Available online at www.sciencedirect.com
ScienceDirect
C. R. Biologies 332 (2009) 336–350
COMPTES RENDUS BIOLOGIES

Genetics / Génétique

ISSCOR: Intragenic, Stochastic Synonymous Codon Occurrence Replacement – a new method for an alignment-free genome sequence analysis

Jan P. Radomski [a,*], Piotr P. Slonimski [b,*]

[a] *Interdisciplinary Center for Mathematical and Computational Modeling, Warsaw University, Pawińskiego 5A, Bldg. D, 02106 Warsaw, Poland*
[b] *Centre de génétique moléculaire du CNRS & Université Pierre-et-Marie Curie (Paris-6), 91190 Gif-sur-Yvette cedex, France*

Received 11 November 2008; accepted after revision 2 December 2008

Available online 3 February 2009

Presented by Jean Rosa

Abstract

Synonymous codons do not occur at equal frequencies. Codon usage and codon bias have been extensively studied. However, the *sequential order* in which *synonymous codons* appear within a gene has not been studied until now. Here we describe an *in silico* method, which is the first attempt to tackle this problem: to what extent this sequential order is unique, and to what extent the succession of synonymous codons is important. This method, which we called **I**ntragenic, **S**tochastic **S**ynonymous **C**odon **O**ccurrence **R**eplacement (ISSCOR), generates, by a Monte Carlo approach, a set of genes which code for the *same amino acid sequence*, and display the *same codon usage*, but have random permutations of the synonymous codons, and therefore different sequential codon orders from the original gene. We analyze the complete genome of the bacterium *Helicobacter pylori* (containing 1574 protein coding genes), and show by various, alignment-free computational methods (e.g., frequency distribution of codon-pairs, as well as that of nucleotide bigrams in codon-pairs), that: (i) not only the succession of adjacent synonymous codons is far from random, but also, which is totally unexpected, the occurrences of *non-adjacent synonymous codon-pair*s are highly constrained, at strikingly long distances of dozens of nucleotides; (ii) the statistical deviations from the random synonymous codon order are overwhelming; and (iii) the pattern of nucleotide bigrams in codon-pairs can be used in a novel way for characterizing and comparing genes and genomes. Our results demonstrate that the sequential order of synonymous codons within a gene must be under a strong selective pressure, which is superimposed on the classical codon usage. This new dimension can be measured by the ISSCOR method, which is simple, robust, and should be useful for comparative and functional genomics. ***To cite this article: J.P. Radomski, P.P. Slonimski, C. R. Biologies 332 (2009).***

Résumé

ISSCOR : une nouvelle méthode pour une analyse des séquences de génome sans alignement. Les codons synonymes n'apparaissent pas à des fréquences égales. L'usage des codons et le biais codonique ont été abondamment étudiés. Par contre, l'ordre dans lequel les codons synonymes se présentent le long d'un gène n'a pas encore été analysé. Cet ordre est-il unique ? A quel point l'enchaînement des codons synonymes non-adjacents est-il important ? Nous présentons ici une nouvelle méthode *in silico* pour aborder ce problème. Dans cette méthode, appelée ISSCOR, on permute, par une approche Monte-Carlo, les codons

* Corresponding authors.
E-mail addresses: janr@icm.edu.pl (J.P. Radomski), slonimski@cgm.cnrs-gif.fr (P.P. Slonimski).

1631-0691/$ – see front matter
doi:10.1016/j.crvi.2008.11.008

synonymes d'un gène. On obtient ainsi un ensemble de séquences nucléotidiques, qui ont le même usage des codons, qui codent pour la même séquence protéique, mais qui diffèrent par l'ordre des codons synonymes. Nous avons analysé la totalité du génome de la bactérie *Helicobacter pylori* (1574 ORFs) et nous démontrons, par différentes approches informatiques (analyse de la fréquence de distribution des paires de codons ainsi que celle des bigrams de nucléotides dans des paires de codons), que : (i) les codons synonymes s'enchaînent dans un ordre déterminé sur de longues distances (douzaines de nucléotides) ; (ii) l'enchaînement des codons synonymes le long d'un gène est en relation directe avec le codage de la protéine ; (iii) les bigrams nucléotidiques situés sur des paires de codons peuvent être utilisés comme une nouvelle méthode, simple et robuste, pour caractériser les gènes et les génomes. ***Pour citer cet article : J.P. Radomski, P.P. Slonimski, C. R. Biologies 332 (2009).***

Keywords: Alignment free analysis; Random codon shuffling; Sequential order of synonymous codons; Synonymous codon replacement

Mots-clés : Analyse sans alignement ; Réarrangement aléatoire des codons ; Ordre séquentiel de codons synonymes ; Remplacement de codons synonymes

1. Introduction

The genetic code is degenerate. The relative frequency with which synonymous codons are used may vary widely from species to species, or from one gene (or a class of genes) to another. A large, and ongoing, body of literature deals with this subject under various headings, such as "codon usage", "codon bias", "codon adaptation", etc. [1–17].

It is of significant interest to ask if, and to what extent, the genetic, molecular and cellular apparatus of each species is geared towards actual codon patterns of each sequence in the genome during translation and protein expression. The first part is obviously rhetorical, as there are plenty of indicators that such differences are not only present, but in fact crucial, and influence the steady state ratio of various proteins. Living organisms have very often quite biased preferences for some synonymous codons over other possible synonymous nucleotide triplets coding for the same amino acids. These differences and their variation have been extensively studied, however, no decisive governing rules have yet been discovered. Frequencies of codons for many species are in close correlation with their genome's GC contents, but the underlying forces governing this are not clear – it might be possible, that it is the GC content which is determining a genome's amino acids predilection for the specific codons being used and their bias. On the other hand it might be that reverse causative relationships are in operation: codons-specific amino acids usage is a driving factor for observed GC contents. Possible factors and forces driving synonymous codons usage postulated so far include, among many others: translational optimization [2–6], mRNA structural effects [7], protein composition [8], and protein structure [9], gene expression levels [2,10], the tRNA abundance differences between different genomes, and tRNA optimization [11–13], different mutation rates and patterns [14]. Also, some other possibilities were hypothesized, like local compositional bias [15], and even gene lengths might play a role too [16].

It is clear, that many interesting biological mechanisms underlie the basic phenomenon of genetic code degeneracy. One of its aspects, however, has not been studied until now, namely, the question dealing with the *sequential order* of occurrence of *synonymous codons*. To what extent this order is characteristic for a gene, to what extent for a set of genes, or a genome. Are there some rules governing such an order? How can one measure the order of synonymous codons, and compare different orders? Obviously, an order of elements in a linear set is a different property, than the frequency of elements in the set. The amino acid composition of a protein (which formally is exactly equivalent to the synonymous codon frequency, or codon usage, of a protein coding sequences) carries much less information than the amino acid sequence of such protein, which in turn is less information intensive than a corresponding nucleotide sequence coding the same protein.

This question can be formulated more precisely. Let us consider a given frequency of synonymous codon usage characteristic for a gene. There is a very large number of different orders in which the synonymous codons can appear sequentially along the gene without changing either the amino acid sequence of the encoded protein, or the codon usage of the gene. For all practical purposes this number is infinite, since the number of permutations of synonymous codons in a gene is comparable to the number of permutations of amino acids in a protein.

However, there are few means available experimentally to actually attempt even simplest direct measurements of the factors involved. Here, we describe an *in silico* method, which, as far as we know, is the first at-

tempt to tackle the problem of the sequential order of synonymous codons. We call it ISSCOR (Intragenic, Stochastic Synonymous Codon Occurrence Replacement) for following reasons: (i) it analyses a original single gene, the nucleotide sequences of an original protein coding sequence (ORF). Of course, after analyzing several individual genes, the results can be computed for a set of genes, or a complete genome; (ii) it is essentially a Monte-Carlo approach. Synonymous codons, which occur at different positions of an ORF are replaced randomly, with the frequencies given by the codon usage of the whole genome. The method generates nucleotide sequences of non-original ORFs, which have identical codon usages, and would encode identical amino acid sequences. It is equivalent to random permutations of the synonymous codon sequence.

We have chosen to test the application of the ISSCOR method on the genome of *Helicobacter pylori*. This organism was selected for two reasons: (i) the *H. pylori* codon usage is not dominated by biased mutation patterns and displays a striking absence for transitionally mediated selection among synonymous codons [17]; and (ii) the *H. pylori* genome shows a striking periodic oscillations of it's nucleotide sequence, and it was hypothesized that these oscillations could be related to the usage of particular synonymous codons for constructing α-helical protein folds [18]. To this end we have retrieved (as of October 2006) from TIGR the complete set of *H. pylori* protein coding sequences, however, due to the needs of the ISSCOR algorithms, only those containing unambiguously assigned nucleotides (A, C, G, and T, in standard notation) have been used – this resulted in 1574 ORFs.

2. The concepts and methods used

2.1. The concept of Intragenic, Stochastic Synonymous Codon Occurrence Replacement

For the reasons outlined briefly above in the Introduction, we describe here the method of calculating the whole genome codon-pair pattern profiles, as well as assessing their significance. Previously [18–21] we have described alignment free approaches to the problem of comparison and analysis of complete genomes, and some techniques enabling us to cope with the sparseness of the n-gram type of genomic information representations. The problem of sparse occurrence matrices is not only present, but even more pronounced when dealing with the number of permutations of the possible synonymous codons. Calculating the set of n-grams for such occurrences will lead to a vector representation, which is severely sparse, especially for higher n-grams lengths, and hence to very poor statistics. To alleviate this problem, we propose here a hybrid approach. Namely, when computing counts of codon-pair patterns – separated by codon sub-sequences of differing length – the actual composition of these spacer sub-sequences will be neglected. However, when such partial counts are used as a composite set, poor statistics are no longer a hindering obstacle, and the complete information about particular n-gram frequencies profile is preserved, albeit in a distributed and convoluted form.

