

生体分子構造解析学特論

シンクロトロン光研究センター

渡邊 信久

第6回

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講義スケジュール

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- 3：二次構造の解明
- 4：DNAの構造
- 5：結晶構造解析法の発展
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High-resolution protein structure analysis

postscript: next 50 years of protein crystallography

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key paper

myoglobin の
2Åの構造解析

STRUCTURE OF MYOGLOBIN
A THREE-DIMENSIONAL FOURIER SYNTHESIS AT 2 Å. RESOLUTION
By Drs. J. C. KENDREW, R. E. DICKERSON, B. E. STRANDBERG, R. G. HART
and D. R. DAVIES*
Medical Research Council Unit for Molecular Biology, Cavendish Laboratory, Cambridge
AND
D. C. PHILLIPS and V. C. SHORE
Davy Faraday Laboratory, The Royal Institution, London

[Nature \(1960\) 185, 422-427](#)

Virus の構造予測

Structure of Bushy Stunt Virus
D. L. D. CASPAR*
Medical Research Council Unit for the
Study of the Molecular Structure of
Biological Systems,
Cavendish Laboratory,
Cambridge.
Jan. 23.

[Nature \(1956\) 177, 476-477](#)

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Nature (1960) 185, 422-427

STRUCTURE OF MYOGLOBIN

A THREE-DIMENSIONAL FOURIER SYNTHESIS AT 2 Å. RESOLUTION

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In the accompanying article⁴ Perutz *et al.* now describe a three-dimensional analysis of the related protein haemoglobin, at a slightly greater resolution, and show that each of the four sub-units of which this molecule is composed bears a close structural resemblance to myoglobin. It is apparent, therefore, that sperm-whale myoglobin possesses a structure the significance of which extends beyond a particular species and even beyond a particular protein.

We now present the results of a second stage in the analysis of sperm-whale myoglobin; in this the resolution has been increased to 2 Å., that is to say, not far short of atomic resolution. The resulting Fourier synthesis is very complicated, and a detailed study of it will take many months; in the meantime, our preliminary findings may be of interest.

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simultaneously. Whereas myoglobin crystals give 400 reflexions having spacings greater than 6 Å., the number of reflexions with spacings greater than 2 Å. is 9,600, each of which has to be measured not only for the unsubstituted protein but also for each of the derivatives. The very much greater number of data posed many problems, both in recording intensities and in computation, and in this stage we relied much more heavily than before on the use of a high-speed computer; it was fortunate that about the time the work began the *Edsac* Mark I computer used viciously was superseded by the very much faster more powerful Mark II.



myoglobin 2Å data set

Dickerson, RE, *Protein Science* (1992) 1, 182-186

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The data for each derivative were recorded on twenty-two precession photographs; a separate crystal had to be used for each photograph to keep radiation damage within acceptable limits. The

function of $\sin \theta$. The co-ordinates of the heavy atoms were further refined using correlation functions⁶ computed by means of programmes devised by Dr. M. G. Rossmann, and finally refined again during the process of phase determination itself. The phases were determined by essentially the same method as before, but owing to the very large number of reflexions the determination was carried out on the computer rather than graphically. The 'best' phases and amplitudes⁷ were computed and used in the final Fourier synthesis, to which a moderate degree of sharpening was applied. In all,

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Earliest Primary Reports of Macromolecular Structures

1958: Myoglobin	6 Å	Kendrew JC, Bodo G, Dintzis HM, Parrish RG, Wyckoff H, Phillips DC. <i>Nature</i> 181 , 662-6.
1960: Hemoglobin	5.5 Å	Perutz MF, FRS, Rossmann MG, Cullis AF, Muirhead H, Will G, North ACT. <i>Nature</i> 185 , 416-22.
1965: Lysozyme	6 Å	Johnson LN, Phillips DC. <i>Nature</i> 206 , 761-3.
1967: Ribonuclease	3.5 Å	Wyckoff HW, Hardman KD, Allewell NM, Inagami T, Johnson LN, Richards FM. <i>J. Biol Chem.</i> 242 , 3984-8.
1968: Papain	2.8 Å	Drenth J, Jansonius JN, Koekoek R, Swen HM, and Wolthers BG. <i>Nature</i> 218 , 929-32.
1971: Insulin	2.8 Å	Blundell TL, Cutfield JF, Cutfield SM, Dodson EJ, Dodson GG, Hodgkin DC, Mercola DA, Vijayan M. <i>Nature</i> 231 , 506-11.

1971: Protein Data Bank established at Brookhaven National Laboratory

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1968: Papain

Drenth J, *et al.* *Nature* **218**: 929-32.

