

The fragile X mental retardation protein and group I metabotropic glutamate receptors regulate levels of mRNA granules in brain

Armaz Aschrafi, Bruce A. Cunningham, Gerald M. Edelman, and Peter W. Vanderklish*

Department of Neurobiology, The Scripps Research Institute, and The Skaggs Institute for Chemical Biology, 10550 North Torrey Pines Road, SBR-14, La Jolla, CA 92037

Contributed by Gerald M. Edelman, December 28, 2004

Fragile X syndrome results from the transcriptional silencing of a gene, *Fmr1*, that codes for an mRNA-binding protein (fragile X mental retardation protein, FMRP) present in neuronal dendrites. FMRP can act as a translational suppressor, and its own translation in dendrites is regulated by group I metabotropic glutamate receptors (mGluRs). Multiple lines of evidence suggest that mGluR-induced translation is exaggerated in Fragile X syndrome because of a lack of translational inhibition normally provided by FMRP. We characterized the role of FMRP in the regulation of mRNA granules, which sediment as a heavy peak after polysomes on sucrose gradients. In WT mouse brain, FMRP distributed with polysomes and granules. EM and biochemical analyses suggested that the granule fraction itself contained clusters of polysomes. In *Fmr1* knockout brain, we observed a significant decrease in the amount of mRNA granules relative to WT mice. This difference appeared to be due to a role of FMRP in regulating the activation of granules during mGluR-induced translation; *in vivo* administration of the mGluR5 antagonist 2-methyl-6-(phenylethynyl)pyridine increased granule content in *Fmr1* knockout mouse brain to levels comparable with those seen in WT brain. In accord with a role of mGluR5 in the regulation of ongoing translation *in vivo*, we observed that the phosphorylation of several initiation factors in response to application of the mGluR1/5 agonist S-3,5-dihydroxyphenylglycine *in vitro* was blocked by methyl-6-(phenylethynyl)pyridine. Together, these data suggest that although large, polysome-containing granules can form in the absence of FMRP, their use in response to mGluR-induced translation is exaggerated.

fragile X syndrome | translation | 2-methyl-6-(phenylethynyl)pyridine

Fragile X syndrome (FXS) is the most prevalent inherited form of mental retardation. It is caused by the pathological expansion of a CGG trinucleotide repeat in the 5'-UTR of the *Fmr1* gene that codes for the RNA-binding protein fragile X mental retardation protein (FMRP), resulting in its transcriptional silencing (for review, see ref. 1). The syndrome is characterized by a broad set of symptoms, including cognitive impairment, autistic behavior, anxiety and compulsive disorders, seizures, and physical manifestations such as macroorchidism (1, 2). Neuroanatomically, FXS is associated with an overabundance of long, thin, and tortuous dendritic spines in cortical regions (3, 4). This synaptic abnormality is observed also in the *Fmr1* knockout (KO) mouse model of FXS (5), although the overall behavioral phenotype of these mice is less severe than expected (6).

The current view of the cellular role of FMRP is that it is involved in the transport and translational regulation of mRNAs critical for the development of neurons and activity-dependent plasticity of their synaptic connections (1, 7, 8). FMRP contains nuclear import and export sequences, and multiple mRNA-binding domains (see ref. 9 and references therein) that mediate interactions between FMRP, and $\approx 4\%$ of mRNA in brain (10–14). FMRP can act as a translational repressor *in vitro* and *in situ*. Studies of the regulation of FMRP targets in *Fmr1* KO

mice suggest complex changes in translation (10, 14–16), including heightened translation of dendritic mRNAs, such as MAP1B (17, 18), that may contribute to alterations in spine morphology. FMRP binds and regulates the translation of its own mRNA as well (11). Stimulation of group I metabotropic glutamate receptors (mGluRs) induces rapid synthesis of FMRP in the synaptodendritic compartment (19, 20). This finding suggests that mGluR-induced translation of FMRP targets is limited at the synapse by a negative-feedback mechanism. In accord with this possibility, a form of translation-dependent long-term depression (LTD) induced by mGluRs is enhanced in *Fmr1* KO mice (21). Stimulation of group I mGluRs also results in a translation-dependent elongation of dendritic spines resembling those seen in fragile X brain (22). These observations motivated the theory that, in FXS, exaggerated mGluR-dependent translation results in synaptic changes that are the proximal causes of cognitive impairment (8).

