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Web Based
Exploratory
Course 101B

IDENTIFYING
EVOLUTION'S DISRUPTIVE ENABLER OF LIFE

(i.e., Identifying the Gurdjieff Enneagram in the Genetic Coded and Noncoded DNA)

COURSE 101B's
or
CHAPTER XII's

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Chapter XII

IDENTIFYING THE DISRUPTIVE ENABLER OF LIFE
or
(Identifying the Gurdjieff Enneagram in the genetic coded and noncoded DNA)

A. INTRODUCTION

As we saw in Figure 84, the numerically derived labels defining the radiant mathematical plan for the mathematically disruptive enabler can be equated to the naturally occurring constants that numerically define the roles of the elementary building blocks of matter/energy. In turn, these defined roles for the elementary building blocks of matter/energy may serve as the disruptive enabler of matter/energy in evolving towards symmetric order, as we know it from the earth's perspective.

Since those six elementary building blocks of matter/energy serve as the building blocks of all the atoms that make up and sustain all molecular matter/energy, expressions of the building blocks' radiant plan for inspiring symmetric order may be identifiable within the universe of molecular matter/energy. If we look for expressions of the disruptive enabler driving towards symmetric order in the ultimate evolutionary culmination of molecular matter/energy, we should then focus on the most evolved class of molecules, namely, the "self-reproducing" macro molecules referred to as the deoxyribonucleic acid or DNA class of molecules, as laid out in this chapter.

DNA molecules have always served as the chemical blueprint for constructing protein molecules (as well as molecular precursors to hormones, vitamins, coenzymes, porphyrins, pigments and neurotransmitters) all of which in turn are used to build and sustain all living organisms.[43] Thus, the DNA class of molecules effectively extends evolution from the phenomenon of molecular matter to the phenomenon of all living organisms.

Fortunately, the chemical blueprint through which DNA translates into the protein components of living organisms always draws its building blocks from the same twenty standard amino acid molecules. Moreover, an organizational matrix of these twenty standard amino acids, called the **"genetic code"**, has always guided the translation between the DNA molecular blueprint and the twenty amino acids. (In other words, the genetic code is like the Rosetta Stone for interpreting DNA). As a result, just as the six elementary building blocks of matter/energy serve as the building blocks of all atoms that make up and sustain all molecules, the twenty standard amino acid molecules serve as the building blocks of all the large protein molecules that make up and sustain all living organisms.

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[43] Any subsequent use of the term proteins in this text is intended to also include precursors to hormones, vitamins, coenzymes, porphyrins, pigments and neurotransmitters.

If the above analogy between the six elementary building blocks of matter/energy as the building blocks of molecular matter/energy and the standard amino acids as the building blocks of living organisms is valid, then the roles numerically defined for the six elementary building blocks of matter/energy in Section XI-B should be manifested or reflected in the roles of the standard amino acids. In other words, to support this analogy, the organizational matrix (i.e. genetic code) guiding the roles of the standard amino acids in constructing living organisms should reflect the guidelines for numerically defining the roles of the six elementary building blocks of matter/energy which were expressed as evolution's disruptive enabler of matter/energy driving towards symmetric order, as presented in Section XI-B. Moreover, since the genetic code guiding the building blocks for living organisms directly evolved from the radiant plan guiding the building blocks of molecular matter/energy, the former can be represented as a direct manifestation of approaching the seventh or final stage of the radiant plan for symmetric order, as presented in Figure 76, just as the latter was represented in Figure 84.

As the first step in demonstrating this analogy, the genetic code in its conventional matrix format is presented in Figure 85 below. This matrix sets out all the possible permutations of the four different groups of atoms called nucleotides (i.e., U, C, A and G), which are sequenced in a long chain format to form the DNA macro-molecules. This sequencing of the DNA's four nucleotides determines which amino acids are to be incorporated into constructing proteins. According to the genetic code, each sequence of three successive nucleotides (called a codon) on the long chain of nucleotides, constituting the coding portion of the DNA molecule, translates to one of the twenty standard amino acids used in constructing proteins.

Said another way, proteins are large molecules made up of various permutations of the twenty standard amino acid molecules. Each section of the DNA molecule (containing multiple codons) which codes a particular protein molecule is referred to as a gene. As such, each DNA molecule represents an extremely large number of genes, each of which codes a different protein molecule. Collectively, these proteins make up and sustain each living organism. In other words, every living entity or organism generally has its own unique DNA macro-molecule which contains the chemical blueprint for constructing every protein making up that living entity.

However, it should be noted that most of an organism's DNA does not constitute genes that directly translate through the genetic code into proteins and is thus referred to as the noncoding or non-gene parts of the DNA. According to the Encyclopedia of DNA Elements (ENCODE), a large public research consortium, the noncoding or non-gene parts of the human DNA primarily regulate gene activity including the many facets of gene expression, transcription and mutation prevention, so that the coding or gene part of the DNA can be properly implemented. The noncoding portion of the DNA will be addressed at the end of Section XII-G below.

FIRST POSITION NUCLEOTIDE

SECOND POSITION NUCLEOTIDE	U	C	A	G	U	C	A	G	U	C	A	G	U	C	A	G
	U	PHE	PHE	LEU	LEU	LEU	LEU	LEU	LEU	ILE	ILE	ILE	MET	VAL	VAL	VAL	VAL
	C	SER	SER	SER	SER	PRO	PRO	PRO	PRO	THR	THR	THR	THR	ALA	ALA	ALA	ALA
	A	TYR	TYR	STP	STP	HIS	HIS	GLN	GLN	ASN	ASN	LSY	LSY	ASP	ASP	GLU	GLU
	G	CYS	CYS	STP	TRP	ARG	ARG	ARG	ARG	SER	SER	ARG	ARG	GLY	GLY	GLY	GLY

THIRD POSITION NUCLEOTIDE

The following abbreviations for the basic amino acids are used in the above genetic code.

FIRST ROW OF CODONS WITH THE NUCLEOTIDE (U) IN THE SECOND POSITION
- Phenylalanine (PHE)
- Leucine (LEU)
- Isoleucine (ILE)
- Methionine (MET)
- Valine (VAL)

SECOND ROW OF CODONS WITH THE NUCLEOTIDE (C) IN THE SECOND POSITION
- Serine (SER)
- Proline (PRO)
- Threonine (THR)
- Alanine (ALA)

THIRD ROW OF CODONS WITH THE NUCLEOTIDE (A) IN THE SECOND POSITION
- Tyrosine (TYR)
- Stop (STP)
- Histidine (HIS)
- Glutamine (GLN)
- Asparagine (ASN)
- Lysine (LYS)
- Aspartic Acid (ASP)
- Glutamic Acid (GLU)

FOURTH ROW OF CODONS WITH THE NUCLEOTIDE (G) IN THE SECOND POSITION
- Cysteine (CYS)
- Stop (STP)
- Tryptophan (TRP)
- Arginine (ARG)
- Serine (SER)
- Glycine (GLY)

Figure 85. The genetic code

As shown in Figure 85 above, the four different types of nucleotides (i.e., U, C, A and G) can combine in every possible sequence of three; therefore, 4^3 or 64 different possible sequences of three nucleotides or codons should theoretically exist.

The methionine (MET) codon is the common initiator or start signal for all proteins. Importantly, methionine, as the starter codon, is the only codon in the genetic code that is not specifically or uniquely programmed for each protein in each living entity. In other words, methionine provides the start signal for initiating the construction of every protein regardless of the organism's DNA.

Importantly, since the 64 codons making up the genetic code represent or draw upon only 20 standard amino acids, most of the amino acids are repeated multiple times within the genetic code.

Structurally, the standard amino acids constituting the genetic code can be classified according to the molecular appendage or side chain, represented by R, attached to the unchanging amino acid molecular group, as shown in Figure 86 below.

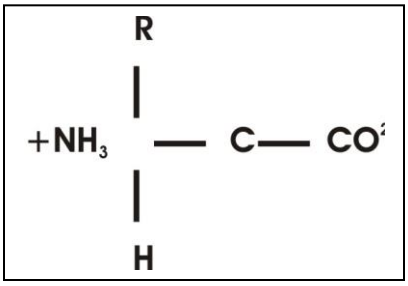

Figure 86. Generic molecular structure of the standard amino acids constituting the genetic code

While each of the amino acid classifications can be associated with many roles, this analysis attempts to identify the most elementary functions for each classification that seems to be common to all living organisms.

The following six sections (i.e., XII-B through G) will, respectively, identify how the six numerical types of the mathematically disruptive enabler (i.e. 1, 4, 2, 8, 5 and 7) can characterize six different groups of codons drawn from the 64 codons making up the genetic code matrix of Figure 85. This identification process will also demonstrate that, after grouping the codons according to the six types, the contiguous and sequential arrangement of these six groups within the genetic code are analogues to the numerical types of the mathematically disruptive enabler as it converges onto the trinitarian triangle in approaching symmetric order. Section H will identify the roles characterized by the three types of the trinitarian triangle (i.e., 3, 6 and 9) within the genetic code and show how the above disruptive enabler converges onto the trinitarian triangle.

BECAUSE VIRTUALLY THE ENTIRE GENETIC CODE IS REPRESENTED BY THE EARLIER DISCUSSED SAME-DIGIT SYMMETRY, THE GENETIC CODE INGENIOUSLY CONFIRMS CONCEPTUALLY THE SPECIFIC ROLES OF, NOT ONLY THE SIX TYPES CONSTITUTING THE DISRUPTIVE ENABLER OF LIFE, BUT ALSO THE THREE TYPES CONSTITUTING THE TRINITARIAN TRIANGLE, AS THE FORMER CONVERGES ONTO THE LATTER. IN DOING SO, THE CONCEPTUAL PREMISE UNDERLYING THIS ENTIRE TRILOGY OF COURSES SEEM TO BE FURTHER CONFIRMED. Also, this process draws upon the special augmentation involving types 9 and 4 in converging towards symmetric order.

Noteworthy, when the six groups representing this disruptive enabler of life interact or converge with the three coordinates representing the trinitarian triangle, the role of the type 6, characterizing open-minded guidance, is disproportionately accentuated over the roles of the trinitarian triangle types 3 and 9.

While the genetic code as the disruptive enabler of life has evolved from the building blocks of matter/energy as the disruptive enabler of matter/energy, keep in mind that all living organisms constructed according to the genetic code must also exist within the constraints of the physical environment constructed according to the underlying disruptive enabler of matter/energy. In other words, the disruptive enabler of matter/energy can be viewed as underlying both the evolutionary micro sourcing of the disruptive enabler of life as well as the evolutionary macro sourcing of the physical environment in which the disruptive enabler of life must exist (see Sections XII-E, F and G).

B. Identifying 1's type within the genetic code

As presented in Section III-E, the numerical type **1** type can be summarized as follows:

- When not redundantly emphasized, **1's** type characterizes the mathematical criterion of equal status without regard for numerical specificity, which represents the basic mathematical criterion governing the low side of randomness.
- When redundantly emphasized, **1's** type characterizes the mathematical criteria of equal status that affirms the perfecting details underlying numerical specificity, which in turn represents the basic mathematical criteria for establishing the high side of symmetric order.
- However, the mathematical criteria of equal status that affirms the perfecting details underlying numerical specificity by definition subsumes the mathematical criterion of equal status, which does not affirm or is indifferent to numerical specificity.

Given this characterization, **1's** type can be identified in the genetic code through the following three considerations.

First, the non-redundantly emphasized version of **1's** type can be identified within the genetic code through the methionine codon (MET) as the criterion for initiating construction of any new protein. As explained in the previous section, this initiating role has nothing to do with the specificity of the living organism's DNA. Of the 64 codons making up the genetic code, the role of the methionine codon as the starter signal or criterion for constructing a protein represents the only codon role that always occur at the same point for every protein in every living organism. Also, because only **1** methionine codon exists in the genetic code (as shown in Figure 87 below), it can be numerically characterized as having a single-digit equivalent value of **1**. In sum, since the **1** methionine codon serves as the initiating criteria for all the proteins of any organism regardless of the specificity of the organism's DNA, the **1** methionine codon represents **1's** non-redundantly emphasized type within the genetic code.

Secondly, the redundantly emphasized version of **1's** type can be identified within the genetic code through the **10** codons representing amino acids where the molecular appendage or side chain R of Figure 86 above is NH_2.[44] All living organisms must incorporate a basic nitrogen metabolism which depends on this group of **10** codons. Moreover, each organism's incorporation of these 10 codons is specifically determined by the organism's DNA.

The amino acids with the NH_2 molecular side chains consist of glutamine (GLN), asparagine (ASN) and arginine (ARG) and are sometimes referred to as amino acid amides. Since there are only three different amino acid amides, they must be repeated to represent **10** codons in the genetic code, as shown in Figure 87 below. The NH_2 molecular side chains enable this group of amino acid amides to serve as the primary organic carriers of the nitrogen involved in an organism's basic nitrogen metabolism. As a result, NH_2 amino acids or amino acid amides serve as the primary nitrogen source in the various biosynthetic pathways or as the primary nitrogen remover from the various biodegradative pathways. In other words, the amino acid amides sustain organisms by facilitating the "appropriate" availability of nitrogen; and as such, the amino acid amides can be viewed as serving as the basic criteria for sustaining the nitrogen-based chemistry of all organisms. Also noteworthy, these criteria for

[44] Appropriately, **10** equates to a single-digit value of **1** (i.e., 10=>1+0=**1**)

"sustaining an organism by facilitating the appropriate availability of nitrogen" is determined as needed for each part of each organism according to the specificity of the organism's DNA. In sum, since the **10** amino acid amides serve as the sustaining criteria for all organisms depending on the specificity of the organism DNA, the **10** amino acid amides codons represent **1's** redundantly emphasized type within the genetic code.

