Wigner-Eckart theorem in the crystal basis
and the organisation of the genetic code

A. Sciarrino

Dipartimento di Scienze Fisiche, Università di Napoli “Federico II”
I.N.F.N., Sezione di Napoli
Complesso di Monte S. Angelo, Via Cintia, I-80126 Napoli, Italy
e-mail: Sciarrino@na.infn.it

To appear in ”Proceedings of VII Wigner Symposium”
University of Maryland, College Park, 24-28 August 2001

Abstract

Modelising the translation errors by suitable mathematical operators in the
crystal basis model of the genetic code and requiring that codons prone to be
misread encode the same amino-acid, the main features of the organisation in
multiplets of the genetic code are described.
I. INTRODUCTION

The storage of genetic information is governed by the DNA, which is formed by four different nucleotides, characterized by their bases: adenine (A) and guanine (G) deriving from purine, and cytosine (C) and thymine (T) coming from pyrimidine. In the double helix structure of DNA there is always a pairing C-G and T-A. The transmission of information from DNA to build proteins is a complex process of transcription and translation [1]. The flow of informations from DNA is transmitted through the RNA which also contains 4 bases, T being replaced by uracile (U). The mRNA (messenger) transmits the information from DNA to the tRNA, which takes part to the protein synthesis. The transcription from DNA to mRNA takes place following the bases complementarity rule: \( A \rightarrow U, T \rightarrow A, G \rightarrow C, C \rightarrow G \). In this context the idea of genetic code emerges giving the connection law translating a sequence of nucleotides in the RNA (here and in the following we shall refer to messenger) into a sequence of amino-acids (a.a.). A triple of nucleotides, codon, is read in the translation process. There are 64 codons, which encode for the 20 a.a. (denoted in the following by their standard shortened notation), which are the building blocks for any protein and for the signal of the end of the protein synthesis (Stop or Non-sense codons). It follows that there is not an one to one correspondence between codons and a.a. and the code is degenerate exhibiting a complex pattern of organisation in multiplets, ranging from sextets to singlets, in particular: for the vertebrate mitochondrial code (VMC) 2 sextets, 7 quartets and 12 doublets; for the eukaryotic or standard universal, code (SUC) 3 sextets, 5 quartets, 2 triplets, 9 doublets and 2 singlets (see Table(I)). For a recent review with a rich bibliography to the original papers see [2].

Codons encoding the same a.a. are called synonymous. Since the discovery of the genetic code three, between many others, puzzling questions have arisen: why does nature use 20 a.a. to build up proteins ? why has the genetic code the peculiar organisation in multiplets ? why is an a.a. encoded by fewer codons than another ? An answer to the last question might be that a.a. more frequently used are encoded by greater multiplets. However such an explanation is weakly supported by the analysis of the data, see Table I see [3]. In particular the sextet encoding for Arg seems really overabundant.

To explain the pattern of the genetic code at least six hypothesis have been put forward [4]:

1. the frozen accident theory, according to which the genetic code is the result of a random event [5]

2. the stereochemical theory, which first idea dates back to 1954, only one year after the discovery of the DNA by Crick and Watson, and was suggested by Gamow [6], according to which the codons assignments are the results of an affinity between the a.a. and the encoding codons [7], [8]

3. the coevolution theory, according to which a.a. most closely related are encoded by close codons, i.e. codons differing by the change of one base [9]

4. the lethal mutation theory according to which the genetic code has evolved minimizing the effect of point mutations of the codons on proteins [10], [11]

5. the translation-error minimization theory according to which the evolution of the genetic code has been governed by the minimization of the errors in the translation process [12], [13]

6. the genetic flexibility theory according to which the genetic code is the outcome of a balance between robustness and mutability [14]
However at my knowledge no quantitative model has been proposed to account either for the number of a.a. either for the structure in multiplets. Efforts have been concentrated to analyse the correspondence codons-a.a.. On this subject a very large literature exists; it is now generally accepted that this correspondence is not causal, but reflects the molecular structure of a.a., even if there is a great debate over the nature of the dominant factors. However in almost all the papers on the subject the number of a.a. and the structure in multiplets of the genetic code are assumed as input elements. The aim of this talk is to propose a mathematical model able to reasonably explain the organisation of the genetic code, i.e. the number and the dimension of multiplets. In a way the proposed model provides a mathematical frame for hypothesis 4) and 5). Clearly indeed a protection against the translation errors is obtained if the codons more prone to be misread encode the same a.a.. The first requirement to set such a mathematical model is to identify codons as mathematical objects, this will be done in the framework of the crystal basis model of the genetic code, which will be briefly recalled in the Sec. 3. To make the paper self-contained in Sec. 2 we recall the crystal basis for $U(q \rightarrow 0)(sl(2))$.

