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Research Article

The Genetic Code: Dissected

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Abstract

Statement of the Problem: By genetic code, it is meant the true genetic code of 24 permutation quadruplets, which is a fabric segmented into quadruplet codons comprising the RNA four bases A,U,G,C (Adenine, Uracil, Guanine, Cytosine).

Dissection is the gory experience of frogs and rabbits and the like of animals, when they become specimens, rather prisoners of war, in the hands of biologists and zoologists prosecuting anatomical studies in laboratories. To all intents and purposes the 24 quadruplet genetic code is now made such a specimen, though not in the hands of the traditional practitioners of dissection, but under a Numerationist from the perspective of Numeration as science of number and arrangement.

Methodology and Theoretical Orientation: Bodies of the animal specimens under dissection are usually cut open with sharp instruments to expose their entrails for visual access in furtherance of anatomical studies. So the 24 quadruplet genetic code whose body is a segmented fabric or string of the RNA four bases A,U,G,C in diverse sequences called codons subjected to separation of its constituent nucleotide base types, though without cutting instruments, because they are amenable to dichotomization in terms of Purines and Pyrimidines.

Findings: The 24 quadruplet genetic code is transformed into a two-winged creature upon dissection. It is now well equipped to reach all its protein-clients whether flying in the air or swimming in the water as the wings are changeable to fins or burrowing in the soil as the fins get withdrawn into its segmented body.

Conclusion and Significance: The opening up of the entrails of specimens through dissection, in the case of the 24 quadruplet genetic code specimen brought forth eight dendritic structures along its entire length at four per side and at two per base type of the four base types in all the quadruplet codons. The significance is that both Chargaff's rules and Watson-Crick's base pairing rules can now be readily verified from the dendritic structure resulting from the dissection effected by dichotomization.

Recommendations: The 24 quadruplet genetic code is recommended to experimental experts in the relevant fields for spelling in order to render it fit for adoption in protein synthesis studies.

Keywords: Dissection; Dichotomization; Codons; Purines; Pyrimidines; Specimen

Introduction

The 24 quadruplet genetic code, our specimen for dissection, is an uncommon one, being neither warm-blooded like rabbits and co, nor cold-blooded like frogs and co of the animal kingdom that are the usual choices of biologists and zoologists who often hold them captives in their laboratories and cut open their entrails at will in prosecution of anatomical studies in advancement of science and knowledge for the common good of mankind. The genetic code even though unblooded, is however corporeal; possessing a 24-segmented fabric for a body, inanimate that is of much interest to a wide range of scientists including Numerationists with the peculiarity of sensitivity to arrangement. The 24-quadruplet genetic code, our specimen, a peculiar body, (inanimate) does not require cutting instruments for its dissection, rather an arrangement centred agency by the name of dichotomization is what is needed for its successful dissection or separation into constituent parts of the four RNA bases of Adenine, Uracil, Guanine, Cytosine (A,U,G,C). The specimen on hand is home-bred in this paper.

Materials and Methods

Materials

The RNA four bases, Adenine, Uracil, Guanine, Cytosine (A,U,G,C) and a square for raising the 24-quadruplet genetic code specimen in situ for dissection.

Methods

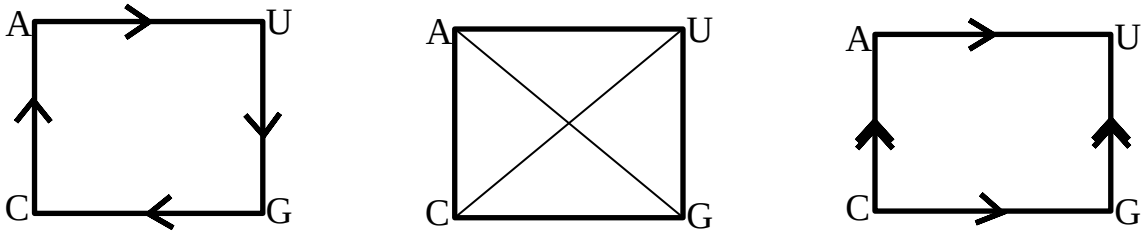
The methods are two: one involving square kinematics view mixing technique for raising the 24-quadruplet genetic code specimen from the RNA four bases, A,U,G,C; and the other involving dichotomization for dissecting the specimen available.

(i) Square kinematics view mixing technique for raising the 24-quadruplet genetic code specimen in situ from the RNA four bases A,U,G,C. A square of convenient size is drawn and the four bases A,U,G,C are individually placed at the four corners as shown in Figure 1 in clockwise direction for sequence.

Figure (1): Square loaded with the RNA four bases A,U,G,C as input set.

The A,U,G,C loaded square is deployed in three ways as depicted in Figure 2 namely:

Figure (2): Three deployments (a), (b), (c) of AUGC loaded square.



a) Sides (b) Diagonals (c) Parallels

Chart (1): Genetic code output computation by Square Kinematics View Mixing Technique.