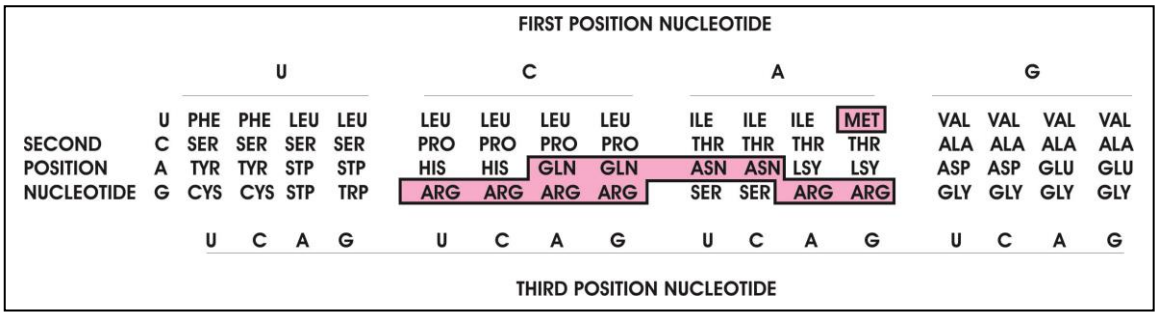

Figure 87. The 1 methionine codon and the 10 amino acid amide codons within the 64 codons of the genetic code

Thirdly, **1's** redundantly emphasized type can be identified within the genetic code is through the 64 codons making up the entire genetic code (also shown in Figure 87), since the most basic criteria for every codon requires that it be drawn from this base of 64 codons specific to each organism's DNA blueprint. Importantly, the 64 codons include the **1** methionine codon and the **10** amino acid amide codons, and that each of these (i.e., the 64, **1** and **10**) represent single-digit equivalent values of **1** (i.e., 64 => 6 + 4 = 10 => 1 + 0 = **1**). This is consistent with the above introductory summary which indicates that the specificity criteria characterized by **1's** redundantly emphasized type (i.e., being included in the 64 codons) subsume the criterion which does not affirm or is indifferent to numerical specificity" (i.e., being started by the methionine codon).

Noteworthy, the genetic code redundantly emphasizes **1's** type in three different ways. This will also be the case with 4's and 7's types (see Sections C and G below) since these three types, when redundantly emphasized, drive towards symmetric order.

C. Identifying 4's type within the genetic code

As discussed in Section V-A, the numerical type **4** characterizes initiating the interactive relationships through multiplying **4** by itself three times or cubing **4** (see Figure 21). In turn this leads to the configuration of interactive relationships between 1's, **4's**, 2's, 8's, 5's and 7's types, referred to as the mathematically disruptive enabler. The mathematically disruptive enabler then graphically approaches convergence onto the trinitarian triangle which interactively relates the 3, 6 and 9 types. Thus, **4's** type characterizes yielding the initiation of the mathematically disruptive enabler as well as its convergence onto the trinitarian triangle. We also saw that the integrative benefit of forming and converging the mathematically disruptive enabler is not exclusive but is equally or collectively available to all the numerical types making up the mathematically disruptive enabler. Also, because of the role of **4's** redundantly emphasized type in initiating symmetric order, it is subjected to the sacrificial death that must accompany the initiation of symmetric order, as discussed in Section III-D.

Given this characterization, **4's** type can be identified within the genetic code through the following three considerations.

First, **4** characterizes the number of different nucleotides (i.e., U, C, A and G) which are interactively sequenced in groups of three to determine each of the 64 codons which make up the genetic code, as described in Section XII-A above. Because the **4** different types of nucleotides can combine in every possible sequence of three, $\mathbf{4^3}$ or 64 different possible sequences of three nucleotides or codons exist.

Also, because the 64 codons are shown in this chapter (see Sections XII-B through G) to represent the six types making up the mathematically disruptive enabler, the process of cubing **4** initiates the interactive relationships that ultimately lead to the genetic code in a similar way that cubing of **4** or **4's** type ultimately initiates the mathematically disruptive enabler, as explained in the introductory paragraph to this section. **In other words, as indicated earlier, the genetic code will be shown to represent evolution's disruptive enabler of life in this chapter.**

Secondly, because the 64 codons in representing the disruptive enabler of life will also be shown in Section XII-H to converge onto the trinitarian triangle, **4** or **4's** type also characterizes this convergence just as it did in the numerical model of Section V-A.

Thirdly, **4** characterizes a group of **4** codons within the genetic code where this group's characterizing molecular appendage or side chain R (see Figure 86) is an extra acid (i.e., CO_2^-). Because they contain an extra acid, the two amino acids represented by these **4** codons (i.e., glutamic acid or GLU and aspartic acid or ASP) are referred to as the acidic amino acids and are delineated within the genetic code matrix, as shown in Figure 88 below. As we saw in the previous section, all organisms assimilate or discard the nitrogen through the NH_2 molecular appendage associated with the amino acid amides. However, this process involves a reversible reaction involving ammonia (NH_3) and the acidic amino acids (glutamic acid and aspartic acid) which are represented by these **4** codons. Since all organisms must extract and return nitrogen from and to ammonia, the capacity of the acidic amino acids to interact with ammonia is the key backup or support function for all organisms. Without this capability, the amino acid biochemistry underlying the genetic code would not be initiated or completed, analogous to the way **4's** type characterizes the initiation and convergence (i.e., completion) of the disruptive enabler discussed above. Moreover, since the acidic amino acids interactively support the amino acid amides, which sustain all parts of all organisms as programmed by each organism's DNA, this group of acidic amino acids also interactively support all parts of all organisms as programmed by each organism's DNA again analogous to the characterization of **4's** type.

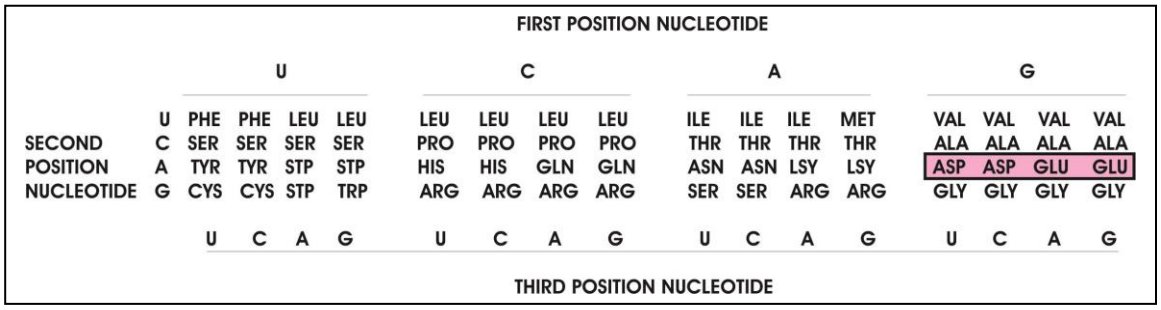

Figure 88. The 4 acidic amino acid codons within the genetic code

The close chemical and functional interaction between the amino acid amines (characterized by 1's type) and the acidic amino acids (characterized by **4's** type) is further re-enforced in the genetic code since these two groups of codons appear next to one another, as shown in Figure 89 below.

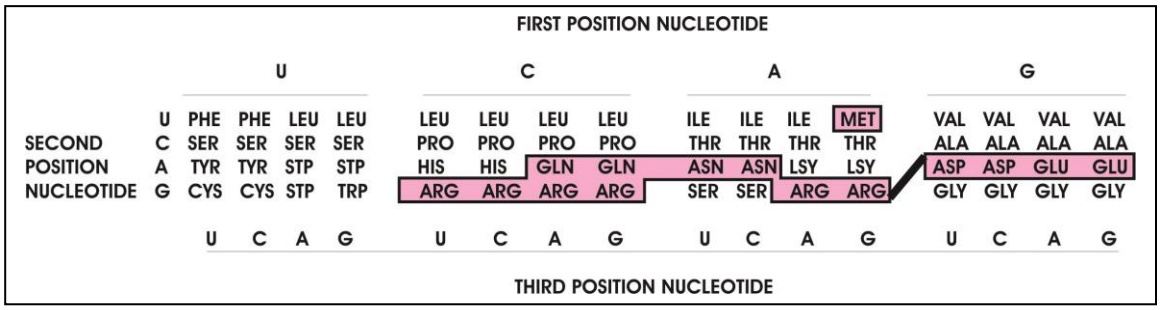

Figure 89. The amino acid amide group (characterized by 1) relates to the acidic amino acid group (characterized by 4)

Lastly, because of the degree to which the acidic amino acids become chemically modified in support all organisms, they may best fulfill the sacrificial death role that accompanies the initiation of symmetric order, as mentioned in the introductory paragraph to this section.

D. Identifying 2's type within the genetic code

As discussed in Sections IV-B, the numerical type **2**, when non-redundantly emphasized, characterizes the interactive connectivity between types which results in mathematically identifying the specificity of the involved types.

Given this characterization, **2's** type can be identified within the genetic code through the following two considerations.

First, **2's** non-redundantly emphasized type characterizes the interactive connectivity of the genetic code through the 20 **standard amino acids** in Figure 85 (i.e., 20 => 2 + 0 = **2**) which are interconnected to produce the proteins for all organisms. As explained in the previous section, 3's and 4's types characterize the implementation of the genetic code since never more than 3 of the 4 available nucleotides can be used to determine each codon which in turn identifies each of the 20 amino acids making up the genetic code. As such, the 20 amino

acids provide a focus on (or identifies) the exclusive role of 3 (or the 3 triangle), as discussed subsequently in Section XII-H. Additionally, since the collection of all the codons will be shown in Section XII-H to represent the six types making up the disruptive enabler, **2's** type, as represented by the 20 standard amino acids, can be viewed as identifying the role of 4's type in characterizing the interactive initiation and convergence of the disruptive enabler.[45]

Secondly, **2** also characterizes a group of 20 **codons** within the genetic code where the associated amino acids tend to have a significantly above average representation (relative to their representation within the genetic code) in proteins that primarily serve to interactively connect or attach various components in making up and identifying the various parts and the "totality" of the organism .[46] Because they interactively connect, the five amino acids associated with these 20 codons are referred to as the interconnecting amino acids and consist of glycine (GLY), serine (SER), threonine (THR), proline (PRO) and lysine (LSY). The first four are among the physically smallest amino acid molecules which should facilitate them coming together to produce the filamentous forms which often characterize the associated interconnecting proteins.[47] The last one (i.e., lysine) is the amino acid with the longest continuous linear side chain of carbon atoms which complements the other molecules in forming interconnecting matrices by providing cross-links.

Some of the better-known examples of proteins with an above average relative representation of these interconnecting amino acids include:

- Collagen used to form a tough matrix for bones and tendons;
- Elastin used to form an elastic matrix for arterial blood vessels and ligaments;
- Fibrinogen and fibronectin used for interconnecting cells;
- Trypsin used to bind to most ingested proteins before cleaving them; and
- Fibron (silk) spun by silkworms to form a cocooning matrix.

Figure 90 delineates below the 20 codons of interconnecting amino acids within the context of the genetic code matrix.

[45] This tends to confirm that **2's** type should functionally follow 4's type within the context of the genetic code consistent with the disruptive enabler, as shown later in Figure 92.

[46] Consistent with the role of interconnecting "different" components, the interconnecting amino acids include amino acids with "different" molecular side chains as opposed to previously discussed groups of amino acids where the molecular side chains were the same for each group. Again, the use of 20 equates to a same-digit equivalent of **2**.

[47] The alanine molecule is small enough to fit into this category and does appear frequently in interconnecting proteins where they share a significant complementary role with the aliphatic amino acids discussed next.

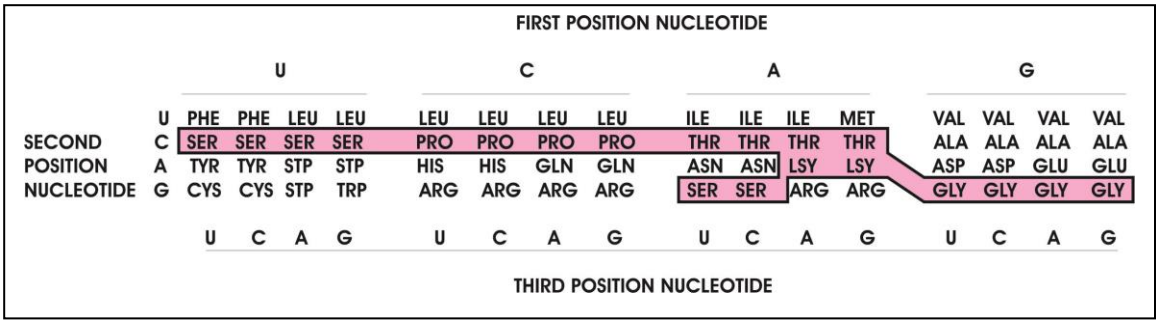

Figure 90. The 20 interconnecting amino acid codons within the genetic code

As will be seen after all of the identifications of the numerical characterizations have been discussed (see Section XII-G), the box enclosing the 20 inter-connecting codons is contiguous or interconnects with the other boxes of codons representing the disruptive enabler (i.e., 1, 4, 8, 5 and 7) in the genetic code matrix. In sum, the interconnective relationships of this group of amino acids enables the components of the living organism to come together and thereby make the total specificity of the living organism and its parts identifiable (i.e., like the gravitational force in the previous chapter). Further, testifying to their contribution to the living organism's total specificity or identity, this group of interconnecting amino acids represents the largest relative representation both within the genetic code matrix and probably within the living organisms.

E. Identifying 8's type within the genetic code

As discussed in Section IX-A and B, the numerical type **8** characterizes the mathematical ability to bring about or produce the greatest change. Eight's type can be analogized to mathematical power or strength as well as the leadership to bring about the greatest change. When non-redundantly emphasized, **8's** type can be analogized to constructive power, strength, or leadership driving towards symmetric order. When redundantly emphasized, **8's** type can be analogized to destructive power, strength, or leadership driving towards randomness.

When non-redundantly emphasized, **8's** type characterizes the mathematical production required to fulfill the mathematical criteria for driving towards the high side of symmetric order as characterized by 1's redundantly emphasized type.