There are only two requirements fundamental for the ISSCOR method: (a) the amino acid sequence of every protein in the whole genome must be strictly preserved; (b) random shuffling of synonymous codons will be performed separately within each codon-degeneracy equivalence group using uniform probability distribution (thus, the codon usage profile for the whole genome, after the synonymous codon shuffling will be preserved within stochastic bounds of uniform probability distribution, and the overall codon usage of the whole genome will not be changed).

For every protein coding gene, with its original nucleotide sequence j_0 in a genome i we generate, by a Monte Carlo approach, a set of equivalent nucleotide strings $(j_1, j_2, j_3, \ldots, j_N)$ which have the following properties:

- they have the same nucleotide lengths as the j_0;
- they have the exactly the same amino acid sequence as the j_0 (i.e., the proteins translated from the $j_1, j_2, j_3, \ldots, j_N$ are identical);
- they have, *on average*, the same codon usage frequencies (i.e., the codon triplet occurrence frequency) as the whole genome, and if the gene under study has no codon bias, the same codon usage as j_0;
- they have in the vast majority of cases a synonymous codon order *different from the original sequence* j_0.

This is an essential point, which merits a commentary. The probability that a given string j_i generated stochastically has the same synonymous codon order as the original j_0 decreases with the product of its length, with a probability limit tending rapidly to zero (e.g., for the gene HP1355, Fig. 1, this probability is less than 10^{-3} for the first six codons, shown in Fig. 1, while the whole gene length is actually 215 codons, thus such probability for this gene is vanishingly small).

Therefore, the ISSCOR method allows comparing the original codon sequence with an ensemble of differ-

	NUCLEOTIDE																																								
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42
ORIGINAL SEQUENCE	a	t	g	g	a	g	a	t	t	a	g	a	a	c	c	t	t	t	t	t	a	g	a	a	c	g	c	g	c	t	t	t	a	a	a	a	g	a	a	g	a	t
SHUF001	a	t	g	g	a	g	a	t	c	a	g	g	a	c	t	t	t	c	t	t	g	g	a	a	a	g	g	g	c	a	t	t	a	a	a	a	g	a	a	g	a	t
SHUF002	a	t	g	g	a	a	a	t	a	a	g	g	a	c	c	t	t	t	t	t	g	g	a	a	a	g	g	g	c	t	t	t	g	a	a	a	g	a	g	g	a	t
SHUF003	a	t	g	g	a	a	a	t	c	a	g	g	a	c	c	t	t	t	t	t	g	g	a	a	c	g	t	g	c	t	t	t	g	a	a	a	g	a	a	g	a	t
SHUF004	a	t	g	g	a	a	a	t	c	c	g	t	a	c	c	t	t	t	t	t	g	g	a	a	a	g	a	g	c	a	c	t	g	a	a	a	g	a	a	g	a	t
...																																										
...																																										
SHUF500	a	t	g	g	a	g	a	t	c	c	g	t	a	c	c	t	t	t	t	t	a	g	a	a	c	g	c	g	c	c	t	t	a	a	a	a	g	a	g	g	a	t
	CODON's NUMBER																																									
	1		2		3		4		5		6		7		8		9		10		11		12		13		14															
	PROTEIN																																									
	M		E		I		R		T		F		L		E		R		A		L		K		E		D													
	CODON USAGE (of the original sequence)																																									
	1.000		0.266		0.494		0.268		0.315		0.788		0.390		0.734		0.244		0.393		0.390		0.771		0.734		0.729													

Fig. 1. Example of synonymous codon replacements by the ISSCOR method, preserving the amino acid sequence of a gene. The beginning of (the first 14 codons) the original, genuine sequence of the gene HP1355 (coding for the nicotinate–nucleotide phosphorylase) is shown in the first line; the synonymous codons are replaced randomly using the frequencies given in the last line. The first run of replacement's (SHUF001) produces the nucleotide sequence, where synonymous codons, which are different from original are shown in red; in successive runs (SHUF002, 003, 004, until 500), other replacements appear (shown in green and blue). The frequency of occurrence of each of the 144 BiHex patterns (Table 3) is calculated for every run of replacements, i.e., separately for sequences SHUF001, 002, . . . , 500; finally the averages, their standard deviations; and deviates are calculated as explained in the text. The amino acid sequences are, of course, identical.

Table 1
The list of all the 144 BiHex patterns analyzed.

	A	C	G	T
A	**A**xx-**A**xx x**A**x-**A**xx xx**A**-**A**xx	**C**xx-**A**xx x**C**x-**A**xx xx**C**-**A**xx	**G**xx-**A**xx x**G**x-**A**xx xx**G**-**A**xx	**T**xx-**A**xx x**T**x-**A**xx xx**T**-**A**xx
	Axx-x**A**x x**A**x-x**A**x xx**A**-x**A**x	**C**xx-x**A**x x**C**x-x**A**x xx**C**-x**A**x	**G**xx-x**A**x x**G**x-x**A**x xx**G**-x**A**x	**T**xx-x**A**x x**T**x-x**A**x xx**T**-x**A**x
	Axx-xx**A** x**A**x-xx**A** xx**A**-xx**A**	**C**xx-xx**A** x**C**x-xx**A** xx**C**-xx**A**	**G**xx-xx**A**x **G**x-xx**A** xx**G**-xx**A**	**T**xx-xx**A** x**T**x-xx**A** xx**T**-xx**A**
C	**A**xx-**C**xx x**A**x-**C**xx xx**A**-**C**xx	**C**xx-**C**xx x**C**x-**C**xx xx**C**-**C**xx	**G**xx-**C**xx x**G**x-**C**xx xx**G**-**C**xx	**T**xx-**C**xx x**T**x-**C**xx xx**T**-**C**xx
	Axx-x**C**x x**A**x-x**C**x xx**A**-x**C**x	**C**xx-x**C**x x**C**x-x**C**x xx**C**-x**C**x	**G**xx-x**C**x x**G**x-x**C**x xx**G**-x**C**x	**T**xx-x**C**x x**T**x-x**C**x xx**T**-x**C**x
	Axx-xx**C** x**A**x-xx**C** xx**A**-xx**C**	**C**xx-xx**C** x**C**x-xx**C** xx**C**-xx**C**	**G**xx-xx**C** x**G**x-xx**C** xx**G**-xx**C**	**T**xx-xx**C** x**T**x-xx**C** xx**T**-xx**C**
G	**A**xx-**G**xx x**A**x-**G**xx xx**A**-**G**xx	**C**xx-**G**xx x**C**x-**G**xx xx**C**-**G**xx	**G**xx-**G**xx x**G**x-**G**xx xx**G**-**G**xx	**T**xx-**G**xx x**T**x-**G**xx xx**T**-**G**xx
	Axx-x**G**x x**A**x-x**G**x xx**A**-x**G**x	**C**xx-x**G**x x**C**x-x**G**x xx**C**-x**G**x	**G**xx-x**G**x x**G**x-x**G**x xx**G**-x**G**x	**T**xx-x**G**x x**T**x-x**G**x xx**T**-x**G**x
	Axx-xx**G** x**A**x-xx**G** xx**A**-xx**G**	**C**xx-xx**G** x**C**x-xx**G** xx**C**-xx**G**	**G**xx-xx**G** x**G**x-xx**G** xx**G**-xx**G**	**T**xx-xx**G** x**T**x-xx**G** xx**T**-xx**G**
T	**A**xx-**T**xx x**A**x-**T**xx xx**A**-**T**xx	**C**xx-**T**xx x**C**x-**T**xx xx**C**-**T**xx	**G**xx-**T**xx x**G**x-**T**xx xx**G**-**T**xx	**T**xx-**T**xx x**T**x-**T**xx xx**T**-**T**xx
	Axx-x**T**x x**A**x-x**T**x xx**A**-x**T**x	**C**xx-x**T**x x**C**x-x**T**x xx**C**-x**T**x	**G**xx-x**T**x x**G**x-x**T**x xx**G**-x**T**x	**T**xx-x**T**x x**T**x-x**T**x xx**T**-x**T**x
	Axx-xx**T** x**A**x-xx**T** xx**A**-xx**T**	**C**xx-xx**T** x**C**x-xx**T** xx**C**-xx**T**	**G**xx-xx**T** x**G**x-xx**T** xx**G**-xx**T**	**T**xx-xx**T** x**T**x-xx**T** xx**T**-xx**T**

ent synonymous sequences-coding for the same amino acids sequence.

2.2. The computational procedure

Mathematically speaking, first, the whole genome's codon usage frequencies are determined for each species i, and on that basis probabilities of replacement are calculated separately for each codon-degeneracy equivalence group d:

$$P_i^k = \frac{u_k}{\sum_{d=1}^{E} u_d} \tag{1}$$

where: P_i^k is the probability that any other codon – from the same degeneracy equivalence group d – will be randomly replaced by the codon k; and u_k is the synonymous codon k triplet frequency for a given amino acid in a whole genome. Therefore, obviously for any given degeneracy equivalence group d, the sum of such probabilities will always be equal to 1.

