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ON THE POLYSACCHARIDE OF FIBRINOGEN AND FIBRIN

by

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It has been observed in the course of amino acid analysis of fibrin hydrolysates that a very marked Molisch reaction could be obtained. In connection with this observation fibrinogen of high purity was prepared from bovine plasma and from plasma of other mammalians by a modified method of our own[1]. Conversion of fibrinogen into fibrin was carried out with bovine thrombin (Hoffman la Roche and Richter) under special conditions[2] in order to facilitate elimination of other protein molecules and of non-protein contaminants. The clot was washed with distilled water, ethanol and ether, and dried *in vacuo* over $CaCl_2$ to constant weight.

For paper chromatography, the fibrin thus prepared was hydrolysed in a water bath at 100° C with $N/2$ H_2SO_4 for 6 to 8 hours. After neutralising with an aqueous solution of barium hydroxide, the resulting $BaSO_4$ was filtered, the filtrate was evaporated *in vacuo*, and the residue dissolved in a small amount of water was subjected to chromatography. Chromatograms were run on Macheray-Nagel paper No. 214 according to the method of PARTRIDGE[3] with butanol-acetic acid and dried. After repeating this process the sugars were located with anisidine phosphate[4].

Three reducing sugars were identified, the spots corresponding to mannose, galactose and glucosamine, respectively[5]. The same three reducing sugars were identified in chromatographic examinations of fibrins of other mammalians (man, horse, sheep and rabbit).

Fibrinogens of different species have also been studied with chromatography. The solutions of fibrinogens containing 95–96% of clottable protein were freed from salts by dialysis against distilled water. The precipitated fibrinogens were washed, dried, and hydrolysed by the method described above. Chromatography showed the presence of the same three sugars as in the case of fibrin.

Although chromatography had shown no qualitative difference between the polysaccharides of fibrinogen and fibrin, the quantitative determination of hexose[6,7] and glucosamine[7] has revealed marked differences between the corresponding fibrinogen and fibrin of all species studied.

TABLE I

HEXOSE AND GLUCOSAMINE CONTENT IN % OF DRY WEIGHT

	n+ *Hexose* %	*n*+ *Glucosamine* %
Bovine fibrinogen	4 1.64 ± 0.02*	2 0.56 ± 0.02*
Bovine fibrin	4 1.33 ± 0.04	2 0.54 ± 0.01
Rabbit fibrinogen	4 1.98 ± 0.03	2 0.59 ± 0.03
Rabbit fibrin	4 1.66 ± 0.02	2 0.60 ± 0.02

n+ No. of determinations; * Standard deviation

It can be seen in the Table that fibrins contain considerably less hexose than do the corresponding fibrinogens, whereas the glucosamine contents are nearly identical.

Evidence obtained in the experiments shows clearly that the demonstrated sugars cannot be contaminations, since they are uniformly found in highly purified materials of different origin. It can be demonstrated in corresponding fibrinogens too and, finally, there is a significant difference between the hexose contents of fibrinogen and fibrin.

The latter result directs attention to the possible role played by the polysaccharide in the conversion of fibrinogen into fibrin. Experiments along this line are in progress.

Details will be published in *Acta Physiol. Acad. Sci. Hung.*

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BOOK REVIEW

Computing methods and the phase problem in X-ray crystal analysis. Report of a Conference held at The Pennsylvania State College, April 6–8, 1950. Edited by RAY PEPINSKY and published by The X-ray Crystal Analysis Laboratory, The Pennsylvania State College, Pa., 1952. Pp. xvii + 390. Price $ 7.50.

A play upon words is justified and irresistible: one must say at once of such an excellent publication that it is on the very wave-front of X-ray structure analysis. Dealing as it does with specialised mathematical, crystallographic, and electronic matters, it hardly calls for detailed notice on the part of this Journal, but that is by no means to suggest that it falls outside its purview. On the contrary, since the book is aimed at overcoming the difficulties inherent in the diffraction analysis of the more complex crystal structures such as those of biological molecules, above all of the proteins, its significance for biophysics and biochemistry is obvious.

Something like half the book comprises papers on the central problem of discovering the *phases* of the waves diffracted by a crystal lattice. The density function describing the periodic atomic distribution can be represented by a three-dimensional Fourier transform whose coefficients are the amplitudes of the X-ray reflections, but unfortunately these are observed primarily as *intensities*; hence, without additional limitations, assumptions and physico-chemical information, the theoretical number of possibilities is infinite. There is no general solution, but considerable progress is being made with more and more complex special cases, and this is pre-eminently the book to tell us how it is being done.

The quest demands all the time better and better methods and devices to minimise the enormous amount of computation involved, and it is to this practical aspect of the problem that the remaining papers are devoted. In particular, there is a long description and discussion of the famous Pepinsky machine, an electronic analogue computer, which is the joy and admiration of visitors to State College. It was, of course, the centre-piece of the 1950 Conference, which must have been not only invaluable but an exceedingly pleasant affair besides, to judge by various photographs and other personal touches with which the report is enlivened. Our thanks and congratulations are due to everyone concerned.

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