Given this characterization, **8's** type can be identified within the genetic code through the group of 17 codons representing only aliphatic amino acids. In this group the molecular appendage or side chain R in Figure 86 consists only of carbon and hydrogen atoms connected together through the simple or "aliphatic" bond. The aliphatic amino acids represented by the 17 codons consist of alanine (ALA), valine (VAL), leucine (LEU), and isoleucine (ILE). Appropriately, the single-digit equivalent value of 17 is **8** (i.e., 17 => 1+7=**8**).

The most elementary applications, for which these aliphatic amino acids appear to be well suited, involve proteins used in converting chemical energy into mechanical or physical energy. Specific examples would include muscle systems which always involve the proteins actin or myosin. Accordingly, the various types of actins appear to have a significantly above average representation of this group of aliphatic amino acids relative to representation of this aliphatic group within the genetic code.

At the cellular level, processes involving the conversion of chemical energy into mechanical or physical energy include the movement, division and change in shape of cells. In addition to actin and myosin, other proteins commonly used in these mechanical or physical work processes include flagellin and tubulin. However, in single cell organisms, flagellin is the primary protein involved in these processes, and of these two proteins, flagellin appears to have a significantly above average representation of aliphatic amino acids relative to the representation of this aliphatic group within the genetic code.[48]

In sum, the aliphatic amino acids can be associated with providing mechanical energy or physical strength to organisms. Moreover, the primary intent of this mechanical energy or physical strength is to sustain an organism in terms of reproducing, getting food and avoiding harm which involves competing with, and overcoming, other cells and/or organisms following the same pursuit. In other words, the aliphatic amino acids can be viewed as essentially producing and sustaining the organism's overall or total physical well being through the application of mechanical energy or strength (i.e., power). Moreover, this physical well being must be determined within the macro physical environment which has evolved according to the underlying disruptive enabler of matter/energy (see last paragraph in Introduction).

When we contrast the introductory paragraph of this section with the immediately preceding paragraph, we see that the latter could well qualify for either the non-redundantly or redundantly emphasized versions of **8's** type, depending on how it is directed. Appropriately, how **8's** type is directed within the genetic code is the subject of the next two sections addressing 5's and 7's types, respectively.

Within the context of the genetic code, as shown in Figure 91 below, the 17 aliphatic amino acid codons are contiguous except for the non-aliphatic amino acid methionine or the "start" codon. The methionine represents the only codon that is not specifically programmed for each protein in each organism (see Section XII-A and B). Because of this non-specificity, the 1 methionone codon represents 1's non-redundantly emphasized type which is subsumed by 1's redundantly emphasized type as the initiator towards symmetric order (see Sections III-B and C and VIII-B). Since 1's and **8's** types are interchangeable at the initiation of symmetric order, the 1 methionine codon is embedded among the 17 aliphatic amino acid codons representing **8's** type (see Section VIII-B).

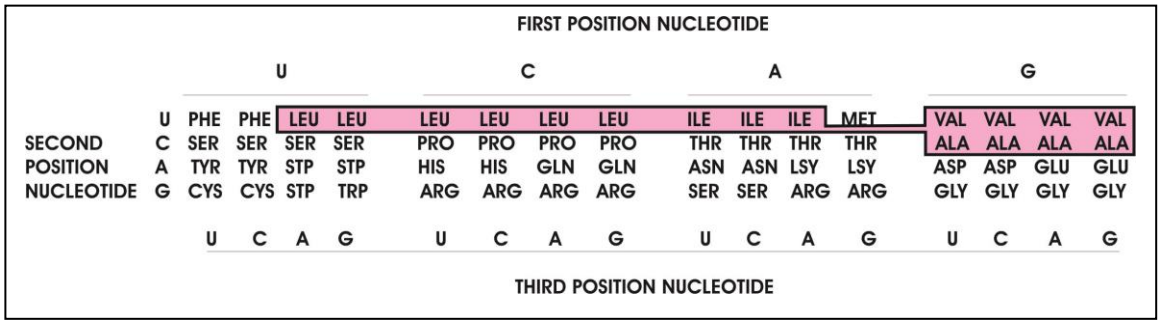

Figure 91. The 17 aliphatic amino acid codons within the genetic code

[48] Interestingly, similar to the above protein group involved with an organism's overall mechanical or physical strength, the immune response protein interleukin-2 precursor, but not the receptor, has an above average relative representation in the aliphatic amino acid group. This might imply a mechanical or physical role for the precursor in connecting with the receptor.

As we saw in the introductory comments to this section, "**8's** non-redundantly emphasized type characterizes the mathematical production required to fulfill the mathematical criteria for driving towards the high side of symmetric order as characterized by 1's redundantly emphasized type". According to Section XII-B, 1's redundantly emphasized type can be identified within the genetic code as providing the criteria for sustaining organisms at the most elementary level by facilitating the appropriate chemical availability of nitrogen. Thus, **8's** non-redundantly emphasized type can be identified in the genetic code as fulfilling the criteria for producing or sustaining organisms by providing for the conversion of chemical energy into mechanical or physical energy.

In regard to the functional relationship between 2's and **8's** types, we saw in the previous section that the 20 codons (which represented 2's type within the genetic code) interactively connect or attach various components in making up the physical totality of the organism. In this section we see that the 17 codons (which represent **8's** type within the genetic code) produce or sustain the various physical components that are connected to form the physical totality. Thus functionally, 2's and **8's** types should sequentially relate to one another which extends the previously discussed sequential relationship of 1's, 4's and 2's types to **8's** type in building towards the disruptive enabler, as shown in Figure 92 below.

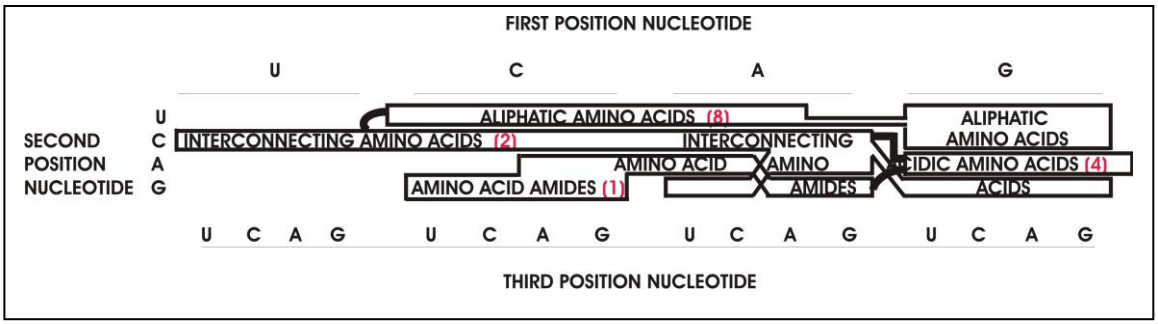

Figure 92. The amino acid amide group (characterized by 1) relates to the acidic amino acid group (characterized by 4) which relates to the interconnecting amino acid group (characterized by 2) which relates to the aliphatic amino acid group (characterized by 8)

Thus far we assumed 8's type within the genetic code is non-redundantly emphasized consistent with transitioning towards symmetric order. However, the genetic code of life may provide greater tolerance for deviations than the zero-tolerance allowed by the building blocks of matter/energy (see Section XI-D). In other words, could a species' representation of 8's type become so redundantly emphasized that the physical strength of such species would allow it to disproportionately dominate the other species constituting the eco-system? Also, since the redundant emphasis of 8's type drives towards randomness, the evolution of a species with a redundant emphasis of 8's type, if carried far enough, could eventually interrupt the eco-system's evolution towards symmetric order.

The only possible species that readily comes to mind with such a disproportionately redundant emphasis on physical strength that it could impact the eco-system evolution towards symmetric order was the reptilian dinosaur family. Indeed, their physical strength allowed them to be the dominant family of species for more than 150 million years. As such,

this reptilian dominance probably slowed the smaller mammalian evolution which ultimately produced the modern homo-sapien.

Interestingly, this dinosaurian domination was corrected through a cataclysmic change in the physical environment from being permissively supportive to becoming very hostile and thus depriving the dinosaurian family of sufficient nourishment to survive. In other words, the above referenced zero tolerance for deviations allowed by the building blocks of matter/energy in representing the disruptive enabler of matter/energy may have eventually modified the physical environment in transitioning towards symmetric order which had the secondary effect of causing the demise of the dinosaur family (see last paragraph in Introduction).

In sum, the genetic code's greater tolerance for deviation in representing the disruptive enabler of life is still limited by the need to comply with the specificity criteria for symmetric order, as characterized by 1's redundantly emphasized type. In the case of the dinosaur family, this specificity criteria for symmetric order was applied by the physical environment constructed according to the underlying disruptive enabler of matter/energy which disproportionately emphasizes the triangular type 9 that is always accompanied by 1's redundantly emphasized type (see Section XI-D).

F. Identifying 5's type within the genetic code

As described in Chapter II, the numerical type **5** characterizes the mathematical conceptualizing which underlies the transition or growth towards symmetric order away from randomness. The former is sensitive to the specificity of the types, the latter is not. Assuming entropy rules, driving towards the high side of symmetric order requires struggling to overcome the low side of randomness.

Given this characterization, **5's** type can be identified within the genetic code through the amino acids that address an organism's growth. Each organism has an optimum growth trajectory depending on its specificity. As such, the organism's growth trajectory provides the conceptual foundation for an orderly or disorderly potential outcome.

Within the amino acids making up the genetic code the aromatic amino acids play the underlying role in managing the organisms' growth by stimulating certain processes. As their label suggests, the common feature of the molecular appendage of this group of amino acids is the aromatic benzene ring which appears in phenylalanine (PHE), tyrosine (TYR) and tryptophan (TRP). As such, the 6-sided structure of the benzene ring could reference the complementary association of 5's and 6's types (see Figure 77 and the associated text). Some of the processes through which derivatives of these aromatic acids play an underlying role in managing the physical organism's growth include:

- light absorption used in the photosynthesis of most plants;
- the biosynthesis of nucleic acids and proteins to produce cells;
- the metabolism of carbohydrates and fats; and
- neurological growth through the production of neurotransmitters.

As shown in Figure 93 below, this group of three aromatic amino acids represents **5** codons within the context of the genetic code and is thus characterized by **5** as the single-digit equivalent value.

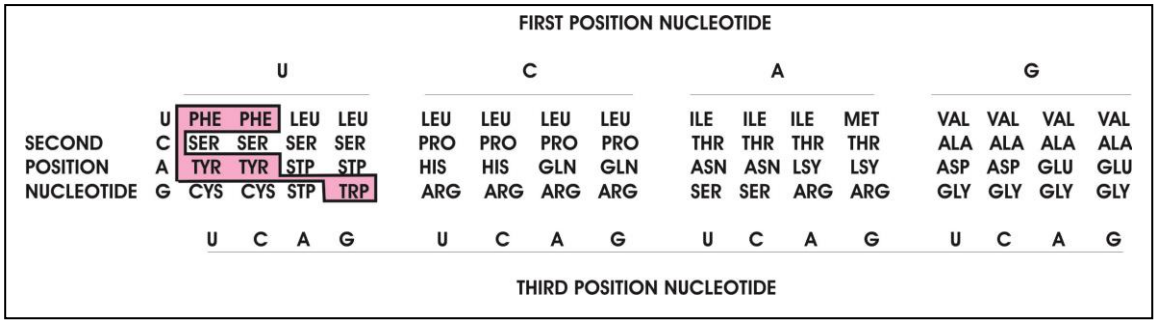

Figure 93. The 5 aromatic amino acid codons within the genetic code

Regarding the role of the aromatic amino acids in the genetic code of humans, the growth processes stimulated by the aromatic amino acid derivatives referred to above (i.e., cell production, fat and carbohydrate metabolism, and neurotransmitter production) can underlie three of the most prevalent chronic diseases or "dysfunctional conditions" in humanity when the growth drivers are not optimally managed. These chronic diseases include:

- **cancer in regard to the biosynthesis of nucleic acids and proteins to produce cells;**
- **coronary disease in regard to the metabolism of fats; and**
- **mental disease in regard to imbalances in neurotransmitters**

Noteworthy, the common denominator of the above-mentioned dysfunctional conditions is that all of them involve non-optimal growth (i.e., non-optimal cell growth, non-optimal growth in fats, and non-optimal growth in a neurotransmitter relative to other neurotransmitters). In these cases, the aromatic amino acid's underlying role in managing growth may be non-optimal relative to the overall potential well being of the human organism. Supportively, the relatively recent cancer drugs Erlotinib and Gefitinib inhibit the epidermal growth factor receptor's tyrosine kinase. Moreover, the use of vitamin D to help restore proper tyrosine activity may be further supportive of this line of reasoning.

Such a conclusion regarding the application of the above aromatic amino acid group would suggest that the genetic code within humanity experienced a very early stage evolutionary regression away from symmetric order. As a result, the application of the genetic code's aromatic acid group within humanity, as characterized by 5's type, became more redundantly emphasized, which would then drive away from symmetric order.

In looking for evidence of such evolutionary regression, we turned to the groun-breaking study published in the May 2010 edition of Science which compared the modern human's DNA with the Neanderthal's DNA. The modern human and Neanderthal separated between 270,000 and 400,000 years ago. Early after their separation the modern human's DNA modified selected sweeps of Neanderthal's DNA. Three of the most important of these gene sweeps addressed the same type of growth functions outlined above as can be seen from the following discussion.

- **The first region swept involved the THADA gene which is associated with metabolism, obesity, type II diabetes and certain cancers**.

- **The second region swept involved the DYRK1A, CADPS2 and AUTS2 genes. DYRK1A is most strongly associated with the above tyrosine (TYR) aromatic amino acid. CADPS2 is associated with the release of neurotransmitters and neuropeptides. When non-optimally expressed, the AUTS2 gene is associated with such psychiatric disorders as alcoholism, attention deficit hyperactivity and autism**.

