A highly conserved sequence in yeast heat shock gene promoters

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The heat shock response in eukaryotes is mediated by the binding of a transcription factor (heat shock transcription factor, HSTF) to a specific DNA sequence (the heat shock element, HSE) found upstream of the TATA box in heat shock promoters (1). The symmetric HSE consensus sequence, derived from a range of sequenced Drosophila, Xenopus and human heat shock genes, is 5' CnnGAAnnTTCnnG 3' (2).

We have recently sequenced the promoter of the Saccharomyces cerevisiae gene encoding the small heat shock gene hsp26 (Bossier et al., submitted for publication). Analysis of this promoter with other sequenced S. cerevisiae heat shock gene promoters has revealed the existence of a highly conserved 8bp sequence:

Hsp Gene		Putative HSE												
HSP26	-357	G	G	T	T	С	T	A	G	A	A	A	G	-346
HSP70	- 356 - 203	C T	A T	T T	T T	C	T C	A A	G G	A A	A A	A A	G G	-345 -192
нѕр84	-237	T	T	T	T	С	T	A	G	A	A	С	G	-226
UBI4	-385 -375	G C	T G	T T	T T	C	T T	A A	G G	A A	A A	C T	G A	-374 -364
PGK1	- 366	G	G	T	T	С	T	G	G	A	A	A	G	- 355
Consensus	5'	n	n	T	T	С	T	A	G	A	A	n	n 3'	

In each case the position of the 8bp sequence is given with respect to the initiator ATG codon.

This sequence is related to the HSE identified by Pelham (1,2), but more closely resembles a sequence (5' nTTCnnGAAn 3') very recently shown to be the key heat shock responsive element in <u>Drosophila</u> (3) where it is found as a dimer. We found no evidence for a dimeric arrangement in S. cerevisiae. The sequence element we describe here is also found in the synthetic HSE sequence used to study the interaction of the S. cerevisiae HŠTF (4).

References

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