The presence of FMRP in polysomes and mRNA granules in brain suggests that it has a role in regulating complexes of translation machinery in dendrites. FMRP is associated with translating polysomes and with stalled polysomes (23–25), suggesting that it gates translation after the initiation step. Such a role of FMRP may be integral to the formation and function of large mRNA granules (heavy-sedimenting particles that contain multiple mRNAs), ribosomes, other mRNA-binding proteins, translation factors, and motor proteins (26–30). Granules are thought to provide a repertoire of mRNAs that are transported into dendrites in a translationally silent state for subsequent site-specific utilization at synapses undergoing protein synthesis-dependent changes (27, 31, 32). Some large mRNA granules contain aggregates of translationally inactive polysomes (27), whereas others appear to lack ribosomes (32). Prolonged depolarization of cortical neurons induces structural changes in granules that suggest that constituent polysomes are being derepressed (27). These changes are accompanied by a shift in the distribution of several dendritic mRNAs into lighter, actively translating polysome fractions. Recent studies identified FMRP as a component of large mRNA granules that also contain stauferin 1 and other factors that are implicated in the transport of mRNAs into dendrites (28, 29). As a component of granules, FMRP may influence the activity-dependent translation of granule mRNAs by regulating preassembled polysomes.

In this study, we used density-gradient fractionation, Western blot analysis, and EM techniques to characterize and compare large mRNA granules in WT and *Fmr1* KO mouse brain. Also, we studied the role of mGluRs in the regulation of granules *in vivo* by using the mGluR5-specific antagonist 2-methyl-6-

Abbreviations: FMRP, fragile X mental retardation protein; DHPG, S-3,5-dihydroxyphenylglycine; MPEP, 2-methyl-6-(phenylethynyl)pyridine; eIF, eukaryotic initiation factor; FXS, fragile X syndrome; mGluR, metabotropic glutamate receptor; KO, knockout; LTD, long-term depression.

*To whom correspondence should be addressed. E-mail: pvanderk@scripps.edu.

© 2005 by The National Academy of Sciences of the USA

Prolonged incubation of slices with MPEP alone reduced eIF4E and eIF4E-BP phosphorylation below control levels, indicating that there is ongoing mGluR5-regulated translation in the culture system. Taken with the results of our *in vivo* studies on the effect of MPEP on granules, these data suggest that the reduction of granules in *Fmr1* KO mice results from the lack of a suppressive influence on ongoing mGluR5-induced translation.

Discussion

In this article, we present evidence that the mRNA granule fraction is reduced significantly in *Fmr1* KO mouse brain, which is thought to have exaggerated mGluR-dependent translation relative to WT brain (8). The granule peak was rapidly reconstituted in the *Fmr1* KO animals upon injection (i.p.) of the mGluR5-specific antagonist, MPEP. This result suggests that suppression of mGluR-induced translation *in vivo* by FMRP stabilizes granules after they are formed. Moreover, it appeared that mRNA granules may serve as a reservoir of translationally arrested polysomes (27) containing FMRP that can be activated or derepressed, resulting in their redistribution to lighter polysome fractions. Overall, our data are consistent with reports showing that FMRP plays an important role in the regulation of local translation from mRNA granules (34), and they support the idea that mGluR-dependent translation is exaggerated in FXS (8, 21, 22).

The Presence of FMRP in mRNA Granules. Two different fractionation protocols yielded granules that cosedimented with FMRP and that had a similar structural appearance: that of a dense, spherical cluster of polysomes. The presence of FMRP in these granules depended on associations with polysomes. Upon disruption of polysomes, granules disappeared, and as reported (24, 33), FMRP was found primarily in the ribosomal fraction, consistent with previous demonstrations of an association of FMRP with the 60S ribosomal subunit (33).

