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The gene encoding the fragile X RNA-binding protein is controlled by nuclear respiratory factor 2 and the CREB family of transcription factors

Karen T. Smith, Robert D. Nicholls1 and Daniel Reines*

INTRODUCTION

Fragile X syndrome results from the loss of functional FMR1 gene product. This protein, FMRP, binds brain mRNA and therefore is important in nucleic acid metabolism [for a review see (1)]. In almost all fragile X patients, disease is due to transcriptional silencing of FMR1 which occurs after expansion of a trinucleotide repeat in the 5′-untranslated region (5′-UTR) of FMR1. Expansion triggers aberrant and permanent DNA methylation and heterochromatin formation and yields an FMR1 promoter that lacks its activators (2–6). Demethylation of FMR1 can be achieved in fragile X cell lines by treatment with 5-azadeoxycytidine which restores transcription factor function and an active state of chromatin (7–11).

In designing strategies to reactivate FMR1 transcription, not only it is important to understand the functions of the silencing factors, but also it is crucial to know the identities and contributions of the transcription factors and co-activators normally controlling FMR1. Silenced FMR1 in fragile X syndrome is marked by a loss of histone acetylation, compared with the active FMR1 gene (8). However, it is not known which proteins are responsible for normally maintaining histone acetylation at active FMR1. In addition, significant questions regarding the exact identities and functions of the transcription factors controlling FMR1 are still unanswered.

Four in vivo footprints were initially identified in the FMR1 promoter in primary and transformed cells of fibroblast and lymphoblast origin (12,13). Several proteins can bind the FMR1 promoter in vitro, including CREB, AP-2, Sp1, nuclear respiratory factor 1 (NRF-1) and upstream stimulatory factors 1 and 2 (henceforth referred to collectively as USF) (14–17). However, these initial studies have left unanswered questions regarding FMR1 transcription in vivo. We have previously shown that Sp1, NRF-1, USF and Max are bound specifically to the active FMR1 promoter in vivo and that Sp1 and NRF-1 were strong synergistic activators of FMR1 transcription (18). Recent work by others has shown that AP-2α may serve as a positive regulator of FMR1 transcription during development (19). Not all transcription factors bound at FMR1 in vivo are positively acting. In addition to Max-mediated repression of FMR1 transcription, we found that USF was unable to activate an FMR1-driven reporter in Drosophila SL2 cells, and indeed, strongly repressed Sp1 and NRF-1 mediated activation of...
FMRI (18). In addition, repression was not dependent on the E-box (18). This result was surprising, since mutation of the E-box has been shown to lower FMRI transcription by ~75% in PC12 cells and it has been speculated that USF operates through this site in vivo (16).

Therefore, it is still unclear which proteins are actually acting through the initially identified footprint over the E-box, which lies nearest to the transcription start site. It has been especially confusing since early experiments showed that a potential cAMP-responsive element (CRE) overlaps this E-box, suggesting that CREB may transduce neuronal stimuli and thereby impact FMRI transcription in brain (14). Despite early evidence, most subsequent reports have either not addressed this issue or obtained data that does not support this finding. For example, two in vivo footprinting reports showed data suggestive of proteins binding the E-box; however, both reports indicated that the partly overlapping CRE site was not occupied albeit neither study examined neuronal cell types (12,13). In addition, EMSA analyses with an FMRI promoter fragment and nuclear extract failed to show that CREB could bind this site (16). Instead, USF bound in vitro to an FMRI promoter fragment and it was suggested that the E-box could be occupied by this factor in vivo (12,13,16). Furthermore, there is no evidence that CREB occupies the FMRI promoter in normal cells nor has there been a functional histone acetyltransferase been identified for this highly acetylated portion of chromatin.

Since our experiments with USF in vivo contradicted the proposed function that USF transactivates FMRI, we have now examined both CREB and USF at FMRI in human cells. USF represses FMRI reporter activity in HeLa cells suggesting that USF does not naturally regulate FMRI transcription through the E-box. Instead, we show occupancy of the active, but not inactive promoter, by the CREB/ATF family of transcription factors in vivo as well as the histone acetyltransferases CBP and p300. Surprisingly, we find that the endogenous FMRI gene in PC12 neuronal-like cells is not cAMP-inducible. We also learned that nuclear respiratory factor 2 (NRF-2) is bound to FMRI in normal but not patient cells and can transactivate the promoter. This is the first implication of this site or transcription factor at FMRI and is congruent with earlier evidence that NRF-1 is known to operate with NRF-2 to coordinately control the transcription of genes involved in mitochondrial respiration and biogenesis (20). These data strongly suggest that CREB/ATF family members and not USF regulate FMRI transcription through the E-box/CRE, and together with NRF-2, positively contribute to FMRI expression. These findings lend new insight into the regulatory network to which the important RNA-binding protein, FMRP, belongs.

