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Sommario	<p>The genetic information is identical within the organism but the mechanisms by which different cell types achieve specialized functions interpreting the same set of instructions is not completely understood. It is now increasingly accepted that the combination of different genomic elements, both promoters and enhancers, favors the recruitment of different TFs, which in turn promotes the assembly of different pre-initiation complexes, guaranteeing heterogeneity in transcriptional outputs across different tissues. Nevertheless, the cis-regulatory elements and the transcriptional rules that control and maintain the expression of constitutively active genes are still poorly characterized. Specifically, whether the constitutive activity of promoters and enhancers relies on entirely distinct or instead shared regulators is unknown. By dissecting the cis-regulatory repertoire of macrophages, we found that the ELF subfamily of ETS proteins selectively bound within 60 bp from the transcription start sites of highly active housekeeping genes. ELFs also bound constitutively active, but not poised macrophage-specific enhancers and promoters. The role of ELFs in promoting constitutive transcription is suggested by multiple evidences: ELF sites enabled transcriptional activation by endogenous and minimal synthetic</p>

promoters; ELF recruitment was stabilized by the transcriptional machinery, and ELF proteins mediated recruitment of transcriptional and chromatin regulators to core promoters. These data indicate that a distinct subfamily of ETS proteins imparts high transcriptional activity to a broad range of housekeeping and tissue-specific cis-regulatory elements, which is consistent with the role of an ETS family ancestor in core promoter regulation in a lower eukaryote.

Localizzazioni e accesso

http://memoria.depositolegale.it/*/http://hdl.handle.net/2434/464938
