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<sup>1</sup>*PSI*, <sup>2</sup>*ETH Zurich*

13:30 – 14:10

**KEYNOTE**

## Multicellularity: Biological and Planetary Perspectives

Andrew Knoll <sup>1</sup>

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The cell is the fundamental unit of life on Earth. The first organisms were most likely unicellular, and numerous clades still complete their life cycles as single cells. That said, multicellularity has arisen many times within Bacteria as well as the Eukarya. Most of these clades can be described as simple multicellular organisms, with cell-cell adhesion but limited communication or differentiation. In these organisms constituent cells remain in more or less direct contact with the external environment, at least during metabolically active stages of the life cycle, and death of individual cells may have only limited impact on the organism as a whole. In contrast, complex multicellularity, defined here operationally as organisms with tissues or organs that circumvent the limitations of diffusion, combine cell-cell adhesion, directed communication between cells and a program of cell differentiation. Organ or tissue failure can doom the whole organism. Such organisms have evolved only about half a dozen times, all within the Eukarya: animals, plants, florideophyte red algae, kelps, and two or more groups of fungi.

While the evolution of multicellularity is a question of biology, it is also one of planetary development, a question of history as well as process. Indeed, a glance at history illuminates the importance of planetary development. While Earth has been a biological planet for most of its history, complex multicellular organisms have populated only the last fifteen percent of that span. Simple multicellular eukaryotes occur in rocks as old as 1600 million years, their evolution perhaps facilitated by resource acquisition, improved predation, or defense against predators. Complex multicellular marine organisms appear ca. 600-575 Ma, coincident with an apparent reorganization of the phosphorus cycle and increases in both primary production and pO<sub>2</sub>. Thus, energetics, modulated by ecology and rooted as much in planetary as in physiological processes, may lie at the heart of macroscopic diversity on Earth-like planets.

14:10 – 14:30

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## Thermal adaptation evolution of the biosphere regulates Earth's long-term climate

Rogger J<sup>1</sup>, Mills B<sup>2</sup>, Gerya T<sup>1</sup>, Pellissier L<sup>1</sup>

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Sustained habitable conditions and the evolution of complex life on Earth depend on efficient climate regulation mechanisms that keep carbon fluxes between geologic reservoirs and the atmosphere-ocean system in balance. The terrestrial biosphere plays an important role in regulating the long-term climate by controlling burial rates of photosynthetically fixed CO<sub>2</sub> as well as by mediating CO<sub>2</sub> consumption through silicate mineral weathering during plant nutrient acquisition, balancing out carbon inputs to the atmosphere-ocean system by volcanism or metamorphism. Current biogeochemical models of the Phanerozoic Earth neglect that the strength of the impact of the terrestrial biosphere on global carbon fluxes is subject to evolutionary dynamics and that it depends on how well the biosphere is adapted to prevailing environmental conditions [1]. Here, we develop a theoretical model to reconstruct million-yearly global organic and inorganic carbon fluxes over the last 400 Myrs. We show that the speed of evolutionary adaptation of the terrestrial biosphere to climatic shifts strongly affects the long-term atmosphere-ocean carbon mass balance. When considering a slow rate of thermal adaptation of the biosphere, resulting in reduced organic carbon burial and especially, strongly reduced silicate weathering rates following temperature shifts, a closer balance of reconstructed Phanerozoic carbon inputs and outputs to and from the atmosphere-ocean system is obtained. Such a balance is a prerequisite to maintain habitable conditions on Earth's surface on a multi-million-year timescale. We argue that the climate evolution of the Phanerozoic Earth is strongly defined by biological and evolutionary processes. Understanding these biological dynamics and how they shape the interactions between Earth's biosphere, geosphere and the climate system may help to understand large shifts in Phanerozoic temperatures and the development of the atmospheric composition of the planet.