MATERIALS AND METHODS

Plasmid construction

Construction of pFMR1-luc, which contains a human FMRI promoter fragment (~272 to +291) driving firefly luciferase expression and mutation of the E-box/CRE in the FMRI promoter have been described previously (18). Mutation of the NRF-2 site in pFMR1-luc was performed by site-directed mutagenesis with the following oligos: 5'-CGTTTCGTTTCCGTAAACGAGAGGCG-3' and 5'-GCCCTCCACGTGTACCGAAACGCG-3' which introduce a HpaI site into the NRF-2 binding site; the mutation was confirmed by sequencing. pACTIN-FL-NRF-1 contains full-length human NRF-1 with an N-terminal FLAG tag and pRL-dA5C contains the Renilla luciferase gene; both constructs are driven by the Drosophila actin 5C promoter and were constructed as described previously (18). A vector expressing full-length rat CREB was a gift from Dr Jerry Boss. Vectors expressing full-length human USF1 (pSV-USF1) or mouse USF2 (pSV-USF2) were gifts from Dr Michele Sawadogo (21). Dominant negative USF (A-USF) expression vector and empty control were gifts from Dr Charles Vinson (22,23). Vectors encoding full-length human NRF-2-alpha (A5C-GABPα), NRF-2-beta (A5C-GABPβ) and ATF-1 (A5C-ATF1) for expression in Drosophila cells, were gifts from Dr Hiroshi Handa (24,25). A luciferase reporter construct containing the human HO-1 promoter (pHOGL3/4.5) was a gift from Dr Anupam Agrawal (26).

Cell culture and transfections

HeLa, SL2 and lymphoblastoid cell culture was carried out as described previously (18). Lymphoblastoid cell lines from a normal male (J-1) and a fragile X male patient (GM3200A) were obtained from Coriell Cell Repositories. J-1 contains an unmethylated 30 CGG repeat allele and GM3200A carries a methylated 530 CGG repeat allele as determined by methylation-sensitive restriction digest and Southern blot analysis (data not shown). PC12 cells were grown in DMEM (Cellgro) with 10% horse serum (Gibco), 5% FetalClone I (Hyclone), 100 U/ml penicillin and 100 μg/ml streptomycin, in a humidified atmosphere at 37°C. HeLa cell transfections were carried out using Lipofectamine Plus (Invitrogen) as described previously (18). Each sample contained 200 ng of either mutant or wild-type pFMR1-luc reporter and 50 ng of the Renilla luciferase reporter pRL-cytomegalovirus (CMV) (Promega). In addition, transfections with wild-type USF contained 250 ng of either pSV-USF1 or pSV-USF2 expression plasmids, or 125 ng of pSV-USF1 and 125 ng of pSV-USF2, or an equal amount of empty expression vector. Alternatively, 100 or 200 ng of A-USF or empty expression vector were included in transfections as indicated. SL2 transfections were performed using Effectene (QIAGEN) as described previously (18). Samples contained 250 ng of either mutant or wild-type pFMR1-luc reporter and 25 ng of the Renilla luciferase reporter pRL-cytomegalovirus (CMV) (Promega). In addition, transfections with wild-type USF contained 250 ng of either pSV-USF1 or pSV-USF2 expression plasmids, or 125 ng of pSV-USF1 and 125 ng of pSV-USF2, or an equal amount of empty expression vector. Alternatively, 100 or 200 ng of A-USF or empty expression vector were included in transfections as indicated. SL2 transfections were performed using Effectene (QIAGEN) as described previously (18). Samples contained 250 ng of either mutant or wild-type pFMR1-luc reporter and 25 ng of pRL-dA5C. Transfections also included one or more of the following, as indicated in each figure: 300 ng of pACTIN-FL-NRF-1, 700 ng of NRF-2 which corresponds to 350 ng of each A5C-GABPα and A5C-GABPβ expression plasmids, 300 ng of ATF-1 expression plasmid (A5C-ATF1) or empty vector. Where necessary, empty expression vector was added to keep total DNA levels constant between samples.

