Hennigan, T., Guliuzza, R., Ingle, M., Lansdell, G. 2023. A creation model of design: application of an interface systems model in key global symbiotic relationships. In J.H. Whitmore (editor), *Proceedings of the Ninth International Conference on Creationism*, pp. 228-241. Cedarville, Ohio: Cedarville University International Conference on Creationism.

A CREATION MODEL OF DESIGN: APPLICATION OF AN INTERFACE SYSTEMS MODEL IN KEY GLOBAL SYMBIOTIC RELATIONSHIPS

Tom Hennigan, Truett McConnell University, The Pilgram Marpeck School of Science, Engineering, Technology, and Math, 100 Alumni Dr., Cleveland, Georgia 30528 USA thennigan@truett.edu

Randy Guliuzza, Institute for Creation Research, P.O. Box 59029 Dallas, Texas 75229 USA rguliuzza@ICR.org

Matthew Ingle, The Master's University, School of Science, Mathematics, Technology & Health, 21726 Placerita Canyon Rd., Santa Clarita, California 91321 USA mingle@masters.edu

Grace Lansdell, Truett McConnell University, The Pilgram Marpeck School of Science, Engineering, Technology and Math, 100 Alumni Dr., Cleveland, Georgia 30528 USA jlansdell5324@truett.edu

ABSTRACT

As biologists explore the astonishing complexities of organisms, it has caused them to rethink their biological understanding, especially with organism relationships. Symbiotic relationships, including mutualists, commensals, and parasites, are long term associations between two or more autonomous creatures. They are crucial for biospheric functioning, health, and biogeochemical processes. Evolutionary models explain how and why symbionts interact and include *game theory*, *biological markets*, and/or *competition- predator/prey* interpretations. While these models give important insights, they depend on naturalistic assumptions of random unguided processes and system self-organization. We propose a model of symbiotic relationships focused on guided interface design. The interface is the boundary, on every autonomous organism, where intimate alliances allow for complex communication and product exchange. Elements of the interface are *authentication*, *protocols*, and *common media* and removal or corruption of one or more elements cause an interface system to collapse or malfunction. This may explain how some commensal and parasitic symbioses have developed since the Fall and how long-term relationships can transition from mutualistic to commensal to parasitic as they respond to changing environmental or symbiont conditions in a fallen world. Here we apply our interface model to globally important mutualists (endomycorrhiza and nitrogen fixation) and parasites (malaria and schistosomiasis). We do not address commensalism because more research is needed in this area. Data suggest that a design interface model accounts for all evolutionary interpretations and adds robust detail describing complexities required for autonomous organisms to form intimate relationships. Creation research gives our God ultimate glory and is worthwhile because his invisible attributes including design, omniscience, and relationship are clearly seen, for He desires to be known from what He has made.

KEY WORDS

interface systems, symbiosis, parasitism, commensalism, mutualism, reverse genetics

I. INTRODUCTION

As biologists explore the *black boxes* of organisms inhabiting our biosphere, detailed complexities being revealed continue to amaze researchers and cause them to rethink biological concepts in areas that include metabolism, organism taxonomy, genetic programming, organism-organism interfaces, organism-environment interfaces, and anatomical/physiological functioning (Behe 2006). For example, consider the new microbial descriptions and surprises being discovered about *giant* viruses and mixotrophic diversity, ecology, and bioremediation (Huang et al. 2021; Li et al. 2022; Schultz et al. 2022). Symbiotic relationships are no exception and these biological discoveries are consistent with intelligent engineering far beyond comprehension.

Historically, symbiotic relationships are long term associations between two or more biologically diverse creatures. However, current research is uncovering a far more complicated picture of a plethora of species interacting in and around organisms that is causing a move to rethink symbiotic modeling, for example, in lichens (Allen and Lendemer 2022). Parasitic relationships occur when an organism takes nutrients from its host, generally not causing harm. Commensal associations have been characterized as at least one of the organisms benefiting and others neither hurt nor benefitted. Investigators realize that commensalism has not been well studied and are suggesting that they are complex and dependent on a variety of ecological phenomena (Mathis and Bronstein 2020). Mutualists are alliances where all benefit. Much discussion surrounding symbiotic relationships has focused on their origins, what constitutes a symbiosis, categories of symbiosis, and how many alliances can transition from one type of relationship to another (Douglas 2010; Hennigan et al. 2022; Paracer and Ahmadjian 2000; Wood and Garner 2009).

The book of Genesis suggests that God initially created organism archetypes fully formed and capable of complex relational interactions that were good and very good (Francis 2003; Francis and Wood 2013; Hennigan 2009A; Zuill 2000; Zuill 2007). Even today, symbiotic relationships are ubiquitous, involve a complex diversity of species, and are at the core of biospheric health and biogeochemical processes. However, the consequences of human rebellion and God's curse resulted in suffering, pain, relational disruption, and death. Evolutionists posit that unguided natural processes resulted in these relationships as they initially evolved and co-evolved via struggle and competition leading to cooperation and system self-organization (Douglas 2010; Hennigan et al. 2022; Lazcano and Peretó 2017; Paracer and Ahmadjian 2000; Perry 1995; Sagan 1967).

Therefore, a creation model of symbiotic relationships is needed within the larger model of young age creation to better explain the complexity of symbiotic relationships within a Design/Fall/Curse paradigm (Guliuzza and Gaskill 2018; Hennigan and Guliuzza 2019). In a recent paper Hennigan et al. (2022) proposed a design model of symbiotic relationships (MOSR) focused on the interface. The interface is the boundary, on each organism, where interactions take place. This model uses human engineered analogues as a basis for describing how two or more autonomous organisms can recognize, cooperate, and regulate resources with one another, in a tightly controlled relationship (Guliuzza and Sherwin 2016). It was suggested that daunting interface requirements needed for organisms to interact may be described more precisely using engineered analogues, rather than the random selection/self-organization explanations put forth in the conventional evolution model.

Applying an engineering approach to biology identifies multiple, bounded individual kinds of self-regulated entities—a host and a microbe—with *no loss* of distinctiveness or identity. Some researchers may believe that hosts and other organisms engage in seamless "interactions," but engineering analysis clearly shows that there really is a seam. To *not* recognize the seam may advance misleading conclusions about autonomy-blurring amalgamations such as human-microbe mosaics, supra-organisms, or trans-human collectives. The understanding of distinct *kinds* of organisms, including humanity, may become fuzzy. In this view, parasites taking nutrients from a host may be a *violation* of distinct boundaries of one entity upon another. This contrasts with mutualism, where all organisms involved are working together to share resources, which may not violate interface boundaries.

We posit that organisms were initially created with interfaces designed for the purpose of enabling sender-receiver relationships. Immune systems are an example of an interface. As will be shown, identification of *non-self* does not automatically activate *immune defense* and the most contemporary research and understanding of immune systems is bearing this out (Guliuzza and Sherwin 2016; Padariya et al. 2021).

With immune systems, identification of non-self will activate protocols that bring on a pre-programmed or *consequential* response that may not involve defense or destruction in any way. If destruction is activated, it is for regulation and control and not necessarily defense. Even so-called *friendly* or *good* microbes are destroyed by the same mechanisms as the *bad* microbes if the *good* ones are not in the locations and/or amounts the host is designed to work with at certain times or under certain environmental conditions. The overwhelming majority of interactions with microbes are mutually beneficial and we suggest discussing symbiotic relationships in terms of a *requester-provider* and *symbiont-symbiont* creation framework.

In this paper we will discuss how researchers are exploring the black box workings of globally important symbionts and highlight a few well researched mutual and parasitic symbioses. Since more research needs to be done on commensalism and relationships can often be on a continuum of mutual, commensal, and parasitic, we will not address commensalism in depth at this time. However, we will allude to it in our discussion below as avenues for future research. We suggest that microbial interface systems were designed to facilitate cooperation and not mortal combat between creatures. Those systems, along with other interfacing mechanisms, are the links making up the myriads of ecological networks enabling creatures to work together in mutually beneficial ways, most of which are still beneficial after the Fall. Some seem to have been corrupted, though more research is needed to determine if actual corruption has taken place. Our Creator and King - Father and Savior - desires to be known. His invisible attributes such as life, design, and intimate relationships are clearly seen and understood, from what has been made (Holy Bible Romans 1:20).

II. SCIENTIFIC, ENGINEERING, AND BIBLICAL CONSIDERATIONS

A. Model organisms and scientific models of symbiosis

Model organisms are non-human species that are scrupulously researched to uncover details of complex biological processes and relationships. There are many that are important in symbiotic research, and they have revealed amazing complexities with diverse organisms that are intimately interacting with each other. Symbiotic model organisms include *Azolla sp.* (water fern), important agricultural legumes such as *Lotus japonicus*, *Medicago truncatula* (barrel clover), *Glycine max* (soybean), *Phaseolus vulgaris* (common bean) and animals such as Porifera (sponges), *Drosophila melanogaster* (fruit flies), *Danio rerio* (zebra fish), *Mus sp.* (mice) and *Aiptasia sp.* (sea anemones) (de Vries and de Vries 2018; Neuhauser and Fargione 2004; Pita et al. 2016; Rädecker et al. 2019; Roy et al. 2020).

Based on findings from model organism research, there are several scientific models that attempt to explain how and why organisms interact in a variety of ways. They include *game theory models* (e.g., prisoners dilemma where hypotheses are formulated to explain why partners may not cooperate even when it benefits them), *biological market models* (e.g., where organisms entering relationships can influence the cost of resources and how much one or both are *willing to pay for it*, depending on location and time of resource interaction), and *competition and predator/prey models* such as Lotka-Volterra modeling (Chess 1988; Frank 1997; Neuhauser and Fargione 2004; van't Padje et al. 2020). While some of these models give important insights into complex symbioses, including how some organisms may interact in a continuum from parasitism to mutualism, interpretations lack the detailed explanations required for how two or more autonomous organisms can enter intimate relationships in intricately complex ways.

