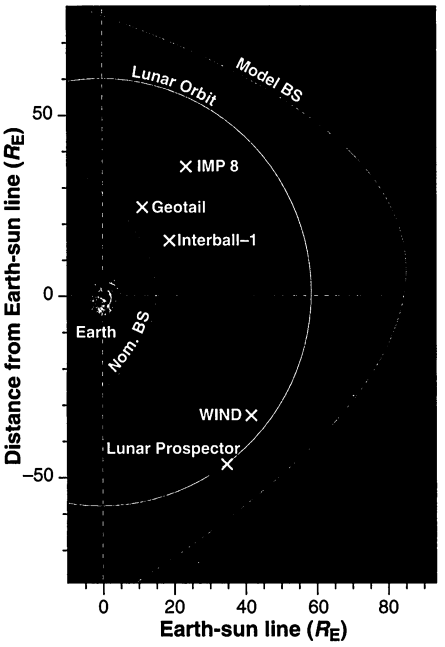

A sunward shift. Positions of various spacecraft at the time when they encountered the outward moving shock front, the "bow shock" (BS). The horizontal axis is the spacecraft distance along the Earth-sun line in units of R_E. The vertical axis is the distance perpendicular to the Earth-sun line. The spacecraft positions have been rotated into the ecliptic plane; spacecraft on the dawn side of Earth are plotted with negative perpendicular distance. White line: lunar orbit. Blue line: nominal (Nom.) position and shape of the bow shock, Pink line: model calculation of the maximum extent of the bow shock during this time period. Earth and the moon are shown at about 3 times their real size.

lar wind electrons (confined to the field lines) direct access to the north polar region. Normally, the solar electron distribution is broadened by collisions; all but the most field-aligned electrons are turned back by the increasing magnetic field as the polar regions are approached. But on this day, a particular part of the solar wind electron velocity distribution (known as the "strahl" because it forms a beam or ray that streams in a narrow cone along the field lines) dominated the distribution. Because the solar wind density was so low, the strahl electrons were relatively unscattered by collisions in the solar wind, and they arrived near Earth in an unusually intense and narrow beam that was able to penetrate into the polar region. The electron collisions with the atmosphere generated "the strongest x-ray emissions ever seen from the polar cap" (D. Chenette, Lockheed-Martin, Palo Alto, CA). The x-rays were observed from the Polar spacecraft, which can view both poles as it orbits Earth. The field polarity was such that electron access to the southern polar region by incoming electrons was not expected, and indeed no x-rays were observed from the south polar regions.

The strahl electrons provided an exciting opportunity to observe the electron distribution deep within the sun's corona. J. Scudder (University of Iowa) suggested that the strahl electrons indicated that substantial electron energy may have been deposited in the lower corona rather than higher up (a situation that is theoretically expected to produce low-mass flux solar wind), resulting in the normal speed but anomalous low-density condition we saw.

The strahl electrons also provided a chance to estimate the temperature at the base of the corona where the electrons were last in collisional equilibrium. The temperature in that region could be deduced from the overly energetic strahl distribution, seen by Wind and by the Hydra experiment on the Polar spacecraft in the tail of Earth's stretched field. Ordinarily, the energy spectrum of the strahl electrons coming into the polar regions decreases above about 1 keV, but in this case the energies exceeded 20 keV, corresponding to temperatures at the coronal base of 10^6 K.

The low solar wind had other effects in regions near Earth. D. Baker and his colleagues (University of Colorado) used data from near-Earth spacecraft to characterize conditions in Earth's Van Allen radiation belts, which are deeply embedded in the magnetosphere. The radiation belts became much more symmetric during the event, with the cometlike tail of the radiation belts apparently disappearing in the process.

Although the density of energetic electrons in the solar wind returned to normal on the following day, the density of very high-energy electrons in the magnetosphere dropped once again the next day and remained severely depleted for nearly 2 months, despite the fact that the solar wind flux had returned to its usual value. This raises interesting questions about the refilling of the radiation belts.

