

Can Irrationality in Mathematics Be Explained by Genetic Sequences as in the Square Root of Ten?

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Abstract

One of the irrational numbers is the square root of ten number. This article researches whether there is a link between the square root of ten number and the genetic sequences. At first, the square root digits of the number ten after the comma are summed one by one. Secondly, the result of the addition corresponds to the nucleotide bases. Thirdly the results thus obtained are expressed as nucleotide bases (A, T, C and G). (A) Adenine, (T) Thymine, (C) Cytosine and (G) Guanine. From this point of view, approximately when the first four hundred digits of the square root of the number ten after the comma are calculated, the resulting gene sequencing is as follows:

[ATAAGTCATAAGTGTATTAGTTTAAAACTG]. Fourthly, at this time, some repetitions were detected exactly like this: as "AGT" and "ATA". Fifthly, after searching this sequence in NCBI (National Biotechnology Information Center), the search result was similar to bony fish, especially *Danio aesculapii*. Lastly, *Danio aesculapii* species is closely related to Zebra fish. In summary, With these results, not only the square root of ten in mathematics, but also many other irrational numbers (as explained by the similar QUANTUM PERSPECTIVE MODEL in previous articles), adding a common perspective to these different sciences; the connection between genetic codes in biochemistry and irrational numbers in mathematics is meaningful and has revealed very valuable results. In other words, with this novel research, a new window has been opened that can lead to new interdisciplinary discoveries.

Subject Areas

Biochemistry, Mathematics, Number Theory

Keywords

Quantum Perspective Model, Danio Kyathit, Danio aesculapii, The Square

Roots of Ten and NCBI (National Biotechnology Information Center)

1. Introduction

Prior to this study, Kevser Köklü had published articles on the Quantum Perspective Model, not only about the square of the speed of light numbers [1], but also with Pi numbers with nucleotide base coded [2]. In addition to these; Pi numbers once again extended version [3], golden ratio numbers [4], Euler numbers [5], square root of two numbers [6], square root of three numbers [7], square root of five numbers [8], square root of seven numbers [9] and Fibonacci numbers [10] were also published by Tahir ÖLMEZ. In summary, the codes of all these irrational numbers (mentioned above) explained by a genetic sequence can be found in this diagram. One of these codes is

[ATAAGTCATAAGTGTATTAGTTTAAAACTG] for the square root of ten number. In sum, this paper attempts to explain whether there is a relationship between the square roots of ten and genetic codes or not? Let's try to explain these similarities and relations of irrational numbers according to genetic sequences.

2. Methods and Discussion

2.1. Methods

In this work, the chemical formulas of nucleotide bases are calculated with regards to atomic numbers of elements. 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) [4].

The atomic numbers of them: Carbon (**C**): 6, Nitrogen (**N**): 7, Oxygen (**O**): 8, Hydrogen (**H**): 1 (Wieser E M *et al.*, 2013) [11]. The chemical structures of bases (**A**, **T**, **C** and **G**) are shown at below (Ölmez T, 2020) [4].

(A) Adenine: C₅H₅N₅: **70**; (T) Thymine: C₅H₆N₂O₂: **66**, (C) Cytosine: C₄H₅N₃O₁: **64**, (G) Guanine: C₅H₅N₅O₁: **78** (Lodish H *et al.*, 2018) [12].

2.2. Discussion

First of all, a paper about Golden Ratio numbers was researched [4]. Then, according to the Quantum Perspective Model, the connection between the

ATOMS/NUCLEOTIDE BASES	C = 6	H = 1	O = 8	N = 7	SUM
ADENINE: C ₅ H ₅ N ₅	5	5	-	5	70
THYMINE: C ₅ H ₆ N ₂ O ₂	5	6	2	2	66
CYTOSINE: C ₄ H ₅ N ₃ O ₁	4	5	1	3	58
GUANINE: C ₅ H ₅ N ₅ O ₁	5	5	1	5	78

Table 1. Representation of nucleotide bases (A, T, C, G) in chemical atoms.

square root of the two [6]/three [7]/five [8]/seven [9] numbers articles were published. Nextly, the relationships between the Pi numbers [3] and Euler's Identitiy [13] and and genetic codes were published. Now, the square root of the number ten and its genetic codes are calculated by this paper.