Antibodies, chromatin immunoprecipitation (ChIP) and forskolin treatment

Antibodies to CBP (A-22), p300 (C-20) and GABP-alpha (H-180) were purchased from Santa Cruz Biotechnology. Phospho-CREB antiserum was a gift from Dr Jerry Boss. ChIP in lymphoblastoid cells was performed as described
Previously (18), ChIP in PC12 cells was done essentially the same way, with a few exceptions. PC12 cells at ~60–80% confluence were grown in DMEM containing 0.5% FetalClone I (HyClone) and treated the next day with 10 μM forskolin (Sigma) or an equal volume of dimethyl sulfoxide (DMSO) for 25 min. Formaldehyde was added to the media for 20 min and whole cell extracts were prepared for ChIP. For the rat c-fos promoter, primers were 5′-CCTACATGCGAGGGTCCACAGAC-3′ and 5′-GAGTGAAGGCACCTCAGTGGC-3′. For the rat FMR1 promoter, primers were 5′-CTCTTTGCGACGAGGACTTG-3′ and 5′-GGCCATAGGCAGACGC-3′. For GABP-alpha ChIPs, primers used to amplify the human Tfam promoter were 5′-CAGAGCTCCAGCCCTGCTTGAC-3′ and 5′-CCTCGGGGGGAGGAATAAGAGC-3′ and primers for the human FMR1 promoter were 5′-CTACGCGGTCCACAAAGGCTCTGGTCG-3′ and 5′-GCAGTCTGACTGACGGAGTGAG-3′. For CBP, p300 and P-CREB ChIPs, primers used to amplify the human FMR1 promoter were 5′-GCTTGTTATAAAAAGGACGGTTGGTG-3′ and 5′-GGTGAAGGCCAGAACATCATCG-3′ and primers for the human FMR1 promoter were 5′-CGACCTCATATCCATGCTCCCTATAAGG-3′ and 5′-CAGATGCTCTCCGGATTCGAT-3′. Cycling conditions were 94°C for 2 min, 33 cycles of 94°C for 45 s, 64°C (for rat and human c-fos and FMR1 promoters) or 68°C (human Tfam and FMR1 promoters) for 50 s and 72°C for 45 s, followed by 72°C for 7 min. PCR products were separated by gel electrophoresis through 1.5% agarose and bands were detected by ethidium bromide staining.

**Quantitative RT-PCR**

Quantitative PCR was performed on a BioRad iCycler using SYBR green. Cycling parameters were 95°C for 3 min, 46 cycles of 95°C for 15 s and 60°C (c-fos, FMR1 and Tfam promoters) or 60°C (FMR1, c-fos and HPRT transcripts) for 50 s, then 1 cycle of 95°C for 50 s and 55°C for 50 s. Primers to amplify the rat FMR1 transcript were 5′-GCTTGTATAAAAAGGACGGTTGGTG-3′ and 5′-GGTGAAGGCCAGAACATCATCG-3′ and primers for the human FMR1 promoter were 5′-CGACCTCATATCCATGCTCCCTATAAGG-3′ and 5′-CAGATGCTCTCCGGATTCGAT-3′. Cycling conditions were 94°C for 2 min, 33 cycles of 94°C for 45 s, 64°C (for rat and human c-fos and FMR1 promoters) or 68°C (human Tfam and FMR1 promoters) for 50 s and 72°C for 45 s, followed by 72°C for 7 min. PCR products were separated by gel electrophoresis through 1.5% agarose and bands were detected by ethidium bromide staining.

**RESULTS**

**USF represses FMR1 promoter activity in mammalian cells**

We have previously shown that USF represses FMR1 reporter activity in Drosophila SL2 cells (18). This result was unexpected, as mutation of the site through which it has been proposed to operate, the E-box/CRE (Figure 1), lowers expression to about 20% of normal in HeLa cells indicating it operates in a positive manner (Figure 2A). This is similar to prior observations in rat PC12 cells (16), and led us to explore the role of USF at FMR1 in human cells. We found that overexpression of USF1, USF2 or a combination of both, repressed FMR1 reporter activity in HeLa cells between 45 and 60% and repression was largely independent of the E-box (Figure 2B). To rule out the trivial possibility that this repression was due to overexpression of USF, we employed a dominant negative USF (A-USF) that binds the endogenous USF proteins and prevents them from interacting with DNA (22). Overexpression of A-USF in HeLa cells did not change FMR1-luc expression although the HO-1 promoter, previously shown to be cAMP-inducible in vivo, and the identities of the likely factors at those sites (12,13). The bent arrow indicates the major transcription start site (61).

