Review

New insights into the regulatory networks of paralogous genes in bacteria

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Extensive genomic studies on gene duplication in model organisms such as Escherichia coli and Saccharomyces cerevisiae have recently been undertaken. In these models, it is commonly considered that a duplication event may include a transcription factor (TF), a target gene, or both. Following a gene duplication episode, varying scenarios have been postulated to describe the evolution of the regulatory network. However, in most of these, the TFs have emerged as the most important and in some cases the only factor shaping the regulatory network as the organism responds to a natural selection process, in order to fulfil its metabolic needs. Recent findings concerning the regulatory role played by elements other than TFs have indicated the need to reassess these early models. Thus, we performed an exhaustive review of paralogous gene regulation in E. coli and Bacillus subtilis based on published information, available in the NCBI PubMed database and in well-established regulatory databases. Our survey reinforces the notion that despite TFs being the most prominent components shaping the regulatory networks, other elements are also important. These include small RNAs, riboswitches, RNA-binding proteins, sigma factors, protein–protein interactions and DNA supercoiling, which modulate the expression of genes involved in particular metabolic processes or induce a more complex response in terms of the regulatory networks of paralogous genes in an integrated interplay with TFs.

Introduction

Gene duplication is one of the main sources of functional divergence in organisms (Babu et al., 2004; Conant & Wolfe, 2008; Gelfand, 2006; Lynch & Conery, 2000; Teichmann & Babu, 2004). In order to fulfil an organism’s metabolic needs, selection processes modify the regulation of the paralogous gene copies, taking advantage of a repertoire of new functions. Duplication events may include genes coding for transcription factors (TFs), permitting a more versatile adaptation of the functional diversity gained from the duplication of structural genes. Different aspects of the evolution of the regulatory networks of paralogous genes have been examined, including the co-evolution of the upstream regulatory regions and their corresponding TFs; the likely consequences of gain, loss, and replacement of TFs in the regulatory networks of paralogous genes (Gelfand, 2006; Teichmann & Babu, 2004); and also the topological and dynamic properties of the regulatory networks (Babu et al., 2006; Balaji et al., 2007; Luscombe et al., 2004). This review will consider the fascinating repertoire of additional mechanisms other than TFs, which help regulate the expression of paralogous genes in Escherichia coli and Bacillus subtilis. This analysis is derived from an extensive compilation of the regulatory information available from the NCBI PubMed database and deposited in the E. coli RegulonDB Release 6.3 (Gama-Castro et al., 2008), B. subtilis DBTBS (Sierro et al., 2008) and Rfam version 9.1 (Gardner et al., 2009) databases.

TFs are essential elements in the regulatory networks of paralogous genes

TFs are the most prominent and usually the only regulatory element taken into account in any of the aforementioned studies because of the important role they play in the regulatory networks of paralogous genes. Teichmann & Babu (2004) formulated a widely accepted evolutionary model portraying the regulation of duplicated genes. In this model, the loss and gain of regulatory interactions may occur following the duplication of either a TF or a target gene, or following the duplication of both a TF and a target gene (Fig. 1a). The Teichmann and Babu model does not

Four supplementary tables are available with the online version of this paper.
question whether the regulatory effect (either activation or repression) of the TFs on the paralogous genes is conserved or changed in any of these instances; it only considers the regulatory interactions. An example of a regulatory conserving effect is found in the E. coli paralogous genes zntA and copA (Group 393, Supplementary Tables S1 and S3), coding for zinc and copper transporters, which are regulated by the paralogous TFs ZntR and CueR, respectively (Yamamoto & Ishihama, 2005a, b) (Fig. 1a). We also identified examples of regulatory systems where the TF is maintained but a different effect is gained (either activation or repression) in one of the paralogous genes. This evolutionary scenario can be observed in the regulation of the E. coli gntK and idnK gluconate kinase genes, involved in the 6-phosphogluconate synthesis which takes place in the Entner–Doudoroff and pentose phosphate pathways, respectively. Although these genes are regulated by the same TFs, CRP, GntR and IdnR, the last TF represses the transcription of gntK, whereas it activates the transcription of idnK (Bausch et al., 2004; Izu et al., 1997) (see Fig. 1b and Group 449 of Supplementary Tables S1 and S3).

