ON THE COMPLETENESS OF GENETIC CODE: PART III

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Abstract. In this third part of the work about the completeness of the genetic code, we present new examples that show that the codon splitting after pyrimidine / purine nucleotides distinctions are followed by specific arithmetical balances of the number of atoms in the amino acid molecules side chains.

The codon splitting in Table 1, under (a), designates a distinction of YYN and RRN codons in dark areas versus YRN and RYN in light areas.[1] The same distinctions we have also under (b), but with further nuance-splitting: YYY, RYY, RYR, YRY, YRR, RRY, RRR.

UUU (F)	UCU(S)	UAU(Y)	UGU(C)
UUC (F)	UCC(S)	UAC(Y)	UGC(C)
UUA (L)	UCA(S)	UAA(ct)	UGA(ct)
UUG (L)	UCG(S)	UAG(ct)	UGG(W)
CUU (L)	CCU(P)	CAU(H)	CGU(R)
CUC (L)	CCC(P)	CAC(H)	CGC(R)
CUA (L)	CCA(P)	CAA(Q)	CGA(R)
CUG (L)	CCG(P)	CAG(Q)	CGG(R)
AUU (I)	ACU(T)	AAU(N)	AGU(S)
AUC (I)	ACC(T)	AAC(N)	AGC(S)
AUA (I)	ACA(T)	AAA(K)	AGA(R)
AUG (M)	ACG(T)	AAG(K)	AGG(R)
GUU(V)	GCU(A)	GAU(D)	GGU(G)
GUC(V)	GCC(A)	GAC(D)	GGC(G)
GUA(V)	GCA(A)	GAA(E)	GGA(G)
GUG(V)	GCG(A)	GAG(E)	GGG(G)
(a) = **286**/308 (296-10/298+10)			

UUU (F)	UCU(S)	UAU(Y)	UGU(C)
UUC (F)	UCC(S)	UAC(Y)	UGC(C)
UUA (L)	UCA(S)	**UAA(ct)**	**UGA(ct)**
UUG (L)	UCG(S)	**UAG(ct)**	**UGG(W)**
CUU (L)	CCU(P)	CAU(H)	CGU(R)
CUC (L)	CCC(P)	CAC(H)	CGC(R)
CUA (L)	CCA(P)	**CAA(Q)**	**CGA(R)**
CUG (L)	CCG(P)	**CAG(Q)**	**CGG(R)**
AUU (I)	ACU(T)	AAU(N)	AGU(S)
AUC (I)	ACC(T)	AAC(N)	AGC(S)
AUA (I)	**ACA(T)**	AAA(K)	AGA(R)
AUG (M)	**ACG(T)**	AAG(K)	AGG(R)
GUU(V)	GCU(A)	GAU(D)	GGU(G)
GUC(V)	GCC(A)	GAC(D)	GGC(G)
GUA(V)	**GCA(A)**	GAA(E)	GGA(G)
GUG(V)	**GCG(A)**	GAG(E)	GGG(G)
(b) = 122+ **164** / 166+**142** (**296**+**10** /298-10)			

Table 1. Distributions of AAs (within four quadruplets of GCT) after nucleotide doublets presented in Table 2 in Part II (Rakočevič, 2015).

(a_1)	(a_2) 158+128 = 296 -10	(b_1)	(b_2)
54 +20+52+32 = 158	170 + 138 = 298+10	YYY 80 + YYR 78 = 158	YYY 80+ YRY 96 = 176
30+28+44+68 = 170	(a_3) YYN 158; RRN 128	RRR 86 + RRY 42 = 128	RYY 70+RRR 86 = 156 (20)
50+40+32+16 = 138	RYN 138; YRN 170	YRY 96 + YRR 74 = 170	YYR 78+RYR 68 = 146 (10)
46+44+34+04 = 128		RYY 70 + RYR 68 = 138	RRY 42+YRR 74= 116 (30)

Survey 1. Atom number balances within amino acid side chains, which follow splitting in Table 1.

[1] Y for pyrimidine, R for purine and N for all four types of nucleotides.