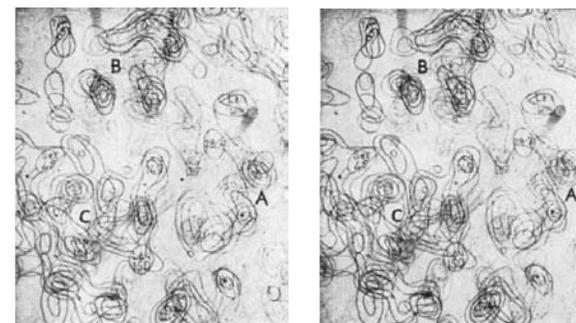


Fig. 1. Pair of stereoscopic photographs of the electron density map.

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1968: Papain

Drenth J, *et al.* *Nature* **218**: 929-32.

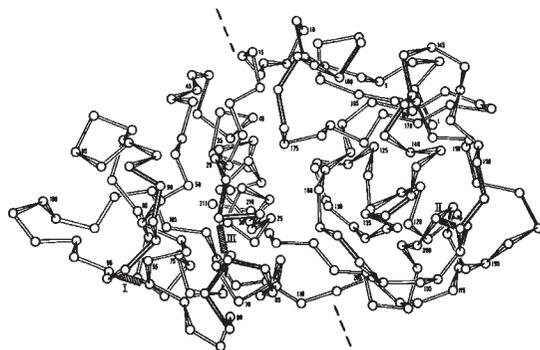


Fig. 4. Perspective drawing of the main chain conformation.

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1971: Insulin

Blundell TL, *et al.* *Nature* **231**(5304):506-11.

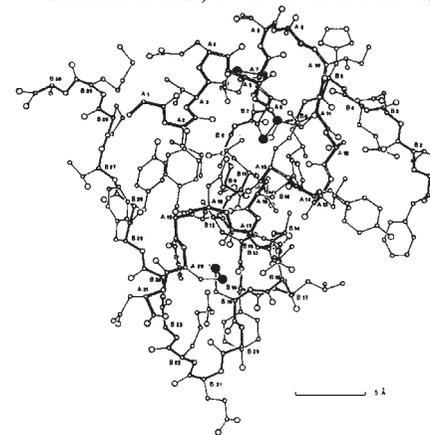


Fig. 3. The atomic position in the insulin molecules.

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その後の蛋白質結晶学

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* より大きいもの

- ウイルス粒子

* より複雑なもの

- リボソーム

* より重要なもの

- 膜蛋白質, 疾病関連蛋白質

* より精密な解析

- プロトン伝達, 電子伝達

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ウイルスの構造解析

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key paper

Nature (1956) 177, 476-477

Structure of Bushy Stunt Virus

D. L. D. CASPAR*
Medical Research Council Unit for the
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All the evidence indicates that the virus has the point-group symmetry $I\bar{3}2$, which implies that it is built up of sixty structurally identical asymmetric units. The molecular weight of bushy stunt virus is about 9 million⁴, of which about 17 per cent is ribonucleic acid⁶; therefore, the molecular weight of the protein part of the asymmetric unit is about 125,000.

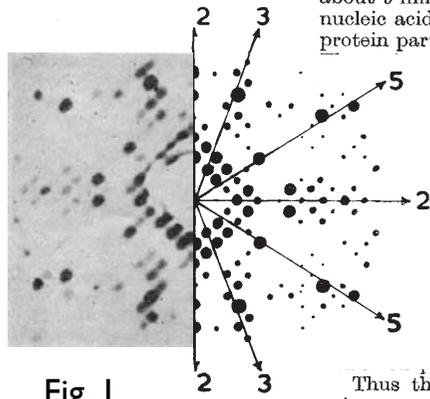


Fig. 1

Thus the X-ray evidence shows that bushy stunt virus possesses sub-units. The number of sub-units is certainly a multiple of twelve and very probably a multiple of sixty. The chemical data suggest that the actual number may be as high as three hundred. I gratefully acknowledge the advice and assistance of Drs. J. D. Watson and F. H. C. Crick.

Tomato bushy stunt virus at 5.5-Å resolution

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 G. Bricogne
 MRC Laboratory of Molecular Biology, Hills Road, Cambridge CB2 2QH, UK

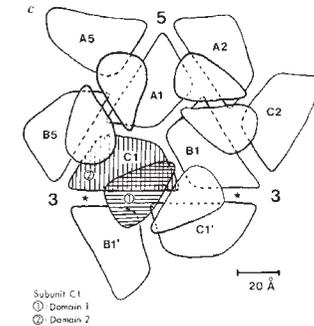
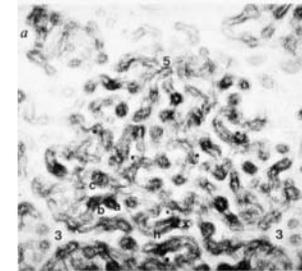


Fig. 2

Tomato bushy stunt virus at 2.9 Å resolution

S. C. Harrison, A. J. Olson, C. E. Schutt* & F. K. Winkler†
 Gibbs Laboratory, Harvard University, 12 Oxford Street, Cambridge, Massachusetts 02138
 G. Bricogne
 MRC Laboratory of Molecular Biology, Hills Road, Cambridge, UK