B. Engineering-based biological research and application

Ironically, just as engineers reproduce manufactured products by reverse engineering and carefully studying their construction and composition, geneticists perform reverse genetics on model organisms to produce a new phenotype. They begin by identifying a gene of interest and bombard certain parts with radiation. This disrupts genetic programming through mutation and causes deleterious effects on symbiotic relationships (Roy et al. 2020).

With the model organism protocol, details of these affected relationships are being elucidated and findings are the inspiration for algorithms that are solving engineering and computer problems. Symbiosis applications include, but are not limited to, increased engineering/computer optimization for pollution emissions, electrical power flow, energy efficient building design, and wireless communication (Abdullahi et al. 2020). Symbiosis researchers hope that their findings will help biologists genetically engineer other organisms that did not have certain abilities previously, to enter functional relationships with other organisms in agricultural and natural communities (de Vries and de Vries 2018). Though there are ethics concerns, genetically engineered relationships would allow organisms to accomplish important nutrient fixation for improving costs, productivity, and sustainability of agricultural practices and improved ecosystem management around the world. This approach is consistent with engineering design, biomimetics, and a supreme Designer behind it all.

Hennigan et al. (2022) hypothesize that at least three engineering-based principles will be the core of interpreting symbiotic observations. *Intentionality (teleology)* is where a search for purpose, and/or invisible characteristics of God (e.g., beauty, relationship, unity, diversity) will drive biological system research; *Internalistic* where biological processes and mechanisms enabling interrelationships and continuous adaptability are innate to organisms and not environmental processes; and *Individualistic* where individual organisms with abilities to identify self from non-self are seen as discreet, interrelated components in the broader ecosystem. This model postulates that the ecosystem is better understood by accounting for the individual roles each organism has and how they interact through operations that are regulated by their highly engineered interface systems.

Researchers emphasize that to understand an interface is to understand how autonomous entities can form intimate alliances and cooperate with one another by communicating in a way that information and product exchanges occur in specific ways (Clark and Petrini 2012). Hennigan et al. (2022) outline the following design elements required for an interface. *Authentication* is a highly regulated and extremely selective process designed to recognize self from non-self. *Protocols* are rules established by the interface designer to *regulate* the relationship. Physical attachment often precedes control but there are other interactions that do not require attachment. The *Common Medium* is a physical condition external to two or more entities. Common media include light, electrical impulses, water, soil, air, and/or various biochemicals. These intricate systems seem to operate in an irreducibly complex and interdependent way (Zuill 2007). Removal of any one of these design elements causes an interface system to effectively cease functioning altogether. Corruption of any element causes a system malfunction. The removal of interface elements and/or system malfunctions may explain how some commensal and parasitic relationships have developed since the Fall. These can also explain how long-term relationships, with the same creatures, can transition from mutualistic to commensal to parasitic, as several phenomena can affect interface elements. The only known origin of interface systems is the mind.

When observing long-term associations, it could look like one species is directly controlling the other, but they are not. Each organism has an interface system, but these systems only directly control the organism to which it belongs. For example, in mutualisms such as nitrogen fixing bacteria and plant roots, several harmonious outcomes are observed. One outcome includes bacteria producing usable nitrogen for the plant and in return, the plant providing carbohydrates for bacteria. Bacteria and plants each have their own identifiable protocols, but the broader interface that enables these protocols to harmonize is not seen. If we searched for where the information underlying specified bacteria/plant harmonization resides, it would not be found within either but comes from the mind of the Designer. We find that explanation more plausible than the conventional (and mystical) assertion that plants and bacteria co-evolved together. But how do we understand system malfunctions, parasitic suffering, and death if a good God created life and relationship?

C. Biblical life and death

Within a biblical worldview, it is important to incorporate concepts of how life and death are defined and how death and suffering fit into a world designed by a good God (Hennigan et al. 2022; Ingle 2015; Wise 2018). The book of Genesis suggests that life and consciousness have characteristics that are not measurable using scientific methodologies. This is consistent with the Author and Creator of life in the cosmos, who is also Spirit, not being physical or measurable (Wise 2018). The scientific implications of life and consciousness being immaterial are profound. What this means is that we can scientifically study the operation of biological functions such as metabolism, adaptation, and organism interactions, and that the operation of these functions are best explained by engineering principles. Yet, consciousness and life itself are not reducible to, derived from, or explained by either biological functions or engineering principles. In addition, Scripture suggests that soul-life found in animals and humans is a different kind of life than other biological taxa (e.g., plants as a food source for humans and animals with soul-life) and that the death brought about by the curse is death of animals and humans (Genesis 1:29-30; Romans 5:12-21; Kennard 2008; Wise 2018). Wise (2019) suggests that biblical death may not only refer to separation, but also cessation of created function and purpose. These concepts are important to discuss and explore in young-age creationism, especially when it comes to describing parasite/parasitoid relations that can cause death and suffering and whether parasites of taxa other than animals and humans were part of God's original and good design (Blaschke 2018; Ingle 2015). More discussion and agreement are needed among young age creationists.

III. MUTUALISTIC SYMBIOSES

Mutualistic symbioses are long-term relationships with two or more organisms working together in a way that all benefit. These associations can be classified as obligate or facultative. In this section we will briefly describe what is currently known about a few globally important relationships that are often the foundation for ecosystem and community health. Human understanding of these complex relationships is growing rapidly, and the data suggest that we are far from fully comprehending any of them. However, what is being elucidated continues to amaze and inspire researchers toward improving human technology, as the complexities in creation far surpass human engineering.

For example, a study by U. C. Berkeley finds that sorghum manipulates soil conditions to promote a beneficial change in microbes on their roots during drought. Over a four month experiment the composition of the microbial community drastically shifted as conditions went from wet to drought. With the onset of drought, sorghum roots released an increased range of carbohydrates and amino acids, as well as secondary metabolites which may include antimicrobials and reactive oxygen species into the soil. The normally dominant microbes (Proteobacteria, Bacteroidetes, and Verrucomicrobia) are poorly suited to these changed conditions and their populations rapidly decrease. *Streptomyces* strains of Actinobacteria are normally present in small numbers but are particularly suited to both the new root products and drought conditions and take over primary colonization of the root system. Sorghum detects the recolonization by Actinobacteria and, through a yet to be identified mechanism, adjusts metabolism again so there is an increase in relative root-to-shoot resource allocation that is correlated with increased root biomass and deeper roots under drought stress. Researchers suggest that these interactions are the result of *cross talk* between sorghum cultivars and microbes (Hunter 2018).

The complex communication and *authentication* operating by sophisticated genetic *protocols*, through soil *media* over a range of moisture conditions, is consistent with a model of interface design.

Mutual symbioses highlighted are mycorrhizal networks and nitrogen fixation.

A. Mycorrhizal networks

The name *mycorrhiza* comes from the Greek meaning *fungus-root*. The term refers to how fungal hyphae connect and interact with plant roots, often forming mutual symbioses. The fungal symbionts improve nutrient uptake and enhance water transfer, seedling development, soil formation, resistance to pathogens, stress resistance, and plant community establishment and in turn, the plant provides crucial carbohydrates (Bonfante and Genre 2010; Hennigan 2009B; Pandey et al. 2019). Hyphae of the mycorrhiza can extend farther than their host plant roots and connect to other mycorrhizal networks forming the *wood-wide-web*, which is responsible for horizontal nutrient movement throughout the community (Anca and Bonfante 2009; Bonfante and Genre 2010).

Two major types of mycorrhizal fungi are ectomycorrhizae (ECM) and endomycorrhizae (EM), and they differ in how they colonize the plant root. Fungal taxa of ECM include species from clades Basidiomycota or Ascomycota and their hyphae connect and grow on the outside of tree and shrub roots forming a *Hartig net* interface where nutrients are exchanged (Anca and Bonfante 2009; Bonfante and Genre 2010; Plett and Stuart 2020). Fungal taxa of EM include species from Glomeromycota where their hyphae penetrate the root cortex of forest trees/shrubs, along with some herbaceous plants, and enter cells forming vesicles. This type of mycorrhizae includes Arbuscular (AM), Ericaceous, and Orchidaceous endomycorrhiza (Bonfante and Genre 2010). We will only discuss arbuscular mycorrhizal symbiosis because it is the most common and well-researched type of mycorrhizal association.

Arbuscular Mycorrhizae (AM) form symbioses with most terrestrial plants (Bonfante and Genre 2010; Chen et al. 2018; Rosendahl 2008). Most of these plants could live without AM fungi, but there are positive benefits to the relationship as the fungal partner increases the plant's ability to resist pathogens, uptake nutrients, and tolerate stress (Bonfante and Genre 2010; Chen et al. 2018). All AM fungi benefit from the association with plants because of the carbon they receive from them (Walder and van der Heijden 2015). Glomeromycota fungi are characterized by their ability to reach the inner cortex of plant roots and form branched arbuscules which are the symbiotic interfaces for nutrient exchange (Bonfante and Genre 2010; Chen et al. 2018). These interfaces are key to understanding how these organisms interact and operate with each other.

In AM symbiosis, the role of the plant-fungal interface is to exchange both signals and nutrients (Roth and Paszkowski 2017). Important molecules involved in signaling are plant metabolites that initiate and maintain AM symbiosis. The metabolome is reprogrammed by the fungus to promote colonization and allows the fungus to obtain carbon from the plant (Kaur and Suseela 2020). The metabolome includes primary metabolites (sugars, organic acids) and secondary metabolites (alkaloids, flavonoids), and changes in the concentration of these compounds depend on the environment, plant species, or fungus species (Machiani et al. 2022). The reprogramming of the plant metabolome can affect the type of relationship exhibited between the plant and the fungus (Kaur and Suseela 2020).

