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The Human Hands Model for the Essentials of the Chemistry of Life

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Abstract Human hands are the model for the neon electron configuration, organic chemistry, protein function and the genetic code structure. The human hands model is investigated for the periodic table. An original genetic code table is presented for the combined vertebrate mitochondrial and universal nuclear genetic codes. The developmental connection between human (vertebrate) mitochondrial and universal (standard) nuclear genetic codes is investigated. The genetic code structure models the bones and joints structure of a human arm.

Keywords: *neon electron configuration, periodic table, organic chemistry, biochemistry, chemistry of life, genetic code table, genetic code structure, human hands structure, models in chemistry, proteinogenic amino acids, protein function*

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1. Introduction

The essentials of the chemistry of life that are investigated are: The neon electron configuration, the periodic table, organic chemistry structure, protein function and the genetic code structure. The intended organic chemistry structure is described and used as an educational tool [1]. The genetic code structure and corresponding genetic code table are original. The chronology of the various items in this article shows the search of the author in finding the model function intended in the title. First, the organic chemistry structure will be connected to the neon electron configuration. The connection raises the question on the nature of the organic chemistry core. The five knowledge pairs of organic chemistry invite to investigate the structure of the five finger pairs of humans. Organic chemistry and human hands have a common structure resembling the neon electron configuration. Consequently, and in reverse, the human hands are the plan model for compound forming forces and organic chemistry. The idea of the human hands model will be investigated further on in connection to protein function, the periodic table and the genetic code structure. Protein function is determined primary by its structure, which is mainly determined by its amino acid sequence. The twenty proteinogenic amino acid side chains are divided in four groups. Each group contains five side chains that each show clear connections to corresponding human fingers. Finally, as a climax, the modeling function of human hands and arms is investigated for the structure of the genetic code.

2. An Organic Chemistry Hierarchy

Organic chemistry is part of the essentials of the chemistry of life as it describes the functional groups of biomolecules, their reactions, and structural properties such as chirality. Everyone who masters organic chemistry is to some extent impressed by its logical structure. Some even write about this logic [2] and J-M. Lehn wrote in his biography [3]: "I was impressed by the coherent and rigorous structure of organic chemistry". The organic chemistry hierarchy exemplifies its logical structure. The presented hierarchy builds the organic chemistry logic up to a climax. The hierarchy uses the electron configuration of neon as a modeling frame around which fundamental organic chemistry knowledge is structured in a perfectly matching knowledge structure, which is summarized as a Neon Electron Configuration Analogy (NECA). Figure 1 shows an overview of the NECA hierarchy. In NECA, organic chemistry topics are hierarchically structured in ten knowledge units that are grouped in five strictly related pairs. NECA presents an attractable, efficient, intriguing, logical, remarkable, simple and unique frame for fundamental organic chemistry. The NECA course structure is in a sense the optimal organic chemistry course structure because of its hierarchical structure that is perfect in line with the neon electron configuration active forces that are present in all carbon compounds. Although the value of the educational tool is not generally accepted, the hierarchy is not yet questioned. I believe this hierarchy cannot be disproved and deserves recognition. In this contribution, the most important question is not if the hierarchy is of educational value or how educational applications could be further developed. It is even not the question if the proposed hierarchy is sufficiently developed. The only question that should arise in view of the NECA structure is if the proposed model for fundamental organic chemistry knowledge is valid or not. The question is: are there fundamental organic chemistry concepts that cannot be sorted into the NECA structure? I believe there will be none.

The analogy is already described in the Supplemental Material two of reference four [4] and is developed as an

educational tool [1]. The tool also describes necessary adaptations that could be done to the traditional curriculum for a better match to NECA. Some of the adaptations are discussed more in detail in supporting publications [5,6,7] and increase the educational power of the tool. The author believes that reference 6 describes perhaps the only existing study of quantitative correlations between boiling points in homologous series and intermolecular forces.

