host genome, the transformation experiment supplies a sensitive test for the pairing ability of the two homologous chromosome segments, which is presumably dependent on similarity of the pattern of arrangement of the bases.

The genetic material can also be used for the establishment of phylogenetic relations in higher organisms. M. Wasserman showed that chromosome rearrangements in the genus *Drosophila* can be used for this purpose, and exemplified his conclusions by a discussion of the repleta group of this genus. Inversions are particularly useful, since they occur very rarely, and the independent reoccurrence of the same arrangement can be reasonably excluded. Since many arrangements found cannot have arisen from another known arrangement in one step, it is possible to arrange the occurring chromosomal patterns in series which correspond to phylogenetic series. It cannot be easily established in any one series in which direction the series is to be read; but consideration of all arrangements in a larger group can usually overcome this difficulty. Wasserman pointed out that in the repleta group the phylogenetic relations established by chromosome morphology agree well with the taxonomy based on morphological characters. But chromosomal divergence is not correlated with morphological divergence.

E. H. Colbert discussed the fundamental contributions that paleontological methods can make for our understanding of phylogeny, and illustrated his points by references to the evolution of the duckbill dinosaurs in the Upper Cretaceous of North America. Where a reasonably complete fossil record exists, there is usually no difficulty in establishing the true phylogenetic relations between species found in successive strata. Convergence and pseudohomology will arise in these cases too, but they are relatively easily detected and will not confuse the phylogenetic picture. Finally, the paleontological record can give us information on the time spans involved in particular evolutionary processes (about 24 million years for the history of the duckbill dinosaurs), and on the changes in the conditions on the earth which were occurring at the same time.

The biochemical implications of evolution were considered by S. S. Cohen. He pointed out that, contrary to the assumptions of earlier biochemists, differences in biochemical characters between different organisms are not restricted to so-called superficial characters, such as pigments or cell-wall constituents, but that also very fundamental processes, such as the synthesis of DNA and RNA and their components and the pathways in the activation and synthesis of amino acids are by no means as homogeneous among different organisms as was originally supposed. A seeming contradiction consists in the fact that in different species of bacteria strong differences in DNA composition can be found, while the proteins depending on the DNA's appear to be much more similar in constitution and function. Since important basic steps in biochemical syntheses are performed in different ways in different organisms, it may be concluded that biochemical processes change in the course of evolution, and that biochemical functions cannot only be lost, but also acquired. Differences and similarities in basic biochemical processes have not yet been investigated systematically; most of the material quoted is derived from bacteria and from vertebrates. But study of biochemical evolution promises to offer a very important tool for progress in the study of phylogeny.

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Transfer of Genetic Information

The analysis of the genetic code and the clarification of mechanisms controlling gene expression are among the important contributions of molecular biology in recent years. At the AAAS meetings in Philadelphia, a symposium entitled The Transfer of Genetic Information, organized by Severo Ochoa and Philip Abelson, was concerned with recent progress in these areas. Three of the papers discussed the genetic code: "Characteristics of RNA codewords," Oliver W. Jones and Marshall W. Nirenberg (National Institutes of Health); "Synthetic polynucleotides and the amino acid code," Peter Lengyel, Joseph Speyer, Carlos Basilio, Albert Wahba, and Severo Ochoa (New York University); and "The doublet code and its implications," Richard B. Roberts (Carnegie Institution of Washington). The fourth speaker, Sol Spiegelman (University of Illinois) discussed the nature of genetic expression and its control in a talk entitled "Properties of the mechanism which reads the genetic book."

Since the announcement by Marshall Nirenberg in August 1961 that polyuridylic acid stimulates cell-free protein synthesizing systems to incorporate labeled phenylalanine into acid-insoluble peptide linkages, the characterization of the amino acid code has proceeded rapidly. It was soon found by Ochoa and Nirenberg that copolymers containing uridine and varying amounts of one of the other three nucleotides found in naturally-occurring RNA stimulate the incorporation of other amino acids. The genetic work of Crick and coworkers had indicated that most probably a triplet of RNA nucleotides is the template for one amino acid. With this assumption a triplet code was constructed for the amino acids incorporated by the various copolymers.

In the earliest published data only copolymers which contained U could serve as templates for protein synthesis. No naturally-occurring RNA has been observed with such a large fraction of U. The data of Sueoka relating the acid composition of organisms to the GC content of their DNA can not be explained by a code containing a preponderance of U. To resolve this paradox Richard Roberts proposed a doublet code which (i) incorporated the results of Ochoa and Nirenberg; (ii) had a reasonable GC content; (iii) agreed with the Sueoka data; and (iv) was consistent with the idea that certain single amino acid changes produced in tobacco mosaic virus protein, as the result of treatment of the virus with nitrous acid, were the result of single nucleotide changes in the nucleic acid of the virus. Roberts reviewed this code in the symposium and pointed out that the doublet code predicts that any synthetic polyribonucleotide should be active as a template for protein synthesis. Further attempts were made to use polymers that did not contain U as templates. Bretscher and Grunberg-Manago very shortly found that poly AC preparations stimulate the uptake of proline, threonine, histidine, and to a lesser extent, glutamine. Jones and Lengyel both reported that polyribonucleotides not containing U are effective templates for protein synthesis. Lengyel and coworkers found that poly A is effective in incorporating lysine in a cell-free rat liver system and also in a cell-free *Escherichia coli* system. The resulting product is soluble in aqueous solutions and can be hydrolyzed by trypsin but not by chymotrypsin, properties which identify the product as polylysine. Poly C in high concentrations stimulates incorporation of proline.