In order to quantify the divergence in the regulation of paralogous genes in E. coli and B. subtilis, BLAST comparisons (Altschul et al., 1990) of their corresponding protein sequence sets were carried out. Based on these comparisons, we identified 477 groups of paralogous genes in E. coli. From this set, 291 groups of paralogous genes were found to be regulated by at least one TF, and for 43 of these (14.8 %) the TFs were shown to have a dual activation/repression effect on their corresponding paralogous target genes (Supplementary Table S3). In B. subtilis this tendency was considerably less. Out of the 483 groups of paralogous genes, we found that 225 groups were regulated by at least one TF, and eight of these (3.6 %) presented at least one TF with a dual activation/repression regulatory activity (Supplementary Table S4). In E. coli, this dual regulatory activity is more frequently found in the groups of paralogous genes regulated by global TFs: ArcA, CRP, FIS, FNR, Hns, IHF and Lrp (Martinez-Antonio & Collado-Vides, 2003) (see Supplementary Table S3). In contrast, only some of the B. subtilis global TFs such as AbrB, CcpA, Spo0A and TnrA (Moreno-Campuzano et al., 2006) exhibit a dual activation/repression activity, whereas others either act always as repressors (CodY, Fur, LexA and YrzC), or always as activators (ComK) (see Supplementary Table S4). Finally, a smaller proportion of local TFs show dual activation/repression regulatory activity on paralogous genes. This is the case for the E. coli NtrC transcription regulator, which represses the transcription of the glutamine transporter subunit glnH gene and activates the transcription of the histidine/lysine/arginine/ornithine transporter hisJ and the lysine/arginine/ornithine transporter argT genes (Zimmer et al., 2000) (Group 27 of Supplementary Table S1).

In order to test the statistical significance of finding a regulatory element (TFs, sigma factors, protein–protein interactions, DNA supercoiling, RNAs and RNA-binding proteins) that regulates two or more paralogous genes in a regulatory network, we carried out a computer simulation procedure, similar to the one performed by Teichmann & Babu (2004), where the regulatory interactions were randomly shuffled. Having performed the randomization process 10 000 times, we compared the mean values of these simulations against the number of interactions in the real regulatory networks of E. coli and B. subtilis (531 and 189 interactions, respectively). These real interactions were found to be significantly different from the average interactions of their corresponding randomized E. coli and B. subtilis datasets (19.5 and 19 standard deviations, $s_d$s, respectively). The statistical significance of two or more paralogous genes being regulated by a similar TF, but having a dissimilar regulation (activation vs repression), was also evaluated. In this case, the distance of the real values from the mean of randomly generated networks in E. coli and B. subtilis was 3.7 and 2 $s_d$s, respectively. Interestingly, when this analysis was performed excluding the global regulators of E. coli (ArcA, CRP, FIS, FNR, Hns, IHF and Lrp) (Martinez-Antonio & Collado-Vides, 2003) and B. subtilis (AbrB, ComK, TnrA, CodY, Spo0A and CcpA) (Moreno-Campuzano et al., 2006), both distances increased significantly, to 6.5 and 3.4 $s_d$s, respectively. These results highlight the evolutionary plasticity of the regulatory networks: not only as a result of the duplication of TFs’ interactions on the regulatory network as previously proposed by Teichmann & Babu (2004), but also as a result of the divergent effect of the TF interactions, activating or repressing the transcription of paralogous genes.

