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Cellular sensing machinery for exogenous and endogenous conditions is differentially encoded on the chromosome and poorly conserved across genomes.



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Short Abstract: Transcriptional factors (TFs) have been classified previously into three classes, depending on the source of their allosteric or equivalent metabolite: TFs of external, internal and hybrid sensing classes. Here we report a chromosomal proximity of transcription factors and their signal genes to sense external conditions in contrast to the components for internal sensing that tend to be distant.

Long Abstract:

Organisms need to have a constant monitoring of the environmental conditions in order to respond correctly to their changes. Physicochemical signals are recognized by the cell as messengers of environmental composition as well as its metabolic state. The binding of transcription factors (TFs) to these specific signals determines their active or inactive conformation and affinities to interact with specific DNA-binding sites or with the rest of the transcriptional machinery. Studies in *E. coli* have shown the influence of DNA supercoiling in gene transcription and the perception of a 3-D spatial structure of the chromatin and its correlation with patterns of gene expression patterns. On the other hand, using statistical analysis and gene expression data it was possible to observe functional associations among neighboring transcription units (TU) where in, most cases a TU coding for a TF was found to be regulating a contiguous non-TF coding TU, and these patterns seem to be conserved in bacteria. In addition, co-regulation of divergent and tandem set of genes is a common theme in *E. coli* but not in *Saccharomyces cerevisiae*. Thus, it seems that there is increasing evidence towards the importance of chromosomal gene organization for the proper functioning of the cell and to precisely co-ordinate its gene expression in different conditions. In this work, we analyze the chromosomal organization and evolutionary conservation of external sensing TFs and their signal genes in comparison to that of internal sensing ones, using a previously developed classification of TFs in *E. coli*. The findings reported here should not only enhance our understanding of the chromosomal positioning and functional organization of internal and external sensing machinery in bacteria but also provide insights to develop strategies for identifying regulatory elements in other organisms.