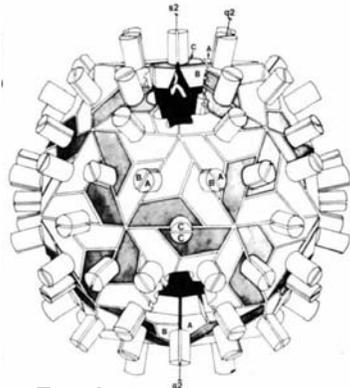


Fig. 1

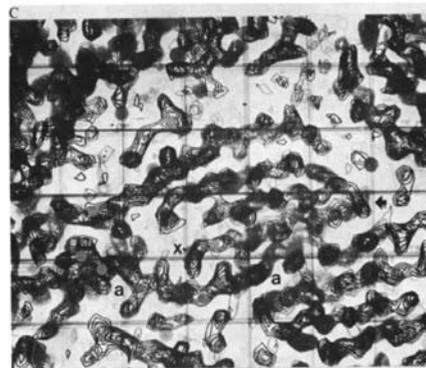


Fig. 2

Tomato bushy stunt virus at 2.9 Å resolution

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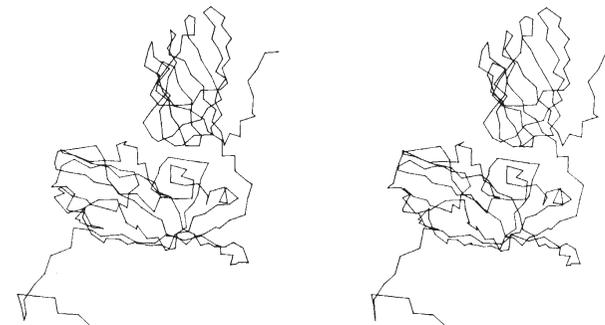


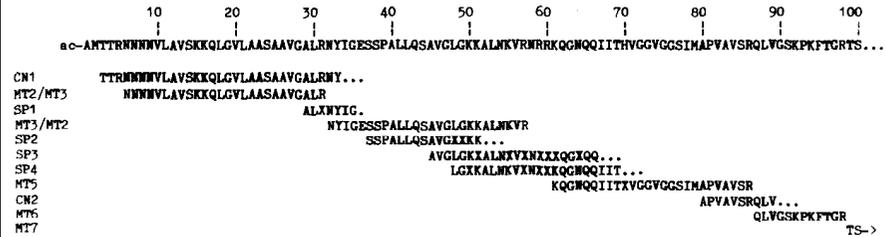
Fig. 3

Structure of Tomato Bushy Stunt Virus

V.† Coat Protein Sequence Determination and its Structural Implications

P. HOPPER¹†, S. C. HARRISON² AND R. T. SAUER¹

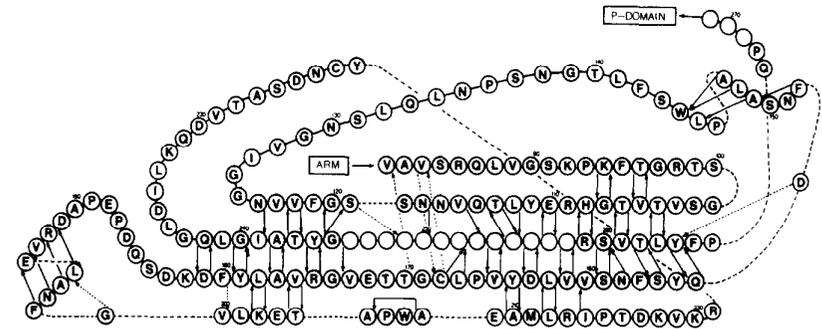
AMINO ACID SEQUENCE OF TBSV 705



Structure of Tomato Bushy Stunt Virus

V.† Coat Protein Sequence Determination and its Structural Implications

Hopper, P., Harrison, S. C., Sauer, R. T., *J Mol Biol* 177 (1984) 701-713



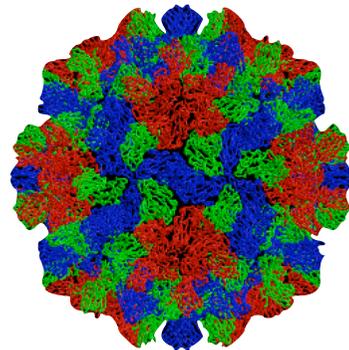
Structure of Tomato Bushy Stunt Virus

V.† Coat Protein Sequence Determination and its Structural Implications

Hopper, P., Harrison, S. C., Sauer, R. T., *J Mol Biol* 177 (1984) 701-713

Resolution : 2.9Å

PDB ID: 2TBV



310 Å

M.W. of major capsid protein : 40,527 Da (180 copies)

Total capsid protein : 7294.86 K Da

