INVESTIGATION OF A NON-CARBON BASED BIOCHEMISTRY AND ITS IMPLICATIONS FOR CELLULAR BIOLOGY

PART I. GLYCINE AND ITS SILICON BASED DERIVATIVES

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Abstract

It has been suggested that since the presumed biochemical evolution of life involves the formation of proteins from amino acids, a similar mechanism could perhaps have also occurred with non-carbon based amino acids. The element most chemically similar to carbon is silicon, although no silicon analogs of amino acids are known to exist. This paper reports a study of bond energetics for glycine, a hypothetical analog in which carbon atoms are replaced by silicon, and other modifications in which the glycine nitrogen and oxygen atoms are replaced by phosphorus and sulphur respectively. Comparison of energy changes are made between reactant molecules and their respective peptide bonded products. The results indicate that the peptide bond formation process is energetically feasible for glycine, but not for the proposed modifications.

Background and Introduction

While efforts to validate the creation mode of origins have embarked upon the vistas of most all areas of science, the one receiving the least attention is that of chemistry. The evolutionary supposition of a “prebiotic soup” has been addressed. Classic experiments of Fox, Orgel, Miller and others have demonstrated that a properly energized, reducing atmosphere of CH_4 , NH_3, H_20, and H_2 can produce certain amino acids (Fox, 1976; Miller and Orgel, 1974; Miller, 1974). However, no polypeptides resembling natural proteins have been produced under laboratory simulations of “prehistoric” conditions (Orgel, 1973, pp. 189-fq; Yockey, 1981; Oro and Kimball, 1961).**

All five of the nucleotide bases have been synthesized by reacting either various combinations of HCN in aqueous solutions, or certain nitriles, including urea and other essential components under controlled heating (Ponnamperuma, 1965; Sanchez, Ferris, and Orgel, 1966; Fox and Harada, 1961; Stephan-Sherwood, Oro, and, Kimball, 1971).

The sugars ribose and deoxyribose have been prepared from alkaline solutions of formaldehyde (Ora and Cox, 1962). Nonetheless, all attempts to combine these compounds together with phosphoric acid or phosphates to produce DNA-like polymers have failed to yield products resembling true biochemically functional polynucleotides. However, Westheimer (1987) still contends that the uniqueness of phosphates in polynucleotides is a choice, of nature dictated by the evolutionary process. Miller (1992) has reviewed the current state of affairs in the theory of biochemical evolution. The available data offer no more supporting evidence than what has been presented in the course of the past 45 years or so.

Creationists and evolutionists alike agree that the basis for the formation of biomolecules is rooted in the uniqueness of the chemistry displayed by the element carbon. This is the only element demonstrating a virtually unlimited capacity for “catenation” (i.e., the property of like atoms bonding to each other and to other kinds of atoms at the same time). In spite of this fact, many non-creationists still make allusions to a parallel biochemistry based on some element other than carbon. Admittedly most of these contentions are usually expressed in rather nebulous terms with little or no concrete substantiating evidence offered in support. However, there is a serious belief on the part of some respected evolutionists that, given appropriate conditions, some other element could replace carbon in its biomolecular function. Ponnamperuma and Woese (Begley, 1979) stated that the large amount of silicates present in clay may have played a major role in the origin of biochemistry when the earth was initially formed (see also Woese, 1979). This was initiated by Bernal (1967) and reiterated more recently in the work of Cairns-Smith (l982).

Consider the following case in point taken from a recent interview made by Frank Miele with Richard Dawkins (Miele, 1995);

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**The subjects of chemical evolution and design in chemical compounds have appeared in the Quarterly previously. See the following selected bibliography: Williams, E. L. 1967. The evolution of complex organic compounds from simpler chemical compounds: Is it thermodynamically and kinetically possible\?: *CRSQ* 4:30-35; Gish, D. T. 1970. The nature of speculations concerning the origin of life. *CRSQ* 7:42-45, 83; Brauer, D. L. 1971. Organic chemistry reflects God’s infinite knowledge. *CRSQ* 8:9-12; Coppedge, J. F. 1971. Probability and left-handed molecules. *CRSQ* 8:163-174; Gish, D. T. 1972. Book review of Biochemical predestination. *CRSQ* 8:277-280; White, A. J. 1972. Uniformitarianism, probability and evolution. *CRSQ* 9:32-37; Gish, D. T. 1979. A consistent Christian-scientific view of the origin of life. *CRSQ* 15:185-203; Trop, M. 1979. Polyamino acid—the missing link. *CRSQ* 15:205-209; Moore, J. N. 1985. Teaching about origin questions: Origin of life on earth. *CRSQ* 22:20-25; Mini-Symposium—Creationist interpretations of chemical organization in time and space. *CRSQ* 22:157-158; Heyes, G. B. 1986. Stereochemical design in lipids. *CRSQ* 23:20-27; Anderson, K. L. 1989. Prebiotic formation on the first cell. *CRSQ* 26:55-60; Lumsden, R. D. 1993. Sources and applications of botanical alkaloids offer evidence of creative purpose and design. *CRSQ* 30:132-140.

