Table 1. Composition of Codons

Amino-acids	Codons	A	U	G	C
I. Polar					
1. Arg	CGC AGA UGC CGA	0·25	0·08	0·33	0·33
2. Asp	GUA GCA GAA	0·45	0·11	0·33	0·11
3. Asp-N	ACA AUA ACU	0·56	0·22	0·00	0·22
4. Glu	GAA GAU GAC	0·45	0·11	0·33	0·11
5. Glu-N	AAC AGA AGU	0·56	0·11	0·22	0·11
6. His	ACC ACU	0·33	0·17	0·00	0·50
7. Lys	AAA AAU	0·83	0·17	0·00	0·00
8. Ser	UCU UCC UCG ACG	0·08	0·33	0·17	0·42
9. Thre	CAC CAA	0·50	0·00	0·00	0·50
10. Tyr	AUU	0·33	0·67	0·00	0·00
	Average over group I	0·43	0·20	0·14	0·23
II. Non-polar					
11. Ala	CCG UCG ACG	0·11	0·11	0·33	0·45
12. Cis	UUG	0·00	0·67	0·33	0·00
13. Gly	UGG AGG CGG	0·11	0·11	0·67	0·11
14. Ileu	UAU UAA	0·50	0·50	0·00	0·00
15. Leu	UUG UUC UCC UUA	0·08	0·58	0·08	0·25
16. Met	UGA	0·33	0·33	0·33	0·00
17. Phe	UUU CUU	0·00	0·83	0·00	0·17
18. Pro	CCC CCU CCA CCG	0·08	0·08	0·08	0·75
19. Try	GGU	0·00	0·33	0·67	0·00
20. Val	UGU UGA	0·17	0·50	0·33	0·00
	Average over group II	0·14	0·40	0·28	0·17
	Total average	0·29	0·30	0·21	0·20

Table 2. The Ratios of the Nucleotides in the Codons

Ratio	Polar amino-acids	All amino-acids	Non-polar amino-acids
U/A	0·47	1·04	2·85
G/C	0·61	1·05	1·64
U/C	0·87	1·50	2·35
G/A	0·33	0·73	2·00
U+G/A+C	0·52	1·02	2·20

amino-acids—by the triplets containing guanine and uracil.

This statement is very rough, being based on simple averaging. There are also few exclusions. However, the difference between the codons of the two groups is well pronounced.

It is easy to show that a mutation of the kind called transition means a transition from A to G or from C to U. The transition can therefore exchange a polar amino-acid for the non-polar one and vice versa. It is not always so in the case of transversion. We can think that the transitions are more dangerous than the transversions. Perhaps the probability of transitions is lower. Our knowledge of these problems is, as yet, very limited. But Freese[4] points out that 80 per cent of the spontaneous mutations of the *T*4-phage are not connected with transitions.

The causes of the differences stated here cannot be explained at present. The structures of A and C have common features—they contain an NH_2-group at the greatest distance from the N-atom linked with ribose. U and G contain a CO-group at the same positions. Perhaps these differences in structure play some role in the interactions of the *s*-RNA with the corresponding amino-acyladenylate at the surface of specific enzyme.

The complete deciphering of the compositions of the codons and of the sequences of the nucleotides in them will make possible a more detailed analysis of this problem.

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Helix-rich Fraction from the Low-sulphur Proteins of Wool

Much has been learnt about the architecture of fibrous proteins such as myosin by controlled proteolysis and the application of physico-chemical and analytical techniques to the fragments obtained in this way[1].

The low-sulphur proteins of wool (*S*-carboxymethylkeratein *A*; SCMKA) resemble myosin in the relatively high proportions that assume the α-helical conformation. Harrap[2] found by optical rotatory dispersion measurements that SCMKA contains about 50 per cent α-helix when dissolved in water and about 60 per cent when dissolved in 2-chloroethanol. It has now been possible, using controlled proteolysis, to prepare fractions containing greater amounts of α-helix.

Solutions of SCMKA, prepared as described previously[2], were digested with crystalline trypsin (1 mg to 100 mg SCMKA) or with pronase P (0·1 mg to 100 mg SCMKA) at *p*H 8·6 in the presence of 0·1 M $CaCl_2$. The *p*H was kept constant and the progress of the reaction was followed by means of a *p*H-stat. With each enzyme the rate curve was characterized by an initially rapid digestion followed by a slower digestion. The digestion was terminated at the desired point, and the larger molecular species precipitated, by adjusting the *p*H to 4·2. The precipitate was recovered by centrifugation, dissolved in 0·05 M sodium borate, dialysed against a portion of the same buffer solution overnight and optical rotatory dispersion measurements made on the solution over the wave-length range 334 to 578 mμ using a Stanley photoelectric polarimeter.

When the optical rotatory dispersion data were plotted in terms of the Moffitt[3] equation, maximum values for $-b_0$ were obtained when the initial rapid digestion was just complete. Pronase digestion produced fractions with $-b_0$ values up to 520 corresponding with approximately 84 per cent α-helix, whereas the product from tryptic digestion gave a $-b_0$ value of 370, indicating an α-helix content in water of only about 60 per cent. The maximum yield of the pronase digestion product prepared under these conditions was about 18 per cent by weight. The b_0 values suggest that the wider specificity of pronase[4] enables the enzyme to rupture peptide linkages nearer to the helical portion of the molecule than is possible with trypsin.

Physico-chemical and analytical data relating to the helix-rich material will be published elsewhere.

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Synthesis of Cellulose by Enzyme Preparations from the Developing Cotton Boll

Recently an enzyme system from mung bean seedlings was described which catalyses the incorporation of radioactivity into cellulose from guanosine diphosphate D-glucose labelled with ^{14}C in the D-glucosyl moiety[1]. The extent of this incorporation was considerably stimulated by the addition of GDP-D-mannose to the reaction mixtures. This effect was later shown to result from the formation of some as yet uncharacterized polysaccharide, probably a glucomannan[2]. The synthesis of this compound also appeared to proceed at a rate many times that at which cellulose was formed by the same preparations. Sugars other than D-glucose, chiefly D-xylose or D-mannose, have been found associated with the cellulosic fractions of most plant species, but cotton fibres consist almost entirely of β-1,4 linked D-glucosyl residues[3]. It was therefore of interest to learn whether ^{14}C-labelled D-glucose from GDP-D-glucose ^{14}C could be incorporated into the cellulose of cotton fibres *in vitro*