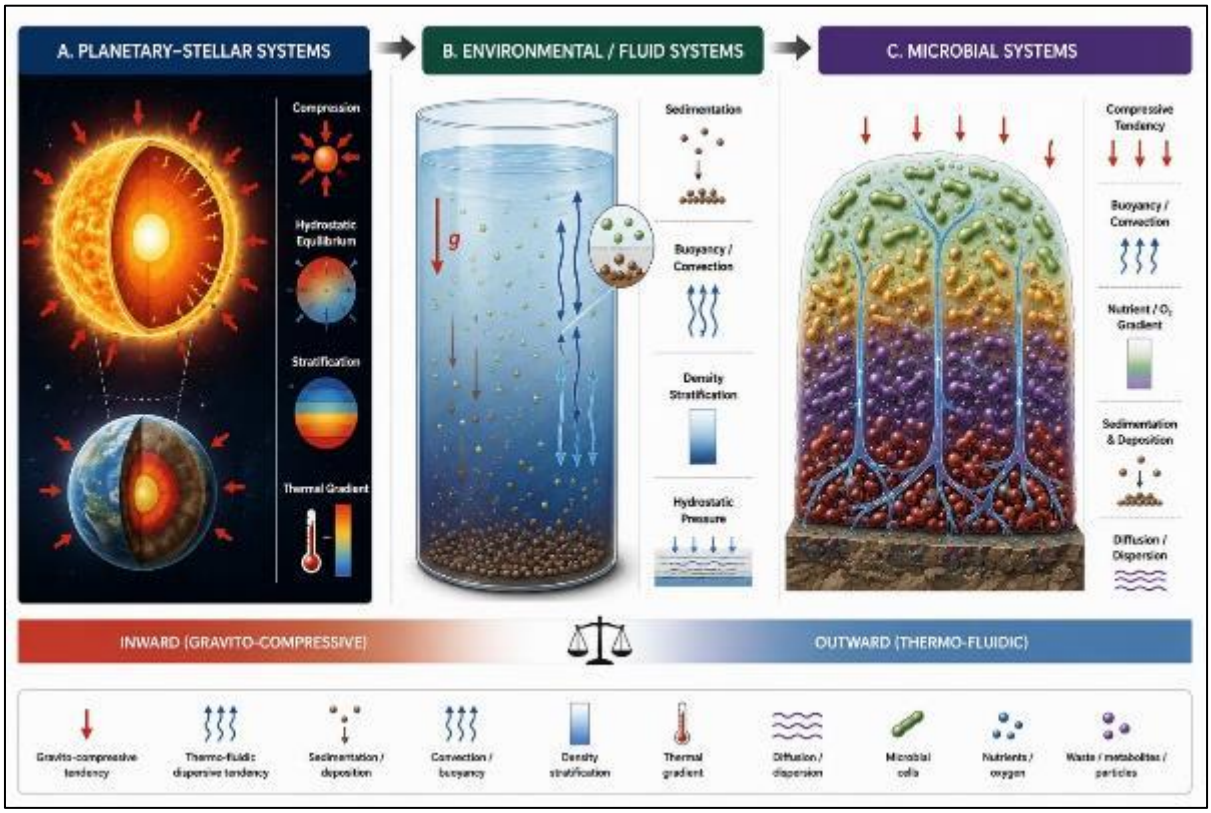

Figure 4 Conceptual schematic illustrating analogical relationships between gravito-compressive organization in planetary–stellar systems, hydrostatic and thermo-fluidic processes in environmental media, and emergent structural organization in microbial systems. The left panel depicts inward compressive tendencies associated with gravity-driven hydrostatic equilibrium, density stratification, and thermal gradients within stars and planets. The central panel illustrates environmental fluid systems characterized by sedimentation, hydrostatic pressure, buoyancy, convection, density layering, and thermo-fluidic redistribution. The right panel represents microbial organization within biofilms and structured communities exhibiting diffusion gradients, nutrient and oxygen stratification, sediment deposition, extracellular polymeric substance (EPS)-mediated cohesion, and metabolically differentiated microzones. The figure conceptually integrates inward gravito-compressive stabilization with outward thermo-fluidic dispersive processes across hierarchical scales, illustrating the proposed interpretation of intrinsic gravitation as a background parameter associated with mass distribution and structural equilibrium within biological and environmental systems.

The present framework therefore proposes that microbial systems exist within dynamic equilibrium between gravito-compressive stabilization, and thermo-fluidic redistribution. This interpretation parallels earlier gravito–thermal propositions advanced for biological systems, embryogenesis, plant architecture, and ecological organization (Bhattacharjee, 2025; Bhattacharjee, 2026). However, the present article applies these concepts specifically to microorganisms and microbial ecosystems.

3.3. Proposed Gravito–Thermal Continuum

Within the proposed framework, microbial organization may be interpreted as emerging from interactions between inward stabilizing tendencies associated with compression, sedimentation, density organization, and structural cohesion, and outward dispersive tendencies associated with thermal redistribution, buoyancy, convection, diffusion, and entropy-driven expansion. This conceptual continuum does not imply that intrinsic gravity ‘singularly’ determines microbial organization, but work as ‘collectively’. It proposes that microbial systems arise through equilibrium among

mass-associated stabilization, osmotic dynamics, diffusion, hydrostatic gradients, thermal transport, and physicochemical redistribution processes in collective manner. Accordingly, intrinsic gravitation is interpreted here as a persistent background parameter associated with organized mass systems and environmental structural stabilization operating continuously alongside thermodynamic and biochemical interactions.

Table 1 Inward organizational versus outward dispersive tendencies as persistent background parameters

Inward organizational tendencies	Outward dispersive tendencies
Compression	Expansion
Sedimentation	Buoyancy
Density stabilization	Thermal agitation
Structural cohesion	Entropic redistribution
Hydrostatic loading	Fluid convection
Colony consolidation	Diffusive spreading

4. Microorganisms Across the Environmental Continuum

Microorganisms inhabit environments whose organization depends fundamentally upon the physical properties of the surrounding medium. For instance, water and lipids differ markedly in their physicochemical properties and consequently influence microbial environments differently. Water (H_2O), with a low molar mass of approximately 18.02 g/mol, is a small polar molecule capable of extensive hydrogen bonding, giving it high density (~1.0 g/cm^3), high specific heat capacity (~4.18 J g^{-1} °C^{-1}), strong cohesion, and excellent solvent capacity. These properties support diffusion, convection, hydrostatic organization, nutrient transport, and thermal buffering within microbial systems. In contrast, lipids generally possess much larger molecular masses (commonly several hundred g/mol), lower density (~0.8–0.9 g/cm^3), lower specific heat capacity, hydrophobicity, and reduced thermal conductivity. Consequently, lipid-rich domains contribute more prominently to buoyancy regulation, membrane formation, insulation, energy storage, and structural compartmentalization rather than rapid thermo-fluidic redistribution.

Similarly, gaseous environments exhibit very low density, high compressibility, rapid thermal fluctuation, and turbulent convection, favouring aerosol suspension and long-distance microbial dispersal. Solid and semi-solid environments such as soils, sediments, biofilms, and ice matrices exhibit comparatively greater confinement, mechanical stabilization, restricted diffusion, and density stratification. Temperature further modifies these environments by regulating molecular motion, viscosity, diffusion rates, and fluid circulation. Within the present gravito–thermal framework, microbial organization therefore emerges through interactions among the physical properties of environmental media, including density, thermal capacity, hydrostatic behaviour, diffusion dynamics, and structural confinement.

4.1. Cosmic and Microgravity Microorganisms

Microorganisms inhabiting extraterrestrial, spacecraft-associated, and simulated microgravity environments provide important experimental systems for examining how altered physical constraint regimes influence biological organization. Unlike terrestrial environments, where gravity continuously and collectively contributes to sedimentation, hydrostatic gradients, buoyancy-driven convection, and fluid stratification, microgravity environments substantially reduce or delayed these processes and thereby alter microbial spatial behaviour, nutrient transport, and physiological adaptation (Nickerson et al., 2004; Klaus & Howard, 2006). Studies conducted aboard orbital platforms and simulated microgravity systems have demonstrated that altered gravitational environments can influence bacterial growth kinetics, virulence, stress responses, biofilm formation, antibiotic susceptibility, quorum signalling, and global gene expression patterns (Wilson et al., 2007; Kim et al., 2013; Zea et al., 2017). Representative microorganisms investigated under microgravity or low-shear modelled microgravity conditions include *Bacillus subtilis*, *Escherichia coli*, *Salmonella enterica*, *Pseudomonas aeruginosa*, and the radiation-resistant extremophile *Deinococcus radiodurans* (Nickerson et al., 2004; Rosenzweig et al., 2010).

Under terrestrial gravity, microbial systems are continuously influenced by downward sedimentation, hydrostatic pressure gradients, buoyancy-associated convection, density stratification, and gravity-mediated fluid redistribution. These processes contribute to nutrient layering, oxygen gradients, colony orientation, and structured biofilm architecture within liquid and semi-solid environments.

In contrast, microgravity substantially reduces or delays sedimentation and buoyancy-driven convection, causing diffusion-mediated transport to become relatively dominant (Klaus et al., 1997). Consequently, suspended particles remain more uniformly distributed, nutrient redistribution becomes less or delayed stratified, fluid mixing alters, and microbial cells experience low-shear fluid environments with modified boundary-layer dynamics. Such changes may influence microbial aggregation, extracellular polymeric substance (EPS) production, and three-dimensional biofilm organization (Zea et al., 2017). Several studies have reported that biofilms formed under microgravity exhibit altered thickness, architecture, and antimicrobial resistance compared with terrestrially grown controls. Within the present gravito–thermal framework, these observations may be interpreted as consequences of altered or delayed equilibrium between intrinsic gravito-compressive organization, and thermo-fluidic redistribution.