Q. Does the existence here on earth of an alternative metabolic "fuel," in some sense make it more probable that there could be life elsewhere in the universe, perhaps using a different base than carbon?

A. (Dawkins) That's surely got to be right, hasn't it? You can speculate in a science fiction way about alternative biochemistry of life, but if you couldn't find anything on Earth moving ever so slightly towards an alternative biochemistry, that would argue against the idea. But when you do find an alternative biochemistry for life here on Earth, that makes it more plausible that somewhere else in the universe there's got to be an alternative form of life.

Q. What then is the *sine qua non* of life? What raw materials and conditions are necessary for life to exist?

A. (Dawkins) Well, you need raw materials that can self replicate. I would have to be more of a chemist than I am to know how likely it is that you are going to get such molecules. I should very much like to direct chemists toward devising an alternative hypothetical chemistry that supports self-replication, a whole alternative system that could, in principle, give rise to life. The fundamental principle that will be required is self-replication. Chemists have begun to look at autocatalytic functions in chemistry where at least some of the prerequisites are present. The *sine qua non*, as you say, is self-replication. I don't know how difficult it would be to achieve that chemically.

Of course, no one knows (except God) what conditions are actually necessary for life to be imparted to a system composed of biomolecules assembled within a cellular matrix. Dawkin's reply to this question specifically addresses the biochemical process of replication involved in cellular reproduction and related processes. Before one can even consider the requirement of "self-replication" in any assumed alternative "biochemistry of life," there is the primary consideration of producing the essential molecular components for constructing protein, RNA- and DNA-like structures. In effect, all carbon atoms in amines, ribose, and nucleotide bases would have to be replaced by some other substituent atom.

The challenge of identifying a viable alternative model chemistry that supports self-replication is the basis for this paper.

Statement of The Problem

The first and most extensive phase of this study has been to investigate the chemical characteristics of various hypothetical amino acid-like molecules, in which the carbon atoms have been substituted by some other chemically similar atoms. The single candidate most likely to chemically mimic carbon is the element silicon (Si), positioned just below carbon in the same Group of Periodic Table of Elements. The Si atom forms a maximum of four chemical bonds as does the C atom, and Si exhibits at least some limited :catenation" ability. A portion of the Periodic Table depicting the pertinent elements relating to this problem is presented in Table I.

The proposed Si substitution will have to be considered in all 20 amino acids crucial to protein structures. I will refer to these hypothetical pseudo-amino acids as "silicino acids." However, the C-N bonds in natural amino acids are chemically different from Si-N bonds in silicino acids. Thus, the replacement of N by phosphorus, which is adjacent to Si in the Periodic Table (see Table I), just as N is adjacent to C, is a logical consideration. It may be that Si-P bonds in silicino acids will have a chemical similarity to the C-N bonds in amino acids.

An additional consideration is the comparison of C=O and C-OH bonds in the carbonyl functional groups of amino acids, to analogous Si=0 and Si-OH bonds in silicino acids. It is anticipated that replacing oxygen by sulfur to yield Si=S and Si-SH bonds, may be preferable counterparts to C=O and C-OH bonds in the acid functional group.

Table I. Second and third period elements of main groups IV, V, VI.

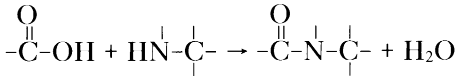
IV	V	VI	
C	N	O	(4 valence electrons – 2s and 2p orbitals)
Si	P	S	(4 valence electrons – 3s and 3p orbitals)

It will be necessary to characterize the structural features and chemical bonding of the silicino acids and compare them to similar properties of amino acids. The current understanding of silicon chemistry suggests that chemical characteristics of silicino acids will be significantly different from amino acids. This work is to demonstrate that these hypothetical biochemical molecular units do not vindicate the evolutionists' supposition of a non-carbon chemistry of life. On the contrary, biochemistry does require the specificity of carbon atoms to provide the necessary biochemical structures and functions. This, however, must be validated with the empirical scientific data presented below.