Because the fungus has morphological similarities to that of a pathogen, the host plant recognizes self from non-self (*authentication*) but goes into a mode with highly restrictive exchanges. As with animals, plants have an immune system—which constitutes the interface system—and, thus, authentication is required (Sanabria et al. 2010). As seen in fungus/plant mutualisms, the protocols of interface systems facilitate a balance between the plant and fungal nutrient needs (Kogel et al. 2006). To have long lasting, mutualistic interactions, mutual protocols facilitate the plant cell's acceptance of the fungal hyphae, and this starts with plant receptor-kinase-mediated transmembrane signaling that recognizes the plant as a cooperative organism (Kogel et al. 2006). The incredibly tight design of the protocols is demonstrated when the plants produce salicylic acid to suppress fungal colonization, but the fungus produces compounds that the plant detects and stops acid production so that the fungus can colonize the plant (Kuar and Suseela 2020). The plant also reorganizes cellular organelles to accommodate fungal structures (Kogel et al. 2006; Bonfante and Genre 2010).

MacLean et al. (2017) discuss three stages for how arbuscular mycorrhizal symbiosis occurs within a host plant. They are perception, transmission, and transcription. These stages correspond to Hennigan et al.'s (2022) *authentication, protocols, and common media* requirements for an interface. The perception stage begins when a plant deprived of phosphorus (P) releases plant hormones called strigolactones into the rhizosphere *medium* of the soil. The AM fungi perceive these hormones and identify the host plant, which leads to the increase in hyphal growth. Fungi will also produce signaling molecules (myc factors) such as chitin oligomers and lipochitooligosaccharides. The transmission stage begins when these myc factors are perceived by the host plant, which activate the common symbiosis pathway. This message is relayed from the plasma membrane to the nucleus through a series of messenger molecule interactions. The *protocols* for the transcription stage are the programmed information found in specific proteins and genes necessary for symbiosis. One example is the Gene OsD14, which increases fungal colonization.

Sometimes, the mutualistic relationship with AM fungi and their host plants can turn parasitic. The relationship is not strictly reciprocal and can change depending on environmental conditions (Walder and van der Heijden 2015). Kogel et al. (2006) describe parasitism in a plant-fungal interaction as an unbalanced symbiosis due to unequal nutrient transfer. Certain environmental conditions can corrupt or change media conditions affecting interface function. Neuhauser and Fargione (2004) found that low soil Phosphorus (P) promotes a mutual relationship between the plant and fungal partner. However, if the soil is fertile, the plant no longer relies on the fungi for nutrients and fungi may *cheat* the plant by taking nutrients from it. Is this an example of cheating or is it consistent with God creating plants as food for other organisms when plants are thriving in high fertility soil?

Walder and van der Heijden (2015) note that resource exchange from the fungus can increase in plants that have a strong sink strength, however, the sink strength of the plant can depend on the efficiency of the plant-fungal interface to exchange these nutrients. If the plant-fungal interface is not functioning properly, resources from the AM fungi may not be transferred to the plant, and it can seem that the fungi is parasitizing the plant. This protocol malfunction is expected in a Fallen world and fits our creation model of symbiotic relationships. The authors also point out the difficulty in determining if a plant is benefiting or being harmed from a mycorrhizal association because of the relational complexity. AM fungi form vast, interconnected networks that have associations with many plants and can provide benefits other than nutrient provision. These other benefits could make up for inadequate nutrient provision from the fungi, and the relationship could be labeled as a *conditional mutualism*.

Lanfranco et al. (2018) discuss possible mechanisms that can affect the type of symbiotic relationship between AM fungi and their host plants. The symbiotic relationship between plants and AM fungi greatly depends on the exchange of nutrients, and these nutrients can act as important signals in the development of the relationship. Sugar is taken from the plant by the fungus, and an important fungal gene involved in this uptake is *RiMST2*. If this gene is silenced, the result is decreased fungal colonization and reduced arbuscular branching. Both the plant and fungi have genes called *PT* genes that are important for P transfer, and if these genes are altered or silenced, the fungus arbuscule lifetime can be shortened. This helps ensure the plant receives P from the fungus and could be a mechanism used by the plant to prevent fungal parasitism. At high P levels, the plant can release phytohormones that reduce AM colonization. It has also been shown that lipid transfer from plant to fungus is important for continuing the relationship (Lanfranco et al. 2018, Wang et al. 2017). Lipids play an important role in the composition of the arbuscular membrane where the interface lies, which affects the functionality of proteins involved in nutrient and signal exchange (Kameoka and Gutjahr 2022). For example, a lipid biosynthesis gene only found in AM host plants is the *FatM* gene, and when it mutates, reduces fungal colonization and arbuscular branching (Roth and Paszkowski 2017). Roth and Paszkowski (2017) argue that the presence of this gene and others in only AM host plants could be a result of evolutionary adaptation of the *symbiotic system*. An MOSR interpretation would suggest that these genetic protocols were put in place by the Creator so that each autonomous organism could interact and exchange nutrients with each other. Disabled protocols can affect nutrient exchange and can cause this mutualism to turn either parasitic or be discontinued.

Change in relationships can also come about in other ways. In an experiment performed by Johnson et al. (2015) they found that light media can reduce plant ability to produce photosynthate for the fungus. Lekberg and Koide (2013) also describe this *cheating* as parasitic. However, plants can prevent such a relationship from occurring by moving carbohydrates to an area of high P concentration in the root, which is where the arbuscular interface lies (Lekberg and Koide 2013; Kaur and Suseela 2020). Relational variability from mutualism to parasitism can be interpreted as *cheating* in certain symbiosis market models. An equally reasonable interface interpretation is consistent with designed protocol response and changing media that determine organism interactions, survival responses, and the Creator's desire for his creatures to thrive even in challenging conditions.

Sorghum is an important food crop because of its extreme drought-tolerance, which affects soil media, which informs relationship interactions at the interfaces. Symbiotic relationships help confer resistance in dry conditions. A 17-week field study subjected two sets of sorghum (*Sorghum bicolor*) reflecting two different genotypes to pre-flowering and post-flowering drought stress and detected changes in the expression of genes related to photosynthesis, and its relationship to fungi on its roots (Varoquaux et al. 2019). A molecular profile of drought response over the growing season was compiled from a dataset of nearly 400 transcriptomes of messenger RNA. These data showed that sorghum rapidly detects and adapts to drought stresses by exquisitely regulating gene expression in 40% of the genome. A total of 10,727 genes were modulated (Manke 2019). The field work also studied the effects of drought on AM fungi, that in non-drought conditions are abundantly concentrated around the roots. During drought, some of the genes, specifically modified by sorghum, changed this symbiotic relationship by downregulating metabolic pathways. This downregulation was associated with the reduced availability of exchangeable products between sorghum and fungi and corresponds to decreased fungal mass in sorghum roots (Varoquaux et al. 2019).

The elements described enabling arbuscular mycorrhizal and sorghum to exchange products and information fit the description of biological interfaces (e.g., authentication, protocols, and media) as first described by Guliuzza and Sherwin (2016).

Mutualism between plants and arbuscular fungi is extremely complex and involves constant communication and signaling between organisms. However, this mutualism can change to parasitism caused in part from issues such as disrupted authentication (signal exchange), degraded protocols (unequal nutrient exchange) or unfavorable environmental media conditions.

B. Nitrogen fixation

Approximately 78% of earth's atmosphere consists of molecular dinitrogen (N_2). In this form, its stability and non-toxicity make it a useful way to store it in the atmosphere. Though nitrogen is required by all organisms for the biosynthesis of life-requiring biomolecules such as DNA, RNA, ATP, and proteins, atmospheric dinitrogen is not usable and must be transformed (fixed) into nitrogen compounds organisms can use. Therefore, nitrogen fixation is a globally important process where dinitrogen is converted into usable ammonia (NH_3) or other important nitrogen compounds. Zuill and Standish (2007) suggested that the biospheric nitrogen cycle system had irreducibly interdependent (complex) properties, evidence of an intelligent Creator. This is because the intricate and global process is mostly accomplished by a diverse suite of organism relationships, with a small percentage produced by lightning (Hill et al. 1980).

The rhizosphere of terrestrial plants is that region of soil that surrounds plant roots. It is a rich ecosystem composed of a plethora of diverse organisms. One of those groups are diazotrophs and they are designed to fix nitrogen. Diazotrophs include several phyla from both Eubacteria and Archaea domains and are further subdivided into root nodule bacteria and plant growth promoting rhizobacteria (Mus et al. 2016).

In turn, plants have a diversity of ways they can associate with diazotrophs and work together for the benefit of their relationship and for the community. The proximity of plant roots and diazotrophs determine the type of association, and their proximity has been delineated into three major categories; *free-living* interactions through soil/water media, *endophytic* where diazotrophs are able to enter plant tissue intercellular spaces, and *endosymbiotic* where diazotrophs are taken into a plant cell and housed within plant synthesized membranes (Mus et al. 2016). Along with these types of relationships, there is evidence that nitrogen fixing associations also occur within fungi and termites (Mullins et al. 2021; Thanganathan and Hasan 2018).

1. Free-living diazotrophs

There is a diversity of free-living diazotrophic prokaryotes in the global rhizosphere. They can be facultative or obligate anaerobes or aerobes and consist of taxa that include proteobacteria, (a recently delineated and controversial phylum of Gram-negative bacteria) and *Cyanobacteria* (National Laboratories of Medicine 2021; Mus et al. 2016). Because these are not classified as symbiotic relationships, and space prohibits detailed discussion, they do fall under relationships where *protocols* do not require attachment (Hennigan et al. 2022). Mus et al. (2016) describe plant roots secreting chemicals into the soil which are detected by plant growth promoting rhizobacteria (PGPR; e.g., proteobacteria). Once detected, these bacteria move toward the roots and when they get into proximity, they have nitrogenase enzymes to transform dinitrogen into metabolically usable NH_3 or NH_4^+ which then enriches the soil and improves the health of the rhizosphere and greater community (Mus et al. 2016; Steenhoudt and Vanderleyden 2000). Hennigan et al. (2022) emphasize that outcomes like increased soil fertility are the result of each autonomous organism's authentication capability of identifying self from non-self, protocols for non-attachment interactions, and relational functioning in soil and growth promoting chemical media. The intelligence required for both plant and PGPR to communicate and respond to one another, for the good of the community, is consistent with an infinitely wise and knowledgeable Designer.

