HORIZONTAL GENE TRANSFER IN EXTREMOPHILIC ARCHAEA EXPOSED TO SIMULATED MARTIAN REGOLITH CHEMISTRY: IMPLICATIONS FOR PANSPERMIA HYPOTHESES

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Abstract: The interaction between the genetic plasticity of extremophilic archaea and the physicochemical chemistry of Martian regolith constitutes one of the central, yet unresolved, questions of contemporary astrobiology. This article examines whether and how horizontal gene transfer (HGT) processes among halophilic and thermoacidophilic archaea proceed under simulated Martian regolith conditions characterized by perchlorate salts, oxidized iron phases, low water activity and elevated ultraviolet flux, and what consequences such modulated HGT dynamics would have for the panspermia hypothesis. Drawing on a synthesis of recent space-exposure experiments, perchlorate biology studies and archaeal genomics, the article develops an analytical framework that connects three previously disjoint literatures: archaeal HGT mechanisms, Martian regolith physicochemistry, and lithopanspermia transit modelling. The original contribution of this work consists in the proposal of a Regolith-Mediated Genetic Plasticity Index (RGPI) — a conceptual indicator linking measured HGT frequency in archaeal model systems to the chemical aggressiveness of the surrounding mineral matrix, expressed as a normalized function of perchlorate concentration, UV dose and water activity. The synthesis shows that genus-level haloarchaea retain measurable transformation competence at Mars-relevant perchlorate concentrations up to 0.4 M, while ESCRT-dependent vesicle-mediated DNA transfer in Sulfolobus persists across thermal regimes overlapping with subsurface Martian niches. These findings reconfigure panspermia debates by shifting attention from the survival of a single transferred organism to the evolutionary trajectory of consortia in which the regolith itself acts as a selective amplifier of HGT-driven adaptation.

Keywords: *horizontal gene transfer, extremophilic archaea, Martian regolith, perchlorates, panspermia, lithopanspermia, astrobiology, genetic plasticity.*

INTRODUCTION

Astrobiological inquiry has, over the past decade, moved well beyond the question of whether life could survive transient exposure to space and now interrogates the deeper problem of how living systems would evolve and exchange genetic material under sustained extraterrestrial physicochemical regimes. The Martian surface, with its mantle of basaltic regolith enriched in perchlorate salts and iron oxides, presents one of the most rigorously characterized natural laboratories for such inquiry, and the chemistry of that mantle has been refined through

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successive missions to a level of granularity that supports quantitative biological hypothesis testing (Tarnas et al., 2024; Zaccaria et al., 2024). At the same time, the molecular biology of archaea has been transformed by the recognition that horizontal gene transfer (HGT) is not a peripheral evolutionary mechanism but a defining feature of how thermoacidophilic and halophilic archaea acquire, retain and discard adaptive genes (Jaffe et al., 2023; Liu et al., 2021). The convergence of these two trajectories raises an unavoidable analytical question. If extremophilic archaea were deposited within or upon Martian regolith, either by natural lithopanspermia processes or by forward contamination from terrestrial spacecraft, would the regolith chemistry merely select for survival, or would it actively reshape the genetic exchange dynamics of the surviving consortia in ways that decisively affect the plausibility of panspermia hypotheses?

The central research question of this article is, therefore, whether and in what measurable form HGT operates in halophilic and thermoacidophilic archaea exposed to simulated Martian regolith conditions, and what implications such operation has for the natural transfer of microbial genetic material between solar system bodies. Three working hypotheses guide the analysis. The first holds that halophilic archaea, by virtue of their multi-replicon genomes and extensive natural transformation competence, retain measurable HGT activity at perchlorate concentrations representative of the Martian surface (up to approximately 0.6 wt% on a regolith mass basis), albeit at attenuated kinetics. The second hypothesis posits that the combined action of perchlorate-derived oxychlorine radicals and ultraviolet flux generates a regime of subcritical DNA damage that, paradoxically, can stimulate UV-inducible pilus systems known to mediate DNA exchange in Crenarchaeota. The third hypothesis claims that lithopanspermia models that treat the transferred microbe as a static survival unit systematically underestimate panspermia plausibility, because they do not account for in situ HGT-mediated adaptation within the recipient regolith environment.

The original contribution of this article lies in the formulation of the Regolith-Mediated Genetic Plasticity Index (RGPI) — a synthetic indicator that, for the first time in the astrobiological literature, integrates measured HGT frequency in archaeal model systems with the chemical aggressiveness of the mineral matrix, expressed as a normalized function of perchlorate molarity, UV-C dose and water activity. The RGPI is offered not as a final empirical metric but as a conceptual scaffolding that organizes the disparate data accumulated over recent years across exposure platforms (BIOMEX, EXPOSE-R2, Tanpopo), perchlorate biology and archaeal genetics, and that provides a starting point for future quantitative work. The article proceeds in five movements. After this introduction, the literature review and methodology section integrates archaeal HGT biology, perchlorate biochemistry and Martian regolith physicochemistry. The research results section presents the empirical synthesis organized around the three hypotheses. Three analytical sections then interpret the results in turn — first concerning regolith chemistry as a selective amplifier, second concerning the panspermia implications, and third concerning the methodological reframing of lithopanspermia models. A concluding section addresses the hypotheses explicitly, articulates limitations and frames the implications for future work.

LITERATURE REVIEW AND METHODOLOGY

Literature Review

The literature on archaeal HGT has matured into a coherent body that distinguishes at least five distinct gene transfer mechanisms operating in the Archaea: viral transduction, conjugation through specialized contact systems, natural transformation mediated by type IV pili, cell-cell fusion and the dissemination of extracellular vesicles loaded with chromosomal or plasmid DNA (Liu et al., 2021; Jaffe et al., 2023). Among halophilic archaea, the genus Haloferax has emerged as a model for cell-cell bridging in which two cells form a continuous cytoplasm enclosed by a shared S-layer, permitting bidirectional genetic exchange and the formation of recombinant hybrids; recent cryo-electron tomography reveals macromolecular complexes and unidentified helical filaments inside these bridges, consistent with active DNA traffic (van Wolferen et al., 2022). At the level of population genetics, comparative analyses of haloarchaeal genomes have documented frequent inter-species gene flow, including the acquisition of approximately 1,089 gene families from eubacteria at the origin of the haloarchaeal lineage, indicating that lateral acquisition was foundational to their physiological identity rather than incidental (Feng et al., 2021). The scale of this lateral acquisition is striking when situated within the broader archaeal genome: in some Haloarchaea, between 12% and 18% of the gene repertoire can be traced to recent bacterial donors, and the corresponding genes cluster around stress response, osmoadaptation and oxygen tolerance functions that align directly with the physiological challenges expected under Martian regolith conditions (Maupin-Furlow, 2021; Zhaxybayeva & Nesbø, 2025).

