condition of chronic systemic inflammation could result in the activation of greater numbers of circulating monocytes. If they are already activated, these cells would be primed for transendothelial migration. This notion is substantiated by the fact that acute SIV infection is associated with increases in both the number of circulating CD16-positive monocytes (*42*) and the number of perivascular macrophages in the brain (*17*). This hypothesis could also help to explain why the best-known predictor of HIV dementia is anemia (*43*). Most important, it suggests that with effective control of systemic HIV replication and consequent macrophage activation, HIV dementia will not develop.

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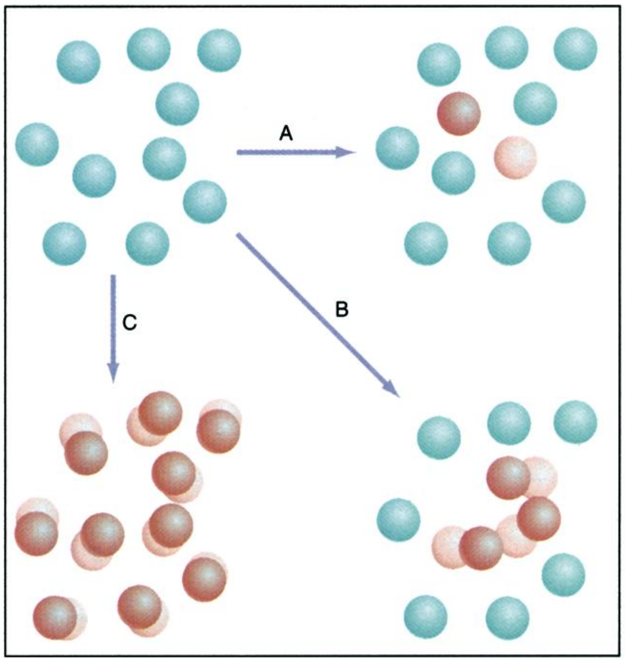
PERSPECTIVES: MATERIALS SCIENCE

Movies of the Glass Transition

M. D. Ediger

When a liquid is cooled, it can solidify in two very different ways. The familiar route produces an ordered crystal. In this case, the change in the mechanical properties of the material from viscous liquid to elastic solid can easily be explained by the change in structure. An equally important but more subtle transformation occurs when crystallization is avoided during cooling. With decreasing temperature, the molecules in the liquid move more and more slowly. In the absence of crystallization, the viscosity of the liquid increases continuously, typically by a factor of 10^{10}. Eventually, molecular motion is frozen on the time scale of laboratory experiments, and a noncrystalline solid—a glass—forms. The structural changes that occur during this cooling are small, and we must look to molecular motion for an explanation for this transformation. Key insights into the motion responsible for the transition to the glass are provided by Weeks *et al.* on page 627 of this issue (*1*) and in a recent report by Kegel and van Blaaderen (*2*).

Understanding the nature of glass formation is an important practical issue that goes far beyond window glass. Glassy pharmaceuticals are more rapidly available to the body than crystals. Saccharide glasses are being used to preserve biological structures (tissues, cells, and enzymes) for storage and transportation. All synthetic polymers form solids that are at least partially amorphous; the properties of materials and devices made from polymers thus depend on the molecular motions responsible for the glass transition. Breakthroughs in our understanding of the glass transition may also impact related fields, including protein dynamics and the flow of granular materials.



How do particles move near the glass transition? For each of the three possibilities shown, the average particle moves 20% of a particle diameter between frames. New particle positions are shown in red; vacated positions are pale red. Motion is either concentrated on one particle (**A**), or distributed across some (**B**) or all particles (**C**). Colloid motion is most like (C), but occurs primarily in a subset of unusually fast particles.

The phenomenology of glass formation has been known for decades (*3*, *4*), but we are still far from understanding the relevant features of molecular motion. Experiments have not allowed us to directly measure how a molecule moves relative to a particular neighbor in a glass or to observe which local structures are prone to reorganization. Therefore, important questions regarding the heterogeneity and cooperativity of molecular dynamics in glasses (see the figure) have remained unanswered. Computer simulations provide the required level of detail, but can only supply limited insight because the relevant time scales are so long.

Kegel and van Blaaderen (*2*) and Weeks *et al.* (*1*) have approached this problem through uniquely powerful experiments on a model glass-forming system made of colloidal spheres suspended in a solvent (*5*). The colloidal glass transi-

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tion is induced by increasing the volume fraction (as opposed to decreasing the temperature in the case of molecular glass formers). The size of one particle is roughly the wavelength of visible light, and therefore confocal microscopy can be used to record the position of each sphere in a large sample as a function of time, thus allowing detailed questions about particle motion to be answered. The trajectories provide a motion picture of particle dynamics, in which the colloids might be regarded as stand-ins ("superatoms") for atoms or molecules. This approach shares an intellectual and technological heritage with the field of single-molecule spectroscopy (*6*).