Deployment of sides, ref. Figure 2 (a)						
Viewing along sides:	From	A	clockwise	AUGC	Line	1
			Fro	CGUA	“	2
“ “ “	From	U	clockwise	UGCA	“	3
			Fro	ACGU	“	4
“ “ “	From	G	clockwise	GCAU	“	5
			Fro	UACG	“	6
“ “ “	From	C	clockwise	CAUG	“	7
			Fro	GUAC	“	8

Deployment of diagonals, ref. Figure 2 (b)						
Viewing along diagonals:	From	A	clockwise	AGCU	Line	9
			Fro	UCGA	“	10
“ “ “	From	U	clockwise	UCAG	“	11
			Fro	GACU	“	12
“ “ “	From	G	clockwise	GAUC	“	13
			Fro	CUAG	“	14
“ “ “	From	C	clockwise	CUGA	“	15
			Fro	AGUC	“	16

Deployment of parallels, ref. Figure 2 (c)					
Viewing the parallels	AU//CG	Horizontals	AUCG	Line	17
		Fro	GCUA	“	18
“ “ “	CG//AU	Horizontals	CGAU	“	19
		Fro	UAGC	“	20
“ “ “	CA//GU	Verticals	CAGU	“	21
		Fro	UGAC	“	22
“ “ “	AC//UG	Verticals	ACUG	“	23
		Fro	GUCA	“	24

Summary of valid products: Lines 1 – 24 = 24 permutation quadruplets.

Factorial 4P4 = 4! = 4 x 3 x 2 x 1 = 24 permutation quadruplets

Production = Prediction = 24 permutation quadruplets

Hence 24 permutation quadruplet genetic code produced as specimen for dissection.

The Second method entails Dichotomization technique for dissecting the 24 quadruplet genetic code specimen as shown in Diagram 1 at the crux of the engagement.

The fabric of the 24 quadruplet genetic code specimen generated by the first method is laid stretched in linear form across the middle of the page with enough room above and below its entire length so as to accommodate the castings of dissection waste on both sides; in other words, the outcome of dichotomization of the constituent RNA four bases of A,U,G,C per codon into Purines and Pyrimidines on opposite sides accompanied by separation of Purines into the two base types of Adenine and Guanine and also the Pyrimidines into the two base types of Uracil and Cytosine as depicted in Diagram 1: The 24 quadruplet genetic code, dissected.

Results

The results are two: one in respect of the production of the 24 quadruplet genetic code specimen from the RNA four bases, A,U,G,C using Square Kinematics View Mixing Technique as shown in Table 1, and drawn from Chart 1, lines 1 – 24. The second result is in respect of the dissected 24 quadruplet genetic code specimen as portrayed in Diagram 1.

