View metadata, citation and similar papers at core.ac.uk

brought to you by CORE

provided by Revistas UPO (Universidad Pablo de Olivade)

Crispr / cpf1 edition in the fission yeast to characterize the regulatory function of 3´UTR RNA loops in transcription termination

- Catalán Casas, Jesús María; Jiménez, Juan (1) y Álvarez Tallada, Víctor (1)

(1) Departamento de Genética, Laboratorio 122, Centro Andaluz de Biología del Desarrollo.

Keywords: CRISPR; Cpf1; wos2; secondary structure; RNA.

ABSTRACT

The wos2 gene encodes for the protein p23, which acts as a co-chaperone in the presence of the protein Hsp90. Their function is to fold proteins during a heat shock stress. This process is very similar both in human and the fission yeast *S.pombe*, our model organism in this project a. It was previously discovered that there exist three mRNA sizes depending on the 3'UTR length. Interestingly, the abundance of each depends on growth temperature. We then hypothesized that the secondary structure of the 3´UTR RNA could dictate the termination site depending on temperature. We are trying to demonstrate this assumption as well as to develop a temperature sensitive switch to control gene expression by inserting the wos2 3'UTR in the 5'UTR of rpl42S59Q gene marker. This allele is resistant to cycloheximide whilst the deletion is not. This way we may easily asses gene expression. To this end, we are using the CRISPR/Cpf1 technology, to engineer the genome region of interest. We are in the process of checking engineered candidates.

REFERENCES

Muñoz, .M., Daga, .R., Garzón, .A. *et al.* Poly(A) site choice during mRNA 3′-end formation in the *Schizosaccharomyces pombe wos2* gene. *Mol Gen Genomics* **267,** 792–796 (2002).

Muñoz, M. J., Bejarano, E. R., Daga, R. R., & Jimenez, J. (1999). The identification of Wos2, a p23 homologue that interacts with Wee1 and Cdc2 in the mitotic control of fission yeasts. *Genetics*, *153*(4), 1561–1572.