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Man and his spaceships

Vehicles for extraterrestrial colonization?

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The resiliency and adaptive ability of microbial life in real time on Earth relies heavily upon horizontal gene transfer. Based on that knowledge, how likely is earth based microbial life to colonize extraterrestrial targets such as Mars? To address this question, we consider manned and unmanned space exploration, the resident microbiota that is likely to inhabit those vehicles, the adaptive potential of that microbiota in an extraterrestrial setting especially with regards to mobile genetic elements, and the likelihood that Mars like environments could initiate and sustain colonization.

By the 1970s, scientists James Lovelock and Lynn Margulis had developed a hypothesis known as the Gaia theory.¹ It proposed that organisms on Earth interact with their inorganic surroundings to form a self-regulating, complex system that contributes to the maintenance of conditions favorable for life on the planet. Whether or not you buy into the Gaian theory, extant Earth is an extraordinary and singular planet inhabiting what appears to be, a sterile solar system. (If not sterile, certainly life, in form and quantity as we know it, inhabits no other neighboring planets). Our singular status in the vacuum of local space raises the question whether exchanges can breach the bounds of our atmosphere, creating conduits with extraterrestrial targets. We've known about the potential for backward contamination for some time. For instance, space debris enters our atmosphere in the form of meteorites continually. Researchers in the origin of life field have long considered the possibility that such events seeded life

on our planet in the beginning and indeed some have considered they may still be doing so.²⁻⁷ Failing hard evidence of that, we've explored meteorites for past extraterrestrial life in fossilized form.^{8,9}

Forward contamination is a different story. Once humankind entered into space exploration the specter for extraterrestrial seeding of Earth based life became a real possibility. We have and do expect to send manned and unmanned spacecraft both to the moon and Mars. There are five active probes on or in orbit around Mars including three orbiters and two rovers. Of the two, Mars is considered to be a more likely candidate either for past life or possible seeding of life. Scientists have argued for the likelihood that Titan and Europa might host life as well but we confine ourselves to Mars in our discussion as it is within the foreseeable future for concentrated exploration, especially regarding manned missions. The question has become, how likely is our potential for seeding another planet and what are the chances it will survive and colonize?^{10,11}

In 2006, a common soil bacterium, *Bacillus*, was found viable and present on spacecraft and in spacecraft assembly rooms that had been subjected to substantial efforts to clean them.¹²⁻¹⁴ One of those Bacilli has since had its genome sequenced and characterized and we have some understanding of its adaptive strategy to the particular challenge of sterilizing UV radiation.¹⁵ But it was troubling that our cleaning efforts were not sufficient in ridding outward bound craft of microbial life and this posed interesting ethical and moral questions. The science community took a closer look at the strategies and

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policies in place that dealt with planet protection.¹⁶

Forward Contamination Relies on Earthly Life Resiliency: So, How Resilient Is It?

We know from the rock record that complex life is amazingly resilient on Earth.¹⁷ Life has never failed to adapt to the new environments, despite near annihilations, although frequently at the expense of previous forms and strategies.¹⁸ It appears that once life got started on this planet it thrived, one way or another. This statement reflects in part on that biology with bones and complex structure which we know can leave a relatively robust history in fossils but it also rests upon the assumption that this is true of the earlier period in Earth's history when microbial life dominated.¹⁹ Because microbial life today is integral to all forms of life (consider especially their elemental recycling),²⁰ the fact that they appear to be the earliest life extant today, and they harbor the very same adaptive machinery at their core as the rest of life on our planet, we can likely assume that they too have been resilient when exposed to catastrophic events as well. However, soft, squishy single cells don't fossilize well. Stromatolites, or the more general term microbialites, are microbial communities that have provided us with the most robust microbial fossil data so far although even these aren't without detractors for validity.^{19,21-23} these communities of diverse microbes show up through various time periods in Earth's history^{21,22} and in fact are still extant today.²⁴ This record points to microbial resiliency in broad terms as they are complex communities adapting to an increasingly oxygenated atmosphere.²⁵

Life then has been resident on most of our planet for most of its 3.5 billion years, at least from the microbial standpoint. And while man might not be able to inhabit every nook and cranny of our planet without some sort of protective intervention, microbial life can. Indeed, it appears that we humans were but unexplored, opportunist, ecologically rich targets for colonization once our ancestors arrived on the biological landscape. The latest results on investigations into

the human microbiome (the total resident microbial population in a particular environment) reveal that microbes inhabit every nook and cranny of our human self to our benefit, if not our survival, certainly to our health²⁶ and vigor. We are repositories for a dynamic, commensal, co-evolving microbiome.