Based on the square root of 10, it can also be obtained as follows: the square root of two [6] is multiplied by the square root of five [8]. The genetic sequence of the square root of the two number is [GGATGACTACGGG**TTT**AGAAA] [6]. The genetic sequence of the square root of the five numbers is

[ATTTATTCAATACATAACCCCATTGA] [8]. But the genetic sequence of the square root of the ten number is

[ATAAGTCATAAGTGTATTAG**TTT**AAAACTG]. The common feature of these sequences is "**TTT**". Now, According to Standard Dna Codon Table, it is Phenylalanine amino acid [14].

3. Calculation of the Square Root of Ten Numbers and Genetic Codes

The first three hundred digits of the square root of ten after the comma are here: The square root of 10 =

 $3.162277660168379331998893544432718533719555139325216826857504852792\\59443863923822134424810837930029518734728415284005514854885603045388\\00146905195967001539033449216571792599406591501534741133394841240853\\16929577090471576461044369257879062037808609941828371711548406328552\\99911859682456420332696160469131433612894979189026652954361267617878\\13500613881862785804636831349524780311437693346719738195131856784032\\3124179540221830804587284461460025357757970282864402902440$ [15].

At first, the first group of the square root numbers of ten after comma was taken. For example 1, 6, 2, 2, 7, 7, 6, 6, 0, 1, 6, 8, 3, 7, 9... and so on. Secondly, all decimal numbers are subjected to the addition process, respectively.

(1+6+2+2+7+7+6+6+0+1+6+8+3+7+9 = 71). The sum of the first group of the root square numbers of ten after comma is "71". Just like as in (A) Adenine: 70 (See also Table 1).

The **first** group of the root square numbers of ten after comma: 1+6+2+2+7+7+6+6+0+1+6+8+3+7+9 = 71 (**A**) Adenine: 70 The **second** group of the root square numbers of ten after comma: 3+3+1+9+9+8+8+9+3+5+4+4 = 66 (**T**) Thymine: 66 The **third** group of the root square numbers of ten after comma: 4+3+2+7+1+8+5+3+3+7+1+9+5+5+5+1 = 69 (**A**) Adenine: 70 The **fourth** group of the root square numbers of ten after comma: 3+9+3+2+5+2+1+6+8+2+6+8+5+7+5 = 72 (**A**) Adenine: 70 The **fifth** group of the root square numbers of ten after comma: 0+4+8+5+2+7+9+2+5+9+4+4+3+8+6 = 76 (**G**) Guanine: **78** The **sixth** group of the root square numbers of ten after comma: 3+9+2+3+8+2+2+1+3+4+4+2+4+8+1+0+8 = 65 (**T**) Thymine: **66** The **seventh** group of the root square numbers of ten after comma: 3+7+9+3+0+0+2+9+5+1+8+7+3 = 57 (**C**) Cytosine: **58** The **eighth** group of the root square numbers of ten after comma: 4+7+2+8+4+1+5+2+8+4+0+0+5+5+1+4+8 = 68 (**A**) Adenine: **70** The **ninth** group of the square numbers of ten after comma: 5+4+8+8+5+6+0+3+0+4+5+3+8+8+0+0 = 67 (**T**) Thymine: 66 The **tenth** group of the square numbers of ten after comma: 1+4+6+9+0+5+1+9+5+9+6+7+0+0+1+5+3 = 71 (**A**) Adenine: **70** The **eleventh** group of the root square numbers of ten after comma: 9+0+3+3+4+4+9+2+1+6+5+7+1+7+9 = 70 (**A**) Adenine: 70 The **twelfth** group of the root square numbers of ten after comma: 2+5+9+9+4+0+6+5+9+1+5+0+1+5+3+4+7+4 = 79 (**G**) Guanine: **78** The **thirteenth** group of the root square numbers of ten after comma: 1+1+3+3+3+9+4+8+4+1+2+4+0+8+5+3+1+6 = 66 (**T**) Thymine: **66** The **fourteenth** group of the root square numbers of ten after comma: 9+2+9+5+7+7+0+9+0+4+7+1+5+7+6 = 78 (**G**) Guanine: **78** The **fifteenth** group of the root square numbers of ten after comma: 4+6+1+0+4+4+3+6+9+2+5+7+8+7 = 66 (**T**) Thymine: 66 The **sixteenth** group of the root square numbers of ten after comma: 9+0+6+2+0+3+7+8+0+8+6+0+9+9+4 = 71 (**A**) Adenine: **70** The **seventeenth** group of the root square numbers of ten after comma: 1+8+2+8+3+7+1+7+1+1+5+4+8+4+0+6 = 66 (**T**) Thymine: 66 The **eighteenth** group of the root square numbers of ten after comma: 3+2+8+5+5+2+9+9+9+1+1+8+5 = 67 (**T**) Thymine: **66** The **nineteenth** group of the root square numbers of ten after comma: 9+6+8+2+4+5+6+4+2+0+3+3+2+6+9 = 69 (**A**) Adenine: **70** The **twentieth** group of the root square numbers of ten after comma: 6+1+6+0+4+6+9+1+3+1+4+3+3+6+1+2+8+9+4 = 77 (**G**) Guanine: **78** The **twenty-first** group of the root square numbers of ten after comma: 9+7+9+1+8+9+0+2+6+6+5+2 = 64 (**T**) Thymine: 66 The **twenty-second** group of the root square numbers of ten after comma: 9+5+4+3+6+1+2+6+7+6+1+7+8 = 65 (**T**) Thymine: **66** The **twenty-third** group of the root square numbers of ten after comma: 7+8+1+3+5+0+0+6+1+3+8+8+1+8+6+2 = 67 (**T**) Thymine: **66** The **twenty-fourth** group of the root square numbers of ten after comma: 7+8+5+8+0+4+6+3+6+8+3+1+3+4 = 69 (**A**) Adenine: **70** The **twenty-fifth** group of the root square numbers of ten after comma: 9+5+2+4+7+8+0+3+1+1+4+3+7+6+9 = 69 (**A**) Adenine: **70** The **twenty-sixth** group of the root square numbers of ten after comma: 3+3+4+6+7+1+9+7+3+8+1+9+5+1+3 = 70 (**A**) Adenine: **70** The **twenty-seventh** group of the root square numbers of ten after comma: 1+8+5+6+7+8+4+0+3+2+3+1+2+4+1+7+9 = 71 (**A**) Adenine: **70** The twenty-eighth group of the square numbers of ten after comma:

5+4+0+2+2+1+8+3+0+8+0+4+5+8+7+2 = 59 (C) Cytosine: **58** The **twenty-ninth** group of the square numbers of ten after comma: 8+4+4+6+1+4+6+0+0+2+5+3+5+7+7+5 = 67 (T) Thymine: **66** The **thirtieth** group of the square numbers of ten after comma: 7+9+7+0+2+8+2+8+6+4+4+0+2+9+0+2+4+4+0 = 78 (G) Guanine: **78** This sequence can be shown as

[ATAAGTCATAAGTGTATTAGTTTAAAAACTG]. Let me try to explain this sequence with the "Quantum Perspective Model". For example, The first group of the square root of ten after comma equal to Adenine (A): 71 with the one more "1" Hydrogen bond (H: 1). (Remember, See Table 1; Adenine (A): 70) This result may mean the sequence of the square root of ten in groups

[ATAAGTCATAAGTGTATTAGTTTAAAAACTG]. The third group of the square root of ten after the comma is regarded as with the lack of one Hydrogen bond (H: 1) Adenine (A): 69; (Remember, See Table 1; Adenine (A): 70) (Because the deviations in the calculation of the square root of ten numbers can be derived from the Adenine (A)—Thymine (T) Hydrogen bonds because of Adenine (A) pairs with Thymine (T) by *two* hydrogen bonds. Cytosine (C)—Guanine (G) pairs with by *three* hydrogen bonds [16]. The reason for the lack of hydrogen bonds: Hydrogen bonding is a very versatile attraction. (Ölmez T, 2020) Hydrogen bonds are relatively *weak and easily broken* by increasing hardness (Farrell R E, 2010) [17]. Hydrogen Bonds are critical for the process of genetic identification and are quantum in nature (Penrose Sir Roger, 2008) [18].

4. Results

After searching the square root of the number ten with the National Biotechnology Information Center (NCBI) databases, several associations with bony fish may be found at the end of this search. What makes *Danio kyathit* [19] different from the others is that its strips are divided into rows of small brown spots. This fish species is closely related to zebrafish [20]. *Danio aesculapii* [21] is its distinguishing feature as the number of shared circular scales, which it has in common only with D. Kerri. Also *Danio aesculapii*, the number of dorsal fins with six branched rays, is the only example of its genus. Generally it differs from other Danio species in that it has six dorsal fins [21]. Especially, when sunlight touches the side of this fish species, it shows a variety of colors [22]. Types of bony fishes are based on *Danio aesculapii* (See Figure 1).

Types of bony fishes are *Paramormyrops kingsleyae*, *Larimichthys crocea* and *Cyprinodon tularosa*.

Types of other living creatures are birds, carnivores, rodents, eudicots, monocots, lizards, bivalves, gastropods, flatworms, beetles, moths, butterflies, walking sticks, bees, butterflies, caddisflies and flies [23] (See **Figure 2**).