Format of The Study

Ten different species of the 20 essential amino acids have been selected from among those contained in the protein insulin. This example was selected because the polymer chains in the primary structure are relatively short, and they incorporate a representative variety of amino acid peptide linkages. These amino acids, presented in Table II, are regarded to be retained in their L-optical isometric conformations (right handed) which are the forms occurring in most natural proteins. With ten per cent parent amino acids and the three modifications of silicino acids for each, there will be a total of 40 molecules to investigate.

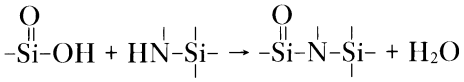
The major points of interest here are the processes of forming peptide and pseudo-peptide bonds. All known peptide bonds involve the process:



$$-\overset{\overset{\displaystyle O}{\|}}{C}-OH + H\overset{|}{N}-\overset{|}{\underset{|}{C}}- \rightarrow -\overset{\overset{\displaystyle O}{\|}}{C}-\overset{|}{N}-\overset{|}{\underset{|}{C}}- + H_2O$$

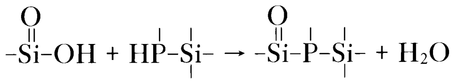
In the case of silicino acids, the parallel processes become:

Modification #1



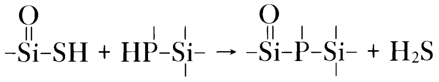
$$-\overset{\overset{\displaystyle O}{\|}}{Si}-OH + H\overset{|}{N}-\overset{|}{\underset{|}{Si}}- \rightarrow -\overset{\overset{\displaystyle O}{\|}}{Si}-\overset{|}{N}-\overset{|}{\underset{|}{Si}}- + H_2O$$

Modification #2



$$-\overset{\overset{\displaystyle O}{\|}}{Si}-OH + H\overset{|}{P}-\overset{|}{\underset{|}{Si}}- \rightarrow -\overset{\overset{\displaystyle O}{\|}}{Si}-\overset{|}{P}-\overset{|}{\underset{|}{Si}}- + H_2O$$

Modification #3



$$-\overset{\overset{\displaystyle O}{\|}}{Si}-SH + H\overset{|}{P}-\overset{|}{\underset{|}{Si}}- \rightarrow -\overset{\overset{\displaystyle O}{\|}}{Si}-\overset{|}{P}-\overset{|}{\underset{|}{Si}}- + H_2S$$

This study compares the energies of the amino acid C-OH bonds and the amino H-N bonds with the energies of the resulting peptide C-N-C bonds vs. H-N bonds vs. Si-N-Si bonds; Si-OH bonds vs. H-P vs. Si-P-Si bonds; and Si-SH bonds vs. H-P bonds vs. Si-P-Si bonds.

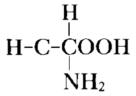
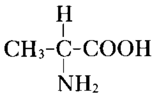
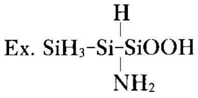
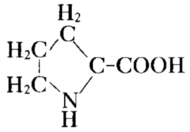
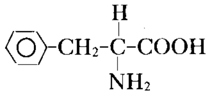
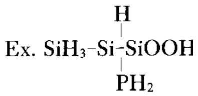
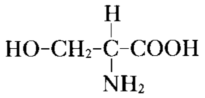
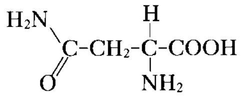
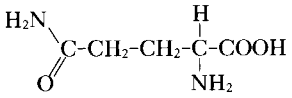
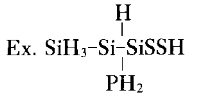
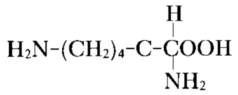
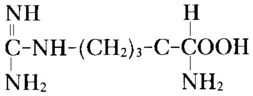
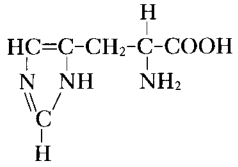
The final portion of this investigation deferred for a subsequent paper, is to calculate the bond energies of the six amino acid segments in the tripeptide portion of the primary structure of insulin, to wit;

Gly–Gln–Arg–Gly–Phe–Phe

A similar calculation will also be carried out with the most stable substituted forms of silicino acids whose structures are analogous to their Gly, Gln, Arg, and Phe counterparts. Thus the relative stabilities of peptide structures derived from natural amino acids can be compared with the pseudo-peptides derived from silicino acids. As inferred from this work, the binding energies of the latter systems are likely to be either too high or too low, in comparison to those of natural peptides, to be biochemically functional.