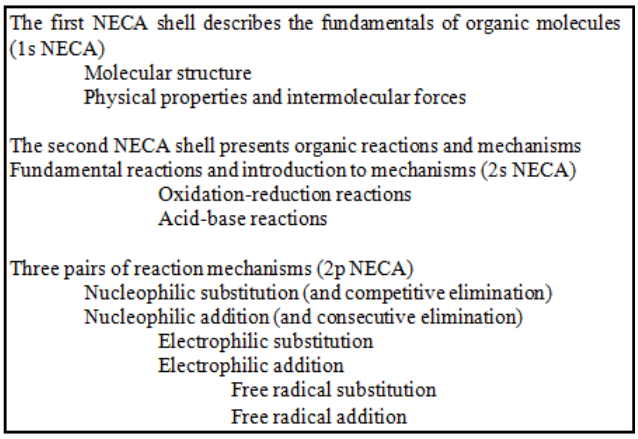

Figure 1. The Neon Electron Configuration Analogy (NECA) of fundamental organic chemistry knowledge. Reproduced with permission of: The Chemical Educator [http://chemeducator.org] [4] and The World Journal of Chemical Education [1]

2.1. The Neon Electron Configuration Structure of Fundamental Organic Chemistry

Because of its coherency, NECA is nearly self-instructing in its simplicity (Figure 1). It is hardly necessary to explain it further on. For further details, the reader could consult reference 1. In this section a few additional comments will be made. The molecular structure and physical properties knowledge pair or 1s shell of NECA is so strongly interconnected that it is even unthinkable to have a molecule without its physical properties. Even the most sophisticated designed organic molecules of the front research find their roots in this section. Professionals consider all intended reactions of NECA as fundamental. They will agree that the 2s NECA reactions, oxidation-reduction and acid-base, are fundamental for the 2p NECA reactions and mechanisms. For many researchers in the field of organic chemistry, the choice of oxidation-reduction in this section will be unexpected at first sight. How can oxidation reactions that you mostly try to avoid in daily practice be fundamental to the mechanism sections? In addition, most textbooks do not use the oxidation level concept that reference 1 needs to implement oxidation-reduction at the 2s NECA level. J. March, of whom the author has the greatest respect for the impressive work that he realized in favor of the chemical community, reserves only the last chapter of his comprehensive book to oxidation-reduction [8].

2.2. The NECA Core

A statement by J.W. Goethe [9], translated by C.L. Eastlake [10] inspired the author to discover the NECA structure of organic chemistry. "*The state in which general physics now is, appears, again, particularly favorable to our labors; for natural philosophy, owing to indefatigable and variously directed research, has gradually attained such eminence, that it appears not impossible to refer a boundless empiricism to one (methodical) center.*"

The author wondered how the boundless empiricism of organic chemistry could point to a methodical center and in this way he discovered the NECA hierarchy. NECA raises questions that will be discussed in this contribution. From a technocratic viewpoint these questions will be unimportant and non-relevant. They will not increase technical applications. But we believe that science goes beyond the economic borders of interests and has a massive impact on the public opinion. In this respect, we may not neglect obvious facts even if they exceed the traditional scientific borders. The chemical knowledge is such a vast and massive entity that it is nearly impossible to overview it in all its detail and extract that what is necessary to see all its implications also when it is in your daily environment. Even the NECA structure of organic chemistry, although so evidently once constructed, was until now out of focus. I believe that the chemical community will also accept the evident insights this contribution makes possible. The non-technocratic questions arise from the fact that it is undeniable that a neon electron configuration points to an atomic core and that the mass differences between neutrons and electrons support the general accepted viewpoint that electrons are derived from split neutrons. The NECA structure faces the scientific community with the following unusual question. What is the nature of the core to which this NECA structure points and from which NECA is derived? The nature of organic chemistry knowledge is idealistic and consists of concepts, theories, reactions, mechanisms, … and ideas related to them and all have an origin connected to humans. According to the mass differences between neutrons, protons and the mass of electrons we could expect a NECA core of ideal nature which is about 1800 times more extensive. In this contribution we will make an attempt to search for the human related nature of the NECA core. Normally, an investigation as is described below should be classified as anthropomorphism. But if the neon electron configuration pattern persists at other knowledge structures of the life sciences and in human connected structures, its impact may not be neglected anymore. Therefore, we will try to find this pattern at other levels. First the finger configuration of the human hands will be investigated.