![Figure 1](https://example.com/figure1.png)

**Figure 1.** Human FMR1 promoter map showing the four binding sites known to be occupied in vivo and the identities of the likely factors at those sites (12,13). The sequence of the overlapping E-box/CRE is shown underneath the site and that of the E-box/CRE mutant used in reporter assays is shown below the wild-type sequence with mutated bases underlined. A question mark above the E-box/CRE represents the unknown factor(s) binding this site in vivo. The bent arrow indicates the major transcription start site (61).
which overlaps the E-box and is well conserved across species (12–14,16). It was initially shown that recombinant CREB can bind an FMR1 promoter fragment in vitro and that overexpression of CREB could increase activity from an FMR1-driven reporter (14). However, subsequent reports suggested that the CRE is not involved in FMR1 transcription, though none directly test CREB’s role in vivo (12,13,16). Since our results suggested that USF is not acting through the E-box, we tested the idea that CRE-binding proteins reside at this site.

Since initial experiments suggested that a CRE-binding protein could act at FMR1 and that this gene may be induced by the cAMP pathway, we employed ChIP using an antibody raised against CREB phosphorylated at Ser 133 (J. Lochamy and J. Boss, manuscript submitted). Indeed, we found that a phosphorylated CREB/ATF family member was bound at the active human FMR1 and c-fos promoters in lymphoblastoid cells, but not at silenced FMR1 in fragile X cells (Figure 3A). This was specific for FMR1, since P-CREB occupied the c-fos promoter in fragile X cells (Figure 3A). Since a P-CREB family member was bound at FMR1, we also tested if the histone acetyltransferases CBP and p300 that bind P-CREB were associated with active FMR1, which shows robust histone acetylation (8). Indeed, both histone acetyltransferases reside at FMR1 and their presence was largely reduced at the fragile X allele (Figure 3B).

We then used undifferentiated PC12 cells to test if the endogenous FMR1 gene is cAMP-inducible. Cells were treated with 10 μM forskolin or DMSO (vehicle). Real-time PCR of endogenous c-fos showed its strong induction (~50-fold) at 1 h post-stimulation (Figure 4A). However, FMR1 and HPRT transcript levels did not change (Figure 4A and data not shown). Even after 24 h, FMR1 mRNA levels remained constant (data not shown) revealing that in contrast to previous suggestions, the endogenous FMR1 gene is not cAMP-inducible in this cell type. We also obtained similar results after KCl/CaCl2 treatment of PC12 cells (data not shown).

Since it has been shown that at c-fos, the phosphorylation of CREB increases in response to forskolin treatment, and this is followed by induction of transcription, we tested if phosphorylation of CREB/ATF at FMR1 changed after forskolin treatment. We found that the CRE-binding proteins at FMR1 and c-fos were phosphorylated in undifferentiated PC12 cells without forskolin treatment (Figure 4B, upper panel). We performed quantitative analyses of P-CREB binding at c-fos and FMR1 and found that in response to forskolin treatment, the increase in occupancy of the phosphorylated CRE-binding protein on FMR1 was ~2.2-fold (Figure 4B, lower left panel), while that on c-fos was ~4.6-fold (Figure 4B, lower right panel).

Identification of a conserved consensus NRF-2 binding site in the FMR1 5′-UTR

Previous FMR1 promoter analysis identified several protein binding sites conserved among species (16). Using homology alignment, we found another evolutionarily conserved transcription factor binding site that had not been previously identified (Figure 5A). The conservation of the GTTT sequences 5′ to the boxed NRF-2 site suggests these bases are also important NRF-2 contacts (Figure 5A). Since recent work has shown
that expression patterns of FMR1-encoded proteins in zebrafish, as well as Xenopus, are conserved compared to humans, we looked to see if the promoter sequences for FMR1 may also be conserved in these animals (27,28). We have now extended the alignment of the FMR1 promoter to include sequences from Danio rerio, Xenopus tropicalis as well as Gallus gallus (Figure 5A). A TATA-like motif and the NRF-2 site are conserved among all species tested, despite variations in the intervening sequence (Figure 5A). In addition, recently available genomic sequence of the zebrafish FMR1 gene shows that, in addition to the TATA-like and NRF-2 elements, sites representing the four in vivo footprints in the human FMR1 promoter are also conserved (Figure 5B).