In this initial paper the data obtained for glycine and the three modifications of its silicino acid counterparts are presented. Subsequent publications will include data for all the cases cited above.

Table II. Select Amino Acids and Presumed Silicino Acids.

Amino Acids		
Glycine (Gly)	 $H-\overset{H}{\underset{NH_2}{C}}-COOH$	*Modification 1:* All C atoms replaced by Si atoms
Alanine (Ala)	 $CH_3-\overset{H}{\underset{NH_2}{C}}-COOH$	 Ex. $SiH_3-\overset{H}{\underset{NH_2}{Si}}-SiOOH$
Proline (Pro)		*Modification 2:* All C atoms replaced by Si atoms; all N atms replaced by P atoms
Phenylalanine (Phe)		 Ex. $SiH_3-\overset{H}{\underset{PH_2}{Si}}-SiOOH$
Serine (Ser)	 $HO-CH_2-\overset{H}{\underset{NH_2}{C}}-COOH$	*Modification 3:* All C atoms replaced by Si atoms; all N atoms replaced by P atoms; all O atoms replaced by S atoms
Asparagine (Asn)		
Glutamine (Gln)		 Ex. $SiH_3-\overset{H}{\underset{PH_2}{Si}}-SiSSH$
Lysine (Lys)	 $H_2N-(CH_2)_4-\overset{H}{\underset{NH_2}{C}}-COOH$	
Arginine (Arg)	 $\overset{NH}{\underset{NH_2}{\overset{\|}{C}}}-NH-(CH_2)_3-\overset{H}{\underset{NH_2}{C}}-COOH$	
Histidine (His)		

Method or Investigation

Since all of the Si modifications to the amino acids are hypothetical, any laboratory synthesis approach to the study of this problem is not feasible. Therein lies the advantage of computational chemistry.

It is possible to employ quantum chemical molecular orbital calculation as the method of investigation. However, such computations are not only lengthy and laborious, but they do not necessarily yield bond energy data of the highest accuracy. Since the main objective of this study is to compare bond energies, it is much more desirable to employ some approach that will provide directly reliable bond energies. Sanderson (1976) described an empirical method for computing bond energies from atomic electronegativities called Stability Ratios (SR). This method yields bond energies with better than 97 percent accuracy.

The stability Ratio is given by the expression

$$SR = D/Di \tag{1}$$

where D is the electron density of the atom in question and Di is the electron density of that atom if its atomic number were the same as that of a noble gas atom in Group 8A of the periodic table of elements (Sanderson, 1976, p. 40). The latter is obtained by interpolation of a plot of the D values for the Group 8A elements. The electron density is evaluated from the expression

$$D = \frac{Z}{\frac{4}{3}\pi r^3} \tag{2}$$

where Z is the number of electrons filling the orbitals of an atom whose atomic number is also Z and $\frac{4}{3}\pi r^3$ is the volume of the total electron cloud about the atom having a nonpolar covalent radius r (Sanderson, 1976, p. 40).

The homonuclear diatomic covalent bond energy (E) for an atom is derived from the expression (Sanderson, 1976, p. 44):

$$E = \frac{37.0(SR)(r)}{n - 0.70} \tag{3}$$

where n = the principal quantum number of the highest occupied orbital for the atom in question, and SR, r have already been defined in equations (1) and (2).

According in Sanderson (1976, p. 78, footnote to Table V-l) the partial charge, q_A, on any atom, A, is

$$q_A = \frac{\Delta S}{\Delta Si} = \frac{S_M - S_A}{2.08\sqrt{S_A}} \tag{4}$$

where S_M is the electronegativity (SR) of the compound, taken as the geometric mean of the SR values of all the atoms in the compound: S_A is the SR value of the atom in question; ΔS_i represents the change in electronegativity for an atom acquiring a unit positive or negative charge. However, I have found that a better procedure for evaluating q_A is not only to consider the difference in the electronegativity of the compound (S_M) and the atom (S_A), but also to include the effects that neighboring bonded atoms have on atom A as well. Thus, the modified expression for the partial atomic charge is

$$q_A = \frac{1}{2.08 n_T \sqrt{S_A}} [S_M - S_A) + (S_B - S_A)n_B + (S_C - S_A)n_C \ldots \text{etc.}] \tag{5}$$

where n_T is the total number of terms in the brackets and n_B, n_C . . . etc. are the numbers of atoms B, C, etc., bonded to atom A. Equation (5) allows for the charge of an atom to vary in different bonding environments as it should be, whereas equation (4) makes no provision for this. However, this does not alter the accuracy of Sanderson's (1976) original approach. As shown below, the net bond energy is partitioned into ionic and covalent contributions, but only the former directly incorporates atomic charges. Any changes in the ionic portion of the bond energy due to charge variation are absorbed by the covalent portion. Thus, the total bond energy is virtually unchanged.