Of the possible scenarios illustrated in the figure, case C is most representative of colloid motion observed near the glass transition. Consistent with inferences made from less direct measurements on molecular glass formers (*7*), small adjustments by a large number of particles allow structural relaxation and flow. However, case C does not even begin to do justice to the complexity of motion near the glass transition. Recent work on molecular glass formers has indicated that dynamics near the glass transition are spatially heterogeneous; that is, dynamics in some parts of the system are orders of magnitude faster than dynamics in other regions a few molecular diameters away (*8*, *9*).

The imaging work on colloidal systems in (*1*) and (*2*) also shows heterogeneity as a dominant aspect of glass transition dynamics. Kegel and van Blaaderen (*2*) report a non-Gaussian van Hove function consistent with the existence of fast and slow subsets of particles on a time scale where the average particle has moved about 25% of a particle diameter. Weeks *et al.* (*1*) report cooperatively rearranging clusters of more than 50 fast-moving particles that seem to dominate structural relaxation [see Fig. 4A in (*1*)]. The properties of these clusters are similar to those found in recent computer simulations (*10*). Further work on colloidal systems may show which features of local structure give rise to the fast population of particles and indicate how these structures might be altered to change the properties of glass formers.

The primary issue regarding the glass transition is the cause of the slow dynamics. Contending viewpoints assert density, entropy, or underlying thermodynamic or dynamic transitions as the major factor in molecular glass formers. A secondary issue is the origin of the spatially heterogeneous dynamics observed as the glass transition is approached. It remains open whether heterogeneous dynamics are fundamentally entwined with slow dynamics or merely a side show to the main event of glass formation.

The amazing detail of the imaging experiments in (*1*) and (*2*) may succeed in answering the above questions for colloidal glass formers. Although not all features of the glass transition in colloids will be applicable to molecular and atomic liquids (*11*), a clear view of this particular system will certainly contribute to understanding the universal features of glass formation.

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PERSPECTIVES: EARTH SCIENCE AND EVOLUTION

Genomics and the Geosciences

Jillian F. Banfield and Charles R. Marshall

Genomics—the mapping and sequencing of genomes and analysis of gene and genome function (*1*)—will revolutionize the biological and possibly the geological sciences. To date, some 21 prokaryotic and 2 eukaryotic (a yeast and a nematode) genomes have been published (*2*), and complete sequences from hundreds, perhaps thousands, of species are anticipated in the next few years. This exploding database holds enormous promise for understanding the coevolution of life and Earth. In particular, genomic data will help to elucidate the biological contributions to modern and ancient geochemical cycles, establish the internal and external driving forces for metabolic and morphological innovation, and assess the relative importance of environmental and biological processes on the coevolution of life and Earth's surface through geologic time.

Geochemical cycles operating near Earth's surface have been altered fundamentally by microbial metabolisms ever since the origin of life. When life first evolved it did so in a context defined by its physical and chemical surroundings. Since then, geochemical cycles operating near Earth's surface have been altered fundamentally by microbial metabolisms. In modern environments, spatially and temporally resolved geochemical distribution patterns and microbial population data can be analyzed simultaneously, allowing the nature of their interdependence to be established. Gene sequence data from large numbers of organisms may, in the long term, reveal sufficient biochemical commonality to allow the development of methods to quantify expression of metabolic pathways at the species or higher level. This will enable us to determine the extent to which chemical reactions such as sulfate reduction, iron oxidation, or organic pollutant degradation are biologically—rather than inorganically—mediated. Changes in the relative importance of biological versus inorganic processes over time and as a function of physical and chemical conditions can thus be determined. In parallel, geological information will be required to decipher the complex character of natural environments that control metabolic and microbial community structure. Some basic controls on microbial population structure have, for example, been identified in iron- and sulfur-dominated systems (*3*). However, in-depth analysis requires understanding of pathways for iron and sulfur oxidation, nitrogen fixation, carbon fixation, metal and acid resistance, etc. Understanding these pathways will be facilitated greatly from analysis of genomic data for members of a wide range of natural microbial populations.

Genomics also offer insights into the evolution of geochemical cycles. For example, models that argue for a predominance of oxygen-poor environments on early Earth are corroborated by molecular phylogenies that place anaerobes close to the root of the tree of life and show that oxygen-inhibited nitrogen fixation existed before the last common ancestor of all living organisms. The emission of oxygen into the atmosphere after the emergence of new, complex photosynthetic systems dramatically changed the distribution and speciation of

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