Then, successively for each codon in a gene the procedure of it's synonymous random replacement is performed based on probabilities according to Eq. (1). Finally, the resulting shuffled sequences are determined, and compared to the original sequence of the gene.

To this end we need, first of all to calculate series of codon-pair pattern[1] occurrence matrices, designed henceforth as O_i^λ, for the original genome i. The method described here is applicable to any genome, and is independent of the respective genome sizes.

The method involves several steps (although, depending on the actual purpose at hand, not all the chain will be always necessary). For completeness sake, we present them here sequentially, to facilitate understanding.

First, for each protein coding sequence, we determine a complete matrix of all codon-pair patterns. Obviously, in a protein coding gene, there are at most 3904 ($61 \times 61 + 61 \times 3$) unique codon-pair patterns. For a given sequence V, and the all codon-spacer lengths, in order to calculate observed values of a particular codon-pair pattern (c_k, c_l), first we need to construct a series of matrices O^λ (occurrence matrices). Each element of

[1] As the repetitive use of the sub-phrase: "codon-pair pattern" may lead to possible confusion, and it might be tedious for the reader, we introduce here the term of *hexon*. Thus, it is important to give, and to distinguish several definitions of some frequently used notions:

Codon-pair: two consecutive codons in the reading frame zero, located on the same strand, and within the same ORF (in the 5′–3′ orientation, i.e., Watson strand); there are $61 \times 61 + 61 \times 3$ such different codon-pairs, and different codon-pairs in an ORF terminated by a stop codon.

Hexon: a codon-pair separated by an arbitrary number of other codons (λ); for $\lambda = 0$ the hexon is an adjacent codon-pair, corresponding to a hexanucleotide while for all other values of λ, the hexon corresponds to non-adjacent codon-pairs; for $\lambda = 1$ the hexon corresponds to a nonanucleotide, for $\lambda = 2$ it corresponds to a dodecanucleotide, etc. (for which only the first and the last codons are specified); in this work we shall explore hexons from $\lambda = 0$ to $\lambda = 32$; i.e., from hexanucleotides, to 102-oligonucleotides, for which there are $3904 \times 33 = 128\,832$ different hexon patterns.

Bigram: is a group of two – out of four possible – symbols (in the context of this work they are A, C, G, and T, clearly corresponding to the four DNA nucleotides).

BiHex: is a *bigram derived from a hexon*; since each codon comprises three nucleotides, in the respective positions 1, 2, 3, and the analysis involves all possible positional combinations of the four nucleotides; at six positions, there are altogether 144 *BiHex patterns* ($3 \times 3 \times 4 \times 4$) for each given value of λ, and 144×33 for all values of λ explored here. Table 1 summarizes all the possible BiHex patterns.

every matrix O^{λ} contains the counted sum of all specific codon-pair patterns (c_k, c_l), separated by a string of other codons present in this sequence, where the λ denotes the number of other codons separating the given codon-pair pattern (c_k, c_l). Using a sliding window of the length $3 * (\lambda + 2)$ nucleotides, and starting at the position m, we would scan the whole sequence V, calculating elements of the matrix by the formula:

$$O^{\lambda}(c_k, c_l, p) = \sum_{m=1}^{M-\lambda-1} f(c_k, c_l, \lambda, m, p), \tag{2}$$

where M is the sequence's length, and

$$f(c_k, c_l, \lambda, m, p) = \begin{cases} 1, & \text{if } V(m) = c_k, \text{ and } V(m+\lambda+1) = c_l, \text{ and} \\ & \text{the codon-pair pattern } (c_k, c_l) \text{ matches} \\ & \text{the pattern of the particular comparison } p, \\ 0, & \text{otherwise.} \end{cases}$$

Comparisons involve matches between the predefined codon-pair patterns, of the first codon c_k, taken together with the second codon c_l.

That is, a particular positional comparison p involves only one nucleotide from the first codon c_k, and one nucleotide from the second codon c_l, ignoring all four remaining nucleotides, which corresponds to a BiHex pattern (see footnote 1). Thus, there are, e.g., nine BiHex patterns containing the adenine (**A**) at any position in a first codon, together with the cytosine (**C**) at any position in a second codon, etc. Obviously, when $\lambda = 0$, one has an adjacent codon-pair pattern (hexanucleotide), for $\lambda = 1$ it is a nonanucleotide, and so on. Note, that since these are ordered counts, each starting at the sequence's 5′-terminus, the matrices O_i^{λ} are not symmetrical, that is the count of the hexon (c_k, c_j) is different from the count of the hexon (c_j, c_k). For each of species i, their hexon counting is repeated for all sequences of the whole genome separately, but the results are then summed up for all sequences, and all respective particular pattern comparisons p. Therefore matrices O_i^{λ} should be considered as a raw, spacer λ dependent, representation of *sui generis* species specific occurrences of their hexons unique patterns.

To make the results independent of a particular genome size (or a subset of genes), we propose to calculate how much the number of actually observed hexons in the original genome, differs from the mean number of the corresponding hexons, observed after performing N random ISSCOR genome permutations, divided by the standard deviation observed in the shuffled genomes:

$$D_{xAx\_\lambda\_Txx} = \frac{O_{\text{occurrences}} - (\sum_n^N R^n_{\text{shuffled}})/N}{STD_{\text{shuffled}}} \tag{3}$$

where:

$D_{xAx\_\lambda\_Txx}$ is a *deviate* of the results for, e.g., the pattern xAx_λ_Txx, that is for the all codon combinations comprising the nucleotide A at the second position in the first codon, and the nucleotide T at the first position of the second codon – the border codons being separated by the number λ of other codons;

$O_{\text{occurrences}}$ are the numbers of the actually observed occurrences for any given hexon in the unperturbed, whole genome;

R^n_{shuffled} are the numbers of occurrences for any given hexon pattern counted *after* codons of the whole genome have been shuffled randomly (as described by the above), thus the R^n_{shuffled}/N is a mean number of such occurrences after the N such random shuffles;

STD_{shuffled} is a standard deviation for all occurrences of a given hexon pattern, after N random shufflings of the whole genome.

We have verified that $N = 500$ is sufficient to ensure satisfactory randomness since the results are practically identical for $N = 500$, 1000, and 1500.

3. Results and discussion

In order to facilitate the comprehension of the BiHex concept, and that of the first results obtained, we shall begin by an example, the detailed analysis of just one particular BiHex pattern: xxG-xxG for $\lambda = 6$. It should be remembered that for all the examined λs there are 4455 ($135 \times 33 = 4455$) different and informative[2] BiHex patterns, all of which have been computed in this work.

*3.1. Detailed description of an example: analysis of just one BiHex pattern "*xxG-xxG*" for* $\lambda = 6$ *demonstrates that specific non-adjacent codon-pairs are strongly constrained in the original protein coding genes*

This BiHex pattern, (where the symbol $^{\circ}BH^{\lambda=6}_{p=131}$, or BH^{6}_{131} in a shorthand notation, denotes the BiHex of the pattern number 131, and with the codon-spacer $\lambda = 6$) can be written explicitly as xxG*yyyyyyyyyyyyyyyyyy*xxG. It corresponds to all the oligonucleotides (24 mers; as previously described, the "x" denotes any nucleotide found in the initial and terminal codons of a given

[2] $144 - 9 = 135$, see explanation in the legend of Table 3. There are therefore nine non-informative BiHex patterns.

BiHex pattern, and the "*y*" denotes any nucleotide constituting the spacer part between the respective initial and terminal codons of such a BiHex pattern), occurring in the reading frame zero, of the *Helicobacter pylori* protein coding genes. The analysis comprises several successive steps:

(1) The number of occurrences of the xxG*yyyyyyyyyyyyyyyyyy*xxG pattern is counted in each of the 1574 original genes (in the example given in Fig. 1 this pattern is absent in the segment shown for the original sequence of the gene HP1355, but it is present in the shuffled sequences SHUFF001, SHUFF002, and SHUFF003, of this gene between the nucleotide positions 6 and 27, 12 and 33, and again 12 and 33, respectively). Altogether there are 21 819 occurrences of the BiHex pattern xxG-λ6-xxG in all the genes of *Helicobacter* ($^{\circ}BH_{p=131}^{\lambda=6} = 21\,819$, Table 2A).

(2) By the use of the ISSCOR method one generates 500 shuffled synonymous sequences for each gene (1574 × 500 nucleotide strings) and then calculates, as previously, the number of occurrences of the same BiHex pattern xxG-λ6-xxG which was found to be present, on average, 20 264 times in the ensemble of permuted sequences ($^{m}BH_{p=131}^{\lambda=6} = 20\,264$, Table 2B).

(3) The difference, $^{d}BH_{p=131}^{\lambda=6}$, in the number of occurrences of this pattern between the observed original sequences, and the calculated average shuffled sequences is highly significant, whether measured by χ^2, or standard deviation $-(21\,819 - 20\,264)^2/20\,264 = 119$, for one degree of freedom the probability is $< 10^{-20}$ (Figs. 2A and 2B), and the deviate is more than 10 standard deviations (Fig. 2B). Therefore, some codon-pair hexons must be *over-represented* in the original genome.

(4) Figs. 2A–2B and Tables 2A–2C prove this point. The BiHex pattern xxG-xxG is constituted by 240 different hexons (i.e., codon-pairs, 15 sense codons xxG upstream, and the same plus the TAG stop codon at the terminal position of an ORF, downstream). *A priori*, hexons can be allocated, by their number of occurrences in the genome, into three classes: (i) those which are significantly more abundant in the original genome than in the shuffled ones, (ii) those where the converse is true, and (iii) those where the difference between the original and the shuffled is too small to be of significance. It is apparent from Tables 2A–2C that the first class of hexons predominates: 29 different hexons occur more frequently in the origi-

Table 2A
Detailed analysis. *Observed* number of occurrences of hexons (i.e. codon-pairs) in the original genome for the BiHex pattern xxG-λ=6-xxG.