Although microorganisms themselves may not generate measurable self-gravity, they normally inhabit gravitationally structured media in which sedimentation, hydrostatic organization, and convection contribute indirectly to environmental stabilization. Reduced-gravity environments therefore provide experimentally valuable systems for examining how diminished or delayed gravito-associated constraints influence microbial organization, diffusion fields, fluid dynamics, and collective behaviour. Radiation-resistant microorganisms such as *Deinococcus radiodurans* are of particular interest because they demonstrate remarkable structural and metabolic resilience under conditions combining microgravity, ionizing radiation, desiccation, oxidative stress, and nutrient limitation (Daly, 2009).

Such organisms extend the concept of microbial environmental continuity from terrestrial ecosystems toward cosmic and astrobiological domains. Consequently, extraterrestrial microbiology and spaceflight-associated microbial ecology may provide important models for investigating the interaction among mass distribution, thermodynamic gradients, fluid organization, and adaptive biological architecture under altered physical constraint regimes.

2.2 Microbial organization under terrestrial gravity (1g) versus microgravity (≈0g)

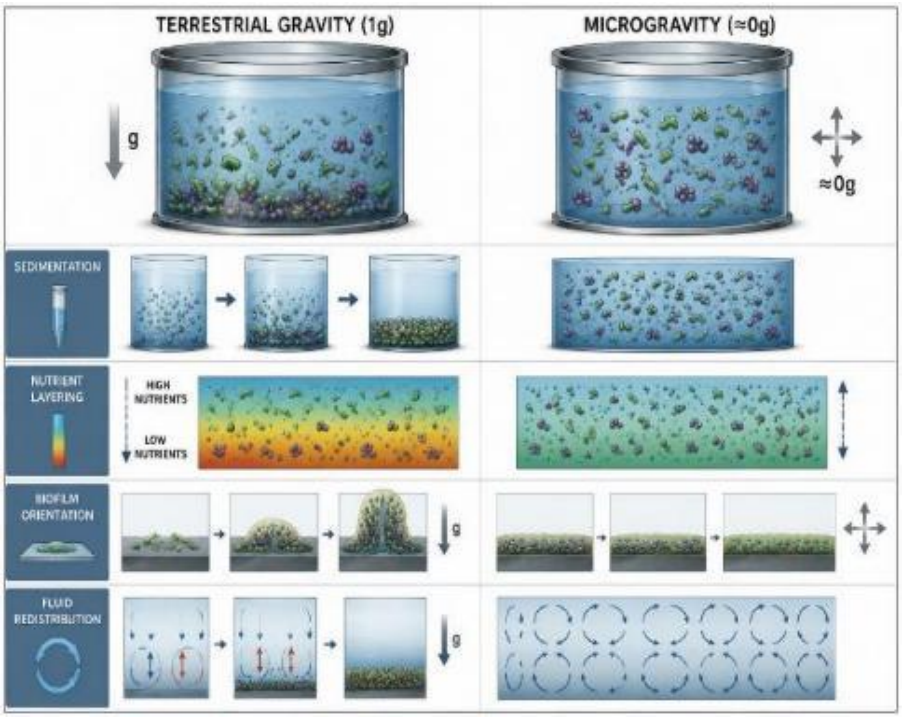

Figure 5 Comparative schematic representation illustrating the influence of gravitational conditions on microbial spatial organization, sedimentation behaviour, nutrient stratification, biofilm orientation, and fluid redistribution. Under terrestrial gravity, microorganisms exhibit instant downward sedimentation, hydrostatic layering, gravity-associated convection, and vertically organized nutrient gradients contributing to structured colony and biofilm architecture. In contrast, microgravity conditions reduce or delay sedimentation and buoyancy-driven convection, resulting in more uniform cellular suspension, altered nutrient distribution, diffusion-dominated transport, and modified biofilm morphology. The schematic conceptually illustrates the dynamic balance between gravito-compressive stabilization and thermo-fluidic redistribution within microbial systems under differing gravitational environments

4.2. Atmospheric Microorganisms

Atmospheric microorganisms constitute an important component of the global microbial continuum and occupy highly dynamic physicochemical environments characterized by turbulent convection, thermal gradients, ultraviolet (UV) radiation, desiccation stress, aerosol suspension, and fluctuating humidity conditions (Womack et al., 2010; DeLeon-Rodriguez et al., 2013).

The atmosphere serves not merely as a passive transport medium but also as a transient ecological habitat supporting metabolically active and dormant microbial populations across multiple altitudinal layers. Airborne microbial assemblages include fungal spores, cyanobacteria, actinomycetes, pollen-associated microbiota, bacterial aerosols, and airborne viruses (Burrows et al., 2009). Representative atmospheric microorganisms include *Bacillus* spores, *Micrococcus* spp., Pseudomonas *syringae*, airborne actinomycetes, and various fungal spores including *Aspergillus* and *Cladosporium* species. Within atmospheric systems, thermo-fluidic processes often transiently dominate over gravitational sedimentation. Turbulent air circulation, convection currents, wind shear, and thermal uplift may maintain microorganisms in aerosol suspension for extended periods despite continuous gravitational settling tendencies (Smith et al., 2013). Consequently, microbial particles may undergo long-distance transport across continents, oceans, and climatic zones. Atmospheric microbial distribution is additionally influenced by particle size, density, hydration state, surface charge, aggregation, and cloud microphysics. Certain bacteria such as *Pseudomonas syringae* function as ice-nucleating organisms and may influence atmospheric precipitation processes by promoting cloud condensation and ice crystal formation (Morris et al., 2014). Such interactions demonstrate the coupling between microbial organization and atmospheric thermodynamic processes.

Within the present gravito–thermal framework, atmospheric microbial systems provide an important example in which thermo-fluidic redistribution and buoyancy-associated suspension transiently counteract gravito-compressive sedimentation. Although gravitational settling continuously acts upon suspended particles, convection, turbulence, and aerosol dynamics may maintain microorganisms within dynamically redistributed atmospheric layers. Atmospheric microbiology therefore illustrates how outward thermo-fluidic forces may temporarily overcome inward sedimentation tendencies within open environmental systems.

4.3. Polar and Cryosphere Microorganisms

Polar and cryospheric ecosystems represent highly constrained microbial environments characterized by low thermal energy, freeze–thaw cycling, reduced liquid water availability, increased viscosity, reduced diffusion dynamics, osmotic stress, and density stabilization within ice matrices (Cavicchioli et al., 2011). Psychrophilic and psychrotolerant microorganisms inhabiting glaciers, sea ice, snowpacks, Antarctic lakes, and permafrost have evolved specialized adaptations enabling survival under prolonged cold stress and restricted molecular mobility. Representative cryospheric microorganisms include *Psychrobacter* spp., Antarctic cyanobacteria, ice-associated algae, cryoarchaea, and cold-adapted fungal communities. Microbial life within frozen systems frequently occurs within brine channels, liquid inclusions, ice grain boundaries, and hydrated microfilms embedded within solid matrices (Price, 2007). These microenvironments impose strong physical constraints on diffusion, nutrient redistribution, hydration, and metabolic exchange. Reduced thermal energy substantially decreases molecular motion and biochemical reaction rates, thereby influencing membrane fluidity, enzyme activity, and transport processes. Simultaneously, freeze–thaw cycles generate repeated osmotic and mechanical stresses affecting cellular integrity and ecological stability. Within cryospheric systems, microbial organization becomes strongly influenced by structurally constrained architectures generated by ice confinement, density stabilization, and restricted diffusion pathways. Microbial populations frequently develop localized clustered distributions within liquid microchannels and nutrient-enriched inclusions, producing heterogeneous microenvironments despite macroscopically frozen conditions.

From the perspective of the present gravito–thermal framework, cryosphere microbiology represents an ecological regime dominated by delayed or reduced thermal redistribution, constrained fluid mobility, density stabilization, and mechanically restricted diffusion. These environments therefore provide important natural models for examining microbial organization under conditions where thermo-fluidic dynamics are minimized or deferred and structural confinement becomes increasingly dominant.

4.4. Aquatic and Marine Microorganisms

Aquatic and marine microbial ecosystems represent some of the clearest examples of gravito–thermal environmental organization because they are continuously structured by interactions among hydrostatic pressure, buoyancy, thermal stratification, nutrient gradients, vertical mixing, sedimentation, and fluid convection (Falkowski et al., 2008). The aquatic water column constitutes a vertically organized physicochemical continuum extending from illuminated surface

layers to aphotic deep-ocean systems characterized by progressively increasing hydrostatic pressure and declining temperature and oxygen availability. Representative aquatic microbial groups include phytoplankton, cyanobacteria, diatoms, dinoflagellates, coccolithophores, heterotrophic bacteria, and marine archaea.

