past 40,000 years, confirms the results from the two ice cores from Dye 3 and Camp Century concerning the fast variations and the transition from the glacial to the post-glacial epoch (*4*). The transition can be investigated in great detail. It is possible to count annual layers back at least 13,000 years, and the thickness of an annual layer is still over 5 cm at the upper end of the transition. The fast climatic variations and the stepwise transition are also confirmed by our American colleagues, who started drilling for their GISP 2 project in summer 1990, about 32 km (ten times the estimated ice thickness) west of Summit. They are using a newly developed drilling technique and in 1992 reached a depth of 2252 m. They will probably reach bedrock in 1993.

From 23 to 25 March, about 50 scientists from GISP 2 and GRIP met in Annecy, France, to compare and discuss the results obtained so far. They did agree that there is ample evidence that the "flickering" of climate during the Ice Age and the termination of the Ice Age in drastic steps are real. The episodic mild periods during the Ice Age were about 7°C warmer than the cold periods but still 5°C colder than the present temperature. The mild periods started with a fast temperature increase within a few decades or even less than a decade, lasted between 500 and 2000 years, and changed afterwards gradually back to the cold climate. It is assumed that these climate changes have been large-scale climatic events, probably typical of the whole North Atlantic region.

The transition from the last glaciation to the post-glacial epoch shows in many respects a similar pattern. There was a fast and drastic temperature increase about 14,500 years ago. After about 1000 years, the temperature started to decrease again and reached cold glacial values again about 12,500 years ago. This return to a cold phase is observed also in peat bogs and lake sediments in Europe and in eastern parts of North America and is called the "Younger Dryas" period. It lasted on the order of 1000 years. About 11,700 years ago, the temperature abruptly increased again, according to the Summit core, by about 6°C.

There is some evidence that the fast climatic changes correlate with changes in the deep water formation in the North Atlantic (*5*). When sea ice disappears, deep water formation increases in the North Atlantic. This again allows an efficient oceanic heat transport into the region by the Gulf Stream, leading to large and fast temperature increases. The mild periods could be terminated by the discharge of considerable amounts of melt water from the expansive continental ice sheets on both sides of the Atlantic, which can reduce the deep water formation and lead to a more extensive ice cover.

If fast climatic changes occur only according to this mechanism, it would be rather good news for mankind. Fast variations would depend on large ice sheets covering North American and Fennoscandinavia that are missing at present. However, with the results from the deeper part of the Summit core, the good news comes to nothing. The last interglacial period, called in Europe the Eem, lasted from about 135,000 to about 115,000 years before the present. It is represented in the Summit core in a depth interval between 2780 and 2870 m below the surface.

The stable isotope record (*6*) indicates that rather drastic climate variations occurred also during this period that were on the order of 2°C warmer than today and which are often suggested as an analog to our climate after a greenhouse warming. It will be a major task for climate modelers to model the fast climatic changes.

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Who Are the Europeans?

Alberto Piazza

In many parts of the world, populations are vanishing as a result of acculturation, urbanization, and migration (*1*). In Europe, populations are moving toward increasing and irreversible amalgamation. Because genetic differences between extant populations are an irreplaceable source of information about our own evolution, the population geneticist is pressed to document existing genomic variation. Fortunately, with molecular biological analyses of variation in DNA, the precision with which populations, their origins, and their interrelations can be defined increases enormously—even with relatively small samples. The populations of Europe are of particular interest: European history, archaeology, and languages are extraordinarily well documented. Moreover, genetic information is being obtained from the copious human fossil records in Europe, raising the possibility of testing hypothetical continuities between old and modern records of human evolution to reconstruct our past more accurately.

In Europe as a whole, the gene frequencies of 34 classical (non-DNA) genetic loci and 95 alleles are intermediate with respect to those of other continents (*2*). However, compared with the aborigines of other continents, Europeans are more homogeneous. The genetic differences between populations, as measured by F_{ST} values (*3*), are lower in Europe (an average of 0.0142) than in other parts of the world (Africa, 0.0520; Asia, 0.0668; America, 0.0755; and Australia, 0.0393). When the genetic information from 26 European populations (Austrian, Basque, Belgian, Danish, Dutch, English, Finnish, French, German, Greek, Hungarian, Icelandic, Irish, Italian, Lapp, Norwegian, Polish, Portuguese, Russian, Sardinian, Scottish, Spanish, Swedish, Swiss, and the former Czechoslovakian and Yugoslavian) is summarized in a phylogenetic tree (*2, 4*), two conclusions are of note: There are seven particularly deviant populations (Lapps, Sardinians, Greeks, Yugoslavians, Basques, Icelanders, and Finnish), and the remaining populations lack a tree-like structure. Both of these findings have a simple interpretation; the European populations have not evolved according to a tree of descent. A basic assumption for giving phylogenetic trees evolutionary meaning is that each of its branches evolves independently from the other ones. This can in principle be true for distant or isolated populations, but it is very unrealistic for Europe, where migrations in both prehistorical and historical times have occurred.