[1] Mills, B.J. et al. Modelling the long-term carbon cycle, atmospheric CO<sub>2</sub>, and Earth surface temperature from the late Neoproterozoic to present day. *Gondwana Research* 67, 172-186. DOI: 10.1016/j.j.gr.2018.12.001

14:30 – 14:50

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## Ediacaran Community Development Suggests a Stochastic Influence on the Early Evolution of Animals

Stephenson N<sup>1</sup>, Delahooke K<sup>1</sup>, Kenchington C<sup>1</sup>, Manica A<sup>1</sup>, Mitchell E<sup>1</sup>

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Modern-day community and ecosystem evolution on Earth is driven by predictable differential patterns in biotic and abiotic variables. Communities develop via succession processes which are largely niche driven. However, previous research has now shown that the first animal communities on Earth were dominated by neutral processes, with stochastic reproduction and dispersal overwhelmingly influencing evolution. It is therefore not known whether community development occurred in early animal communities and what this meant for community dynamics and evolution of the first animals. Here, we show that early animal systems did experience a maturation process, but that there are no consistent signals of composition or individual species dominance. We propose that randomness in community development had a profound effect on the evolution of the first animal life on Earth, rather than the directional and systematic dynamics observed in modern ecosystems. Early animals would therefore not have been predictably exposed to the same combinations of different species, but instead encountered random variation leading to irregular patterns of interactions and evolutionary pressures within a community. This random variation suggests that the point at which systematic niche processes became dominant in animal ecosystems on Earth may be impingent on random biotic and abiotic events. The influence of stochastic events on evolution indicates that the transition from neutral- to niche-dominance on Earth was likely temporally unpredictable, and as such evolutionary dynamics on other planets may not replicate an Earth-like system. Therefore, without the specific evolutionary events that happened on Earth, life on other planets may be markedly different dependant on planet-specific dynamics that drive evolution.

14:50 – 15:10

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## The costs and benefits of multicellular group formation in algae

Kapsetaki S<sup>1,2</sup>, West S<sup>2</sup>

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The first step in the evolution of complex multicellular organisms involves single cells forming a cooperative group. Consequently, to understand multicellularity, we need to understand the costs and benefits associated with multicellular group formation. We found that in the facultatively multicellular algae *Chlorella sorokiniana*: (1) the presence of the flagellate *Ochromonas danica* or the crustacean *Daphnia magna* leads to the formation of multicellular groups; (2) the formation of multicellular groups reduces predation by *O. danica*, but not by the larger predator *D. magna*; (3) under conditions of relatively low light intensity, where competition for light is greater, multicellular groups grow slower than single cells; (4) in the absence of live predators, the proportion of cells in multicellular groups decreases at a rate that does not vary with light intensity. These results can explain why, in cases such as this algae species, multicellular group formation is facultative, in response to the presence of predators.

15:10 – 15:30

67

## How BioEncounters at the microscale prime microbial interactions

Slomka J<sup>1</sup>

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Microbial life critically depends on cell-cell or cell-resource encounters: these microscale processes control the rate of many fundamental ecological and evolutionary functions. A prominent example are the encounters among phytoplankton in the ocean that lead to the formation of marine snow following a phytoplankton bloom, an important process which fuels the “biological pump,” the vertical export of carbon to the deep ocean. Another example is horizontal gene transfer between bacteria by conjugation, a key driver of bacterial evolution that is primed by cell-cell encounters followed by a plasmid-mediated gene exchange. Microscale encounters are nearly always modeled as encounters between inanimate spheres, borrowing from physical models of gasses, coagulating colloids and rain formation. However, I will show here that these physics-based approaches fail to account for important traits of microorganisms, for example cell elongation, and I will outline how more realistic models of encounters and aggregation can contribute to our understanding of fundamental ecological and evolutionary processes controlled by microbes. For example, cell shape, in conjunction with buoyancy and turbulence, can increase encounter rates and thus speed up the formation of marine snow by elongated phytoplankton nearly ten-fold: this result provides a mechanistic explanation for the rapid clearance of blooms of elongated phytoplankton species. I will then describe our recent experimental efforts to measure the probability that a bacteria-bacteria encounter results in a plasmid transfer – a key parameter that determines the rates of data exchange and thus genetic innovation between bacteria.

### Exploring the influence of plants on Phanerozoic climate using a deep time dynamic vegetation model

Gurung K<sup>1</sup>, Mills B<sup>1</sup>

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Land plants are key contributors to global primary production and influence atmospheric CO<sub>2</sub> levels. Over the Phanerozoic, terrestrial vegetation and its interaction with atmospheric carbon likely exerted control, to some degree, on climate. However, representation of the terrestrial biosphere over geological timescales and paleogeography in biogeochemical models is limited and poorly understood.