The codon splitting in Table 2, under (a), designates a further codons distinction, valid for first and second doublets in four doublet-quadruplets, presented in Table 2, in Part II. The same distinctions we have also under (b), but valid for third and fourth doublets in four doublet-quadruplets, presented in Table 2, in Part II of this work.

UUU (F)	UCU(S)	UAU(Y)	UGU(C)
UUC (F)	UCC(S)	UAC(Y)	UGC(C)
UUA (L)	UCA(S)	UAA(ct)	UGA(ct)
UUG (L)	UCG(S)	UAG(ct)	UGG(W)
CUU (L)	CCU(P)	CAU(H)	CGU(R)
CUC (L)	CCC(P)	CAC(H)	CGC(R)
CUA (L)	CCA(P)	CAA(Q)	CGA(R)
CUG (L)	CCG(P)	CAG(Q)	CGG(R)
AUU (I)	ACU(T)	AAU(N)	AGU(S)
AUC (I)	ACC(T)	AAC(N)	AGC(S)
AUA (I)	ACA(T)	AAA(K)	AGA(R)
AUG (M)	ACG(T)	AAG(K)	AGG(R)
GUU(V)	GCU(A)	GAU(D)	GGU(G)
GUC(V)	GCC(A)	GAC(D)	GGC(G)
GUA(V)	GCA(A)	GAA(E)	GGA(G)
GUG(V)	GCG(A)	GAG(E)	GGG(G)

(a) = (60+**66**/70+**84**)
126/154

UUU (F)	UCU(S)	UAU(Y)	UGU(C)
UUC (F)	UCC(S)	UAC(Y)	UGC(C)
UUA (L)	UCA(S)	UAA(ct)	UGA(ct)
UUG (L)	UCG(S)	UAG(ct)	UGG(W)
CUU (L)	CCU(P)	CAU(H)	CGU(R)
CUC (L)	CCC(P)	CAC(H)	CGC(R)
CUA (L)	CCA(P)	CAA(Q)	CGA(R)
CUG (L)	CCG(P)	CAG(Q)	CGG(R)
AUU (I)	ACU(T)	AAU(N)	AGU(S)
AUC (I)	ACC(T)	AAC(N)	AGC(S)
AUA (I)	ACA(T)	AAA(K)	AGA(R)
AUG (M)	ACG(T)	AAG(K)	AGG(R)
GUU(V)	GCU(A)	GAU(D)	GGU(G)
GUC(V)	GCC(A)	GAC(D)	GGC(G)
GUA(V)	GCA(A)	GAA(E)	GGA(G)
GUG(V)	GCG(A)	GAG(E)	GGG(G)

(b) = (74+**68**/84+**88**)
142/172

Table 2. Distributions of AAs within eight (a), plus eight (b) squares of GCT, after nucleotide doublets presented in Table 2 in Part II of this work. The Table under (a) corresponds with Table 3, and Table under (b) with Table 4 in Part II of this work.

(a_1) = (60+ **66** / 70+**84**) [126/154];	(b_1) = (74+ **68** / 84+**88**) [(142/172);	(a_2) 60 = 10 x 6 66 = 11 x 6 70 = 10 x 7 84 = 12 x 7
(I NY 60 + II NY 70 = 130) (140-10) (I NR **66** + II NR **84** = 150) (140+10)	(III NY 74 + IV NY 84 = 158) (157+1) (III NR **68** + IV NR **88** = 156) (157–1)	
I NY 60 + I NR **66** = 126 I NR **66** + II NY 70 = 136 I NY 60 + II NR **84** = 144 II NY 70 + II NR **84** = 154	III NY 74 + III NR **68** = 142 III NR **68** + IV NY 84 = 152 III NY 74 + IV NR **88** = 162 IV NY 84 + IV NR **88** = 172	(b_2) 142+154 = 296 152+144 = 296 162+136 = 298 172+126 = 298

Survey 2. Atom number balances within amino acid side chains, which follow splitting in Table 2.

REFERENCE

Rakočević, M. M. (2015) On the Completeness of Genetic Code: Part II, viXra:1501.0117.