2. Intercellular endophytes

Many diazotrophic bacteria (e.g., *Azoarcus, Herbaspirillum, Gluconacetobacter, and Nostoc*) can enter plant tissue through openings such as lenticels, stomata, or root cracks without causing damage and tripping a defense response (Mus et al. 2016). For this reason, they are classified as endophytes. Endophytes are ubiquitous and can be facultative or obligate, mutualistic, commensal, or parasitic, and have been identified in all plant species to date (Mus et al. 2016; Hardoim et al. 2015). Nitrogen fixing cyanobacteria (*Nostoc sp.*) are also associated with some bryophytes (e.g., mosses and liverworts), fungi, lichens, and cycads (palm-like gymnosperms), and do not form root nodules (de Vries and de Vries 2018; Mus et al. 2016).

Details differ depending on species associations, but general patterns can be described across diverse associations. For example, relationships begin with highly complex communication via *authentication* in soil or water *media*. Plants can attract nitrogen-fixing symbionts with flavonoids and/or a diversity of polysaccharides that function as signal molecules that symbionts detect, recognize, and respond to in a variety of ways (de Vries and de Vries 2018). Not all signal molecules have been identified and in the case of *Nostoc* relationships, signal molecules are also called hormogonia-inducing factors (HIF). HIF are detected in soil or water *media* and transform *Nostoc* non-motile vegetative cells into motile cells called hormogonia. Hormogonia communicate with other plant molecular signals and move toward the plant by gliding over wet surfaces or viscous substrates. When hormogonia reach the plant host, they differentiate again into unique, thick-walled cells called heterocysts and enter plant tissue. Research into structural defects on the surface of polysaccharide signal molecules suggests that some of these symbiotic associations fail because these defects prohibit *authentication* (Mus et al. 2016). This is consistent with Hennigan et al. (2022) when they discussed that failure of one or more interface components would result in deleterious effects on symbiotic associations.

de Vries and de Vries (2018) outline the intricate components needed once symbionts enter the plant where each symbiont is tightly controlling their respective interfaces. Several *protocols* have been described for how they do this and they are regulated both transcriptionally and at a protein level where proteins regulate other proteins, undergo modification, and/or use available non-protein cofactors that assist with reactions. Nitrogen fixing genes (*nif*) can be regulated by nitrogen fixing proteins such as *nifA*. For example, the protocols for the nitrogenase enzyme complex alone are intricate. Two key components that make up the enzyme complex are nitrogenase reductase and nitrogenase. Nitrogenase reductase consists of two identical building blocks (subunits) coded by *nifH* while nitrogenase is composed of two identical β subunits (β2) coded by *nifK* and two α subunits (α_2) coded by *nifD*. Another protein, *nifL*, can interact with *nifA*, depending on environmental cues that are detected by sensors on the diazotroph and plant (Hennigan and Guliuzza 2019). Appropriate gene expression is also dependent on *nifS* and *nifU* proteins regulating fixation rates with the help of cofactors.

For dinitrogen to be transformed into useful plant compounds other genomic/proteomic protocols are required for anaerobic conditions and high ATP rates. This is because oxygen inactivates nitrogenase and a lot of energy is required for these biochemical reactions. Research also suggests that sugars involved with cyanobacteria are not just signal molecules but are also important in providing a nitrogenase pathway through the pentose-phosphate biochemical pathway (de Vries and de Vries 2018; Mus et al. 2016). But, to produce high ATP rates, high oxygen concentrations are also needed. Therefore, these autonomous organisms must tightly regulate gene expression so that the proper chemical environment, monitoring of environmental variables (e.g., temperature, N_2 concentration, O_2 concentration, light, plant growth), efficient resource exchange, and exchange rates result in healthy functioning for one another. In *Nostoc*, the genomic and proteomic *protocols* are programmed to synthesize unique heterocyst cells that become the anaerobic chambers required for nitrogen fixing reactions. Requirements include; three cell walls for oxygen impermeability, nitrogenase production, retention of photosystem I for ATP production, dismantling of photosystem II so that oxygen production stops, upregulation of glycolytic enzymes, and synthesis of special proteins for scavenging remaining oxygen (de Vries and de Vries 2018).

There is a unique endophytic association with aquatic ferns (*Azolla sp.*) and cyanobacteria (*Nostoc sp.)* worth highlighting. Similar authentication and genetic/proteomic protocols discussed above are still relevant and complex. However, rather than a continual attraction and interaction of *Nostoc* symbionts recruited from the environment, symbionts are inherited via vertical transfer and always found in *Azolla* leaf tissue (de Vries and de Vries 2018).

Though much research is still needed to understand the *Azolla/Nostoc* nitrogen fixing relationship, de Vries and de Vries (2018) outline our understanding to date. As with all types of mutualistic symbiosis *Nostoc* and *Azolla sp.* require a highly complex and tightly controlled communication with one another because they undergo several complex stages of symbiosis that includes transferring inoculum sexually and asexually, but also control pathogens that can remove fixed nitrogen for themselves. Generation to generation vertical inheritance has provided a stable relationship between the two and has provided continuity in this relationship for 66 to 100 million years based on conventional dating. Humans have recognized *Azolla* spp. for thousands of years as a fertilizer in rice agriculture and recent data suggest this symbiosis can increase agricultural yield by 200% (de Vries and de Vries 2018).

3. Intracellular endosymbionts

Fabaceae is considered the third largest flowering plant family and includes the legumes of the world (Roy et al. 2020). Many global members of this family enter the most complex and intricate nitrogen fixing symbiosis with microbes. They are known as nodule forming endosymbionts. These microbes proceed through a typical, yet to be fully understood, relationship progression, similar to what was described above, but also includes authentication and protocols for determining self from non-self (recognition), protocols for physical interaction between entities (penetration), protocols for diverse growth structures (e.g., cell division stimulation of nodules), and protocols for morphological/physiological changes and diversification in the endosymbiont (Mus et al. 2016, Roy et al. 2020). Nodule forming endosymbioses is one of the best studied relationships using model species such as the soybean (*Glycine max*) and common bean (*Phaseolus vulgaris*). The following description is a summary of our current understanding of these interactions.

Roy et al. (2020) outline the following general steps for nitrogen fixing rhizobia to enter relationally tight interactions with leguminous plants. They include the importance of authentication where complex signaling mechanisms trigger gene expression in both partners so that partners can identify and determine relationship parameters while immune system responses exclude other microorganisms. This authentication process is a considerable undertaking because the soil medium is full of compatible and incompatible microorganisms and plants use complex signaling to distinguish them. Protocols are involved with coordinating bacterial access to epidermal and cortical cells, stimulating root cell mitosis and nodule formation, manufacturing thousands of symbiosomes that are specialized organelles that house bacteroids which are the anaerobic chambers for Nitrogen fixation, and modifying plant tissue for providing nutrients to bacteroids (Clúa et al. 2018; Roy et al. 2020).

Early signaling molecules include legumes producing flavonoids into the soil medium. Rhizobia detect and recognize these signals and they synthesize lipochitooligosaccharides (Nod factors) which allows the plant to recognize the bacteria, which triggers the plant to synthesize welcome signals to the symbiont. Complex genetic protocols express thousands of genes which express large numbers of chemical signaling pathways, from both organisms, so that this partnership will be successful. These genetic protocols and signal pathways reorganize several key anatomical structures in the plant for a successful symbiosis. For example, root hairs, cytoskeleton for root hair reorientation, cell wall degradation, and membrane invagination are all required for microbial entrance into the plant and are tightly controlled by genetic and hormonal interactions modifying these structures that are still being illuminated (Clúa et el. 2018; Roy et al. 2020). Plant hormones such as cytokinins and auxins control nodule organogenesis depending on concentrations and ratio of the two. These parameters determine timing and location of nodule cell division (Roy et al. 2020).

Soil media characteristics affect the efficiency of these relationships and include concentrations of water, phosphate, and sulfate. Metal ions in soil such as iron, molybdenum, zinc, and copper are crucial cofactors required in symbiotic nitrogen fixation metabolism. As limiting factors, they can directly or indirectly affect the process and cause negative effects for the bacteria, plants, or both. This, in turn, can affect how we view the symbiosis as mutual, commensal, or even parasitic.

Mutualistic symbioses are ubiquitous in the biosphere and space prohibits descriptions of the many other intricate relationships being revealed. Data suggest that an interface MOSR is consistent with the relational complexities being discovered including, but not limited to, termite gut physiology, algal/amphibian symbioses, fungus farming ants, lichens, fish gut microbiomes, bacteria/squid relationships, Cnidarian/dinoflagellates (e.g., coral reefs), sponges, and symbiont mediated insecticide resistance (Allen and Lendemer 2022; da Costa et al. 2019; de Vries and de Vries 2018; Graham et al 2014; Kikuchi et al. 2012; Kim et al. 2014; Levy et al. 2021; Neuhauser and Fargione 2004; Pita et al. 2016; Rädecker et al. 2019; Roy et al. 2020, Tarnecki et al. 2017). We predict that our model will be a helpful starting point for future creation investigators for producing robust interpretations of highly complex organism interactions and ecosystem networks, from a young-age biblical worldview.

IV. PARASITIC ASSOCIATIONS

Parasitic associations are generally defined as long-term relationships where one organism takes nutrients from another. Though there are exceptions, parasites may not cause harm. From a MOSR perspective, removal of any one of the interface elements (e.g., authentication, protocols, or common medium) causes an interface system to cease functioning. Corruption of any element causes a system malfunction. These disruptions can explain how parasitic relationships have developed and how they can transition from mutualistic to commensal to parasitic.

Two parasitic relationships are discussed in depth below: malarial protozoans *Plasmodium* spp. and schistosomiasis protozoans (*Schistosoma* spp.).

