studies indicated that, as with the related enzyme 2-hydroxybutyrate dehydrogenase, both the polar choline head group and the hydrocarbon chains are involved in the binding of the lipid to the protein.

These specific lipid-protein complexes are probably examples of allotropic interactions. This form of complexing may explain aspects of the behaviour of these enzymes *in vivo*.

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Biological Activity of Double-Stranded Ribonucleic Acid Fragments

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Fungal viruses containing double-stranded RNA have been detected in a number of *Penicillium* species, and all of them tested as yet have been found to possess the capacity to induce interferon in animals and to give protection against infection by different viruses (for review see Colby, 1971). The double-stranded RNA responsible for these effects has been studied with respect to the importance of molecular weight for biological activity.

Double-stranded RNA isolated from *Penicillium chrysogenum* virus (Lemke & Ness, 1970; Buck *et al.*, 1971) has been fragmented in three different ways: (a) by digestion with ribonuclease III; (b) by digestion with high concentrations of pancreatic ribonuclease A in high salt concentration; (c) by ultrasonic disintegration.

Degradation was followed by viscosity measurements, polyacrylamide-gel electrophoresis and sucrose-density-gradient analysis. With the exception of some special mild conditions, breakdown was always random, producing a heterogeneous mixture of fragments of a rather wide size range. Optimal conditions for obtaining relatively large fragments with no traces of intact material have been worked out. The 'melting' temperature, T_m , was practically unchanged after degradation, suggesting that the breakdown products were still double-stranded.

The capacity of the RNA to induce interferon was diminished even after mild degradation, though at the same time the toxicity increased as compared with that of the intact RNA. (These changes were observed in a virus-sensitive strain of mice, BSVS.) As similar results were obtained whichever method of degradation was used, but the results varied with the degree of degradation, it would seem that biological activity is dependent on molecular weight rather than on the intact structure of any particular site in the RNA molecule.

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Resolution of Supercoiled Deoxyribonucleic Acid Structures by Light-Scattering

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There is, at present, considerable interest in and uncertainty about both the exact tertiary structure of supercoiled DNA and the possible transitions occurring on alteration of the secondary structure by, for example, dye titration (Bauer & Vinograd, 1968; Wang, 1969; Revet *et al.*, 1971; Dean & Lebowitz, 1971). Previous techniques used have been mainly hydrodynamic, requiring small amounts of material, but providing rather ambiguous answers to the problem of tertiary-structure determination.

Light-scattering requires larger amounts of material, but supplies a direct numerical parameter of tertiary structure, the root-mean-square radius, and also a complete simple interference curve on which further calculations can be made.

We have undertaken a light-scattering study of bacteriophage ϕ X174-RFI DNA in attempts to differentiate between different possible structures, such as (a) the straight interwound model, (b) the toroidal model (Gray, 1967) and (c) the interwound Y-shaped model as seen in electron micrographs.

The experiments were performed on pure bacteriophage ϕ X174-RFI DNA in BPES buffer (Krasna & Harpst, 1964), pH 6.8, at 25°C by using a refractive-index increment of 0.166 ml/g (Krasna, 1970).

Results were as follows. The number of superturns/molecule was -11.8 ± 1.6 ; in further calculations it was assumed to be an integer, 12. The molecular weight of bacteriophage ϕ X174-RFI DNA was $3.17 \times 10^6 \pm 0.19 \times 10^6$, significantly lower than the value of twice 1.7×10^6 previously reported for single-stranded bacteriophage ϕ X174 DNA (Sinsheimer, 1959). The root-mean-square radius was 103.5 ± 12 nm.

To extract further information from the scattering experiment, we predicted reciprocal particle scattering factors, $P(\theta)^{-1}$, for each of the models mentioned above, having dictated their dimensions with the experimental root-mean-square radius and molecular

weight. This gives unique dimensions for models (a) and (b), but for the Y-shapes several varieties of arm lengths and interarm angles must be considered.

$P(\theta)^{-1}$ was calculated from the formula (Guidushek & Holtzer, 1958):

$$P(\theta) = \frac{1}{N^2} \sum_n \sum_m^N (\sin hr_{nm}/hr_{nm})$$

where r_{nm} is the absolute value of the vector between the n th and m th scattering points. This was evaluated on a digital computer, and the results were plotted as $P(\theta)^{-1}$ against $\sin^2(\theta/2)$ for comparison with the experimental points.

Our conclusion was that, although the fit was not total, the experimental data corresponded best to a Y-shape molecule of equal arm lengths of four supercoils (185.6 nm), cross-sectional arm radii of 15.05 nm and an angle of 120° between each arm.

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as a measure of the number of cells present. The method depends on the enhancement of the fluorescence of ethidium bromide (2,7-diamino-10-ethyl-9-phenylphenanthridinium bromide) that occurs when the dye binds to double-stranded nucleic acids (Le Pecq *et al.*, 1964; Le Pecq & Paoletti, 1966, 1967). We measure the fluorescence intensity before and after treatment with deoxyribonuclease; this makes the method specific for DNA.

The procedure is more economical in terms of the starting material (i.e. the granulocytes) used than methods (Burton, 1956; Giles & Myers, 1965) that employ the diphenylamine reaction.

The values obtained for the DNA content of human granulocytes by the present method is 6–7 pg/cell. This agrees with the values reported by previous workers, who have used less sensitive methods and larger numbers of cells (Mandel *et al.*, 1950; Metais *et al.*, 1951; Davidson *et al.*, 1951).

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The Measurement of the Deoxyribonucleic Acid Content of Human Granulocytes

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We are currently studying some aspects of protein synthesis in human granulocytes (Andrews *et al.*, 1971). These cells have a strong tendency to form clumps when they are resuspended for biochemical studies, having been previously separated from heparinized whole blood by dextran sedimentation and differential centrifugation through an albumin solution. This makes their enumeration with either a haemocytometer or the Coulter counter unreliable, so that a cell count is a poor parameter against which to express the results of relatively more precise biochemical investigations.

We have developed a method of measuring the DNA content of as few as 1×10^6 human granulocytes with a coefficient of variation of about $\pm 3\%$. This enables the amount of DNA present to be used

Metabolism of Prostaglandin E_1 by Human Plasma

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Prostaglandins have been found in human blood in certain pathological conditions (see, e.g., Williams *et al.*, 1968) and during labour (Karim, 1968), but there has been a lack of evidence for their presence in normal human blood. We have, however, now demonstrated the presence of prostaglandins in normal human blood (Greaves & McDonald-Gibson, 1972). During this study an enzymic prostaglandin E_1 -metabolizing system in human plasma became apparent.

[5,6- 3H]Prostaglandin E_1 was added to fresh blood (final concn. 10 ng/ml). Plasma was separated and prostaglandins and metabolites were extracted and