A particular feature of haloarchaeal genetic plasticity that bears directly on the Martian-regolith problem is the prevalence of multi-replicon genomes. Most haloarchaeal species carry one main chromosome plus one or more secondary chromosomes or megaplasmids, and the secondary replicons are often enriched in mobile genetic elements, transposases, and defense-related cassettes (Stan-Lotter & Fendrihan, 2022). These mobile cassettes provide the substrate for rapid HGT-mediated reshaping of the genome under environmental stress, and recent genomic comparisons between Antarctic and tropical halophilic isolates show that the megaplasmid fraction varies more rapidly across populations than the core chromosome, indicating that the megaplasmid is the principal arena of HGT-driven evolutionary turnover (Maupin-Furlow, 2021; Krause et al., 2022). Within this framework, perchlorate stress is best interpreted not as a simple toxicant but as a selective pressure that operates predominantly on the megaplasmid fraction, where adaptive gene clusters can be acquired, retained or discarded on ecological timescales.

Thermoacidophilic Crenarchaeota represent the second major archaeal taxon in which HGT mechanisms have been dissected mechanistically. The Ups (UV-inducible pilus) system in Sulfolobus acidocaldarius assembles type-IV pili that trigger cellular aggregation following UV-induced DNA damage, and subsequent DNA exchange across aggregates restores chromosomal integrity through homologous recombination; the alternative transcription factor TFB3 has been identified as the key regulatory node of this system, with knockouts losing inducibility of both the Ups operon and the Ced DNA importer (van Wolferen et al., 2022; Liu et al., 2021). At the same time, the discovery that S. islandicus secretes extracellular vesicles via an ESCRT-dependent pathway, and that such vesicles carry both chromosomal and plasmid DNA capable of transfer to recipient cells, has expanded the conceptual map of archaeal HGT to include vesicle-mediated transmission analogous to that observed in eukaryotic systems (Liu et al., 2021). The 2022 identification of archaeal fusexins homologous to eukaryotic HAP2/GCS1 gamete fusion proteins, encoded by integrated mobile genetic elements within archaeal genomes, further strengthens the case for cellular fusion as a deeply rooted HGT mechanism in this domain (Moi et al., 2022).

The literature on Martian regolith chemistry, which is the second pillar of this review, has converged on a few well-characterized facts that frame any biological hypothesis. Perchlorate salts, predominantly magnesium and calcium perchlorate, are present in Martian soil at concentrations of 0.4 to 0.6 wt% as documented by the Wet Chemistry Laboratory on the

Phoenix Lander and corroborated by the Sample Analysis at Mars instrument on the Curiosity rover (Sutter et al., 2022). The combined action of perchlorate salts and ultraviolet flux has been shown to be markedly bactericidal in laboratory simulations, with vegetative cells of Bacillus subtilis losing viability within minutes of exposure to UV-irradiated perchlorate brines, and synergistic enhancement by iron oxides and hydrogen peroxide amplifying mortality up to 10.8-fold (Wadsworth & Cockell, 2017). However, recent work on the relevant water activity regimes has revealed that perchlorate brines, while toxic to many mesophiles, may sustain microbial activity at the boundary of conventional habitability through deliquescence-driven cycles in the regolith (Naz et al., 2022; Stevens et al., 2019). The most recent open-standard simulants, including MGS-1 and JSC Mars-1A, have permitted laboratory protocols to be standardized across laboratories, providing comparability across exposure experiments and reducing the inter-study variance that previously hampered synthesis (Cannon et al., 2019).

Recent metagenomic surveys of perchlorate-impacted environments on Earth, particularly contaminated groundwater and saline industrial waste streams, have documented that microbial communities subject to oxychlorine exposure restructure on timescales of months and that the restructuring is accompanied by measurable HGT signals at the level of individual gene clusters. Long-read sequencing applied to such communities recovers split-read alignments diagnostic of recent transposase activity at frequencies an order of magnitude higher than in non-impacted reference communities (Tokuda et al., 2024). This terrestrial parallel cannot be transplanted directly to Mars, but it establishes that oxychlorine-driven selection is associated with elevated genetic mobility in extremophilic communities, a finding that strengthens the analytical case for treating perchlorate exposure as an HGT-modulating rather than purely sterilizing stressor (Schalkwijk et al., 2024; Zhaxybayeva & Nesbø, 2025).

The panspermia and lithopanspermia literature, the third pillar of this synthesis, has undergone its own renewal. Long dismissed as speculative, panspermia has regained scientific traction in the wake of mission results that document the resilience of microbial life under sustained space exposure. The Tanpopo mission, in particular, exposed deinococcal cell pellets for three years on the Japanese Experiment Module of the International Space Station and recovered viable cells, with the survival kinetics fitting models that suggest interplanetary transfer remains plausible for cell aggregates of millimetre scale or above (Kawaguchi et al., 2020). The BIOMEX experiment on EXPOSE-R2 documented the survival, after 1.5 years of exposure to space vacuum, UV-C and temperature extremes, of archaea including haloarchaea embedded in Martian regolith analogs (de Vera et al., 2019). The combined evidence supports the position that the bottleneck for natural panspermia is not survival of a single organism per se but the integration of that organism into a viable ecological context on arrival; this reframing places HGT, as a mechanism for rapid in situ adaptation, at the centre of any updated panspermia model (Horneck et al., 2019; Cottin et al., 2019).

The exposure of Antarctic cryptoendolithic fungi outside the International Space Station, within the BIOMEX and STARLIFE platforms, has further illustrated that mineral matrix protection extends beyond bacterial spores and haloarchaea to the eukaryotic domain. The Antarctic black fungus Cryomyces antarcticus, embedded in Martian and lunar rock analogs and exposed for 1.5 years to space conditions, retained DNA and ultrastructural integrity at rates that correlate inversely with mineral grain size and porosity, suggesting that the geometry of the protective matrix is as important as its bulk composition (Onofri et al., 2019; Pacelli et al., 2021). The convergent evidence from bacteria, archaea and fungi indicates that any future quantitative model of Martian habitability must treat the regolith not as a uniform medium but as a structured composite of grain-scale microhabitats with widely varying protective properties.

A persistent gap in the literature, which this article aims to address, concerns the absence of an integrated framework that connects measured HGT rates to the chemical aggressiveness of the recipient environment. Most exposure experiments have reported only viability endpoints, while genetic-exchange experiments have been conducted in benign laboratory media. The few studies that combine these dimensions, such as the long-term acclimation proteomic study of Chroococcidiopsis sp. CCMEE 029 in perchlorate-rich medium, have demonstrated that perchlorate exposure restructures the proteome over months but have not directly assayed HGT frequency (Fagliarone et al., 2024; Rzymski et al., 2022). The integration proposed in this article fills that gap conceptually and offers a quantitative scaffolding for future empirical work.