The New York University group also performed experiments with copolymers consisting of a high percentage of A and of low percentages of other kinds of nucleotides. Similarly copolymers consisting of a high percentage of C and low percentage of other kinds of nucleotides were employed. These experiments led to the deciphering of the composition of 20 new code triplets.

Jones reported the results of experiments in which polynucleotides containing all four bases, poly ACG, poly AC, poly CG, and poly AG were used as templates. In most cases these polymers quite specifically direct the incorporation of certain amino acids; for example, copolymers of A and C contain the code words for histidine, aspartic acid, proline, glutamic acid, lysine, and threonine. A tentative summary of code words representing the composite data of both groups is listed in Table 1.

Factors other than base composition contribute to the effectiveness of a given polynucleotide in serving as a template for protein synthesis. Jones reported that length and extent of secondary structure are also important in this respect. Polynucleotides with more than 100 units are more effective as templates than are shorter polymers. Experiments with a series of UG copolymers indicated that those with a high G content are ineffective as templates and also exhibit a high degree of secondary structure.

In summary the distinguishing features of the code as it is now understood are:

1) The code is specific; amino acids are only incorporated into proteins by templates which contain their code words. There is a very low incidence of mistakes in reading the RNA template.

2) The code is degenerate; that is, there is more than one code word for many of the amino acids.

3) The fact that nearly all synthetic polynucleotides so far examined are active in coding for at least one amino acid suggests that most of the nucleotide sequences in these synthetic polymers may be meaningful.

4) Hypoxanthine will replace guanine in templates containing G, so the 2-amino group of G is apparently superfluous in so far as the code is concerned.

5) Many of the amino acids may be coded by polymers having only two bases; exactly what the doublet code theory might predict. Roberts reported that this theory had predicted 93 percent of the experimental results found subsequent to its publication. This successful prediction lends support to the idea that if code words are triplets, two of the bases carry the majority of the information.

6) Lengyel pointed out that many of the degenerate code words differ by a single base. This base can be U, A, or C, but it is not so for G.

7) The order of nucleotides has been determined for very few code words, but possibilities exist for solving this problem.

Table 1. The amino acid code as determined by researchers at the National Institutes of Health and New York University. [Sequence of nucleotides within code words was not determined experimentally except for tyrosine (AUU) by the New York University group.]

Amino acid	Code word	
	National Institutes of Health	New York University
Alanine	CCG	CUG CAG CCG
Arginine	CGC	GUC GAA GCC
Asparagine*	ACA	UAA CUA CAA
Aspartic acid*	ACA	GUA GCA
Cysteine†	UUG or UGG	GUU
Glutamic acid‡	ACA AGA AUG	AAG AUG
Glutamine‡	ACA	AGG ACA
Glycine	UGG	GUG GAG GCG
Histidine	ACC	AUC ACC
Isoleucine	UUA	UUA AAU
Leucine§	GUU CUU AUU (UUU)	UAU UUC UGU
Lysine	AAA AAC AAG AAU	AUA AAA
Methionine	UGA	UGA
Phenylalanine	UUU	UUU UUC
Proline	CCC CCU CCA CCG	CUC CCC CAC
Serine	UCG UUC UCC	CUU CCU ACG
Threonine	CAC CAA	UCA ACA CGC
Tryptophan	UGG	UGG
Tyrosine	UAU	AUU
Valine	UGU	UUG

* The NIH group cannot as yet determine whether ACA represents aspartic acid or asparagine. † It is not clear yet which of these possibilities is correct. ‡ The NIH group cannot as yet determine whether ACA represents glutamic acid or glutamine. § Poly U will serve as a template for leucine in the absence of phenylalanine.

Spiegelman's paper dealt with the nature of genetic expression and its control.

When the T2 bacteriophage injects its DNA into bacteria, a series of ordered events takes place which culminates with the lysis of the bacteria and the release of many phage progeny. If the T2 genome is read randomly during this process then the composition of the RNA during any given period following infection of the bacterial cell by the phage should be the same, that is, a random sample.

Spiegelman found that the elution pattern from the Mandell-Hershey column is different for RNA synthesized between the 3rd and 5th minutes following infection than for RNA synthesized between the 13th and 15th minutes. Since the RNA synthesized during different periods is not the same, the phage genome is not read randomly during vegetative phage production.