Microbial distribution within aquatic systems is strongly influenced by thermoclines, haloclines, nutrient stratification, and buoyancy-associated transport processes. Surface euphotic zones receive solar radiation supporting photosynthetic microbial communities including cyanobacteria and algae, whereas deeper aphotic zones are dominated increasingly by heterotrophic bacteria, chemolithotrophs, and pressure-adapted archaea (Azam & Malfatti, 2007). Many planktonic microorganisms possess specialized adaptations that partially counteract gravitational sinking tendencies. These include gas vacuoles, lipid accumulation, altered colony morphology, reduced density structures, flagellar motility, and active vertical migration (Walsby, 1994). Such adaptations enable microorganisms to maintain position within optimal thermal and nutrient layers despite continuous sedimentation forces. Consequently, buoyancy functions as a major counteractive mechanism opposing downward gravito-compressive redistribution within aquatic ecosystems. Marine microbial communities additionally exhibit pronounced vertical ecological stratification associated with oxygen gradients, hydrostatic compression, nutrient availability, and thermal layering. At increasing depths, hydrostatic pressure rises substantially, influencing membrane organization, protein stability, enzymatic activity, and microbial metabolism (Bartlett, 2002). Deep-sea microbial systems therefore represent environments where gravito-compressive hydrostatic organization becomes increasingly dominant. Within the present gravito–thermal framework, aquatic microbial ecosystems illustrate dynamic equilibrium between downward sedimentation and hydrostatic stabilization, and upward buoyancy, convection, and thermo-fluidic redistribution. The resulting environmental stratification generates vertically differentiated microbial architectures across aquatic thermoclines and ecological layers.

4.5. Vertical stratification of microbial communities across aquatic thermoclines

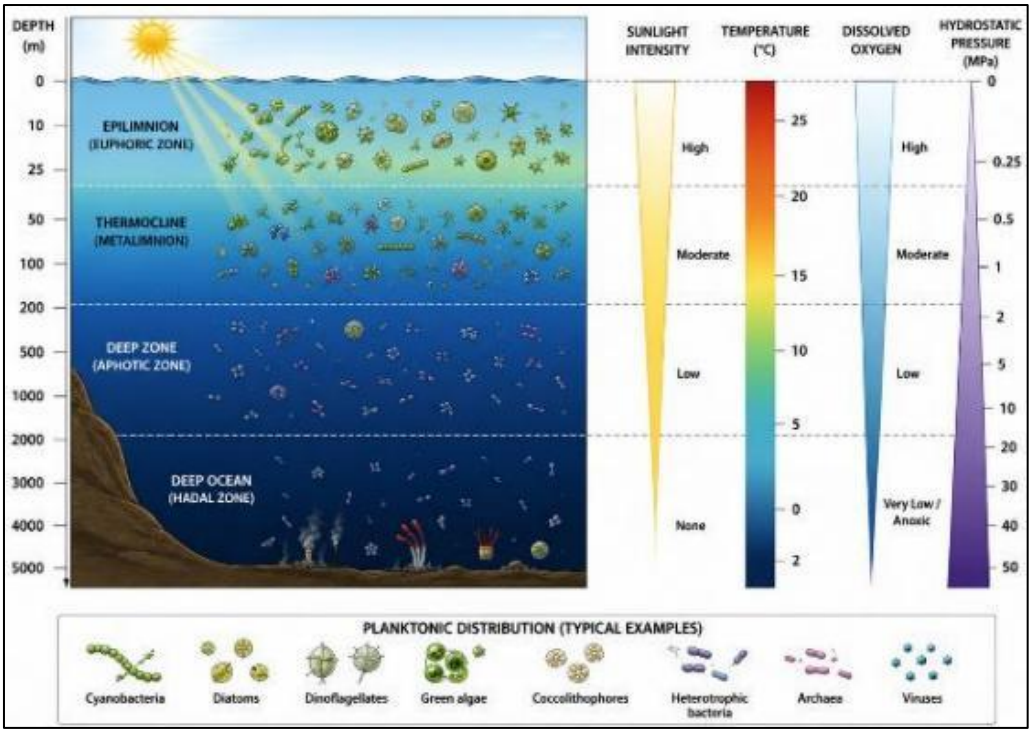

Figure 6 Conceptual representation illustrating microbial distribution and environmental gradients across the aquatic water column from surface euphotic zones to deep oceanic and hadal environments. The schematic depicts progressive reduction in sunlight penetration, temperature, and dissolved oxygen with increasing depth, accompanied by increasing hydrostatic pressure and density stabilization. Distinct microbial communities occupy different thermal and physicochemical layers, including cyanobacteria, algae, and photosynthetic plankton in illuminated surface waters; mixed microbial populations within thermocline-associated transition zones; and pressure-adapted heterotrophic bacteria, archaea, and deep-sea microorganisms in aphotic high-pressure environments. The figure highlights interactions among thermal stratification, buoyancy regulation, nutrient gradients, sedimentation, hydrostatic compression, and ecological adaptation within vertically organized aquatic gravito–thermal systems

4.6. Hydrothermal Vent Microorganisms

Deep-sea hydrothermal vent ecosystems represent some of the most extreme and physically dynamic microbial habitats known on Earth. These environments occur along tectonic spreading centres and submarine volcanic systems where superheated mineral-rich fluids emerge from the oceanic crust under conditions of immense hydrostatic pressure, geothermal heating, chemical disequilibrium, steep thermal gradients, and reduced solar influence (Corliss et al., 1979; Jannasch & Mottl, 1985). Hydrothermal systems provide compelling examples of coupled gravito–thermal organization because they exist at the interface between inward hydrostatic compression generated by the overlying water column, and outward geothermal convection driven by thermal and chemical energy release from the lithosphere. Representative hydrothermal microorganisms include sulphur-oxidizing bacteria, methanogenic archaea, sulphate-reducing microorganisms, thermophilic chemolithotrophs, and hyperthermophilic archaea such as *Pyrolobus fumarii* and *Methanopyrus kandleri* (Stetter, 1996). Unlike surface ecosystems dependent upon photosynthesis, hydrothermal microbial communities derive energy primarily through chemosynthesis involving sulphur oxidation, methane metabolism, hydrogen utilization, iron cycling, and other redox-driven reactions (Takai et al., 2006). These microbial systems occupy environments characterized by intense hydrostatic loading, mineral precipitation, fluid turbulence, and fluctuating thermal micro gradients.

Hydrothermal fluid circulation continuously redistributes dissolved minerals, gases, and thermal energy through convection-driven transport, while simultaneously generating localized ecological niches supporting highly specialized microbial populations. Within vent chimneys and mineralized biofilms, microorganisms frequently develop structurally organized communities associated with porous mineral matrices, thermal gradients, diffusion limitation, and fluid-channel architectures. Such systems illustrate strong interactions among pressure, thermal transport, mineral interfaces, density-dependent stratification, and microbial ecological adaptation.

Within the present gravito–thermal framework, hydrothermal vent ecosystems may therefore be interpreted as environments where gravito-compressive hydrostatic stabilization and thermo-fluidic geothermal redistribution coexist in dynamic equilibrium. These systems provide particularly important models for understanding microbial organization under coupled conditions of compression, heat transfer, fluid circulation, and geochemical energy exchange.

4.7. Soil and Rhizospheric Microorganisms

Soil ecosystems represent highly heterogeneous gravito–thermal environments in which microorganisms interact continuously with mineral particles, capillary water films, gas-filled pore spaces, organic matter, root exudates, and fluctuating thermal conditions (Young & Crawford, 2004). Unlike relatively homogeneous aquatic systems, soils exhibit complex microscale architectures generated through gravitational sedimentation, particle aggregation, hydration gradients, thermal cycling, capillary transport, and gas diffusion. Representative soil and rhizospheric microorganisms include *Rhizobium*, actinomycetes, *Nitrosomonas*, mycorrhizal fungi, cyanobacteria, and phosphate-solubilizing bacteria. Microbial distribution within soils is strongly influenced by pore geometry, water retention, nutrient diffusion, oxygen availability, and mechanical confinement. Rhizospheric environments are particularly dynamic because plant roots continuously modify surrounding physicochemical conditions through osmotic gradients, exudate secretion, ion exchange, hydraulic redistribution, and localized nutrient enrichment (Philippot et al., 2013).

Root-associated microbial communities therefore inhabit highly structured microenvironments where fluid transport, diffusion limitation, and hydration gradients interact continuously with biological activity. Capillary water movement within soils further contributes to microbial redistribution and localized stratification, while repeated wetting–drying cycles generate fluctuating osmotic and mechanical stresses. Soil aggregates frequently function as confined microbial microhabitats exhibiting pronounced gradients in oxygen, pH, hydration, nutrient concentration, and metabolite accumulation.

Within the present gravito–thermal framework, soil microbial systems may be interpreted as environmentally confined physicochemical architectures in which gravitational settling, capillary transport, thermal fluctuation, osmotic regulation, and diffusion collectively shape microbial organization. Rhizospheric ecosystems particularly demonstrate the coupling among biological activity, fluid transport, hydrostatic micrograd ients, and structurally constrained ecological organization.

4.8. Biofilms as Gravito–Thermal Architectures

Biofilms represent one of the strongest biological examples supporting the present gravito–thermal framework because they exhibit highly organized spatial architectures arising through coupled interactions among diffusion, mechanical

stabilization, hydration, nutrient transport, hydrostatic microenvironments, and physicochemical gradients (Costerton et al., 1995; Flemming et al., 2016). Biofilms are structured microbial communities embedded within extracellular polymeric substance (EPS) matrices attached to surfaces or interfaces. Unlike freely suspended planktonic cells, biofilm-associated microorganisms exist within mechanically stabilized and diffusion-regulated environments characterized by layered organization, nutrient gradients, oxygen stratification, waste accumulation, hydrostatic microchannels, and density-dependent spatial differentiation. Representative biofilm-forming microorganisms include *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Escherichia coli*, and numerous mixed-species microbial consortia.