Why periods of very low density wind occur remains unknown. It is interesting to note, as N. Crooker (Boston University) pointed out, that such low wind flux periods tend to appear on the ascending portion of the solar activity cycle, a period in which we are in now (*2*). Discussions of low solar wind flux periods will undoubtedly occupy solar physicists for years to come.

References and Notes

1. American Geophysical Union Fall Meeting, San Francisco, CA, 13 to 17 December 2000, sessions SM11A, SM21E, and SM22C.
2. See, for example, www.oulu.fi/~spaceweb/textbook for general background on solar physics.
3. I wish to thank J. Scudder at Iowa and A. Szabo at NASA/Goddard Space Flight Center for their help with this Perspective.

SOURCE: A. STABO/NASA/GSFC

PERSPECTIVES: GENOMICS

The End of the Beginning

Sydney Brenner

In classical experimental genetics, where many of us began, we could not assert the existence of a wild-type gene until a mutant version with an altered function had been isolated. For Mendel to say that there was a factor for tallness, he first had to find heritable dwarf variants that suffered from a lack of tallness. This genetics began with inherited changes in phenotype that provided, if not knowledge, then at least a classification of the functions of genes, and it used genetic complementation experiments to discover how many genes were involved in dictating each phenotype. But, if one asked how many genes were required to make a bacteriophage or a bacterium or a fly or a mouse, no answer could be given.

A quarter of a century ago, the advent of new methods to analyze genomes directly changed the field of genetics. When the genome of bacteriophage lambda was first sequenced, it allowed the enumeration of all of the open reading frames (DNA sequences that potentially can be translated into protein). Some of these were in genes that encoded proteins whose functions had been thoroughly explored, whereas others encoded new proteins that were not essential for the growth of bacteriophage in the laboratory.

Proteins are the workhorses of biological systems, and deepening functional analyses of organisms requires that their proteins be purified and characterized. By sequencing the genome of a complex organism, the amino acid sequences of all of the proteins are obtained, so to speak, in one blow, thus avoiding the terrifying prospect of separating and purifying all of the proteins, and sequencing them by laborious methods. Cloning the genes into expression vectors allows us to make large amounts of the proteins for study and, what is more, we can make mutations in them and study the consequences without ever going back to the original genome.

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As time progressed, and methods of DNA sequencing improved, sequencing moved to larger and larger genomes. Although sequencing the human genome was contemplated quite early on, and sequencing of the *Caenorhabditis elegans* worm genome was begun as a continuation of the mapping program, what emerged next were the sequences of bacterial genomes, and the sequence of yeast, the latter accomplished by a European group effort. The sequence of the yeast genome was published in 1997, that of *C. elegans* in 1998 and, now, in three reviews in this issue (pages 2185, 2196, and 2204), we have the complete sequence of the 125-megabase genome of the fruit fly *Drosophila* (*1–3*).

When large-scale sequencing projects were first discussed in the mid-1980s, it was clear that a resource much larger than the average research laboratory, as well as improvements in technology, would be required. Walter Gilbert was the first to suggest a sequence factory—I seem to remember the number of 250 for the technicians that would be needed—but most of our colleagues were bitterly opposed to this idea. One, I remember, advocated the cottage industry model, hoping that the sequence of the genomes of organisms would be accomplished by many scientists working on individual genes. However, building factories with increased automation and very large computer resources has provided an answer to large-scale genome sequencing.

In their review, Adams *et al.* (*1*) provide a list of gene functions in *Drosophila*, classified by the proteins deduced from the genomic sequences into the now familiar classes (of which "unknown" and "hypothetical" are the most common). Rubin and colleagues (*3*) compare the *Drosophila* genome sequence with that of yeast and *C. elegans*, the only other eukaryote genomes sequenced so far. It should be noted that the fly has fewer genes than the worm; the genome sequence predicts about 14,200 proteins for *Drosophila* as opposed to 18,400 for *C. elegans*.

