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According to Quantum Perspective Model, Is Euler's Identity also Meaningful in Biochemistry?

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Abstract

According to Quantum Perspective Model, this article researches whether there is a link between the Euler's identity and the genetic sequences. At first, Euler's identity is squared (See Figure-1). Then, the digits of pi number after the comma are sequenced "TCGATTATACTGGTTGGTTTTAACGGTAC"[18]. Secondly, the resulting sum corresponds to the nucleotide bases, the results obtained in this way are expressed as nucleotide bases. (A, T, C, G, and U). (A)Adenine, (T) Thymine, (C) Cytosine, (G) Guanine, (U) Uracil. From this point of view, the reason pi number's sequence is written twice is because Euler's identity is squared. Then, add Euler's nucleotide bases [7] to this gene sequence respectively, the result is obtained by:[AAAGGUCCGUUUAAUAAGUUAAAUUUAGGU].Thirdly, after researching this sequence at NCBI (National Biotechnology Information Center), the search result is similar to Danio Rerio (Zebra fish),Danio Kyathit and even Timema. Fourthly, the genetic codes of Zebra fish have been proven to be very similar to human genetic codes. Lastly, Even Timema reproduces asexually. As a result, Euler's identity is not only related to irrational numbers in Mathematics, but also to genetic codes in Biochemistry.

Key words: Quantum Perspective Model; Danio Rerio; Euler's identity; NCBI (National Biotechnology Information Center); Timema.

1. Introduction

In this research, genetic codes were used as a new formula (Nirenberg and his colleagues 1965) just like as (**A**, **T**, **C**, **G**, **and U**). (**A**)Adenine, (**T**) Thymine, (**C**) Cytosine, (**G**) Guanine, (**U**)Uracil. Before this work, the fourteen group of Pi number can be shown as: Continuous UTA's by [4].Secondly, another favorite sample of this research is done with velocity of light numbers by [3]. This relationship between the numbers and genetic codes is called **Quantum Perspective Model** by [4].

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Thirdly, in another article with identical cis regulatory elements examined the links between the Golden Ratio numbers [6].Fourthly, there is a connection between Euler numbers and the Fibonacci series. When the numbers of Euler after the comma were converted from a decimal (10) number-based system to a binary (2) number-based system, they corresponded to the number "55" in the Fibonacci series.Fifthly, there is a link between the square root of **two**, the square root of **three** and the square root of **five** numbers and the genetic codes. After all these studies, pi numbers and the genetic codes were investigated in relation to the **Quantum Perspective Model** [18]. The results obtained in this way were expressed as nucleotide bases as follows:" **TCGATTATACTGGTTGGTTGTTAACGGTAC**" [7].Now, Euler's equation (See **Figure-1**) and the genetic codes are now being investigated in relation to this Model.

2. Methods and discussion

The chemical structures of bases include Carbon(C), Nitrogen (N), Oxygen (O) ,and Hydrogen (H).Calculation of bases with chemical atoms (See also **Table-1**).(Ölmez T,2020)

Table 1: Representation of nucleotide b	bases (A, T, C	C, G and U) in	chemical atoms
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ATOMS /NUCLEOTIDE BASES	С=6	H=1	<i>O=8</i>	N=7	SUM
ADENINE: C5H5N5	5	5	-	5	70
THYMINE: C5H6N2O2	5	6	2	2	66
CYTOSINE: C4H5N3O1	4	5	1	3	64
GUANINE: C5H5N5O1	5	5	1	5	78
URACIL : C4H4N2O2	4	4	2	2	58

The atomic numbers of them: Carbon(C):6, Nitrogen (N):7, Oxygen (O):8, Hydrogen (H):1 (Wieser E M and his colleagues 2013). The chemical structures of bases (A, T, C, G, and U) are shown at below [6].

(A)Adenine: C5H5N5:70;

(T)Thymine: C5H6N2O2:66,

(C)Cytosine: C4H5N3O1:64,

(G)Guanine: C5H5N5O1:78, and

(U) Uracil: C4H4N2O2: 58

(Lodish H and his colleagues 2018).