A. Malaria protozoans

Disease is nothing new to our species. Humans have been fighting pathogens with varying levels of success since the Fall when death entered creation. Malaria may be one of the oldest human diseases, discussed in dozens of ancient writings, including Hippocrates and Herodotus (Bruce-Chwatt 1988). Few human diseases have impacted human history the way malaria has. This disease contributed to the end of conquests by Alexander the Great, the fall of Greek civilization, the failure of some crusades, and killed more soldiers in World War II than actual warfare (Bruce-Chwatt 1988). Historians and lay people have always connected swamps and fevers, believing the causative agent of sickness to be “bad air” or *mal aria*. By the end of the 19th century, pioneering work by physicians illustrated that *Plasmodium* spp. are responsible for the unique pathologies of malaria. One of these physicians, Ronald Ross, was awarded the Nobel Prize for medicine in 1902 for his discovery of mosquitos as the vector of *Plasmodium* (Bruce-Chwatt 1988). While there are several species in the genus, the deadliest is *Plasmodium falciparum.*

This parasite causes malignant tertian malaria and accounts for 50% of all malaria cases. *Plasmodium falciparum* triggers fever paroxysms where people suffer a fever every third day with temperatures often reaching 104°F (40°C) or higher (Edington 1967). Many of the patients never feel well in between paroxysms, some with continuous fevers and others with 24 to 36 hour long *hot periods* as compared with the 8 to12 hour periods with other species of *Plasmodium* *(*Edington 1967). Most sufferers experience feelings of being unwell (malaise) such as body aches, chills, and a loss of appetite. The fevers can be so intense that teeth chatter to the point of cracking and the bed rattles with the shivering. With this most virulent of the *Plasmodium* species, the disease can cause severe anemia and develop into cerebral malaria that is often fatal. More than 3.2 billion people live in areas with malaria risk, with more than 200 million infected at any given time (World Health Organization [WHO] 2016). The disease is only limited by the geographic distribution of species of *Anopheles* mosquitoes capable of transmitting the parasite (WHO 2016).

When the mosquito feeds on its human host, *P. falciparum* individuals migrate from the salivary glands of the mosquito into the human bloodstream. Parasites migrate to the liver and reproduce at a prodigious rate. At this stage, some argue that the *Plasmodium* individuals have a commensal existence, not harming the host. In fact, some species of *Plasmodium* can avoid causing disease in the host for decades (Markus 2012). Once the individuals start moving through the life cycle, the symptoms appear quickly. A single protozoan delivered from a mosquito can generate millions of individuals after several rounds of reproduction. Parasites pour out of the liver and immediately infect red blood cells, feeding on the hemoglobin. In addition to destroying the red blood cells, the feeding produces an insoluble molecule called hemozoin. This dark pigment is diagnostic and triggers the human body to release tumor necroses factor (TNF), which causes the fevers and most of the pathology related to the disease. Parasites leave ruptured red blood cells and continue to infect new rounds of cells or are ingested by mosquitoes and potentially transmitted to new hosts. In many *P. falciparum* infections, more than half of all red blood cells contain parasite individuals. It is no wonder this parasite causes such a debilitating and deadly disease. How did something like this come from a creation full of life that the Creator would call *very good*?

1. Design interface

P. falciparum individuals and humans are locked in an intimate symbiotic relationship. These relationships are like dances that have turned into wrestling matches. Both members of this parasitic relationship operate as autonomous beings capable of recognizing self and not losing distinct boundaries. Merozoites of the parasite contain several unique surface proteins, including merozoite surface protein 1 (Hoessli et al. 2003). This protein, in addition to marking the membrane as belonging to *P. falciparum,* is integral for parasite invasion of erythrocytes. Additionally, the parasite cells seek out the opposite sex to complete sexual reproduction. After several cycles of asexual reproduction within red blood cells, some of the parasites develop into macrogametocytes (female) or microgametocytes (male). If these cells are consumed by mosquitos having a blood meal, the microgametocyte will exflaggelate (cast off their flagella) in the gut of the mosquito and locate the macrogametocyte to fertilize. Human cells contain several cell markers and receptors for recognizing self, many of which are the focus of tremendous research. At least two of these markers are used by *P. falciparum* to recognize the specific human cells they need to invade for completing the life cycle.

Many protocols for this symbiosis have been discovered and described. The wrestling match between *P. falciparum* and humans seems to be rather one sided, with malaria helping make mosquitos the most dangerous animals on Earth. Two points in the *P. falciparum* life cycle require the parasite to contact the host cell, invade it, and ultimately take control of it. The parasitic cells contain receptors that recognize and bind surface protein on both hepatocytes for the exoerythrocytic cycle and red blood cells in the erythrocytic cycle. This ensures that the parasite invades the correct cell type required for completing the life cycle. Human cells seem to exert little to no control of *P. falciparum* cells. In fact, humans generate antibodies that prevent the immune system from keeping the parasites from invading erythrocytes (Guevara Patiño et al. 1997). It is like a wrestler tying his wrists together to prevent him from putting his opponent in an arm bar. The only real attempt from the human body to control the invader is to release TNF after monocytes or macrophages bind the parasite, triggering a raging fever and debilitating body aches.

This relationship between *P. falciparum* and humans takes place in the common medium of the human bloodstream interstitial space around hepatocytes, and within human cells. The parasites thrive in each of these chemical environments as do human cells in the absence of the parasite. *P. falciparum* individuals are so adept at thriving in these vertebrate environments that they trigger the production of antibodies discussed above that prevent human cells from blocking the erythrocytic invasion (Guevara Patiño et al. 1997). The chemical environment changes dramatically once the immune system reacts to the presence of the parasite. Human cells and *Plasmodium* cells struggle to thrive under the conditions created by TNF. While the body may kill the parasites and prevent further cycles, it does so at the expense of its own flourishing.

2. Original design interface

Most readers of Genesis 1, if believing it to be historical narrative, cannot reconcile a relationship like this with a creation that God would declare "very good." While both members of the symbiotic relationship have the six characteristics of life, they do not seem to be experiencing the flourishing encompassed in *nephesh* life. It seems that the death God declared would come as soon as Adam and Eve ate of the tree of life has distorted the design and purpose of this relationship. Research indicates that each of the species of *Plasmodium* may have moved into humans independently (Prugnolle et al. 2011). *Plasmodium falciparum* seems to have originated in gorillas, and switched hosts when *Anopheles* transmitted them to humans. It is interesting that *P. falciparum* demonstrates an ability to take control of cells in human systems and can thrive in the chemical environment within human cells. This indicates that the design in these symbionts is robust enough to use receptors different than those they were specifically designed to interface with. It seems the parasite can be used in a variety of engineered systems with varying levels of success. In fact, *Plasmodium* species are notorious for host switching, sometimes contributing to terrible pathology in the new hosts. These new hosts, including humans with *P. falciparum* seem to be unable to control the parasite because they were not designed to interface with them. It is quite possible that no organism was designed to interface with *Plasmodium* spp. Most research indicates that all *Plasmodium* spp. and similar parasites in other genera originated from coccidians that completed the entire life cycle within a single host. Coccidians are the largest subclass of Apicomplexan protists and are obligate intracellular parasites of animal intestinal tracts (Marugan-Hernandez et al. 2021). This ancestor likely evaded host immune response or was held in check by host cell control. It is likely that this ancestor and its vertebrate host had a well-developed interface like those seen in the mutualistic relationships discussed previously. As death entered creation, interface components broke down and symbionts entered foreign systems.

B. Schistosomiasis

Schistosoma mansoni, and other species of blood fluke flatworms in this genus, cause a disease known as schistosomiasis. Like malaria, schistosomiasis has been known for as long as humans have been leaving records. One major difference between the two is the large size of *Schistosoma* spp. when compared to *Plasmodium* spp. Both *Schistosoma* larva and adult, and the durability of the eggs, mean the parasite leaves more lasting evidence behind. In fact, at least 50 records of this disease exist in Egyptian papyri, and Egyptian mummies often contain calcified eggs of the worms (Di Bella et al. 2018).

Physicians in Napoleon's army recorded pathology of schistosomiasis, and within 50 years, Theodor Bilharz discovered evidence of the worm responsible for infecting more than a fourth of all people in Egypt (Di Bella et al. 2018). English surgeons found the parasite in an ape dying in the London Zoo and by World War I both disease and the blood fluke were well known across Europe (Roberts et al. 2012).

Schistosomian blood flukes are some of the most feared parasites in the world, with more than 800 million people at risk. It is likely that more than 200 million people are currently infected with schistosomiasis, with 125 million symptomatic, and 20 million with severe disease (Di Bella et al. 2018). The most common sign of schistosomiasis is bloody urine (most common with *Schistosoma haematobium*) or bloody diarrhea. During the acute phase of infections, the patient suffers from fever, fatigue, headache, malaise, muscle aches, lymphadenopathy (swollen lymph nodes), and gastrointestinal discomfort. If the disease moves to the chronic phase, hosts suffer from bloody urination or diarrhea with abdominal pain and lethargy. In some *S. mansoni* and *S. japonicum* infections, eggs block the hepatic portal system and cause ascites, which is a build-up of fluid in the belly.

The pathology of *Schistosoma* spp. is uniquely caused primarily by eggs. While adult worms in the veins present plenty of antigen to the immune system, the release of eggs triggers the immune response and pathology associated with the disease. One response is the production of various white blood cells that include eosinophils, neutrophils, and macrophages. These contribute to the formation of an aggregation of macrophages, called granulomas, around the eggs (Roberts et al. 2012). The formation of granulomas contributes to the release of TNF that causes the pathology of the acute phase. The pathology of the chronic phase is usually the result of the granulomas lodging in vessels or triggering the production of fibroblasts. In heavy infections, with massive fibroblast development, the intestinal wall and/or bladder wall become ulcerated (Roberts et al. 2012). This ulceration can lead to genital and kidney involvement, and even urinary tract blockages, secondary bacterial infections, bladder cancer, and bladder calcification. This is another parasite that is both common and devastating. There is little doubt that something has gone wrong with original *Schistosoma* relationships as death entered creation.