II. REMINDER OF $U(q \rightarrow 0)(SL(2))$

For self constience, let me recall the definition and main properties of $U_q(sl(2))$ and of the $q$-tensor operator, see, e.g., [17]. $U_q(sl(2))$ is defined by the following commutation relations

$$[J_+, J_-] = [2J_3]_q$$

$$[J_3, J_\pm] = \pm J_\pm$$

where

$$[x]_q = \frac{q^x - q^{-x}}{q - q^{-1}}$$

In the following we shall omit the lower label $q$.

The deformed enveloping algebra $U_q(sl(2))$ is endowed with an Hopf structure. In particular the coproduct is defined by

$$\Delta(J_3) = J_3 \otimes 1 + 1 \otimes J_3$$

$$\Delta(J_\pm) = J_\pm \otimes q^{J_3} + q^{-J_3} \otimes J_\pm$$

The Casimir operator can be written

$$C = J_+ J_- + [J_3][J_3 - 1] = J_- J_+ + [J_3][J_3 + 1]$$

For $q$ generic, i.e. not a root of unity, the irreducible representations (irrep.) are labelled by an integer or half-integer number $j$ and the action of the generators on the vector basis $|jm>$, $(-j \leq m \leq j)$, of the IR is

$$J_3 |jm> = m |jm>$$

$$J_\pm |jm> = \sqrt{[j \mp m][j \pm m + 1]} |j, m \pm 1> = F^\pm(j, m) |j, m \pm 1>$$
From eqs.(3)-(7) it follows

\[ C \vert jm \rangle = [j] [j + 1] \vert jm \rangle \]  \hspace{1cm} (8)

Let us recall the definition of \(q\)-tensor operator for \(U_q(sl(2))\). An irreducible \(q\)-tensor of rank \(j\) is a family of \(2j + 1\) operators \(T^j_m\) \((-j \leq m \leq j\)) which transform under the action of the generators of \(U_q(sl(2))\) as

\[ q^{J_3}(T^j_m) \equiv q^{J_3} T^j_m q^{-J_3} = q^m T^j_m \]  \hspace{1cm} (9)

or

\[ [J_3, T^j_m] = m T^j_m \]  \hspace{1cm} (10)

\[ J_{\pm} (T^j_m) \equiv J_{\pm} T^j_m q^{J_3} - q^{-J_3 \pm 1} T^j_m J_{\pm} = F^{\pm} (j, m) T^{j \pm 1}_m \]  \hspace{1cm} (11)

In deriving the above equations use has been made of the non trivial coproduct eq.(4). The \(q\)-Wigner-Eckart (\(q\)-WE) theorem now reads:

\[ <JM \vert T^j_m \vert j_1 m_1 > = (-1)^{2j} \frac{<J \vert T^j \vert j_1 >}{\sqrt{2J + 1}} < j_1 m_1 jm \rangle \]  \hspace{1cm} (12)

or

\[ T^j_m \vert j_1 m_1 > = (-1)^{2j} \sum_{J=|j-j_1|}^{j+j_1} \frac{<J \vert T^j \vert j_1 >}{\sqrt{2J + 1}} < j_1 m_1 jm \rangle \]  \hspace{1cm} (13)

Let us study now the limit \(q \to 0\). From the definition eq.(3) we have

\[ [x]_{q \to 0} \sim q^{-x+1} \hspace{1cm} x \neq 0 \]  \hspace{1cm} (14)

So it follows that

\[ F^{\pm} (j, m)_{q \to 0} \sim q^{-j+1/2} \]  \hspace{1cm} (15)

\[ [j] [j + 1]_{q \to 0} \sim q^{-2j+1} \]  \hspace{1cm} (16)