Divergence of paralogous genes may include the modification or acquisition of new regulatory mechanisms, changes in gene dosage (Gu et al., 2002), subdivision of ancestral functions and the evolution of new functions (Conant & Wolfe, 2005, 2002; Li et al., 2005), implying that alterations in gene expression precede potential changes in function. Furthermore, it has been postulated that paralogous genes which diverge in function contribute to evolutionary innovation at a biochemical level (Evangelisti & Wagner, 2004; Gu et al., 2005, 2002; Zhang et al., 1998). In order to corroborate these observations, we analysed the metabolic divergence of paralogous genes. By identifying the differences in the assigned biochemical reaction or metabolic pathway, we were able to show that 198 (42 %) of the paralogous groups in E. coli have a known metabolic function, according to the KEGG database (Gu et al., 2005, 2002; Kanehisa et al., 2008). From this set, we identified 53 groups (27 %) that possess members which share the same metabolic pathway.
and perform the same enzymic reactions; 64 groups (32%) which are formed exclusively from proteins that belong to different pathways; and 26 groups (13%) which are entirely constituted of proteins that are part of the same pathway, although they take different metabolic steps. Intermediate cases of groups partially formed by any of the above categories were found on 55 occasions (28%). Slightly different tendencies were observed in the 485 groups of paralogous genes in *B. subtilis*. Finally, duplication events may not be restricted to individual
Alternative sigma, anti-sigma and anti-anti-sigma factors may also be part of the regulatory network of paralogous genes

Transcription regulation by alternative sigma factors, anti-sigma factors and anti-anti-sigma factors is a common strategy used by various organisms in order to accomplish different cellular processes, including (i) the regulation of specific biogenesis processes, such as flagellar biosynthesis in E. coli, which is regulated by σ^{38} (Chilcott & Hughes, 2000); (ii) the response to a metabolic requirement, as occurs when E. coli grows in nitrogen-deprived conditions and gene transcription depends on σ^{54} (Reitzer & Schneider, 2001); (iii) the response to different kinds of stress factors, as in heat shock stress in E. coli, which is regulated by σ^{32}, or in the case of general stress in B. subtilis, which is regulated by σ^{B} (Hecker et al., 2007); (iv) synchronized transcription at a specific growth stage, as occurs in the stationary phase of E. coli, where transcription is regulated by σ^{38} (Hengge-Aronis, 2002); and (v) coordinated cell differentiation processes, such as B. subtilis forespore formation, whose regulation depends on genes transcribed by σ^{E}, σ^{F}, σ^{A}, σ^{H} and σ^{K} (Kroos & Yu, 2000). Although in general each of the sigma factors recognizes clearly distinguishable promoter sequences and thus transcribes different groups of genes, in E. coli the stationary-phase σ^{38} and its paralogous counterpart, the housekeeping σ^{70}, may share overlapping sets of target genes (Typyas et al., 2007). The presence of cis-acting elements located in the promoter region, as well as the activity of trans-acting proteins, establishes whether a promoter is recognized by RNA polymerase containing σ^{38} or σ^{70}. This transcription regulation based on σ^{38} and σ^{70} constitutes a clear example of an extension of the Teichmann and Babu model, where the regulatory network grows by the duplication of regulatory elements other than TFs, which modulate the expression of common gene targets.

According to our compiled data referring to the regulatory networks of paralogous genes, there are 100 out of 477 (21%) groups in E. coli and 144 out of 483 (30%) groups in B. subtilis that are regulated by alternative sigma, anti-sigma or anti-anti-sigma factors (Supplementary Tables S1 and S2). In order to evaluate the statistical significance of finding a sigma factor which regulates two or more paralogous genes, we repeated the simulation procedure performed in the TF analysis, using the sigma factor interaction as input data. Our statistical analysis shows that these sigma factor interactions on paralogous genes in E. coli and B. subtilis were highly significant, as they registered 18 and 6.8 SDs above the mean shown by those obtained in the corresponding randomized regulatory networks. The regulatory model of paralogous genes based on sigma factors is illustrated by the stress response and the early sporulation stage of B. subtilis, which both depend on the paralogous sigma factors σ^{B} and σ^{F}. The regulatory network of these systems also involves a set of paralogous anti-sigma and anti-anti-sigma factors and represents an excellent example of an extension of the Teichmann and Babu model, where the regulatory elements are not TFs. In a first instance, the transcriptional role of σ^{B} and σ^{F} on their target genes is inhibited by the binding of the anti-sigma factors RsBW and SpoIAB (Group 232, Supplementary Tables S2 and S4), respectively. In a second instance, these paralogous anti-sigma factors are negatively regulated by the anti-anti-sigma factors RsBV and SpoIIA (Group 313, Supplementary Tables S2 and S4). Finally, the transcription of the genes that encode these paralogous anti-anti-sigma factors depends on the paralogous sigma factors σ^{A} and σ^{E} (Hecker et al., 2007) (Fig. 1c).