2.3. The NECA Finger Configuration of the Human Hands and Organic Chemistry Fingers

The five electron pairs of the neon electron configuration and the five knowledge pairs of organic chemistry that point to a human related core invites to investigate the configuration of the five finger pairs of human hands. Human hands are most important in bond making actions of humans as are electrons in chemical bonds. The human fingers are sensitive to individual variations. Nevertheless, a common configuration is generally accepted according to the specific name of each

finger. Due to the mirror image shape of both hands, the ten fingers are paired two by two. The implantation of the thumb in the palm of the hand is much lower than the four other fingers. Among the latter four fingers, the implantation of the pinky finger is also clearly lower than the other three fingers (index, middle and ring finger), all three being implanted nearly at the same height. By first inspection, at least 10% of the population shows this implantation pattern. In most people, the index and middle finger are implanted the highest and the ring finger slightly lower. Measurement of distances from the implantation sites of the fingers to the hand carpus shows no significant differences between these two groups of persons. The reason behind this observation is that all humans have both implantation conformations and that we can rather easily switch between them. When folding both hands together (like for praying) each finger on both hands forms a perfectly matching antiparallel pair and as such both hands together form a spherical structure. The implantation pattern of the fingers invites for a comparison with the neon electron configuration pattern. The two paired thumbs correspond to the $1s^2$ electrons; the two paired pinky fingers to the $2s^2$ electrons; and the three other pairs of fingers correspond to the $2p^6$ electrons. The s-character of thumb and pinky finger is indicated by their outside position in the hand. Outside position and lower implantation in the palm of the hand for the thumb and pinky fingers correspond with fundamental 1s and 2s levels of the neon electron configuration as are the 1s and 2s NECA level fundamental in organic chemistry reactions. The thumb is very fundamental for the fine finger skills. SMS-users usually use their thumbs for mobile text editing. The pinky finger strongly resembles the three other fingers just as both the 2s and 2p NECA levels point to reactions and consequently have common properties. The p-orbitals point more to the nucleus than the spherical s-orbitals and correspondingly the three middle fingers also point more to the hand carpus as they are in its extension. The human hands are operational tools for the most versatile types of actions. They point to an acting person. Because of the analogy correspondence between the configuration of human hands and the NECA structure of organic chemistry, NECA indicates organic chemistry in action. The ten knowledge units of NECA are like organic chemistry fingers. Organic chemistry is by this reasoning a potentially acting organism of thoughts that acquires physical hands by the persons who are dedicated to it. Consequently and in reverse, the human hands are the plan model for compound forming forces of the neon electron configuration and for organic chemistry by its NECA structure. The analogy between human fingers and the neon electron configuration invites us to search for chemical fingers next to the NECA organic chemistry fingers. The most typical molecules in actions are proteins. The next section demonstrates such a search for protein fingers.

3. Proteinogenic Amino Acid Fingers

In biochemistry, proteins are the acting agents by excellence. There is no biochemical function possible without direct influence or action of proteins. Proteins operate in the first place by means of the 20 proteinogenic amino acid residues. Secondly, proteins act by mean of non-protein cofactors (prosthetic groups), just like humans act with tools. We may say that proteins act, handle, by hand and feet and have therefore 20 fingers; i.e. 20 amino acid side chains. If we observe the immense difference in the way of action between proteins and humans, a perfect match between human fingers and amino acid side chains may look utopic but we nevertheless will try to demonstrate it. Three arguments will be discussed to convince even the most skeptics. First, we must find four hands that each demonstrates five amino acid fingers. The number of fingers and toes is already in accordance with the number of amino acids. The four protein hands are a division of amino acid side chains in four groups. Figure 2 shows these four groups: 1) non-cyclic non polar-, 2) non-cyclic uncharged polar-, 3) non-cyclic charged polar- and 4) cyclic side chains.