- **The third region swept involved the RUNX2 gene which is believed to act as a "master switch" regulating a number of other genes associated with the development of cells that build bones (osteoblasts)**.

Since these three genetic regions are so involved in orchestrating the earliest growth stages of modern humans, their modifying sweeps occurred early after modern humans separated from Neanderthals. Likewise, should modern humans experience some form of genetic regression, these same regions should be among the first to be impacted.

According to the Science study, modern humans did indeed experience a genetic regression between 50,000 and 80,000 years ago when they interbred with the Neanderthals after having been separated for over 200,000 to 300,000 years. The regressive reconnecting or interbreeding caused 1% - 4% of the modern human's DNA to flow from the Neanderthal's DNA. While the overall impact was only 1% – 4%, to the extent it first emphasized the above three genetic regions the regressive or dysfunctional impact on the early growth stages influenced by these three genetic regions could be disproportionate.

Also, noteworthy, the above referenced regressive interbreeding first occurred as the modern humans migrated from Africa and entered the Middle Eastern region, but before migrating to the other parts of the earth. As a result, virtually all modern humans have experienced this regressive gene flow except for the direct ancestors of the originating Africans who never interbred with modern humans carrying the regressive representation of Neanderthal DNA. Also, to the extent interbreeding between Neanderthals and modern humans occurred at subsequent points in time would not alter the above outcomes but could influence their intensities. Note, the February 2016 issue of Nature reported that Neanderthals and modern humans interbred as early as 100,000 years ago; however, the progeny of this interbreeding became extinct and is not part of our present-day ancestry. Ongoing research in this area confirms and expands upon the above theses.

While the earlier discussed dinosaurian regression in type 8 was subsequently corrected through the evolutionary specificity of the physical environment which was constructed according to the underlying disruptive enabler of matter/energy, no such correction has yet occurred for humanity's above regression in type 5 (see Section XII-E). Accordingly, the process for remediating this regression is addressed in Course 101C.

In regard to the sequential placement of the **5** codons representing the aromatic amino acids, given their role in managing the growth of the physical organism, they should sequentially relate to the group of aliphatic amino acid codons since the latter group characterizes the production or sustenance of the organism's overall physical well being, as explained in the previous section. This sequential relationship is presented in Figure 95 following the discussion of 7's type.

Since the most elementary or simplest expression of the abstract mathematical concept of symmetric order, as characterized by 5's type, is same-digit symmetry (see Section II-B), it should be manifested in the above 5 aromatic amino acid codons in Figure 93. Accordingly, the pairs of phenylanine (PHE) and tyrosine (TYR) codons in Figure 93 can be viewed as a manifestation of same-digit (or same-codon) symmetry. Likewise, just as any of the nine digits constituting the circle of symmetric order can be repeated to express same-digit symmetry (see Section II-B), so too are all the codons constituting the genetic code repeated to express same-digit (or same-codon) symmetry, except for two codons, namely, tryptophan (TRP) and methionine (MET). In both cases they serve to introduce the other repeating amino acid codons. Specifically, the non-repeating tryptophan codon (TRP) can play an initiating role in the synthesis of the other two repeating aromatic amino acid codons [i.e., phenylanine (PHE) and tyrosine (TYR) for this group representing 5's type]. Likewise, the non-repeating methionine codon (MET) is the common initiator or start signal for all proteins. As such, it was included as the initiating member of the group of codons representing 1's type in characterizing the initiating criterion for symmetric order (see Section XII-B). Appropriately, same-digit symmetry represents both the conceptualization and criteria roles for introducing the symmetric order orientation as characterized by types 5 and 1, respectively (see Section III-D, Double-edged sword / tongue metaphor). Accordingly, tryptophan (TRP) and methionine (MET) as the initiating members of the groups of codons representing types 5 and 1, respectively, can be viewed as initiating the same-digit (or same-codon) symmetry which is represented by all the other repeating codons constituting the genetic code and discussed in depth in Section XII-I.

Importantly, while same-digit symmetry occurs when any digit on the symmetric circle is viewed as being paired with itself, this same-digit pairing process can draw from more than two repeating digits. Accordingly, the same-codon pairing process, represented in Section XII-I, draws from more than two repeating codons.

IN OTHER WORDS, SINCE THE GENETIC CODE SERVES AS THE CONCEPTUAL GATEWAY AND INTRODUCTORY CRITERIA FOR ALL CODED DNA, SIMILAR TO THE ROLES OF SAME-DIGIT SYMMETRY (see Sections II-B and III-D), THE GENETIC CODE CAN BE PRESENTED AS SAME-DIGIT OR SAME-CODON SYMMETRY IN REGARD TO INTRODUCING THE SYMMETRIC ORDER ORIENTATION.

G. Identifying 7's type within (and outside of) the genetic code.

As presented in Section X-C, when redundantly emphasized, the numerical type **7** characterizes defining the mathematically radiant framework or plan for establishing the mathematically disruptive enabler.

The **7** remaining codons, which are identified in Figure 94 below, can be viewed as characterizing **7's** redundantly emphasized type and are appropriately **7** in number. These **7** codons consist of the last two amino acids to be reviewed, namely cysteine (CYS) and histidine (HIS), as well as a special stop or STP codon, the roles of which are outlined below as two separate subgroups. The first consists of cysteine and histidine accounting for four of the 7 codons and the second consists of three STP codons.

Regarding the first subgroup, the most elementary functions of both cysteine and histidine seem to involve "defining and determining" an organism's framework of interfaces, whether approached from an inwardly or outwardly direction. Accordingly, these two amino acids can be grouped together within the organization of the genetic code and referred to as the "defining" amino acids. However, the molecular designs of these two amino acids are quite different from each other.

When viewed from an inwardly direction, the cysteine and histidine subgroup defines the organism's framework of interfaces such that its constituents or components optimally interact or converge to actually form the organism. On the other hand, when viewed from an outwardly direction, this subgroup defines the organism's framework of interfaces such that the organism optimally interacts or converges with external factors.

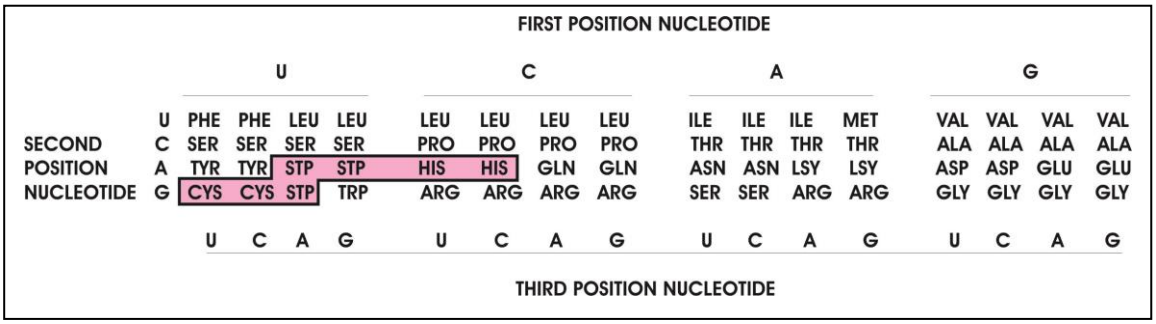

Figure 94. The 7 defining (amino acid) codons within the genetic code

Beginning with cysteine, it is differentiated by the bonding characteristic of the sulfur contained in its molecular appendage. As indicated above, cysteine plays a significant role in protein applications which help to broadly define or determine an organism's inwardly and outwardly focused framework of interfaces or exchanges. Through these bonding interfaces or exchanges an organism can radiate its overall framework or plan. Four examples of this role are outlined below with the very pervasive classes of proteins which have an above average relative representation of cysteine, namely, keratins, interleukins, integrins and insulin.[49]

[49] Above average relative to the representation of cysteine (or histidine) within the genetic code.

- **Keratins define the overall organism's exchanges in radiating with its external environment by serving as a key structural and defining component in the organism's interface with the external environment. The external interfaces include hair, fur, wool, feathers, reptilian skin or scales, nails, the membrane of eggshells, the reddish pigmentation in skin and roots, and even the retinal material in eyes. Paradoxically, external interfaces also include the linings of airways and digestive tracts since they are interfacing with external inputs (i.e., air and food). Moreover, this structural and defining interface role extends to the linings of other organs and surfaces where keratins are found. Generally, all of these linings or interfaces contain or are associated with epithelial cells or tissues.**

- **Interleukins are cytokins or signaling proteins that mediate communication between cells particularly in stimulating immune response. They also regulate cell growth, differentiation and motility.**

- Integrin molecules span the outer membrane of all the cells making up an organism and define or determine the cells' framework of extracellular associations as well as radiating the signal or informational exchanges with these extracellular associations.[50]

- The primary function of the multifunctional insulin could be viewed as defining and radiating the glucose exchange for organisms. The actual mechanism may most often involve an insulin molecule bonding at the membrane interface with a molecule rich in the growth oriented, aromatic amino acid tyrosine, discussed earlier. Interestingly, histidine (which is discussed below) also has an above average relative representation in insulin.

This interfacing of the cysteine rich molecule with a molecule rich in the growth oriented, aromatic amino acid tyrosine is also found in keratins and this functionally supports the contiguous placement of the groups of defining and aromatic acids in the genetic code, as shown in Figure 95. Also noteworthy, in all four cases the exchanges (i.e., in radiating via light, heat, intercellular information, glucose, etc.) involving the cysteine rich proteins apply to the entire organism; thus, cysteine's defining roles can be viewed as also applying to the entire organism.

Another way in which organisms define their radiant environmental boundaries is through the rejection of alien substances. While cysteine plays a role in many of the molecules involved in these biochemical defenses, another well known player in the early front line of defense is the histidine amino acid or its metabolic counterpart histamine.[51] The histidine within a cell can directly respond to an alien substance by releasing and radiating histamine to connect with or chelate the alien material and thus combat the attack.

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[50] Horwitz, A.F. ;" Integrins and Health"; Scientific American 1997.

[51] Regarding an example of cysteine's role in biochemical defenses, the disulfide bonds between cysteine residues provide the key bridges between the four chains making up all classes of immunoglobulin. Immunoglobulin or antibody molecules play a foundational role in the immune response against antigens. Noteworthy, the histidine activity associated with immunoglobulin can be induced by interleukins.

Or, under certain circumstances the histidine can serve as a neural inhibitor suppressing the response.[52]

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[52] **To the extent that proteins rich in growth or aromatic amino acids support growth rates non-optimal to the overall well-being of an organism (or species of organisms) as described in Section XII-F, the proteins rich in defining amino acids (particularly cysteine) would correspondingly not be able to fully define the framework of boundaries for optimizing the growth of the organism. In the human organism their failure might manifest itself as a breakdown of the immune response system. On the other hand, because of this latent possibility for non-optimal growth, the proteins rich in defining amino acids can also overreact to the threat of anticipated non-optimal growth which may not occur and thus result in a dysfunctional or even destructive reaction.**

One such example would be the celiac autoimmune disease where the finger-like villi of the small intestine flatten out and damage the epithelial lining of the intestine when a celiac eats gluten. As a consequence, the damaged villi can lose their ability to absorb nutrients into the bloodstream. Since the villi contain keratins which (as we saw above) serve as a "key structural and defining component in the organism's interface with the external environment", possibly a keratin deficiency or imbalance is contributing to this condition. Moreover, this deficiency or imbalance may be augmented by the villi's inability to absorb carotene foods which convert into Vitamin A which in turn controls the keratin gene expression.

To test this hypothesis, the author of this Trilogy, who is a celiac and highly intolerant of gluten (as well as cow's milk), experimentally consumed beta-carotene daily. Within a short period of time he became completely tolerant of gluten as well as cow's milk so long as he continued to take the beta-carotene. Noteworthy, he had been and continued taking Vitamin D which can influence interleukin activity in stimulating immune response, as discussed above. When his Vitamin D consumption was interrupted, the beta-carotene therapy became ineffective. Moreover, to be effective, the intakes of the beta-carotene and Vitamin D should be sufficiently spaced to allow for the beta-carotene to convert into Vitamin A so that both Vitamins A and D are present at the same time. Note, another celiac sufferer duplicated the author's experience.

Since, initially, discontinuance of either the beta-carotene or Vitamin D caused the celiac conditions to return within a short period of time, celiac patients may suffer from deficiencies of both Vitamins A and D. However, after about two years this was no longer the case in that the intestinal celiac conditions did not return after discontinuing either or both vitamins.

Also, the author had a deep digital myxoid cyst on a toe joint for several years that resisted all treatments to bring about healing, short of surgical intervention. Again, after about nine months of the above described beta-carotene / Vitamin D therapy healthy tissue has replaced the cyst.

Another example involved the epithelial rich eye tissue, after a year of this therapy the growth in the author's cataracts, seem to slow, if not stop.

IN SUM, THE BETA-CAROTENE AS VITAMIN A CONTROLS THE EXPRESSIONS OF KERATINS IN THE EPITHELIAL TISSUES WHICH INTERACT WITH MANIFESTATIONS OF INTERLEUKINS THAT ARE INFLUENCED BY VITAMIN D, SO THAT APPARENTLY THE DAMAGED EPITHLIAL TISSUES IN THE INTESTINE, TOE JOINT AND EYE WERE FAVORABLY IMPACTED.

A KEY QUESTION GOING FORWARD IS TO WHAT EXTENT CAN THIS SYNERGISTIC THERAPY OVER TIME ADDRESS COMPROMISED EPITHELIAL CELLS OR TISSUES THROUGHOUT THE BODY, SUCH AS IN TUMORS SINCE MOST CANCERS START IN EPITHELIAL TISSUES.