4.9. Layered gravito–thermal architecture of microbial biofilms

Within mature biofilms, diffusion limitation generates pronounced physiological heterogeneity across relatively short spatial distances (Stewart & Franklin, 2008). Surface layers frequently contain oxygen-rich aerobic populations, whereas deeper regions progressively develop oxygen depletion, anaerobic microzones, reduced nutrient availability, slower metabolic rates, and increased metabolite accumulation. The EPS matrix contributes significantly to structural cohesion, hydration retention, mechanical stability, diffusion regulation, and protection against environmental stress. Simultaneously, interconnected hydrostatic microchannels facilitate localized fluid redistribution, nutrient circulation, and metabolite transport throughout the biofilm architecture.

Biofilms therefore exhibit emergent multicellular-like spatial coordination despite lacking centralized developmental control systems. Such organization arises through interactions among diffusion gradients, osmotic regulation, hydrostatic microenvironments, thermo-fluidic transport, and mechanically stabilized structural organization.

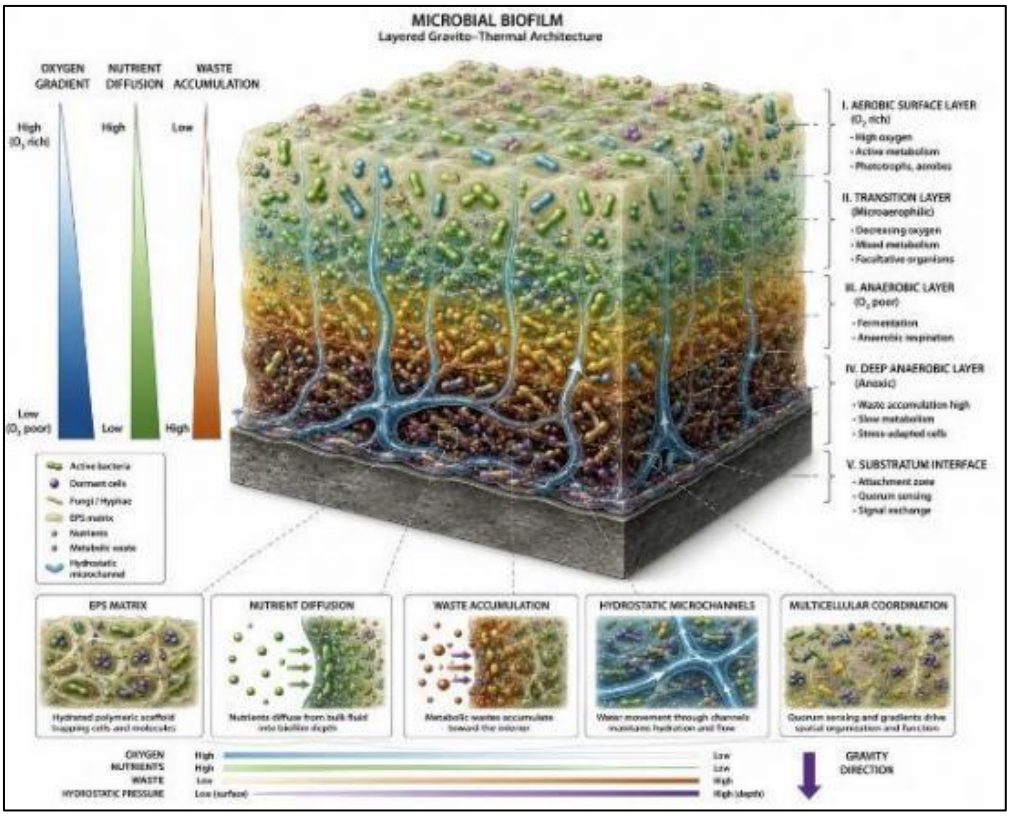

Figure 7 Conceptual illustration showing the spatial and physicochemical organization within a mature microbial biofilm. The schematic demonstrates vertical oxygen gradients, inward nutrient diffusion, progressive waste accumulation toward deeper layers, extracellular polymeric substance (EPS) matrix formation, and interconnected hydrostatic microchannels facilitating localized fluid circulation and metabolite transport. Surface regions are characterized by higher oxygen availability and active aerobic metabolism, whereas deeper layers exhibit oxygen depletion, reduced diffusion, anaerobic microenvironments, and increased metabolic waste accumulation. The EPS matrix contributes structural cohesion, hydration retention, and mechanical stabilization, while microchannels enable thermo-fluidic redistribution within the biofilm architecture. Collectively, the layered organization illustrates emergent multicellular-like spatial coordination arising through interactions among gravito-compressive stabilization, diffusion gradients, hydrostatic organization, thermo-fluidic transport, and ecological adaptation

Within the present gravito–thermal framework, biofilms may be interpreted as highly organized microbial infrastructures in which gravito-compressive stabilization, thermo-fluidic redistribution, diffusion limitation, and environmental confinement collectively generate complex ecological architectures.

4.10. Host-Associated Microorganisms

Host-associated microbial communities inhabit some of the most physiologically structured microbial environments known in nature. These microbiotas exist within thermally regulated systems, fluid transport networks, hydrostatic compartments, pressure fields, immune boundaries, and chemically differentiated tissues (Turnbaugh et al., 2007). Representative host-associated microbiomes include gut microbiota, oral microbiota, skin-associated microorganisms, respiratory microbiota, and reproductive tract microbial communities. Within multicellular hosts, microorganisms encounter continuously regulated temperature, osmotic balance, fluid circulation, nutrient supply, oxygen gradients, and immune-mediated selective pressures.

The gastrointestinal tract particularly exhibits pronounced spatial stratification associated with pH variation, oxygen limitation, peristaltic fluid transport, mucus-layer organization, and nutrient gradients.

Similarly, pulmonary microbiota inhabits mechanically dynamic environments influenced by airflow, hydration, and gas exchange, whereas skin-associated microorganisms experience fluctuating hydration, temperature, and salinity conditions.

Host tissues therefore function as macro-scale gravito–thermal ecosystems integrating hydrostatic transport, thermoregulation, biochemical signalling, and mechanically structured physiological compartments. Within the present framework, host-associated microbiomes may be interpreted as highly organized ecological systems embedded within larger biological architectures where thermal regulation, fluid dynamics, pressure gradients, and structural confinement collectively shape microbial organization and ecological stability.

4.11. Deep Earth Biosphere

The deep subsurface biosphere represents one of the most extreme microbial environments known, extending through deep sediments, fractured crustal rocks, aquifers, petroleum reservoirs, and lithospheric interfaces beneath Earth's surface (Whitman et al., 1998; Edwards et al., 2012). Microorganisms inhabiting these systems survive under conditions characterized by high hydrostatic pressure, geothermal gradients, mineral interfaces, extreme nutrient limitation, low energy flux, anoxic environments, and prolonged fluid confinement. Representative deep biosphere microorganisms include methanogenic archaea, sulphate-reducing bacteria, chemolithotrophs, hydrogenotrophic microorganisms, and pressure-adapted anaerobic communities. Unlike surface ecosystems driven primarily by photosynthesis, deep biosphere microbial systems depend largely upon geochemical energy, hydrogen production, mineral redox reactions, methane cycling, and radiolytic processes (Lin et al., 2006). Fluid movement within deep geological systems is often extremely restricted, resulting in prolonged physicochemical isolation and strong environmental confinement. Microbial metabolism proceeds under conditions of low diffusion, slow nutrient turnover, elevated compression, and persistent geothermal influence. Consequently, deep subsurface microorganisms may represent some of the most compression-dominated microbial systems presently known.

Within the present gravito–thermal framework, the deep biosphere may be interpreted as the terminal end of a planetary microbial continuum in which hydrostatic compression, geological confinement, geothermal gradients, and density stabilization become dominant organizing constraints. These systems therefore provide important models for understanding microbial persistence and organization under extreme long-term physicochemical stabilization regimes.