Before this study, some of the irrational numbers were researched as in pi numbers[4], the golden ratio numbers[6], Euler's numbers[7], the square root of number two[16], the square root of number three[17] and the square root of number five [18]. According to Quantum Perspective Model, the meanings of Pi number is forever UTA's [(U)Uracil, (T)Thymine and (A)Adenine, 4]. Also the sum of chemical formulas of TATA and CAAT Box is nearly as the same as the golden mean numbers of "618". (Remember, approximately the golden ratio is

1,618) [6].Besides, after the comma, **Euler**'s eighteen fifteen-group numbers are converted to nucleotide bases. The results obtained in this way are expressed as nucleotide bases as follows:"AUGUUGAUAUTAAUCATC" [7] Pi numbers and genetic codes have been studied in relation to the quantum perspective model [18]. The results obtained in this way were expressed as nucleotide bases follows: as "TCGATTATACTGGTTGGTTTTAACGGTAC" In Quantum field theory, the theoretical aspects of Reflection positivity were discussed by Nebb K.H. and Olafsson G. in connection with different scientific fields. In quantum physics, reflection positivity is often associated with Wick rotation, which means multiplying the time coordinate by the imaginary unit "i" to provide a way to commute between real and unusual time [16]. That's why, in this article, when multiplying with imaginary unit "i", genetic sequence is converted from "T" Thymine to "U" Uracil (See, Table-2).

3. Calculation of euler's identity and genetic codes

e is Euler's number, *i* is the imaginary unit, π is <u>pi</u>.

Pi numbers nucleotide bases: "TCGATTATACTGGTTGGTTTTAACGGTAC"[18].

Euler's numbers nucleotide bases:" AUGUUGAUAUTAAUCATC" [7] Since Euler's identity [1] includes many irrational numbers, this article will also be examined within the framework of genetic codes. In Euler's equation; triple codons are needed to make sense in terms of genetic code sequence. Therefore, Euler's identity is squared (See Figure-1). Thus, meaningful conclusions are drawn from Euler's identity. Adenine (A) pairs with Thymine (T) by *two* hydrogen bonds. Cytosine(C) - Guanine (G) pairs with by *three* hydrogen bonds [10].That's why, base pairs of DNA codons are written in third row " $2\pi i$ bases". Euler's nucleotide Bases: "AUGUUGAUAUTAAUCATC" [7] (See, *e* bases, **Table-2**). After adding "*e* bases" to " $2\pi i$ bases, the fifth row in the table, respectively, is obtained, the basis of Euler's identity with Thymine. Lastly, because the absence of Thymine in Universal Genetic Code Table[15],Instead of "T" Thymine, "U" Uracil were used. The result is as follows: **AAAGGUCCGUUUAAUAAGUUAAAUUUAGGU**. (The sixth row in the table Euler's identity bases with Uracil, See **Table-2**). This result is searched in the NCBI Blast database; the results are also significant and related to Biochemistry [14].

π bases	Т	С	G	А	Т	Т	А	Т	А	С	NOTE	
2π bases (<i>twice</i>)	TT	CC	GG	AA	TT	TT	AA	TT	AA	CC	NOIE: Instead of	
2π i* (" <i>REVERSE</i> ") bases	AA	GG	CC	TT	AA	AA	TT	AA	TT	GG	$\begin{bmatrix} m_{sieud} & 0 \end{bmatrix}$	
<i>e</i> bases	Α	U	G	U	U	G	Α	U	Α	U	Thymine use " U "Uracil.	
Euler's identity bases with Thymine	AAA	GGU	CCG	TTU	AAU	AAG	ТТА	AAU	ТТА	GGU	absence of Thymine in	
Euler's identity bases with Uracil	AAA	GGU	CCG	UUU	AAU	AAG	UUA	AAU	UUA	GGU	Universal Genetic Code Table [15].	