One might have teleological arguments with the Gaia theory but it correctly identifies the two key factors one has to consider for the kind of survival and colonization we see on Earth: the evolutionary-produced innovations that allow for an adaptive biology and the environments that tolerated, contributed, initiated, certainly participated in that evolution. When considering potential for Earth seeding extra-terrestrially, we have to tease out how important and necessary, dependent or interdependent those two factors are in two separate contexts: unmanned missions harboring microbial stowaways and manned missions with the highly integrated and regulated microbiome packaged in its own Gaian-like transportable vehicle, man. Either way, it's all about the limits of adaptability.

Amazing Biology, How Majestic Is Your Evolution

In the eukaryotic world, sexes and mating clearly established a mechanism that insured diversity in the face of extreme environmental trial. The near annihilations recorded in rock and fossil spurred morphological novelty and unprecedented diversity in eukaryotes. While we don't actually know the mechanism that allowed this to occur, there is a theme of sorts in the solution involving bilateralism. HOX genes are the basic genetic solution for the mapping problem in assigning directionality for cell differentially in metazoans today.^{27,28} HOX gene strategy leads to a quite elegant explanation for the diversity we frequently see in fossils. While circumstantial and without any basis for the "why" HOX genes might have bridged some innovative divide that was fixed in metazoans, it's satisfyingly consistent that the genetics as we understand them, bolster the argument. One might say that HOX genes were to bilateral entities what wheels were to anything

that rolls. Variation on a theme was a powerful engine of diversity given catastrophic events.

However, prokaryotes are different. Clonal entities with identical genetics and relatively small genomes, the default evolutionary strategy of diversity occurring piecemeal through mutational happenstance was a strategy requiring large populations, lots of time, and strict vertical inheritance. Early pioneers in the field of bioinformatics, such as Margaret Dayhoff, discounted the likelihood that whole sections of genes moved randomly through microbial genetic landscapes.²⁹ No one anticipated the extensive utilization of a native genetic engineering process, horizontal gene transfer. As sequencing technology of nucleic acids became practical and cheap the databases detailing prokaryotic genome content indicated that there was a great deal more going on in microbial genomes than point mutations, just as promiscuous and as likely to produce diversity and adaptive potential as eukaryotic sex. The mechanism(s) were different³⁰ but horizontal gene transfer almost guaranteed adaptive evolution in real time.³¹ Bioinformatics defined a whole suite of mobile elements that served as environmental vectors for bringing in or taking out strips of genetic material to neighboring prokaryotic entities,^{32,33} be they related or not. The methodology of antibiotic resistance is a prime example of bacterial adaptation fueled in real time.³⁴⁻³⁶ The fact that previously innocuous gut bacteria could become pathogenic through genetic islands³⁷⁻³⁹ further focused our thinking on just how fluid bacterial genomes could be.^{40,41}

Horizontal gene transfer explained the rapid adaptive response to changing ecologies. The key was an expansive genetic resource. Microbial communities are diverse in constituency and thrive in huge numbers. Researchers have estimated the number of prokaryotes and viruses found in various environments, e.g. oceans and lakes,⁴²⁻⁴⁴ dirt,⁴⁵ and the human gut.⁴⁶⁻⁴⁹ For reference, the most current estimates for the ocean floor is 2.9×10^{29} cells or ten million trillion microbes for every person on the planet.⁴⁴ This provides a perspective on the desperate need to understand microbiology in terms of populations⁵⁰ if

we were to get a handle on how obligatory horizontal gene transfer might be to the adaptive process.⁵¹ In a further complication, prokaryotes and their parasitic viruses have the potential for travel abroad⁵²⁻⁵⁵ making the genetic resource global. In a Gaian Earth like ours, as long as the possibility to eke out a living in any little crevice or water spot exists, the potential for finding the adaptive genetic resource is possible, if not guaranteed.

In the last two decades several scientific activities have come to bear upon the mechanisms that provide adaptation in the microbial world and our understanding of the evolution of diversity in prokaryotes. They bear directly on the chances of survival of forward contamination.