Recent reports that FMRP associates with polysomes in brain have not detected a granule peak (23, 24). This result has led to the suggestion that granules may be an artifact of the culture preparation originally used to characterize them. However, many reports that characterize FMRP-containing complexes as polysomes or smaller entities also show evidence for FMRP in pellet fractions. Thus, it is possible that large mRNA granules with sedimentation properties similar to those observed here and elsewhere (27, 28, 32) might have been observed if broader sucrose gradients had been used or if fractionation methods had been altered to retain heavier material. The recent purification of FMRP-containing granules by two methods (28, 29) and colabeling of identified components *in situ* provides critical support for the existence of large mRNA granules and for FMRP as a component protein.

Our data provide additional support for the existence of granules in that their abundance is linked to the presence of FMRP and to the activity of receptors that elicit many phenomena that are altered in the absence of FMRP. Moreover, we could not detect granules in liver and testis. There is no *a priori* reason to predict that these tissues would be less subject to generating artifactual associations of translation machinery than brain. Also, note that the heavy granule peak is discrete, suggesting that granules may exhibit a degree of structural regularity. If granules were artifactual in origin, they might be expected to display a broader range of sizes.

The presence of FMRP in the granule fraction may reflect a number of roles of this mRNA-binding protein in the regulation of translation. Our data suggest that one role is to suppress granule mRNAs, regulating their translation in response to synaptic activity. Several lines of evidence indicate that FMRP is a translational suppressor of specific mRNAs (36, 37), and its presence in transport granules may ensure that mRNA cargos

are not translated at inappropriate sites or times (34). Further characterization of effectors of FMRP-mediated suppression in granules, such as components of the microRNA pathway (38), will aid in evaluating this possibility. It has already been shown that the noncoding dendritic RNA, BC1, and several mRNAs presumably suppressed in dendrites by FMRP-BC1 interactions are present in granules (16, 28). FMRP could also regulate the composition of granules; it associates with other mRNA-binding proteins, and dimerization of FMRP with the human homolog of zipcode binding protein 1 (IMP1) on mRNA is sufficient to induce the formation of larger mRNA-containing granules (39). Last, the presence of NLS and NES sequences in FMRP suggests a role in mRNA transport. However, *in situ* hybridization analyses of the distributions of several mRNAs present in granules found no difference between WT and *Fmr1* KO mice, suggesting that FMRP does not have a major role in transport of mRNAs packaged into granules (28, 40).

Reduction of the Heavy mRNA Granule Peak in *Fmr1* KO Mice. We observed a reduction in the heavy mRNA granule peak resolved from brain lysates of *Fmr1* KO mice relative to WT mice. This reduction could reflect a lack of FMRP-mediated translational suppression in the KO brain, and a commensurate shift of polysomes sequestered in a silent state into dense granules to a less dense fraction of translating polysomes. The alternative notion that FMRP may be a key structural component that is critical for the assembly of some granules seems to be less likely because, after treatment with the mGluR5 antagonist, granules in KO mice were as abundant as in WT mice. Moreover, the EM analyses did not reveal obvious structural differences in granules from *Fmr1* KO, compared with WT mouse brain, and the granules that were present in these animals had similar sedimentation properties. These observations suggest that granules can form properly in *Fmr1* KO mice but that they may be “unpacked” at a faster rate than in WT brain.

The granule peak was not entirely absent in the KO brain. Studies of the relative distributions of mRNA-binding proteins found in granules (32, 34, 41) suggest that the mRNA granule pool is heterogeneous. If the sucrose-gradient-fractionation method resolves most heavy granules equally without disruption, then it is likely that most heavy granules contain FMRP.