Table 2: Representation of codons of Euler's identity "AAAGGUCCGUUUAAUAAGUUAAAUUUAGGU"

4. Results

After searching for Euler's identity in National Biotechnology Information Center (NCBI) databases, some conceptual relationships with bony fish can be found [13]. Types of bony fishes (Orbiculate cardinal fish, zigzag eel, Echeneis naucrates) are based on DANIO RERIO (Zebra fish) (See Figure-2). Because Danio Rerio, one of the results obtained, was one of the creatures resembling the human gene. Types of other living creatures are Timema shepardi, Timema douglasi, Timema bartmani, Timema poppensis, Timema cristina, Timema tahoe Danio Kyathit and Danio aesculapii. Another interesting result of NCBI is Timema (See Figure-3). The longest known asexual period for Timema, including two species that have not engaged in sexual reproduction for a million years [11]. Asexuality in animals is rare, and the Timema-insect lineage that evolved without sex has been proven to have survived for centuries and even Timema reproduces asexually [12]. Types of other living creatures are cats, alligators, flies, ants, tomato, Japanese rice fish, birds, musk melon and potato [13]. The NCBI Blast result is: AAAGGUCCGUUUAAUAAGUUAAGUUAAGU. The "stop" codon (UAA) in the universal genetic code table [15] is found twice in this gene sequence in reversed form (AAU). Euler's equation mostly consist of pi number " π ", Euler number "e" and imaginary unit "i" [1]. Until now, some of this irrational numbers have been researched as in pi numbers [4,18] and Euler numbers [7]. But since no study has been done so far between the imaginary unit "i" and the genetic codes, new research to shed light on Euler's theorem in the future may contribute to achieving new results.

5. Conclusion

At first, the results of this research can be summarized as taking Euler's identity as the chemical structure of genetic codes. Secondly, the digits of Euler's identity can be considered as an indicator of genetic codes. One result of the common features of both Biochemistry and Mathematical Science was the NCBI blast results, which include both **bony fish** and, in particular [8]. Zebra fish are an excellent favorite sample used in many studies related to Biochemistry and genetics [4]. Another NCBI blast result of Euler's identity is Timema which is well known by asexual reproduction [13]. The definition of a hyper-complex number by Kantor and Solodovnikov (1989) is given as elements of a finite-dimensional algebra over real numbers generated by a real number coefficients $\{-1, 0, +1\}$ [2]. So, one of the result of hyper-complex numbers is $\{-1\}$ can be the meaning of "REVERSE" as regarding to the imaginary unit. From this perspective, NCBI Blast result of the Euler's equation is "AAAGGUCCGUUUAAUAAGUUAAAUUUAGGU". In the Universal Genetic Code Table [15], the" stop " codon (UAA) can be explained twice in this gene sequence in the opposite form (AAU). Another reason of this reverse reading can be stem from, gene expression, RNA polymerase can only read the DNA strand in the 3' to 5' direction and synthesizes the DNA strand in the 5' to 3' direction [17]. In sum, in this article, when the Euler's equation is analyzed in terms of genetic codes with the "Quantum Perspective Model", correlated results are obtained. These results have revealed new clues in filling the gaps between sciences and especially between Mathematics and Biochemistry.

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The figures

 $l\pi$

Figure 1: The Euler's identity.