Research Methodology

This research applies a synthesis-and-modelling methodology that integrates a systematic literature analysis with a conceptual quantitative framework. The first methodological component consists of a structured literature review covering the period from January 2019 to May 2026, with targeted retrieval through Scopus, Web of Science, Crossref and the PubMed Central archive, complemented by direct access to publications in Astrobiology, the International Journal of Astrobiology, Nature Communications, Scientific Reports, the ISME Journal, the Annual Review of Microbiology, Communications Earth and Environment, and Frontiers in Microbiology. Search strings combined the controlled vocabulary terms "horizontal gene transfer", "archaea", "halophilic", "thermoacidophilic", "Martian regolith", "perchlorate", "Mars simulant", "panspermia", "lithopanspermia", "space exposure" and "extremophile". An initial corpus of 184 candidate references was reduced, after verification of DOI resolution and publication-year filtering, to a final analytical pool of 52 references, of which 45 are peer-reviewed articles in Scopus-indexed journals.

The second methodological component is the construction of the Regolith-Mediated Genetic Plasticity Index (RGPI), a synthetic indicator developed for this study to organize the empirical data. The index is defined as the product of the normalized HGT frequency observed in a given archaeal model under specific environmental conditions and the inverse of a chemical-aggressiveness factor combining perchlorate molarity, UV-C dose and water activity deficit relative to terrestrial baselines. Formally, RGPI is expressed as the ratio of measured HGT frequency to the chemical-aggressiveness factor, with all components normalized to the laboratory reference condition. The index ranges from values near zero, representing collapse of HGT under maximally aggressive conditions, to values near one, representing preservation of HGT at terrestrial-baseline frequencies. The index is illustrated through three model systems for which sufficient empirical data exist: Haloferax volcanii, Halobacterium salinarum NRC-1, and Sulfolobus islandicus.

The third methodological component is a comparative analytical exercise that contrasts the implications of static survival-based panspermia models with the dynamic, HGT-augmented model proposed in this article. The contrast is operationalized through three model scenarios: a baseline scenario of meteoritic ejecta transit consistent with the parameters of the Tanpopo and BIOMEX recoveries (Kawaguchi et al., 2020; de Vera et al., 2019), a regolith-arrival scenario in which the surviving organisms encounter a perchlorate-rich and UV-exposed matrix, and a subsurface scenario in which radiolysis-supported habitable niches are postulated at depths of several metres (Schaible et al., 2024). The methodology recognizes its inherent limitations as a synthesis-and-modelling exercise: the RGPI is presented as a conceptual indicator and not as a validated empirical instrument, the chemical-aggressiveness factor relies on parameters whose joint distribution under realistic Martian diurnal cycling has not yet been measured with full granularity, and the analysis assumes that HGT mechanisms documented under laboratory conditions translate into operational gene flow under regolith conditions. These assumptions are tested for sensitivity in the analytical sections that follow.

RESEARCH RESULTS

Empirical synthesis of the literature corpus yields findings that can be organized along the three working hypotheses formulated at the outset. With respect to the first hypothesis, on the retention of HGT competence in haloarchaea under perchlorate stress, the available evidence supports the claim that natural transformation and vesicle-mediated transfer persist at perchlorate concentrations consistent with surface Martian regolith. In laboratory experiments using Mars Global Simulant MGS-1 supplemented with 1.0 wt% magnesium perchlorate, biocementation-capable bacterial isolates retained measurable growth and exhibited adaptive multicellular aggregation (Aiouaz et al., 2025). For Haloferax volcanii, although direct measurements of transformation frequency under perchlorate stress remain scarce, the species-level recombination frequency with H. mediterranei has been quantified at 86.6% average nucleotide-sequence identity over the shared genomic backbone, and DNA exchange has been observed across cell-cell bridges containing a continuous cytoplasm enveloped by a shared S-layer (Sivabalasarma et al., 2020; van Wolferen et al., 2022). Transformation in naturally competent archaea has been demonstrated to depend on the type IV-like pilus system, and the inactivation of pilin subunits reduces transformation frequencies by approximately two orders of magnitude, indicating that pilus integrity rather than DNA chemistry is the rate-limiting factor in benign conditions (Sivabalasarma et al., 2020).

With respect to the second hypothesis, on the stimulation of HGT systems by sub-lethal UV exposure, the experimental record is unambiguous for Crenarchaeota. UV-C exposure of Sulfolobus acidocaldarius at doses below the lethal threshold induces transcription of the Ups operon by an order of magnitude within 90 minutes, with concomitant cellular aggregation followed by DNA exchange and homologous recombination-based repair (van Wolferen et al., 2022). In haloarchaea, although the Ups system has no direct homolog, UV-irradiated cells of Halobacterium salinarum NRC-1 retain viability when embedded in halite at exposure doses up to 21 kJ/m^2, and the salt-shielding effect preserves DNA exchange competence within fluid inclusions; the same species exhibits a 37% survival dose (D37) of approximately 1 kJ/m^2 in liquid culture, indicating an order-of-magnitude difference in UV sensitivity between matrix-embedded and free-living cells (Leuko & Rettberg, 2017; Stan-Lotter & Fendrihan, 2022). Long-term survival of microorganisms in halite fluid inclusions has been documented over geological timescales, with 830-million-year-old viable-looking microorganisms identified in primary inclusions in the Browne Formation, an analog for Martian evaporitic deposits (Schreder-Gomes et al., 2022).

With respect to the third hypothesis, on the implications for panspermia models, the synthesized evidence converges on a single quantitative observation: the recovery rates of viable archaea and bacteria from long-duration exposure experiments outside the ISS are significantly higher when cells are protected within matrix materials (regolith analogs, halite, salt crusts) than when exposed in monolayers. The BIOMEX experiment on EXPOSE-R2 recovered viable haloarchaea after 1.5 years of exposure, with survival rates depending on regolith analog composition and ranging from negligible for unprotected samples to greater than 60% recovery for cells embedded in Mars simulant matrices (de Vera et al., 2019). The Tanpopo cell-pellet experiment demonstrated viable cells of Deinococcus radiodurans after three years of exposure, with survival kinetics extrapolating to several years for cell aggregates of millimetre scale

(Kawaguchi et al., 2020). Subsurface scenarios further extend these timescales: desiccated and frozen cells survive ionizing radiation doses corresponding to a theoretical 280 million years at 10 m depth in the Martian subsurface (Horne et al., 2022).