Among the genetically most deviant populations, Lapps, Sardinians, and Basques are of special interest. Although Lapps are heavily mixed with Scandinavians, a fraction of them retain a phenotype characteristic of northern Siberian people, in particular the Samoyed, who speak a language of the same non–Indo-European (Uralic) family. Classical genetic polymorphisms show Lapps to be an admixture, in which European genes predominate, but genes in common with people from the Uralic region may reach between 20% and 50% (*5*).

The island of Sardinia has been settled for at least 10,000 years (*6*). The local population had reached substantial numbers (200,000 or more) 3000 years ago, before other foreign colonizers, the Carthaginians, arrived in the south of the island. There were no Greek settlers in Sardinia at the time of

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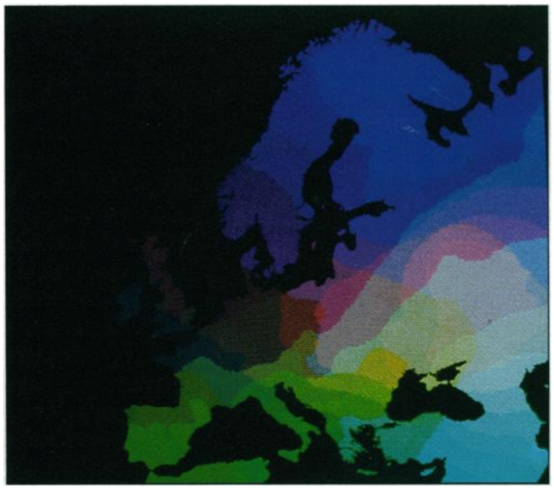
Greek colonization of the western Mediterranean. The Roman occupations had little genetic consequence; however, it did change the language, which was originally non–Indo-European. Some genetic similarity with more direct descendants of Paleolithic people from Europe, such as Basques or Caucasians (*7*), indicates that the first settlers of Sardinia may have been Paleolithic (*6*). The arrival of Neolithic farmers from the Middle East and genetic contributions from both Phoenicians and Carthaginians may help to explain why Sardinians show a primary genetic resemblance to Lebanese, and secondarily (but only by a small amount) to that of Italians, their closest geographic neighbors, who have contributed to the island's colonization since late Roman times.



Genetic gradients. The three principal components of European genetic variability were originally represented by shadings of green, blue, and red. Their computer synthesis gives this trichromic picture. [Reprinted with permission from (*4*), © 1993 Princeton University Press]

Basques, who live in southwestern France and in northwestern Spain, are probably the most direct descendants of the earliest post-Neanderthal settlers of Europe. Their unique language has no known relative in Europe except for languages of the North Caucasian family (*8*). Caucasian is also believed to have an ancient relation with the American NaDene and the East Asian Sino-Tibetan linguistic families (*9*). If so, this group of languages may be a very ancient protophylum that spread east in northern Asia and west in Europe during the Paleolithic around 40,000 years ago. There is a marked genetic similarity among people living today in the regions with Basque place names, and these people are remarkably different from the people of the rest of western Europe. These same areas also show the greatest concentration of cave art from the upper Paleolithic. Very likely, the genetic and linguistic uniqueness of Basque is a product of the isolation of western Europe from eastern Europe at the time of the last glaciation, which peaked around 18,000 years ago, and may have limited considerably genetic and cultural exchange between the two halves of Europe (*10*).

As trees of descent have little use in areas that, like Europe, have had a very active network of genetic exchange, alternative methods of analysis have been used. A useful approach has been application of the classical statistical technique of the principal component analysis, namely geographic contour mapping of the highest principal axis scores by smoothing the original gene frequency data over the whole geographical surface. This method can resolve the genetic picture of Europe into a number of "genetic landscapes," each of which is likely the memory of a particular historical scenario (*11*). The three most informative landscapes can be represented by the shadings of different colors and their computer-generated composition given in a trichromic picture: one image thus summarizing the three landscapes. An updated version of this synthetic map is shown in the figure. The predominant component (green) is a gradient that originates in the Middle East and is directed to the northwest. As confirmed by others (*12*), this gradient was generated by a migration of Neolithic farmers from the Middle East that started about 10,000 years ago, moved west along the coast of the Mediterranean and northwest via the Balkans and central Europe to France, England, and Scandinavia. This gradient is the result of continuous, partial admixture of the expanding farmers with local hunter-gatherers, in a process that lasted about 4000 years, as originally suggested by Ammerman and Cavalli-Sforza (*13*).