The impact of evolutionary forces on the topological structures known as motifs has been analysed for different kinds of networks (Shen-Orr et al., 2002); for example biological regulatory networks (Kashkan & Alon, 2005; Shen-Orr et al., 2002) and paralogous gene networks (Teichmann & Babu, 2004). It has been reported that duplication of an entirely feed-forward motif (a topological
structure where a TF regulates a second TF, and both TFs simultaneously regulate a target gene) has not been observed in the regulatory networks of model organisms, although single genes generated by duplication could be part of a new feed-forward or other kind of motif. For example, in *B. subtilis* the paralogues $\sigma^F$ and $\sigma^S$ are part of different feed-forward motifs. In the first case, $\sigma^F$ forms a feed-forward motif with the anti-anti-sigma factor SpoIIAA and the anti-sigma factor SpoIAB, as $\sigma^F$ regulates the expression of SpoIIAA and SpoIAB, whereas SpoIIAA modulates the expression of SpoIAB. In a similar manner, the second feed-forward loop is formed by $\sigma^E$, PhoP and PhoR, which are involved in phosphate uptake, post-exponential growth phase and other stress responses (Pragai et al., 2004). Duplication events, or mutations in the duplicated regulatory genes or in the regulatory target sites, can generate new feed-forward motifs useful for the rewiring of the regulatory networks of the paralogous genes, which favours the adaptation process of the organism as it responds to niche adaptation (Gelfand, 2006).

Protein–protein interactions modulate the activity of paralogous proteins

The regulatory networks evolved by gene duplication are not exclusively regulated at the level of transcription initiation. The activity of paralogous proteins can also be significantly post-translationally modified by protein–protein interactions. This kind of regulation is mainly represented by the two-component signal-transduction systems. Most of these systems consist of a membrane-bound histidine kinase that senses a specific environmental signal and catalyses the transfer of a phosphate group to its corresponding response regulator, inducing its activation. An example of this regulation is found in *E. coli* by the paralogous TFs GlnG and AtoC, involved in the transcriptional activation of genes in response to nitrogen limitation and the catabolism of short-chain fatty acids, respectively. The regulatory activity of these TFs depends on their corresponding paralogous histidine kinases GlnL and AtoS (Lioliou et al., 2005; Ninfa & Magasanik, 1986) (see Fig. 1d and Group 8 of Supplementary Tables S1 and S3). Another well-characterized example of the regulation of paralogous proteins by protein–protein interaction is observed in the chemotactic response of *E. coli*. In this case CheR and CheB cause the post-translational regulation of the methyl-accepting chemotaxis proteins Trg, Tap, Tar, Aer and Tsr, paralogous proteins that undergo changes in their methylation state in response to chemical stimuli, thus establishing the swimming pattern (Ferris & Minamino, 2006) (See Group 41 of Supplementary Tables S1 and S3). From our set of paralogous genes, we found nine groups regulated by protein–protein interactions in *E. coli* and nine groups in *B. subtilis* (Supplementary Tables S1 and S2). The numbers of post-translationally interactions that involve one regulator modulating the activity of two or more paralogous genes in *E. coli* and *B. subtilis* were 16 and 12, respectively. Despite the fact that these interactions represent only a small fraction of their corresponding regulatory networks, we found these values to be statistically significant, as they are 23.5 and 15.5 sds above the means of the corresponding *E. coli* and *B. subtilis* randomly generated networks. It is worth mentioning that these protein–protein interactions in the networks of paralogous genes have great hierarchical relevance in terms of the overall regulatory networks, since the modified proteins commonly correspond to regulatory proteins that in turn regulate the transcription of many other genes or interact among these to form a cascade of transcriptional regulation, as in the cases of PhoP/PhoQ, RstA/RstB and PhoB/PhoR, two-component systems that respond to acidic conditions in *E. coli* (Ogasawara et al., 2007).