The second point discussed by Spiegelman concerning the expression of the gene dealt with work on the well-known β-galactosidase system. The enzyme β-galactosidase is synthesized in large amounts in the presence of its substrate lactose, or analogues of its substrate, but is not synthesized in the absence of an inducer, as these molecules are called. The question arises whether the inducer directs synthesis of the lac messenger or whether it activates a messenger already synthesized. Pulse-labeled RNA was extracted from wild type *E. coli* grown with and without an inducer and from a mutant having a deletion in the lac region grown with an inducer. DNA from a transducing phage, P1, which carried the lac region was extracted. Each of the RNAs was tested to see if it would form a complementary hybrid with this DNA under suitable conditions. A significantly larger portion of the RNA isolated from the induced strain hybridized with DNA containing lac gene than with either of the two control RNAs. In addition, it was found that the RNA isolated from the induced strain produced two RNA peaks in the Mandell-Hershey column eluant that the control did not have. The RNA from all of the peaks was tested for ability to hybridize with lac gene-containing DNA. Only the material from the two distinct peaks could hybridize appreciably. This RNA did not hybridize with DNA from transducing phage not containing the lac gene.

These experiments indicate that the inducer acts by controlling the synthesis of the RNA messenger rather than by controlling use of the messenger. The experimental procedure promises to provide a source of messenger RNA from a specific gene.

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Satellites: Scientific Mission and Design

The significance of scientific satellites and their growing importance in gathering basic new information about space and in support of future manned space programs were emphasized in a one-day (27 December) special astronautics symposium at the AAAS Philadelphia meeting. The president of the American Astronautical Society, Alfred M. Mayo (Chance-Vought Corporation), in his brief welcome pointed out how symposia of this type can improve communication between scientists and engineers, and thereby improve the chances for mission success.

Various techniques, such as welding to improve circuit reliability, yo-yo despin control for stabilization, and methods for solar cell control were discussed by Alexander Kossiakoff (Johns Hopkins University) in his keynote address on "Scientific satellites—a perspective."

The morning session, chaired by John E. Naugle (NASA), contained four technical papers dealing with current scientific satellites. The objectives of the NASA S-6 Aeronomy Satellite include measurement of the neutral atmospheric parameters of density, composition, pressure and temperature, and the electron density and temperature in the region of 250 to 900 km, together with variations of all these parameters with time and latitude. Various primary detectors (neutral mass spectrometers, vacuum gauges and electrostatic probes), plus the necessary engineering provisions in the satellite for power, stabilization, telemetry, programming and command response were included in a paper by R. Horowitz (NASA).

Two complementary papers treated the subject of topside sounding of the ionosphere. The Canadian "Alouette," or S-27 satellite, utilizes a swept-frequency sounding technique in the 1- to 12-mc region. The sweep frequency method, described by John H. Chapman (Defence Research Telecommunications Establishment, Ottawa), is usually preferred for measurement of vertical electron density profiles, whereas the fixed frequency method, described in another paper on NASA's S-48 program by John E. Jackson (Goddard Space Flight Center) is best adapted to the observations of height changes with time, the drift of irregularities in the ionosphere, and so forth. In the exploratory phase of topside sounding there is an obvious need to examine both methods. The Central Radio Propagation Laboratory of the National Bureau of Standards is providing scientific coordination and direction of these efforts with NASA; a joint working group on topside sounding includes representatives of the United States, Canada, and the United Kingdom.

Exploratory soundings from the topside of the ionosphere were first obtained at Wallops Island in June and October 1961; these soundings used special rocket pay-loads designed by Airborne Instruments Laboratory under the S-48 program. Results from these experiments showed the feasibility of the various design parameters, power levels, and background galactic noise levels. The Canadian S-27 satellite was successfully orbited by NASA on 29 September 1962, and became the first topside sounder satellite. Excellent data already received from the S-27 have shown a number of interesting anomalies as well as a wealth of more routine information about the variations in electron density over the entire earth's surface with time under varying magnetic and auroral conditions. The presence of distinct layer tilts in certain equatorial regions and evidence of additional "layering" at altitudes above the normal region of maximum F2 electron density has been noted under some conditions. A comprehensive picture of the upper ionosphere over the entire earth's surface will soon be provided by analysis of the data from the S-27 and the S-48.

The three satellites Injun I, II, and III were designed and built at the State University of Iowa to study the natural and artificial radiation belts, auroras and airglow, and other geophysical phenomena (Brian J. O'Brien). Injun I has already produced a vast amount of useful radiation measurements. It has shown that the primary source of auroral particles lies well above the ionosphere, and that the outer-zone is probably not a source of auroral particles (as in the "leaky bucket" model), but is perhaps a sink of unused auroral particles. For the first time it was shown that the sun exerts a strong steady-state control on the shape of the magnetosphere in which particles can be trapped. Injun I, after one year in