Increased mRNA Granule Levels After *in Vivo* Injection of MPEP. Administration of MPEP to *Fmr1* KO mice brought the low level of granules in these animals to levels approximately equal to those seen in WT mice injected with MPEP. This result is significant because it suggests that mGluR5-induced translation from granules is an ongoing process in mouse brain that occurs at a higher rate in the absence of FMRP. Our studies on translation-factor phosphorylation, as well as other reports on the regulation of translation machinery by mGluRs (42, 43), indicate that mGluRs have a strong activating effect on translation initiation. Thus, increased levels of granules after MPEP treatment may be due to an attenuation of translation-factor activity. In WT, changes in the distribution or posttranslational modification of FMRP may be involved also. It has been shown that stimulating mGluRs causes FMRP to uncouple from *Fmr1* target mRNA (34) and that a fraction of phosphorylated FMRP is present in stalled polysomes (25). In the *Fmr1* KO mouse, compensating activities of the structurally related FXRs or phosphorylation of eukaryotic elongation factor 2 (eEF2) may be responsible for stalling polysomes to regenerate granules (44). Phosphorylation of eEF2 mediates translational suppression in various circumstances, and it can be induced by the activity of NMDA-type glutamate receptors, which may dominate its regulation when mGluR signaling is inhibited.

Significance for Translational Regulation in FXS. The “mGluR theory” of FXS holds that exaggerated mGluR-dependent translation leads to changes in synaptic plasticity and structure that are the proximal causes of symptoms (8). These synaptic changes may include an exaggeration of LTD (21) and other events that have been linked to mGluR-dependent translation, such as control of intrinsic neuronal properties and seizure thresholds (45, †), spine elongation (22), and the priming of LTP consolidation (42, 46). Our data support this theory and suggest that, in particular, translation of mRNAs transported in the form of large, polysome-containing granules is exaggerated in FXS. Also, the ability of MPEP to restore the heavy granule fraction in *Fmr1* KO mice supports the notion that antagonists of mGluRs may be efficacious in treating many symptoms of FXS (8).

How well antagonism of mGluRs can offset changes caused by a lack of FMRP will be determined in part by whether FMRP regulates mGluR-induced translation exclusively. Multiple receptors at glutamatergic synapses induce translation, and their signaling can converge onto common points of translation control. However, there is reason to believe that mechanisms for differential translation exist at synapses (47). At least three forms of long-term synaptic efficacy change require local translation for their consolidation: LTD, LTP, and potentiation

induced with the brain-derived neurotrophic factor. These plastic changes differ in valence, induction and expression mechanism, associated spine-shape changes, and longevity. Thus, it is reasonable to assume that they require distinct translational responses. For example in hippocampus, where LTD is exaggerated in the *Fmr1* KO mouse, no differences in LTP have been observed. Moreover, there is evidence that selective utilization of mRNAs in dendrites can arise from differences in receptor signaling and translation factor modulation.

If the set of mRNAs bound by FMRP were to overlap extensively with that regulated by mGluRs, then mGluR antagonists could impact a broad set of symptoms in FXS. Studies of the FMRP target mRNAs provide some basis to address this issue. Identification of mRNAs bound by FMRP in heavy granules, and the set of mRNAs selectively translated in response to mGluR activation may clarify this issue further. Last, the changes in mRNA granule peak size described here may provide a convenient biological marker with which to evaluate the effects of candidate therapeutic compounds on components of the translation machinery in *Fmr1* KO mice.

We thank Dr. Robert Bauchwitz (Columbia University, New York) for providing hybrid (C57 X FVB) *Fmr1* KO mice, Dr. Malcolm Wood for assistance with EM studies, and Katherine Woodard for excellent technical assistance. This research was supported by a grant from the Fragile X Research Foundation (to P.W.V.), National Institutes of Health Grants HD09635-31 (to G.M.E.) and HDL6550-23 (B.A.C.), and the Skaggs Institute for Chemical Biology (A.A.).

[†]Chuang, S., Yan, Q., Bauchwitz, R. P. & Wong, R. K. S. (2004) *Soc. Neurosci. Abstr.* **228.5**.