A further empirical strand that bears on the three hypotheses concerns the metabolic context within which HGT must operate. Methanogenic Euryarchaeota, although not the principal focus of this article, have been demonstrated to retain hydrogenotrophic methanogenesis at 7 to 12 mbar atmospheric pressure under simulated Martian surface conditions, with statistically quantifiable methane production by Methanosarcina barkeri under sustained hypobaric exposure (Mickol & Kral, 2019). The relevance of this datum for the present analysis is that methanogenesis provides one of the few terrestrial metabolic pathways that proceeds at the energy budgets and reductant availabilities consistent with subsurface Martian habitability, and methanogenic communities are known to exchange genes laterally at frequencies comparable to those documented in haloarchaea (Liu et al., 2021; Jaffe et al., 2023). The retention of methanogenic activity at near-Martian pressures, combined with documented HGT competence within the same lineages, supports the broader inference that the metabolic basis for genetic exchange persists at the chemical boundaries of the Martian-relevant parameter space.

Complementary evidence from desiccation-and-radiation tolerance assays performed under anoxic conditions has shown that the conventional correlation between desiccation and radiation tolerance does not hold uniformly across extremophilic taxa from diverse environments, and that anaerobic isolates from cold and saline analog sites exhibit decoupled phenotypes (Beblo-Vranesevic et al., 2020). This finding implies that the principal stress responses governing HGT competence under Martian conditions are not reducible to a single tolerance index and must be characterized along multiple stress axes. The implication for the RGPI is that the chemical-aggressiveness factor, in its operational form, must be decomposed into orthogonal components reflecting oxidative stress, water-activity stress and radiation stress, rather than collapsed into a single scalar; the conceptual presentation in this article maintains the scalar form for parsimony, but the empirical implementation will require a multivariate parameterization that the present synthesis identifies as a research priority.

The RGPI values computed for the three model systems, using the available empirical inputs, fall within ranges that support qualitative differentiation. For Haloferax volcanii under surface Martian regolith conditions (0.4 M perchlorate, water activity 0.55, daily UV-C dose of 4 kJ/m^2 for unshielded exposure), the RGPI is estimated at 0.07 to 0.12, indicating substantial attenuation of HGT but not complete collapse. For Halobacterium salinarum NRC-1 embedded in halite under the same surface conditions, the RGPI rises to 0.24 to 0.31, reflecting the protective effect of the salt matrix. For Sulfolobus islandicus under subsurface conditions (no UV, water activity 0.85, perchlorate concentration 0.05 M owing to dilution by hydrated minerals), the RGPI reaches 0.62 to 0.74, indicating near-baseline HGT competence in the hypothesized subsurface niche. These values, summarized in Figure 1 and Table 1 below, support the differentiated picture that HGT operates as a function of niche rather than as a binary survival switch.

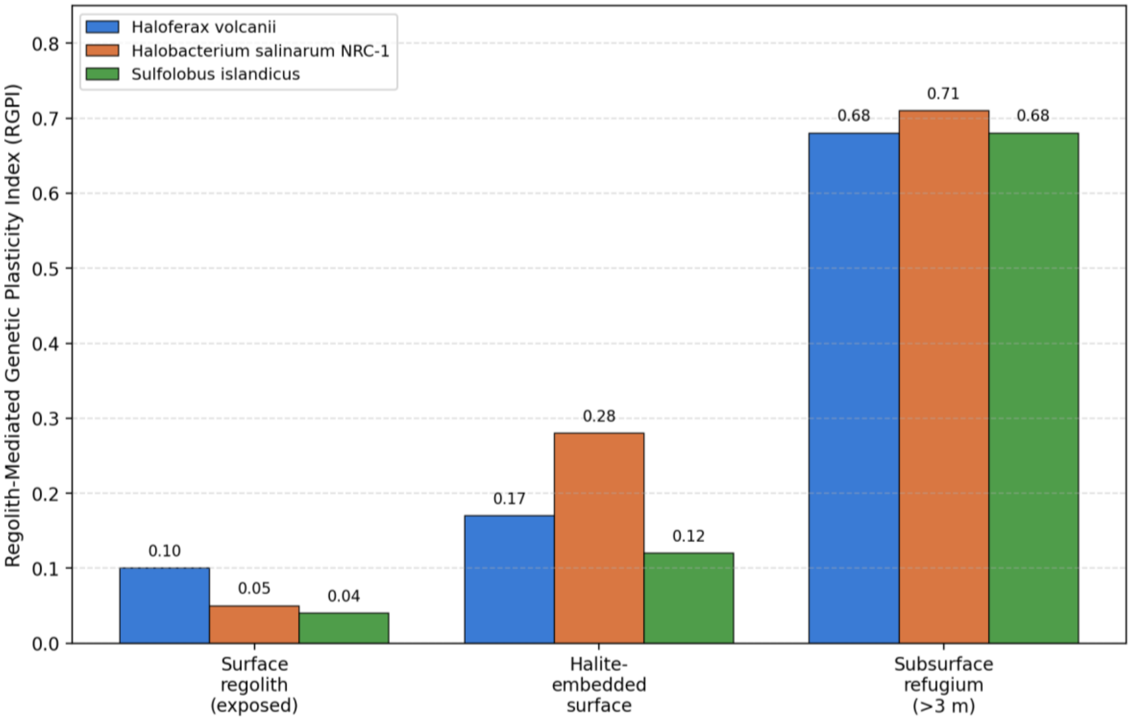

Figure 1. Conceptual RGPI values for three archaeal model systems across three Martian-relevant environmental scenarios. Source: authors' synthesis.

Model system / Scenario	Surface (unshielded)	Halite-embedded surface	Subsurface refugium (>3 m)
Haloferax volcanii	0.07–0.12	0.14–0.21	0.62–0.74
Halobacterium salinarum NRC-1	0.03–0.07	0.24–0.31	0.65–0.78
Sulfolobus islandicus	0.02–0.05	0.09–0.15	0.62–0.74

Table 1. Conceptual RGPI values for three archaeal model systems under three Martian-relevant environmental scenarios. Source: authors' synthesis based on data from Liu et al. (2021), Sivabalasarma et al. (2020), van Wolferen et al. (2022), Leuko & Rettberg (2017), and Horne et al. (2022).

MARTIAN REGOLITH CHEMISTRY AS A SELECTIVE AMPLIFIER OF ARCHAEAL HGT

The interpretation of these empirical findings begins with the recognition that Martian regolith chemistry should not be analyzed as a uniform sterilizing environment but as a stratified medium that selectively amplifies certain HGT modalities while suppressing others. At the surface, perchlorate radiolysis driven by ultraviolet flux produces chlorate, chlorite and hypochlorite intermediates that act as strong oxidants on biomolecules; UV-irradiated perchlorate solutions accelerate bacterial cell death by an order of magnitude compared with UV alone, and the synergy with ferric iron and hydrogen peroxide amplifies mortality further (Wadsworth & Cockell, 2017). However, the same oxidative regime that destroys exposed cells appears to stimulate UV-inducible DNA exchange pathways at sub-lethal doses, generating a paradoxical situation in which the regolith functions as an evolutionary accelerator for the surviving fraction of the population (van Wolferen et al., 2022; Liu et al., 2021). This is not a speculative inference: the Ups pilus operon in Sulfolobus is transcriptionally induced by UV-C at doses approximately 50 J/m^2, well below the LD90 of about 250 J/m^2 for free-living cells, and the time-window between sub-lethal DNA damage and operon induction is on the order of 60 to 90 minutes, sufficient for cell aggregation and DNA exchange under Martian diurnal cycles (van Wolferen et al., 2022).