The second (in importance) genetic landscape of Europe is represented in the figure by the blue color. It shows a north to south gradient correlated with latitude, and hence probably with temperature, but also correlated with a partition of Europe into two linguistic areas, Indo-European and Uralic. People speaking Uralic languages may have spread westward along the Arctic coast from an unknown area of origin. Today Samoyeds, who speak a Uralic language, live not far from the Arctic Ocean east of the Urals. The Uralic speakers west of the Urals remained in Arctic areas but mixed largely with the presumably more numerous speakers of Indo-European languages from northern Russia. Although the original language survived, the original genetic types of the extreme western Uralic speakers of Finland are in fact highly diluted.

The third genetic landscape of Europe (red in the figure) suggests the origin of another expansion in an area where archaeological data place the beginnings of the "Kurgan" culture developed by pastoral nomads of the Eurasian steppes starting around 6300 years ago. Gimbutas (*14*) suggested that the spread of this culture is associated with the migrations of the first Indo-European speakers. This hypothesis is in contrast to the alternative suggestion by Renfrew (*15*) that Indo-European languages came to Europe from Anatolia with the spread of farmers (green gradient), but these alternative views are not easy to test. Sokal and co-workers (*16*) attempted to examine the correlations between genetic and linguistic expansions postulated by Renfrew and by Gimbutas, but they found no correlation for either. They calculated partial correlations between frequencies of single genes and possible routes of expansions, with geographic distances held constant. Analysis of the data with synthetic maps reaches different conclusions: The third (red) genetic landscape shows a significant association with a possible homeland of a population of Proto-Indo-European speakers in the Kurgan region. It is worth considering, however, that this finding is really not incompatible with an Anatolian origin. Both may be correct: The Kurgan migration may have occurred subsequent to the spread of agriculture to the steppes.

Diffusion of people entails the spread of their culture, including the language: Some correlation between genetic and linguistic patterns is expected in the cases where transmission of language implies a real moving of individuals. Indeed Barbujani and Sokal (*17*) found a correlation between linguistic and genetic discontinuities in Europe. In most cases (22 out of 33) there were also physical barriers (for example, mountains or the sea) that may be the cause of both genetic and linguistic boundaries. It remains for future research to investigate if, in the remaining cases, linguistic boundaries have generated or enhanced the genetic ones, or if both are the consequence of political, cultural, and social boundaries that have played a role similar to that of physical barriers.

Much more of the history and prehistory of Europe can be understood by an accurate study of its human population genetics. This knowledge may contribute greatly to European archaeology, history, and linguistic information, and the synthesis of all these perspectives will be especially illuminating. Modern genetic techniques bring analysis to an unprecedented degree of sophistication. Europe is in a unique position to promote the molecular study of human variation because of the outstanding richness and depth of its human and scientific resources. We hope this opportunity will be grasped with enthusiasm by European and non-European scientists.

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ROSAT—A New Look at the X-ray Sky

Joachim Trümper

During the last 30 years x-ray astronomy has become one of the cornerstones of observational astrophysics. At x-ray wavelengths, we see the "hot universe"—objects at temperatures of millions to billions of degrees. We also see large concentrations of relativistic electrons interacting with dense photon fields or magnetic fields. Often the emission of x-rays is connected with explosive events. The brightest objects in the x-ray sky are neutron stars and black holes in the process of accreting matter.

The field of x-ray astronomy has evolved in steps. Major milestones include the 1962 rocket experiment in which the brightest steady x-ray source in the sky was discovered (*1*); the Uhuru satellite, launched in 1971, which was the first astronomy satellite to perform an all-sky survey at x-ray wavelengths (*2*); and the Einstein observatory (1978), the first satellite-borne x-ray telescope, which led to a gain in sensitivity and angular resolution by orders of magnitude (*3*).