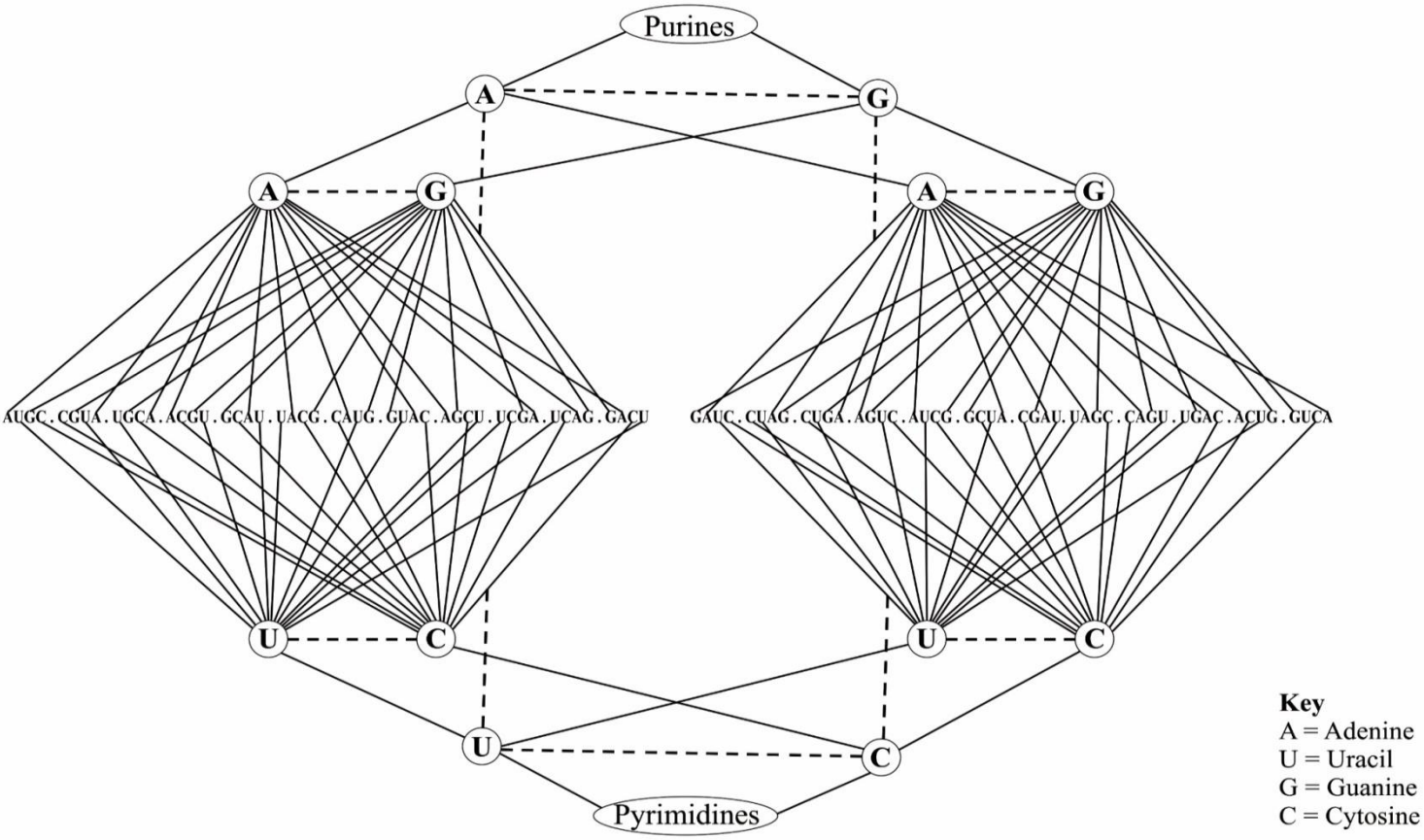
Diagram 1 showing the dissected 24 quadruplet genetic code specimen, is a two-winged creature bearing an axis segmented into 24 quadruplet codons. The 24 quadruplet genetic code is thereby greatly enriched structurally or anatomically by the dissection exercise.

Table (1): 24 quadruplet genetic code specimen produced in situ.

S/N	Codons	Source Ref. Chart 1	Remarks
1	AUGC	Line 1	Segmented
2	CGUA	" 2	
3	UGCA	" 3	Specimen
4	ACGU	" 4	
5	GCAU	" 5	Fabric
6	UACG	" 6	
7	CAUG	" 7	In
8	GUAC	" 8	
9	AGCU	" 9	Lateral
10	UCGA	" 10	
11	UCAG	" 11	Packing
12	GACU	" 12	
13	GAUC	" 13	
14	CUAG	" 14	

15	CUGA	"	15	
16	AGUC	"	16	
17	AUCG	"	17	
18	GCUA	"	18	
19	CGAU	"	19	
20	UAGC	"	20	
21	CAGU	"	21	
22	UGAC	"	22	
23	ACUG	"	23	
24	GUCA	"	24	

Diagram 1. The 24-quadruplet genetic code specimen, dissected.



Discussion

The discussion is centred on the exploration of pre-dissection and post-dissection 24 quadruplet genetic code specimen by pentadic characterization,

application as conveyed in Table 2: Dissection Data of the 24-quadruplet genetic code (in linear form) specimen.

featuring the five parameters of identity, structure, function, operation and

Table 2: Dissection Data of 24-quadruplet genetic code specimen

Pentadic Characterization	**24 quadruplet genetic code dissection specimen**		**Remarks**
Parameters	Pre-dissection ref. Table 1	Post-dissection, ref. Diagram 1	
1. Identity	24 quadruplet genetic code in block format	24 quadruplet genetic code in linear form in dentritic rendition	
2. Structure	24 permutation quadruplet codons of RNA four bases in lateral alignment i.e. codons lying side to side.	AGCU square of RNA bases in three locations	
3. Function	Workforce of strength 24 quadruplet codons for servicing protein synthesis in plants and animals	Demonstration of Chargaff's rule (1) and Watson-Crick's base pairing rules (2). In addition to bearing AGCU square as seed of genetic code life.	
4. Operation	Utilizing collinearity with protein types one to one correspondence between 24 quadruplet codons and 20 amino acids of protein type/4 control signals to fix 20 amino acids in sequence during protein synthesis	AGCU square can undergo view mixing to regenerate 24 permutation quadruplets genetic code, apart from illustration of genetic code dichotomization into Purines and Pyrimidines	
5. Application	Proliferation and diversification of protein types in the course of protein synthesis	Clarification of Chargaff's rules and Watson-Crick's base pairing rules in addition to proliferation and diversification of protein types as the fabric during protein syntheses remains intact, despite the dissection. Also the representation of additional morphology known as dendritic morphology to the 24-quadruplet genetic code	

Inspection of the dissected 24 quadruplet genetic code as depicted in Diag. 1 shows the validation of Chargaff's rules and Watson-Cricks base pairing rules viz:- Chargaff's rules: In the DNA the number of Adenines (A) is always equal to the number of Thymines (T) i.e. A = T, and the number of Guanines (G) is always equal to the number of Cytosines (C) i.e. G = C. That in turn means the number of Purines (A+G) always equals the number of Pyrimidines (C+T) i.e. A+G = C+T. The same is true of the RNA four bases A,U,G,C that feature in the genetic code specimen where Thymine (T) is replaced by Uracil (U).