AS TO WHY THIS THERAPY HAS NOT BEEN PREVIOUSLY DISCOVERED, THE LITERATURE INDICATES THAT BOTH VITAMIN A AND VITAMIN D HAVE BEEN EXTENSIVELY TESTED AS SEPARATE THERAPIES; HOWEVER, WE COULD FIND NO EVIDENCE THAT THEY HAD BEEN

We now turn to the second subgroup of the **7** defining (amino acid) codons, namely the three STP or stop codons. The STP codons do not represent amino acids but do define the appropriate place or sequence to stop or terminate the chain of amino acids in constructing the protein molecules. Like the methionine or MET codon in starting the protein molecule, the STP codons apply to every protein molecule in every organism. However, unlike the role of the methionine codon (which is the same or non-specific for each protein molecule, see Section XII-B), the role of the STP codons is specifically programmed by the DNA molecule for every protein in every organism.

Given the above boundary defining roles for the STP subgroup of codons, the defining codon group (characterized by **7's** type) logically occupies the final position to complete the disruptive enabler (i.e., 1, 4, 2, 8, 5 and **7**), as shown in Figure 95 below. Also, since the cysteine / histidine subgroup does not reject nitrogen as an alien substance, it defines the acceptance of the nitrogen-based chemistry underlying the group of amino acid amide codons (characterized by 1's type, see Section XII-B). Thus, the defining codon group (characterized by **7's** type) is also shown in Figure 91 as relating back to the group of amino acid amide codons (characterized by 1's type) which facilitates the disruptive enabler becoming repeatable.

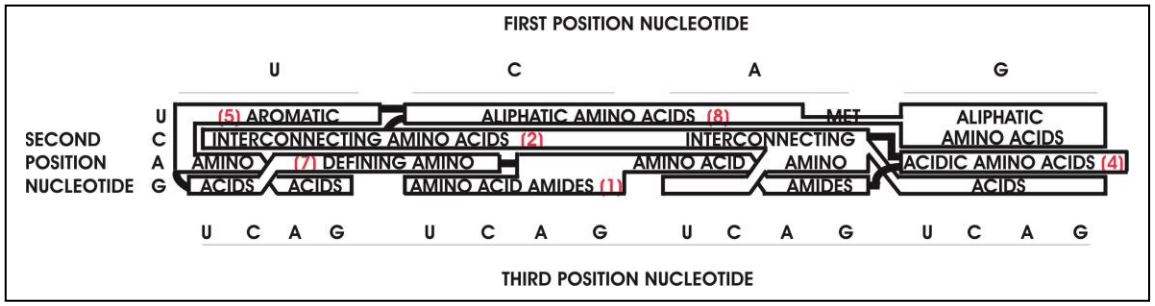


Figure 95. The genetic code's implementation of the disruptive enabler, where the amino acid amide group (characterized by 1) relates to the acidic amino acid group (characterized by 4) which relates to the interconnecting amino acid group (characterized by 2) which relates to the aliphatic amino acid group (characterized by 8) which relates to the aromatic amino acid group (characterized by 5) which relates to the defining (amino acid) group (characterized by 7) which relates to the amino acid amide group and thus repeats the 1/7th disruptive enabler.

PREVIOUSLY TESTED AS AN INTEGRATED, SYNERGISTIC THERAPY.

Regarding the next step, the First Analysis Institute has been sponsoring three years of very supportive efficacy studies (both in vitro and mouse based) with the University of Chicago's Celiac Center and the University of Illinois at Chicago's Pharmacognosy Laboratory. This is part of a broader educational effort by the Institute focused on the role of cysteine rich proteins, e.g. keratins and interleukins, in healthcare issues arising from regressions in applying the genetic code to humans.

THIS INTEGRATED THERAPY MAY HAVE TOXIC SIDE EFFECTS AND HAS NOT BEEN APPROVED BY ANY MEDICAL AUTHORITY.

Noteworthy, in the above matrix of the genetic code, the groups of amino acids representing 5's and 4's counterbalancing opposite types are on opposite sides of the genetic code matrix and those representing the 8's and 1's counterbalancing opposite types are on the top and bottom of the matrix, leaving the groups of amino acids representing the **7's** and 2's counterbalancing opposite types occupying opposite positions inside the genetic code matrix. This is consistent with the numerically derived disruptive enabler where 5's and 4's and 8's and 1's opposite types bracket the **7's** and 2's opposite types, as shown in the many figures of the disruptive enabler throughout this course trilogy. At the same time, the pairs of complementary types (i.e., 5 and 7, 8 and 1, as well as 4 and 2) are complementarily situated in Figure 95 somewhat similar to the many figures of the disruptive enabler throughout this course trilogy. Further, in the above generic code matrix, each group of amino acids representing the opposite types 5's and 4's as well as 8's and 1's has, respectively, its own or the same molecular side chain; whereas, each group of amino acids representing **7's** and 2's opposite types has a mix of different molecular side chains (see Sections XII-B through G).

Turning back to the noncoding or non-gene parts of the DNA, introduced earlier in Section XII-A, they too involve an overall "defining and determining" role as characterized by 7's type. According to the Encyclopedia of DNA Elements (ENCODE), a large public research consortium, the noncoding or non-gene parts of the human DNA primarily regulate gene activity including the many facets of gene expression, transcription and mutation prevention so that the coding or gene parts of the DNA can be properly implemented.

While, we do not yet know enough about the various individual roles of the noncoding parts of the DNA to delineate the specific "defining and determining" roles, as characterized by 7's type, the noncoding portions are increasingly being identified as pathways to causing hereditary diseases, particularly autoimmune diseases (also, see footnote 52).

Moreover, since the noncoding parts of the DNA lead to implementing the coding parts of the DNA, significant portions of the noncoding DNA also include "junk" DNA which represents effectively interim cul-de-sac's in the long journey to ultimately evolve an organism's DNA. In other words, these cul-de-sac's of DNA can be viewed as the residue of the trial and error process in guiding or determining the evolution of DNA, as characterized by 7's type.

The way in which the noncoding DNA leads to implementing the coded DNA could be analogous to the way in which the transitional iterations lead to establishing the mathematically disruptive enabler. Even though both schemas originate as part of type 7's characterization, so little is known about the former that it can't be compared in any detail with the latter. Thus, to the extent possible, Figure 95a below applies the schematic for the transitional iterations leading to establishing the mathematically disruptive enabler to the noncoding DNA leading to implementing the coded DNA.

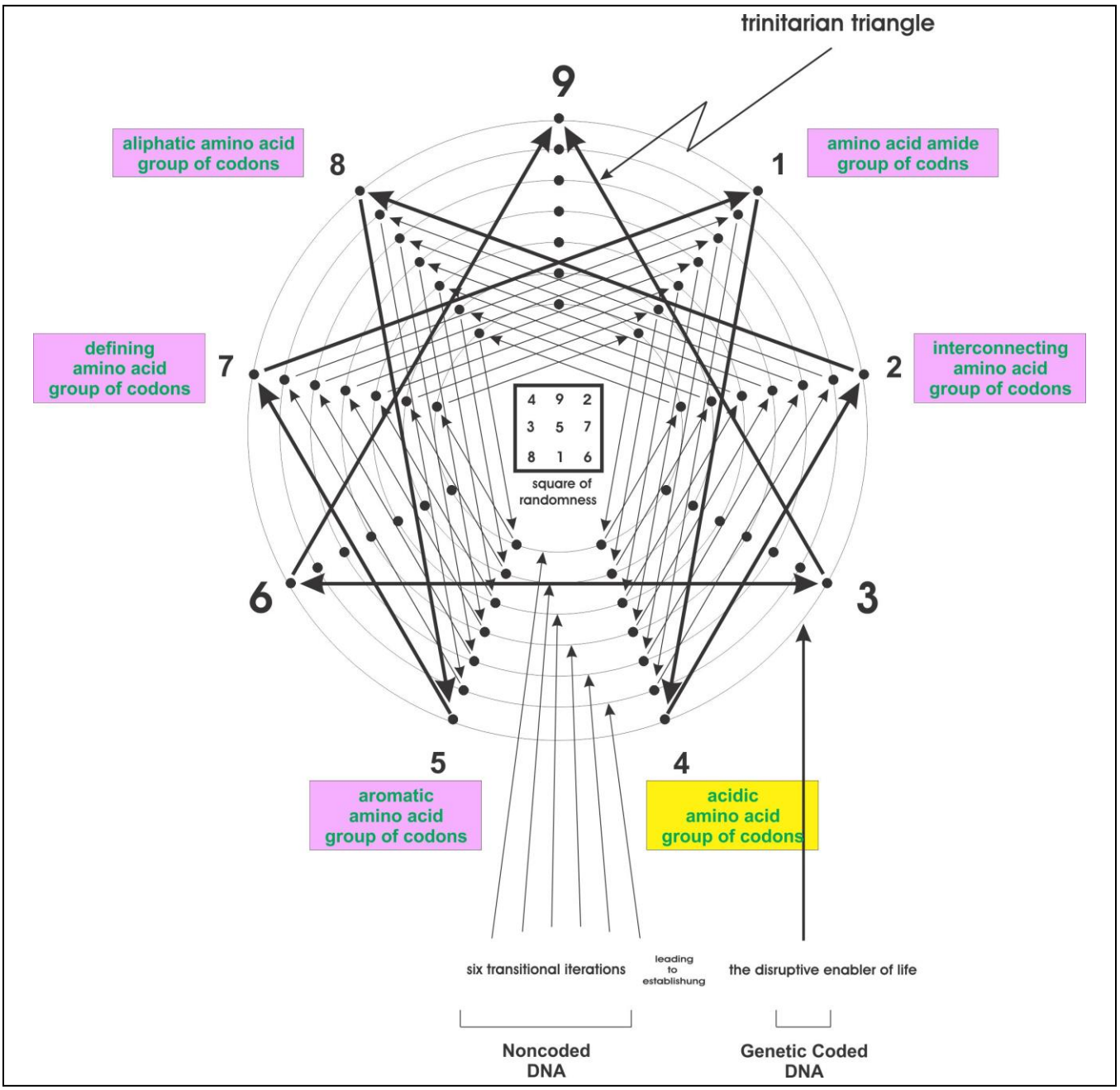


Figure 95a. incorporating the noncoded DNA leading to the genetic coded DNA to represent the disruptive enabler of life

Importantly, of further interest would be to better understand the noncoding roles of the DNA in defining the framework of boundaries for limiting the impact of evolutionary regression, such as manifested in the immune response system referenced in footnote 52.

H. Identifying the trinitarian 3, 6 and 9 types within the genetic code

H-i. THE TRINITARIAN TYPE 3

As described in Section VI-A, the numerical type **3**, when redundantly emphasized, characterizes the exclusive, but subtle, mathematical factor underlying both the interactive relationships of the trinitarian triangle as well as the structure of symmetric order. Also, because 2's type focuses on the exclusivity of the interactive relationships of the trinitarian triangle, 2's type essentially focuses on the exclusivity of **3's** type (see Section IV-B). Similarly, because 4's type converges onto the trinitarian triangle, 4's type essentially converges onto **3's** type (see Section V-A). In other words, **3's** type is complementary to 2's and 4's types; but, it is always accompanied by the latter (see Section VI-A and B).

Given this characterization, **3's** type can be identified within the genetic code through the following three considerations.

First, as explained in Section XII-A, each sequence of **3** successive nucleotides (called a codon) on the coding portion of the DNA molecule, translates to one of 20 standard amino acids used in constructing proteins. In other words, **3** is the factor underlying the interactive relationships making up the coding portion of the DNA molecule which in turn underlies the entire genetic code because every codon constituting the coding portion of the DNA molecule is based on **3**.

Secondly, since the 20 standard amino acids will only accept a coding sequence (i.e., codon) of **3** nucleotides in constructing every protein for every organism, the 20 standard amino acids create a focus on the exclusive role played by **3** as the factor underlying all the interactive relationships making up the DNA molecule. Since the 20 standard amino acids are characterized by 2's type (see Section XII-D), 2's type also characterizes the genetic code's focus on the subtle exclusivity of **3's** type in underlying the interactive relationships making up the DNA molecule.

Thirdly, as presented in Section XII-C, 4 or 4's type characterizes the number of different nucleotides which are interactively sequenced in groups of **3** to determine each of the genetic code's 64 codons. Moreover, when 4's and **3's** roles are viewed together within the context of the genetic code, 4's role can be viewed as one of converging onto **3's** role which again is very much consistent with their respective types, as discussed in the above introductory paragraph.

Fourthly, the dimensional characteristic of the genetic code matrix most closely associated with **3's** type is the vertical columns, since each column consists of 4 codons that can represent 4's type which in turn always accompanies **3's** type (see Figure 85). Thus, the column labels, which represent the third position nucleotide, must also be associated with **3's** type (see Figures 96 and 96a below).

H-ii. THE TRINITARIAN TYPE 9

As discussed in Sections IX-B and E, the symmetric order version of the numerical type **9** characterizes the independent, unifying mathematical totality encompassing all **9** types. Also, manifestation of **9's** type must incorporate features of the complementary type 1, because the latter always accompanies the former.

Given this characterization, the independent, unifying completeness of the genetic code is best conveyed by the totality of the 64 codons making up the genetic code. However, the methionine or MET codon must be treated differently. Unlike the other 63 codons, the methionine codon is not specifically programmed for each protein in each organism and thus represents the only randomness version of a type in the genetic code and in this case applies to 1's type (see Section XII-A and B). Recall from Section III-E that the symmetric order oriented version of 1's type must subsume the randomness-oriented version of 1's type and thus the reason for including MET codon in the genetic code. Appropriately, the symmetric order version of 1's type is represented by the 64 total codons (i.e., 64 => 6 + 4 = 10 => 1 + 0 = 1), as discussed in Section XII-B. However, the randomness oriented MET codon must be excluded from the totality of symmetric order represented by the genetic code. Accordingly, the remaining 63 codons represent a single-digit equivalent value of **9** (i.e., 63 => 6 + 3 = **9**) and thus can represent **9's** type with the genetic code. Again note, the inter-play between 1's and **9's** complementary types is very consistent with the numerical derivation of the later in Chapter IX which showed that **9's** type is always accompanied by 1's type (but at the same time differentiating between the randomness and symmetric order oriented versions).

