ple grains or crystals with different crystallographic orientations that are separated by grain boundaries. As a result of plastic deformation, the original grains are subdivided into smaller grains separated by dislocation (line defect) networks. Moreover, commercial alloys always contain impurities that can form precipitates, which are small particles with a different composition and crystal structure than the matrix.

Schmidt et al. have determined the absolute crystallographic orientation, position, volume, and shape of a recrystallizing grain in deformed aluminum. Their work shows that the shape of a recrystallizing grain in aluminum is more or less spherical as it starts to grow, in accordance with general belief, but as it grows the grain progresses in different directions with different speeds and in a jerky fashion. The mobility of the grain boundary, which is an important parameter in models, is unambiguously determined and shown to be anisotropic. The authors show that the jerky movement of the grain boundary reflects the inhomogeneous distribution of dislocations in the deformed aluminum matrix. Knowledge about the density, distribution, and arrangement of the dislocation in the deformed matrix and their influence on the growth of an individual grain, as measured by Schmidt et al., is of utmost importance in understanding recrystallization phenomena.

The authors measured the recrystallization process in exceptional detail, which is of great value for theoreticians because theory and experiment can now be compared at the elementary level of a single grain. Characterizing microstructures in 4D opens great opportunities in other fields of materials science. For example, it should now be possible to study the underlying mechanisms of solidification, solid-state phase transformations, and precipitation of a wide range of materials. As a result, the 3DXRD technique will contribute to the development of materials with superior properties and optimal production routes.

References and Notes
7. Supported by the Dutch Technology Foundation (STW) of the Netherlands Organization for Scientific Research (NWO).

GENOMICS

The Chimpanzee Genome—A Bittersweet Celebration
Maynard V. Olson and Ajit Varki

These are exciting times for those interested in human origins. After almost a century of knowledge gleaned from the excavation of hominid bones in East Africa, the draft sequence of the chimpanzee genome is now providing a flood of molecular data that may shed new light on human origins. The challenge of integrating these molecular data with the fossil record and with behavioral studies of great apes was on full display during a recent symposium at the University of California, San Diego (1).

Most speakers discussed one of three principal sources of data: a Japanese-led analysis of chimpanzee chromosome 22 (2); a private-sector initiative at Celera Genomics to sequence most of the exons of the chimpanzee genome (3); and the National Human Genome Research Institute (NHGRI)–funded project to produce a rough-draft sequence of the whole chimpanzee genome (4). Although the recent release of the draft sequence by the Washington University and MIT/Broad Institute sequencing centers (4) was the primary impetus for this symposium, many other aspects of our closest evolutionary relative also were explored.

Yoshiyuki Sakaki (RIKEN Genomics Sciences Center) represented the Japanese-led effort. Although this project analyzed only ~1% of the chimpanzee genome, it provides the first look at long-range comparisons with the human genome based on complete high-quality sequence. The long-range organization of chimpanzee chromosome 22 is nearly identical to that of its human homolog, chromosome 21. The level of single–base pair substitutions between the two species is only 1.44%. However, there are tens of thousands of insertion-deletion variants, including one 200-kbp human-specific duplication. Many sequence variations between the chimpanzee and human lineages are attributable to differing activities of large numbers of retrotransposons.

Andy Clark (Cornell University), representing Celera’s exon sequencing effort, discussed chimpanzee-human comparisons of inferred protein sequences. Interestingly, proteins involved in amino acid catabolism showed a big positive selection signal in the human lineage, whereas those involved in neural development did not. This finding reminds us that diet and pathogens are dominant selective forces for all species. Other genes undergoing rapid positive selection in the human lineage include those encoding proteins that are involved in hearing, such as α-tectorin, a structural inner-ear protein. Evan Eichler (Case Western Reserve University), who based his analysis on the rough-draft whole-genome sequence, emphasized the same point. He reported major deletions in the chimpanzee genome, totaling at least 8 Mbp, which include a number of genes associated with immunity and inflammation. Eichler also discussed the presence in the chimpanzee of many copies of a retroviral provirus that is absent from the human genome. Its presence in chimpanzees, bonobos, gorillas, and Old World monkeys—but not humans, orangutans, and gibbons—suggests multiple, independent instances of horizontal transmission. This serves as another

M. V. Olson is at the University of Washington Genome Center, Departments of Medicine and Genome Sciences, Seattle, WA 98195, USA. A. Varki is at the Glycobiology Research and Training Center, Departments of Medicine and Cellular and Molecular Medicine, University of California at San Diego, La Jolla, CA 92093, USA. E-mail: mvo@u.washington.edu; a1varki@ucsd.edu
Perspectives

Washington) reflected on changing ideas perspectives. Mary-Claire King (University of coverage of both historical and future per-

ging to be a difficult task (compared the chimp and human genomes is learning about human uniqueness by com-

during recent human evolution (this gene has undergone positive selection changes in amino acid coding and a pattern of nucleotide polymorphisms that suggest this gene has undergone positive selection during recent human evolution (Despite these fascinating findings, it is clear that learning about human uniqueness by com-

Paradigm shifts and genotype-phenotype relationships held center stage, two talks on classical aspects of chimpanzee bi-

Although genomes and genotype-phenotype relationships held center stage, two talks on classical aspects of chimpanzee bi-

er monitor faster, and more reliably, than his graduate students!

The symposium ended on a somber note with a talk by Caroline Tutin (University of Stirling, UK) about the desperate plight of the great apes in the wild. Tutin has spent much of her career studying chimpanzees in Gabon. A combination of deforestation, hunting, and disease threaten the imminent collapse of these seriously endangered pop-

References and Notes

1. “Sequencing the Chimpanzee Genome: What Have We Learned?” 12th March 2004, San Diego, CA. Sponsored by The UCSD Project for Explaining the Origin of Humans and supported by the G. Harold and Leila Y. Mathers Charitable Foundation.


4. Unpublished data from the Washington University and MIT/Broad Institute Sequencing Centers (directed by Rick Wilson and Eric Lander, respectively) are pub-


