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Large-scale computational and statistical analyses of high transcription potentialities in 32 prokaryotic genomes

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ABSTRACT

This article compares 32 bacterial genomes with respect to their high transcription potentialities. The σ70 promoter has been widely studied for *Escherichia coli* model and a consensus is known. Since transcriptional regulations are known to compensate for promoter weakness (i.e. when the promoter similarity with regard to the consensus is rather low), predicting functional promoters is a hard task. Instead, the research work presented here comes within the scope of investigating potentially high ORF expression, in relation with three criteria: (i) high similarity to the σ70 consensus (namely, the consensus variant appropriate for each genome), (ii) transcription strength reinforcement through a supplementary binding site—the upstream promoter (UP) element—and (iii) enhancement through an optimal Shine-Dalgarno (SD) sequence. We show that in the AT-rich *Firmicutes*' genomes, frequencies of potentially strong σ70-like promoters are exceptionally high. Besides, though they contain a low number of strong promoters (SPs), some genomes may show a high proportion of promoters harbouring an UP element. Putative SPs of lesser quality are more frequently associated with an UP element than putative strong promoters of better quality. A meaningful difference is statistically ascertained when comparing bacterial genomes with similarly AT-rich genomes generated at random; the difference is the highest for *Firmicutes*. Comparing some *Firmicutes* genomes with similarly AT-rich *Proteobacteria* genomes, we confirm the *Firmicutes* specificity. We show that this specificity is neither explained by AT-bias nor genome size bias; neither does it originate in the abundance of optimal SD sequences, a typical and significant feature of *Firmicutes* more thoroughly analysed in our study.

INTRODUCTION

This article addresses potentially high ORF expression related to σ70-like promoters, in bacterial genomes. In these genomes, a single enzyme, the RNA polymerase, is responsible for the synthesis of all RNA types. The core holoenzyme $\alpha^2\beta\beta'$ is competent for transcribing a specific region of the DNA strand into an RNA molecule. However, transcription can only be initiated (at the so-called +1 transcription site) through a temporary biochemical complex. This complex is composed of the four previous subunits and of a protein, the σ factor, the primary one being σ70. As one of the simplest known bacterial models, *Escherichia coli* K-12 has been subjected to intensive research, especially with regard to transcription (1–8). Knowledge was therefore gained about the *E. coli* σ70 factor's binding sites. Their consensuses are, respectively, TTGACA and TATAAT, in the 5′ to 3′ direction. The optimal fixation of the RNA polymerase requires that the site with the consensus TTGACA should be located between 35 bp and 30 bp or thereabouts upstream of the first transcribed nucleotide. This former site is thus called the −35 box. The Pribnow box, TATAAT, is called −10 box for similar reasons. These sites are separated by 15–21 bp in the known functional promoters, the canonical σ70 promoter being characterized by the optimal distance of 17 bp. Various methods and softwares devoted to the prediction of functional promoters in *E. coli* genome have been developped (9–12) (to restrain to a few examples). We do not mention here the numerous softwares designed to uncover a motif common to a set of biological sequences.

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Not only is the RNA polymerase conserved through evolution in bacteria, but also there seems to be a *single* σ70 factor, responsible for housekeeping gene transcription, across the bacterial kingdom (13–14). Both points legitimate searches for σ70-like binding sites in other prokaryotic genomes (15–17). Furthermore, the number of complete prokaryotic genomes sequenced has increased at a high speed (594 in october 2007), which allows genome-wide computational investigations. In the domain of *in silico* analyses related to σ70 factor transcription, a reference contribution showed that σ70 promoter-like sequences are present throughout the kingdom of prokaryotic organisms (18). This former study demonstrated that the density of promoter-like sequences is high within regulatory regions, in contrast to coding regions and regions located between convergently transcribed genes. For instance, an average of 38 promoter-like sequences was computed for *E. coli*, within each 250 bp subregion located upstream of the start codon (SC).

In vivo, transcriptional regulations are known to compensate for promoter weakness (19–20). For example, Huerta and Collado-Vides established that more than 50% of experimentally verified promoters are not the promoters with the highest scores when scoring relies on the proximity to the canonical promoter, both in terms of consensus similarity and optimal bp distances between boxes (9). This statement was checked on the 111 promoters constituting a training set designed in a former work (15). On the other hand, in *E. coli* genome, it has been shown that mutations in the −10 box or the −35 box that bring the promoter sequence closer to the σ70 consensus tend to increase the strength of the promoter, and conversely, mutations decreasing homology to the σ70 consensus tend to lower the promoter strength (1). Thus, the more similar to the canonical σ70 promoter, the more potentially strong this promoter would be, with the noteworthy exception that the *consensus* promoters may actually be weak because RNA polymerase binds them so strongly that it cannot escape (21). Therefore, it is attractive to study and compare genomes from the point of view of potentially high transcription, allowing for mismatches, under a minimal similarity constraint. This large-scale comparative analysis is feasible through an *in silico* approach.

No computational method can capture the biological features and environmental conditions involved *in vivo*, to predict functional *strong* promoters. Besides, even for the most intensively studied prokaryotic genome, *E. coli*'s, the available repositories of σ70 promoters do not provide annotations about promoter strength. The measurement of promoter activity in cellular or cell-free expression systems cannot be applied on a large scale. ChIP on chip assays allow the identification of transcription factor binding sites, under given environmental conditions, but high-throughput promoter strength measurement cannot be implemented using this technique. Thus, before such large-scale array experimentations may be conducted on the 32 genomes we are interested in, an *in silico* genome-comparative analysis focused on intrinsically high transcription potentiality is worth being performed.

