

THE TORTOISE VERSUS THE HARE: COMPUTER SIMULATION OF EUENDOLITHIC MICROBIAL ALTERATION TEXTURES. N. R. Banerjee^{1*}, J. Lee¹, M. R. M. Izawa¹, and K. Tiampo¹, ¹Dept. Earth Science, University of Western Ontario, 1151 Richmond St. London, Ontario, Canada N6A5B7 *neil.banerjee@uwo.ca

Introduction: Microbial trace fossils consisting of hollow or mineralized tubules and/or granules in basaltic glass have been reported from rocks of a wide range of ages [1-7]. These structures are interpreted from multi-technique observational approaches to be the result of microbial glass dissolution [1-7]. Laboratory experiments have been successful in producing pitting textures on sterile volcanic glass surfaces but generation of tubular alteration morphologies on laboratory timescales remains elusive [cf. 2]. Here we use a computer model to simulate the production of euendolithic microbial alteration textures in basalt glass. Our model produces textures that are qualitatively and quantitatively similar to those observed in natural glass bioalteration studies. This allows us to make predictions about what factors may control tubular bioalteration and suggests time is an important factor.

Motivation: Our model is inspired by growth models such as diffusion limited aggregation, where a number of particles move through space while observing some restrictions [8]. The evolution of such a model is marked off in discrete time steps where all particles update their state simultaneously [9]. Growth and particle models can generate very complex patterns, even exhibiting fractal behavior. We set out to investigate whether a simple simulated environment based upon the postulated mechanisms of microbial glass bioalteration could reproduce the variety of complex textural features observed in natural glassy volcanic rocks [1,2,7].

Computer Simulated Microbial Alteration Textures (COSMAT): The program has 10 adjustable parameters: the size of the glass-exterior interface surface (length and width); the maximum number of microbe etcher colonies, hereafter referred to as 'microbes' for simplicity; the maximum lifespan of an individual colony; the mortality rate; the division rate; the mean and variance of the direction of microbe motion into the glass; and the mean and variance of the length of each step into the glass. COSMAT begins by generating a random surface, which represents the interface along which colonization might occur. In nature this could represent a fracture in glass or an exterior surface. Random points on this surface are then chosen as colonization points for microbes (i.e., where etching will begin). The final step of the initialization chooses several additional user-defined parameters that control the future evolution of the system (i.e., the 'rules').

After initialization, the model is moved forward in discrete time steps over which each microbe will make forward movement, or die, reflecting the postulated requirement that the microbes must etch glass to survive, either through the liberation of nutrients, energy, or both. At the beginning of each forward step, the displacement vector of each microbe is oriented in a particular direction, with one 'hard' constraint: the microbe must move into the glass, not toward the exterior. An adjustable parameter controls the tendency to continue moving in the initial direction. Once a direction is chosen, a step length is chosen uniformly between a given minimum and maximum, and the microbe attempts to step forward. In the basic model this attempt always succeeds.

A variant has been designed where the microbe can detect a collision with another tube and change course. Collision avoidance is justified in terms of microbial behaviour and metabolism: a ~30 nm thick SiO₂-rich, nutrient depleted zone has been detected surrounding bioalteration textures [11]. Such a depleted layer could inhibit etching, perhaps because the glass is more polymerized and/or resistant to etching, and/or because it would not be metabolically favourable to etch such depleted glass. The fact that microbial etchings in basaltic glass do not intersect has been reported in numerous petrographic studies and is an argument for their biological origin [1,2,5]. By analogy, observations of worm burrows in sediments and sedimentary rocks indicate that they rarely, if ever, cross and this is attributed to biological behaviour.

At each time step, there is a probability of the tubules bifurcating (i.e., probability of cell/colony division). If a division event occurs, a second microbe is introduced and begins its own path. This new microbe continues from the same point as the original, but chooses an independent direction. At each step, each microbe has a small adjustable probability of dying. If it dies, then it no longer adds steps to its path and does not bifurcate. A microbe also dies if it reaches the maximum age, which is another user-defined parameter.

Model fit to observations: The division rate, lifespan and mortality in the model strongly influence the morphology of the etch structures. In particular, it is observed that rapid division and high mortality (live fast, die young) leads to small, knotted structures that closely resemble observed granular alteration textures in basaltic glass in laboratory

experiments and nature [2,5]. Conversely, slow division and long life spans favour the production of long, sub-parallel groups of tubules, highly reminiscent of tubular bioalteration textures only observed in nature. This model observation is consistent with arguments, based on diffusion, for the necessity of long division times for the microbes responsible for producing tubular bioalteration textures. At slow division rates diffusion could be responsible for transfer of nutrients and waste along long tubules without starvation or poisoning of the microbes, respectively. A possible intermediate case, with higher incidence of tubule bifurcation and convoluted tubule morphology, is also observed.

The paths the etchers take can also be influenced by a probability function on the material. That is, a heterogeneous material is created by dividing the original medium into separate regions. Each partition is assigned a value which represents the difficulty for a microbe to move through that region. Qualitatively, this ranges from “impossible” to “unimpeded”. If this feature is added to the model, it shapes the probability function of the direction a microbe chooses to move. For example, if a perfect barrier is set up in the material and a microbe approaches it, then the probability of moving in the direction of the barrier drops to zero. In effect, the microbe will be forced to avoid such ‘inedible’ materials.

The earliest version of the model had no such material probability function and so effectively assigned a value of “unimpeded” to all points. Physically, this corresponds to etching into homogeneous basaltic glass. A further development will be to include a variety of different substrate materials, physically corresponding to minerals and void spaces (phenocrysts and vesicles) in the glass. Many scenarios may be envisaged including: ‘edible’ glass with ‘inedible’ inclusions, ‘inedible’ glass with ‘edible’ inclusions (perhaps corresponding to a more felsic glass with Fe-rich inclusions), and varieties of inclusions which are more or less ‘edible’, perhaps corresponding to the different nutrient/energy availability in minerals such as olivine, pyroxene, plagioclase, oxides, sulfides, and glass.

Quantifying bioalteration textures: The success of this model in qualitatively reproducing not only the variety of structures observed in natural glasses, but specific features that can be linked to the particular parameters of the model, led us to perform a more detailed quantitative analysis on the spatial properties of both the observed data and the model. In addition, we can study their variation in the model with different parameter values. Finally, the temporal evolution of the model can be quantified using additional techniques, popularized in the field of complexity theory, which can be used to evaluate the

effect of various model parameters on the evolution of these structures.

Spatial properties of the long, sub-parallel tubule structures can be evaluated through either the box counting dimension and/or the Hausdorff dimension scaling laws, and various cluster analysis techniques [12-14]. Here the correlation between these values in the data, natural glasses, and the behaviour of the model, are studied and the particular parameter values that present statistics that match these values are evaluated in order to provide insight into the biological processes.

Temporal statistics are more difficult to evaluate for phenomena such as this. One measure of the nature of the fluctuations in a time series is given by the Hurst coefficient, which provides a sensitive method for revealing long-run correlations in random time series [15,16]. Once the appropriate parameter ranges that provide a good fit to the natural glasses are determined from the above spatial statistics, different techniques can be used to calculate this coefficient for simulated time series from our model. In addition, a complementary scaling analysis, the diffusion entropy analysis (DEA), that focuses on the scaling exponent of the diffusion generated by the fluctuations of a time series, is performed in order to determine the characteristics of these time series [17,18].

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