100 Years of X-Rays

MS24.01.01 THE DISCOVERIES of X-RAYS by ROENTGEN and DIFFRACTION by von LAUE B.W. Batterman, Applied & Engineering Physics, CHESS, Cornell University, Ithaca, New York.

It took 17 years after Roentgen's discovery of X-Rays in 1895 until the realization and verification that X-Rays were a form of light whose wavelengths were comparable to the spacings between atoms in crystals.

Laue's experiment showed that X-Rays are diffracted by crystals and gave birth to the field of X-Ray Crystallography, which provides us jobs, consumes our interest, and brings us to Seattle.

MS24.01.02 CRYSTALLOGRAPHIC REMINISCENCES, THE EARLY DAYS. Cecil Arnold Beevers, Chemistry Department, University of Edinburgh, Edinburgh, EH9 3JJ, England

I have had a long history of contacts with the subject of Crystallography, and with Practitioners of the Art, from pre- X-ray days to the time when the Digital Computer took over. In the earlier years there were, of course, fewer workers and it was relatively easy to know them all. Some of us had to make their own X-ray tubes and cameras, and to spend much time devising means of reducing the labour of the long calculations. The main strategy was "Trial and Error", often long continued. The International Congresses every three years provided a most pleasant way of knowing what was going on. I was able to attend no less than ten of these, each with its unique flavour and its opportunity to travel and broaden the mind.

The paper describes some of the human contacts in my Crystallographic Experience.

MS24.01.03 CRYSTAL STRUCTURE DETERMINATION. Isabella L. Karle, Laboratory for the Structure of Matter, Naval Research Laboratory, Washington, D. C. 20375-5341, U.S.A

A rapid glance into the past will be presented describing some of the procedures and personalities that were involved in the dramatic changes that have taken place in the ease and scope of crystal structure analyses. The replacement of eye-estimation of intensities of diffraction spots on film by rapid automated data collection, the replacement of the desk calculator with supercomputers and associated computer programs, and the progression of structure determination from trial-and-error methods to Patterson and vector-search functions, to direct phase determination, particularly for structures lacking any atoms heavier than oxygen, have contributed to the rapid determination of structure, conformation and molecular assembly for molecules containing up to several hundred atoms. In retrospect, elements of processes were introduced into structure determination before they acquired a name in other arenas, such as the concept of "fuzzy logic" in practical phase determination and computer graphics representing molecules and mathematical functions.

MS24.01.04 COMPUTING IN CRYSTALLOGRAPHY: THE EARLY DAYS. Robert Langridge, Computer Graphics Laboratory, University of California, San Francisco, CA 94143, and Department of Biochemistry and Biophysics, Oregon State University, Corvallis, OR 97331, USA. Jenny P. Glusker, Institute for Cancer Research, Fox Chase Cancer Center, 7701 Burholme Avenue, Philadelphia, PA 19111, USA.

"It is unworthy of excellent men to lose hours like slaves in the labor of calculation which could safely be relegated to anyone else if machines were used" Leibniz (1671)

"As soon as an Analytical Engine exists, it will necessarily guide the future course of science" Babbage (1864)

"The purpose of computing is insight, not numbers" Hamming (1962)

Detailed numerical calculations have been the life blood of our field since it began, and computations for X-ray crystallography rank among the pioneering applications of stored program digital computers, revolutionizing our work and making possible the application of large-scale direct methods to smaller molecules and the determination of the complex architectures of structures of the magnitude of viruses. Furthermore, the numbers generated by these calculations, particularly for large biological molecules, are almost incomprehensible without the now routine use of interactive three dimensional computer graphics to visualize the results and to help generate the insight which the numbers alone cannot provide.

Although the date of origin of the modern computer cannot be fixed as precisely as that of the discovery of X-rays, the celebration of the 50th anniversary of the introduction of ENIAC now being held in Philadelphia illustrates how short is the history of computers. After a brief summary of pre-ENIAC computing, we recall the first use of EDSAC at Cambridge in 1951 by Bennett and Kendrew for protein crystallography, and select some highlights of the early days of the exciting and productive association between computers and crystallographers.

MS24.01.05 WHY HAVE CRYSTALLOGRAPHIC DATABASES? Dr. Olga Kennard, Cambridge Crystallographic Data Centre, 12 Union Road, Cambridge CB2 1EZ, England

Crystallographers have a long tradition of bringing together the experimental results of structure analyses in databases. These cover proteins, organic and inorganic compounds, metals and alloys. With the continuing increase in the number of structure determinations it seems pertinent to ask why we have these databases. The talk will examine their origin, development and future directions. Of necessity, each of these databases can not be covered in detail, and will mainly be illustrated by reference to the Cambridge Structural Database. The questions raised, however, are sufficiently general to be applicable to all crystallographic databases.

MS24.01.06 PROTEIN CRYSTALLOGRAPHY. Michael G. Rossmann, Department of Biological Sciences, Purdue University, West Lafayette, IN 479071392

It was not clear in the early 50's that proteins would have unique structures rather than be colloidal aggregates. Nevertheless, early attempts at determining the structures of proteins included studies of lysozyme (Linus Pauling), insulin (Dorothy Hodgkin) and hemoglobin (Max Perutz), stimulated by the availability of diffracting crystals. W.T. Astbury, J.D. Bernal, I. Fankuchen and others were starting to elucidate some features of proteins, such as the α- and ß-structures in fibers and even the structure of the rod-shaped tobacco mosaic virus.

Perutz had demonstrated that hemoglobin contained rod-like structures and that these rods were probably Pauling's α-helices. He had also tried a variety of innovative techniques to solve the phase problem using the shrinkage of cell dimensions produced by drying and the changes in structure amplitudes caused by alterations in salt concentration.

Bragg had intuitively used the isomorphous replacement method in solving the structure of Na and KCl. J.M. Robertson had demonstrated the possibility of isomorphous replacement in the study of phthalocyanines. Perutz, in the face of skepticism, showed that heavy atoms could diffuse into crystals and produce measurable differences in the diffraction pattern. In 1953, he was able to produce a map of horse hemoglobin in projection, having phased the centric monoclinic (h0l) reflections. It was to take another 6 years before a three-dimensional 5.5 Å map was possible. That required a group of young assistants to measure with rulers hundreds of maxima representing Bragg reflections. All these had to be sorted and used in a home-built computer having the equivalent of only 10Kbytes of memory. In the meantime, John Kendrew had made progress in the structure determination of myoglobin. In 1959, it was possible to recognize the extraordinary evolutionary conservation of the globin fold in comparing the three-dimensional structures of myoglobin and hemoglobin, as well as seeing the atomic details of Pauling's α-helix. The techniques developed for these first protein structure determinations are still the essence of today's technology.