In our work, we intentionally focus on the subset of putative strong σ70 promoters already potentially favoured by the presence of an optimal Shine-Dalgarno (SD) sequence (GGAGG). The presence of the SD sequence has been ascertained for a large number of bacteria (22) and it was established that the extent to which a SD sequence is conserved relates to its translation efficiency (23). Besides, our study also puts emphasis on strength transcription reinforcement through the upstream promoter (UP) element presence. The UP element is an enhancer for transcription and thus for ORF expression (24–25). In about 3% of *E. coli* promoters, an UP element has been identified upstream of the −35 region, conferring additional strength to the promoter. The high conservation of the domain of the alpha subunit of the RNA polymerase involved in the interaction with the UP element suggests that the UP element consensus should be valid throughout the bacterial kingdom. To our knowledge, in addition to *E. coli* genome, the UP element has been experimentally identified in *Bacillus subtilis* (26), *Vibrio natriegens* (27) and *Bacillus stearothermophilus* (28). UP elements were previously taken into account by PlatProm algorithm (29); to our knowledge, the only other work devoted to *in silico* identification of σ70 promoter-like sequences harbouring an UP element is by M. Dekhtyar, A. Morin and V. Sakanyan (Sakanyan, personal communication.).

In this article, we perform a comparison of the frequencies observed for the putative strongest promoters over 32 bacterial genomes. We distinguish two strength levels, depending on the relaxation allowed with respect to the canonical σ70 promoter, and combine them with either mandatory or optional UP element presence. Thus, we perform four genome-comparative studies. We discuss the statistical significance of our results through comparisons with randomly generated genomes, highlighting and elucidating the specific case of *Firmicutes*.

SYSTEMS AND METHODS

Genome analysis upon request

For each genome studied, BacTrans[2] (http://www.sciences.univ-nantes.fr/lina/bioserv/BacTrans2/) takes as an input the Fasta genome sequence provided by GenBank (http://www.ncbi.nlm.nih. gov/genomes/lproks.cgi) together with the corresponding genome annotation. For each gene encoding a protein, the tool first extracts the subregion spanning to 350 nucleotides upstream of SC's first nucleotide. Then, occurrences of the σ70 promoter binding sites are searched for under constraints relative to: (i) bp distances between binding sites or distances between binding sites and translation signals playing the role of 'anchors' and (ii) the maximal number of mismatches allowed with respect to each consensus. In GenBank files, the only location annotation available is that of the SC. Hence, for each gene, the SC is considered a right anchor and each region upstream of SC is scanned to retrieve in priority the structured motif [*UP element*] <3-18> [−35 *box*] <15-20> [−10 *box*] <10-200> [*SD*] <2-10> [*SC*] (described in the 5′ to 3′ direction),

where *SD* denotes the Shine-Dalgarno sequence and $[box_1] < d_{min} - d_{max} > [box_2]$ states the minimal and maximal bp distances allowed between the two boxes concerned. Actually, the full motif identification is performed in the 3′ to 5′ direction, successively considering each possible occurrence of the current box as a right anchor. In the absence of any UP element, the structured motif [−35 *box*] <15-20> [−10 *box*] <10-200> [*SD*] <2-10> [*SC*] is looked for.

For each genome, the consensuses used have been adapted from *E. coli* σ70 promoter, relying on the work of Huerta and co-workers (18). These authors first identified a pair of Position-Specific Scoring Matrices (PSSMs), corresponding to the −35 and −10 boxes, associated with an interval of minimal and maximal bp distances, best describing *E. coli* σ70 functional promoters (see latter reference, Matrix_18_15_13_2_1.5 in Figure 2). Second, for any genome other than *E. coli*, they normalized the frequencies of the pair of *E. coli* PSSMs, using the *a priori* nucleotide probabilities characterizing this genome. Then, they relied on the normalized PSSM pair, to identify a set of promoter-like sequences within each genome. Finally they computed the −10 and −35 consensuses for each genome. In our study, for each genome, the consensuses retained are the subsequences of the consensuses of Huerta and co-workers, corresponding to the locations of the canonical TTGAC and TATAAT *E. coli* consensuses. We were careful to set accordingly the optimal bp distance between the −10 and the −35 boxes. As a result, the two −10 consensus TATAAT and TAAAAT have been used, respectively, for 20 and 12 genomes; TTGAC, TTGAA and TTTAA were the three −35 consensuses used to scan 6, 18 and 8 genomes, respectively (see Supplementary Appendix 1). A value of 200 bp was chosen for the maximal distance between *SC* and *SD*; it was selected on the basis of the average 5′UTR region's length (50 or thereabouts, with variations between 0 and 200). The UP consensus used is that of *E. coli*, AAAWWTWTTTTNNAAAA (The genuine UP element has NN and NNN, respectively, as 5′ and 3′ termini).

For each binding site, minimal similarity is described through a maximal number of mismatches allowed. Notation $(err(UP), err(-35\ box), err(-10\ box))$ specifies the maximal numbers of mismatches allowed with regard to the UP element, the −35 box and the −10 box, respectively. Given this notation, two mismatch constraints are retained in our study; they are described as follows: **(4,2,1)** and **(4,3,2)**. From now on, the two mismatch constraints **(4,2,1)** and **(4,3,2)** will be, respectively, denoted *CI* and *CII*. *CI* is more stringent than *CII*. Finally, four configurations will be considered in our analysis: *CI*, UP element required; *CII*, UP element required; *CI*, UP element optional; *CII*, UP element optional. The requirement of a greatest specificity for the −10 box compared to the −35 box is modeled after observations relative to functional σ70 promoters.