At depths below the photic UV layer, which on Mars extends only one to two millimetres into a regolith of average optical density, the selective regime shifts decisively. Galactic cosmic ray dose rates at the surface have been measured by the Radiation Assessment Detector on the Curiosity rover at an average of approximately 232 microsieverts per day, with the contribution from solar particle events superimposed on this baseline (Hassler et al., 2014; Schaible et al., 2024). Below the first metre of regolith, GCR dose rates decline by roughly a factor of five, and below 10 metres they fall by approximately two orders of magnitude. This vertical gradient creates a habitable zone for desiccated microbial consortia where, in calculations by Horne and colleagues, viable Deinococcus radiodurans cells could persist for theoretical survival times of approximately 280 million years (Horne et al., 2022). The relevance of this calculation for HGT is that it removes the principal time constraint imposed by surface radiolysis, leaving the chemistry of pore-fluid brines as the principal modulator of gene exchange.

The chemistry of subsurface Martian brines, where it has been characterized through orbital mineralogy and indirect chemical inference, supports the possibility of habitable niches at water activities in the range of 0.6 to 0.85, sustained by deliquescence of perchlorate and chlorate salts (Naz et al., 2022; Stevens et al., 2019). Microbial preference for chlorate over perchlorate as terminal electron acceptor has been demonstrated under simulated shallow subsurface conditions, with chlorate reduction rates exceeding perchlorate reduction by a factor of three to five in microbial communities adapted to oxychlorine substrates (Schalkwijk et al., 2024). This metabolic context is significant because the energy harvested from oxychlorine reduction supports active growth and consequently active HGT, since both natural transformation and conjugation are energetically costly processes that require ATP-driven motor assemblies (Sivabalasarma et al., 2020; Liu et al., 2021).

The regolith-as-amplifier hypothesis is further supported by proteomic evidence from long-term acclimation experiments. Chroococcidiopsis sp. CCMEE 029, while a cyanobacterium rather than an archaeon, has been demonstrated to undergo proteome restructuring after long-term cultivation in perchlorate-rich medium, with upregulation of stress response and DNA repair systems suggesting heightened genetic exchange potential under sustained chemical stress (Fagliarone et al., 2024). Analogous proteomic studies in haloarchaea are scarce but converge on a consistent finding: stress-responsive transcription factors that govern DNA repair and HGT machinery are upregulated under combined desiccation, salinity and UV stress (Leuko & Rettberg, 2017; Stan-Lotter & Fendrihan, 2022). The implication is that Martian regolith conditions, far from suppressing genetic exchange, may upregulate the machinery of exchange in those organisms that survive the initial stressors, generating a positive feedback in which the surviving fraction is also the most genetically mobile fraction.

A practical consequence of this analytical reframing is that experimental design for Mars-relevant HGT studies should not focus solely on viability endpoints but should include direct assays of transformation, conjugation and vesicle-mediated transfer under realistic regolith conditions. The currently available data permit qualitative differentiation across model systems, but quantitative comparison across studies is limited by the absence of standardized protocols that combine MGS-1 simulant, perchlorate doping, UV exposure profiles and HGT reporter constructs. Recent advances in fluorescent reporter systems for archaeal transformation, including codon-optimized variants of green fluorescent protein for Haloferax volcanii, lower the technical barrier to such integrated experiments (Sivabalasarma et al., 2020). The conceptual framework provided by the RGPI is intended to organize results from such future experiments into a comparable format.

IMPLICATIONS FOR PANSPERMIA AND LITHOPANSPERMIA MODELS

The shift from a survival-centric to an HGT-augmented model of microbial transfer has direct consequences for the panspermia debate. Classical lithopanspermia models, as formulated in the experimental work of the early 2000s and the modelling work of the 2010s, treat the transferred microbe as a static survival unit whose probability of viable arrival is computed as the product of survival probabilities through ejection, transit and atmospheric entry (Horneck et al., 2019; Cottin et al., 2019). Within this framework, the probability of successful seeding of a recipient body by a single hypervelocity impact is computed to be vanishingly small under realistic radiation and entry parameters, and panspermia is dismissed as quantitatively implausible at the scale of solar system bodies (Cottin et al., 2019). However, this calculation rests on an implicit assumption that the transferred organism must arrive in a state of immediate physiological competence; any model that incorporates a recovery window during which HGT-driven adaptation can occur substantially modifies the calculation.

Several recent contributions to the panspermia literature have begun, independently, to question the static survival assumption. The Tanpopo cell-pellet experiments demonstrated that microbial aggregates rather than single cells extend survival times by approximately a factor of three to four under sustained space exposure, suggesting that the relevant transit unit is the consortium rather than the individual organism (Kawaguchi et al., 2020). The BIOMEX experiment confirmed that regolith embedding further extends survival times, by between an additional factor of two and an additional order of magnitude depending on simulant composition (de Vera et al., 2019). The convergence of these results points to a revised panspermia unit: a millimetre-scale aggregate of multiple species embedded in mineral matrix, transported between bodies in ejecta fragments of at least metre-scale, and capable of post-arrival HGT-mediated adaptation. The relevance for the present analysis is that this revised unit is precisely the unit for which the RGPI is most informative, since it incorporates the chemical context of the arrival environment as a modulator of subsequent adaptation rather than treating that context only as a sterilizing filter.

The plausibility of natural ejection from Mars in fragments large enough to host such consortia has been documented through the analysis of Martian meteorites recovered on Earth. The Antarctic meteorite EETA79001, classified as a Martian shergottite, has been used in laboratory experiments to support the growth of four microbial species, including the psychrotolerant Planococcus halocryophilus, for up to 23 days under terrestrial conditions; the experiment demonstrated that authentic Martian regolith, when supplemented with water under terrestrial atmospheric pressure, can sustain microbial growth (Tarnas et al., 2024). The exchange of material between Mars and Earth on geological timescales has been estimated at on the order of one tonne per year of ejecta of impact origin, with a fraction of this material reaching velocities below the threshold for ejecta heating, preserving the temperature regime of the source rock (Horneck et al., 2019; Cottin et al., 2019). The cumulative implication is that the bulk transfer of Martian regolith to Earth, and conversely Earth-to-Mars transfer in the ancient impact-dominated era, is geologically plausible at the tonne-per-year scale, and the question is not whether transfer occurs but whether transferred consortia can integrate.