2.3 Grand microbial continuum from cosmic microgravity to deep Earth biosphere

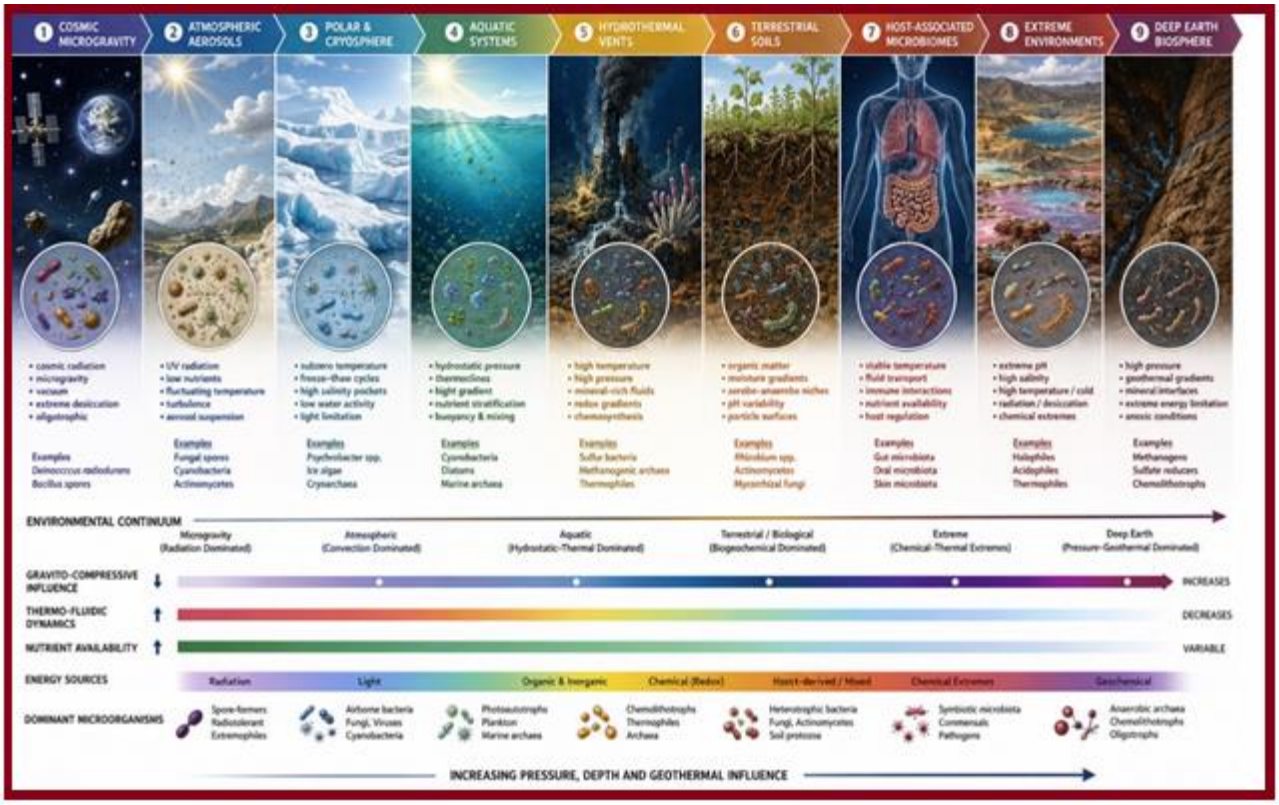

Figure 8 Conceptual overview illustrating the distribution of microorganisms across a continuous environmental and gravito–thermal spectrum extending from extraterrestrial microgravity systems to deep lithospheric biospheres. Representative ecosystems include cosmic space, atmospheric aerosols, polar cryospheres, aquatic systems, hydrothermal vents, terrestrial soils, host-associated microbiomes, chemically extreme habitats, and deep subsurface environments. Environmental transitions are depicted relative to changing dominant organizing factors including radiation exposure, thermal gradients, hydrostatic pressure, nutrient availability, buoyancy, convection, geochemical interfaces, structural confinement, and compressive geological forces. Representative microbial groups—including bacteria, archaea, fungi, planktonic microorganisms, extremophiles, chemolithotrophs, symbiotic microbiota, and anaerobic deep biosphere communities—are shown along the continuum. The schematic highlights the proposed balance between gravito-compressive stabilization and thermo-fluidic redistribution as a unifying biophysical framework underlying microbial organization across diverse ecological domains.

4.12. Microorganisms That Challenge the Common Principle

Although numerous microbial systems exhibit organization consistent with gravito–compressive stabilization and physicochemical stratification, not all microorganisms conform uniformly to simple sedimentation-driven or compression-dominated behaviour. Several microbial groups possess adaptations that actively counteract, modify, or transiently overcome gravitational settling and density-dependent redistribution. These exceptions are important because they demonstrate that microbial organization emerges through dynamic negotiation between compressive stabilization and dispersive or motile counterforces rather than through unidirectional gravitational control alone.

Planktonic cyanobacteria provide a classical example of buoyancy-mediated counteraction to gravitational sinking. Many cyanobacteria possess intracellular gas vacuoles that reduce cellular density and permit vertical migration within aquatic water columns (Walsby, 1994). Such buoyancy-regulating structures enable microorganisms to maintain optimal positions relative to sunlight, nutrient gradients, thermal layers, and oxygen availability.

Similarly, motile protozoa and flagellated microorganisms actively resist passive sedimentation through swimming behaviour, taxis mechanisms, and cytoskeletal motility systems. Chemotaxis, phototaxis, gravitaxis, and rheotaxis enable microorganisms to navigate dynamically across environmental gradients despite continuous hydrostatic and sedimentation-associated constraints (Fenchel, 2002).

Airborne fungal spores and microbial aerosols represent additional systems in which thermo-fluidic and atmospheric processes transiently dominate over gravitational settling. Turbulent convection, thermal uplift, wind circulation, and aerosol suspension can maintain microbial particles within atmospheric layers for prolonged periods, facilitating long-distance transport across continents and climatic systems (Womack et al., 2010).

Biofilm dispersal cells provide another important example of transient escape from structurally stabilized microbial architectures. Mature biofilms frequently release planktonic dispersal populations through enzymatic EPS degradation, hydrodynamic shear, nutrient limitation, and active motility responses (Kaplan, 2010).

Likewise, hydrothermal vent microorganisms inhabiting convection-dominated geothermal systems experience intense upward fluid transport capable of partially offsetting sedimentation and hydrostatic stabilization. Thermal convection, mineral-rich plume circulation, and turbulent vent flow create highly dynamic physicochemical environments where microbial redistribution occurs continuously despite extreme pressure conditions.

Within the present gravito–thermal framework, such exceptions strengthen rather than weaken the proposed interpretation because they demonstrate that microbial systems continuously negotiate between inward compressive stabilization, and outward dispersive or redistributive processes. Microbial organization therefore emerges not from static gravitational control but through dynamic equilibrium among sedimentation, buoyancy, motility, convection, diffusion, and environmental constraint.

5. Proposed Unified Principle

The present framework proposes that microbial organization may be interpreted as emerging through coupled interactions among gravito-compressive stabilization, thermo-fluidic redistribution, hydrostatic regulation, diffusion dynamics, and ecological constraint. To summarize this conceptual relationship, a generalized heuristic expression may be proposed:

$$MO = G_c + T_f + H_p + D + E$$ where:

MO = microbial organization
Gc = gravito-compressive tendency
Tf = thermo-fluidic redistribution
Hp = hydrostatic pressure in granular active poroelastic microbial mass
D = diffusion dynamics in granular active poroelastic microbial mass
E = environmental/ecological constraints

This expression is not intended as a predictive mathematical law but rather as a heuristic conceptual framework integrating multiple physical and ecological determinants contributing to microbial organization across scales.

Within this interpretation gravito-compressive tendencies contribute toward structural stabilization, sedimentation, and density organization; thermo-fluidic processes promote redistribution through convection, buoyancy, and heat-driven transport; hydrostatic forces influence fluid-mediated organization; diffusion governs nutrient transport and spatial heterogeneity; and environmental constraints define ecological boundaries and physicochemical stability. The proposed framework therefore attempts to integrate microbial ecology, fluid mechanics, hydrostatics, thermodynamics, environmental physics, and systems biology into a unified interpretive architecture.

6. Discussion

Microbial systems, built up through granular active poroelastic microbial process, exist within highly organized physicochemical environments structured by hydrostatic pressure, thermal gradients, diffusion dynamics, fluid transport, osmotic balance, sedimentation, and environmental confinement. Across ecological domains ranging from atmospheric aerosols and aquatic thermoclines to biofilms, hydrothermal vents, host-associated microbiomes, and deep lithospheric biospheres, microorganisms continuously interact with these coupled physical constraints while simultaneously modifying their surrounding microenvironments.

The present gravito–thermal framework interprets microbial organization as an emergent outcome of dynamic interactions among compressive stabilization, thermo-fluidic redistribution, diffusion-mediated transport, hydrostatic

organization, and ecological adaptation. Within this perspective, intrinsic gravitation is considered as a collective background structural parameter associated with density stabilization, sedimentation, hydrostatic layering, environmental compression, and large-scale mass organization across environmental systems. Simultaneously, thermal and fluid-mediated processes including convection, buoyancy, osmotic expansion, diffusion, and entropy-driven redistribution continuously generate counteractive dispersive tendencies. Microbial architecture therefore emerges through equilibrium between structural consolidation and environmental redistribution across multiple scales of biological organization.

This framework integrates observations from mechanobiology, microbial ecology, hydrostatics, thermodynamics, fluid mechanics, environmental microbiology, and systems physics. Biofilms, stratified aquatic microbial systems, cryospheric communities, hydrothermal vent ecosystems, and microgravity-associated microbial behavior collectively demonstrate that microbial organization is strongly influenced by physicochemical gradients and structural environmental architectures. Rod-shaped bacteria, filamentous growth patterns, sediment-associated colonies, and diffusion-regulated biofilms further illustrate the role of mechanical stabilization, confinement, and directional physicochemical stress distribution in shaping microbial morphology and ecological structure.

The proposed "Grand Microbial Continuum" extending from cosmic microgravity environments to deep Earth biospheres highlights progressive transitions among buoyancy, sedimentation, hydrostatic compression, geothermal influence, thermal stratification, and environmental confinement. Rather than functioning as isolated ecological systems, these environments may be interpreted as interconnected physical continua exhibiting varying balances between compressive stabilization and thermo-fluidic redistribution. Recent investigations into gravitation at sub-millimeter scales, granular organization, nonequilibrium systems, and emerging quantum gravity approaches further indicate that physical organization at microscopic and mesoscale levels remains incompletely understood (Adelberger et al., 2003; Carney et al., 2021). Future advances in mesoscale biophysics and complex systems theory may therefore provide deeper insight into how weak structural constraints interact with biological organization across environmental scales. The present framework aims to stimulate interdisciplinary discussion regarding the role of physical constraint regimes in microbial ecology and biological organization while encouraging integration between microbiology, environmental physics, thermodynamics, and systems-level biophysical interpretation.

2.4 Conceptual Highlights

- Microorganisms as Physicochemical Architectures

Microorganisms are interpreted not solely as biochemical entities but as physicochemically organized systems governed by interactions among mass distribution, thermal gradients, hydrostatic pressure, diffusion, osmotic balance, and environmental confinement.

- Intrinsic Gravitation work as a Background Structural Constraint

Intrinsic gravitation is interpreted conservatively as a background parameter.