Hereafter, we denote *sp* the number of strong σ70 promoter-like sequences obtained from a given genome, when the presence of the UP element is optional. Similarly we define *upsp* when the UP element is required. From now on, we will refer to sp_{CI}, sp_{CII}, $upsp_{CI}$ and $upsp_{CII}$.

Scoring function used

In the sequel, $err(b)$ denotes the number of mismatches observed with respect to the consensus box b; d_1 denotes the bp distance observed between the −35 box and the −10 box; d_2 denotes the bp distance observed between the UP element and the −35 box. The score is calculated as follows: $score = 0.60\ err(-10\ box) + 0.40\ err(-35\ box) + t_1 + err(UP) + t_2$, where $t_1 = 0$ if d_1 belongs to [17–19] else $t_1 = 5 * d_1$, and $t_2 = 0$ if d_2 ranges in interval [6–8] else $t_2 = 3 * d_2$. When no UP element can be identified, the score is merely computed as: $score = penalty + 0.60\ err(-10\ box) + 0.40\ err(-35\ box) + t_1$. The penalty value is set in order to systematically favour a candidate with an UP element within the regulatory region. This scoring function takes into account the specificity increase of the −10 box with respect to the −35 box. The choice of the coefficients 0.6 and 0.4 may be debatable. The most important point remains that the ratio between these coefficients be consistent with the behaviour of RNA polymerase as observed through functional promoters. Besides, we wished to emphasize the UP element weight, in the case when two promoter candidates harbour an UP-like element. Therefore, we assigned a value of 1 to the coefficient of the UP element. Finally, BacTrans[2] outputs 0 or 1 putative SP per gene encoding a protein. The scoring function is one of the six major differences with the approach by Dekhtyar *et al.* (V. Sakanyan, personal communication). For an enumeration of the differences, the reader is referred to https://hal.archives-ouvertes.fr/hal-00153303/en/.

Comparison with randomly generated genomes

For each bacterial genome considered in this study, we compare the *sp* value (respectively, *upsp* value) observed with respect to the corresponding value expected *on average* for a similarly AT-rich genome generated at random. This latter artificial genome is only constrained to have the same following characteristics as the prokaryotic genome considered: same total number of genes coding for proteins and same proportions of A, C, T and G nucleotides in the 350 nucleotide-long region upstream of the SC. Due to the high bp distance allowed between the −10 box and the SD sequence (200), and the numbers of mismatches allowed, the calculation of the theoretical expected value would not be tractable. Thus, for each genome, and under the four conditions studied, we computed the minimum, maximum, mean and standard deviation for *sp* and *upsp* values, over 100 such randomly generated genomes. Scanning the largest batch of genomes (1400 artificial genomes) required no more than two days and a half under *CII* conditions. To evaluate whether two distributions are statistically different when the latter are not of the Gaussian type and when their variances are not in the same order of magnitude, we relied on the Wilcoxon test. The H_0 hypothesis is stated as follows: the populations from which the two distributions are taken have identical median values. This test first ranks all $n_1 + n_2$ values from both distributions (n_1 and n_2) combined, then sums the ranks on each distribution, *ws* being the smallest sum and *ws′* being computed as $n_1(n_1 + n_2 + 1) - ws$.

If either *ws* or *ws′* is smaller than the theoretical value mentioned in Wilcoxon tables for n_1 and n_2 and an *a priori* level of significance, then hypothesis H_0 is rejected. We also computed the *Z*-score as the absolute difference between the number of SPs *obs* observed in the prokaryotic genome and the average number M_{emp} of promoters computed from the 100 artificial genomes, divided by the standard deviation σ_{emp} computed over these 100 latter genomes: $Z\text{-score} = |obs - M_{emp}| / \sigma_{emp}$, where *obs* is an *spCI* value (respectively, *spCII*, *upspCI*, *upspCII* value). Again, statistical significance will be discussed, this time, with respect to several *Z*-score thresholds.

RESULTS AND DISCUSSION

Are potentially strong σ70 promoter-like sequences frequent?

The 32 genomes compared belong to ten *Firmicutes*, 13 *Proteobacteria*, 3 *Actinobacteria*, 2 *Spirochaetales*, 1 *Chlamydia* and 3 other taxa outside latter phyla. We draw the reader's attention to the case of small genomes: *Borrelia burgdorferi* (0.91 Mbp), *Chlamydophila pneumoniae* (1.22 Mbp), *Mycoplasma genitalium* (0.58 Mbp), *Mycoplasma pneumoniae* (0.81 Mbp), *Rickettsia prowazekii* (1.11 Mbp) and *Treponema pallidum nichols* (1.13 Mbp). All previous six species are either obligate intracellular pathogens, symbionts or animal commensal parasites and have undergone massive gene decay, as well as numerous genomic rearrangements. The presence of functional σ70 promoters is disputable in these genomes. Hereafter the two *Firmicutes M. genitalium* and *M. pneumoniae* will be referred to as *Mollicutes*. Nevertheless, except for *R. prowazekii*, these genomes were investigated in the reference work of Huerta and co-workers (18). We will follow this line, taking great care regarding the discussion. The total number of genes *g* encoding proteins in a genome and the size of this genome are proven to be correlated over the 32 genomes studied (linear correlation coefficient: 0.93). To escape the size bias when comparing genomes, we define the percentage *p*1 ($p1 = 100 \times sp/g$). The top section of Figure 1 (A and B) depicts the variations of *sp* values and *p*1 percentages through genomes (also see Supplementary Data, Appendix 2). For illustration, the output files relative to *E. coli* genome are provided (see Supplementary Data, Appendix 3).