5. Conclusion

At first, the summary of this research can be summarized as the expression of

Homo sapiens 3 BAC RP11-784B9 (Roswell Park Cancer Institute Human BAC Library) complete sequ.	<u>Homo sapiens</u>	42.1	42.1	70%	1.1	100.00%	181158	AC109129.3
PREDICTED: Nothoprocta perdicaria ubiquitin specific peptidase 53 (USP53), mRNA	Nothoprocta pe	40.1	40.1	66%	4.4	100.00%	4720	XM_026034587.1
Scophthalmus maximus chromosome 12	Scophthalmus	40.1	40.1	66%	4.4	100.00%	24811384	CP026254.1
Gari tellinella genome assembly, chromosome: 6	<u>Gari tellinella</u>	40.1	40.1	66%	4.4	100.00%	98983066	OV277861.1
PREDICTED: Varanus komodoensis solute carrier family 10 member 7 (SLC10A7), transcript variant X	. Varanus komod	40.1	40.1	66%	4.4	100.00%	7387	XM_044430844.1
Malus domestica genome assembly, chromosome: 14	Malus domestica	40.1	40.1	66%	4.4	100.00%	32239075	OU745004.1
Malus domestica genome assembly, chromosome: 14	Malus domestica	40.1	76.3	66%	4.4	100.00%	32470335	OU744966.1
Malus domestica genome assembly, chromosome: 14	Malus domestica	40.1	40.1	66%	4.4	100.00%	32241094	OU744555.1
Malus sylvestris genome assembly, chromosome: 14	Malus sylvestris	40.1	110	73%	4.4	100.00%	30380474	OU696516.1
Malus domestica genome assembly, chromosome: 14	Malus domestica	40.1	76.3	66%	4.4	100.00%	31671675	OU696690.1
Sphecodes monilicornis genome assembly, chromosome: 9	Sphecodes mo	40.1	40.1	66%	4.4	100.00%	27521247	OU565292.1
Ypsolopha scabrella genome assembly, chromosome: 9	Ypsolopha scab	40.1	40.1	80%	4.4	95.83%	31020244	OU342969.1
Ypsolopha scabrella genome assembly, chromosome: 2	Ypsolopha scab	40.1	40.1	66%	4.4	100.00%	32863811	OU342962.1
Ochlodes sylvanus genome assembly, chromosome: 19	Ochlodes sylva	40.1	40.1	66%	4.4	100.00%	11776845	FR990142.1
Pieris rapae genome assembly, chromosome: 16	Pieris rapae	40.1	40.1	80%	4.4	95.83%	10179501	LR990598.1
Danio kyathit genome assembly, chromosome: 1	Danio kyathit	40.1	40.1	66%	4.4	100.00%	78371624	LR812519.1
Danio aesculapii genome assembly, chromosome: 14	Danio aesculapii	38.2	38.2	90%	18	92.59%	56859170	LR812497.1
Danio aesculapii genome assembly, chromosome: 8	Danio aesculapii	38.2	74.3	66%	18	100.00%	55069896	LR812495.1
Pseudochaenichthys georgianus genome assembly, chromosome: 9	Pseudochaenic	38.2	38.2	63%	18	100.00%	48837966	LR792554.1
Canis lupus familiaris breed Labrador retriever chromosome 10a	Canis lupus fa	38.2	72.4	63%	18	100.00%	69938001	CP050591.1

Figure 1. The NCBI (National Biotechnology Information Center) result for nucleotide sequence "ATAAGTCATAAGTGTATTAGTTTAAAACTG" [23].