From eqs.(3) and (15) it follows that the action of the generator \(J_{\pm}\) is not defined in the limit \(q \to 0\). Let us define

\[ \bar{J}_{\pm} = \Gamma_0 J_{\pm} \]  \hspace{1cm} (17)

where

\[ \Gamma_0 = C^{-1/2} \]  \hspace{1cm} (18)

\[ \Gamma_0 \vert jm \rangle = ([j] [j + 1])^{-1/2} \vert jm \rangle \]  \hspace{1cm} (19)

These operators are well behaved for \(q \to 0\). Their action in the limit \(q \to 0\) will define the crystal basis:
\[ \tilde{J}_+ |jm > = |j, m+1 > \quad \text{for} \quad -j \leq m < j \]  
\[ \tilde{J}_- |jm > = |j, m-1 > \quad \text{for} \quad -j < m \leq j \]  
\[ \tilde{J}_+ |jj >= \tilde{J}_- |j, -j >= 0 \]  

It is also possible to define a Casimir operator in the crystal basis
\[ \tilde{C} = (J_3)^2 + \frac{1}{2} \sum_{n \in \mathbb{Z}_+} \sum_{k=0}^{n} (\tilde{J}_-)^{n-k}(\tilde{J}_+)^n(\tilde{J}_-)^{k} . \]  

such that
\[ \tilde{C} |jm >= j(j+1) |jm > \]  

Then I can define \( \tau_{j}^{m} \)-tensor or crystal operator \( \tau_{j}^{m} \) by:
\[ J_3(\tau_{j}^{m}) \equiv m \tau_{j}^{m} \quad \tilde{J}_\pm (\tau_{j}^{m}) \equiv \tau_{j \pm 1}^{m} \]  

Clearly, if \( |m| > j \) then \( \tau_{j}^{m} \) has to be considered vanishing. In the following I shall omit to explicitly write the tilde. The tensor product of two representations in the crystal basis is given by \ref{eq:tensor_product}. Theorem - If \( B_1 \) and \( B_2 \) are the crystal bases of the \( M_1 \) and \( M_2 U_{q \to 0}(sl(2)) \)-modules, for \( u \in B_1 \) and \( v \in B_2 \), we have:
\[ \tilde{J}_-(u \otimes v) = \begin{cases} \tilde{J}_-u \otimes v & \exists n \geq 1 \text{ such that } \tilde{J}_-^n u \neq 0 \text{ and } \tilde{J}_+^n v = 0 \\ u \otimes \tilde{J}_-v & \text{otherwise} \end{cases} \]  
\[ \tilde{J}_+(u \otimes v) = \begin{cases} u \otimes \tilde{J}_+v & \exists n \geq 1 \text{ such that } \tilde{J}_+^n v \neq 0 \text{ and } \tilde{J}_-^n u = 0 \\ \tilde{J}_+u \otimes v & \text{otherwise} \end{cases} \]  

So the tensor product of two crystal basis is a crystal basis and the states of the basis of the tensor space are pure states. In other words, in the limit \( q \to 0 \) all the \( q \)-Clebsch-Gordan \( (q\text{-CG}) \) coefficients vanish except one which is equal to \( \pm 1 \). The Wigner-Eckart theorem eq.\( \ref{eq:wigner_eckart} \) now reads
\[ \tau_{j}^{m} |j_{1}m_{1} >= <J||T^j||J_{1} > |J, m_1 + m > \]  

where the value of \( J \) (\( |j_1 - j| \leq J \leq j_1 + j \)) depends on the value of \( m_1 \) and \( m \) and of the order in which the tensor product of irreps. \( (jm) \) and \( (j_1m_1) \). In the following the irrep. \( (jm) \) will be considered as the second one.

**III. THE MATHEMATICAL MODEL**

In the crystal basis model of the genetic code \ref{eq:crystal_basis} the 4 nucleotides are assigned to the 4-dim fundamental irrep. \( (1/2, 1/2) \) of \( U_{q \to 0}(sl(2) \oplus sl(2)) \) with the following assignment for the values of the third component of \( \tilde{J} \) for the two \( sl(2) \) which in the following will be denoted as \( sl_{H}(2) \) and \( sl_{V}(2) \):
\[ C \equiv (\frac{1}{2}, \frac{1}{2}) \quad T/U \equiv (\frac{1}{2}, \frac{1}{2}), \quad G \equiv (\frac{1}{2}, -\frac{1}{2}) \quad A \equiv (-\frac{1}{2}, -\frac{1}{2}) \]  

and the codons, triple of nucleotides, to the 3-fold tensor product of \( (1/2, 1/2) \). We report in Table\( \ref{table:codon_assignment} \) the assignment of the codons to the different irreps. The mathematical model mimicking the translation errors is essentially based on the following Assumption:
Two codons are prone to translation error if their corresponding states in the crystal basis model are connected by the action of a suitable crystal tensor operators \( \tau_{H,m}^{j} \otimes \tau_{V,m}^{\prime} \) of \( U_{q} \rightarrow 0 (sl_{H}(2) \oplus sl_{V}(2)) \) in the sense of the Wigner-Eckart theorem.