As a first result, we check that the number of putative strong promoters identified increases when constraints are relaxed from *CI* to *CII*. Secondly, we observe that for the AT-rich genomes of *Firmicutes*, putative SPs are over-represented under the two constraints *CI* and *CII*. This differentiates *Firmicutes* from all other genomes studied. Nonetheless, among *Firmicutes*, the numbers of SPs may differ in high proportions (1 to 4 under *CI* and *CII* constraints); *Streptococcus pneumoniae* is always characterized by the lowest value whereas *B. subtilis*, *Oceanobacillus ihenyensis* and *Clostridium perfringens* happen to show peaks depending on the constraint. The differentiation between *Firmicutes* and other genomes holds for *p*1 percentage. The non-*Firmicutes* genomes pointed out by the highest *p*1 percentages (over 5%) are *Aquifex aeolicus*, *Thermotoga maritima* and *B. burgdorferi*. Thirdly, a more thorough examination shows that the genomes with the highest numbers of genes (*g*) are not necessarily those with the highest numbers of putative strong promoters (*sp*). The percentage *p*1 is variable and no linear correlation can be shown to exist between *sp* and *g*. More comments are provided in Supplementary Appendix 4, including a brief report about investigating the nature of genes associated with putative SPs.

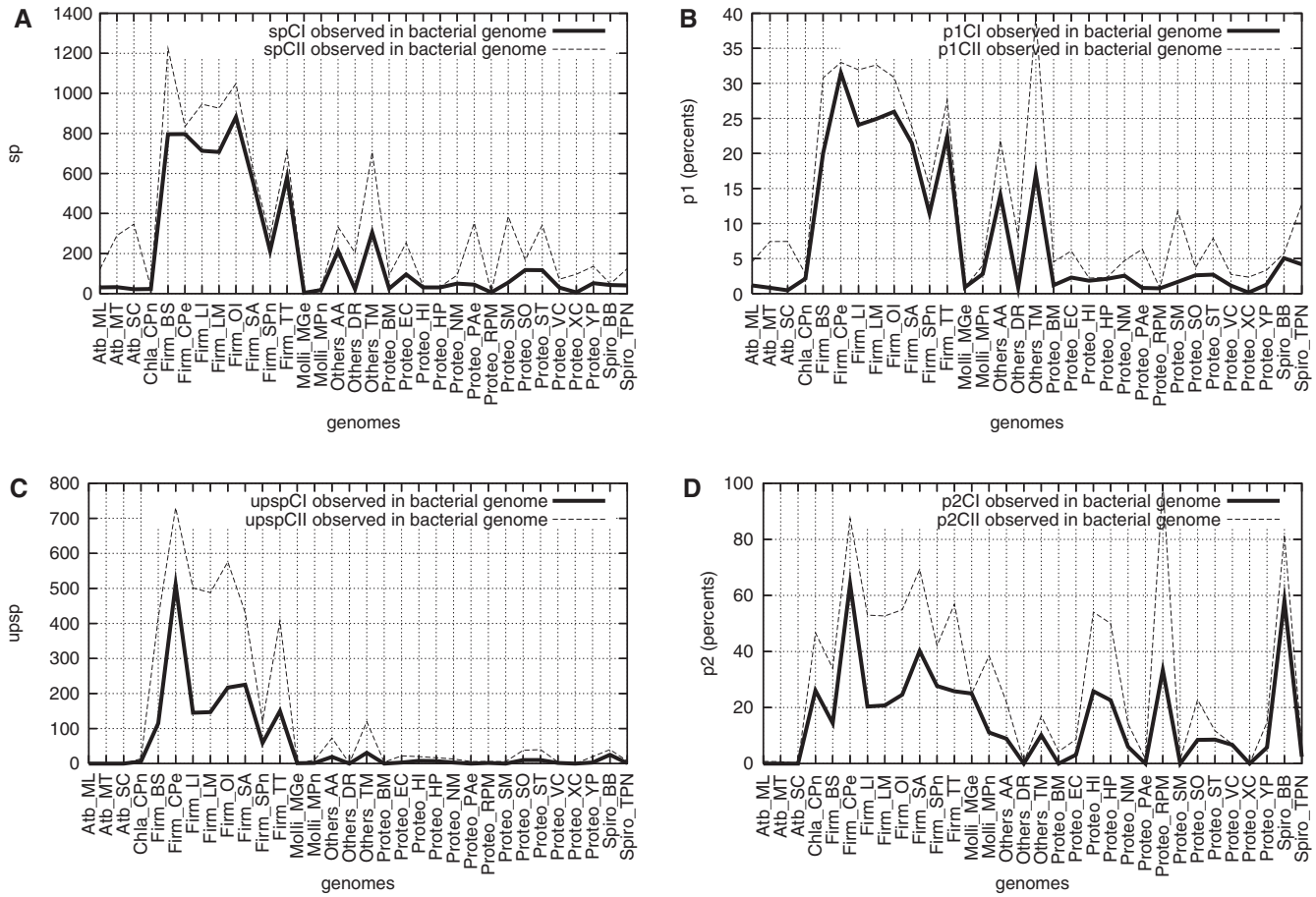
The high AT-richness of *Firmicutes* could justifiably be suspected to yield these high numbers of σ70 promoter-like sequences. Indeed, we show that AT-content does not interfere much with *p*1: over the 32 genomes, the linear correlation coefficient between $p1_{CI}$ and AT-content is **0.52**; the correlation coefficient between $p1_{CII}$ and AT-content is equal to **0.30**, which was expected indeed under relaxed constraints allowing more blurred occurrences of the σ70 promoter model. When we take into account all bacteria but *Firmicutes*, such coefficients go down to 0.26 (*CI*) and −0.14 (*CII*), respectively. When the 10 AT-richest genomes are considered (*Firmicutes*), the coefficients are 0.27 and 0.20, respectively. Anyway, in the latter case, 10 is a borderline value regarding correlation analysis validity.

