Effects of heat and UV radiation in the mobilization of transposon *mariner-Mos1*

Cell Stress and Chaperones

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Table S1. Primer sequences used for gene amplification in RT-qPCR analyses.

MAR 308_F	5' GTGAACGGTGGTTTCAACG 3'
MAR 490_R	5' AGCGATTGGAAACTGCTTGT 3'
HSP70_F	5' GCTGACGTTCAGGATTCCAT 3'
HSP70_R	5' CGGAGTCTCCATTCAGGTGT 3'
EF1_F*	5' CAAGCCAGGCATGGTCGTC 3'
EF1_R*	5' ACGGACACGTTCTTCACGTT 3'
RPL17_F*	5' CCCTCCTTTTCGTTTTCGTT 3'
RPL17_R*	5' GTGTTGTCGGCACAGTTCAT 3'
GPDH_F*	5' GAGGTGGCTGAGGGCAACTT 3'
GPDH_R*	5' AACCTCCACGGCATCAGCAT 3'

F: forward primer, R: reverse primer

*Genes used for mRNA normalization input

Re-analysis of promoter region of *mariner-Mos1* element.

Nowadays more sequences and new bioinformatics tools are available for gene sequences analysis. For these reasons we have re-analyzed the promoter regions of *mariner-Mos1* element. The core promoter elements were described by Jacobson et al. (1986) and the putative heat-shock element (HSE) by Chakrani et al. (1993) These authors performed a search for the consensus sequence of HSE (CTgGAAtnTTCtAG) in sequences of *Hsp* genes (*Hsp22*, *Hsp23, Hsp26, Hsp27, Hsp27, Hsp68, Hsp68, Hsp83* and *Hsp70*) of *Drosophila* and compared with element *copia*. Chakrani et al. (1993) found 57% of homology among the sequence consensus and *mariner-Mos1*.

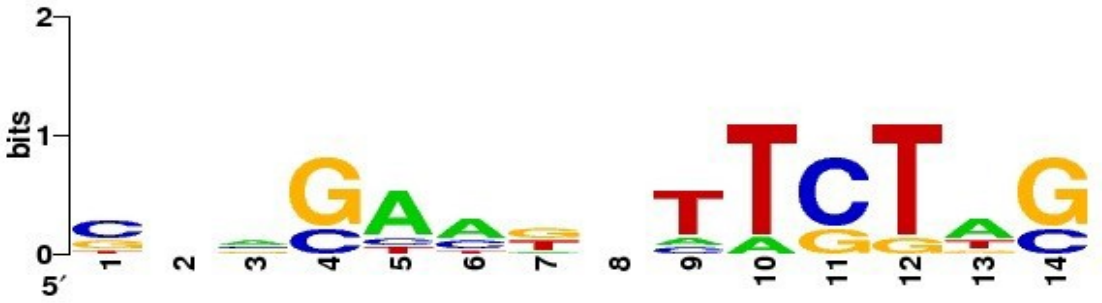
We performed this analysis again. First, the sequences of all *Hsp* genes above were downloaded from database (Flybase) and confirmed by BLAST in the database *D. simulans* genome (GenBank), consisting our sequence dataset. After, using the UGENE software (Okonechnikov et al. 2012) we searched for the sequence of HSE described by Strand and McDonald (1985)(CtgGAAtnTTCtAG) and the canonical HSE sequence nTTCnnGAAnnTTCn (Åkerfelt et al. 2010) in our dataset. We identified the HSE in each gene, and the frequency of each acid nucleic was calculated with the applicative WebLogo (Crooks et al. 2004).

As can be seen in the Figure 1S, we found a HSE for *Drosophila Hsp* genes similar as previously described by Strand and McDonald (1985) CtgGAAtnTTCtAG. The Drosophila HSE maintains partial similarities with the canonical HSE (nTTCnnGAAnnTTCn).

The analyzes in the *mariner-Mos1* 5' UTR region allow us find the region previously described by Chakrani et al (1993), with 57% of homology with HSE consensus or 86% if considering variations observed in conserved sites. A new putative HSE was found in 63 bp downstream of the first one (Fig2S). Although there are differences to the former, the homology of this new HSE with the HSE consensus is also 57%.

The putative promoter core elements of *mariner-Mos1* are also indicated in Fig 2S. Judging by our *in silico* analysis, the *mariner-MOS1* element has a promoter region that can be activated by heat-shock factor (HSF), as previously suggested by Chakrani et al (1993).

A



B

Figure 1S- A) LOGO sequence of *Drosophila* Heat-shock Elements (HSE) obtained in our analysis; B) Canonical HSE (Åkerfelt et al 2010) .

*5'**ccaggtgtacaagtagg**GAATgTcGGT**tcgaacatatagatgtctcgcaaacgtaaatatttaccgattgtcataaaa*
ctttgaccttgtGAAGtgTCaACcttgactgtcgaaccaccatagtttggcgcaaattgagcgtcataattgttttctctcagtg
cagtcaacatgtcga…3'

Fig 2S. **Heat-shock elements (HSE) in the 5' UTR *mariner-Mos1* sequence**. Terminal Inverted Repeated (TIR), bold letters; HSE described by Chakrani et al (1993), highlighted in blue; new HSE, yellow; The core promoter elements are underlined (in order: TFIIB recognition element, TATA box, initiator and start codon.

References

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