- O'Donnell, W. T. & Warren, S. T. (2002) *Annu. Rev. Neurosci.* **25**, 315–338.
- Hagerman, R. J., Amiri, K. & Cronister, A. (1991) *Am. J. Med. Genet.* **38**, 283–287.
- Hinton, V. J., Brown, W. T., Wisniewski, K. & Rudelli, R. D. (1991) *Am. J. Med. Genet.* **41**, 289–294.
- Irwin, S. A., Galvez, R. & Greenough, W. T. (2000) *Cereb. Cortex* **10**, 1038–1044.
- Comery, T. A., Harris, J. B., Willems, P. J., Oostra, B. A., Irwin, S. A., Weiler, I. J. & Greenough, W. T. (1997) *Proc. Natl. Acad. Sci. USA* **94**, 5401–5404.
- Yan, Q. J., Asafo-Adjei, P. K., Arnold, H. M., Brown, R. E. & Bauchwitz, R. P. (2004) *Genes Brain Behav.* **3**, 337–359.
- Antar, L. N. & Bassell, G. J. (2003) *Neuron* **37**, 555–558.
- Bear, M. F., Huber, K. M. & Warren, S. T. (2004) *Trends Neurosci.* **27**, 370–377.
- Adinolfi, S., Bagni, C., Musco, G., Gibson, T., Mazzarella, L. & Pastore, A. (1999) *RNA* **5**, 1248–1258.
- Darnell, J. C., Jensen, K. B., Jin, P., Brown, V., Warren, S. T. & Darnell, R. B. (2001) *Cell* **107**, 489–499.
- Schaeffer, C., Bardoni, B., Mandel, J. L., Ehresmann, B., Ehresmann, C. & Moine, H. (2001) *EMBO J.* **20**, 4803–4813.
- Alvarez, G., Ramos, M., Ruiz, F., Satrustegui, J. & Bogonez, E. (2003) *J. Neurosci. Res.* **73**, 260–269.
- Hinds, H. L., Ashley, C. T., Sutcliffe, J. S., Nelson, D. L., Warren, S. T., Housman, D. E. & Schalling, M. (1993) *Nat. Genet.* **3**, 36–43.
- Brown, V., Jin, P., Ceman, S., Darnell, J. C., O'Donnell, W. T., Tenenbaum, S. A., Jin, X., Feng, Y., Wilkinson, K. D., Keene, J. D., et al. (2001) *Cell* **107**, 477–487.
- Miyashiro, K. Y., Beckel-Mitchener, A., Purk, T. P., Becker, K. G., Barret, T., Liu, L., Carbonetto, S., Weiler, I. J., Greenough, W. T. & Eberwine, J. (2003) *Neuron* **37**, 417–431.
- Zalfa, F., Giorgi, M., Primerano, B., Moro, A., Di Penta, A., Reis, S., Oostra, B. & Bagni, C. (2003) *Cell* **112**, 317–327.
- Lu, R., Wang, H., Liang, Z., Ku, L., O'Donnell, W. T., Li, W., Warren, S. T. & Feng, Y. (2004) *Proc. Natl. Acad. Sci. USA* **101**, 15201–15206.
- Zhang, Y. Q., Bailey, A. M., Matthies, H. J., Renden, R. B., Smith, M. A., Speese, S. D., Rubin, G. M. & Broadie, K. (2001) *Cell* **107**, 591–603.
- Todd, P. K., Mack, K. J. & Malter, J. S. (2003) *Proc. Natl. Acad. Sci. USA* **100**, 14374–14378.
- Weiler, I. J., Irwin, S. A., Klintsova, A. Y., Spencer, C. M., Brazelton, A. D., Miyashiro, K., Comery, T. A., Patel, B., Eberwine, J. & Greenough, W. T. (1997) *Proc. Natl. Acad. Sci. USA* **94**, 5395–5400.
- Huber, K. M., Gallagher, S. M., Warren, S. T. & Bear, M. F. (2002) *Proc. Natl. Acad. Sci. USA* **99**, 7746–7750.