Are potentially strong σ70 promoter-like sequences harbouring an UP-like element frequent?

We now define percentage *p*2 as follows: $p2 = 100 \times upsp/sp$. The bottom section of Figure 1 (C and D) depicts the variations of *upsp* and *p*2 among the 32 micro-organisms, under *CI* and *CII* constraints (also see Supplementary Data, Appendix 2). The output files relative to *E. coli* genome are provided (see Supplementary Data, Appendix 5).

Again, detailed complements to the present paragraph may be found in Supplementary Appendix 4. We first show that the differentiation between *Firmicutes* and other genomes holds, but it is more subdued for *p*2 percentage than for *p*1 percentage. Secondly, we observe that σ70 promoter-like sequences of relatively 'lesser quality' (constraint *CII*) are more frequently associated with an UP-like element than sequences of 'better quality' (constraint set *CI*) (Figure 1(C and D)): the ratio $p2_{CII}/p2_{CI}$ is calculable for 24 genomes and its average is 2.13; the average computed for all *Firmicutes* but *Mollicutes* is 2.07. Thirdly, we show that some genomes characterized by a low number of strong promoters show in contrast a high (*p*2) percentage of them harbouring an UP element, whatever the constraint (see Supplementary Appendix 4 for more details).

We calculate a correlation coefficient between $p2_{CI}$ and AT-content of **0.84** when all 32 genomes are considered; the correlation between $p2_{CII}$ and AT-content is similarly high (**0.87**). A high correlation is still observed when *Firmicutes* are not taken into account (0.82 and 0.86, respectively). In contrast with the case when no UP element was required, the 10 *Firmicutes* clearly show a correlation between *p*2 and AT-content (0.87 and 0.65, respectively). As expected, a stronger correlation is



Atb_ML:	Mycobacterium leprae tn
Atb_MT:	Mycobacterium tuberculosis h37rv
Atb_SC:	Streptomyces coelicolor a3 (2)
Chla_CPn:	Chlamydophila pneumoniae ar 39
Firm_BS:	Bacillus subtilis 168
Firm_CPe:	Clostridium perfringens str13
Firm_LI:	Listeria innocua
Firm_LM:	Listeria monocytogenes strain EGD
Firm_OI:	Oceanobacillus iheyensis hte831
Firm_SA:	Staphylococcus aureus mw2
Firm_SPn:	Streptococcus pneumoniae r6
Firm_TT:	Thermoanaerobacter tengcongensis
Molli_MGe:	Mycoplasma genitalium G37
Molli_MPn:	Mycoplasma pneumoniae M129
Others_AA:	Aquifex aeolicus vf5
Others_DR:	Deinococcus radiodurans r1
Others_TM:	Thermotoga maritima
Proteo_BM:	Brucella melitensis 16m
Proteo_EC:	Escherichia coli k12
Proteo_HI:	Haemophilus influenza rd kw20
Proteo_HP:	Helicobacter pylori j99
Proteo_NM:	Neisseria meningitidis mc58
Proteo_PAe:	Pseudomonas aeruginosa pa01
Proteo_RPM:	Rickettsia prowazekii madrid e
Proteo_SM:	Sinorhizobium meliloti 1021
Proteo_SO:	Shewanella oneidensis mr1
Proteo_ST:	Salmonella typhimurium lt2
Proteo_VC:	Vibrio cholerae n16961
Proteo_XC:	Xanthomonas campestris atcc 33913
Proteo_YP:	Yersinia pestis
Spiro_BB:	Borrelia burgdorferi b31
Spiro_TPN:	Treponema pallidum nichols

Figure 1. Frequencies of genes harbouring a putative strong promoter (SP), under four constraint sets, in 32 prokaryotic genomes. See text, Subsection "Genome analysis upon request" for the definition of *CI* and *CII* constraints. (**A**) and (**B**): UP element optional; (**C**) and (**D**): UP element required. Along the x-axis, the following phyla and groups are encountered: *Actinobacteria*, *Chlamydia*, *Firmicutes* (among which *Mollicutes*), "Others" group, *Proteobacteria*, *Spirochaetales*. (A) *y*-axis: number of genes harbouring a SP (*sp*); (B) *y*-axis: ratio $p1$ of genes harbouring a SP (*sp*) to the total number of genes encoding proteins in the genome (g), $p1 = 100 \times sp/g$; (C) *y*-axis: number of genes identified with an **UP** element harboured in the SP (*upsp*); (D) *y*-axis: ratio $p2$ of the number of genes with an UP element in the SP (*upsp*) to the number of genes with a SP (*sp*), $p2 = 100 \times upsp/sp$.

observed for $p2$ with respect to $p1$, since 7 out of the 17 nucleotides of the UP element consensus are nucleotides A, 5 are nucleotides T and 3 are A or T (W).

We now recapitulate the results obtained regarding AT-richness influence on $p1$ and $p2$: (i) depending on the species considered, AT-richness interferes but moderately so long as the UP element is not considered ($p1$); (ii) on the contrary, AT-content and percentage $p2$ are highly correlated. A pending question is then: does AT-richness alone entail high *upspCI* and *upspCII* values? To answer this question, we will in particular compare *Firmicutes*' genomes with similarly AT-rich genomes generated at random.