Observed	**AAG**	**ACG**	**AGG**	**ATG**	**CAG**	**CCG**	**CGG**	**CTG**	**GAG**	**GCG**	**GGG**	**GTG**	**TAG**	**TCG**	**TGG**	**TTG**	***Sum***
AAG	250	65	109	172	61	28	15	41	224	168	236	292	10	34	65	294	*2064*
ACG	84	56	45	112	30	22	1	23	79	97	137	131	1	28	32	147	*1025*
AGG	93	40	61	83	20	17	3	24	86	83	78	127	2	29	38	122	*906*
ATG	189	96	98	254	76	35	10	50	207	226	224	321	9	46	77	358	*2276*
CAG	67	26	20	60	22	6	6	22	61	61	60	80	0	12	24	80	*607*
CCG	33	14	13	41	16	10	4	8	27	36	37	61	1	9	15	60	*385*
CGG	9	6	4	11	7	3	1	4	12	14	18	20	2	2	3	16	*132*
CTG	40	21	17	49	7	6	3	10	41	51	59	54	1	11	25	59	*454*
GAG	228	82	95	154	47	24	12	50	248	178	186	245	5	31	48	231	*1864*
GCG	201	78	99	218	56	31	15	42	178	275	267	326	7	41	73	331	*2238*
GGG	205	117	91	220	62	37	17	42	209	290	330	349	4	49	89	338	*2449*
GTG	298	136	102	310	66	71	12	48	239	326	367	477	9	68	124	444	*3097*
TCG	43	25	19	47	15	4	0	7	34	34	41	51	2	13	13	69	*417*
TGG	67	38	32	80	16	16	5	13	53	78	102	111	4	17	37	95	*764*
TTG	280	146	119	298	87	39	16	78	275	299	361	437	11	63	103	529	*3141*
Sum	*2087*	*946*	*924*	*2109*	*588*	*349*	*120*	*462*	*1973*	*2216*	*2503*	*3082*	*68*	*453*	*766*	*3173*	*21 819*

The codon-pairs should be read from the left (column) to the right (row); e.g., the hexon GTGyyyyyyyyyyyyyyyyyyTTG corresponds to a 24-mer, and occurs 444 times, etc.

Table 2B
Detailed analysis. *Calculated* averages of occurrences of hexons (i.e. codon-pairs) in the shuffled genome for the BiHex pattern xxG-λ=6-xxG.

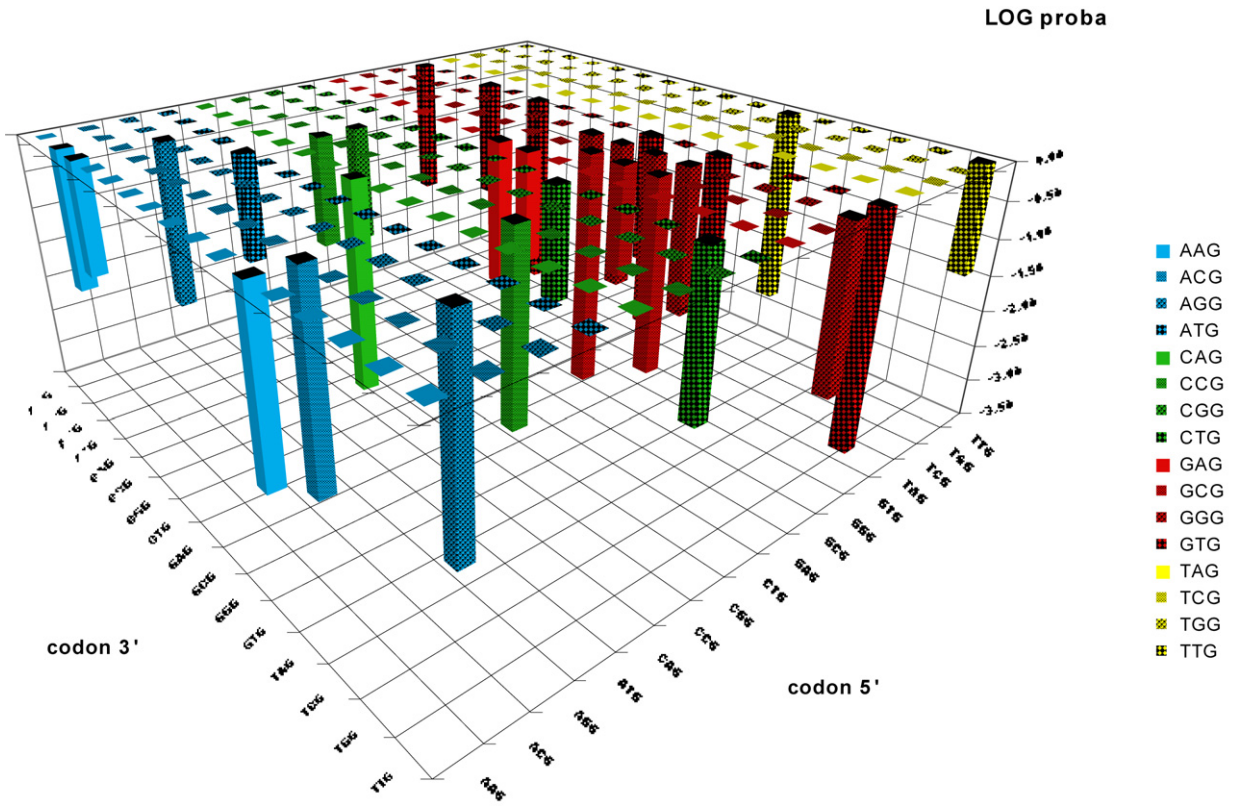
Averages	**AAG**	**ACG**	**AGG**	**ATG**	**CAG**	**CCG**	**CGG**	**CTG**	**GAG**	**GCG**	**GGG**	**GTG**	**TAG**	**TCG**	**TGG**	**TTG**	***Sum***
AAG	240	89	88	159	62	31	11	42	206	189	196	273	9	36	66	288	*1985*
ACG	94	57	37	102	28	17	5	21	82	106	105	121	3	19	35	143	*972*
AGG	84	37	42	84	23	13	5	17	77	80	91	114	3	16	34	117	*837*
ATG	200	103	93	254	59	33	12	54	191	221	240	312	5	45	77	369	*2269*
CAG	60	26	24	50	20	10	3	11	54	51	51	70	2	11	16	77	*536*
CCG	31	19	13	35	9	6	2	7	29	31	33	42	1	6	15	49	*328*
CGG	10	5	5	10	3	2	1	2	10	10	11	14	0	2	4	15	*105*
CTG	42	19	17	43	11	7	2	10	37	43	44	59	2	9	14	71	*430*
GAG	221	84	82	139	55	28	10	35	217	172	172	219	6	33	48	238	*1759*
GCG	191	97	84	222	53	34	11	45	171	224	234	276	6	39	68	305	*2059*
GGG	182	119	85	219	51	34	11	43	171	250	282	304	5	44	85	292	*2177*
GTG	256	130	110	272	67	49	14	55	222	285	331	409	9	54	107	378	*2749*
TCG	36	19	16	42	11	5	2	9	32	40	41	52	1	8	14	61	*390*
TGG	64	34	29	80	15	12	4	14	53	72	88	103	3	13	37	99	*720*
TTG	289	129	121	294	74	47	15	71	252	292	306	404	11	58	100	483	*2947*
Sum	*2001*	*968*	*846*	*2005*	*539*	*328*	*107*	*435*	*1805*	*2068*	*2226*	*2773*	*67*	*392*	*721*	*2984*	*20 264*

As in Table 2A: the calculated average number of occurrences for the hexon GTGyyyyyyyyyyyyyyyyyyTTG corresponding to a 24-mer, and occurs 378 times, etc.

Table 2C
Detailed analysis. Yates corrected χ^2 values for the difference between the *Observed* and the *Calculated* occurrences of hexons (i.e. codon-pairs) for the BiHex pattern xxG-λ=6-xxG.