Noteworthy, all the repeating codons (except one of the 3 STP codons) repeat along the horizontal rows and are discussed in the following Section XII-I. Also, as discussed earlier, the repeating codons are analogous to the repeating digits of the same-digit symmetry. Since each of the nine digits can be represented by their respective same-digit symmetry, the totality of the independent unifier, characterized by 9 best encompasses the 9 different same-digit symmetries. Thus, the 9 characterization or type is best associated with horizontal rows represented by the second position nucleotide (see Figure 96 and 96a below).

H-iii. THE TRINITARIAN TYPE 6

Refer to "Identifying the Enneagram in the Genetic Code to Enable Novel Health Care Discoveries", page 20.

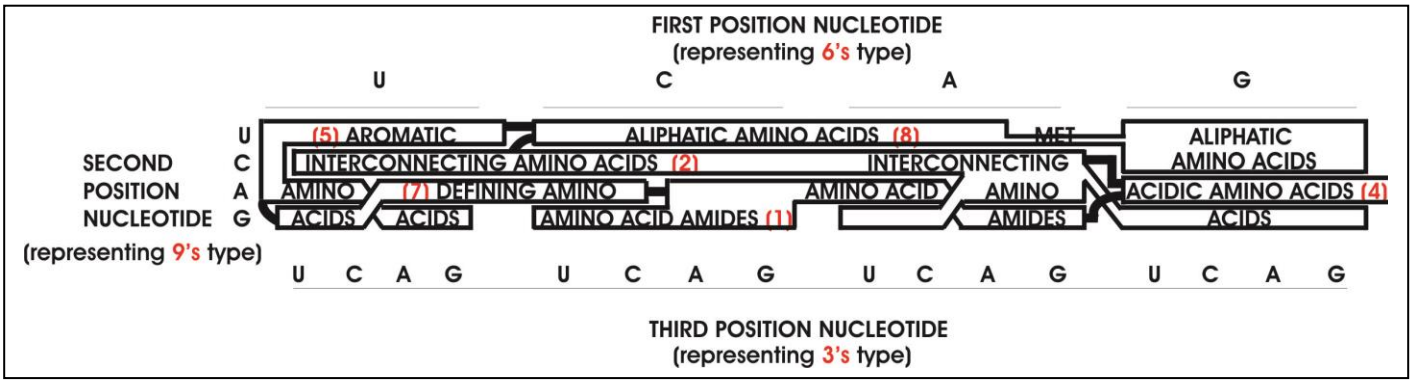


Figure 96. <u>The genetic code's implementation of evolutions disruptive enabler of life converging onto the trinitarian types 3, 6 and 9</u>

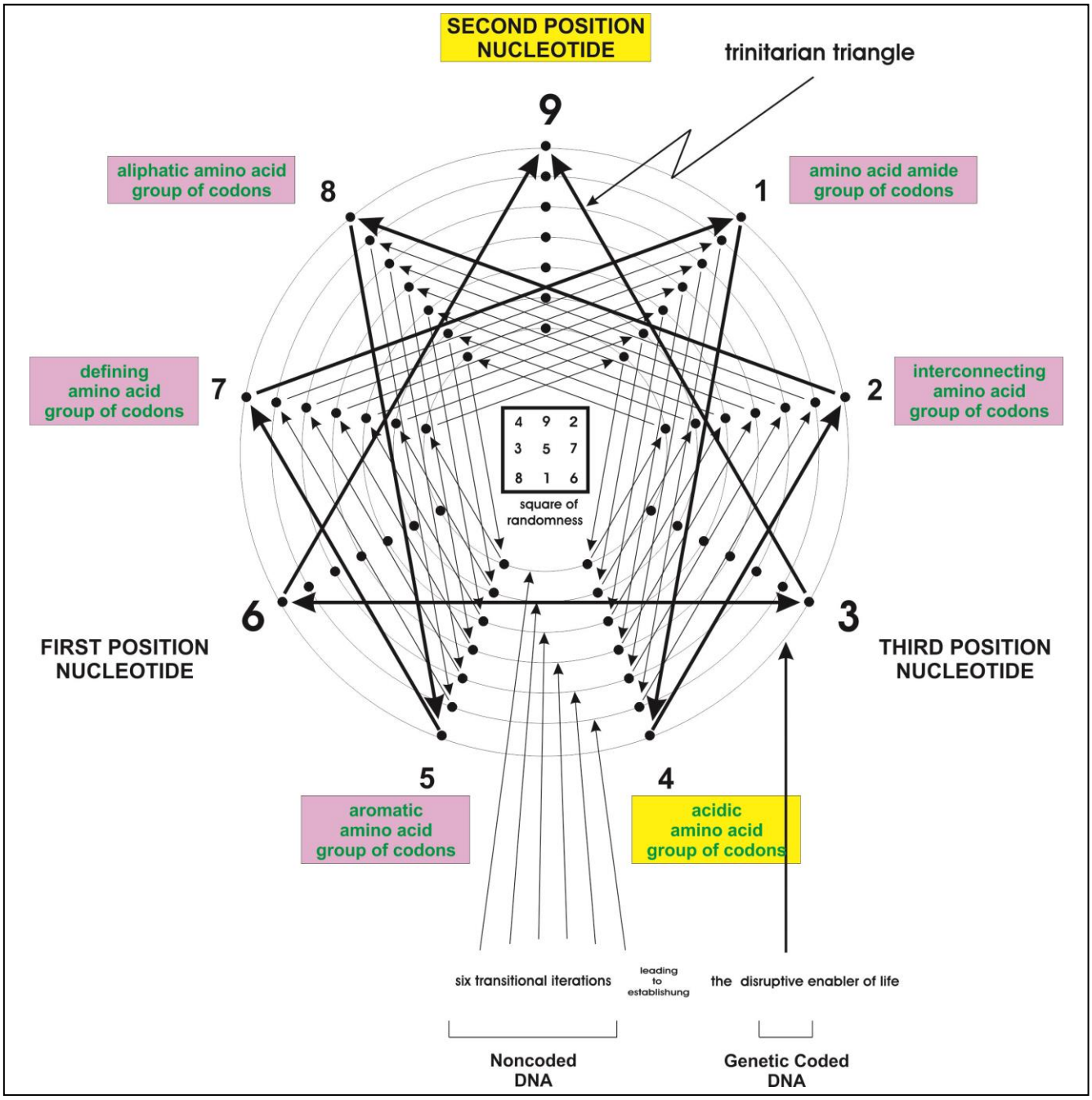


Figure 96a. Incorporating the noncoded DNA leading to implementing the genetic coded DNA to represent the disruptive enabler of life converging onto the trinitarian types 3, 6 and 9

or

IDENTIFYING THE GURDJIEFF ENNEAGRAM IN THE GENETIC CODED AND NONCODED DNA

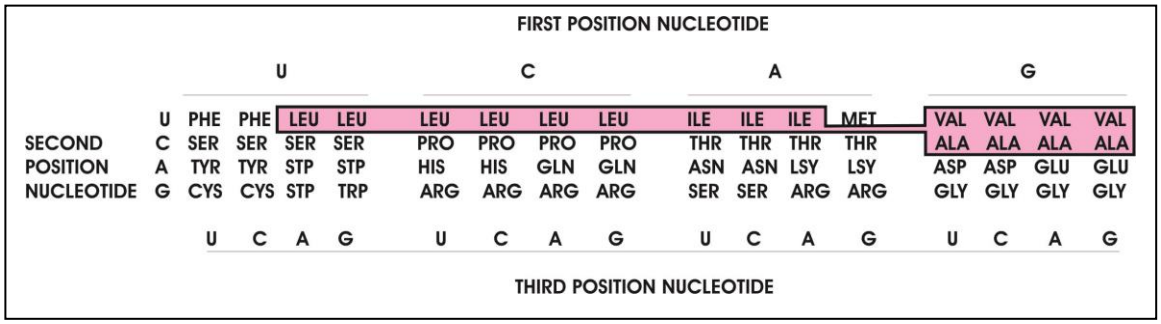
Also noteworthy, the genetic code provides another representation for 6's type similar to the way 9's type was addressed. Recall from the previous section that the totality characterized by 9's type was represented by the genetic code's total codons (i.e., 64) after removing the MET codon representing 1's randomness oriented type which always accompanies the complementary type 9 having 63 codons equating to the single-digit equivalent value of 9 (i.e., 63 => 6 + 3 = 9). Likewise, these 63 codons can transition to represent **6's** type after removing the three STP (non-amino acid) codons representing 7's type which always accompanies the complementary type **6** leaving 60 codons equating to the single-digit equivalent value of **6** (i.e., 60 => 6 + 0 = **6**), see Section XII-G. Similar to the MET codon which initiates the series of amino acids forming all proteins, the STP codons terminate these same series. **Importantly, while the three STP codons where shown in Section XII-G to represent 7's type they will be shown below in Section XII-I to also refer to 3's type which is the reason for viewing the 60 codons (representing 6's type) separately from the 3 STP codons (referring to 3's type or the counterbalancing opposite to 6's type). In other words, just as the MET codon (because of its randomness orientation) was differentiated from the symmetric totality characterized by the complementary type 9, so too the STP codons (because they refer to the counterbalancing type 3) are differentiated from the complementary type 6.**

I. Analyzing same-digit symmetry or same-codon symmetry

As indicated earlier at the end of Section XII-F, the genetic code serves as the conceptual gateway and introductory criteria for all coded DNA similar to the roles of same-digit symmetry in regard to introducing the symmetric order orientation. As such, the genetic code should be analyzed from the perspective of same-digit or same-codon symmetry.

– **Analyzing same-codon symmetry from the perspective of the fully implemented type 8**

The fully implemented type 8 characterizes producing the disruptive enabler converging onto the trinitarian triangle and is represented in the genetic code by the group of 17 aliphatic amino acid codons (see Section VIII-B and Figure 91 which is repeated below).



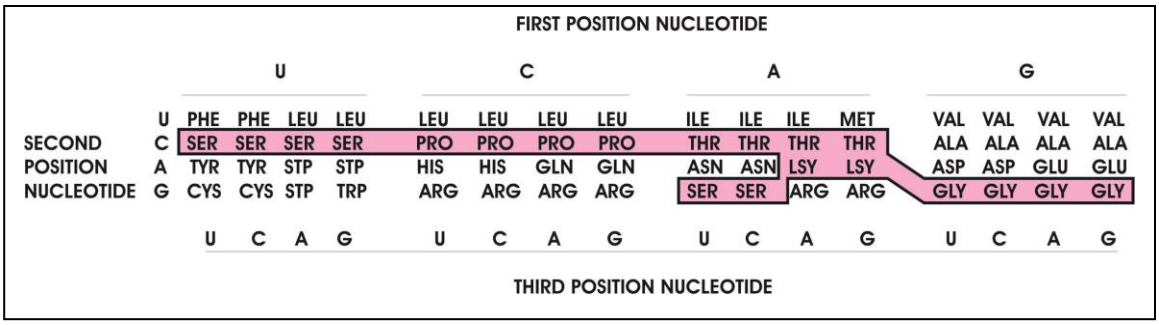
Repeating Figure 91. The 17 aliphatic amino acid codons within the genetic code representing the fully implemented type 8

Accordingly, this group of 17 aliphatic amino acid codons refers to the trinitarian triangle onto which the disruptive enabler converges by the set of 6 repeating leucine (LEU) codons representing the trinitarian type 6, the set of 3 repeating isoleucine (ILE) codons representing the trinitarian type 3, and the totality of these two sets of codons (i.e., 6 + 3 = 9) representing the trinitarian type 9,

Moreover, 8's type characterizes the completed production of the converging disruptive enabler while the redundantly emphasized type 4 characterizes this overall converging process. Accordingly, this is represented within the 17 aliphatic amino acid codons by the two sets of 4 repeating codons [i.e., valine (VAL) and alanine (ALA)] (see Section VIII-B). Also, since this trinitarian presentation is self-contained within type 8's production-oriented characterization, it can be viewed as disproportionately focusing on the trinitarian type 9 with its complementary production-oriented characterization (see Figure 77).

– **Analyzing same-codon symmetry from the perspective of 2's type identifying the exclusivity of the trinitarian types**

Type 2 characterizes identifying the exclusivity of the trinitarian types 3, 6 and 9 and is represented in the genetic code by the group of 20 interconnecting amino acid codons (see Section IV-B and Figure 90 which is repeated below).