1. Design interface

Unlike the relationship between malarial parasites and humans (ignoring the parasite going into the dormant hypnozoite), the relationship between *Schistosoma* spp. and humans can last for years and even decades. The adult worms and humans are engaged in something more like two organisms that have identified themselves but have a truce. During this truce, both species maintain autonomy and present their identities using cell surface and secreted proteins. Crosnier et al. (2022) found more than 100 proteins unique to the cell surface and secretions of *Schistosoma mansoni*. Additionally, schistosomatids are somewhat unique in that they have separate sexes. Most parasitic species of Phylum Platyhelminthes are monoecious, possessing both male and female gonads and producing male and female gametes. Having separate sexes, require females to seek out males or never mature and starve to death. Once they find them using cell markers found on the surface of and by protein secreted by males, the females enter a canal in the male body and live out their lifecycle.

Schistosome parasites, like *Plasmodium* individuals, must survive in two physiologically and chemically distinct hosts. They survive in humans, mostly by evasion of the immune system and not by taking control of the host. However, they do employ some host control mechanisms. The first of these allows the cercariae (larval stage) to penetrate through the epidermis, basement membrane, and dermis to reach blood vessels underneath. While dodging immune cells in the skin, the parasites secrete materials that break down cell-cell junctions in the human tissues allowing them to take the three-day long journey through the incredible barrier (Hambrook and Hanington 2021). When dodging the immune cells does not work and the worms need to exert more control on individual immune cells or the entire immune response, they release immune modulators such as the anti-inflammatory protein *Sm16/SmSLP/SmSPO-1*. This renders the immune system useless in preventing the complete penetration by the worm through the outer defense. Interestingly, many Schistosomatids of birds, such as flukes in the genus *Ornithobilharzia,* cannot stop the inflammation response in humans and never make it through the skin. Instead, they die in the skin and trigger a great deal of inflammation causing “swimmer’s itch” (Ingle and Aaron 2015). After the worms have made it through the skin and journey through the human body to reach the place they transform into adults, the relationship with the immune system changes. The adult worms live in vessels that carry blood away from the intestines (*S. mansoni and S. japonicum*) or bladder (*S. haematobium*). To get the eggs out of the host, the parasite must induce the immune system to form granulomas around the eggs and carry the granuloma through the lining of the intestines or bladder where the granuloma containing eggs can be extruded in feces or urine (Schwartz and Fallon 2018). Like the situation with malaria, human cells have little to no control over the parasites other than to try to eliminate them. The immune resistant tegument of *Schistosoma* spp. makes this very difficult (Hambrook and Hanington 2021).

Schistosomatids thrive in the bodies of vertebrates, inflecting birds and mammals. The parasites find an abundant food source in venule erythrocytes draining organs and manipulate the chemical environment to their advantage (Hambrook and Hanington 202; Ingle and Aaron 2015). At least three genera of Family Schistosomatidae complete the life cycle in mammals, with *Schistosoma* functioning well in humans. Data suggest that as many as 70% of the larvae may die as they enter an adult by penetrating the skin and traveling the entire blood stream, moving through lung capillaries. The working of a non-corrupted immune system acting as an interface is demonstrated as it helps the parasite develop properly with interleukin-7 helping worms complete their journey through the human body and helping female worms produce more eggs (Wolowczuk et al. 1999). But this host-worm relationship has been corrupted. Extreme pathology results from an exuberant inflammatory response primarily from the effects of TNF coupled with blockages from the granulomas containing parasite eggs. The worms suffer only if the host dies because of the infection.

2. Original design interface

Family Schistosomatidae may be a holobaramin, representing a single created kind that has diversified into genera and species since the Fall (Ingle and Aaron 2015; Wood and Murray 2003). Because we would expect a created kind that God would call *very good* to benefit the host, it seems likely that this group was created to benefit the host (Ingle 2015). Therefore, it seems likely that this group was created to live in birds, but the robust design allowed them to switch hosts into mammals (Ingle and Aaron 2015). It seems that the switch to mammals put the symbiont into a host that was equipped to exert control and keep the parasites from becoming too abundant. That is one of the known functions of certain protocols of an interface system. These new hosts’ inflammatory response becomes dysregulated when eggs are released and avoid blockages. It should be noted that many humans (especially those that live in areas where *Schistosoma* spp. are endemic) show reduced pathology with the parasite compared with others. This can be explained when remembering that the pathology is almost exclusively the result of the human inflammatory response and not the parasite itself. As Family Schistosomatidae has diversified through time, it has become more specialized with species infecting a smaller variety of hosts. The more specialized the species of Schistosomatidae, the more severe the pathogenicity (Ingle and Aaron 2015). Data suggest that as schistosomatid authentication and protocols have consistently deteriorated from the original ancestor, relational disruption has occurred resulting in harmful parasitism.

V. CONCLUSIONS

How do two autonomous entities with distinct boundaries work together? This question is answered with a principle of design indispensable to engineering practice. For two autonomous entities with distinct boundaries to work together, they must be connected by an interface with three distinctive elements: authentication mechanisms, standardized protocols, and a mutually accessible medium to all entities involved. There are several implications based on this principle being true. The interface designer’s *thorough knowledge* of *all* systems to be integrated is essential. Creationists and ID advocates should begin to accentuate this point when making the case for an engineering-based approach to biology. This greatly compounds the “what-is-the-source-of-information” question. It is difficult enough to come up with a plausible evolutionary explanation for the information carried by DNA. Now, a natural explanation would have to be offered to explain the source of information controlling two or more entities—all linked together in massive ecological webs—and the complete set of logic involved remains a major part to be elucidated (unlike, for example, the information for genetic logic switches located in DNA). Evolutionists simply appeal to explanations that it evolved and coevolved. Engineering analysis eliminates these mystical appeals in standard biological descriptions and identifies true engineering causality in condition-consequence processes. Engineering analysis identifies extensive integration of interdependent, yet distinctly innate, systems, which makes the explanation of coevolution far less plausible.

ACKNOWLEDGMENTS

We would like to thank Dr. Steven Gollmer and the anonymous reviewers for their helpful and insightful suggestions on earlier manuscripts.

REFERENCES

Abdullahi, M., M.A. Ngadi, S.I. Dishing, S.M. Abdulhamid, and M.J. Usman. 2020. A survey of symbiotic organisms search algorithms and applications. *Neural Computing and Applications* 32:547-566.

Allen, J.L. and J.C. Lendemer. 2022. A call to reconceptualize lichen symbiosis. *Trends in Ecology and Evolution* 37, no. 7:582-589.

Behe, M.J. 2006 (2nd Edition). *Darwin's Black Box: The Biochemical Challenge to Evolution.* New York: Free Press.

Bergquist, R., and D.J. Gray. 2019. Schistosomiasis elimination: beginning of the end or a continued march on a trodden path. *Tropical Medicine and Infectious Disease* 4, no.2:76

Blaschke, J. 2018. Toward a young earth model of parasite evolution. *Journal of Creation Theology and Science Series B: Life Sciences,* 8, no. 1:1-5.

Bonfante, P. and I. A. Anca. 2009. Plants, Mycorrhizal Fungi, and Bacteria: A Network of Interactions. *Annu. Rev. Microbiol.* 63:363-83.

Bonfante, P. and A. Genre. 2010. Mechanisms underlying beneficial plant-fungus interactions in mycorrhizal symbiosis. *Nature Communication* 1:48.

Booth, N.J., P.M.C. Smith, S.A. Ramesh, and D.A. Day. 2021. Malate transport and metabolism in nitrogen-fixing legume nodules. *Molecules* 26, no. 22 (November): 6876. DOI: 10.3390/molecules26226876

Chen, M., M. Arato, L. Borghi, E. Nouri, and D. Reinhardt. 2018. Beneficial services of mycorrhizal fungi-from ecology to application. *Front. Plant Sci.* 9:1270.

Chess, D.M. 1988. Simulating the evolution of behavior: The iterated prisoner's dilemma problem. *Complex Systems* 2:663-670.

Clark, K. J. and B.M. Petrini. 2012. Capturing and analyzing interface characteristics Parts 1&2: *IBM Developer Works*.

Clúa, J., C. Roda, M.E. Zanetti, and F.E. Blanco. 2018. Compatibility between legumes and rhizobia for the establishment of a successful nitrogen-fixing symbiosis. *Genes* 9, no. 125:1-21. DOI: 10.3390/genes9030125.

Crosnier, C., C.H. Hokke, A.V. Protasio, C. Brandt, G. Rinaldi, M.C.C. Langenber, S. Clare, J.J. Janse, S. Wilson, M. Berriman, M. Roestenberg, and G.J. Wright. 2022. Screening of a library of recombinant *Schistosoma mansoni* proteins with sera from murine and human controlled infections identifies early serological markers. *Journal of Infectious Diseases* 225, no. 8:1435-1446.

da Costa, R.R., S.M.E. Vreeburg, J.Z. Shik, D.K. Aanen, and M. Poulsen. 2019. Can interaction specificity in the fungus-farming termite symbiosis be explained by nutritional requirements of the fungal crop? *Fungal Ecology* 38:54-61. DOI: 10. 1016j.funeco 2018.08.009.

de Vries, S. and J. de Vries. 2018. Azolla: A modern system for symbiotic Nitrogen fixation and evolutionary developmental biology. In H. Fernandez (editor), *Current Advances in Fern Research*, pp. 21-46. Switzerland, AG: Springer International Publishing Part of Springer Nature.

Douglas, A.E. 2010. *The Symbiotic Habit.* Princeton: Princeton University Press.

Francis, J.W. 2003. The organosubstrate of life: A creationist perspective of microbes and viruses, " *Proceedings of the Fifth International Conference on Creationism*: Vol. 5, Article 40: 433-444. https://digitalcommons.cedarville.edu/icc_proceedings/vol5/iss1/40 accessed on 25 September 2022.

