



Gene expression profiles in the cerebellum of transgenic mice over expressing the human *FMRI* gene with CGG repeats in the normal range

J.J. Fernández¹, R. Martínez¹, E. Andújar², M. Pérez-Alegre³, A. Costa¹, V. Bonilla-Henao¹, F. Sobrino¹, C.Ó. Pintado⁴ and E. Pintado¹

¹Department of Medical Biochemistry and Molecular Biology, University Hospital Virgen Macarena, University of Seville, Spain

²Genomics Unit, Andalusian Molecular Biology and Regenerative Medicine Centre, CSIC, Seville, Spain

³Genomics Unit, Andalusian Molecular Biology and Regenerative Medicine Centre, Seville, Spain

⁴Breeding and Research Animal Center, University of Seville, Seville, Spain

Corresponding author: E. Pintado
E-mail: elizabet@us.es

Genet. Mol. Res. 11 (1): 467-483 (2012)

Received July 20, 2011

Accepted October 17, 2011

Published March 1, 2012

DOI <http://dx.doi.org/10.4238/2012.March.1.4>

ABSTRACT. Modifications in the GABA pathway are considered to be responsible for motor alterations in animal models for fragile X-associated tremor ataxia syndrome. We analyzed the expression profile in the cerebellum in a transgenic mouse model that over expresses the human *FMRI* gene with CGG repeats in the normal range. We used the “GeneChip Mouse Gene 1.0 ST Array” from Affymetrix analyzing 28,853 well-described and -characterized genes. Based on data from the comparative analysis of the expression profile, we detected a significant gradient with a P value <0.1 and changes in expression equal to or greater than 1.5 times compared to the control mouse genes. There were significant changes in the expression of 104 genes, among which 72% had decreased and 28% had increased expression. With the exception

of *GabarapL2*, no changes in expression of genes from the GABA pathway were observed, which may explain the absence of an altered motor phenotype in these mice. These results further support the view that toxic effects in fragile X-associated tremor ataxia syndrome are due to expansion of CGG repeats rather than increased mRNA levels, since in the transgenic mice the *FMRI* mRNA levels were increased 20-100 times compared with those of control littermates.

Key words: Animal model; Microarrays; *FMRI*; Cerebellum; FXTAS