The preceding examples demonstrating the regulatory role of the two-component system proteins provide evidence of the relevance of protein–protein interactions in the evolution of the regulatory networks of paralogous genes in *E. coli* and *B. subtilis*. It has been documented that the sensor domain of the histidine kinases is subject to a faster evolutionary process than that of the DNA-binding domain of the response-regulator proteins (Alm et al., 2006). The plasticity of these elements in terms of their capacity to change their regulatory specificity as they respond to the adaptive process may include gene duplication and specialization (Commichau & Stulke, 2008). Furthermore, it has been proposed that two-component proteins acquired through duplication may undergo subsequent domain shuffling, permitting the development of novel genetic diversity. This may happen more quickly than that manifested by two-component systems acquired by horizontal gene transfer, as these proteins are more likely to retain their original functions (Alm et al., 2006; Wanner, 1992; Yosef et al., 2009). To sum up, massive duplication followed by shuffling, faster evolution in the sensor protein domain, and probably horizontal gene transfer, all have a significant influence on the evolution of protein–protein interactions and on the architecture of regulatory networks in bacteria.

RNA and RNA-binding proteins are important factors involved in shaping the regulatory networks of paralogous genes

The important role played by RNA molecules in gene regulation has been recently documented. In bacteria, RNA molecules can regulate either in cis, e.g. as riboswitches that are located in the 5‘ untranslated leader region (Winkler & Breake, 2005) or in trans, acting as diffusible products which act by base pairing with their target mRNAs, resulting in changes in their translation or stability (Gottesman et al., 2006). We identified the participation of RNA elements in 28 and 52 groups of paralogous genes in *E. coli* and *B. subtilis*, respectively (Supplementary Tables S1 and S2), by means of computational analysis, using the co-variance models from the Rfam database (Gardner et
RNA-binding proteins can also be included in the regulatory networks of genes generated by duplication. An example of this is found in the carbon catabolite repression system in \textit{B. subtilis}, which makes possible the preferential utilization of easily metabolizable carbon sources, such as glucose. Fig. 1(f) shows the regulation of the paralogous genes \textit{bgIP} and \textit{sacP}, which code for the permeases responsible for the transport of the \textit{\beta}-glucoside salicin and sucrose, respectively (Group 36 of Supplementary Table S2). The transcriptional regulation of these genes is based on the paralogous RNA-binding proteins LiCT and SacT, which can bind and disrupt potential ribonucleic acid anti-terminators located in the upstream regions of the \textit{bgIP} and \textit{sacP} genes (Schilling \textit{et al.}, 2006). As previously carried out for other regulatory elements, a statistical analysis was undertaken for the RNA regulatory interactions of \textit{E. coli} and \textit{B. subtilis}. Despite the participation of RNA elements in different paralogous groups, we only found 12 examples of an RNA element regulating two or more paralogous genes in \textit{B. subtilis}. This value registers 11.6 SDs above the mean of their corresponding randomized regulatory networks.