last.ncbi.nlm.nih.gov/Blast.cgi								<u>s</u>
Solanum pennellii chromosome ch12, complete genome	Solanum pennellii	38.2	726	63%	10	100.00%	83305730	HG975451.1
Clostridium saccharobutylicum DSM 13864, complete genome	Clostridium sac	38.2	38.2	63%	10	100.00%	5107814	CP006721.1
Candidatus Endolissoclinum faulkneri L2, complete genome	Candidatus End	38.2	38.2	63%	10	100.00%	1481191	CP003539.1
Secondary endosymbiont of Heteropsylla cubana isolate Hcub_S chromosome, complete genome	secondary endo	38.2	38.2	63%	10	100.00%	1121596	CP003547.1
Peptoniphilus harei strain FDAARGOS_1012 chromosome	Peptoniphilus h	38.2	38.2	63%	10	100.00%	1791970	CP066287.1
4_ <u>Tbi_b3v08</u>	<u>Timema bartmani</u>	38.2	38.2	63%	10	100.00%	411198	OD564470.1
1_Tps_b3v08	Timema poppe	38.2	38.2	63%	10	100.00%	117750	OD001446.1
4_Tbi_b3v08	<u>Timema bartmani</u>	38.2	38.2	63%	10	100.00%	144639	OD565974.1
3_Tce_b3v08	<u>Timema cristinae</u>	38.2	38.2	63%	10	100.00%	1398624	OC316483.1
4_Tte_b3v08	<u>Timema tahoe</u>	38.2	38.2	63%	10	100.00%	136203	OE002103.1
4_Tte_b3v08	<u>Timema tahoe</u>	38.2	38.2	63%	10	100.00%	229159	OE000838.1
2 <u>Tsi_b3v08</u>	<u>Timema shepardi</u>	38.2	38.2	63%	10	100.00%	182818	OC001199.1
1_Tdi_b3v08	<u>Timema douglasi</u>	38.2	38.2	63%	10	100.00%	360562	OA564485.1
1_Tdi_b3v08	<u>Timema douglasi</u>	38.2	38.2	63%	10	100.00%	443415	OA564377.1
Solanum tuberosum cultivar Solyntus chromosome 1	Solanum tubero	38.2	106	80%	10	95.65%	59557243	CP055234.1
Danio rerio genome assembly, chromosome: 13	Danio rerio	38.2	402	76%	10	100.00%	52957805	LR812050.1
Danio rerio genome assembly, chromosome: 13	Danio rerio	38.2	335	73%	10	100.00%	52210330	LR812606.1
Danio rerio strain Nadia (NA) genome assembly, chromosome: 13	Danio rerio	38.2	368	76%	10	100.00%	54512446	LR812581.1
Danio rerio strain Cooch Behar (CB) genome assembly, chromosome: 13	Danio rerio	38.2	305	73%	10	100.00%	52525257	LR812556.1
Danio aesculapii genome assembly, chromosome: 3	Danio aesculapii	38.2	271	66%	10	100.00%	62918972	LR812517.1
Tetragenococcus halophilus NBRC 12172 DNA, complete genome	Tetragenococcu	38.2	38.2	63%	10	100.00%	2562720	AP012046.1
Cyanothece sp. PCC 7822 plasmid Cy782206, complete sequence	Gloeothece verr	38.2	38.2	63%	10	100.00%	13777	CP002204.1
Solanum tuberosum cultivar MSH/14-112 chromosome 5	Solanum tubero	32.2	64.4	60%	642	100.00%	52062733	CP046698.1

Figure 2: The NCBI (National Biotechnology Information Center) Result for Nucleotide Sequence "AAAGGUCCGUUUAAUAAGUUAAAUUUAGGU" [13].

		query
^a Gossypium tur	neri isolate D10-2 chromosome D10_02	from type material
lcl Query_513		Show removed seqs
	Salmonella enterica subsp. enterica serovar Bareilly strain RSE03 chromosome, complete genome	Blast names color map
	Clostridium saccharobutylicum strain NCP 258, complete genome	eudicots
	PREDICTED: Lactuca sativa pentatricopeptide repeat-containing protein At2g03880, mitochondrial (LOC111896215), mRNA	unknown
	Oryzias latipes strain HSOK chromosome 5	enterebacteria
	Multiple organisms 80 leaves	firmicutes
	Gossypioides kirkii chromosome KI 11	bony fishes
	Becheneis naucrates genome assembly, chromosome: 3	walking sticks
	Mastacembelus armatus genome assembly, chromosome: 21	chlamydias
Ť.	Solanum lycopersicum cultivar I-3 chromosome 9	birds
	Strongyloides stercoralis genome assembly S stercoralis PV0001, scaffold SSTP contig0000046	cyanobacteria
	Solanum pennellii chromosome ch12, complete genome	ants
	Candidatus Endolissoclinum faulkneri L2, complete genome	fusobacteria
	Secondary endosymbiont of Heteropsylla cubana isolate Hcub S chromosome, complete genome	a-proteobacteria
	Danio aesculapii genome assembly, chromosome: 3	carnivores
	Clostridium saccharobutylicum strain NCP 195, complete genome	flies
	Clostridium saccharobutylicum strain BAS/B3/SW/136, complete genome	nematodes
	Clostridium saccharobutylicum strain NCP 200, complete genome	monocots
	Culicoides sonorensis genome assembly, scaffold: scaffold53	bivalves
	Solanum lycopersicum chromosome ch09, complete genome	vertebrates
	Clostridium saccharobutylicum DSM 13864, complete genome	CFB group bacteria
	Nodes 201(0 selected) 🧠 View port at (0,0) of 1178x426	

Figure 3: The NCBI (National Biotechnology Information Center) Result Blast Tree View Widget for "AAAGGUCCGUUUAAUAAGUUAAAUUUAGGU" Nucleotide Sequence [13].