Yates Chi^2	**AAG**	**ACG**	**AGG**	**ATG**	**CAG**	**CCG**	**CGG**	**CTG**	**GAG**	**GCG**	**GGG**	**GTG**	**TAG**	**TCG**	**TGG**	**TTG**	***Sum***
AAG	0.34	**6.36**	**4.77**	0.99	0.00	0.27	1.12	0.01	1.56	2.30	**8.07**	1.27	0.06	0.04	0.01	0.11	*3.09*
ACG	0.87	0.01	1.75	0.91	0.14	1.00	2.21	0.19	0.06	0.64	**9.53**	0.69	nc	3.75	0.12	0.10	*2.84*
AGG	0.97	0.11	**7.85**	0.00	0.19	1.19	0.70	2.65	0.91	0.10	1.65	1.33	nc	**10.11**	0.41	0.14	*5.63*
ATG	0.58	0.46	0.26	0.00	**4.37**	0.11	0.10	0.21	1.21	0.08	0.98	0.23	nc	0.00	0.00	0.30	*0.02*
CAG	0.67	0.00	0.63	1.93	0.09	1.00	nc	**9.84**	0.83	1.66	1.45	1.39	nc	0.06	3.22	0.08	*9.33*
CCG	0.06	0.98	0.00	0.75	**4.62**	1.64	nc	0.02	0.11	0.57	0.38	**8.68**	nc	0.73	0.00	2.37	*9.68*
CGG	0.08	0.17	0.14	0.00	nc	nc	nc	nc	0.32	1.31	3.21	1.83	nc	nc	nc	0.01	*6.43*
CTG	0.05	0.14	0.00	0.70	0.96	0.04	nc	0.00	0.30	1.48	**4.43**	0.33	nc	0.47	**7.03**	1.81	*1.29*
GAG	0.17	0.02	1.97	1.46	1.07	0.41	0.21	**6.44**	**4.38**	0.16	1.07	2.87	0.01	0.07	0.00	0.17	*6.19*
GCG	0.44	3.51	2.55	0.04	0.12	0.15	1.26	0.14	0.24	**11.53**	**4.39**	**9.03**	0.03	0.04	0.32	2.15	*15.46*
GGG	2.83	0.01	0.36	0.00	2.26	0.19	3.20	0.00	**7.98**	**6.28**	**7.83**	**6.42**	0.12	0.37	0.16	**7.22**	*33.89*
GTG	**6.76**	0.21	0.56	**5.25**	0.01	**9.62**	0.14	0.84	1.24	**5.61**	3.74	**11.16**	0.02	3.51	2.53	**11.18**	*43.83*
TCG	1.32	1.29	0.44	0.38	1.28	0.18	1.14	nc	0.05	0.85	0.00	0.01	nc	3.11	0.04	1.05	*1.77*
TGG	0.07	0.34	0.25	0.00	0.06	0.86	0.16	nc	0.00	0.36	2.20	0.50	nc	1.20	0.01	0.11	*2.62*
TTG	0.28	2.17	0.01	0.05	2.26	1.19	0.00	0.67	1.94	0.12	**9.78**	2.54	0.01	0.28	0.05	**4.35**	*12.69*
Sum	*3.65*	*0.48*	*7.01*	*5.33*	*4.37*	*1.31*	*1.54*	*1.63*	*15.61*	*10.58*	*34.37*	*34.34*	*0.01*	*9.18*	*2.78*	*11.94*	*119.27*

The χ^2 values, which are significant at the probability threshold of 0.05, are shown in bold; nc: the χ^2 values are not calculated since the corresponding average occurrence numbers are smaller than 5. The χ^2 for the Hexon GTGyyyyyyyyyyyyyyyyyyTTG is 11.18 for one degree of freedom, etc.

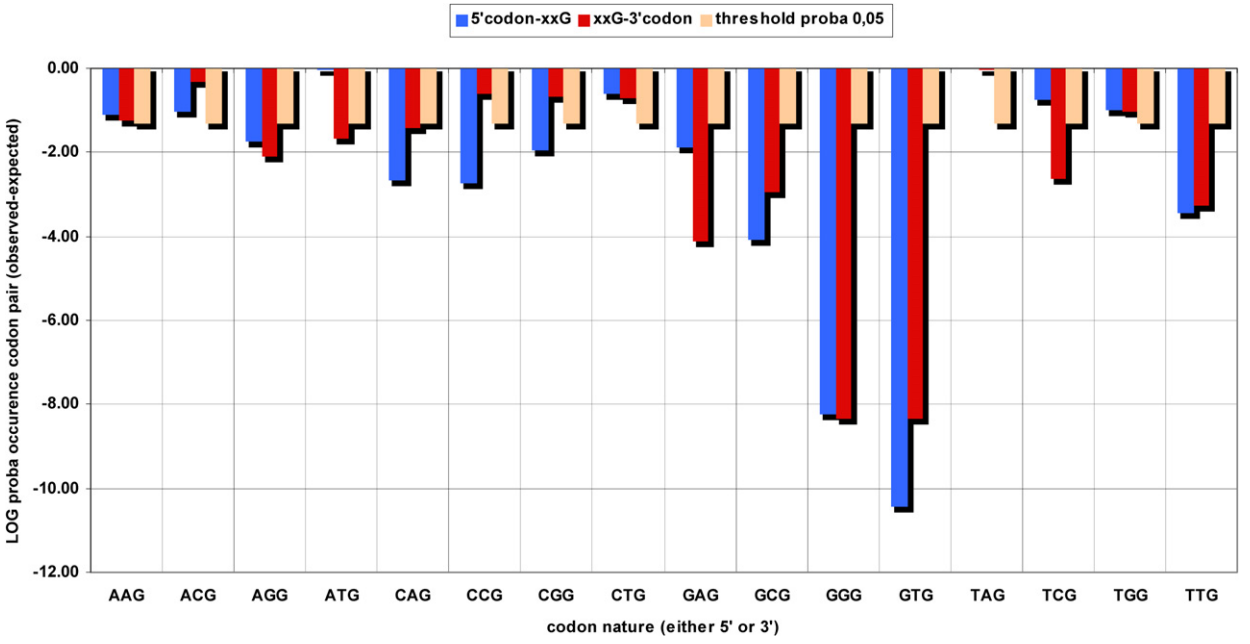


(A)

Fig. 2A. Probability of occurrence by chance of codon-pairs corresponding to the BiHex pattern xxG-λ=6-xxG. The probabilities (shown on a vertical axis in a log. scale) of occurrence by chance of the 240 hexon patterns were calculated from the χ^2 values given by Table 2C (only the patterns giving probabilities < 0.05 are shown). The patterns should be read in the order: codon 5′–codon 3′; thus the probability for the pattern TTGyyyyyyyyyyyyyyyyyyGCG is close to 10^{-3}, and that of GTGyyyyyyyyyyyyyyyyyyTTG is close to 10^{-4}, etc.

nal gene sequences than in the shuffled ones, and only one hexon (AAG-ACG) occurs less frequently. This result explains not only that the BiHex pattern xxG-λ=6-xxG is more abundant in the original, (observed) values than in the expected, (calculated from the shuffled) ones. It points also to the notion that the observed over-represented hexons exceed very strongly the expected values: the individual χ^2 values, in the majority of cases, are greater than 7 (which corresponds to the E values $< 10^{-2}$), and in several instances, e.g., GCG-λ=6-GCG, GTG-λ=6-GTG, GTG-λ=6-TTG, the χ^2 values are greater than 11, for one degree of freedom, E values $< 10^{-3}$. Figs. 2A and 2B summarize the significance of individual hexons, and allows one to draw a few conclusions. Individual hexons are not distributed evenly, but rather in groups, which display some common characteristics. For instance, hexons containing CGG codon are never over-represented in their occurrence, and those containing ACG are very rarely over-represented. In contrast, hexons containing GGG or GTG codons are frequently over-represented. When the 240 different, individual hexons are divided into 16 simpler categories, by summing up the number of occurrences of all hexons containing a given codon, either at the 5′ or at the 3′ terminus of the respective polynucleotide chain, a very clear picture is obtained (Fig. 2B). Original gene sequences differ from the average permuted ones mainly by a higher frequency of codon-pairs containing either GGG or GTG, and less frequently by those containing TTG, GCG, GAG, while all the remaining hexons which contain other xxG codons, represent only a very minor contribution.

Contrary to numerous studies on the occurrence and the biases of *adjacent* codon-pairs [22–27], the analysis of *non-adjacent* codon-pairs is extremely limited. Only one study deals with this problem [23]. Based upon limited data available at that time (non-complete genome sequences of *E. coli*, *S. cerevisiae*, and *H. sapi-*



(B)