On February 24, 1988, Richard Lenski began an experimental evolution study using 12 populations of genetically identical *E. coli* which reproduced only asexually (without bacterial conjugation).^{56,57} The idea was to sample each population each day and inoculate fresh media with the previous day's population. The experiment is still tracking and the populations reached the milestone of 50,000 generations in February 2010. At various points, analyses of the evolutionary trajectory have been taken.⁵⁸⁻⁶⁰ Specifically, the questions addressed have been to know how rates of evolution varied over time, how repeatable evolutionary events were in identical environments, and how phenotypic changes are reflected in the genotype. To summarize to date the results of this elegant experiment, each population is thought to have generated hundreds of millions of mutations over the first 20,000 generations but Lenski estimates that only 10 to 20 beneficial mutations were fixed in each population and less than 100 total point mutations (including neutral ones) were fixed. Between 31,000 and 31,500 generations, one population evolved a citrate-using variant (a characteristic that is often used to distinguish *E. coli* from *Salmonella*) and there was evidence that this ability could re-evolve from earlier time points in this lineage, at a rate of occurrence of once per trillion cells. Lenski explains this through Stephen J Gould's argument that "historical contingency can have a profound and lasting impact" on the course of evolution.⁶¹

These experiments are certainly evidence that point mutations provide adaptive potential in pure culture situations. In summary though, we note that for a mutation to become fixed in the population, it required tens of thousands of generations and trillions of cells and the nutrient availability in which to conduct the experiment.

Once bioinformatics moved out into the field the microbiology community strived to identify bacterial species, or ecotypes, by what they did in their environment.⁶²⁻⁶⁴ This seemed sensible because organismal identity in prokaryotes was part historical inheritance and part horizontal. We accepted as fact that diversity was rapidly sparked by horizontal gene transfer and was at play everywhere. Even if the genetic machinery that provided the adaptive innovation was borrowed, for microbes it was indicative of that organism's role in its environment. This was important because even though the tenets of population biology don't mesh well with entities that don't have barriers that can define species precisely in the classic sense, for bacteria it aided in our ability to identify community members in a particular environment.

For bacterial communities then, one needed to appreciate the diversity within the community (expressed in this combination of vertical and horizontal genetic ecotype terms), the community as a whole, and the broader environment itself: what each have to offer in the way of commodity and challenge, respectively. For each individual in the community, the intra- and inter community environment had to be utilized to sustain growth and reproduction while adapting. Under these considerations, microbial population biology has made some good progress. The work at Cuatro Ciénegas Bolson is an example of that progress.⁶⁵⁻⁶⁷ Briefly, the CCB combines geographical isolation, long-term continuity and strong local selection pressures (especially from phosphorus limitation) creating high levels of endemic microbial biodiversity (in the form of locally unique microbiota).^{65,68-73} Recognizing that extensive HGT can provide a means for evolutionary innovation and adaptation, it can also obliterate local diversification by homogenizing

the populations, especially when outside genetic resources are not obtainable due to geographic isolation. While the unique factors of CCB are good at producing locally adapted endemic species and a lot of diversity while doing so, they require a long-term stable environment in which to do it in.

Therefore, given what we know about the efficiency and the occurrence of the adaptive processes for microbial entities on Earth, how does this speak to our concern for contamination?

The Lonely Microbe on an Even Lonelier Planet

Crisler et al.⁷⁴ recently conducted an experimental regime exposing certain microbial populations to conditions that simulated the surface of Mars. Mars surface environmental parameters include extremes in salinity, temperature, desiccation, radiation, a diurnal cycle that includes alternate freezing and thawing, low water activity, and a thin, anoxic atmosphere.⁷⁵ If water ice in permafrost regions should melt or water vapor condense, brines would likely result that are nearly saturated in $MgSO_4$.⁷⁶ Using bacterial populations from the Great Salt Plains, Crisler and colleagues lightly inoculated (below 0.05 OD at 600 nm) the most halotolerant members to a variety of experimental regimes. (A back of the envelope calculation can estimate that the number of cells in a light inoculation is about 55 million.⁷⁷) They demonstrated that aerobic, halotolerant bacteria could grow in the high concentrations of $MgSO_4$ estimated for Martian soils. However, they found that exposure to cyclic drying and rewetting or freezing and thawing was a limiting factor for the growth of these terrestrial organisms. They could not survive.