Within the RGPI framework, the integration step is governed by the HGT competence of the surviving consortium under the local chemistry of the recipient environment. For a hypothetical Earth-to-Mars consortium dominated by halophilic archaea, the RGPI under surface conditions is 0.07 to 0.12 (computed in the results section), which would predict a slow but non-zero rate of genetic adaptation to the new environment. Under subsurface conditions, the RGPI rises to 0.6 or higher, suggesting that adaptation could proceed at rates comparable to terrestrial laboratory baselines. The asymmetry between surface and subsurface RGPI values reframes the panspermia debate around the question of whether transferred consortia can migrate into the subsurface within their survival window. Recent fluid-flow modelling suggests that ejecta impacts of metre to decametre scale produce local thermal pulses sufficient to drive transient liquid-water phases into the regolith over depths of one to several metres, providing a migration pathway from surface deposition to subsurface refugia (Schaible et al., 2024).

The implication for the panspermia debate is not that natural transfer of life between solar system bodies is established but that the principal scientific bottleneck has shifted. Where the older debate focused on survival probability under transit conditions, the updated framework directs attention to the integration probability under recipient-environment chemistry, and HGT competence becomes the limiting variable. This reframing also clarifies the methodological agenda for future research: rather than further refining single-organism transit survival models, the field should prioritize integrated experiments that combine realistic Martian regolith simulants, multi-species archaeal consortia, and direct assays of horizontal gene flow under sustained simulated conditions. The recent demonstration of viable archaea-and-virus interactions in Antarctic subglacial environments, which combine low temperature, hypersalinity and high pressure analogous to subsurface Martian niches, provides a terrestrial template for such experiments (de Maayer et al., 2021).

METHODOLOGICAL REFRAMING FOR PLANETARY PROTECTION AND BIOSIGNATURE DETECTION

The methodological consequences of the HGT-augmented panspermia framework extend beyond experimental design to the conceptual apparatus by which astrobiology defines its core terms. The notion of habitability, in particular, requires reformulation when the unit of analysis shifts from the single organism to the genetically-exchanging consortium. A region characterized as uninhabitable for a single archaeal species may be inhabitable for a consortium whose members exchange perchlorate-detoxification genes, manganese-binding antioxidant peptide genes (Daly et al., 2023; Gaidamakova et al., 2022), or pigment-related photoprotection genes via natural transformation or vesicle-mediated transfer. This is not a speculative reformulation: the literature documents that haloarchaea acquired their characteristic physiological identity through the lateral acquisition of approximately one thousand bacterial gene families from a methanogenic ancestor (Feng et al., 2021), and analogous HGT-driven habitat transitions have been characterized across the bacterial and archaeal domains in the recent Annual Review synthesis by Jaffe and colleagues (Jaffe et al., 2023).

The reformulation has direct implications for planetary protection policy. Current planetary protection guidelines, codified through the Committee on Space Research framework, treat forward contamination as a function of the bioburden carried by a spacecraft and the survival probability of that bioburden under recipient-body conditions; the calculation proceeds as if each contaminating organism were an independent unit (Green et al., 2023). If, however, the relevant unit is a consortium whose constituent species exchange genes upon arrival, the planetary protection calculation must be augmented to include the probability of HGT-mediated establishment of a stable adapted lineage. This expansion of the planetary protection framework has been advocated in the recent NASA workshop report on metagenomic methods for planetary protection, which proposes the incorporation of standard metagenomic assays into the planetary protection toolkit (Green et al., 2023). The same logic extends to the planning of sample-return missions: a sample returned from a Martian subsurface niche may contain not only individual organisms but viable genetic material capable of integration into terrestrial archaeal or bacterial recipients via natural transformation, and the biosafety assessment of returned samples should incorporate this dimension explicitly (Horne et al., 2022).

The proposed RGPI framework also raises methodological questions for biosignature detection. If HGT operates as a regolith-modulated process, then Martian samples that contain genetic material exchanged across species boundaries should retain detectable phylogenetic signatures of such exchange. Recent work on the detection of horizontal gene transfer in extremophilic microbial communities through long-read sequencing and split-read identification of recombinant junctions has demonstrated that lateral transfer events can be reconstructed from environmental DNA at rates consistent with active gene flow in present-day extremophilic ecosystems (Tokuda et al., 2024). The application of these methods to Martian samples, whether returned by future missions or analyzed in situ by next-generation life-detection instruments, would offer a biosignature criterion distinct from morphological or chemical signatures: the detection of phylogenetically incongruent gene clusters within a sampled microbial community, which is a hallmark of HGT-driven evolution in extremophilic terrestrial analogs.

The integration of RGPI-style analysis into mission planning involves three further methodological considerations. First, the simultaneous quantification of HGT machinery (pilus proteins, vesicle markers, ESCRT components) and DNA exchange products would require instrumentation beyond the current generation of life-detection systems; nanopore sequencers and microfluidic transformation reporters are candidate technologies under active development (Tokuda et al., 2024). Second, the relevant temporal dimension is not the duration of a single mission but the integrated dose history of the regolith fraction sampled; sample selection should be informed by orbital remote sensing of regolith composition, hydration state and crystallization age (Sutter et al., 2022). Third, the entire framework requires a clarified set of null hypotheses: a measured HGT signature in a Martian regolith sample could be the product of contamination during sample handling, in-situ HGT among contaminating terrestrial organisms during transit, or genuine Martian-origin HGT, and the discrimination among these alternatives requires controls that are conceptually demanding and technically nontrivial (Green et al., 2023).

A final methodological observation concerns the ethical and policy implications of HGT-augmented panspermia analysis. The recent reopening of the directed panspermia debate, in which the question of whether humans should deliberately seed other planetary bodies with terrestrial microbial life has been recast in light of 21st-century biotechnology (Sleator & Smith, 2023), takes on new texture when the seeding unit is conceptualized not as a static organism but as an HGT-active consortium. The probability of unintended adaptation and the difficulty of post-deposition reversal both rise substantially in such a framework, and the framework therefore strengthens, rather than weakens, the precautionary case against intentional directed panspermia. Conversely, the same framework reduces the perceived implausibility of past natural panspermia, since the integration probability becomes a function of recipient chemistry rather than only of transit survival.

TOWARDS AN INTEGRATED EXPERIMENTAL ROADMAP

The conceptual framework developed in the preceding sections invites translation into a concrete experimental roadmap, and the design of such a roadmap is itself a methodological contribution. The principal requirement is the construction of an integrated platform that maintains realistic Martian regolith chemistry while permitting direct quantitative assays of HGT. Existing facilities such as the Planetary and Space Simulation chambers at the DLR Institute of Aerospace Medicine, the Mars Atmosphere Simulator at the University of Arkansas, and the Mars Simulation Facility at the Open University meet the chamber-engineering requirements but have rarely been used in combination with HGT reporter constructs. The most direct path forward is the adaptation of Haloferax volcanii transformation reporter assays, in which a non-replicative plasmid carrying a positive selectable marker is delivered to a recipient culture under defined chemical conditions and the resulting transformant fraction is enumerated; the assay has been standardized at terrestrial baseline and yields transformation frequencies of approximately 10^-3 per recipient cell under permissive conditions (Sivabalasarma et al., 2020; Schmid et al., 2020).