Old geneticists knew what they were talking about when they used the term "gene", but it seems to have become corrupted by modern genomics to mean any piece of expressed sequence, just as the term algorithm has become corrupted in much the same way to mean any piece of a computer program. I suggest that we now use the term "genetic locus" to mean the stretch of DNA that is characterized either by mapped mutations as in the old genetics or by finding a complete open reading frame as in the new genomics. In higher organisms, we often find closely related genes that subserve closely related, but subtly different, functions. Thus, vertebrate genomes contain three different genetic loci specifying three different aldolase enzymes. In *Drosophila*, we have one aldolase "genetic locus" that produces three different aldolases by variable splicing of the messenger RNA. Indeed, this is clearly part of the genomic style of the fly. *Drosophila* has one myosin locus that produces all of the different heavy chains by variable splicing; in contrast, *C. elegans*, with simpler muscle systems, has four different myosin genes. We have to appreciate this before we can make sense of gene numbers. It also leads one to be cautious about the commonly accepted generalization that it takes four invertebrate genomes to make a vertebrate. The science of genomics is still in its infancy, and we will have to acquire far more sophisticated views of genomes and their evolution before we can answer such questions as why the fly has 352 zinc-finger genes but the worm has only 132.

The analysis of genome sequences gives us a comprehensive protein parts list and it short-cuts the massive amount of work that would have been required to characterize each protein individually. But there is one important piece of information that is almost totally missing: the sequence information that specifies when and where and for how long a gene is turned on or off. This switching information—which I call the left-hand value of the gene by analogy with the address of a computer location—cannot be deduced from the sequence. It is absolutely essential information because in complex organisms, evolution does not proceed by enlarging the protein inventory but rather by modulating the expression of genes.

The functional properties assigned to the protein products of genes are centered on what might be called molecular functions. These can be specified whenever a protein is found to be similar to one for which the function has been determined by conventional biochemical methods. It is the way one learns to speak a natural language by listening to other speakers, and is not the result of some elaborate computation. Quite often there is little connection between these molecular functions and the classical assignments of function by phenotype (which are at the level of the organism). The middle ground—that is, the participation of proteins in the physiology of cells and how cells contribute to the function of the organism—is a gap that still remains to be closed.

The problems faced by pre- and post-genomic genetics are therefore much the same—they all involve bridging the chasm between genotype and phenotype. Genome sequencing represents only a new beginning and not an end in itself. It is useful to have and will help us to answer the many questions that still lie ahead. Yeast, *C. elegans*, and *Drosophila* have large constituencies of researchers who will make good use of the genome sequence and, in the coming years, will tell us what it all means.

References
1. M. D. Adams *et al.*, *Science* **287**, 2185 (2000).
2. E. W. Myers *et al.*, *Science* **287**, 2196 (2000).
3. G. M. Rubin *et al.*, *Science* **287**, 2204 (2000).

PERSPECTIVES: ANTHROPOLOGY

Age, Sex, and Old Goats

Curtis W. Marean

The Zagros mountains that run through western Iran and northeastern Iraq are a harsh highland environment of craggy and precipitous limestone ridges and deeply incised valleys. Few large mammal species find this habitat attractive—that is, apart from wild goats and sheep that nimbly negotiate these rocky crags. About 40,000 years ago, Neanderthals started to hunt goats and sheep at some sites in the Zagros mountains. After they became extinct, their human successors continued this hunting pattern. But at some point, there was a critical shift in the relation between hunters and hunted, resulting in the gradual domestication of wild animals. Exactly when this shift happened has been hotly debated. Now, Zeder and Hesse, reporting on page 2254 of this issue (*1*), persuasively argue that humans began to domesticate wild goats about 10,000 years ago (see the figure). With modern goat skeletons as a guide, they examined assemblages of ancient goat bones from the Zagros and assigned them an age at death and a sex.

Our human ancestors began to domesticate wild animals through herd management. They first controlled the movements of animals, and then introduced selective breeding and regulation of the sex ratio and age structure of the herds. With time and efficient selective breeding, domesticated species underwent shifts in the frequency of certain groups of genes, resulting in anatomical changes. In the case of goats, this included changes in horn shape, the

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