Finally, the normalized ratio ρ of the number of promoter-like sequences (associated with an optimal SD) to the number of genes harbouring an optimal SD sequence has been calculated under all four conditions (see Supplementary Appendix 4, Table 4.1). The first observation drawn from Table 4.1 is that *CII* conditions

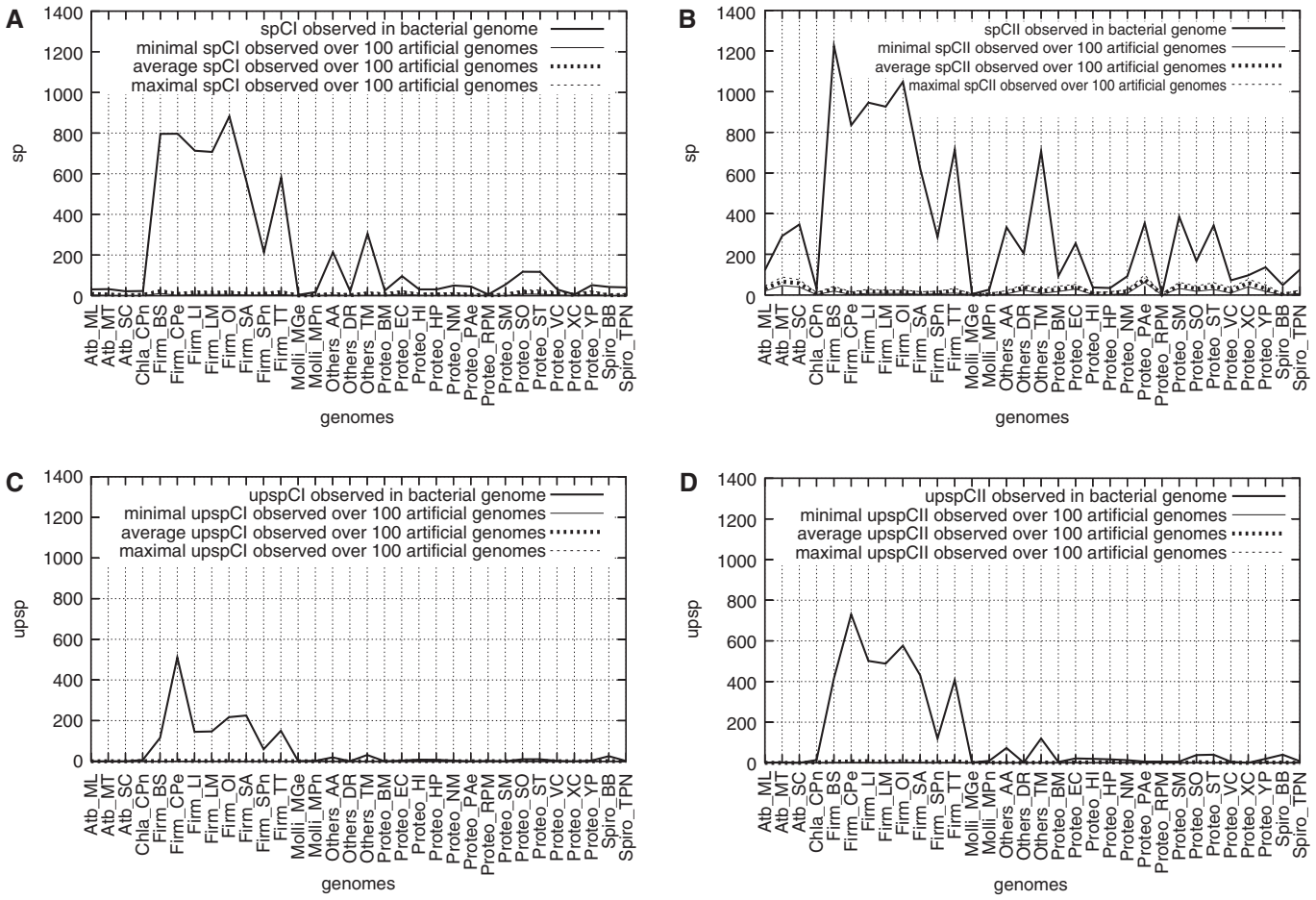


Figure 2. Observed bacterial genome values versus minimal, average and maximal values observed over 100 similarly AT-rich genomes generated at random, for *sp* and *upsp*, respectively, under four constraint sets. See Figure 1 for definition of *sp* and *upsp*, and for genome abbreviations. See text, Subsection "Genome analysis upon request" for the definition of *CI* and *CII* constraints. (A): *CI*, UP element optional; (B): *CII*, UP element optional; (C): *CI*, UP element required; (D): *CII*, UP element required.

do not entail any selection, thus leading to the conclusion that *CII* conditions alone are not adequate for potentially strong promoter description. Moreover, interestingly, under all three other conditions (*CI* and *CII*, UP element required; *CI*, UP element optional), this normalized ρ ratio is always significantly higher in *Firmicute* genomes than in non-*Firmicute* genomes. Therefore, we have indisputably confirmed the existence of a meaningful bias for frequencies of σ70 promoter-like sequences associated with optimal SDs, in *Firmicute* genomes.

Comparing observations in bacterial genomes with expectations in randomly generated genomes

For each genome, we compare the frequency of putative SPs with that obtained for a similarly AT-rich 'average' genome generated at random (Figure 2). For comparison purposes, a common scale is used in the four pictures of Figure 2 (The reader interested in details is referred to Supplementary Data, Appendix 6, for a magnification relative to artificial genomes' results).