The division is not yet used, but is nevertheless very logical. This unusual division is made possible by the amino acid formulas. These formulas convince or they do not. The following will show to what extent they will convince. In each group, we look from left to right for the corresponding thumb, index, middle, ring, and pinky amino acid finger. The most deviating amino acid is chosen as the thumb and the smallest as the pinky finger. In group 3, cysteine not only deviates by its sulfur element, but also because it is only partly charged at physiologic pH. In group 4, proline cannot be depicted as a side chain and it causes rigidity in the protein conformation, therefore it is the most deviating in its group and corresponds to a protein thumb. Group 4 puts histidine on the ring finger position because of its structural correspondence with tryptophan, although it is somewhat smaller than phenylalanine. Histidine greatly deserves the ring finger position according to its most important functionality. Best known are the distal and proximal histidines in hemoglobin. Each group contains, apart from the thumb, two pairs of amino acids that resemble each other most. One pair corresponds to the middle and ring fingers and the other pair to the index and pinky fingers. The second and third argument will be discussed together and are regarding the correspondence of the two structural related amino acid pairs with the chosen fingers. Two properties of the real fingers not including the thumb will demonstrate the choice of these two pair amino acid fingers. For most people, there is a correspondence in the decreasing length of respectively middle, ring, index and pinky fingers with the chain length of the corresponding amino acid fingers, except the already mentioned histidine position in group 4. The histidine exception demonstrates the human finger length exceptions on the normal finger length distribution. The index finger can point most easily from the fist out to a specific direction without causing strain on the other fingers that must stay in the fist position. Repeat this experiment with the other fingers except for the thumb. The other fingers can also point to the same specific direction but with increasing strain for respectively pinky finger, middle and ring finger. Both properties, chain length and pointing strain, stress the connection between the index and pinky finger pair. Consequently, middle and ring fingers form the second pair. These two finger pairs correspond with the two pair

of structural related amino acid fingers in each of the four amino acid groups (hands). In this way, we convincingly sort the 20 proteinogenic amino acids into four hands that each has five clearly defined amino acid fingers. Consequently and in reverse, the human hands are the plan model for protein function because the amino acid sequence determines the protein conformation, which determines the function.

In this comparison, the chirality of human hands is not demonstrable. Protein fingers do not have the same mirror symmetry of our two hands, but 19 of them occur as L-amino acids. In some way, protein functioning resembles human functioning. Managers, estate agents, teachers… act comparable as enzyme proteins, they all catalyze the process in which they are involved. The analogy correspondence between amino acids side chains and human fingers that show a NECA structure in the human hand may be of use in predicting protein conformations from amino acid sequences or in explaining solved protein conformations.