Here, we couple a new deep-time vegetation model (FLORA) to a spatially-resolved long-term climate-chemical model (SCION [1]). FLORA improves upon the spatial representation of plant productivity over the Phanerozoic. The dynamic feedback created between local climatic conditions and vegetation biomass allows us to explore the impact of vegetation on organic carbon burial and spatial weathering rate amplification, and thus atmospheric CO<sub>2</sub> concentration over the Phanerozoic. We show that continental aridity during the Triassic and Jurassic restricted CO<sub>2</sub> drawdown and created a hotter climate. Conversely, continental dispersal in the Cretaceous allowed the terrestrial biosphere to sequester more carbon, countering high rates of tectonic degassing and mediating climate. By improving the representation of the terrestrial biosphere and creating local climatic interactions, the new SCION predictions better match available proxy data and highlight the importance of a comprehensive vegetation model within long-term climate-chemical models. Further improvements to the model involve the addition of plant functional types, ecological interactions and terrestrial nutrient cycling. Future work aims to use these models to explore the impact of land colonisation and plant evolution on Phanerozoic climate change.

[1] Mills, B. J. W., Donnadieu, Y. & Godd ris, Y., (2021), *Gondwana Research* 100, 73-86.  
doi:10.1016/j.gr.2021.02.011



## High-affinity interactions between amino acids and phyllosilicates: Observations from the biosphere-geosphere interface

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<sup>1</sup>*Geological Institute, ETH Zurich*, <sup>2</sup>*Biogeochemistry Research Center, JAMSTEC*

Earthen and extraterrestrial matrices comprise complex mixtures of minerals and organic matter. Among these organic constituents, amino acids represent a commonality in both environments and are widely considered prerequisite to the origin of life (Degens, 1964). Amino acids are composed of amino and carboxyl functional groups associated with a carbon skeleton and exhibit a wide molecular range from hydrophilic to hydrophobic profiles. The affinity between silicates and amino acids is a controlling factor in producing nitrogenous molecule diversity as well as carbon skeletal elongation reactions (Vinogradoff et al., 2020). Cutting edge investigations on geologically recent matrices showcase direct evidence on the role of phyllosilicates for modulating the preservation of amino acids in the sedimentary record. Observed for the first time in nature using techniques developed by teams at ETH Zurich and JAMSTEC using high-resolution chromatographic isolation and subsequent measurement of amino acid-specific radiocarbon, these preservation patterns largely reflect molecular-level interactions consistent with experimental and theoretical knowledge (Blattmann & Ishikawa, 2020). With an organic geochemical approach to the geological principle of uniformitarianism utilizing the present as a key to the past, we posit that these synergetic interactions between organic molecules and silicate minerals operated similarly on primordial Earth with implications for the spatial disposition and chemical stabilization/modification of life's prebiotic building blocks.

### References:

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- Degens, E.T. (1964) Genetic relationships between the organic matter in meteorites and sediments. *Nature* 202, 1092-1095.
- Vinogradoff, V. et al. (2020) Impact of phyllosilicates on amino acid formation under asteroidal conditions. *ACS Earth and Space Chemistry* 4, 1398-1407.

## Stochastic versus deterministic drivers of early animal evolution.

Mitchell E<sup>1</sup>

<sup>1</sup>*University Of Cambridge*

The evolution of animals was one of the most important evolutionary transitions in the history of life on Earth, with widespread animals appearing around 600 million years ago (Ma) during the Ediacaran time period. However, the drivers behind the origins and early evolution of these animals are unresolved. Fortunately, the eco-evolutionary dynamics of these Ediacaran animals can be investigated because the fossil preservation during this time is exceptional with thousands of these sessile organisms preserved in-situ, as censuses of their communities. This exceptional preservation enables the use of quantitative ecological approaches to test the relative importance of stochastic versus deterministic (environmental) processes for Ediacaran community dynamics. In the oldest Ediacaran animal communities, stochastic processes dominate with deterministic processes exerting limited influence, in contrast with the deterministic and niche-dominated dynamics of modern marine ecosystems. The dominance of stochastic processes suggests that early metazoan diversification may not have been driven by systematic adaptations to the local environment, but instead may have resulted from stochastic demographic differences. This stochastic dynamic changes for younger Ediacaran communities, which were heavily influenced by local environmental patchiness, and also saw a significant increase in competition within and between different species. These environmental interactions are deterministic or predictable. Further analyses of all known Ediacaran communities show that throughout the Ediacaran there is increasing environmental specialisation and ecological complexity, paving the way for more familiar animals to rise in the Cambrian. This change in eco-evolutionary dynamics throughout the first animals of the Ediacaran, from stochastic to deterministic, raises the intriguing possibility that other key evolutionary events and dynamics may be a mixture of random chance and predictable responses to the biosphere, and that the origins of animals themselves may not have been inevitable.