We start our analysis focusing on the *CI* case. Figure 2A (*CI*) shows that strong σ70 promoter-like sequences are significantly more frequent in *Firmicutes* genomes than in corresponding artificial genomes. From now on, we distinguish the two *Mollicutes* from the other eight *Firmicutes*. Given as quadruplets (minimum, maximum, **average**, standard deviation), *Z*-scores are as follows: *Firmicutes* except *Mollicutes*: (81.3, 308.5, **193.0**, 66.1); *Proteobacteria*: (1.0, 32.4, **16.0**, 9.5). We check that the eight *Firmicutes*' *Z*-scores are above threshold 140, except for *Listeria monocytogenes* (81.3). Concerning the 12 large *Proteobacteria* genomes studied, 10 have their *Z*-scores above threshold 7, among which 6 have their *Z*-scores above threshold 15. In particular, the *Z*-score obtained for *E. coli* genome is 21.7.

When restraining our examination to the 26 species with large genomes, under condition *CI*, we observe that 24 genomes have their *Z*-scores over threshold 7, among which 15 have their *Z*-scores over threshold 15 and finally 10 *Z*-scores exceed threshold 80. For a detailed description relative to sp_{CII}, $upsp_{CI}$ and $upsp_{CII}$ values (Figure 2; B, C and D), the reader is referred to Tables 6.1 through 6.4 in Supplementary Appendix 6. Table 6.3 focuses on *E. coli*. We recapitulate the main results and conclusions in the following paragraph.

First, we confirm that, except for the slightly more subdued case of *L. monocytogenes*, *Firmicutes* clearly show a specific trend, with *Z*-scores above thresholds 160, 100 and 150, respectively, under *CII* condition (UP optional), and *CI* and *CII* conditions (UP required). Yet, under all four conditions, the *Z*-scores calculated for *L. monocytogenes* stay rather high (they range in interval [69, 93]). Secondly, relaxing the constraint from *CI* to *CII* entails no decrease of the *Z*-score (see Supplementary Appendix 6, Table 6.1). At first sight, this is not a trivial result, as the opposite was expected instead. But *CII* condition alone has been shown to be under-constrained. Therefore, no valid information can be drawn from the *Z*-scores, in this case. Besides, the number of putative SPs harbouring an UP element, observed in the average random genome under *CI* condition, drastically decreases down to 0 for 26 species out of 32. Under this latter condition, it is obvious that both observed and expected $upsp_{CI}$ distributions strongly differ from one another. More rigorously, and more generally, the Wilcoxon test successively performed on $p1_{CI}$, $p2_{CI}$ and $p2_{CII}$ allows us to conclude that the difference between observed values and values expected by chance is statistically significant under all three conditions, for the 0.05 threshold. Thus, the σ70 promoter-like sequences retrieved in bacterial genomes are not due to mere chance. Additionally, Table 6.2 in Supplementary Appendix 6 enables evaluation of the statistical significance for each non-*Firmicute* genome with respect to the *Z*-score thresholds 7, 15 and 80. Table 6.4 recapitulates the number of large genomes for which statistical significance is ascertained with regard to these thresholds: at least half of them under *CI* condition, for threshold 15, which we consider a high threshold; nearly all of them for threshold 7. Finally, since similarly AT-rich average genomes generated at random are far from yielding such high frequencies as those observed for the eight corresponding *Firmicutes* genomes, AT-richness is clearly not the reason for the *Firmicutes* specificity.

Another lead is thoroughly examined to attempt to explain the *Firmicutes* difference. Due to the lack of space, we refer the reader to Tables 6.6 and 6.7 in Supplementary Appendix 6. We demonstrate therein that the *Firmicutes* difference is neither explained by genome size bias. Summarizing, in this section, we have characterized the statistical significances for all genomes, under four conditions of stringency, and with respect to three *Z*-score thresholds. We have proven the existence of a specificity for *Firmicutes* (large) genomes with regard to our definition of potentially high transcription. Moreover, this specificity is neither an artefact due to high AT-richness nor to differences in gene numbers between genomes.

Discussing the *Firmicutes* case

To explain the fact that putative strong σ70 promoters appear much more frequently in *Firmicutes* than in other bacteria, including—paradoxically—*E. coli*, we recall that we adopted the consensus GGAGG. In *E. coli*, GGAGG is a very strong SD sequence; more frequent SDs are the submotifs GGAA, GGAG, GAGG, AGGA and AAGG (30, 23). On the other hand, ribosomes from many Gram-positive bacteria depend much more stringently upon a strong SD interaction for initiation (31). For instance, in *B. subtilis* genome, most SD sequences are close to the consensus sequence AAAGGAGG (32). This, we suggest, could be the reason for the abundance of putative SPs in *Firmicutes* genomes. This point has been investigated further. We show that the percentage p_{bact} of genes associated with an optimal SD sequence ranges between 2.21% and 39.8% for the 26 large genomes. Immediately behind *T. maritima*, which shows the highest ratio, the eight large *Firmicutes* genomes rank first with respect to this p_{bact} ratio ([15.3%, 32.6%]). The percentages p_{rand} expected for similarly AT-rich genomes generated at random have been calculated. The calculus is described in Supplementary Appendix 7. The p_{bact} and p_{rand} distributions are proven statistically different through a Wilcoxon test (threshold 0.05). Furthermore, the correlation coefficient between p_{rand} and AT-richness is −0.97, over the 32 artificial genomes. This high negative value was expected, since the optimal SD sequence is enriched with four G nucleotides. In contrast, the correlation coefficient between p_{bact} and AT-richness is low when computed over the 32 bacterial genomes (0.22). This point argues in favour of the biological significance of such GGAGG sequences in the close neighbourhood of SCs. Moreover, regarding this criterion, the Wilcoxon test also ascertains the statistical significance of the difference between the eight *Firmicutes* and the 18 other species with large genomes. This difference is reflected by the *Z*-scores. *Z*-scores range in interval [3.2, 363.9] when all genomes are considered (mean: 86.9, standard deviation: 103.1). The *Z*-scores calculated for the eight large *Firmicutes* genomes range between 86.8 (*S. pneumoniae*) and 363.9 (*C. perfringens*). When all large genomes but *Firmicutes*' are considered, the mean and standard deviation are, respectively, equal to 41.8 and 40.0. Outside the *Firmicutes* taxon, *T. maritima* and *A. aeolicus* are the only two bacteria showing as outstanding *Z*-scores as *Firmicutes* (respectively, 168.7 and 106.2). Again, we emphasize that both previous genomes are also characterized with high AT percentages (54.6% and 57.6%), which confirms a bias for the presence of optimal SD sequences in some genomes.