- Dynamic Equilibrium Between Compression and Dispersion

Microbial organization emerges through equilibrium between inward gravito-compressive tendencies (sedimentation, hydrostatic loading, structural cohesion), and outward thermo-fluidic tendencies (convection, buoyancy, diffusion, entropy-driven redistribution).

- Collective Action of Various Physical Constraints that Shape Microbial Organization

Confinement, diffusion limitation, peptidoglycan mechanics, osmotic pressure, hydrostatic microenvironments, and environmental geometry collectively influence microbial morphology, colony structure, biofilm architecture, and ecological stratification.

- Biofilms as Strong Models of Gravito–Thermal Organization

Biofilms represent emergent multicellular-like systems exhibiting layered oxygen gradients, nutrient diffusion, extracellular polymeric substance (EPS)-mediated structural cohesion, hydrostatic microchannels, and physiologically differentiated microzones.

- Environmental Continuum from Cosmos to Deep Earth

Microbial life exists across a continuous gravito–thermal environmental spectrum extending from extraterrestrial microgravity systems and atmospheric aerosols to polar cryospheres, aquatic thermoclines, hydrothermal vents, terrestrial soils, host-associated microbiomes, and deep lithospheric biospheres. Despite profound ecological diversity, these habitats exhibit interconnected organizational principles involving hydrostatic pressure, thermal gradients, diffusion dynamics, buoyancy, sedimentation, structural confinement, and physicochemical stabilization, thereby supporting the concept of a unified "Grand Microbial Continuum."

- Microgravity as an Experimental Window

Spaceflight and simulated microgravity experiments demonstrate altered sedimentation, convection, biofilm architecture, virulence, and gene expression, supporting the importance of environmental physical organization in microbial behaviour.

- Hydrothermal and Deep Biosphere Systems as Compression-Dominated Regimes

Hydrothermal vents and deep subsurface ecosystems represent environments where hydrostatic compression, geothermal gradients, mineral interfaces, and constrained diffusion become dominant organizing constraints.

- Exceptions Strengthen the Framework

Cyanobacterial buoyancy, motile protozoa, airborne spores, and biofilm dispersal systems demonstrate that microbial life continuously negotiates between compressive stabilization and dispersive counterforces rather than obeying rigid gravitational organization alone.

2.5 Fundamental Biophysical Processes

- Mass Distribution: Spatial arrangement of matter according to density, composition, and structural packing. Influences sedimentation, stratification, and structural stabilization.
- Thermal Gradients: Differences in temperature across space driving heat transfer, convection, molecular motion, and ecological stratification.
- Hydrostatic Pressure: Pressure exerted by overlying fluids or materials, increasing with depth and contributing to compression and environmental stabilization. $\frac{dP}{dr} = -\rho g$
- Diffusion Dynamics: Passive movement of molecules along concentration gradients regulating nutrient transport, gas exchange, and metabolite redistribution. $J = -D\nabla C$
- Osmotic Regulation: Movement of water across semipermeable boundaries balancing solute concentration and cellular turgor pressure.
- Environmental Confinement: Physical restriction within pores, matrices, biofilms, sediments, tissues, or ice structures influencing diffusion, organization, and microbial architecture.

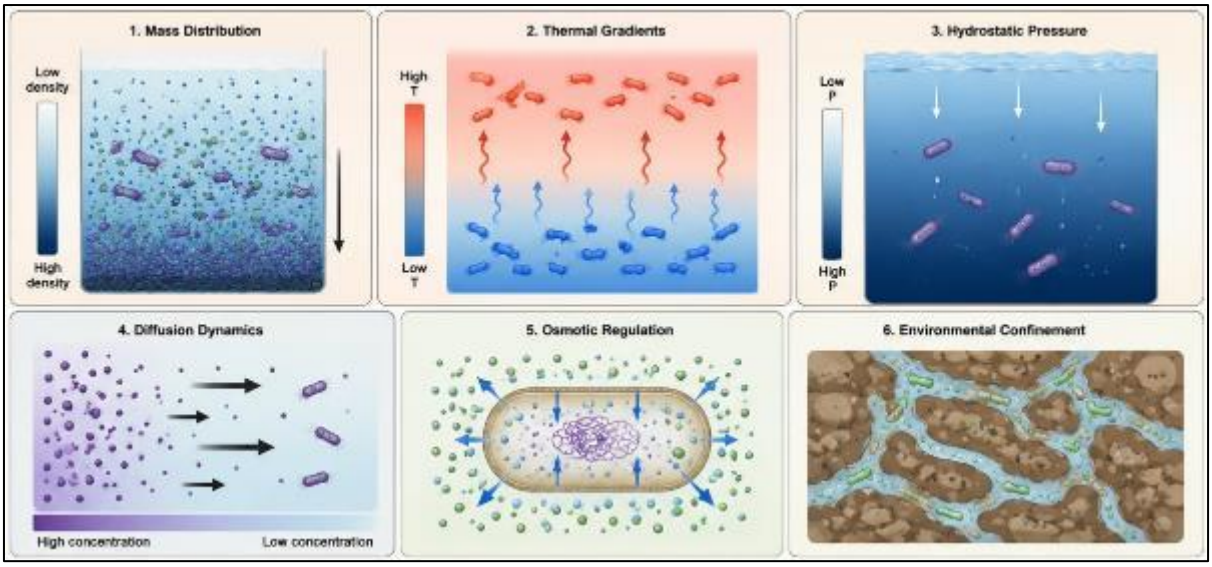

Figure 9 Demonstration of key Physical Processes: 1. Mass distribution, 2. thermal gradients, 3. hydrostatic pressure, 4 diffusion dynamics, 5. osmotic regulation, 6. environmental confinement

- Dynamic Gravito–Thermal Equilibrium
  - Inward Intrinsic Gravito–Compressive Stabilization: Associated with compression, sedimentation, density stabilization, hydrostatic loading, structural cohesion.
  - Outward Thermo–Fluidic Redistribution: Associated with convection, buoyancy, diffusion, osmotic expansion, entropy-driven dispersion. This equilibrium governs microbial organization across environmental systems.

Figure 10. Demonstration of key Physical Processes: (a). Inward Intrinsic Gravito–Compressive Stabilization, (b). Outward Thermo–Fluidic Redistribution

- Principal Counteractive Processes
  - Convection: Bulk fluid movement driven by thermal or density differences, redistributing heat, nutrients, and microorganisms.
  - Buoyancy: Upward force opposing sedimentation in fluids; important in planktonic suspension and gas-vacuole regulation.
  - Diffusion: Spontaneous molecular spreading from higher to lower concentration regions.
  - Osmotic Expansion: Water influx causing outward cellular pressure and volumetric expansion.
  - Entropy-Driven Redistribution: Natural tendency toward molecular dispersal, mixing, and reduction of concentration gradients.

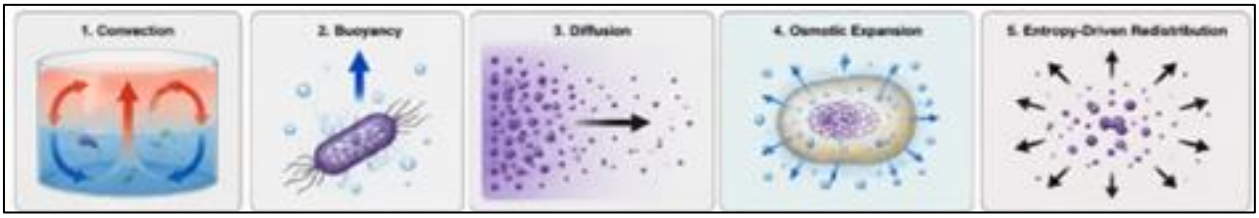

Figure 11.Demonstration of key Physical Processes: 7. Convection, 8. buoyancy, 9. diffusion, 10. osmotic expansion, 11. entropy-driven redistribution

2.6 Collective gravity driven backgrounds of structural parameters

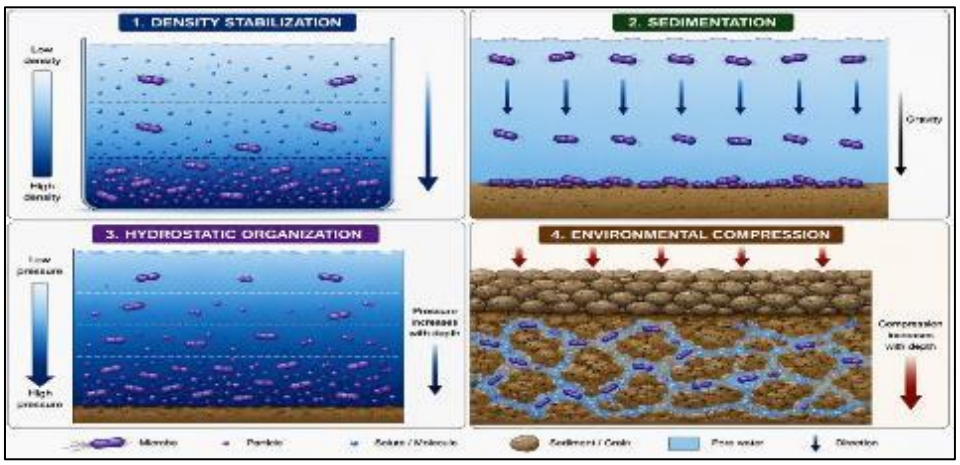

Figure 12 Demonstration of key Physical Processes: 12 Density stabilization, 13. sedimentation, 14. hydrostatic organization, 15. environmental compression

3. Conclusion

Microorganisms may be interpreted as components of a continuous gravito–thermal environmental spectrum extending from extraterrestrial microgravity systems and atmospheric aerosols to aquatic thermoclines, cryospheric habitats, hydrothermal vents, terrestrial soils, host-associated microbiomes, and deep lithospheric biospheres. Across this continuum, microbial organization emerges through coupled interactions among mass distribution, thermal gradients, hydrostatic pressure, diffusion dynamics, osmotic regulation, environmental confinement, and ecological adaptation.