icer arietinum chromosome Ca5	
icer anetinum chromosome Ca5	Show removed set
icer arietinum chromosome Ca5	
 Papaver somniferum clone scf7180001502001 genomic sequence Myripristis murdjan genome assembly, chromosome: 4 Spirosoma sp. CJU-R4 chromosome, complete genome Gadus morhua genome assembly, chromosome: 11 Digitaria exilis genome assembly, chromosome: 9A Multiple organisms 28 leaves Cyanobacterium aponinum PCC 10605 chromosome, complete genome PREDICTED: Bombyx mandarina pyridoxal kinase (LoC114249930), mRNA Leptospira welli strin (CJDO6 chromosome I, complete sequence Danio rerio genome assembly, chromosome: 2 Panio rerio genome assembly, chromosome: 2 Botnyits cinerae B05.10 chromosome BCIN12, complete sequence Botryits cinerae B05.10 hypothetical protein (BCIN_12g05770), mRNA PREDICTED: Seriola Ialandi dorsalis PDZ domain-containing protein GIPC1-like (LOC111653697), mRNA Multiple organisms 8 leaves Danio rerio genome assembly, chromosome: 2 Danio rerio genome assembly, chromosome: 2 Botryits cinerae B05.10 hypothetical protein (BCIN_12g05770), mRNA Multiple organisms 8 leaves Danio rerio genome assembly, chromosome: 2 Danio rerio strain Nadia (NA) genome assembly, chromosome: 2 Danio rerio strain Nadia (NA) genome assembly, chromosome: 2 Danio rerio strain Nadia (NA) genome assembly, chromosome: 2 Danio rerio strain Nadia (NA) genome assembly, chromosome: 2 Danio rerio strain Nadia (NA) genome assembly, chromosome: 2 Danio rerio strain Nadia (NA) genome assembly, chromosome: 2 Danio rerio strain Nadia (NA) genome assembly, chromosome: 2 Zebriafish DNA sequence from clone CH211-12E1 in linkage group 2, complete sequence Geosporobacter ferrineducens strain IRF9 chromosome, complete genome PREDICTED: Phoca vitulina zinc finger and AT-hook domain containing (ZFAT), transcript variant X1, mRNA 	e Blast names color n bony fishes eudicots flowering plants rodents CFB group bacter monocots a-proteobacteria firmicutes g-proteobacteria bats whales & dolphin butterfiles cyanobacteria batseria ascomycetes carnivores unknown enterobacteria flatworms
Multiple organisms 41 leaves	even-toed ungul

Figure 2. The NCBI (National Biotechnology Information Center) result blast tree view widget for "ATAAGTCATAAGTGTATTAGTTTAAAACTG" nucleotide sequence [23].

the square root of the number ten, about the first four hundred digits after the decimal point, with bases in DNA. Secondly, these found bases in DNA are scanned in the NCBI database and meaningful results are tried to be obtained. A common feature of the NCBI blasts is the result of bony fish, particularly *Danio rerio* (Zebra fish) (Also, See Table 2).

Irrational Numbers	NCBI Results	Genetic Sequence		
√2 [6]	Danio rerio, Timema, Bony fish	GGATGTCTATTGAGTGACAA		
√3 [7]	Denticle Herring, Bony fish, Bats	GGATGACTACGGGTTTAGAAA		
√5 [8]	Danio rerio (Zebra fish), Bony fish	ATTTATTCAATACATAACCCCATTGA		
√7 [9]	<i>Danio rerio, Danio aesculapii</i> , Bony fish	GATTUCCCAUTAGAGTTAUTAGTTTGATT		
√10	Danio Kyathit, <i>Danio aesculapii</i> , Bony fish	ATAAGTCATAAGTGTATTAGTTTAAAACTG		
Pi Numbers (as a 22/7) [2]	Danio rerio (Zebra fish), Bony fish	UTA		
Pi Numbers (as an extended form) [3]	<i>Danio rerio</i> (Zebra fish), Bony fish, Timema, Danio Kyathit	TCGATTATACTGGTTGGTTGTTAACGGTAC		
Euler's Identity [13]	Danio Kyathit, <i>Danio rerio</i> (Zebra fish), Bony fish, Timema	AAAGGUCCGUUUAAUAAGUUAAAUUUAGGU		
Euler's Numbers [10]	<i>Danio rerio</i> (Zebra fish), Bony fish, bat coronavirus	AUGUUGAUAUTAAUCATC		
Golden Ratio Numbers (only "618") [4]	Bony fish, Denticle Herring	CAAT Box "GGCCAATCT"; TATA Box "TATAAAA"		

Table 2. The NCBI (National Biotechnology Information Center) summary and genetic sequences of some irrational numbers.

Thirdly, *Danio aesculapii* has a similar appearance to Zebrafish [22] (See Figure 2). Fourthly, Since Zebra fish have the ability to regenerate heart and lateral hair cells in their larval stages; they can contribute to a replication crisis in biomedical research, providing a useful *scientific model* as an organism [20]. Fifthly, although there is no periodic sequence of irrational numbers, in this paper a periodic sequence has been obtained in terms of genetic sequences, just as in "AGT" and "ATA". Remember, this sequence can be shown as

[ATAAGTCATAAGTGTATTAGTTTAAAACTG]. Finally, this study may shed light on the genetic sequences to be obtained, in biochemistry not only to explain the square root of the number ten with genetic codes, but also to explain other irrational numbers with the same property.

Conflicts of Interest

The author declares no conflicts of interest.

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