\textbf{The regulatory networks of paralogous genes are influenced by DNA supercoiling}

Coordinate gene expression involves several hierarchical levels that comprise local control of individual genes or operons, multiple operons within a regulon and multiple regulons within a stimulon. It has been proposed that the highest level of hierarchical gene regulation is mediated by DNA supercoiling, which serves as a global regulator of gene expression (Hatfield & Benham, 2002). Although chromosomal DNA has slight negative supercoiling, the degree of supercoiling can be modulated by the action of DNA topoisomerases, in response to a wide variety of altered nutritional and environmental conditions, including temperature (Grau \textit{et al.}, 1999), osmolarity (Cheung \textit{et al.}, 2003; Grau \textit{et al.}, 1994), oxidative stress (Weinstein-Fischer \textit{et al.}, 2000), aerobic to anaerobic growth shift (Hsieh \textit{et al.}, 1991) and growth stage in either \textit{E. coli} (Cheung \textit{et al.}, 2003) or \textit{B. subtilis} (Bird \textit{et al.}, 1992). DNA supercoiling adjusts the basal levels of expression of all genes whose transcription depends on promoters that are directly sensitive to supercoiling (Hatfield & Benham, 2002) or indirectly, acting in combination with some TFs or sigma factors. This is the case for some genes, where transcription by \(\sigma^{34}\) depends on the superhelical densities, occurring as a function of growth conditions (Bordes \textit{et al.}, 2003). This fine-tuning of regulation by DNA supercoiling is also found to form part of the regulatory networks of paralogous genes. According to our data survey, in \textit{E. coli} there are 15 groups of paralogous genes where regulation is directly modulated by DNA supercoiling. Interestingly, three of these groups correspond to DNA-binding transcriptional regulators which in turn exert a regulatory control on other genes within the network, thus expanding the regulatory response in a hierarchical manner. One of

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\textit{et al.}, 2009). As an example of the RNA molecules recognized, Fig. 1(e) shows the regulation of the \textit{E. coli rpoH} and \textit{rpoS} paralogous genes (Group 374 of Supplementary Table S1), which code for the \(\sigma^H\) and \(\sigma^\beta\) sigma factors, respectively. The translation of \textit{rpoH} is under the regulation of a \textit{cis}-acting RNA element located in the coding sequence of the \textit{rpoH} gene. At low temperatures, this thermo-regulator folds into a secondary structure which overlaps and sequesters the ribosome-binding site (RBS), inhibiting \textit{rpoH} translation (Narberhaus \textit{et al.}, 2006) (Fig. 1e). In contrast, the regulation of \textit{rpoS} depends on a set of \textit{trans}-acting small RNAs, in response to different kinds of stress factors, such as low temperature (DsrA), osmotic shock (RprA) and oxidative shock (OxyS). Interestingly, RprA and DsrA have a positive effect on \textit{rpoS} translation by destabilizing a secondary structure that sequesters the RBS, whereas OxyS has a negative effect on translation, by an unidentified mechanism (Gottesman \textit{et al.}, 2006) (Fig. 1e).