We assume, on phenomenological grounds see [11], [20], [21], that there is a hierarchy in the occurrence of translation errors and, in order of decreasing intensity, we consider:

1. the transitions, in particular \( C \rightarrow U \) or \( G \rightarrow A \), concerning nucleotides in the 3rd position
2. the transversions, in particular \( C \rightarrow G, U \rightarrow A \) and \( C \rightarrow A \), in the nucleotides in 3rd position.
3. the transitions (resp. transversions) concerning nucleotides in 1st position
4. the transitions (resp. transversions) concerning nucleotides in 2nd position
5. the mutation induced by the transitions (resp. transversions) on the first two nucleotides

Transitions (transversions) of the nucleotide in the middle position are far weaker than transitions (transversions) in other positions.

The hierarchy in the translation errors mechanisms means that a multiplet formed in a level is frozen; in the subsequent levels, the merging of two whole multiplets in a larger structure is possible, if it is induced by the relevant tensor operator. If the transition is allowed only for some member of a multiplet, there is conflict between the choice of merging the multiplet in a larger one, so decreasing the variety of encoded a.a. but increasing the protection or preserving the multiplets decreasing the level of protection. In this case, the formation of larger structures will generally take place or not according to the rule to protect the weakest codons, i.e. the codons more inclined to be misread. I assume that misreading of nucleotide C or A is the most common. Let me emphasize that we want to build the most simple model in which the codons, which are most subject to reading errors, are synonymous; in this spirit the explicitly analysed transitions \( (C \rightarrow U, G \rightarrow A) \) or transversions \( (C \rightarrow G, U \rightarrow A, C \rightarrow A) \) have not to be considered as the only possible misreadings, but as the representatives which allow the most simple modelisation. For simplicity I consider only the transversions decreasing or leaving unchanged the value of \( J_{H,3} \). Finally, it is clear from the Table[1][I] that there are generally more than one irrep. labelled by the same value of \((J_{H}, J_{V})\) whose content in the constituent nucleotides is different. The transformation properties of a crystal tensor operator determine which states are related each other, only according to the irreps. to which the states belong to. To take into account someway the multiplicity of irreps., generally, the choice of the rank of the tensor operator will depend on the position of the misread nucleotide and on the irrep. to which the codon belongs to. The transitions and the transversions are modelised by the following crystal tensor operator, the value of the component being determined by the labels of the nucleotides, see eq.(29):

\[
C \rightarrow U \quad \text{or} \quad G \rightarrow A \quad \tau_{H,-1}^{1} \otimes \tau_{V,0}^{a} \quad (30)
\]

\[
C \rightarrow G \quad \text{or} \quad U \rightarrow A \quad \tau_{H,0}^{b} \otimes \tau_{V,-1}^{1} \quad (31)
\]

\[
C \rightarrow A \quad \tau_{H,-1}^{c} \otimes \tau_{V,-1}^{d} \quad (32)
\]

where the values of the rank \( a, b, c \) and \( d \) depend on the position inside the codons of the misread nucleotide and on the irreps. to which the codons belong, see next section. The above
choice for the horizontal (resp. vertical) part of the crystal vector operator in eq. (30) (resp. eq. (31)) is indeed the most simple choice according to the change in the labels of the states of codons for transitions (resp. transversions), see eq. (29). The choice of the rank of the vertical (resp. horizontal) part of the crystal operator in eq. (30) (resp. eq. (31)), as well as the tensor operator modelising the transversion \( C \rightarrow A \), is somewhat arbitrary. The value of the rank of the operator modelising the translational errors in 2nd position will be generally assumed larger than the one describing errors in 1st position and the latter one will be generally assumed larger than the one describing errors in 3rd position, so to model the less frequent misreading.