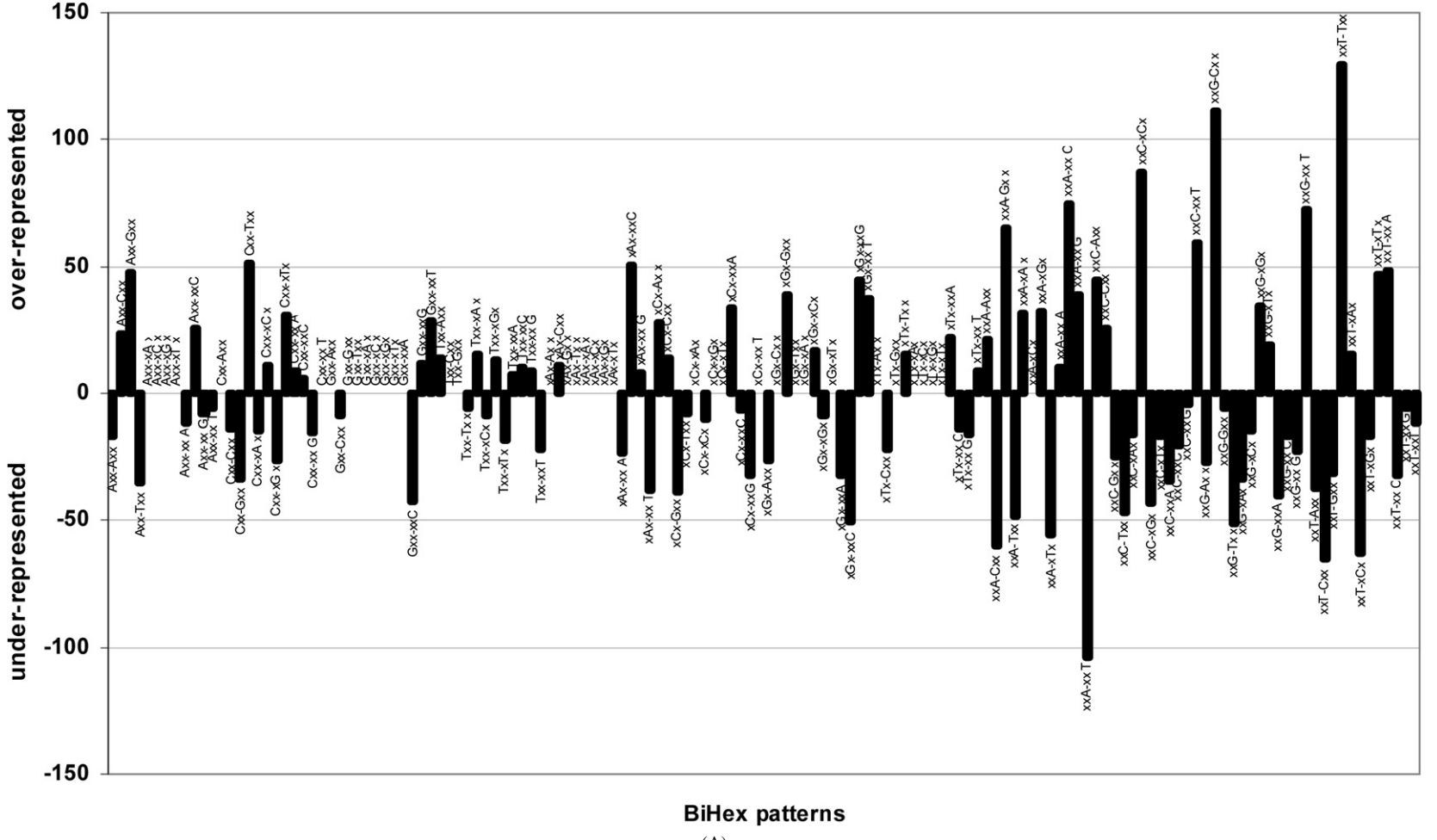
Fig. 2B. Probability of occurrence by chance of groups of codons pairs, corresponding to the BiHex pattern xxG-λ=6-xxG. The number of occurrences of all hexons beginning (in blue) with the codons given in the abscissa, or those terminated (in red) by them, were summed up for the original genes (Table 2A) and for the permuted ones (Table 2B). The χ^2 and probabilities were calculated, and the latter are shown on the ordinate in a log scale. Thus, the probability for the GTG-λ=6-xxG pattern is close to 10^{-10}, etc.

ens) Hatfield and Gutman observed that the occurrence of non-adjacent codon-pairs is non random at long distances. Their data were obtained by pooling together all the possible 3904 codon-pairs into one bin only. The authors conclude that "the basis of this effect remains a mystery". As far as we know, no analysis of this problem has been continued. Here we have shown that the different synonymous codon-pairs, specific for different distances, are responsible for the distant codon-pairs biases.

3.2. *Perusal of all the informative 135 BiHex patterns for* $\lambda = 0$ *demonstrates, that all six positions of a pair of adjacent codons are constrained*

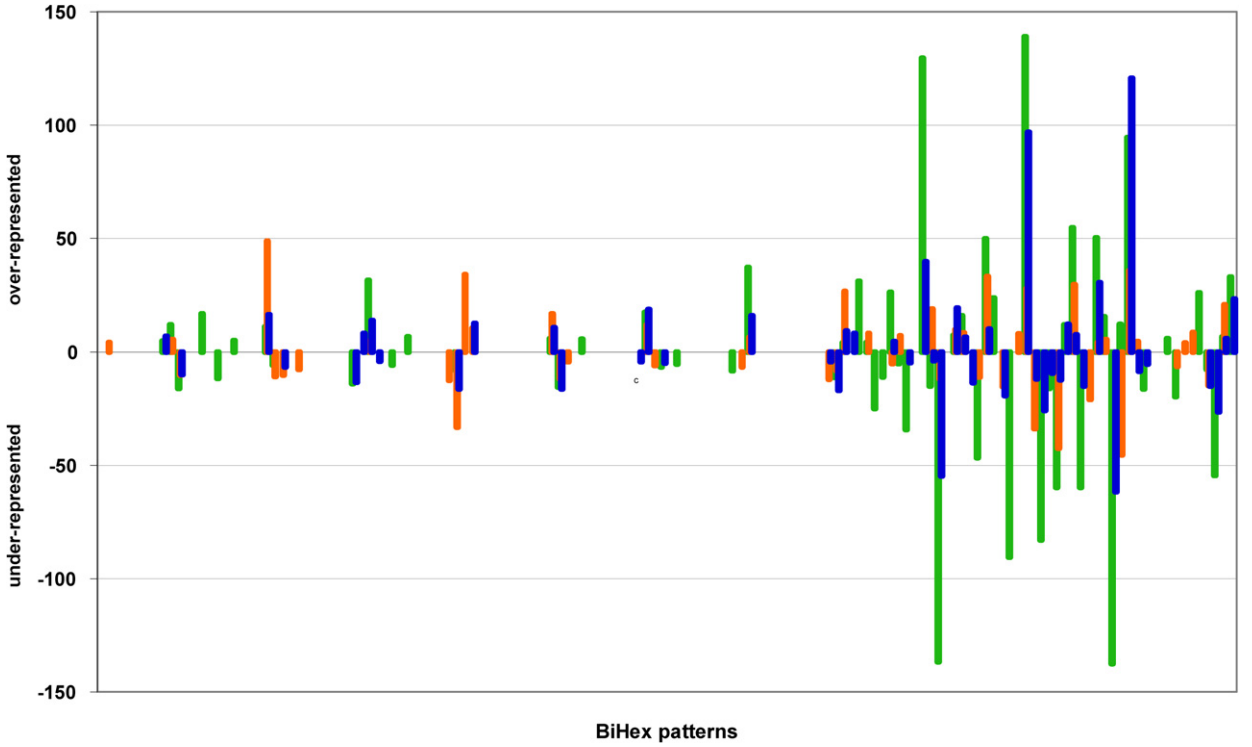
It would be very tedious and undigestable to analyze in depth, in a manner analogous to that shown in Tables 2A–2C, all the 135 BiHex patterns listed in Table 1, for all the spacer codons λ from 0 to 32 (which would represent an equivalent of $135 \times 33 \times 3 = 13\,365$ such individual tables!). Furthermore, this is not in the scope of the present article, which aims rather at the description of a novel method in computational biology of genomes. We believe that the introduction of the BiHex notation, both as a concept, and as a new method of computation, will be a successful shorthand for the description of profound and unexpected discoveries of the genuine, original order of synonymous codons whose nature and evolutionary significance remains to be understood. The results shown in Figs. 3A, 3B illustrate this notion.

A majority of BiHex patterns (109/135) significantly deviate in the adjacent codon-pairs, i.e., $\lambda = 0$ (Figs. 3A, 3B). Both over-represented and under-represented BiHex patterns are present in comparable numbers and with comparable amplitude of their deviates (compare, e.g., the BiHex pattern xxT-Txx, which is over-represented by more than 100 standard deviations (STD), with the pattern xxA-xxT, which is under-represented by more than 100 STD in the original gene sequences. The E values for such amplitudes are smaller than 100^{-100}. It should be remembered, from the complete analysis of the BiHex pattern xxG-xxG (*vide supra*), that if a given BiHex pattern is strongly deviating, then numerous codon-pairs corresponding to such a pattern must be strongly deviating too, all in the same direction (i.e., all in "plus", or in all "minus"). Therefore, one can conclude, that hexanucleotides xxTTxx (and also xxGCxx, xxAGxx, xxCAxx, etc.; Figs. 3A, 3B), in the reading frame 0, are strongly over-represented, while at the same time the hexanucleotides xxTCxx, xxGTxx, and xxTAxx, are



(A)

Fig. 3A. BiHex patterns significantly deviating in the original genome for the adjacent codon-pairs (codon-spacer $\lambda = 0$). The number of occurrences of the BiHex patterns for $\lambda = 0$ (here, hexons correspond to hexanucleotides) are calculated for the original genome, and compared with their corresponding average number of occurrences in the 500 ISSCOR permutations (Eq. (3)). The difference, between original and the averaged permuted number of occurrences, is expressed in standard deviation units (STD). For clarity, we plot the deviates in two opposite directions – the patterns over-represented in the original above the zero line, and these under-represented below the zero line; with the negative sign. All BiHex patterns shown significantly deviate from randomness, some of them more than 100 STD (e.g., xxT-Txx – over-represented; and xxA-xxT – under-represented).



(B)

Fig. 3B. Examples of BiHex patterns significantly deviating in the original genome for the non-adjacent codon-pairs. The order of BiHex patterns, on the abscissa, is the same as in Fig. 3A, but their symbols are omitted for clarity, the numbering of patterns is given in Table 3. The ordinate shows the χ^2 values calculated for the difference between the observed occurrences, and the calculated occurrence averages after 500 ISSCOR permutations. Only the significant averages (probabilities < 0.05) are shown. For clarity, the χ^2 values are plotted in opposite directions – the patterns over-represented in the original are above the zero line, and the under-represented below the zero line. The values corresponding to the codon-spacers: $\lambda = 3$ are green, for $\lambda = 5$ are orange, and for $\lambda = 6$ are blue. Notice, that χ^2 value of 10 corresponds to the probability of 10^{-3}, that of 20 to 10^{-6}, that of 50 to 10^{-12}, and that of 140 to 10^{-32}.

under-represented in the *H. pylori* protein coding genes. It is well known that the fourth position [11,12] of a pair of adjacent codons is strongly constraint because of the properties of the translation machinery, and the interactions between the ribosomal A and P sites. It is therefore not surprising that the above-observed deviations, *which all deal with the fourth position*, are detected. The ISSCOR method and the BiHex concept simply allow to sieve out rapidly the nature of nucleotides present at the fourth position, pinpointing the nature of the nucleotides upstream, at the 1st, 2nd or 3rd position of hexanucleotides in the reading frame zero, and to estimate the statistical significance of the observed associations.