Francis, J.W. and T.C. Wood. 2013. A creationist perspective on the origin of pathogenic vibrio cholerae and vibrio cholerae Toxin (CT). The Proceedings of the Seventh International Conference on Creationism 7 Article 29. https://digitalcommons.cedarville.edu/icc_proceedings/vol7/iss1/29 accessed on 25 September 2022.

Frank, S.A. 1997. Models of symbiosis. *American Naturalist* 150:S80-S99.

Graham, E.R, Z.M. McKie-Krisberg, and R.W. Sanders. 2014. Photosynthetic carbon from algal symbionts peaks during the latter stages of embryonic development in the salamander *Ambystoma maculatum*. *BMC Research Notes* 7:664-767.

Guavara Patiño, J.A., A.A. Holder, J.S. McBride, and M.J. Blackman. 1997. Antibodies that inhibit malaria merozoite surface protein-1 processing and erythrocyte invasion are blocked by naturally acquired human antibodies. *Journal of Experimental Medicine* 186, no. 10:1689-1699.

Guliuzza, R.J. and P.B. Gaskill. 2018. Continuous environmental tracking: an engineering framework to understand adaptation and diversification. In J.H. Whitmore (editor), *Proceedings of the 8th International Conference on Creationism*, pp.158-184, Pittsburg, Pennsylvania: Creation Science Fellowship.

Guliuzza, R. J. and F. Sherwin. 2016. Design analysis suggests that our "immune" system is better understood as a microbe interface system. *Creation Research Society Quarterly* 53:123–139.

Hambrook J.R., and P.C. Hanington. 2021. Immune evasion strategies of schistosomes. *Frontiers in Immunology* 11:624178.

Hardoim, P.R., L.S. van Overbeek, G. Berg, A.M. Pirttilä, S. Compant, A. Campisano, M. Döring, and A. Sessitsch. 2015. The hidden world within plants: Ecological and evolutionary considerations for defining functioning of microbial endophytes. *Microbiology and Molecular Biology Reviews* 79, no. 3:293-320. DOI: 10.1128/MMBR.00050-14.

Hennigan, T. 2009 A. Toward a biblical basis for ecology, with application in mycorrhizal symbiosis in orchids. *Journal of Creation* 23, no.1:78-85.

Hennigan, T. 2009 B. Toward an understanding of arbuscular mycorrhizal symbioses within a creation model of ecology: implications for godly stewardship and sustainable agriculture. *Answers Research Journal* 2:21-27.

Hennigan, T. and R.J. Guliuzza. 2019. The continuous environmental tracking hypothesis-application in seed dormancy and germination in forest ecosystems. *Journal of Creation* 33, no. 2:59-65.

Hennigan, T., R. Guliuzza, and G. Lansdell. 2022. Interface systems and continuous environmental tracking as a design model for symbiotic relationships. *Journal of Creation* 36, no. 2:97-105.

Hill, R.D, R.G. Rinker, and H.D. Wilson. 1980. Atmospheric nitrogen fixation by lightning. *American Meteorological Association* 37, no.1:179-192. DOI: 10.1175/1520-0469.

Hoessli, D.C., M. Poincelet, R. Gupta, S. Ilangumaran, and N. Din. 2003. *Plasmodium falciparum* merozoite surface protein 1 glycosylation and localization to low-density, detergent-resistant membranes in the parasitized erythrocyte. *European Journal of Biochemistry* 270: 366-375.

Huang, L., Xing, X., Zhou, P. *et al.* 2021. Mixotrophic bacteria for environmental detoxification of contaminated waste and wastewater. *Appl Microbiol Biotechnol* 105 6627–6648. DOI: https://doi.org/10.1007/s00253-021-11514-5.

Hunter, A. K. 2018. Microbes in soil help sorghum stay strong against droughts https://www.insidescience.org/news/microbes-soil-help-sorghum-stay-strong-against-droughts accessed on 19 August 19 2022.

Ingle, M. E. 2015. Parasitology and creation. *Answers Research Journal* 8:65-75.

Ingle, M.E., and M. Aaron. 2015. A baraminic study of the blood flukes of Family Schistosomatidae. *Answers Research Journal* 8: 327-337.

Johnson, N.C., G.W.T. Wilson, J.A. Wilson, R.M. Miller and M.A. Bowker. 2015. Mycorrhizal phenotypes and the law of the minimum. *New Phytologist* 205, no. 4:1473-1484. DOI: https://doi.org/10.1111/nph.13172.

Jones, N. 2013. Food fueled with fungi. *Nature* 504(7479):199. https://www.nature.com/news/food-fuelled-with-fungi-1.14339?keywords=3+6 accessed on 1 September 2022.

Kameoka, H., C. Gutjahr. 2022. Functions of lipids in development and reproduction of arbuscular mycorrhizal fungi. *Plant and Cell Physiology* 63, no. 10: 1356-1365. DOI: https://doi.org/10.1093/pcp/pcac113.

Kaur, S and V. Suseela. 2020. Unraveling arbuscular mycorrhiza- induced changes in plant primary and secondary metabolome. *Metabolites* 10, no. 8:335. DOI: 10.3390/metabo10080335.

Kennard, D. (2008). Hebrew Metaphysic. *Answers Research Journal* 1:169-195.

Kikuchi, Y., M. Hayatsu, T. Hosokawa, A. Nagayama, K. Tago, and T. Fukatsu. 2012. Symbiont-mediated insecticide resistance. *PNAS* 109, no. 22:8618-8622. DOI: 10.1073/pnas.1200231109.

Kim, E., Y. Lin, R. Kerney, L. Blumenberg, and C. Bishop. 2014. Phylogenetic analysis of algal symbionts associated with four North American amphibian egg masses. PLos One 9 no. 11: e108915. DOI: 10.1371/journal.pone.0108915.

Koch, R.A, G.M. Yoon, U.K. Aryal, K. Lail, M. Amirebrahimi, K. LaButti, A. Lipzen, R. Riley, K. Barry, B. Henrissat, I.V. Grigoriev, J.R. Herr, and M.C. Aime. 2022. Symbiotic nitrogen fixation in the reproductive structures of a basidiomycete fungus. *Current Biology* 31, no. 17: 3905-3914. DOI: 10.1016/j.cu.2021.06.033.

Kogel, K.H., P. Franken, and R. Hückelhoven. 2006. Endophyte or parasite - what decides? *Current Opinion in Plant Biology* 9:358-363.

Lanfranco, L., V. Fiorilli, C. Gutjahr. 2018. Partner communication and the role of nutrients in the arbuscular mycorrhizal symbiosis. *New Phytologist* 220: 1031-1046.

Lazcano, A. and J. Peretó. 2017. On the origins of mitosing cells: A historical appraisal of Lynn Margulis endosymbiotic theory. *J. Theor. Biol.* 434:80-87.

Lekberg, Y. and R.T Koide. 2014. Integrating physiological, community, and evolutionary perspectives on the arbuscular mycorrhizal symbiosis. *Botany* 92: 241-251.

Levy, S., A. Elek, X. Grau-Bové, S. Menéndez-Bravo, M. Iglesias, A. Tanay, T. Mass, and A. Sebé-Pedrós. 2021. A stony coral cell atlas illuminates the molecular and cellular basis of coral symbiosis, calcification, and immunity. *Cell* 184, no. 11:2973-2987. DOI: 10.1016/j.cell.2021.04.005.

Li, Q., Edwards, K.F., Schvarcz, C.R. *et al.* 2022. Broad phylogenetic and functional diversity among mixotrophic consumers of *Prochlorococcus*. *ISME J* 16:1557–1569. DOI: https://doi.org/10.1038/s41396-022-01204-z.

Machiani, M.A., A. Javanmard, R.H. Machiani, and A. Sadeghpour. 2022. Arbuscular mycorrhizal fungi and changes in primary and secondary metabolites. *Plants* 11 no. 17: 2183. DOI: 10.3390/plants11172183.

MacLean A.M., Bravo A., Harrison M.J. 2017. Plant signaling and metabolic pathways enabling arbuscular mycorrhizal symbiosis. *Plant Cell*. 10:2319-2335. DOI: 10.1105/tpc.17.00555. Epub 2017 Aug 30. PMID: 28855333; PMCID: PMC5940448.

Manke, K. 2019. Genomic gymnastics help sorghum plant survive drought. Posted on news.berkeley.edu December 2, 2019, accessed August 19, 2022. https://news.berkeley.edu/2019/12/02/genomic-gymnastics-help-sorghum-plant-survive-drought/.

Marugan-Hernandez, V., G. Sanchez-Arsuaga, S. Vaughan, A. Burrell, and F.M. Tomley. 2021. Do all coccidia follow the same trafficking rules? *Life* 11:909. DOI: https://doi.org/10.3390/life11090909.

Mathis, K.A. and J.L. Bronstein. 2020. Our current understanding of commensalism. *Annual Review of Ecology, Evolution and Systematics* 51:167-189.

Mullins, A., T. Chouvenc, and N-Y. Su. 2021. Soil organic matter is essential for colony growth in subterranean termites. *Nature: Scientific Reports* 11:21252. DOI:10.1038/41598-021-00674-z.

Mus, F, M.B. Crook, K. Garcia, A. G. Costas, B.A. Geddes, E.D. Kouri, P. Paramasivan, M-H. Ryu, G.E.D. Oldroyd, P.S. Poole, M.K. Udvardi, C.A. Voight, J-M. Ané, and J.W. Peters. 2016. Symbiotic nitrogen fixation and the challenges to its extension to nonlegumes. *Applied and Environmental Microbiology* 82, no. 13:3698-3710.

National Laboratories of Medicine: National Center for Biotechnology Information. NCBI Taxonomy to include phylum rank in taxonomic names, 2021. Retrieved June 13, 2022, from NCBI Taxonomy to include phylum rank in taxonomic names - NCBI Insights (nih.gov).