The bonding radius, r_b of an atom having a partial charge q is obtained from the atom's nonpolar covalent radius, r, with the relation (Sanderson, 1976, p. 80):

$$r_b = r - B_q \tag{6}$$

where B is an empirical size parameter for the shrinking of a positively charged atom or the expansion of a negatively charged atom. Pertinent values of B are presented by Sanderson (1976, p. 82, Table V-2).

The total bond energy, BE, for any two bonded atoms, e.g., A and B, is given by the equation (in kcal/mol)

$$BE(A,B) = E_C(AB) + E_i(AB) \tag{7}$$

where E_C is the covalent part of the bonding energy and E_i is the ionic contribution.The E_C term is obtained from Sanderson (1976, pp. 99-100):

$$E_C(AB) = \frac{R}{R_O}(E_{AA}E_{BB})^{\frac{1}{2}} t_C \tag{8}$$

where R = the sum of the homopolar covalent radii and R_O the observed bond distance, or the one computed by applying equation (6), in angstrom units, t_c = the fractional covalent character of the bond given by $t_c = (1 - t_i)$, with t_i the fractional ionic character. For two atoms, A and B, having charges q_A and q_B respectively

$$ti = \frac{q_A - q_B}{2}. \tag{9}$$

If more than one B atom, n_B, is bonded to A, then t_i is given by

$$t_i = \frac{q_A - q_B n_B}{(1 + n_B)}. \tag{10}$$

The ionic contribution to the bond energy is obtained from

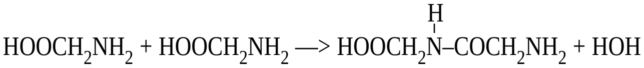
$$E_i(AB) = \frac{332 q_A q_B\, t_i}{R_O} \tag{11}$$

where the factor 332 converts energy units (ergs to kcal/mol).

Equations (7)-(11) may be applied for any number of bonds between adjacent atoms. The pertinent data for the atoms of the compounds of interest in this study are presented in Table III.

Results and Discussion

According to the following chemical equation, formation of the dipeptide glycine-glycine



$$HOOCH_2NH_2 + HOOCH_2NH_2 \longrightarrow HOOCH_2\overset{H}{N}\text{–}COCH_2NH_2 + HOH$$

requires the cleavage of a C-OH bond on one glycine molecule and the cleavage of an N-H bond on the other glycine, while the products involve the formation of one N-C peptide bond and one H-OH bond. The pertinent bond energies have been calculated employing the methodology described above. These data are included in Table IV together with silicino acid derivations listed as modifications 1, 2, and 3 in Table II.

Table III. Data for bond energy calculations.

Energy	SR	r[a]	E[b]	B
H	3.55	0.32	104.2	0.974
C	3.79	0.77	83.2	0.486
N	4.49	0.74	94.8	0.311(+), 0.063(–)
O	5.21	0.70	103.9	0.240
Si	2.84	1.17	53.4	0.587
P	3.43	1/10	60.7	0.404(+), 0.132(–)est.
S	4.12	1.04	69.0	0.681(+), 0.222(–)

[a] angstrom units (i.e., 10^{-8} cm).

[b] kilocalories per mole = kcal/mol.

Table IV. Pertinent bond energy data for glycine and its silicino acid derivatives.

Compound	Bond	BE[a]	E^b_{BB}	E^c_{BF}
H_2NCH_2COOH	–C–OH	105.7		
	–N–H	87.2	192.9	
$HOOCCH_2NHCOCH_2NH_2$	–N–C	89.1		
H_2O	H–OH	107.3		196.4
		$\Delta H^d = 3.5$		
H_2NSiH_2SiOOH	–Si–OH	115.6		
	–N–H	91.0	206.6	
$HOOSiSiH_2NHSiOSiH_2NH_2$	–N–Si	92.3		
H_2O	H–OH	109.6		201.9
		$\Delta H = 4.7$		
H_2PSiH_2SiOOH	–Si–OH	118.6		
	π			
–P–H	79.5	198.1		
$HOOSiSiH_2PHSiOSiH_2PH_2$	–P–Si	64.4		
H_2O	H–OH	109.3		173.7
		$\Delta H = 24.4$		
H_2PSiH_2SiSSH	–Si–SH	75.9		
	–P–H	79.1	155.0	
$HSSSiSiH_2PHSiSSiH_2PH_2$	–P–Si–	63.0		
H_2S	H–SH	74.3		137.3

[a] All bond energies (BE) in kcal/mol units.