Let's estimate that in our efforts to clean spacecraft, we leave 20,000 *Bacillus* spores aboard. (Spacecraft clean room requirements are much more stringent than this: the Goddard clean room has a class-10,000 rating, indicating that any cubic foot of air has no more than 10,000 particles floating around in it larger than 0.5 microns. A bacterium is roughly 1.0 micron, *Bacillus* spores are 0.8

microns.) Once on Mars (or really anywhere else that is not Earth-like) they must at once continue to reproduce and adapt. We imagine that in Earth terms, Mars is even more barren of nutrients than places like the CCB therefore the adaptive challenge for microbial stowaways would be huge; much more challenging than bringing citrate across a membrane, utilizing an alternate sugar, or conserving resources by scavenging components of community members. Given the results from the Crisler et al. study, we know that the community would have to endure and survive several challenging ecological parameters, not limited to repeated thawing and freezing in the occasional, near saturated brine, and all in an unfamiliar atmosphere, one that was not oxidizing. If the reliance for adaptive progress relies on point mutations, we have some idea of how long they must survive if challenged minimally; years. We have no estimates if the challenges are multiple and simultaneous as the Mars surface would necessitate. Without a diverse community, gene transfer, possibly the primary engine of bacterial diversity for real time adaptive evolution on Earth would be a non sequitur. The genetic repertoire that makes Earth microbiology so responsive to environmental change is not available extra-terrestrially, if the only stowaways are a few other, nearly identical clones. Add to that geographically isolation and fewer resources to sustain any amount of evolution and Earth based life on Mars will go extinct, if indeed it ever was able to colonize.

What about Dirty Man and His Space Plans?

Human beings are a collection of roughly 10 trillion cells, each cell containing about 23,000 genes. Estimates for the human microbiome indicate that humans play host to another 100 trillion microbial cells, each with their own suite of genes, in the neighborhood of 5–8 million non-human genes.^{78,79}

We have learned very recently that while the human body may define the environmental landscape, it's the combination of human and microbes participating, equally and fully, in a functional and

integrated community that are dictating outcomes with and beyond the human genetic repertoire.^{49,80,81} Depending upon the community of microbes inhabiting our gut,⁴⁹ we may or may not develop diabetes^{78,82} Our nutritional status and access to essential vitamins are determined not just by diet but our microbial gut repertoire.^{83,84} If our gut microbial diversity is low or changes in constituency, it can lead to obesity and inflammatory bowel disease.^{49,82,85} Alternatively, if the vaginal microbial diversity is high it can lead to bacterial vaginosis.⁸⁶ There is a “morbid union” between our cardiovascular system, disease, and diet, with our gut microbiota playing a much bigger role in supplying chemical signals that unconsciously impact our food choices.⁸⁷ Immune disorders, including dermatitis, have been linked to our gut microbiota⁸⁸ and indeed colon commensal microbiota participate and even educate our immune system with regards to autoimmunity.⁸⁹ The microbiome that sets up residency during infancy and in the first three years impacts the rest of life^{88,90,91} and at the end of life if we should end up in a nursing home, our gut microbiota not only dictates our quality of life but can actually contribute to our frailty.^{90,92}

Several research groups are studying the structural and functional configuration for a normal, healthy, geographically dispersed, human microbiome population over time^{49,79,81,93} with interesting conclusions. Our individual microbiomes are unique to us with distinct microbial species dominating the various niches of our bodies. They are dynamic in community structure over time, both in healthy and diseased individuals. From a metabolic standpoint, our microbiomes are doing much the same thing in each of us just with a different microbial constituency. Therein lays our microbiomic individuality, our differing and individual adaptive potential to ecological challenges. Ethnicity, geography, diet and early microbial exposure all play a role in our resident biota along with certain driving physical factors such as oxygen, moisture, pH, host immunological factors, and microbial interactions (e.g., mutualism or competition).⁹⁴ We are far more than the sum of our human parts, we are indeed that and

our microbiota all at once; a mutualistic host-microbial relationship supported through the homeostatic properties of the human body.²⁶

Given the appreciation for the diversity and the population size we carry around with us in our microbiome alone, the genetic repertoire represented by a single human being, let alone a space crew, improves our prospects for forward contamination than a few thousand *Bacillus* left on a spacecraft. Perhaps the news is even more sobering. Mounting evidence indicates that our bodies are hot spots with regards to horizontal gene transfer and our resident microbiome.^{95,96} Smillie et al.⁹⁷ estimate a 25-fold more HGT between human-associated bacteria than among ecologically diverse non-human isolates. The host-microbiome consortium exhibits a delicate, hyper dynamic, but relatively controlled relationship integral to the human immune system dependent upon the long-term adaptation to its local as well as global environment. But outside of that Gaian paradise, things change.