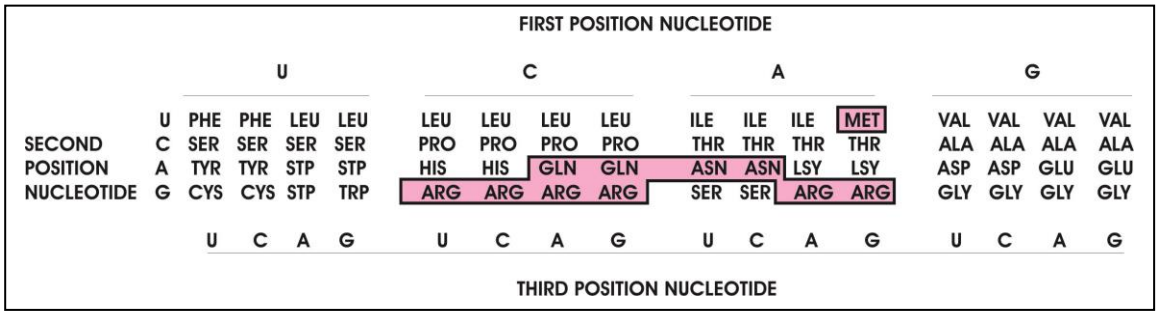


Repeating Figure 90. The 20 interconnecting amino acid codons within the genetic code representing type 2

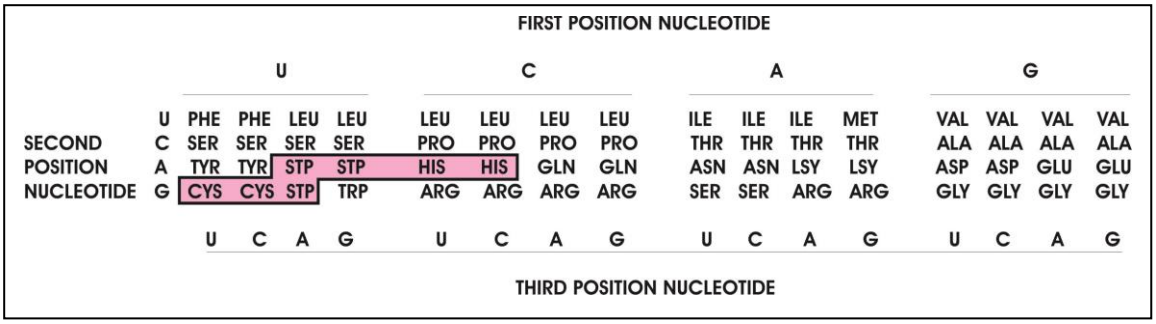
Accordingly, within this group of interconnecting amino acids are three sets of 4 repeating codons [i.e., proline (PRO), threonine (THR) and glycine (GLY)] referring to the trinitarian type 3 and its continual accompaniment with 4's type (i.e., 3 x 4 = 12 => 1 + 2 = 3, see Sections VI-A & B), a set of 6 repeating serine (SER) codons referring to the trinitarian type 6, and the totality of these four sets (i.e., 3 x 4 = 12 + 6 = 18 => 1 + 8 = 9) refers to the trinitarian type 9. Also, since this trinitarian presentation is self-contained within the group of interconnecting amino acid codons representing type 2's interactive characterization and draws heavily upon the complementary type 4's interactive characterization for presenting type 3, it can be viewed as disproportionately focusing on the trinitarian type 3 with its complementary interactive characterization (see Figure 77).

– **Analyzing same-codon symmetry from the perspective of all the disruptive enabler's types except the fully implemented type 8**

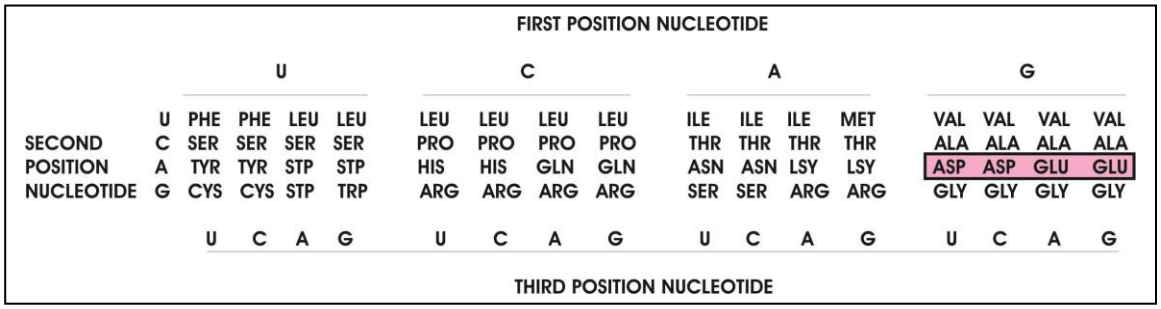
The remainder of the repeating codons within the genetic code can be divided into a set of 6 repeating arginine (ARG) codons drawn from Figure 87 (repeated below) referring to the trinitarian type 6, a set of 3 repeating stop (STP) codons drawn from Figure 94 (repeated below) referring to the trinitarian type 3, and nine sets of 2 repeating codons constituting the remainder of the genetic code referring to the trinitarian type 9 (i.e., 2 x 9 = 18 => 1 + 8 = 9) drawn from Figures 87, 94, 88 and 93 (repeated below) as well as Figure 90 (repeated above).



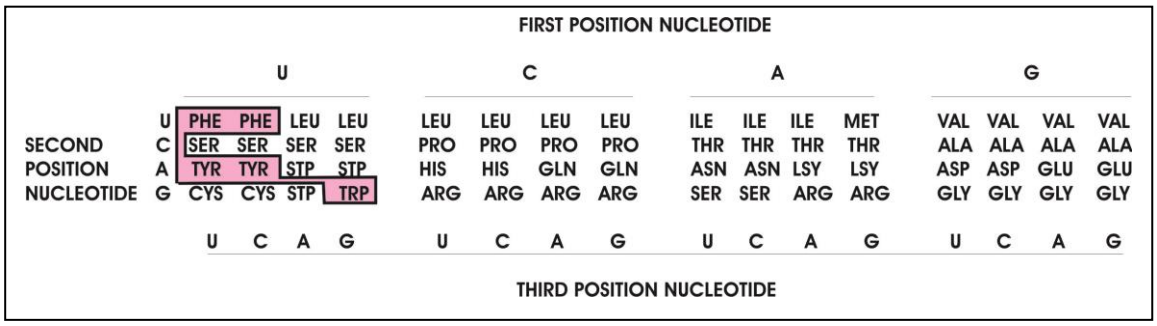
Repeating Figure 87. The 10 amino acid amide codons within the genetic code representing type 1



Repeating Figure 94. The 7 defining (amino acid) codons within the genetic code representing type 7



Repeating Figure 88. The 4 acidic amino acid codons within the genetic code representing type 4



Repeating Figure 93. The 5 aromatic amino acid codons within the genetic code representing type 5

Importantly, the use of nine sets of 2 repeating codons from five of the six groups of amino acid codons conveys that 2's type characterizes both identifying the specificities of (as well as interconnecting with) the various types making up the disruptive enabler, in addition to identifying the trinitarian types, as we saw immediately above (see Section IV-B). However, the group of codons representing 8's type does not include a set of 2 repeating codons because 2's type does not identify the fully implemented type 8 after it is no longer interchangeable with 1's type (see Section IV-B). However, 2's type does indeed identify type 8 as the sixth type so long as it is interchangeable with 1's type which is conveyed by this perspective.

Moreover, since this perspective's trinitarian presentation involves all six types making up the disruptive enabler (i.e., type 8 is included while interchangeable with type 1), it can be viewed as disproportionately affirming the trinitarian type 6's characterization of the guiding focus for the overall convergence of the disruptive enabler until 8's type is no longer interchangeable with 1's type.

– ANALYZING SAME-CODON SYMMETRY FROM THE PERSPECTIVE OF 4's TYPE

When the repeating codons of the genetic code are viewed from the perspective of the redundantly emphasized type 4, we see the following nine sets of 4 repeating codons representing 4's type, as shown in Figure 96b below.

Nine sets of 4 repeating codons referring to 4's type characterizing the initiation and convergence of the disruptive enabler of life	The nine sets of 4 repeating codons are embedded in the groups of amino acid codons representing the following types respectively drawn from Figures 93, 88, 87, 94, 90 and 91 (repeated above)

TOP (OR INITIATING) GROUP	
PHE, PHE, TYR, TYR HIS, HIS, CYS, CYS GLN, GLN, ASN, ASN ASP, ASP, GLU, GLU	5 7 1 4
BOTTOM (OR CONVERGENCE) GROUP	
PRO, PRO, PRO, PRO THR, THR, THR, THR GLY, GLY, GLY, GLY VAL, VAL, VAL, VAL ALA, ALA, ALA, ALA	2 2 2 8 8

Figure 96b. The genetic code's same-digit or same-codon symmetry from the perspective of 4's redundantly emphasized type characterizing the initiation and convergence of the disruptive enabler of life

- TOP (OR INITIATING) GROUP

Since the top group represents type 4 characterizing the initiation of the disruptive enabler, the top group of repeating codons must reflect that type 7 can be divided into type 1 with the outcome equating to type 4. Moreover, the identification of this process must be characterized by 2's type (see Section IV-B). Furthermore, during this initiation of the disruptive enabler types 1 and 8 must be interchangeable which also is identifiable by type 2's (again see Section IV-B). For further confirmation of this process, recall from Section X-C's Plan for Establishing the Disruptive Enabler - Step 2 that the fourth stage of the plan characterized by 7's type goes into or divides into the third stage characterized by 1's type to equate to the second stage characterized by 4's type.

✶ Moving forward with this background in mind, the type 7 divisor is represented by the 16 repeating codons constituting the most basic

components of the top group (i.e., 16 => 1 + 6 = 7), as shown in Figure 96b. As such, these most basic or granular components of the top group should serve as the type 7 divisor.

- Continuing with this same logic, when the top group is viewed as a whole or single (i.e., 1) entity, it should represent 1's type which can then be divided into (or by) the above constituents or components representing 7's type.

- The outcome equating to type 4 is represented by the 4 rows of the top group where each row incorporates the individual repeating codons as its granular constituents consistent with being the quotient of this overall division process.

- Type 2's characterization identifying this process is represented by the eight sets of 2 repeating codons where each set is a constituent of both the top group and each row, but at the same time each set incorporates the individual repeating codons as its granular constituents consistent with identifying each of the factors making up the entire division process.

- Because there are 8 sets of the two repeating codons making up the single (i.e., 1) top group, they also identify the embedded interchangeability between 8's and 1's types during the initiation of the disruptive enabler, as represented by the top group.

- The redundant emphases of types 7, 4 and 1 are conveyed by their characterizations being represented by, not only the overall top group of repeating codons (as described above), but also the individual rows (as shown in the right-hand column of Figure 96b). Specifically, the fourth row representing 7's type relates to or goes into the third row representing 1's type (see paragraph preceding Figure 95) which then in turn relates to or yields the second row representing 4's type (see the paragraph preceding Figure 88 and the paragraph preceding Figure 89).

- The non-redundantly emphasized type 5, which conceptualizes the initiation of the disruptive enabler, is non-redundantly represented (i.e., only once) by the first row of the top group.

In sum, all six types of the initiating disruptive enabler are represented by the top group.

- BOTTOM (OR CONVERGENCE) GROUP

Turning to the bottom or second group, the repeating codons constituting this group must reflect the conceptualization and then the yielding and production of the final convergence of the disruptive enabler onto the trinitarian triangle, as characterized by types 5, 4 and 8, respectively. For further confirmation of this process, recall from Section X-C's Plan for Establishing the Disruptive Enabler - Step 2, that the sixth stage of the plan characterized by type 2 goes into or divides into the fifth stage characterized by type 8 to equate to either 5's or 4's type depending on whether 8's type is still interchangeable with 1's type (i.e., 1's

type ÷ 2's type => 5's type) or non- interchangeable (i.e., 8's type ÷ 2's type => 4's type). In other words, the seventh or final stage is characterized initially by 5's type and then by 4's type. Moreover, since 5's and 4's types are counterbalancing opposites, the production of which is characterized by 8's type (see Section VIII-A), 8's type also characterizes producing the disruptive enabler converging onto the trinitarian triangle and thereby fulfilling its role in characterizing the fifth stage.

- Moving forward with this background in mind, just as the type 7 divisor was represented by the 16 repeating codons constituting the top group, the type 2 divisor is represented by the 20 repeating codons constituting the bottom group (i.e., 20 => 2 + 0 = 2). Likewise, just as the type 1 entity to be divided was represented by the top group being viewed as a single (i.e., 1) entity, this type 1 entity to be divided is represented by the bottom group being viewed as a single entity. Further, just as the outcome equating to 4's type was represented by the 4 rows of the top group, the outcome equating to 5's type is represented by the 5 rows of the bottom group.

- Because the interchangeability of types 1 and 8 is transitioning to the type 8 becoming no longer interchangeable, the last two rows of the bottom group shown in Figure 96b represent the non-interchangeable type 8 entity to be divided similar to the way the type 1 entity was divided above. Thus, to be consistent the type 2 divisor must be represented by the first three rows of the bottom group. In this case, the outcome equating to 4's type is represented by the 4 repeating codons making up each of the 5 rows of the bottom group.

Further adherence to the above referenced Section X-C's Plan for Establishing the Disruptive Enabler is provided by the top and bottom groups of repeating codons representing counterbalancing opposites (i.e., 4 vs. 5 rows, 16 => 1 + 6 = 7 vs. 20 => 2 + 0 = 2 repeating codons, and 1 vs. 8 focuses), the totality of which is characterized by type 9. NOTE, WE HAVE SEEN THIS AUGMENTATION PROCESS INVOLVING TYPES 9 AND 4 IN CONVERGING TOWARDS SYMMETRIC ORDER (AS REPRESENTED BY THERE BEING 9 SETS OF 4 REPEATING CODONS IN FIGURE 96b) INVOLVING THE FINE STRUCTURE CONSTANT IN DEFINING THE DISRUPTIVE ENABLER OF MATTER/ENERGY (SEE SECTION XI-A). HOWEVER, THIS IS THE FIRST TIME WE HAVE SEEN THIS ASSOCIATION BETWEEN THE TYPES 4'S AND 9'S PERSPECTIVES ALSO INCORPORATE THE SAME-DIGIT OR SAME-CODON PHENOMENON.

– ANALYZING FROM THE PERSPECTIVE OF 7'S TYPE

SINCE WE EARLIER SAW THAT 6'S TYPE CHARACTERIZES FROM THE PERSPECTIVE OF THE MATHEMATICALLY DISRUPTIVE ENABLER VERSUS 3'S TYPE CHARACTERIZING FROM THE PERSPECTIVE OF THE TRINITARIAN TRIANGLE, TYPE 6'S ACCOMPANIMENT WITH TYPE 7 (AS A MEMBER OF THE MATHEMATICALLY DISRUPTIVE ENABLER) IS MUCH MORE REFLECTIVE OF THE DISRUPTIVE ENABLER'S PERSPECTIVE THAN TYPE 3'S ACCOMPANIMENT OF TYPE 4. MOREOVER, THIS REFLECTIVENESS OF THE DISRUPTIVE ENABLER

THROUGH THE ACCOMPANIMENT WITH THE REDUNDANTLY EMPHASIZED TYPE 7 IS EVEN FURTHER INTENSIFIED BECAUSE THE TRINITARIAN TYPE 6 IS NOT REDUNDANTLY EMPHASIZED; WHEREAS, THE TRINITARIAN TYPE 3 IS REDUNDANTLY EMPHASIZED (SEE SECTION X-D).THEREFORE, BECAUSE THE REPEATING SAME-CODON SYMMETRY DOES NOT REFER DIRECTLY TO 7'S TYPE IMPLIES THAT SUCH AN UNUSUAL DEGREE OF INTENSIFICATION OF 7'S TYPE MUST BE REPRESENTED BY THE NONCODING OR NON-GENE PARTS OF THE DNA. ACCORDINGLY, THE NONCODING PORTION, WHICH IS CHARACTERIZED BY 7'S TYPE, CONSTITUTES MOST OF AN ORGANISM'S DNA (SEE SECTIONS XII-A AND G).