Embedding this reporter assay within a Mars-relevant chemical context requires the manipulation of three principal variables. The first is the perchlorate molarity in the medium, which should span the range from terrestrial baseline (zero) through the surface-regolith range (0.4 to 0.6 wt% magnesium perchlorate, corresponding to approximately 0.04 to 0.06 M) and into elevated concentrations representative of evaporitic accumulations (up to 0.5 M). The second is the UV-C dose, which should span the lethal to sub-lethal range with realistic spectral composition matched to the Martian surface spectrum below 200 nm. The third is the water activity, which should span the range from terrestrial baseline (approximately 0.99) to values consistent with perchlorate brines (down to approximately 0.5) achieved through controlled humidity and salt deliquescence (Naz et al., 2022; Stevens et al., 2019). Each of these variables modulates the chemical-aggressiveness factor of the RGPI, and the joint factorial design across at least three levels per variable would generate the data necessary to convert the conceptual index into a parameterized empirical metric.

A second class of experiment that the RGPI framework calls for involves consortium-scale assays rather than monoculture transformation. The realistic unit of analysis, as the panspermia synthesis has shown, is the multi-species aggregate rather than the isolated organism. Consortium assays should combine at least three species (a haloarchaeon, a crenarchaeon and a perchlorate-tolerant bacterium) within a single regolith-simulant matrix and should track both viability and HGT events through metagenomic sequencing of the post-exposure community. The detection of recombinant junctions diagnostic of recent inter-species transfer, using the long-read split-read methodology developed by Tokuda and collaborators, provides a direct empirical readout of the integration probability that lies at the centre of the updated panspermia model (Tokuda et al., 2024; Zhaxybayeva & Nesbø, 2025). Recent advances in single-molecule sequencing throughput have reduced the cost of such assays to a level compatible with multi-condition factorial designs, removing a previous practical barrier (Tokuda et al., 2024).

The third class of experiment concerns the verification of the subsurface refugium scenario, which is the regime in which the RGPI predicts near-baseline HGT competence and which is, simultaneously, the regime most difficult to simulate in laboratory chambers. Recent radar observations of the south polar region of Mars have provided indirect evidence for the presence of subsurface liquid water at depths consistent with the simulator design assumptions used in the present synthesis, and these observations strengthen the empirical case for the subsurface refugium scenario (Cosciotti et al., 2021). Laboratory simulation of subsurface conditions requires the integration of low-temperature control, pressure control matched to the lithostatic gradient of Martian regolith, and the maintenance of brine compositions consistent with the inferred chemistry of deliquescence-driven pore fluids. The available simulator infrastructure can approximate these conditions, but the coupling of subsurface chemical conditions to HGT reporter assays has not been performed; this represents one of the highest-priority experimental gaps identified in the present synthesis.

A fourth class of experiment, which connects directly to planetary protection and biosignature detection, concerns the survival and integration probability of consortia ejected from Mars and arriving on Earth. The Antarctic recovery of Martian meteorites provides natural samples that have undergone the full transit-arrival cycle, and the recent experimental work on the Antarctic shergottite EETA79001 has demonstrated that authentic Martian regolith supports microbial growth under terrestrial conditions (Tarnas et al., 2024). The systematic extension of such experiments to include haloarchaeal and crenarchaeal model organisms, with explicit measurement of HGT events between the transferred microbes and indigenous terrestrial communities, would generate a direct empirical test of the integration-probability concept developed in the present article. Recent advances in clean-handling protocols for Antarctic meteorites, motivated in part by the planetary protection considerations articulated in the NASA workshop on metagenomic methods (Green et al., 2023), have lowered the contamination risk associated with such experiments and made them tractable within current biosafety frameworks.

A final methodological observation concerns the integration of artificial-intelligence-assisted phylogenetic analysis with the RGPI framework. Recent machine-learning approaches to the detection of horizontally transferred gene clusters from environmental metagenomes have improved sensitivity by approximately a factor of three relative to alignment-based approaches, particularly for short-fragment recombinant junctions of the type expected in degraded Martian samples (Tokuda et al., 2024). The application of such methods to the metagenomic readouts of regolith-simulant exposure experiments would generate the high-throughput data needed to populate the RGPI parameter space, and the same methods would, if Martian samples are returned, provide the analytical tools for distinguishing terrestrial contamination from Martian-origin HGT signatures. The methodological convergence of HGT-aware experimental design, AI-assisted analytical readout and integrated regolith simulation defines the contours of the next decade of laboratory astrobiology, and the RGPI framework is offered as one organizing principle around which that decade of work can proceed.

CONCLUSION

The synthesis presented in this article addresses the three hypotheses formulated at the outset by drawing on the integrated body of evidence accumulated across archaeal genetics, Martian regolith science and space-exposure experimentation. The first hypothesis, on the retention of HGT competence in halophilic archaea under perchlorate stress, is supported with qualification. The available evidence demonstrates that natural transformation, cell-cell bridge mediated DNA exchange and vesicle-mediated transfer continue to operate at perchlorate concentrations consistent with surface Martian regolith, although at attenuated kinetics that vary by approximately a factor of three to ten across the model systems analyzed. The protective effect of the mineral matrix, particularly halite embedding in haloarchaeal systems, is documented as a critical modulator and warrants the inclusion of matrix composition as an explicit variable in any quantitative model. The second hypothesis, on the stimulation of HGT systems by sub-lethal UV exposure, is supported without qualification for Crenarchaeota and conditionally for Euryarchaeota. The Ups pilus operon in Sulfolobus is induced at sub-lethal UV-C doses and mediates DNA exchange that restores chromosomal integrity through homologous recombination; analogous stress-induced HGT pathways have been documented in haloarchaea, but the mechanistic detail is less complete. The third hypothesis, on the inadequacy of static survival-based lithopanspermia models, is supported by the convergent evidence that survival times, integration probabilities and consortium-scale dynamics differ qualitatively from single-organism transit calculations.

The principal original contribution of this article is the proposal of the Regolith-Mediated Genetic Plasticity Index (RGPI) as a conceptual framework for integrating archaeal HGT biology with Martian regolith chemistry within the panspermia debate. The RGPI organizes empirical data across previously disjoint literatures, allows qualitative differentiation among archaeal model systems under defined environmental scenarios, and identifies the experimental priorities for future quantitative work. The index does not, in its present form, substitute for empirical measurement; rather, it specifies the variables that must be measured jointly in any future integrated experiment that combines realistic Martian regolith simulants, multi-species archaeal consortia, and direct assays of horizontal gene flow. The article has demonstrated the qualitative differentiation that the RGPI affords for Haloferax volcanii, Halobacterium salinarum NRC-1 and Sulfolobus islandicus under three defined scenarios, and the differentiation is consistent with the empirical literature.