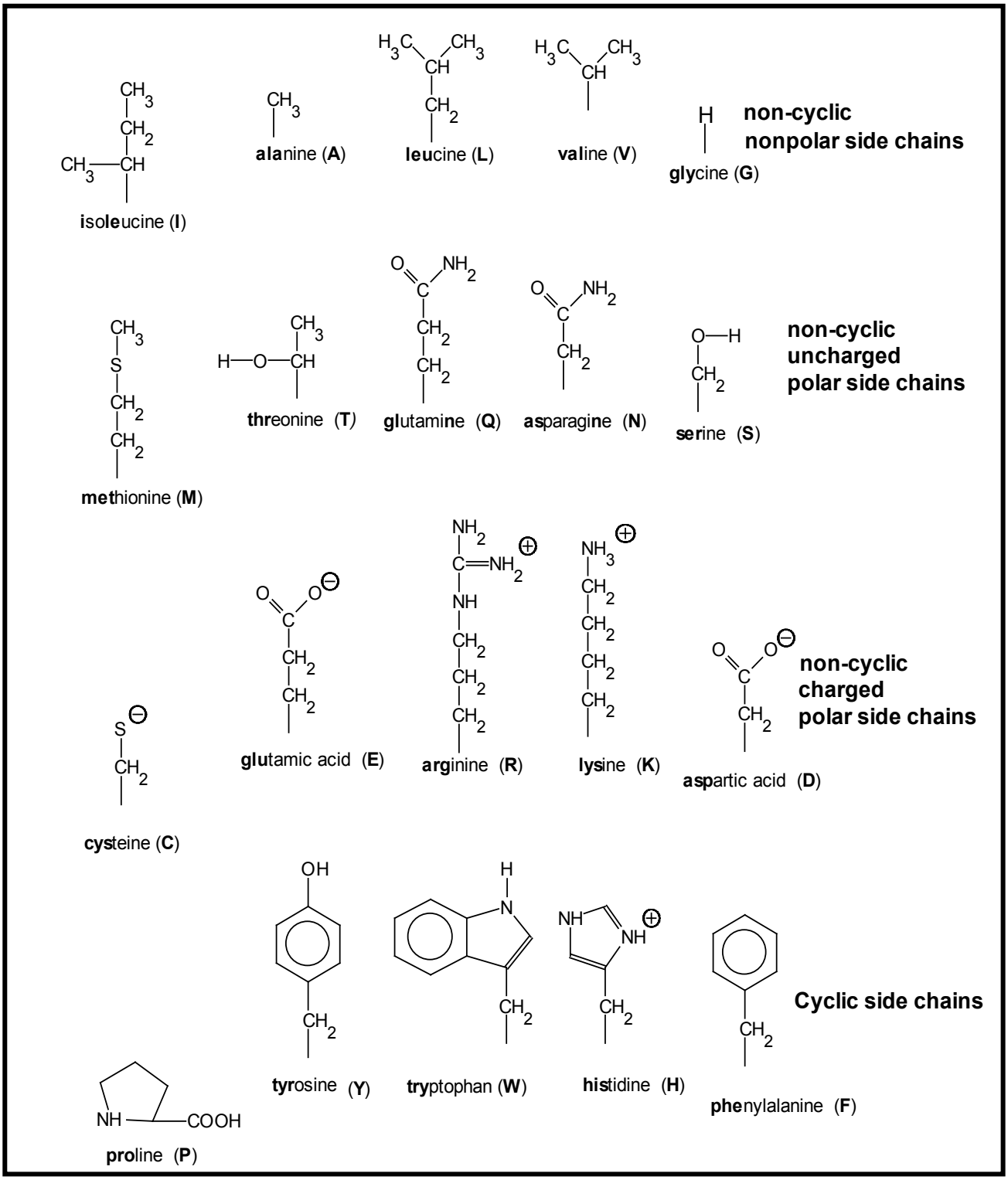

Figure 2. The proteinogenic amino acid fingers

4. Periodic Table Fingers

The search for periodic table hands and feet needs four extraordinary groups of chemical elements, periods or groups. The number of chemical periods is not in line with such a search. Periodic table fingers and toes are ideally searched for among the elements that are essential for the human body. Unfortunately, the search for essential chemical elements is not completely finished. Some of the proposed essentials may have only a positive influence on life. Ten essential elements clearly can be sorted into two groups of five elements. The first group of five elements is composed of the five elements in the proteinogenic amino acids: C, H, O, N and S. The second group contains the ion forming elements in main groups: Na, K, Mg, Ca and Cl. The next ten elements are: P, Fe, Zn, Co, I and Cr, Cu, Mn, Mo, Se. These 20 essential elements are in line with most essential element tables. Unfortunately, the basis on which the latter ten elements could be sorted in two groups is less clear and some research will claim additional essentials.

The periodic table groups are a second way for detecting a correspondence to fingers and toes. We should find twenty groups sorted into four related super sets composed of five periodic table groups. The standard periodic table is divided into 18 groups. If we would extract the lanthanides and the actinides as separate groups, we already would have the necessary twenty groups. Four logical super sets are not easily formed with these 20 groups. Furthermore, lanthanides and actinides are not very relevant for the life sciences. Another option seems to be inevitable. It has always been a problem to sort hydrogen into a group of the periodic table. Hydrogen does not match the group 1 (IA) properties and is so dominantly present in the biosphere that hydrogen deserves the status of a separate group. Helium, the noble gas configuration of hydrogen in its compounds, deviates by its non-octet structure from all other noble gases and therefore needs to share the same status as hydrogen. Hydrogen and helium are evolutionary the cosmic source elements by excellence. The latter determination further supports the choice of hydrogen and helium as extraordinary groups. By this reasoning, we also obtain the necessary twenty groups. How can we sort them in four logical limb representing sets of five groups? The ten transition metal groups are rather logically split into two sets of five groups. One from group 3 (IIIB) to group 7 (VIIB) and the other from group 8 (VIIIB) to group 12 (IIB). A third set contains the groups 1 (IA), 2 (IIA), 16 (VIA), 17 (VIIA), and 18 (VIIIA) except helium. This set contains the typical ion forming elements and connects them to their corresponding noble gases. The last set contains groups 13 (IIIA), 14 (IVA), 15 (VA), hydrogen and helium. The first two sets contain most oligo elements and the last two super groups contain all the macro elements of the human body and most macro elements of the earth. By this organization, the macro elements connect humans to the earth and make sets three and four resembling the feet. Whereas the transition elements are cofactor tools in protein including enzyme functions, which will be better manipulated by hands.