Watson-Crick's base pairing rules

2(A/Ux12) lines and 2(G/Cx12) lines per genetic code sequence of 24 quadruplet codons is evident i.e.24 lines of A matched by 24 lines of U and 24 lines of G matched by 24 lines of C across the axis of the genetic code specimen.

Findings

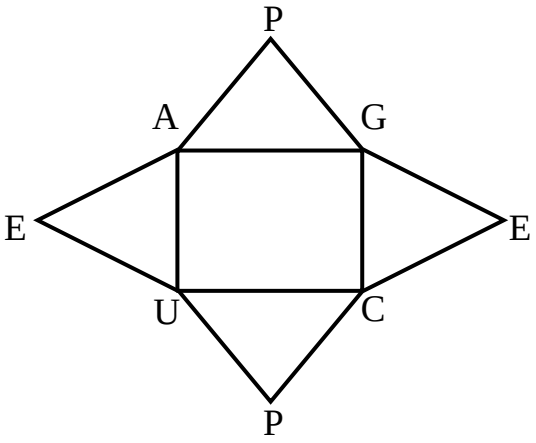
The findings of the genetic code dissected, like the Discussions are also centred on the Dissection Data, trying to portray the thoroughness and benefits of the dissection carried out on the axial body of the inanimate genetic code specimen for the first time.

The thoroughness is evident in Diagram 1, the post-dissection specimen, that all the 96 base units in four types making up the 24 permutation quadruplet codons full length of the specimen are affected individually as they are conveyed through the 96 dendritic veins to eight sites: four on either side of the segmented axis and two per base type in accordance with designations as Purines and Pyrimidines in opposite sides of the axis of the specimen.

The benefits are actual as well as figurative apparently. The actual include the clarification of Chargaff's rules and Watson-Crick's base pairing rules as noted under Table 2. The figurative benefits issue from the physical configuration of the aftermath of dissection, ref. Diagram 1. We see the genetic code, the protein type synthesizer turned into a two-winged creature, that can go along with its clients for protein supply namely birds in the air or along with fishes in the water, when the wings change to fins or along with worms in the soil when the fins are withdrawn into its segmented axial fabric. So the genetic code is duly adapted to flying, swimming and burrowing through dissection wrought by dichotomization. Also additional morphology known as dendritic morphology is prepared for the 24-quadruplet genetic code.

The 24 quadruplet codons of the genetic code specimen unanimously underwent the gory experience of dissection with all their belongings in a single file, but emerged with magnified strength and concentration so that one representative quadruplet codon AGCU (9th segment of the specimen) is now in three locations: two on ground and one air-borne cabled as evident in Diagram 1, in the aftermath of dissection. As a matter of fact, that surviving AGCU codon carried in a square AGCU in three locations of the dissected genetic code ref. Diagram 1 bears the framework for genetic code dichotomization based on Chargaff's rules and Watson-Crick's base pairing rules for expediting the dissection of the genetic code, as per Figure 3, below.

Figure (3): AGCU codon square, framework for genetic code dichotomization for expediting genetic code dissection.



Key: A = Adenine, G = Guanine, C = Cytosine, U = Uracil, P = Purine, Py = Pyrimidine, E = Erwin Chargaff

Notes: AG = Northern horizontal, holding the two Purines; Adenine and Guanine
UC = Southern horizontal, holding the two Pyrimidines; Uracil and Cytosine
AU = Western vertical, (a) holding A and U in equal amount
GC = Eastern vertical, (i) holding G and C in equal amounts, (ii) pairing G with C and A with U in support of both Watson-Crick's base pairing rule, and Chargaff's rule also.

Conclusion and Significance

The anatomy of the 24 quadruplet genetic code is now denuded, made bare to all and sundry by dissection. Moreover, the dissected genetic code is identified as dendritic morphology of the 24-quadruplet genetic code, alongside two others named lito-morphology and kinomorphology in "Genetic Code: Mapping Base Kinematics in Quadruplet Codons" by W. B. Bozegha (2018) published by Acta Scientific. The significance of the dissection is remarkable in that both Chargaff's Rule and Watson-Crick's base pairing rule are clearly portrayed and demonstrated.

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