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.

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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 chimp chromosome 22 (*2*); a private-sector initiative at Celera Genomics to sequence most of the exons of the chimp genome (*3*); and the National Human Genome Research Institute (NHGRI)–funded project to produce a rough-draft sequence of the whole chimp 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 chimp and human lineages are attributable to differing activities of large numbers of retrotransposons.

Andy Clark (Cornell University), representing Celera's exon sequencing effort, discussed chimp-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

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reminder that a dominant force shaping primate genomes has been the proliferation of mobile elements of various kinds.

Providing an overview of the rough-draft whole-genome sequence, Robert Waterston (University of Washington) discussed evidence for the possible rapid evolution of genes involved in host defense, using protease genes as an example. Discussing another aspect of primate interactions with the environment, Svante Paabo (Max Planck Institute, Leipzig) provided new data from his work on olfactory receptor genes (*5*). All great apes appear to have been steadily losing members of this large gene family, but the rate of gene loss in the human lineage is exceptional. Enhancements in human cognitive capacity, and perhaps also the acquisition of bipedalism, may have diminished the need for an acute sense of smell. Paabo also reprised his work on the transcription factor FOXP2 (*6*). Mutations in the human *FOXP2* gene are associated with an autosomal dominant form of dysarthria (difficulty in articulating speech). The human *FOXP2* gene shows changes in amino acid coding and a pattern of nucleotide polymorphisms that suggest this gene has undergone positive selection during recent human evolution (*6*). Despite these fascinating findings, it is clear that learning about human uniqueness by comparing the chimp and human genomes is going to be a difficult task (*7*).

The symposium also provided broad coverage of both historical and future perspectives. Mary-Claire King (University of Washington) reflected on changing ideas about human-chimpanzee relationships since her pioneering work with Alan Wilson in the 1970s comparing molecular similarities between the two species (*8*). Pascal Gagneux (San Diego Zoological Society) summarized evidence from decades of work showing that the chimp and bonobo are our nearest relatives, followed by the gorilla and orangutan. Symposium co-organizer Ajit Varki (University of California, San Diego), with Chaitanya Baru (San Diego Supercomputer Center), outlined early efforts to complement the chimpanzee genome project with a "Great Ape Phenome Project" (*9*). This initiative aims to organize all extant data—currently difficult to find—about phenotypic differences among the great apes.

Although genomes and genotype-phenotype relationships held center stage, two talks on classical aspects of chimpanzee biology and ecology are likely to have left the strongest impressions. Tetsuro Matsuzawa (Kyoto University) described his career-long studies of chimpanzee behavior, carried out both in the wild and in captivity. His studies in West Africa have captured the way in which particular types of tool use are culturally transmitted, that is, passed on to other members of the same chimp community. He showed film footage of a young chimp imitating every detail of an adult's use of a large stone to crack extremely hard nuts. In addition to documenting natural behavior, Matsuzawa showed examples of chimpanzees in his laboratory in Kyoto. These individuals are able to carry out certain interactive tasks at a computer 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 populations. In his summary remarks, symposium co-organizer Maynard Olson (University of Washington) urged scientists to look for ways to channel some of their enthusiasm for understanding the similarities and differences between humans and their closest kin into urgent conservation efforts. Both Tutin and Matsuzawa emphasized that if great apes are to survive in the wild, their preservation will be won one replanted tree and one reordered priority at a time.

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