## Experimental evolution under extraterrestrial conditions

McGinnis D<sup>1,2</sup>, Ibelings B<sup>1,2</sup>, Thomas M<sup>2</sup>, Bolmont E<sup>1,2</sup>

<sup>1</sup>Center Life in the Universe, <sup>2</sup>University of Geneva

Life is defined by the capacity of Darwinian evolution. Experimental evolution has proven to be one of the most powerful tools to study the mechanisms of evolution on Earth (e.g. Lenski et al. 2017). Evolution that drove the diversification of life from a simple and homogenous beginning. We aim to perform experimental evolution and observe which geno- and phenotypic traits will be favored under conditions found on different planets. For this we assume that there is a core to life that is similar on Earth and elsewhere, so that presently the best model system to study Life in the Universe are life-forms found on Earth. There are many organisms (facultatively) adapted to life in the absence of oxygen (e.g. methanogens, yeast, e.g. Beatty et al. 2005 for an example). Some of these function with very simple substrates, for example methane production occurring from hydrogenotrophic processes, where the substrates could be from expelled biogases of other organisms or by carbonate rock erosion ( $4\text{H}_2 + \text{CO}_2 \rightarrow \text{CH}_4 + 2\text{H}_2\text{O}$ ). These processes also alter the balance of the stable C isotopes in the system ( $\delta^{13}\text{C}$ ).

From this perspective, we propose conducting experiments on organism evolution in alternative environments (various substrates and initial atmospheres, such as  $\text{H}_2 + \text{N}_2$  mixture or  $\text{CO}_2$ ). Besides quantifying the organism's evolutionary trajectory, we propose to monitor - using existing equipment in Department Forel from the university of Geneva - the various gases consumed or produced by these organisms, i.e. to investigate what types of atmospheric gas compositions could suggest the presence of life on extra-terrestrial worlds. Studies have shown growth of unicellular prokaryotes and eukaryotes under conditions found on other planets, like the  $\text{H}_2$  dominated atmosphere of rocky exoplanets (Seager et al. 2020), so the potential for experimental evolution is present.

We will present this project, which will start in Septembre-Octobre of this year and which will bring elements of answers on two major questions:

- What are the key traits that evolve when life adapts to non-earth like conditions and what is the nature of the underlying mutations?
- What are the biosignatures found as a consequence of the evolution of new traits? Are they unique signatures of life?

## Motile cilia and eukaryogenesis by comparative structural studies

Ishikawa T<sup>1,2</sup>, Noga A<sup>1</sup>

<sup>1</sup>PSI, <sup>2</sup>ETH Zurich

Cilia are appendage-like organelles of eukaryotes with ~300nm diameter and 5~20 µm length. There are two types of cilia – motile and immotile. Motile cilia have unique structure composed of nine microtubule doublets surrounding two single microtubules, called “9+2”, and powered by dynein, ATP-driven motor proteins. This 9+2 structure of motile cilia is shared from unicellular algae to human, suggesting that the origin of this organelle is widely common, and maybe can be tracked back to the last eukaryotic common ancestor (LECA). Probably motile cilia were acquired by unicellular cells at the early stage of eukaryogenesis, since they were necessary for them to swim toward light and nutrition, and evolved to be in multicellular organisms with various functions. In human, motile cilia function in tracheae, oviducts, brain, sperm and embryos. Defect of motile cilia causes various diseases (primary ciliary dyskinesia).

Interestingly the base part of cilia, called the basal body, which determines nine-fold symmetry and becomes the seed of ciliogenesis, is the same organelles as centriole, the center of microtubule cytoskeleton for cell division. It is still an open question, either the basal body was recycled as the center of cell division, or the centriole was used to be a core of ciliogenesis. Variety of questions regarding origin of motile cilia are unanswered as well – Were cilia originated from other already existing microtubule-based organelles, or brought by other organisms with endosymbiotic or syntrophic mechanisms? Did motile cilia appear first and evolved to immotile cilia, or vice versa? Etc.

Our group has been working on questions regarding motile cilia and the basal body, using comparative structural studies by cryo-electron microscopy, combined with genetic/phylogenetic approaches. Our structural analyses gave mechanistic insight of motile cilia, but also suggestion how motile cilia have been evolving in the history of eukaryotes. In this presentation, we will show our comparative studies on large motor and regulatory complexes from cilia and discuss from evolutionary viewpoints.