Experiments designed to measure the effects of microgravity on *Bacillus* species and rates of HGT through conjugation have not been conclusive; weightlessness could not be shown to increase the rate but neither was inhibition observed.⁹⁸ More work needs to be done to understand the possible effects of weightlessness and HGT on microbial communities. We've known for some time that astronaut immune systems, especially their T-cells which are specialized white blood cells known to interact with our microbiota^{84,89} are dysfunctional in less than Earth gravity situations for extended periods of time.⁹⁹⁻¹⁰¹ Not unlike the affect that HIV has on the human immune system,^{102,103} once you lose the ability to proliferate T-cells you've short circuited the entire immune response.

Hurtling toward Mars, with months of antigravity destabilizing a coherent, functioning, already quite dynamic host-microbiome supraorganism, each crew member harboring 5–8 million non-human genes, we have substantially altered the adaptive capacity that HGT conferred on us by Earth's ecology. The genetic resource at our disposal is substantial. The homeostasis borne of tens of

thousands of years of adaptive evolution on the human-microbiome is now much different.

Once there with an extended stay of at least a year we will be protecting ourselves with space suits and habitats that supply an artificially buffered and homeostatic environment. Meanwhile, our bodies teaming with microbes in charge of our immune systems, the odds of inoculating Mars with a genetic repertoire that could adapt to Martian ecology is at least substantially better than the unmanned scenario previously described. How would the seeding proceed? The most likely contamination would be waste disposal, especially the microbiome residing in our gut. We'd need a thoughtful, precise plan for sewage disposal. We could save it for the trip back home, create a surface sanitary dump, destroy it, or bury it. We know that Mars is largely inhospitable on its surface so the worse choice we could make would be to bury it. The best hope we have in finding life on Mars is remnants of one either alive or in stasis underground. If this be the case, burying our waste products expands the possibilities of some kind of experiment that far outstrips our current knowledge of how diversity and mating might be achieved with Earth life, let alone alien life.

If Mars Along with the Rest of the Solar System Seems to be Sterile, Why Worry?

Indeed, why worry? It's this author's contention that the very fact that the majesty and bounty of life as we know it is not presently resident on neighboring planets says something about the possibility of that occurrence in and of itself. Despite our best or worst efforts in providing the opportunity in manned or unmanned visits to seed Mars or other neighboring solar system bodies, it seems doubtful that colonization is inevitable, at least in the present solar system environment. The most likely scenario presented here involves subsurface contamination and yet, one of the few places on our planet that we truly believe life is abundant and yet undiscovered, deep under the sea floor, a dark biosphere where the sun

never reaches, remains more a hope than a reality.¹⁰⁴

True to the Gaia hypothesis, we really aren't life entities evolving without context in just any old inorganic environment. We rely on gravity, liquid water, plate tectonics, ready energy, and our unique position in our solar system to ensure a buffered and comparatively genteel environment in which to explore the power of evolution.

If the impossible did happen, what would it actually mean? Given that we understand the unique strategies that microbial Earth life use to diversify and adapt, it's almost certain that if some part of 20,000 clonal *Bacillus* survived, they would likely have devised a whole other strategy than anything that is currently employed on Earth. We'd have to decide whether or not that event constituted a new origin of life, a window into the way life could seed and succeed, some kind of a historical contingency recovered from a time when Mars was full of life, or a rewind of that mysterious time in Earth's history when life indeed came from a common ancestor pool of non-diversified entities.

If it's dirty man and the refuse from his whacked out immune system that seeds successfully, at a minimum we'd probably need to revise our planet protection strategies. Maximally, it would be the finest testament to Earth life's inherent resiliency, whether the seeding produced some sort of conjugation between resident but unknown Mars life or a colonization of solely Earth based life.

In 1967, The United Nations *Treaty on Principles Governing the Activities of States in the Exploration and Use of Outer Space, Including the Moon and Other Bodies* states that our exploration should be conducted as to avoid harmful contamination. The UN consults with the International Council of Science on policies to provide guidelines for planet protection. Not knowing whether or not what we carried in our bodies or on our spaceships was harmful to Mars would render each of these seeding scenarios as unethical in practice. They would, however, provide unparalleled experimental results. Perhaps the most telling result would be not just the seeding, but if successful, long-term colonization was the result. In the advent

of such an outcome, we would have to rethink one of the basic tenets of life as we understand it, the close association of life and its environment, an environment in the case of Earth that is as dynamic as life itself.

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No potential conflicts of interest were disclosed.

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