[b] E_{BB} = sum of all BE for bond breaking process, in kcal units.

[c] E_{BF} = sum of all BE for bond formation process, in kcal units.

[d] $\Delta H = -(E_{BF} - E_{BB})$, the net enthalpy for the reaction.

As can be seen from Table IV, the formation of a peptide bond from two glycine molecules is a slightly endothermic process, requiring only 3.5 kcal of energy. This is even less energy than that computed for the —N——H----O— hydrogen bond energy (4.4 kcal) between the two glycine molecules. Hence it is understood that the peptide bond formation process occurs efficiently at low energy, without even interrupting the critical intermolecular hydrogen bonding so important to the stability of protein structures.

The hypothetical silicino acid counterpart of glycine enters into pseudo-peptide Si-N bond formation requiring an endothermic energy input of 4.7 kcal. Thus the total energies of the bond breaking processes exceed the total energies of the bond formation process, so that the stability of the products will not be maintained in any spontaneous chemical reaction. While 4.7 kcal is not a large energy perturbation, it is sufficient to disrupt hydrogen bond formation, even if it could be compensated for by some other chemical means.

To be precise, the free energy change, ΔG, is the correct thermodynamic criterion for a reaction to be favorable. The entropy, which is not included in these bond enthalpy calculations, does make a contribution to the thermodynamic process, but it is usually small relative to the enthalpy. For example, the entropies of gaseous C and Si are 37.8 and 40.1 cal/mol-deg respectively, which amounts to an entropy difference of only 2.3 cal/mol-deg. This contributes just 0.7 kcal/mol to the free energies at an ambient temperature of 298K. If the substitution of C by Si in glycine is regarded to not alter the overall molecular geometry (as is reasonable), then the entropy will differ by only C and Si entropies *per se.* Thus, the net entropy contribution will be merely 5 percent of the total difference in ΔH for both C and Si analogues of glycine (see Table IV).

In conclusion, the implications of these results, admittedly limited at present by initial findings reported herein, are that replacements of carbon by silicon in glycine and subsequent peptide bond formation are not energetically feasible processes. Since living cells are known to have very specific protein structures formed from natural carbon based amino acids, it appears that any chemical deviations from this design may not suffice for producing viable cellular structures.

Of course, nothing stated at this point is definitive, since data have been obtained for only one amino acid and its silicon counterparts. Further work is currently in progress to determine whether the results obtained with glycine will also be forthcoming with the nine other essential amino acids comprising the structure of a model peptide.

Acknowledgement

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BOOK REVIEWS

The Great Dinosaur Extinction Controversy by Charles Officer and Jake Page. 1996. Helix Books. Addison-Wesley Publishing. New York. 209 pages. Hardcover $25.00.

Reviewed by Carl R. Froede Jr.*

What killed the dinosaurs and exactly when did this occur in Earth's past? The controversy rages on as impactors and volcanists wage open warfare on each other in the printed media. A creationist perspective on this controversy is outlined in Froede and De Young (1996). Although acknowledging that they have the less popular theory, Officer and Page provide new information to the reader about this very popular issue. This book levels serious charges against the impact modelers ranging from the inappropriate hype of "imminent earth-ending impacts" touted by NASA (so necessary to secure government program dollars to search for earth-crossing asteroids) to blatant and willful ignorance to consider or accept an opposing and better supported scientific position. This easy to read book clearly presents counter evidences which insist on a volcanic end to the dinosauria and the termination of the Cretaceous Period. Officer and Page provide the reader with a brief but thorough review of the impact theory and then begin dismantling the key evidences used to support it. If the new volcanist issues raised by Officer and Page are not addressed by the impactors it will suggest that the impact theory is one of the most embarrassing displays of non-science in recent history, akin to cold-water fusion. Within the conclusions section of their book Officer and Page present the "symptoms of a degenerative emerging scientific research program or hypothesis." Symptom by symptom they walk the reader through this sequence as it relates to the impact hypothesis. They reveal that much of the evidence used to support the Cretaceous-Tertiary boundary impact extinction event is pseudo-science. These same symptoms also fit the evolution hypothesis. I highly recommend this book to anyone interested in this topic.