In general, the number of RNA molecules acting in \textit{cis} as riboswitches on the regulatory networks of paralogous genes is greater in the Firmicute \textit{B. subtilis} than in the Proteobacterium \textit{E. coli}. Indeed, there are \textit{B. subtilis} riboswitches that do not exhibit a counterpart in \textit{E. coli}, which is the case for the T-box element, regulating different kinds of genes involved in amino acid biosynthesis, transport and charging onto their corresponding tRNAs (Gutierrez-Preciado \textit{et al.}, 2005, 2009). On the other hand, the regulation of paralogous genes by \textit{trans}-acting RNA elements is particularly important in \textit{E. coli} and other Gram-negative bacteria, where it has been related to the response to different stress factors such as the aforementioned low temperature (DsrA), osmotic shock (RprA) and oxidative shock (OxyS), in addition to the stress caused by iron limitation (RyhB) and the accumulation of glucose phosphate (SgrR) (reviewed by Gottesman, 2005). In fact, there is an important bias of these small RNAs to regulate paralogous gene coding for outer-membrane proteins involved in stress response, previously described (see Groups 19, 58 and 278 of Supplementary Tables S1 and S3). Interestingly, some of these small RNAs have been generated by duplication, as is the case of \textit{E. coli} OmrA RNA, which is accumulated in the late stationary phase, whereas its paralogous counterpart, OmrB, is transiently expressed in the early stationary phase (Guillier \textit{et al.}, 2006). In higher organisms such as rice, it has been proposed that some pseudogenes may have acquired novel regulatory roles as antisense small RNAs, after being duplicated (Guo \textit{et al.}, 2009). Duplication of regulatory RNA elements is not restricted to \textit{trans}-acting RNAs, but may include \textit{cis}-acting riboswitches. Such is the case with tandem T-boxes located in the regulatory regions of the tryptophan biosynthetic operons in \textit{Bacillus anthracis}, \textit{Bacillus cereus}, \textit{Bacillus halodurans} and other Gram-positive bacteria. It has been proposed that these tandem riboswitches may expand the range of regulation of their respective transcription units (Gutierrez-Preciado \textit{et al.}, 2005).
these groups includes the OxyR regulator involved in the oxidative stress response (Group 4, See Supplementary Tables S1 and S3). In addition, we found groups of paralogous genes coding for transporters of amino acids and other types of metabolite, as well as genes coding for prophage proteins (Supplementary Tables S1 and S3). It is interesting that all the genes whose expression is reported to be modulated by DNA supercoiling belong to different paralogous groups; thus no statistical analysis was carried out to determine the probability of finding this regulatory element acting on two or more different gene targets.

**Different kinds of regulatory elements simultaneously participate in the regulatory networks of paralogous genes**

The response to different external and metabolic signals on the part of the regulatory networks of paralogous genes involves the integration of multiple kinds of regulatory elements, acting at different levels. An excellent example of this kind of regulatory integration is found in the *E. coli* paralogous porins OmpC and OmpF (Group 58 of Supplementary Table S3) in response to medium osmolality, temperature and oxidative stress (Guillier et al., 2006; Pratt et al., 1996). Fig. 2 summarizes the different regulatory layers and types of regulatory elements of this system, which comprise: (i) regulation at transcription initiation by at least 11 TFs that act directly on *ompC* and *ompF*, or indirectly regulate the transcription of other regulatory elements of the system; (ii) regulation at translation initiation, accomplished by a set of small antisense RNAs; (iii) post-transcriptional control of the RNA chaperone StpA on *micF* RNA, by the induction of its degradation; and (iv) post-translational modification of protein activity, as is the case in OmpR activation, by means of its phosphorylation by the histidine kinase EnvZ.

Furthermore, Fig. 2 shows that a single regulatory element may act at different levels on more than one target gene. For example, H-NS may directly regulate *ompC* expression by blocking its transcription and indirectly regulate *ompF* translation by repressing the transcription of the *micF* antisense RNA. Interestingly, a specific TF may have a dual activity on its target genes and may act as a transcription activator or repressor, as a result of its interaction with other regulatory elements of the system. This is the case with OmpR, where the active state depends on its phosphorylation by EnvZ, in response to osmolarity. At a low concentration of OmpR-P (low osmolarity), transcription of *ompF* is activated. At high osmolarity, the concentration of OmpR-P increases and the protein binds to additional low-affinity sites, blocking the transcription of *ompF* (Pratt et al., 1996).

![Fig. 2](image-url)
Concluding remarks

The compilation and analysis of regulatory elements in paralogous genes of model organisms has led us to extend the original model of the evolution of regulatory networks, which took only TFs into account, to a model of more general type, which includes other regulators such as small RNAs, riboswitches, RNA-binding proteins, sigma factors, protein–protein interactions and DNA supercoiling. Despite the fact that TFs are the most extensively used element in regulatory networks, the extended repertoire of other regulatory mechanisms has resulted in a significant increase in the versatility of the network, accurately modulating the organism’s gene expression. Our analysis of the model organisms E. coli and B. subtilis is consistent with previous observations (Conant & Wolfe, 2008) regarding the relevance of the regulatory networks of paralogous genes in the process of adaptation of an organism in response to changing environments.

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