Anyway, such bias exists for all genomes. For example, in the light of the previous explanation, we now explain the scarcity of putative SPs associated with optimal SD sequences, in *E. coli*, through the low p_{bact} percentage of 6.2% observed. Though, the percentage expected is 0.9%. The bias measured through the *Z*-score is 37.9. Therefore, this point suggests that even in *E. coli*, hazard would only contribute for 15% (0.9/6.2) to yield false positive optimal SD sequences. Finally, considering the criteria retained in our analysis (high intrinsic transcription potentiality combined with strong SD interaction), we conclude that *Firmicutes* would appear as genomes more favoured by nature, especially with respect to other similarly AT-rich genomes.

Putative strong promoters versus experimentally verified functional promoters in *E. coli* genome

In vivo, activation by various factors is ascertained to compensate for promoter weakness. However, it is not known whether some functional promoters might also be intrinsic strong promoters. So far, data compilations relative to experimentally verified functional promoters are only available for *E. coli* genome, through two repositories, RegulonDB and PromEC (33–34). Therefore, we could compare the putative strong promoters identified by BacTrans^2 software in *E. coli* genome with known *E. coli* functional promoters. For this purpose, we compiled our own σ70 promoter dataset from 5.8 RegulonDB release (september 2007, http://regulondb.ccg.unam.mx/data/PromoterSet.txt.) and PromEC database (http://margalit.huji.ac.il/). We checked that *E. coli* known functional promoters are intrinsically weaker than all putative SPs retrieved by our software BacTrans^2, which was expected (see Supplementary Appendix 8).

Experimental verification of putative strong promoters identified in *T. maritima* genome

The hyperthermophilic model *T. maritima* has been intensively studied (35–36). In the context of a former study, the activity of 13 putative strong promoters harbouring an UP element has been measured in *E. coli* cell free extracts (37). The present work thereby benefits from these experimentations. The protocol used is described in Supplementary Appendix 9. Seven putative strong promoters harbouring an UP element identified by BacTrans^2 were thus tested. Four were identified under the most constrained condition *CI* (*TM*1016, *TM*0373, *TM*0477, *TM*1667). The other three were identified under *CII* condition (*TM*0032, *TM*1429, *TM*1780). All of them promote protein synthesis, indicating that they are all functional promoters. Moreover, except *TM*0032, all provided a higher protein yield than that of the well-studied pTac promoter. *TM*0477 has been shown to be twice as strong as others regarding protein yield. Therefore, six potentially strong promoters among the seven tested do really favour high expression in *E. coli* cell free extracts.

CONCLUSION

Our work contributes to shedding new light on potentially high ORF expression in prokaryotic genomes, focusing on potentially high transcription combined with the presence of an optimal SD sequence. Our approach also puts emphasis on transcription initiation potentially enhanced through UP-like elements. In itself, this latter feature introduces originality with respect to other genome-comparative studies devoted to bacterial promoters. Moreover, genomes were compared in a rather unusual way, that is on the basis of their frequencies of intrinsically SP candidates, upstream of genes coding for proteins. Besides, our analysis clearly departs from other works, since it considers four different conditions of stringency and discusses in each framework the statistical significance of the presence of σ70 promoter-like sequences. Under all four conditions, we identified the species showing statistically significant differences between the bacterial genome and an average similarly AT-rich genome generated at random. Thus, specific features typical for *E. coli* promoters were used to extract promoter-like signals from other genomes and statistically significant differences were revealed on the basis of this approach. In particular, *Firmicutes* would appear as genomes more favoured by nature with respect to other genomes, including the cases when an UP-like element is required. A rigorous discussion allowed us to dismiss AT-richness and genome size bias as determining factors to explain the *Firmicutes* specificity. We have shown that this specificity is neither explained by the typical abundance of optimal SD sequences in *Firmicutes'* large genomes, thus revealing another *Firmicute* bias, unknown so far. Besides, so far, the UP element has been identified by experimentation in four genomes. Thus, our comparative study also brings novel knowledge about the statistical significance of the presence of putative σ70 promoters enhanced with an UP-like element, in various genomes.

The generic software platform BacTrans^2 currently provides such putative strong promoters for 45 genomes. These data may be of interest to select a subset of promoters for experimental characterization and possible further use in biotechnological applications. In this latter field, inserting in cellular or cell-free expression systems regulatory regions including promoters enhanced with an UP element and an optimal SD sequence may be advocated, instead of inserting artificial binding sites in a synthetic sequence. A more thorough study of high translation potentiality related to high transcription potentiality in prokaryotic genomes is attractive and is currently under work. Finally, BacTrans^2's genericity allows the user to analyse genomes with respect to any other super-motif consisting of three or four boxes.

SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online.

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