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The Quark and the Jaguar by Murray Gell-Mann. 1994. W. H. Freeman. New York. 392 pages. $l5.95.

Reviewed by Eugene F. Chaffin*

This work is a popular-level exposition of rationalistic evolutionism. The jaguar is used in the title as a metaphor for what is termed a "complex adaptive system." The book attempts to treat biology, physics, economics, linguistics, child development, computers, and a host of other subjects under this one umbrella. Murray Gell-Mann, the author, received the Nobel Prize in physics for his work on elementary particle theory. He introduced the idea of a "quark." Three quarks make up a nucleon, according to the results of group theory, a branch of mathematics with which Gell-Mann is highly skilled. His genius was in relating the re-

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sults of group theory to the maze of data which emerges from high energy physics experiments. However, no equations are relied on in this book to make the points.

In the early pages of the book, Gell-Mann defines *algorithmic information content* as the length of the shortest program that can produce a particular message string. Somewhat later in the discussion he defines *effective complexity* as the length of a concise description of the regularities of a system. With these definitions, he builds a picture of a universe which organizes itself, first into the elementary particles of the standard model, then into galaxies, single-celled life, multi-celled life, mammals with immune systems, humans, human societies, computers, humans with their brains wired together (p. 370), etc. The book concludes with an imagined "world in which humanity as a whole and the rest of nature operate as a complex adaptive system to a much greater degree than we do now."

Of course, it is well-known that Dr. Gell-Mann is an anticreationist. In several places in the book he charges creationists with misinterpreting the second law of thermodynamics and expresses his belief that matter has an innate ability to organize itself. He sometimes refers to *frozen accidents* as a way to explain various circumstances. One example is the question of why certain biological molecules are invariably left-handed in living systems. A frozen accident arises from the combination of simple fundamental laws and the operation of chance. He uses the example of the succession of Henry VIII to the English throne by the circumstance of the death of his brother. In other words, the development of complex systems sometimes reaches a crucial point in history where a chance occurrence affects all future events in a decisive fashion. In this way, Gell-Mann attempts to explain away creationist arguments such as Paley's watch. He wishes to assign to matter an ability to organize itself. In other words, the book defines several new terms, discusses various complex adaptive systems using these terms, and concludes that Paley's watch could assemble itself: If it were not for our need to understand the directions in which the evolutionary establishment is headed, I would call this book a waste of time. However, one should realize that Gell-Mann is no longer a professor at California Institute of Technology, but now works at a place called the Santa Fe Institute, which he helped to start. This institute involves biologists, economists, physicists, etc. in thinking about complex adaptive systems, the future of mankind, and other high level thoughts. One would hope that such an institution would finally recognize that a Designer was involved in origins of and destiny of our planet. Based on this book, it does not seem that such an outlook on life has yet emerged at the Santa Fe Institute.

Catastrophic Plate Tectonics: A Global Flood Model of Earth History by Steven A. Austin, John R. Baumgardner, D Russell Humphreys, Andrew A. Snelling, Larry Vardiman, and Kurt P. Wise. 1996. Geology Education Materials, P.O. Box 712679, Santee, CA 92072. Slide collection, script, and supporting articles. $89.95 + $4 S&H.

Reviewed by Lane P. Lester*

This review should begin with a disclaimer: I am a biologist, not a geologist. It is that distinction that led me to obtain this excellent set of materials, because I found myself in need of additional content for my college general biology course. George Howe, Dennis Englin, and I are working on a biology textbook from the creation point of view, and I have decided to add a longer study of the history of life, pre-Flood and post-Flood. However, in order to study the history of life, one must begin with a study of the history of the earth. The materials reviewed here are very helpful.

The model presented by the authors is one in which the earth was created with a single giant continent which broke into separate land masses during the Flood. Although the model has a few resemblances to the evolutionist model of continental drift, it is framed in terms of the catastrophic effects of the Flood rather than the presumed long ages of evolution. The power of the model lies in the way that it accounts for so many of the earth's features, a number of them more satisfactorily than the evolutionist model.

The package includes 80 35mm slides, nicely filling a single standard slide tray. A script is provided in which each slide is described. You should not assume, however, that you could present this program by merely reading the script, unless you're speaking to a group of geologists. Steve Austin, the author of the script, has included a lot of technical information to make it possible to deal with questions that might arise. Anyone using this package will need to prepare a presentation with a particular audience in mind. Another point to be considered is that, although the authors of this package are six highly-qualified Ph.D.'s, not all creation scientists agree that this is the best model of earth history. Therein lies one of the attractions of slides over other media: It is easy to present the material in a variety of ways.