IV. OUTCOME OF THE MODELISATION OF TRANSLATION ERRORS

In the following I use the standard notation: \( X,Y,N \) denoting any nucleotide, \( Y = C, U \) (pyrimidine), \( R = G, A \) (purine).

1. Misreading of 3rd nucleotide

The transitions in 3rd position in the codons \( XZC \) and \( XZG \), are modelised by the operator given by eq. (30) with \( a = 0 \): (in the following the equations have to be read by the western rule from left to right)

\[
\psi(XZC) \circ (\tau_{H,-1}^1 \otimes \tau_{V,0}^0) \implies \psi(XZU) \tag{33}
\]

\[
\psi(XZG) \circ (\tau_{H,-1}^1 \otimes \tau_{V,0}^0) \implies \psi(XZA) \tag{34}
\]

We get the splitting of the 64 codons in 32 doublets of the form \( XZR \) and \( XZY \).

The transversions in 3rd position in the codons \( XZC \) and \( XZU \) are modelised by the following operators:

\[
\psi(XZC) \circ (\tau_{H,0}^b \otimes \tau_{V,-1}^1) \implies \psi(XZG) \tag{35}
\]

\[
\psi(XZU) \circ (\tau_{H,0}^b \otimes \tau_{V,-1}^1) \implies \psi(XZA) \tag{36}
\]

\[
\psi(XZC) \circ (\tau_{H,-1}^b \otimes \tau_{V,-1}^1) \implies \psi(XZA) \tag{37}
\]

where in eqs. (35), (36), (37) \( b = 2 \) if the first two nucleotides (dinucleotide) \( XZ \) are: CA, GA, CG, UG, UA, UU, AU, AA, GG, AG) t and \( b = 1 \) otherwise.

We get the merging of 16 doublets in 8 quartets, the quartets being the codons whose the first two nucleotides are: CC, CU, CG, UC, GG, GC, GU, and AC.

2. Misreading of 1st nucleotide

The transitions are modelised by the operators eq. (30) with \( a = 1 \):

\[
\psi(CXN) \circ (\tau_{H,-1}^1 \otimes \tau_{V,0}^1) \implies \psi(UNX) \tag{38}
\]

\[
\psi(GXN) \circ (\tau_{H,-1}^1 \otimes \tau_{V,0}^1) \implies \psi(AXN)
\]

We get the merging of the doublet UUR and the quartet CUN in a sextet (encoding Leu).

The transversions in first position are modelised by the operators:

\[
\psi(CXZ) \circ (\tau_{H,0}^c \otimes \tau_{V,-1}^1) \implies \psi(GXZ) \tag{39}
\]

\[
\psi(UXZ) \circ (\tau_{H,0}^c \otimes \tau_{V,-1}^1) \implies \psi(AXZ) \tag{40}
\]

\[
\psi(CXZ) \circ (\tau_{H,-1}^c \otimes \tau_{V,-1}^1) \implies \psi(AXZ) \tag{41}
\]
where \( c = 1 \) if the codons CXZ and UXZ belong to the same irrep. and \( c = 2 \) otherwise.

As a consequence the doublet AGR merges into the quartet CGN forming another sextet (encoding Arg).

3. Misreading of central nucleotide

The transitions are modelised by the operators eq. (30) with \( a = 2 \):

\[
\begin{align*}
\psi(XCN) \circ (\tau_{H,-1}^1 \otimes \tau_{V,0}^2) &\implies \psi(XUN) \\
\psi(XGN) \circ (\tau_{H,-1}^1 \otimes \tau_{V,0}^2) &\implies \psi(XAN)
\end{align*}
\]

No modification of the previous established pattern comes out.

We modelise the transversions as

\[
\begin{align*}
\psi(XCZ) \circ (\tau_{H,0}^1 \otimes \tau_{V,-1}^2) &\implies \psi(XGZ) \\
\psi(XUZ) \circ (\tau_{H,0}^2 \otimes \tau_{V,-1}^2) &\implies \psi(XAZ) \\
\psi(XCZ) \circ (\tau_{H,-1}^c \otimes \tau_{V,-1}^2) &\implies \psi(XAZ)
\end{align*}
\]

where \( c = 1 \) if the codons XCZ and XUZ belong to the same irrep. and \( c = 2 \) otherwise. It turns out that one should expect the fusion in a sextet of the quartet UCN and of the doublet UGY. This sextet does not appear, but as we shall see below the quartet UCN indeed merges with the doublet AGR. One should also expect the fusion in a sextet of the quartet CCN and the doublet CAY, which indeed does not happen. Both these results suggest that indeed the misreading of the central nucleotide is a very weak effect, if not enhanced by the simultaneous misreading of the first nucleotide.