Within this framework, intrinsic gravitation contributes toward density stabilization, sedimentation, hydrostatic organization, structural cohesion, and environmental compression, while thermo-fluidic processes generate redistributive tendencies through convection, buoyancy, diffusion, osmotic expansion, and entropy-driven dispersion.

Microbial systems therefore exhibit dynamic equilibrium between inward structural stabilization and outward environmental redistribution. This balance becomes visible across multiple biological and ecological scales including molecular crowding, peptidoglycan-mediated morphology, biofilm stratification, planktonic buoyancy regulation, hydrothermal convection systems, and deep subsurface compression-dominated microbial ecosystems.

The proposed “Grand Microbial Continuum” provides an integrative environmental perspective linking microorganisms across diverse habitats through shared physicochemical organizational principles. By combining microbiology with hydrostatics, thermodynamics, fluid mechanics, environmental physics, and systems ecology, the present work attempts to provide a broader biophysical interpretation of microbial organization across planetary environmental systems.

Future investigations involving microgravity experiments, hydrostatic gradient systems, biofilm mechanics, sedimentation dynamics, diffusion-regulated microbial architectures, and mesoscale biophysical modeling may further clarify how environmental physical constraints contribute to microbial adaptation and organization across ecological continua.

Compliance with ethical standards

Acknowledgments

The author acknowledges the contribution of his deceased spouse Mrs. Sukla Bhattacharjee, for her constant inspiration and support on all fronts during long odd and even hours of companion while advancing the historic concept.

Disclosure of conflict of interest

The author declares that there is no conflict of interest.

4. References

[1] Anderson, E.M. (1951) The dynamics of faulting and dike formation with application to Britain. Oliver and Boyd, 2nd Edition, Edinburgh,

[2] Azam F, Malfatti F. Microbial structuring of marine ecosystems. *Nat Rev Microbiol*. 2007 Oct;5(10):782-91. doi: 10.1038/nrmicro1747. Erratum in: Nat Rev Microbiol. 2007 Dec;5(12):966. PMID: 17853906.

[3] Baross, J.A., Hoffman, S.E. (1985) Submarine hydrothermal vents and associated gradient environments as sites for the origin and evolution of life. *Origins Life Evol Biosphere* 15, 327–345. https://doi.org/10.1007/BF01808177.

[4] Bartlett DH. (2002 Pressure effects on in vivo microbial processes. *Biochim Biophys Acta*. Mar 25;1595(1-2):367-81. doi: 10.1016/s0167-4838(01)00357-0. PMID: 11983409.

[5] Bhattacharjee, I.R. (1988) Gravity Dictates Life-Death and Biological Growth (also agricultural productivity) Introductory Concept: ISBN-13: 9788170193203.

[6] Bhattacharjee, Iresh Ranjan (2013) Self Gravity: The Major Investigation Gap in Life Science (Part I). *WebmedCentral Biophysics*; 4(6): WMC004279. doi: 10.9754/journal.wmc.2013.004279.

[7] Bhattacharjee, Iresh Ranjan (2013) Self Gravity: The Major Investigation Gap in Life Science (Part II). *WebmedCentral Biophysics*; 4(6): WMC004296. doi: 10.9754/journal.wmc.2013.004296.

[8] Bhattacharjee Iresh Ranjan (2025). Grand Evolutionary Continuum of Mass: Parallels Across Stars, Earth, and Human on Intrinsic Gravitation Mechanisms. *IJARESM* 13 (1), 20–35. https://doi.org/10.56025/IJARESM.2024.121224020

[9] Bhattacharjee Iresh Ranjan, Shaptadvipa Bhattacharjee (2026) Intrinsic Gravitation as a Physical Layer of Genetic Expression Mass, Torque, and Repeatability from RNA Dynamics to Development, J*ournal of Novel Research and Innovative Development JNRID* (www.JNRID.org), ISSN:2984-8687, Vol.4 (1) pp 158-66, https://doi.org/10.56975/jnrid.v4i1.701972 ; https://tijer.org/jnrid/viewpaperforall.php?paper=JNRID2601016

[10] Bhattacharjee Iresh Ranjan (2026) Intrinsic Gravitation as a Universal Structural Constraint in Biophysical Framework to Plant Systems and Agriculture, *International Journal of Creative Research Thoughts (IJCRT)*, ISSN:2320-2882, 14 (2), pp.102-120, http://www.ijcrt.org/papers/IJCRT2602599.pdf. https://doi.org/10.56975/ijcrt.v14i2.302005

[11] Bhattacharjee Iresh Ranjan (2026) Embryogenesis as Gravito-Thermo-Biophysical Process, *International Journal of Scientific Development and Research IJSDR.* ISSN:2455-2631, 11(4) pp 698-722, https://ijsdr.org/papers/IJSDR2604348.pdf, https://doi.org/10.56975/ijsdr.v11i4.309403

[12] Burrows, S. M., Elbert, W., Lawrence, M. G., and Pöschl, U (2009 Bacteria in the global atmosphere – Part 1: Review and synthesis of literature data for different ecosystems, *Atmos. Chem. Phys.*, 9, 9263–9280. https://doi.org/10.5194/acp-9-9263-2009.

[13] Cavicchioli R (2002). Extremophiles and the search for extraterrestrial life. *Astrobiology*. 2(3):281-92. doi: 10.1089/153110702762027862. PMID: 12530238.

[14] Corliss JB, Dymond J, Gordon LI, Edmond JM, von Herzen RP, Ballard RD, Green K, Williams D, Bainbridge A, Crane K, van Andel T H (1979) Submarine thermal sprirngs on the galapagos rift. *Science*. 16;203(4385):1073-83. doi: 10.1126/science.203.4385.1073. PMID: 17776033.

[15] Costerton JW, Lewandowski Z, Caldwell DE, Korber DR, Lappin-Scott HM. (1995) Microbial biofilms. *Annu Rev Microbiol*. 1995; 49:711-45. doi: 10.1146/annurev.mi.49.100195.003431. PMID: 8561477.

[16] Daly MJ (2009) A new perspective on radiation resistance based on Deinococcus radiodurans. *Nat Rev Microbiol*.7(3):237-45. doi: 10.1038/nrmicro2073. Epub 2009 Jan 27. PMID: 19172147.

[17] DeLeon-Rodriguez N, et al (2013). Microbiome of the upper troposphere: species composition and prevalence, effects of tropical storms, and atmospheric implications. *Proc Natl Acad Sci* U S A. 12;110(7):2575-80. doi: 10.1073/pnas.1212089110. Epub 2013 Jan 28. PMID: 23359712; PMCID: PMC3574924.

[18] Edwards, Katrina J.; Becker, Keir; Colwell, Frederick (2012). The deep, dark energy biosphere: Intraterrestrial Life on Earth. *Annual Review of Earth and Planetary Sciences*, 40, 551–568. DOI: 10.1146/annurev-earth-042711-105500.

[19] Falkowski PG, Fenchel T, Delong EF (2008) The microbial engines that drive Earth's biogeochemical cycles. *Science.* 23;320(5879):1034-9. doi: 10.1126/science.1153213. PMID: 18497287.

[20] Fenchel T (2002) Microbial behavior in a heterogeneous world. Science. 10;296(5570):1068-71. doi: 10.1126/science.1070118. PMID: 12004118.

[21] Flemming HC, Wingender J, Szewzyk U, Steinberg P, Rice SA, Kjelleberg S (2016). Biofilms: an emergent form of bacterial life. *Nat Rev Microbiol.* 11;14(9):563-75. doi: 10.1038/nrmicro.2016.94. PMID: 27510863.

[22] Flores, P., McBride, S. A., Galazka, J. M., Varanasi, K. K., & Zea, L. (2023). Biofilm formation of Pseudomonas aeruginosa in spaceflight is minimized on lubricant impregnated surfaces. *Npj Microgravity*, 9(1), 66. https://doi.org/10.1038/s41526-023-00316-w.

[23] Hoehler TM, Jørgensen BB. (2013) Microbial life under extreme energy limitation. *Nat Rev Microbiol*. 11(2):83-94. doi: 10.1038/nrmicro2939. PMID: 23321532.

[24] Huang KC, Mukhopadhyay R, Wen B, Gitai Z, Wingreen NS. (2008) Cell shape and cell-wall organization in Gram-negative bacteria. *Proc Natl Acad Sci U S A.* 9;105(49):19282-7. doi: 10.1073/pnas.0805309105. Epub 2008 Dec 2. PMID: 19050072; PMCID: PMC2592989.

[25] Jannasch HW, Mottl MJ. (1985) Geomicrobiology of deep-sea hydrothermal vents. *Science.* 23;229(4715):717-25. doi: 10.1126/science.229.4715.717. PMID: 17841485.

[26] John Conrad Jaeger, Neville G. W. Cook, Robert Zimmerman (2007). Structural geology (2nd ed.). ISBN: 978-0-632-05759-7. Wiley-Blackwell New York.

[27] Kaplan JB. (2010) Biofilm dispersal: mechanisms, clinical implications, and potential therapeutic uses. *J Dent Res.* 89(3):205-18. doi: 10.1177/0022034509359403. Epub 2010 Feb 5. PMID: 20139339; PMCID: PMC3318030.