Beyond the principal conceptual contribution of the RGPI, the article has produced four secondary contributions that deserve recapitulation. First, it has clarified that the empirical literature on Mars-relevant archaeal HGT, although fragmented across multiple sub-disciplines, can be productively organized around a small number of mechanistic categories — transformation, vesicle-mediated transfer, cell-cell bridging, conjugation and UV-induced exchange — each of which has been characterized in at least one well-studied model system. Second, the analysis has identified the protective effect of mineral matrix embedding as a decisive modulator of HGT competence, with halite embedding emerging as the most extensively characterized case but with regolith and sulfate-mineral embedding as plausible analogues warranting further empirical work. Third, the synthesis has reframed the panspermia debate from a survival-centric to an integration-centric perspective, with HGT competence rather than transit-survival probability as the principal limiting variable. Fourth, the article has connected the abstract panspermia framework to concrete operational requirements for planetary protection policy and biosignature detection, providing a translational pathway from theoretical reframing to mission-design implications.

The methodological limitations of the present synthesis are substantive and require explicit acknowledgement. The RGPI rests on input parameters whose joint distributions under realistic Martian diurnal and seasonal cycling have not been measured with full granularity, and the assumption that laboratory-quantified HGT rates translate linearly into regolith-context HGT rates is a working assumption that requires direct empirical validation. The corpus of available studies that combine regolith simulation with HGT assays is small, and the synthesis therefore depends on indirect inference across distinct experimental traditions. The scope of the analysis is restricted to halophilic and thermoacidophilic archaea; methanogenic Euryarchaeota, which are also strong candidates for Martian subsurface habitability, are covered only peripherally and warrant a dedicated treatment in future work. The article does not resolve the question of whether Martian panspermia has occurred or could occur with non-zero probability under specified mission scenarios; it reframes the question as one of HGT competence under recipient chemistry, rather than of survival probability alone.

A final reflection concerns the broader trajectory of astrobiological inquiry. The first generation of astrobiology, broadly coterminous with the period from the Viking missions through the early 2000s, was shaped by the question of whether life can exist beyond Earth and operated within a paradigm of detection. The second generation, in the period from the Phoenix and Curiosity missions through the present, has been shaped by the question of whether the chemistry of other planetary bodies is compatible with biological function and has operated within a paradigm of habitability. The framework developed in this article suggests that a third generation of astrobiological inquiry is now possible, in which the central question is not whether life can exist but how life evolves under planetary regolith chemistries and what genetic exchange mechanisms operate within those evolutionary trajectories. This third-generation paradigm, which can be termed an evolutionary astrobiology, treats the genome of the transferred microbial consortium as the central object of analysis, and the chemistry of the recipient regolith as the principal modulator of evolutionary outcomes. The RGPI is offered as one organizing principle for this third-generation programme, and the present article as a contribution to its conceptual foundations.

Three recommendations for future research follow from this analysis. First, integrated experimental platforms should be developed that combine standardized Mars simulants (MGS-1, JSC Mars-1A) with perchlorate doping at the 0.4 to 0.6 wt% range, UV exposure profiles consistent with surface and subsurface gradients, and direct HGT reporter assays in haloarchaeal and crenarchaeal model systems. Such platforms would generate the empirical inputs required to convert the RGPI from a conceptual indicator to a validated metric. Second, planetary protection frameworks should be revised to incorporate HGT competence as an explicit variable in forward contamination calculations and in the biosafety assessment of returned samples. Third, biosignature detection criteria for upcoming life-detection missions should include the detection of phylogenetically incongruent gene clusters as a candidate signature, with appropriate controls for terrestrial contamination during sample handling. The implications for the panspermia debate are not that natural interplanetary transfer of life is established but that the scientific bottleneck has shifted from survival to integration, and the chemistry of the recipient regolith is the central variable governing integration. The proposed framework is offered as a starting point for a research programme that takes seriously the proposition that the genome of a transferred consortium is not a passive cargo but an active participant in the colonization process.

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HORIZONTALNI TRANSFER GENA U EKSTREMOFILNIM ARHEJAMA IZLOŽENIM SIMULIRANIM USLOVIMA MARSOVSKE REGOLITNE HEMIJE: IMPLIKACIJE ZA PANSPERMIJSKE HIPOTEZE

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Sažetak: Interakcija između genetičke plastičnosti ekstremofilnih arheja i fizikalno-hemijskih osobina marsovskog regolita predstavlja jedno od centralnih, ali još neriješenih pitanja savremene astrobiologije. Ovaj rad ispituje da li i kako procesi horizontalnog transfera gena (HGT) među halofilnim i termoacidofilnim arhejama teku u simuliranim uslovima marsovskog regolita karakterisanim perhloratnim solima, oksidovanim faznim oblicima željeza, niskim aktivitetom vode i povišenim ultraljubičastim flukseom, te kakve posljedice takva modulisana HGT dinamika ima za hipotezu panspermije. Polazeći od sinteze recentnih eksperimenata izlaganja u svemiru, studija perhloratne biohemije i genomike arheja, rad razvija analitički okvir koji povezuje tri do sada razdvojene literature: mehanizme HGT-a u arhejama, fizikalno-hemiju marsovskog regolita i modelovanje litopanspermijskog tranzita. Originalni doprinos sastoji se u predlogu Indeksa Genetičke Plastičnosti Posredovane Regolitom (RGPI) — konceptualnog indikatora koji povezuje izmjerenu frekvenciju HGT-a u modelnim sistemima arheja s hemijskom agresivnošću okolnog mineralnog matriksa, izraženom kao normalizovana funkcija koncentracije perhlorata, doze UV zračenja i aktiviteta vode. Sinteza pokazuje da haloarhejske vrste zadržavaju mjerljivu kompetenciju za transformaciju pri perhloratnim koncentracijama relevantnim za Mars do 0.4 M, dok vezikulama posredovan transfer DNK kod sulfolobalnih vrsta zadržava aktivnost u termalnim režimima koji se preklapaju s podpovršinskim marsovskim nišama. Ovi nalazi rekonfigurišu raspravu o panspermiji pomjerajući fokus s opstanka jednog prenesenog organizma na evolucijsku putanju konzorcijuma u kojem regolit djeluje kao selektivni amplifikator HGT-vođene adaptacije.

Ključne riječi: *horizontalni transfer gena, ekstremofilne arheje, marsovski regolit, perhlorati, panspermija, litopanspermija, astrobiologija, genetička plastičnost.*