5. The Human Arm and Hands Model for the Genetic Code Developmental Structure

Our investigation on the genetic code developmental structure is restricted to the universal or standard code and to the vertebrate mitochondrial code. These two codes also apply to humans. Most genetic code variants are mitochondrial variants and a few are nuclear variants [11]. The variants are situated in invertebrates and micro-organisms. It is remarkable how little the various variants differ from each other and from the standard code. In open access, the quest for the origin of the genetic codes is reviewed in reference [12]. Strongly simplified, the focus of the search for the origin is mainly based on evolutionary connections and on structural properties of the coded amino acid residues. The connections between the two vertebrate codes (mitochondrial and nuclear) are mostly reduced to a simple statement of the differences. We investigate the structural connection between the two vertebrate codes and present this connection as “the genetic code developmental structure”. Both codes operate in the same cells and, as a logical consequence, they are structural connected. In this section, we will discover this structural connection. We will make use of a genetic code table that is helpful in making the investigated connections clear. This table is an original genetic code table for the combined mitochondrial and universal genetic codes of vertebrates.

5.1. Vertebrate Mitochondrial and Universal (Standard) Nuclear mRNA Genetic Code in one Table

Table 1 is mainly based on synonymous codon structures or codon variables. The sixteen combinations of the first and the second nucleotide (ab combinations) of a codon triplet are shown in columns one and three. The column headings abN, abPy and abPu are codon variables that indicate for each ab combination respectively 4, 2 and 2 synonymous codons with respectively the four nucleotides (N) as the third base or the two pyrimidines (Py) U and C or the two purine (Pu) bases A and G. A spliced abN variable corresponds to two abPy and two abPu codons. Column two shows 32 codons for eight amino acids, which is half of all the 64 codons. The mitochondrial and the universal code are identical in the non-colored cells. Turquoise highlight is specific for the mitochondrial and yellow highlight is specific for the universal code. The mitochondrial code is fully described with abN, abPy and abPu codons. The number of each the abPy and abPu mitochondrial codons is of course 16. The 4 mitochondrial stop codons are abPu codons; CCPu and UCPu. Amino acids that have six synonymous codons are in bold text.

5.2. Genetic Code Developments

The investigated genetic code structure is the result of a development process. The comparison of the mitochondrial and the universal code indicates a development from mitochondrial towards universal code. Both codes have

two paired development steps in common: The abN and the spliced abN codons. Half of the mitochondrial code (32 codons) consists of 8 ab combinations of abN structure (8 times four synonymous codons). The other half (32 codons) consists of 8 ab combinations of the spliced abN structure (8 times two synonymous abPy and 8 times two synonymous abPu codons). The next step is the transformation of the mitochondrial code into the universal code. In this transformation one abPy and three abPu mitochondrial codon pairs are concerned corresponding to eight codons; respectively, the AUPy Ile codons, the AUPu Met codons, the UGPu Trp codons and the AGPu stop codons. Five universal codons that code for amino acids: one AUG Met codon, one UGG Trp codon, and three AU(N-G) Ile codons, and also the UAG stop codon, do not show the abPy and abPu structure anymore. In Table 1, they are shown at the bottom of the table. After the transformation, the number of paired abPy and abPu nuclear codons is respectively 14 and 12. The mitochondrial isoleucine codon pair is converted to three codons for the nuclear code at the expense of one mitochondrial AUA Met codon. The genetic code development progresses from the more general codon variables (abN, abPy and abPu) to specific codons. The common operation site of both vertebrate codes (in the same cell) and the overlapping common structure (described in this section) support the idea that both codes have a common origin.