[28] Kim W, Tengra FK, Young Z, Shong J, Marchand N, Chan HK, Pangule RC, Parra M, Dordick JS, Plawsky JL, Collins CH. (2013) Spaceflight promotes biofilm formation by *Pseudomonas aeruginosa*. *PLoS One.* 29;8(4):e62437. doi: 10.1371/journal.pone.0062437. PMID: 23658630; PMCID: PMC3639165.

[29] Klaus D, Simske S, Todd P, Stodieck L. (1997) Investigation of space flight effects on *Escherichia coli* and a proposed model of underlying physical mechanisms. Microbiology (Reading). 143 (Pt 2):449-455. doi: 10.1099/00221287-143-2-449. PMID: 9043122.

[30] Klaus DM, Howard HN. (2006) Antibiotic efficacy and microbial virulence during space flight. *Trends Biotechnol.* 24(3):131-6. doi: 10.1016/j.tibtech.2006.01.008. Epub 2006 Feb 7. PMID: 16460819.

[31] Koch AL. (1983) The surface stress theory of microbial morphogenesis. *Adv Microb Physiol* ;24:301-66. doi: 10.1016/s0065-2911(08)60388-4. PMID: 6364728.

[32] Lin LH, Wang PL, Rumble D, Lippmann-Pipke J, Boice E, Pratt LM, Sherwood Lollar B, Brodie EL, Hazen TC, Andersen GL, DeSantis TZ, Moser DP, Kershaw D, Onstott TC. (2006) Long-term sustainability of a high-energy, low-diversity crustal biome. *Science*. 20;314(5798):479-82. doi: 10.1126/science.1127376. PMID: 17053150.

[33] Merino N, Aronson HS, Bojanova DP, Feyhl-Buska J, Wong ML, Zhang S, Giovannelli D. (2019) Living at the Extremes: Extremophiles and the Limits of Life in a Planetary Context. *Front Microbiol*. 15; 10:780. doi: 10.3389/fmicb.2019.00780. Erratum in: Front Microbiol. 2019 Aug 13; 10:1785. doi: 10.3389/fmicb.2019.01785. PMID: 31037068; PMCID: PMC6476344.

[34] Michael T. Madigan, John M. Martinko, Kelly S. Bender, Daniel H. Buckley, David A. Stahl. (2021) Brock Biology of Microorganisms. Hoboken, NJ: Pearson Education ISBN 9780321649638 (student).

[35] Morris CE, Conen F, Alex Huffman J, Phillips V, Pöschl U, Sands DC. (2014) Bioprecipitation: a feedback cycle linking earth history, ecosystem dynamics and land use through biological ice nucleators in the atmosphere. *Glob Chang Biol*.;20(2):341-51. doi: 10.1111/gcb.12447. Epub 2013 Nov 26. PMID: 24399753.

[36] Nickerson CA, Ott CM, Mister SJ, Morrow BJ, Burns-Keliher L, Pierson DL (2000). Microgravity as a novel environmental signal affecting *Salmonella enterica serovar Typhimurium* virulence. *Infect Immun*.;68(6):3147-52. doi: 10.1128/IAI.68.6.3147-3152.2000. PMID: 10816456; PMCID: PMC97548.

[37] Nickerson CA, Ott CM, Wilson JW, Ramamurthy R, Pierson DL. (2004) Microbial responses to microgravity and other low-shear environments. *Microbiol Mol Biol Rev*.68(2):345-61. doi: 10.1128/MMBR.68.2.345-361.2004. PMID: 15187188; PMCID: PMC419922.

[38] Persat A, Nadell CD, Kim MK, Ingremeau F, Siryaporn A, Drescher K, Wingreen NS, Bassler BL, Gitai Z, Stone HA. (2015) The mechanical world of bacteria. *Cell.* 21;161(5):988-997. doi: 10.1016/j.cell.2015.05.005. PMID: 26000479; PMCID: PMC4451180.

[39] Philippot L, Raaijmakers JM, Lemanceau P, van der Putten WH. (2013) Going back to the roots: the microbial ecology of the rhizosphere. *Nat Rev Microbiol*. 11(11):789-99. doi: 10.1038/nrmicro3109. Epub 2013 Sep 23. PMID: 24056930.

[40] Price PB. (2007) Microbial life in glacial ice and implications for a cold origin of life. *FEMS Microbiol Ecol.* 59(2):217-31. doi: 10.1111/j.1574-6941.2006.00234. x. PMID: 17328118.

[41] Purcell EM. (1977). Life at low Reynolds number. *Am. J. Phys*. 45, 3–11. https://doi.org/10.1119/1.10903

[42] Rosenzweig JA, Ahmed S, Eunson J Jr, Chopra AK. (2014) Low-shear force associated with modeled microgravity and spaceflight does not similarly impact the virulence of notable bacterial pathogens. *Appl Microbiol Biotechnol*. 98(21):8797-807. doi: 10.1007/s00253-014-6025-8. Epub 2014 Aug 23. PMID: 25149449; PMCID: PMC4199916.

[43] Rothleitner, C. (2021) Ultra-weak gravitational field detected. *Nature*.; 591(7849): 209-210. doi: 10.1038/d41586-021-00591-1. PMID: 33692552.

[44] Smith DJ, Jaffe DA, Birmele MN, Griffin DW, Schuerger AC, Hee J, Roberts MS. (2012) Free tropospheric transport of microorganisms from Asia to North America. *Microb Ecol*. 64(4):973-85. doi: 10.1007/s00248-012-0088-9. Epub 2012 Jul 4. PMID: 22760734.

[45] Sreepadmanabh, M., Ganesh, M., Sanjenbam, P., Kurzthaler, C., Agashe, D., & Bhattacharjee, T. (2024). Cell shape affects bacterial colony growth under physical confinement. *Nature Communications*, 15(1), 9561. https://doi.org/10.1038/s41467-024-53989-6.

[46] Stetter KO. (1996) Hyperthermophiles in the history of life. *Ciba Found Symp.*;202:1-10; discussion 11-8. PMID: 9243007.

[47] Stewart, P. S., & Franklin, M. J. (2008). Physiological heterogeneity in biofilms. *Nature Reviews Microbiology*, 6(3), 199-210. https://doi.org/10.1038/nrmicro1838

[48] Stoodley P, Sauer K, Davies DG, Costerton JW. (2002) Biofilms as complex differentiated communities. *Annu Rev Microbiol.* 56:187-209. doi: 10.1146/annurev.micro.56.012302.160705. Epub 2002 Jan 30. PMID: 12142477.

[49] Takai, K., Nakamura, K., Toki, T., Tsunogai, U., Miyazaki, M., Miyazaki, J., Hirayama, H., Nakagawa, S., Nunoura, T., & Horikoshi, K. (2008). Cell proliferation at 122°C and isotopically heavy CH_4 production by a hyperthermophilic methanogen under high-pressure cultivation. *Proceedings of the National Academy of Sciences,* 105(31), 10949-10954. https://doi.org/10.1073/pnas.0712334105

[50] Turnbaugh PJ, Ley RE, Hamady M, Fraser-Liggett CM, Knight R, Gordon JI. (2007) The human microbiome project. *Nature.* 18;449(7164):804-10. doi: 10.1038/nature06244. PMID: 17943116; PMCID: PMC3709439.

[51] Vollmer W, Blanot D, de Pedro MA. (2008) Peptidoglycan structure and architecture. *FEMS Microbiol Rev.* 32(2):149-67. doi: 10.1111/j.1574-6976.2007.00094. x. Epub 2008 Jan 8. PMID: 18194336.

[52] Vollmer W, Blanot D, de Pedro MA. (2008) Peptidoglycan structure and architecture. *FEMS Microbiol Rev.* 32(2):149-67. doi: 10.1111/j.1574-6976.2007.00094. x. Epub 2008 Jan 8. PMID: 18194336.

[53] Walsby AE. (1994) Gas vesicles. *Microbiol Rev.* 58(1):94-144. doi: 10.1128/mr.58.1.94-144.1994. PMID: 8177173; PMCID: PMC372955.

[54] Whitman WB, Coleman DC, (1998) Wiebe WJ. Prokaryotes: the unseen majority. *Proc Natl Acad Sci U S A*. 9;95(12):6578-83. doi: 10.1073/pnas.95.12.6578. PMID: 9618454; PMCID: PMC33863.

[55] Wilson JW*, et al* (2007) Space flight alters bacterial gene expression and virulence and reveals a role for global regulator Hfq. *Proc Natl Acad Sci U S A.* 9;104(41):16299-304. doi: 10.1073/pnas.0707155104. Epub 2007 Sep 27. PMID: 17901201; PMCID: PMC2042201.

[56] Womack, A. M., Bohannan, B. J. M., & Green, J. L. (2010). Biodiversity and biogeography of the atmosphere. *Philos Trans R Soc Lond B Biol Sci* 365 (1558): 3645–3653. https://doi.org/10.1098/rstb.2010.

[57] Zea L, Larsen M, Estante F, Qvortrup K, Moeller R, Dias de Oliveira S, Stodieck L and Klaus D (2017) Phenotypic Changes Exhibited by E. coli Cultured in Space. *Front. Microbiol*. 8:1598. doi: 10.3389/fmicb.2017.01598

5. Authors short Biography

Dr. Iresh Ranjan Bhattacharjee (ORCID: 0000-0003-4599-4021) is an Indian scientist and independent theorist working on biophysical interpretations of biological systems. His research integrates intrinsic gravitation, thermodynamics, and fluid-mediated mechanics, culminating in the Grand Evolutionary Continuum of Mass (2025). His recent work focuses on embryogenesis as a gene-regulated, mechanically executed morphogenetic process among others.