Much richer in unexpected results are the comparisons concerning the 5th and the 6th position of adjacent codon-pairs. In several particular patterns the 5th position of an, in frame, hexanucleotide is vastly over-represented (e.g., xxTxTx, xxCxCx, CxxxTx, and xxGxGx), while in others (e.g., xxGxAx, xxCxGx, and CxxxGx) it is strongly under-represented. In the 6th position, again numerous highly significant deviations are observed. The xxAxxT hexanucleotide is the most strongly deviating one amongst all analyzed. Its occurrence in the *Helicobacter* genes is the least frequent. Just the opposite is true for the hexanucleotides xAxxxC, xxAxxC, and xxGxxT, which are amongst the most frequently occurring; and the most significant patterns. There is no point here, however, in enumerating such a simplified catalogue. What our results demonstrate, is that *all positions in a pair of adjacent codons are important, which means that the order of synonymous codons is an intrinsic characteristics of a genuine genome*, and that this order can not be too dissimilar between different individual genes. Otherwise, the global occurrences of BiHex patterns would have been scrambled, and no significant deviations could have been uncovered in the complete set of genomic sequences. It is important to repeat once more, that the random permutations of synonymous codons by the ISSCOR method allow us to disentangle the significant deviations from

Table 3
Numbering of all the 144 BiHex patterns, and amino acids corresponding to synonymous codon replacements by the ISSCOR method.

No.	BiHex	5′	3′	No.	BiHex	5′	3′	No.	BiHex	5′	3′	No.	BiHex	5′	3′	No.	BiHex	5′	3′	No.	BiHex	5′	3′
1	Axx-Axx	R;S	R;S	*25*	Gxx-Axx	–	R;S	*49*	xAx-Axx	–	R;S	*73*	xGx-Axx	S	R;S	*97*	xxA-Axx	aa_12	R;S	*121*	xxG-Axx	aa_11	R;S
2	Axx-Cxx	R;S	L;R	*26*	Gxx-Cxx	–	L;R	*50*	xAx-Cxx	–	L;R	*74*	xGx-Cxx	S	L;R	*98*	xxA-Cxx	aa_12	L;R	*122*	xxG-Cxx	aa_11	L;R
3	Axx-Gxx	R;S	–	*27*	Gxx-Gxx	–	–	*51*	xAx-Gxx	–	–	*75*	xGx-Gxx	S	–	*99*	xxA-Gxx	aa_12	–	*123*	xxG-Gxx	aa_11	–
4	Axx-Txx	R;S	L;S	*28*	Gxx-Txx	–	L;S	*52*	xAx-Txx	–	L;S	*76*	xGx-Txx	S	L;S	*100*	xxA-Txx	aa_12	L;S	*124*	xxG-Txx	aa_11	L;S
5	Axx-xAx	R;S	–	*29*	Gxx-xAx	–	–	*53*	xAx-xAx	–	–	*77*	xGx-xAx	S	–	*101*	xxA-xAx	aa_12	–	*125*	xxG-xAx	aa_11	–
6	Axx-xCx	R;S	S	*30*	Gxx-xCx	–	S	*54*	xAx-xCx	–	S	*78*	xGx-xCx	S	S	*102*	xxA-xCx	aa_12	S	*126*	xxG-xCx	aa_11	S
7	Axx-xGx	R;S	S	*31*	Gxx-xGx	–	S	*55*	xAx-xGx	–	S	*79*	xGx-xGx	S	S	*103*	xxA-xGx	aa_12	S	*127*	xxG-xGx	aa_11	S
8	Axx-xTx	R;S	–	*32*	Gxx-xTx	–	–	*56*	xAx-xTx	–	–	*80*	xGx-xTx	S	–	*104*	xxA-xTx	aa_12	–	*128*	xxG-xTx	aa_11	–
9	Axx-xxA	R;S	aa_12	*33*	Gxx-xxA	–	aa_12	*57*	xAx-xxA	–	aa_12	*81*	xGx-xxA	S	aa_12	*105*	xxA-xxA	aa_12	aa_12	*129*	xxG-xxA	aa_11	aa_12
10	Axx-xxC	R;S	aa_15	*34*	Gxx-xxC	–	aa_15	*58*	xAx-xxC	–	aa_15	*82*	xGx-xxC	S	aa_15	*106*	xxA-xxC	aa_12	aa_15	*130*	xxG-xxC	aa_11	aa_15
11	Axx-xxG	R;S	aa_11	*35*	Gxx-xxG	–	aa_11	*59*	xAx-xxG	–	aa_11	*83*	xGx-xxG	S	aa_11	*107*	xxA-xxG	aa_12	aa_11	*131*	xxG-xxG	aa_11	aa_11
12	Axx-xxT	R;S	aa_15	*36*	Gxx-xxT	–	aa_15	*60*	xAx-xxT	–	aa_15	*84*	xGx-xxT	S	aa_15	*108*	xxA-xxT	aa_12	aa_15	*132*	xxG-xxT	aa_11	aa_15
13	Cxx-Axx	L;R	R;S	*37*	Txx-Axx	L;S	R;S	*61*	xCx-Axx	S	R;S	*85*	xTx-Axx	–	R;S	*109*	xxC-Axx	aa_15	R;S	*133*	xxT-Axx	aa_15	R;S
14	Cxx-Cxx	L;R	L;R	*38*	Txx-Cxx	L;S	L;R	*62*	xCx-Cxx	S	L;R	*86*	xTx-Cxx	–	L;R	*110*	xxC-Cxx	aa_15	L;R	*134*	xxT-Cxx	aa_15	L;R
15	Cxx-Gxx	L;R	–	*39*	Txx-Gxx	L;S	–	*63*	xCx-Gxx	S	–	*87*	xTx-Gxx	–	–	*111*	xxC-Gxx	aa_15	–	*135*	xxT-Gxx	aa_15	–
16	Cxx-Txx	L;R	L;S	*40*	Txx-Txx	L;S	L;S	*64*	xCx-Txx	S	L;S	*88*	xTx-Txx	–	L;S	*112*	xxC-Txx	aa_15	L;S	*136*	xxT-Txx	aa_15	L;S
17	Cxx-xAx	L;R	–	*41*	Txx-xAx	L;S	–	*65*	xCx-xAx	S	–	*89*	xTx-xAx	–	–	*113*	xxC-xAx	aa_15	–	*137*	xxT-xAx	aa_15	–
18	Cxx-xCx	L;R	S	*42*	Txx-xCx	L;S	S	*66*	xCx-xCx	S	S	*90*	xTx-xCx	–	S	*114*	xxC-xCx	aa_15	S	*138*	xxT-xCx	aa_15	S
19	Cxx-xGx	L;R	S	*43*	Txx-xGx	L;S	S	*67*	xCx-xGx	S	S	*91*	xTx-xGx	–	S	*115*	xxC-xGx	aa_15	S	*139*	xxT-xGx	aa_15	S
20	Cxx-xTx	L;R	–	*44*	Txx-xTx	L;S	–	*68*	xCx-xTx	S	–	*92*	xTx-xTx	–	–	*116*	xxC-xTx	aa_15	–	*140*	xxT-xTx	aa_15	–
21	Cxx-xxA	L;R	aa_12	*45*	Txx-xxA	L;S	aa_12	*69*	xCx-xxA	S	aa_12	*93*	xTx-xxA	–	aa_12	*117*	xxC-xxA	aa_15	aa_12	*141*	xxT-xxA	aa_15	aa_12
22	Cxx-xxC	L;R	aa_15	*46*	Txx-xxC	L;S	aa_15	*70*	xCx-xxC	S	aa_15	*94*	xTx-xxC	–	aa_15	*118*	xxC-xxC	aa_15	aa_15	*142*	xxT-xxC	aa_15	aa_15
23	Cxx-xxG	L;R	aa_11	*47*	Txx-xxG	L;S	aa_11	*71*	xCx-xxG	S	aa_11	*95*	xTx-xxG	–	aa_11	*119*	xxC-xxG	aa_15	aa_11	*143*	xxT-xxG	aa_15	aa_11
24	Cxx-xxT	L;R	aa_15	*48*	Txx-xxT	L;S	aa_15	*72*	xCx-xxT	S	aa_15	*96*	xTx-xxT	–	aa_15	*120*	xxC-xxT	aa_15	aa_15	*144*	xxT-xxT	aa_15	aa_15

The table lists all BiHex patterns in the same order as it is given in Figs. 2A, 2B and 3A–3B. The correspondence between respective amino acids, which are affected by the synonymous codon replacements by the ISSCOR method are listed as well. This correspondence will be explained by an example – consider the BiHex pattern #2. This pattern, Axx-Cxx, corresponds to replacements of either the codon:

(i) Arg (AGG or AGA), by Arg codon CGx (upstream); or by
(ii) Ser (AGT or AGC), by Ser codon TCx (upstream); or by
(iii) Leu codon CTx, by Leu codon TTA, or TTG (downstream); or by
(iv) Arg codon CGx, by Arg codon AGA, or AGG (downstream).