4. Misreading of two nucleotides

The transition and transversion of the first (second) nucleotide is modelised by the same operator used for the translation or transversion on the first nucleotide. In the following we denote with a lower label the position of the nucleotide where the operator acts. The action of the two-nucleotides operators has to be computed in the following way: as first step one has to compute the action of the operator labelled by I giving rise to a ”virtual” state with the labels assigned by the action of the relevant operator on the initial state of the codon, then one considers the action of the operator labelled by II on the ”virtual” state and gets the labels of the final state. If these labels denote, see Table(II), the state corresponding to the codon, the misreading is allowed. As an example let us compute

\[
\psi(CCN) \implies \psi(UUN)
\]

\[
\begin{align*}
(i) \quad \psi(CCN) \circ (\tau_{H,-1}^1 \otimes \tau_{V,0}^1)_{(vir)} &\implies \psi(UCN)_{(vir)} \\
(ii) \quad \psi(UCN)_{(vir)} \circ (\tau_{H,-1}^1 \otimes \tau_{V,0}^2)_{II} &\implies \psi(UUN)
\end{align*}
\]

We get the merging the doublet AGR with the quartet UCN giving rise to the third sextet (encoding Ser).
V. CONCLUSIONS

The outcome of the proposed mathematical model is a pattern of organisation in: 3 sextets, 5 quartets, 13 doublets which is very close to the pattern of the VMC and SUC codes. In particular it differs from the last one for the absence of the breaking of two doublets into singlets, which may reasonably be seen as a minor effects. A more refined analysis, see [15], indeed gives hints for:

- the breaking of the doublets
- the choice of the Stop codons
- the similarity of the physical chemical properties of a.a. encoded by codons prone to misreading

The number and dimension of multiplets seem to be the outcome of a strategy addressed to keep as many as different amino acids with a reasonable protection against translation errors.

As final remark, in [15], a discussion of the dependence of the obtained results from the choice of tensor operators mimicking the misreading shows that there is a dependence, but the main bulk is left unmodified.
REFERENCES

[1] M. Singer, P. Berg, *Genes and Genomes*, Editions Vigot, Paris (1992).
[2] B.K. Davies, Prog.Biophys.Mol.Biol. 72 (1999) 157.
[3] D.T. Jones, W.R. Taylor, J.M. Thornton, CABIOS 8 (1992) 275.
[4] O.P. Judson, D. Haydon, J.Mol.Evol. 49 (1999) 539.
[5] F.H.C. Crick, J.Mol.Biol. 38 (1968) 367.
[6] G. Gamow, Nature 173 (1954) 318.
[7] S.R. Pelc, Nature 207 (1965) 597.
[8] C.R. Woese, D.H. Dugre,, S.A. Dugre, M. Kondo, W.C. Saxinger Cold Spring Harbor Symp.Quant.Biol. 31 (1966) 723.
[9] JT-F. Wong, Proc.Natl.Acad.Sci. USA 72 (1975) 1909.
[10] T.M. Sonneborn, in V. Bryson, H.J. Vogel Eds. "Evolving genes and proteins", Academic Press, New York (1965), 377.
[11] C.J. Epstein, Nature 210 (1966) 25.
[12] C.R. Woese, Proc.Natl.Acad.Sci. USA 54 (1965) 1546.
[13] A.L. Goldberg, R.E. Wittes, Science 153 (1966) 420.
[14] T. Maeshiro, M. Kimura, Proc.Natl.Acad.Sci. USA 72 (1975) 1909.
[15] A. Sciarrino, *A Mathematical Model Accounting for the Organisation in Multiplets of the Genetic Code*, math-ph/0102022
[16] L. Frappat, A. Sciarrino, P. Sorba, Phys.lett.A 250 (1998) 214.
[17] L.C. Biedenharn, M.A. Lohe, *Quantum Group Symmetry and q-Tensor Algebras*, World Scientific, Singapore (1995)
[18] V. Marotta, A. Sciarrino, J. Math. Phys. 41 (2000) 5735, math.QA/9811143
[19] M. Kashiwara, Commun. Math. Phys. 133 (1990) 249.
[20] S.M. Friedman, I.B. Weinstein, Proc.Natl.Acad.Sci. USA 52 (1964) 988.
[21] S.J. Freeland, L.D. Hurst, J.Mol.Evol. 47 (1998) 238.
TABLE I. Relative frequency (R.f.) \(10^{-3}\) of occurrence of 20 amino-acids (a.a.) and the number (N) of corresponding encoding codons.