Table 1. Vertebrate Mitochondrial and Universal Nuclear mRNA Genetic Code in one Table

		Spliced abN		
ab	abN	ab	abPy	abPu
GC	Ala, A	UU	Phe, F	**Leu, L**
CG	**Arg, R**	AA	Asn, N	Lys, K
GG	Gly, G	GA	Asp, D	Glu, E
CU	**Leu, L**	CA	His, H	Gln, Q
CC	Pro, P	UA	Tyr, Y	stop
UC	**Ser, S**	AG	**Ser, S**	**Arg, R** stop
AC	Thr, T	UG	Cys, C	Trp, W
GU	Val, V	AU	Ile, I	Met, M
No of AA	8		7 8	5 6
ab	G	A	(N-G)	
UG	Trp, W	stop		
AU	Met, M		Ile, I	

Table legend: see section 5.1.
ab is the first and the second nucleotide of a codon triplet.
U, C, A and G are the single letter abbreviations for nucleotides.
N, Py and Pu represent respectively four, two pyrimidine and two purine nucleotides as third base in a codon triplet.
AA is amino acids. The 20 AA are shown in three and one letter abbreviations, AA full names are in Figure 2.
Turquoise highlight is specific for the mitochondrial and yellow highlight is specific for the universal code.
Amino acids that have six synonymous codons are in bold text, except. the four mitochondrial Arg codons.

5.3. The NECA Structure of the Genetic Code; Connection to the Neon Electron Configuration and the Human Hands

The described genetic code development resembles in its structure the neon electron configuration. The general abN and the spliced abN codon variables are the fundamental ideas of the genetic code but not yet specific codons, they are the 1s level of the genetic code structure. From the 8 mitochondrial codons that are connected to the universal code transformation by their corresponding codon variables, the two paired AUPy codons correspond to the 2s level and the 6 remaining codons, the 2p level, of the transformation are three pairs of abPu codons. In Table 1, the turquoise color for the specific codons of the mitochondrial code stress attention on this 2s and 2p level structure. By this, we demonstrate the NECA structure of the genetic code structure and indicate its core origin (compare with section 2.2. The NECA Core). Previously, we already have described the connection between the neon electron configuration and the structure of the human hands. In this way, the human hands also model the genetic code.

5.4. Connection to the Structure of a Human Arm

The numerical properties of the genetic code development are numerical analogous to the development of the number of bones in a human arm limb from upper arm to fingertips (1, 2, 8, 5 and 14). Note that the abN variable corresponds to one bone (the humerus) and the two spliced abN variables to two bones (radius and ulna). The 8 mitochondrial codons connected to the nuclear transformation correspond to 8 wrist carpels, the 5 nuclear codons of the transformation that code for amino acids correspond to 5 meta carpels and the 14 nuclear abPy codons correspond to the 14 phalanges. The transition between each step of the genetic code development corresponds to a limb joint. In summary, the bones and connected joints are: humerus, elbow, radius and ulna, wrist, 8 wrist carpels, hand joint, 5 meta carpels, finger joint and 14 finger(thumb)phalanges including the interphalangeal joints. The number of wrist carpals (8) and of ankle tarsals (7) differs. A few tarsals grown together during embryonic development because of the more specialized function of the food compared to the more flexible hand. The genetic code development may be of use for a Goethean metamorphose study of the bones for a human arm limb. The UAG stop codon is not part of the mitochondrial code but is a result of the transformation into the standard code, it possibly indicates also the stop of the bone metamorphose in the human arm.

6. Conclusion

The human hands are the model for five major chemistry principles that are basic to the life sciences: The compound forming forces of the neon electron configuration, the periodic table, organic chemistry structure, the twenty proteinogenic amino acid fingers that determine protein function, and the human hands and arm structure in the genetic code developmental structure. Consequently, the human hands model five essential levels in the hierarchy of the life sciences chemistry. The NECA structure of the vertebrate codes points to a core origin in a similar way as the NECA structure for organic chemistry and the NECA structure for the implantation sites of the human fingers. Possibly the same holds for the 20 proteinogenic amino acid side chain fingers.

This contribution invites for further research to detect human connected structures in chemistry and in the life

sciences. The neon electron configuration analogy of human hands together with the proteinogenic amino acid fingers is possibly of use in predicting protein conformations from amino acid sequences or in explaining solved protein conformations.

Abbreviation

NECA Neon Electron Configuration Analogy

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