In other words, the BiHex pattern #2 (Axx-Cxx) comprises synonymous codon replacements involving only two amino acids, arginine or serine of the upstream codon; and leucine or arginine of the downstream codon. On the other hand, permutations constituting, e.g., BiHex pattern #117, comprise altogether 15 different amino acids of the upstream codon, and 12 amino acids of the downstream codon.

The nature of amino acids involved in replacements at the 3rd position of synonymous codons corresponds to:

aa_11 to the: Ala, Arg, Gln, Glu, Gly, Leu, Lys, Pro, Ser, Thr; and Val;
aa_12 to the: Ala, Arg, Gln, Glu, Gly, Ile, Leu, Lys, Pro, Ser, Thr, and Val;
aa_15 to the: Ala, Arg, Asn, Asp, Cys, Gly, His, Ile, Leu, Phe, Pro, Ser, Thr, Tyr, and Val.

The nine BiHex patterns: #27, #29, #32, #51, #53, #56, #87, #89, and #92, are not informative since their occurrences are not changed by the synonymous codon replacements (e.g., when the codon-pair GAG-GAA is replaced by the pair GAA-GAA, or GAA-GAG, or GAG-GAG, the number of occurrences of the pattern #27 Gxx-Gxx is not changed).

the basal noise. They change neither the codon usage frequencies, nor the amino acid or protein sequences. They *earmark and measure* "pure" properties of the sequential order, and not the frequencies of the constituents (codons, amino acids) of that order.

In a comprehensive survey of codon-pair biases across ORFs from 16 genomes, Buchan et al. ([12], and references therein), have concluded that tRNA properties help shaping adjacent codon-pair preferences. Our results are compatible with this interpretation. They strengthen, however, the idea that the basis of selection of codon-pairs depends not only on the tetranucleotide combinations, but on the complete hexanucleotide combinations (with its first and last positions as well). Interestingly, our results were obtained with *Helicobacter pylori*, which is an organism amongst the least affected by the tRNA-based translational selection of synonymous codons [12,17].

3.3. Perusal of BiHex patterns at long range distances demonstrates that the sequential order of synonymous codons is constrained in a specific manner all along protein coding genes

Fig. 3A gives examples and demonstrates the "pure" order aspects at long-range distances along the genes. Highly significant deviations can be observed and measured for non-adjacent codon-pairs separated by 3, 5, or 6 codon spacers λ. Although less striking in their amplitude of differences than those observed for the adjacent codon-pairs (i.e., $\lambda = 0$), their significance leaves no doubt. Several BiHex patterns from the original genome differ from those of the permuted ones from 5 up to 15 STD units. These differences occur as well in the positive direction (over abundance), as in the negative direction (under abundance). These deviations correspond to E values smaller than 10^{-10}. Importantly, for each set of distances along the genes a different set of significant BiHex patterns is detected. One can see, in the examples shown in Fig. 3A, that the BiHex patterns deviating at $\lambda = 5$ (orange) frequently do not coincide with those deviating at $\lambda = 6$ (blue). The property of "*sui generis*" constraints is therefore always true at long range, but the nature of specific codon-pairs, which are constrained at long distances *is different*. Just one example, the comparison of a 21-mer ($\lambda = 5$) oligonucleotide, and a 24-mer ($\lambda = 6$) oligonucleotide, illustrates this notion. We have verified, by the in depth analysis of the BiHex pattern xxG-xxG (*vide supra*), that this is true for the 240 codon-pairs, which constitute this pattern. These codon-pairs, which are conspicuous in the 24-mers, and significantly over-represented (Table 3), are not necessarily those, which are conspicuous and over-represented in 21-mers (data not shown), and vice versa.

In conclusion the remarkable and singular properties of polynucleotide chains described in this work are properties of the sequential order of synonymous codons within a gene, which must be under selective pressure. This sequential order is thus superimposed on the classical codon usage frequencies. This new dimension can be measured by the ISSCOR method, which is simple, robust, and should be useful for comparative and functional genomics.

Acknowledgements

J.P.R. was partially supported by the EU project SSPE-CT-2006-44405, also J.P.R. and P.P.S. were partially supported from the 352/6.PR-UE/2007/7 grant. We would like to thank Dr. C.J. Herbert for looking over the English. This contribution was presented for the first time at the international symposium "The Logic of Gene Regulation Networks" in the honor of Prof. René Thomas, Brussels, May 30–31, 2008.

References

[1] C.R. Woese, The Genetic Code – The Molecular Basis for Genetic Expression, Harer & Row Publishers, NY, 1967.
[2] R. Grantam, C. Gautier, M. Gouy, R. Mercier, A. Pave, Codon catalog usage and the genome hypothesis, Nucl. Acids Res. 8 (1980) r49–r62.
[3] O.G. Berg, C.G. Kurland, Growth rate-optimized tRNA abundance and codon usage, J. Mol. Biol. 270 (1997) 544–550.
[4] A. Carbone, F. Kepes, A. Zinovyev, Codon bias signatures, organization of microorganisms in codon space and lifestyle, Mol. Biol. Evol. 22 (2005) 547–561.
[5] M. Dries, R. Savva, L. Wernish, Solving the riddle of codon usage preferences: a test for translational selection, Nucl. Acids Res. 32 (2004) 5036–5044.
[6] A.S. Novozhilov, Y.I. Wolf, E.V. Koonin, Evolution of genetic code: partial optimization of a random code for robustness to translation error in a rugged fitness landscape, Biol. Direct, 2007, http://www.biology-direct.com/content/2/1/24.
[7] M. Zama, Codon usage and secondary structure of mRNA, Nucl. Acids Symp. 22 (1990) 93–94.
[8] D.W. Collins, Relationship between G+C in silent sites of codons and amino acids composition of proteins, J. Mol. Evol. 36 (1993) 201–213.
[9] A.A. Adzubei, I.A. Adzubei, I.A. Krashennikov, S. Neidle, Non-random usage of 'degenerate' codons related to protein three-dimensional structure, FEBS Lett. 399 (1996) 78–82.
[10] P.M. Sharp, G. Matassi, Codon usage and genome evolution, Curr. Opin. Genet. Dev. 4 (1994) 851–860.
[11] T. Ikemura, Codon usage and tRNA content of unicellular and multicellular organisms, Mol. Biol. Evol. 2 (1985) 13–34.
[12] J.R. Buchan, L.S. Aucott, I. Stansfield, tRNA properties help shape codon-pair preferences in open reading frames, Nucl. Acids Res. 34 (2006) 1015–1027.

[13] M.V. Rodnina, W. Wintermeyer, Fidelity of aminoacyl-tRNA selection on the ribosome: Kinetic and structural mechanisms, Annual Review of Biochemistry 70 (2001) 415–435.
[14] N. Suoeka, Directional mutational pressure, selective constraints, and genetic equilibria, J. Mol. Evol. 34 (1992) 95–114.
[15] M.A. Antezana, M. Kreitman, The nonrandom location of synonymous codons suggests that reading frame-independent forces have patterned codon preferences, J. Mol. Evol. 49 (1999) 36–43.
[16] A. Eyre-Walker, M. Bulmer, Reduced synonymous substitution rate at the start of enterobacterial genes, Nucleic Acids Res. 21 (1993) 4599–4603.
[17] B. Lafay, J.C. Atherton, P.M. Sharp, Absence of translationally selected synonymous codon usage bias in *Helicobacter pylori*, Microbiology 146 (2000) 851–860.
[18] P.P. Slonimski, Periodic oscillations of the genomic nucleotide sequences disclose major differences in the way of constructing homologous proteins from different procaryotic species, C. R. Biol. 330 (2007) 13–32; Erratum in: C. R. Biol. 330 (2007) 188.
[19] A. Krzywicki, P.P. Slonimski, Formal analysis of protein sequences. I. Specific long range constraints in pair associations of amino acids, J. Theoret. Biol. 17 (1967) 136–158.
[20] J.P. Radomski, P.P. Slonimski, Genomic style of proteins: concepts, methods and analysis of ribosomal proteins from 16 microbial species, FEMS Microbiol. Rev. 25 (2001) 425–435.
[21] J.P. Radomski, P.P. Slonimski, Primary sequences of proteins from complete genomes display a singular periodicity: Alignment-free N-gram analysis, C. R. Biol. 330 (2007) 33–48.
[22] G.W. Hatfield, G.A. Gutman, Nonrandom utilization of codon-pairs in *Escherichia coli*, Proc. Natl. Acad. Sci. 86 (1989) 3699–3703.
[23] G.W. Hatfield, G.A. Gutman, Codon-pair utilization bias in bacteria, yeast, and mammals, in: D.L. Hatfield, B.J. Lee, R.M. Pirtle (Eds.), Transfer RNA in Protein Synthesis, CRC Press, 1992.
[24] B. Irvin, J.D. Heck, G.W. Hatfield, Codon-pair utilization biases influence translational elongation step times, J. Biol. Chem. 270 (1995) 22801–22806.
[25] L.S. Fooley, M. Yarus, Codon contexts from weakly expressed genes reduce expression in vivo, J. Mol. Biol. 209 (1989) 359–378.
[26] S. Boycheva, G. Chkodrov, I. Ivanov, Codon-pairs in the genome of *Escherichia coli*, Bioinformatics 19 (2003) 987–998.
[27] G. Moura, M. Pinheiro, R. Silva, I. Miranda, V. Afreixo, G. Dias, A. Freitas, J.L. Oliveira, M.A. Santos, Comparative context analysis of codon-pairs on an ORFeome scale, Genome Biol. 6 (2005) R28.