American Crystallographic Association (ACA) Annual Meeting, Cincinnati, OH, July 20-24, 2019 Michael Rossmann (1930-2019): phase extension and *ab initio* phasing

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1988 1992

Canine Parvovirus (CPV)

 Full particle and empty capsids: Jun Tsao, Hao Wu, Michael Chapman, Mavis Agbandje, Walter Keller, Kathy Smith, Ming Luo, Tom Smith, Richard Compans, Colin Parrish.



- Parvoviruses negative sense ssDNA viruses and are pathogenic.
- Canine parvovirus is a remarkable example of the emergence of a new viral pathogen, likely from feline panleukopenia virus (FPV).
 - Identified in 1978; become pandemic in a few months; endemic in all populations of domestic and wild canids that have been examined.
 - Genetic recombination mapping shows that four coding and three noncoding changes within the coat protein region can endow FPV with the ability to replicate in dogs.

Structure determination of CPV: data collection

- Icosahedral symmetry with triangulation number (T) = 1.
- P2₁ with cell dimensions a = 263.1, b = 348.9, c = 267.2 A, and β = 90.8°
- Data collected at CHESS and Daresbury.
 - Oscillation angles from 0.3° to 0.7° ; > 2.8 Å resolution; one virion/au.
 - Very low resolution data collected by increasing the crystal-to-film distance from 100 to 300 mm
- Crystals were randomly oriented, indexed by the auto-indexing procedure of Sangsoo Kim developed while at Purdue.
- Refinement of crystal orientation, intensity measurements, scaling, postrefinement, and averaging were accomplished with the Purdue processing program package.
- Latter two formed some of the basis for modern data processing software.

Structure determination of CPV: ab initio phasing $\beta \neq 90^{\circ}$ α , $\gamma = 90^{\circ}$ Rotation Fit to ideal 2, 3, 5-fold axes (2-fold almost parallel with b) function symmetry ~129 Å radius at Spherical Native Patterson Fitting to low resolution data: near (0.25, y, 0.25) packing outer radius (128 Å, or 122 Å) and inner radius (85 Å) Starting 20 Å SIR (5%) at 8 Å Refine virus position Phase extend to 9 Å $K_{2}PtBr_{6}$ (5%) Phase extension to 3.25 Å Negative Pt holes **Difference Fourier** (phases 180° shifted) (60 steps, 3 cycles at each step)

Structure determination of CPV: model building and DNA

- Traced and sequence fitted on a stack of transparencies; Wrong hand; FRODO (T. A. Jones).
- Most of the nucleic acid (as in other spherical viruses) is not seen. In CPV some DNA structure is visible where icosahedral symmetry has been imposed on it by internal binding to the coat protein.
- A total of 11 nucleotides were built into this density. Since this occurs in each of the 60 icosahedral asymmetric units of the virus, there are a total of 660 visible bases, or 13 percent of all of the encapsidated DNA.



Influence of a life time

- Michael was a virtuoso in solving structures
 - Advanced crystallography course, Thursday evening discussion, working closely with us – synchrotron trips, project discussions, Fortran programming, writing papers
- Support us to go to meetings
- Support us for collaborations:
 - 1) John Innes Institute, UK
 - 2) University of Kentucky
- Personal development

Cauliflower mosaic virus (CaMV)



- Always interested in you; in order to graduate: swimming, driving
- Unwavering enthusiasm for life and almost childlike curiosity

Tributes to Michael Rossmann: Let the legacy continue

- Arnold E, Wu H, Johnson JE (2019). Michael G. Rossmann (1930-2019), pioneer in macromolecular and virus crystallography: scientist, mentor and friend. *Acta Crystallogr D Struct Biol*. 75: 523-527
- Wu H, Arnold E (2019). Michael G. Rossmann (1930-2019). Nat Struct Mol Biol. [Epub ahead of print]
- Chuan (River) Xiao, Liang Tong (2019). Michael G. Rossmann (1930-2019). *Structure* in press
- Johnson JE (2019)...

Mila Mountain (Lhasa, Tibet) 2012





Japan, 2008



Morocco, 2009

Lhasa, 2012



Parade of Students: Rossmann Symposium 2017