WHILE THE GENETIC CODE MUST EXHIBIT SOME DEGREE OF FLEXIBILITY TO AT LEAST ACCOMMODATE CHANGES IN THE PHYSICAL ENVIRONMENT, HOW DOES THE GENETIC CODE PREVENT REGRESSING WHICH PRIMARILY REPRESENTS FAILURE TO COMPLY WITH THE PLAN FOR SYMMETRIC ORDER AS CHARACTERIZED BY TYPE 7 ? TO THE EXTENT THIS COMPLIANCE REACHES BEYOND THE CODING AND THE EXTENSIVE NONCODING PARTS OF THE DNA CHARACTERIZED BY TYPE 7, THIS SUBJECT IS FURTHER DISCUSSED IN COURSE 101C, WHICH MAY HAVE INTERESTING IMPLICATIONS FOR GENETIC ENGINEERING.

- **Analyzing from the perspective of the non-repeating codons representing 5's and 1's types**

In regard to the only two non-repeating codons of the genetic code [i.e., tryptophan (TRP) and methionine (MET) representing 5's and 1's types], they serve to introduce the other repeating amino acid codons by characterizing the conceptualization and criteria roles of same-digit or same-codon symmetry (see last paragraph of Section XII-F).

- **Number of repeating codons are either three and six or two and four**

As presented above, the genetic code uses only three and six repeating codons to directly convey the trinitarian types because the totality characterized by the trinitarian type 9 is never limited to itself. Likewise, the genetic code utilizes only two and four repeating codons from the disruptive enabler types because 2's and 4's types represent the two interactive characterizations as opposed to the non-interactive characterizations represented by 5's and 7's types (see Figure 77). In other words, the interactive mathematical processes of multiplication and division characterized by 4's and 2's types, respectively, can be directly factored while the non-interactive mathematical processes of addition and subtraction characterized by 5's and 7's types, respectively, cannot be directly factored (see Course 101A). Eight repeating codons are not utilized because the repeating-codon symmetry addresses 8's type both as interchangeable and non-interchangeable with 1's type.

Figure 96b below updates Figure 96a to incorporate both the same-digit or same-codon symmetry (i.e., green print) as well as the special augmentation process involving types 9 and 4 in converging towards symmetric order (yellow background).

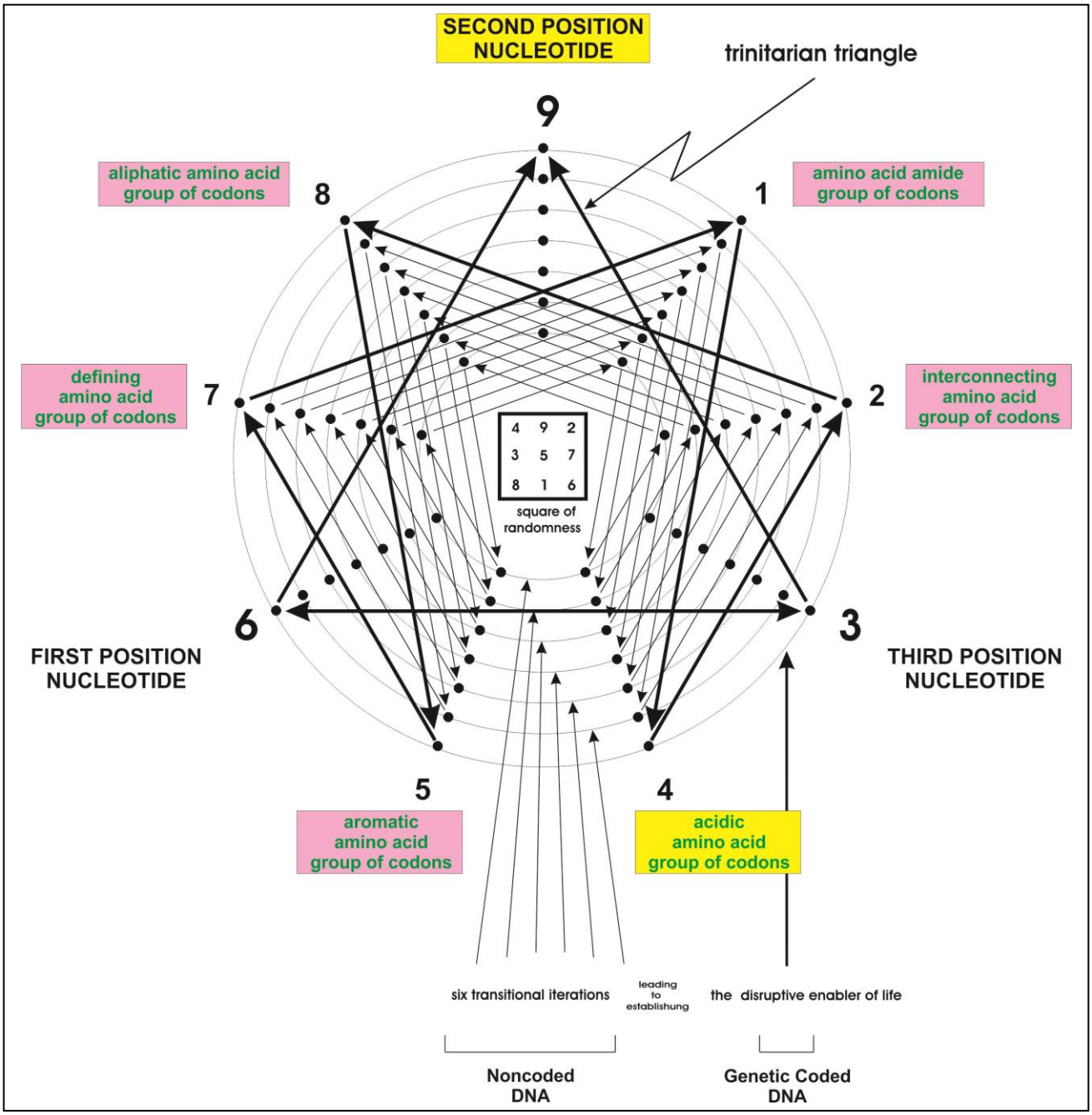


Figure 96b. Incorporating the noncoded DNA leading to implementing the genetic coded DNA to represent the disruptive enabler of life converging onto the trinitarian types 3, 6 and 9

or

IDENTIFYING THE GURDJIEFF ENNEAGRAM IN THE GENETIC CODED AND NONCODED DNA

(While Gurdjieff died before the discovery of the genetic code, he did illustrate his Law of Seven in the periodic table of chemical elements.)

J. To summarize:

The first six sections (i.e., XII-B through G), respectively, identified how the six numerical types of the mathematically disruptive enabler (i.e. 1,4,2,8,5 and 7) can characterize the 64 codons making up the genetic code matrix of Figure 85. This identification process also demonstrated that, after grouping the codons according to the six numerical types, the contiguous and sequential arrangement of these six groups within the genetic code are the same as the numerical sequence of the mathematically disruptive enabler as it converges onto the trinitarian triangle in approaching symmetric order. Thus, the genetic code can be viewed as being incorporated into evolution's disruptive enabler of life somewhat similar to the way in which the particle types of matter and energy were incorporated into evolution's disruptive enabler of matter/energy.

Importantly, while the genetic code or the genetic coding parts of the DNA can be primarily identified as evolution's disruptive enabler of life, the noncoding or non-gene parts of the DNA (i.e., not manifested by the genetic code) also involve an overall "defining and determining" role as characterized by 7's type. However, we do not yet know enough about the various individual roles of the noncoding parts of the DNA to delineate the specific "defining and determining" roles even though the noncoding portion may constitute most of an organism's DNA.

Section H identified the roles characterized by the three types of the trinitarian triangle (i.e., 3, 6 and 9) within the genetic code and presented how the above disruptive enabler of life converges onto the trinitarian triangle [see Figure 96a]. In this process the genetic code disproportionately accentuates the guiding focus role characterized by 6's type.

SECTION I SHOWS HOW THE GENETIC CODE INGENIOUSLY UTILIZES THE REPETITION OF SAME-DIGIT OR SAME-CODON SYMMETRY TO CONFIRM CONCEPTUALLY THE SPECIFICITIES OR SPECIFIC ROLES OF, NOT ONLY THE SIX TYPES CONSTITUTING THE DISRUPTIVE ENABLER, BUT ALSO THE THREE TYPES CONSTITUTING THE TRINITARIAN TRIANGLE, AS THE FORMER CONVERGES ONTO THE LATTER. IN DOING SO, THE CONCEPTUAL PREMISE UNDERLYING THIS ENTIRE TRILOGY OF COURSES SEEMS TO BE FURTHER CONFIRMED. Also, this process draws upon the special augmentation involving types 9 and 4 in converging towards symmetric order.

Because the trinitarian type 6's accompaniment with the complementary type 7 is much more extensive than types 3's and 9's accompaniments with their complementary types 4 and 1, respectively, (see Section VII-A and B), the genetic code's disproportional accentuation of type 6 means that type 6's more extensive accompaniment with type 7 is correspondingly accentuated even further (including the roles of the noncoding parts of the DNA). Therefore, because the repeating same-codon symmetry does not refer directly to 7's type implies that such an unusual degree of accentuation of 7's type must be represented by the noncoding or non-gene parts of the DNA. Accordingly, the noncoding portion, which is characterized by 7's type, constitutes most of an organism's DNA (see Sections XII-A and G).

While the genetic code must exhibit some degree of flexibility to at least accommodate changes in the physical environment, how does the genetic code prevent regressing which primarily represents failure to comply with the plan for symmetric order as

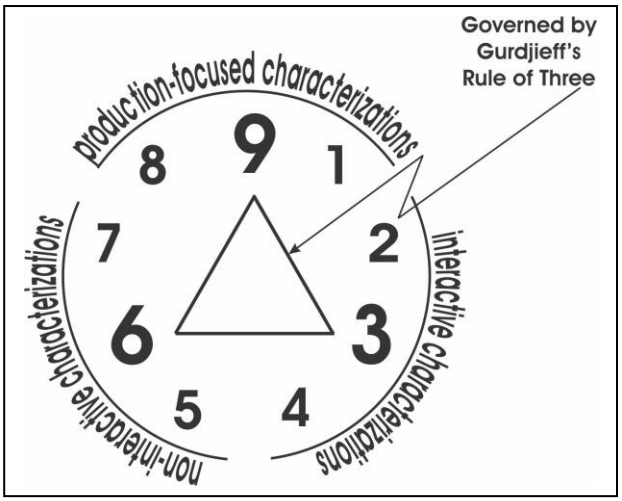
characterized by type 7 ? Indeed, two fundamental examples were addressed where the genetic code appears to have reversed orientation from symmetric order towards randomness. To the extent this compliance reaches beyond the coding and noncoding parts of the DNA characterized by type 7, this subject is further discussed in Course 101C, which may have interesting implications for genetic engineering.

While the genetic code as the disruptive enabler of life has evolved from the building blocks of matter/energy as the disruptive enabler of matter/energy, keep in mind that all living organisms constructed according to the genetic code must also exist within the constraints of the physical environment constructed according to the underlying disruptive enabler of matter/energy. In other words, the disruptive enabler of matter/energy can be viewed as underlying both the evolutionary micro sourcing of the disruptive enabler of life as well as the evolutionary macro sourcing of the physical environment in which the disruptive enabler of life must exist (see Sections XII-E, F and G).

Identifying the Gurdjieff Enneagram in Language Formation

In searching for the highest-level manifestation or application of the Gurdjieff Enneagram in humanity, short of the human personality discussed in the next chapter, syntax generation in language formation is an excellent candidate. Syntax generation begins when two syntactic objects combine to form a new syntactic unit. In turn, the new syntactic unit can hierarchically combine with another syntactic unit as part of an endlessly recursive process. Noam Chomsky called this process Merge and claims it distinguishes language from other cognitive faculties and is unique to the modern human specious.

Merge involves three basic components which can be compared (or even analogized) to the three basic characteristics of the Enneagram as governed by Gurdjieff Law of Three Principles, Focus or Ways, as introduced in Figure 19 and summarized below in the repeat of Figure 77.



Repeat of Figure 77. Categorizing the types based on their complementary characterizations

As shown above, on the right side of Figure 77, the Enneagram can characterize the interactive connectivity including the resulting specificity of two or more types converging towards symmetric order. This could be analogized to the Merge component interfacing with the interactive sensorimotor systems which involve all the various externally oriented morphological considerations.

As shown above on the left side of Figure 77, the Enneagram can characterize the non-interactive connectivity including the conceptualizing, guiding and planning of two or more types converging towards symmetric order. This could be analogized to the Merge component interfacing with the non-interactive and internally oriented systems involving conceptualizing, hierarchical guiding and planning considerations.

As shown above at the top of Figure 77, the Enneagram can characterize producing a unifying totality according to the criteria of symmetric order. This could be analogized to the Merge CPU component which encompasses the basic compositional production of human language.

To summarize, the above outlined interactive, non-interactive and production components of both the Enneagram and the Merge system of human language formation lend themselves to a triangular representation governed by the Gurdjieff Law of Three.

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