A quick viewing of the slides along with the script turned up a few nuisances. The slides come in "slide photo pages" as part of the looseleaf binder of materials, and they are not keyed for proper insertion into a slide tray. The script contains inconsistent usage of the metric and English systems of measurement; it would have been helpful to have included both throughout. Typographic errors in the script are rare, but most would have been caught by the use of a computer

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spell checker. Some of the text slides could have used more text, e.g., one which had only "Post-Flood Geology" on it should have also included from the script, "(1) tectonics, (2) volcanism, (3) sedimentation, (4) erosion, and (5) global cooling."

A very valuable part of this package's design is the inclusion of two articles describing the model proposed by the authors. The first, with the same title as the package, is a technical presentation published in *Proceedings of the Third International Conference on Creationism* (1994). I am grateful for the second article, "Plate Tectonics: Have the Continents Really Moved Apart," from *Creation Ex Nihilo Technical Journal* (1995), which is somewhat less technical and quite readable. I am sure that, with the help of these articles, when I teach this topic it will seem as though I really know what I am talking about.

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The Mythmaker's Magic: Behind the Illusion of "Creation Science" by Delos B. McKown. I993. Prometheus Books. Buffalo, NY. 180 pp. $12.00.

Reviewed by George Sanctuary*

McKown, head of the Philosophy Department at Auburn University, has written this book in a continuing ten-year effort to thwart, or even destroy, the influence of "scientific creationism" in public education. In his introduction he divides the "world's people" into two classes: 1) ". . . those who tend to base their beliefs on facts . . . ," and 2) ". . . those who acquire their beliefs dogmatically . . . who alter or dismiss facts to fit their preexisting faith." He says his book is for the first group, about those who belong to the second group

To accomplish his purpose, McKown occasionally uses biblical arguments, which are derived without a belief in the inerrancy of the scriptures. He is convinced that "Scientific Creationists" are dressing up their biblical doctrine in the "trappings of science" (p. 41). He refers to their creedal statements to support this conviction. McKown says that biblical theories of origins are fanciful tales when compared to Big Bang theorizing. He states, "None can be expressed mathematically as Einstein, for example, expressed the relationship of energy to mass in his famous equation, $e = mc^2$. In modern scientific cosmology, any successful TOE (Theory Of Everything) will, on the contrary, be mathematically expressible" (p. 51).

I can understand where McKown is coming from, even though I accept a literal understanding of the Bible. He believes in a naturalistic origin of everything, without the need for biblical revelation. Unfortunately, he does not seem to recognize that this is a form of faith in itself.

Bible believers can learn two things from this book. First, we need to make it clear to all people that our faith is in the God of the Bible, and in His word. This is nothing to be ashamed of, or to be hidden. Secondly, creationists need to develop a simple, mathematically expressible theory for the creation of the universe — that not only fits in with the biblical account of creation, but also satisfies the observable evidence. It is true that this will involve making certain assumptions. But we know that many cosmological assumptions have been made with the Big Bang theory to explain celestial observations. These assumptions are like a creedal statement for a naturalistic origin of the universe.

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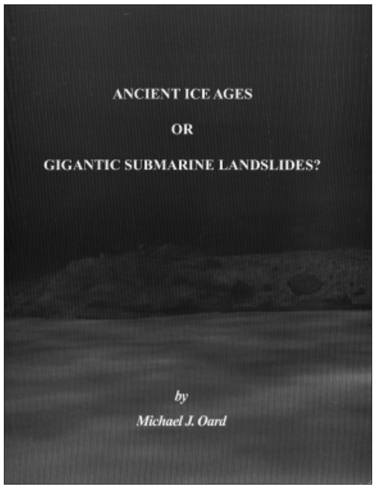

NEW BOOK

Mainstream scientists present many geological challenges to creationists. One of the main geological challenges is pre-Pleistocene ice age, which group into four main periods of geological time: 1) mid Precambrian, 2) late Precambrian, 3) late Ordovician, and 4) late Paleozoic. Their evidence consists of hardened till-like rocks associated with other "diagnostic" features sandwiched between sedimentary rocks. How can an ice age occur in Flood sediments, or as some creationists believe in pre-Flood sediments for the Precambrian cases? Davis Young in *Christianity and the Age of the Earth*, pages 90-91, considers pre-Pleistocene ice ages one of the main geological arguments against the Flood. In this compact book, the hypothesis of pre-Pleistocene ice ages is analyzed and challenged, and an alternative is presented: gigantic submarine landslides during the Genesis Flood.