- Vanderklish, P. W. & Edelman, G. M. (2002) *Proc. Natl. Acad. Sci. USA* **99**, 1639–1644.
- Khandjian, E. W., Huot, M. E., Tremblay, S., Davidovic, L., Mazroui, R. & Bardoni, B. (2004) *Proc. Natl. Acad. Sci. USA* **101**, 13357–13362.
- Stefani, G., Fraser, C. E., Darnell, J. C. & Darnell, R. B. (2004) *J. Neurosci.* **24**, 7272–7276.
- Ceman, S., O'Donnell, W. T., Reed, M., Patton, S., Pohl, J. & Warren, S. T. (2003) *Hum. Mol. Genet.* **12**, 3295–3305.
- Antic, D., Lu, N. & Keene, J. D. (1999) *Genes Dev.* **13**, 449–461.
- Krichevsky, A. M. & Kosik, K. S. (2001) *Neuron* **32**, 683–696.
- Kanai, Y., Dohmae, N. & Hirokawa, N. (2004) *Neuron* **43**, 513–525.
- Village, P., Marion, R. M. & Ortin, J. (2004) *Nucleic Acids Res.* **32**, 2411–2420.
- Ohashi, S., Koike, K., Omori, A., Ichinose, S., Ohara, S., Kobayashi, S., Sato, T. A. & Anzai, K. (2002) *J. Biol. Chem.* **277**, 37804–37810.
- Keene, J. D. & Tenenbaum, S. A. (2002) *Mol. Cell* **9**, 1161–1167.
- Antic, D. & Keene, J. D. (1998) *J. Cell Sci.* **111**, 183–197.
- Siomi, M. C., Zhang, Y., Siomi, H. & Dreyfuss, G. (1996) *Mol. Cell Biol.* **16**, 3825–3832.
- Antar, L. N., Afroz, R., Dichtenberg, J. B., Carroll, R. C. & Bassell, G. J. (2004) *J. Neurosci.* **24**, 2648–2655.
- Angenstein, F., Greenough, W. T. & Weiler, I. J. (1998) *Proc. Natl. Acad. Sci. USA* **95**, 15078–15083.
- Li, Z., Zhang, Y., Ku, L., Wilkinson, K. D., Warren, S. T. & Feng, Y. (2001) *Nucleic Acids Res.* **29**, 2276–2283.
- Laggerbauer, B., Ostareck, D., Keidel, E. M., Ostareck-Lederer, A. & Fischer, U. (2001) *Hum. Mol. Genet.* **10**, 329–338.
- Jin, P., Alish, R. S. & Warren, S. T. (2004) *Nat. Cell Biol.* **6**, 1048–1053.
- Rackham, O. & Brown, C. M. (2004) *EMBO J.* **23**, 3346–3355.
- Steward, O., Bakker, C. E., Willems, P. J. & Oostra, B. A. (1998) *NeuroReport* **9**, 477–481.
- Tiruchinapalli, D. M., Oleynikov, Y., Kelic, S., Shenoy, S. M., Hartley, A., Stanton, P. K., Singer, R. H. & Bassell, G. J. (2003) *J. Neurosci.* **23**, 3251–3261.
- Francesconi, W., Cammalleri, M. & Sanna, P. P. (2004) *Brain Res.* **1022**, 12–18.
- Shin, C. Y., Kundel, M. & Wells, D. G. (2004) *J. Neurosci.* **24**, 9425–9433.
- Scheetz, A. J., Nairn, A. C. & Constantine-Paton, M. (2000) *Nat. Neurosci.* **3**, 211–216.
- Sourdet, V., Russier, M., Daoudal, G., Ankri, N. & Debanne, D. (2003) *J. Neurosci.* **23**, 10238–10248.
- Raymond, C. R., Thompson, V. L., Tate, W. P. & Abraham, W. C. (2000) *J. Neurosci.* **20**, 969–976.
- Vanderklish, P. W. & Edelman, G. M. (2005) *Genes Brain Behav.*, in press.