| a.a. | R.f. | N | a.a. | R.f. | N | a.a. | R.f. | N | a.a. | R.f. | N | a.a. | R.f. | N |
|------|------|---|------|------|---|------|------|---|------|------|---|------|------|---|
| Leu  | 91   | 6 | Glu  | 62   | 2 | Arg  | 51   | 6 | Tyr  | 32   | 4 |      |      |   |
| Ala  | 77   | 4 | Thr  | 59   | 4 | Pro  | 51   | 4 | Met  | 24   | 1 |      |      |   |
| Gly  | 74   | 4 | Lys  | 59   | 2 | Asn  | 43   | 2 | His  | 23   | 2 |      |      |   |
| Ser  | 69   | 6 | Ile  | 53   | 3 | Gln  | 41   | 2 | Cys  | 20   | 2 |      |      |   |
| Val  | 66   | 4 | Asp  | 52   | 2 | Phe  | 40   | 2 | Trp  | 14   | 1 |      |      |   |
TABLE II. The vertebral mitochondrial code. The upper label denotes different irreducible representations. In bold character the amino acids which are encoded differently in the eukaryotic or standard code: UGA, AUA, AGR encoding respectively for Ter, Ile and Arg.

| codon | a.a. | $J_H$ | $J_V$ | $J_{3,H}$ | $J_{3,V}$ | codon | a.a. | $J_H$ | $J_V$ | $J_{3,H}$ | $J_{3,V}$ |
|-------|-----|-----|-----|-----|-----|-------|-----|-----|-----|-----|-----|-----|
| CCC   | Pro | $\frac{2}{3}$ | $\frac{2}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | UCC   | Ser | $\frac{2}{3}$ | $\frac{2}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| CCU   | Pro | $\frac{1}{3}$ | $\frac{2}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | UCU   | Ser | $\frac{1}{3}$ | $\frac{2}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| CCG   | Pro | $\frac{2}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | UCG   | Ser | $\frac{2}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| CCA   | Pro | $\frac{1}{3}$ | $\frac{2}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | UCA   | Ser | $\frac{1}{3}$ | $\frac{2}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| CUC   | Leu | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | UUC   | Phe | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| CUU   | Leu | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | UUU   | Phe | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| CUG   | Leu | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | UUG   | Leu | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| CUA   | Leu | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | UUA   | Leu | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| CGC   | Arg | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | UGC   | Cys | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| CGU   | Arg | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | UGU   | Cys | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| CGG   | Arg | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | UGG   | Trp | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| CGA   | Arg | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | UGA   | Trp | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| CAC   | His | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | UAC   | Tyr | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| CAU   | His | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | UAU   | Tyr | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| CAG   | Gln | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | UAG   | Ter | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| CAA   | Gln | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | UAA   | Ter | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| GCC   | Ala | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | ACC   | Thr | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| GCU   | Ala | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | ACU   | Thr | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| GCG   | Ala | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | ACG   | Thr | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| GCA   | Ala | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | ACA   | Thr | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| GUC   | Val | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | UAC   | Ile | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| GUU   | Val | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | AUU   | Ile | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| GUG   | Val | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | AUG   | Met | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| GUA   | Val | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | AUA   | Met | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| GGC   | Gly | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | AGC   | Ser | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| GGU   | Gly | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | AGU   | Ser | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| GGG   | Gly | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | AGG   | Ter | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| GGA   | Gly | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | AGA   | Ter | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| GAC   | Asp | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | AAC   | Asn | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| GAU   | Asp | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | AUA   | Asn | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| GAG   | Glu | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | AAG   | Lys | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |
| GAA   | Glu | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | AAA   | Lys | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ | $\frac{1}{3}$ |