A new era of x-ray astronomy began on 1 June 1990 when the German satellite ROSAT was boosted into the sky over Florida by an American rocket. Since then, ROSAT has made a wealth of discoveries on the hot and relativistic matter in our universe. The acronym ROSAT stands for Röentgen Satellite, named after Wilhelm Conrad Röntgen, who discovered x-rays in 1895 in Würzburg and won the first Nobel Prize in Physics in 1901. The satellite was conceived at the Max-Planck-Institut für Extraterrestrische Physik (MPE), which has also taken the scientific lead in this international project (*4*). The satellite comprises two powerful instruments: a large German x-ray telescope sensitive to photon energies from 0.1 to 3 keV and a smaller British extreme ultraviolet (EUV) telescope covering the adjacent band between 25 and 100 eV (Table 1). With these telescopes, the frontiers in x-ray and EUV astronomy could be shifted dramatically.

The first half-year of the mission was devoted to an all-sky survey, the first to use imaging x-ray telescopes and the first at all in the EUV. This survey brought a large jump in the number of sources; whereas 840 sources were known from High-Energy Astronomical Observatory 1 (HEAQ-1), a preliminary analysis of the ROSAT survey yielded some 60,000 x-ray sources (*5*) and 384 EUV sources (only a dozen were known before) (*6*). The ROSAT survey includes almost every kind of astrophysical object. The largest classes are active galactic nuclei (>25,000), normal stars (>20,000), clusters of galaxies (~5000), and normal galaxies (a few hundred).

In addition, the x-ray survey revealed the large-scale structure in the sky connected with the distribution of hot and cool gas in our galaxy and some 100 new supernova remnants were found in x-rays (*7*), whereas only about 50 had been known before. Owing to the "unlimited field of view" of the survey, the large galactic structures and old supernova remnants could be mapped as a whole, and the spectral resolution of the image detectors allowed measurement of their temperature distributions for the first time in detail. A special highlight was the discovery of sharp conical structures in supernova remnants (such as Vela) (Fig. 1), indicative of Mach cones produced by clumps of matter moving with Mach numbers of ~3 in the hot interstellar medium.

This enormously productive survey took only half a year. For more than 2 years, ROSAT has been used for detailed observations of selected sources, with some 3400 observations made so far for hundreds of guest observers all over the world. Compared with its famous predecessor, the Einstein observatory, ROSAT imaging offers a substantial increase in sensitivity (factor 3–10), angular resolution (factor 10), spectral resolution (factor 2.5), and imaging quality.

In the well-known Crab nebula, structural features were discovered that reflect the beaming geometry of the Crab pulsar's ultra-relativistic electron and positron wind, which carries particles with energies up to ~10^{14} eV. Several other pulsars were observed at x-ray energies that had been sought for a long time, such as the Vela and Geminga pulsars.

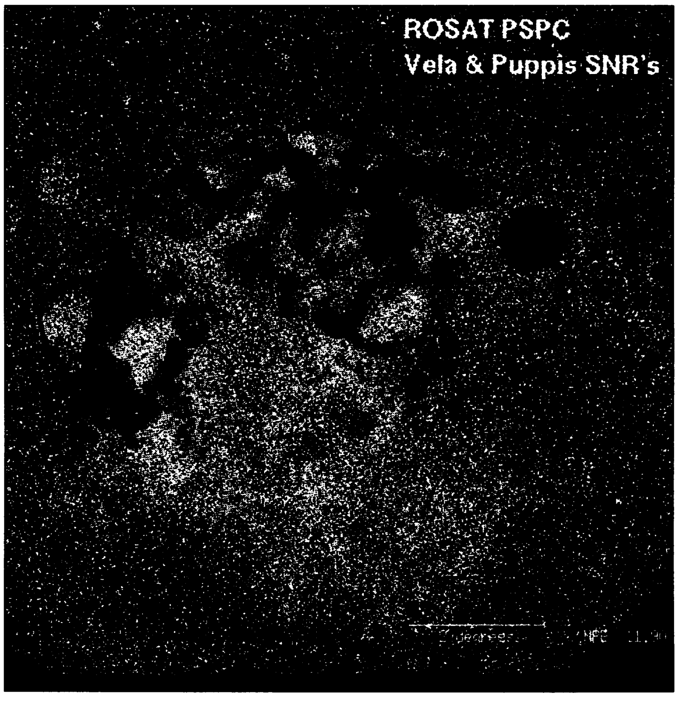

Fig. 1. X-ray shocks. Color map of Vela and Puppis A supernova remnants. Supersonic wakes preceding the main shock front are seen in the east (left), west, and north.

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