Neuhauser, C. and J.E. Fargione. 2004. A mutualism-parasitism continuum model and its application to plant-mycorrhizae interactions. *Ecological Modeling* 177:337-352. DOI:10.1016/j.ecolmodel.2004.02.010.

Pandey, D., H. K. Kehri, I. Zoomi, O. Akhtar, and A. K. Singh, 2019. Mycorrhizal fungi: Biodiversity, ecological significance, and industrial applications. *Recent Advancement in White Biotechnology through Fungi* 181-199.

Paracer, S. and V. Ahmadjian, 2000. *Symbiosis: An Introduction to Biological Associations.* Oxford, Oxford University Press Inc.

Perotto, S., S. Daghino, and E. Martino. 2018. Ericoid mycorrhizal fungi and their genomes: another side to the mycorrhizal symbiosis? *New Phytol.* 220:1141-1147.

Perry, D.A. 1995. Self-organizing systems across scales. *Trends in Ecology and Evolution*. 10, No. 6:241-244.

Pita, L, S. Fraune, and U. Hentschel. 2016. Emerging sponge models of animal-microbe symbiosis. *Frontiers in Microbiology*. 7:1-8. DOI: 10.3389/fmicb.2016.02102.

Plett, K. L., and E. K. Stuart, 2020. Digging Deeper: In Search of the Mechanisms of Carbon and Nitrogen Exchange in Ectomycorrhizal Symbiosis. *Front. Plant Sci.* 10:1658.

Prugnolle, F., P. Durand, B. Ollomo, L. Duval, F. Ariey, C. Arnathau,

J. Gonzales, E. Leroy, and F. Renaud. 2011. A fresh look at the origin of *Plasmodium falciparum,* the most malignant malaria agent. *PLoS Pathogens* 1001283.

Rädecker, N., J.E. Chen, C. Pogoreutz, M. Herrera, M. Aranda, and C. R. Voolstra. 2019. Nutrient stress arrests tentacle growth in the coral model *Aiptasia. Symbiosis.* 78:61-64.

Rosendahl, S. 2008. Communities, populations, and individuals of arbuscular mycorrhizal fungi. *New Phytologist* 178:253-266.

Roth, R., and U. Paszkowski. 2017. Plant carbon nourishment of arbuscular mycorrhizal fungi. *Current Opinion in Plant Biology* 39:50-56.

Roy, S, W. Liu, R.S. Nandety, A. Crook, K.S. Mysore, C.I. Pislariu, J. Frugoli, R. Dickstein, and M.K. Udvardi. 2020. Celebrating 20 years of genetic discoveries in legume nodulation and symbiotic nitrogen fixation. *The Plant Cell* 30, no. 1:15-41. DOI: 10.1105/tpc.19.00279.

Sagan, L. 1967. On the origins of mitosing cells, *J. Theor. Biol.* 14:225-274.

Sanabria, N.M, J. Huang, and I. A. Dubery. 2010. Self/nonself perception in plants in innate immunity and defense. *Self Nonself* 1(1):40-54. DOI: 10.4161/self.1.1.10442.

Schulz, F., Abergel, C. & Woyke, T. 2022. Giant virus biology and diversity in the era of genome-resolved metagenomics. *Nat Rev Microbiol* 20 721–736. DOI: https://doi.org/10.1038/s41579-022-00754-5.

Schwartz, C., and P.G. Fallon. 2018. Schistosoma "eggs-iting" the host: granuloma formation and egg excretion. *Frontiers in Immunology* 10:3389.

Snow, R.W. 2015. Global malaria eradication and the importance of *Plasmodium falciparum* epidemiology in Africa. *BMC Medicine* 23.

Steenhoudt O., J. Vanderleyden. 2000. Azospirillum, a free-living nitrogen-fixing bacterium closely associated with grasses: genetic, biochemical and ecological aspects. *FEMS Microbiol Rev* 24:487–506. DOI: 10.1111/j.1574-6976.2000.tb00552.x.

Stubbendiek, R.M., H. Li, and C.R. Currie. Convergent evolution of signal-structure interfaces for maintaining symbioses. *Current Opinion in Microbiology* 50:71-78.

Tarnecki, A.M., F.A. Burgos, C.L. Ray, and C.R. Arias. 2017. Fish intestinal microbiomes: Diversity and symbiosis unravelled by metagenomics. *Journal of Applied Microbiology* 123:2-17. DOI: 10.1111.jam.13415.

Thanganathan, S. and K. Hasan. 2018. Diversity of nitrogen fixing bacteria with various termite species. *Pertanika J. Trop. Agric. Sc.* 41, no. 3:925–940.

Thompson, L.R., K. Nikolakakis, S. Pan, J. Reed, R. Knight, and E.G. Ruby. 2017. Transcriptional characterization of *Vibrio fischeri* during colonization of juvenile *Euprymna scolopes.* 2017. *Environmental Microbiology* 19, no.5:1845-1856. DOI: 10.1111/1462-2920.13684.

van't Padje, A., G.D.A. Werner, and E.T. Kiers. 2020. Mycorrhizal fungi control phosphorus value in trade symbiosis with host roots when exposed to 'abrupt' crashes and 'booms' of resource availability. *New Phytologist* 229:2933–2944. DOI: 10.1111/nph.17055.

Varoquaux, N., B. Cole, C. Gao, G., Pierroz, C.R. Baker, D. Patel, M. Madera, T. Jeffers, J. Hollingsworth, J. Sievert, Y. Yoshinaga, J. A. Owiti, V.R. Singan, S. Degraaf, L. Xu, M.J. Blow, M.J. Harrison, A. Visel, C. Jansson, K.K. Niyogi, R. Hutmacher, D. Coleman-Derr, R.C. O'Malley, J.W. Taylor, J. Dahlberg, J.P. Vogel, P.G. Lemaux, & E. Purdom. 2019. Transcriptomic analysis of field-droughted sorghum from seedling to maturity reveals biotic and metabolic responses. *Proceedings of the National Academy of Sciences* 116, no. 152: 27124-27132 https://doi.org/10.1073/pnas.1907500116].

Vohnik, M. 2020. Ericoid mycorrhizal symbiosis: theoretical background and methods for its comprehensive investigation. *Mycorrhiza* 30: 671-695.

Walder, F., M. G. A. van der Heijen. 2015. Regulation of resource exchange in the arbuscular mycorrhizal symbiosis. *Nature Plants* 1, no. 11: 1-7.

Wang, W., J. Shi, Q. Xie, Y. Jiang, N. Yu, E. Wang. 2017. Nutrient Exchange and Regulation in Arbuscular Mycorrhizal Symbiosis. *Molecular Plant* 10, no. 9: 1147-1158.

Watkinson, S. C. 2016. Mutualistic Symbiosis Between Fungi and Autotrophs. *In the Fungi (Third Edition)*, pp. 205-243.

Wise, K.P. 2019. Biblical death as a cessation of function. *Journal of Creation Theology and Science Series B Life Sciences,* 9:1-7.

Wise, K.P. 2018. *Devotional Biology: Learning to Worship the Creator of Organisms*. Nashville, Compass Classroom.

Wolowczuk, I., S. Nuttun, O. Roye, M. Delacre, M. Capron, R.M. Murray, F. Trottein, and C. Auriault. 1999. Infection of mice lacking interleukin-7 (IL-7) reveals an unexpected role for IL-7 in the development of the parasite *Schistosoma mansoni*. *Infection and Immunity* 67, no 68: 4183-4190.

Wood, T.C., and M.J. Murray, 2003. Understanding the pattern of life: origins and organization of the species. Edited by K. Wise. Nashville, Tennessee: Broad & Holman Publishers.

Wood, T.C. and P.A. Garner (Editors). 2009. *Genesis Kinds: Creationism and the Origin of Species, Issues in Creation No. 5,* Eugene: Wipf and Stock, 163-192.

Xu, et al. 2018. Drought delays development of the sorghum root microbiome and enriches for monoderm bacteria. *Proceedings of the National Academy of Sciences* 115, no. 18: E4284–E4293. www.pnas.org/cgi/doi/10.1073/pnas.1717308115.

Zuill, H. 2000. Ecology, biodiversity, and creation. *CEN Technical Journal* 14, no. 2:82-90.

Zuill, H. and T.G. Standish. 2007. Irreducible interdependence: An ic-like ecological property potentially illustrated by the nitrogen cycle. *Origin-GRI* 60:6-40.

THE AUTHORS

Tom Hennigan is Associate Professor of Ecology at Truett McConnell University. His particular research interests focus on forest ecology and complex relational interactions. He has an A.A.S. in forest technology from the New York State Forest Ranger School, a B.S. in natural resources management from the University of Alaska, an M.S. in education from Syracuse University, and an M.P.S. in environmental and forest biology from SUNY College of Environmental Science and Forestry. He has taught ecology for over 20 years and has studied in the Galápagos. A product of creation evangelism, he has authored numerous articles, and a book.

Dr. Randy Guliuzza has a B.S. in Engineering from the South Dakota School of Mines and Technology, a B.A. in theology from Moody Bible Institute, an M.D. from the University of Minnesota, and a Master of Public Health from Harvard University. Dr. Guliuzza served nine years in the Navy Civil Engineer Corps and is a registered Professional Engineer. In 2008, he retired as a lieutenant colonel from the Air Force, where he served as 28th Bomb Wing Flight Surgeon and Chief of Aerospace Medicine, and joined ICR as National Representative. He was appointed President of ICR in 2020.

Matthew E. Ingle is an Adjunct Associate Professor at The Master's University. His particular research interests include parasitology, especially how parasites impact host behavior and ecology. He has a

B.S. in biology from The Master's College, a M.S. in natural science from Loma Linda University, and a PhD in biology from Loma Linda University. He has taught at numerous universities for more than 10 years and has authored several articles and book chapters.

Grace Lansdell is an undergraduate biology major at Truett McConnell University. She has many scientific interests, including ecology, botany, astronomy, and volcanology. As she narrows down these interests, her goals are to pursue both Masters and Ph.D. degrees for the purposes of contributing important insights to the Creation Model.