The NRF-2 site is positively acting and NRF-2 stimulates the FMR1 promoter

We tested the function of the putative NRF-2 site in the human FMR1 promoter. Mutating four bases in the binding site (Figure 5A) reduced FMR1 promoter activity to 40% of wild-type in HeLa cells showing the importance of this site for FMR1 expression (Figure 6A). To test if FMR1 was a bona fide NRF-2 target, we asked if NRF-2 was bound to active FMR1 in human cells. Using ChIP and an antibody against its DNA-binding (alpha) subunit, we found that NRF-2 is bound to FMR1 in vivo (Figure 5A). As expected for an activator of transcription, NRF-2 was not bound at the silenced, expanded FMR1 allele in patient cells, although it occupies the active Tfam promoter in these cells (Figure 6B).

We have previously shown the importance of NRF-1 in FMR1 transcription (18). NRF-1 often works at promoters with NRF-2; this is especially well documented for numerous nuclear-encoded mitochondrial genes (20,29). To test NRF-2’s transcriptional activity at FMR1, we asked whether NRF-2 could activate the FMR1 promoter in SL2 cells which have previously proven successful in assessing the function of this transcription factor (25,30–32). As expected, transfection of either NRF-2-alpha or NRF-2-beta alone had no effect on FMR1 transcription (data not shown). However, co-transfection of both subunits activated the FMR1 promoter between 1.7- and 3.1-fold (Figure 7A and B). We then tested if NRF-1 and NRF-2 could work together at FMR1 and found that they activated transcription additively (Figure 7A). Since members of the CREB/ATF family have been shown to work with NRF-2 to synergistically activate transcription, we wanted to test if this occurred at FMR1 (25). Indeed, we found that ATF-1 activates FMR1 transcription synergistically with NRF-2 (Figure 7B). This result is similar to that obtained with CREB and NRF-2 (data not shown). Importantly, mutation of either the E-box/CRE or the NRF-2 binding site abolished activation by ATF-1 and NRF-2 (Figure 7B).

**DISCUSSION**

The precise roles and relative importance of the many transcription factors implicated in FMR1 promoter function is controversial. Early reports suggested that FMR1 is regulated by cAMP signaling, perhaps through CREB (14). Here we show that CRE-binding proteins play a role in FMR1 transcription, however the endogenous gene is not induced in a manner such as that observed for the immediate early c-fos gene. These data are consistent with our findings that USF does not appear to operate through this region of the promoter resolving the paradox that a protein resides at this site but that USF does not activate this promoter. It is also worth noting that Drosophila SL2 cells accurately predicted how USF
proteins would act at the \textit{FMR1} promoter in a human cell line, showing that this is a useful cell line for studying these human transcription factors (18). Due to the overlapping nature of the E-box and the CRE, it is unlikely that both could be occupied at the same time by different transcription factors. However, we cannot rule out the possibility that this overlapping site could be differentially used by E-box binding factors and CRE-binding proteins in different cell types. To date, there is no direct \textit{in vivo} evidence that USF is positively acting through the E-box/CRE site at \textit{FMR1} in any cell type and c-Myc is not present at \textit{FMR1} \textit{in vivo} though other E-box binding proteins could play a role (18). \textit{In vitro}, USF can bind to an \textit{FMR1} promoter fragment and induce bending of an \textit{FMR1} promoter fragment (16,17). Curiously, our previous

\begin{figure}
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\includegraphics[width=\textwidth]{figure4.png}
\caption{\textit{FMR1} transcription is not cAMP-inducible. (A) Real-time PCR quantification of endogenous \textit{FMR1}, \textit{HPRT} and \textit{c-fos} transcripts in PC12 cells with or without 1 h of forskolin stimulation. (B) Phosphorylation of CREB/ATF at \textit{FMR1} increases 2-fold after forskolin induction of PC12 cells. ChIP was performed with P-CREB antiserum on DMSO- or forskolin-treated PC12 cells. PCR was performed to amplify the rat \textit{FMR1} and \textit{c-fos} promoters (top). Quantification of P-CREB binding was performed by real-time PCR (bottom). Error bars represent ±1 standard deviation. For \textit{FMR1} real-time analysis, two independent IPs are represented, each with duplicate real-time PCR. For \textit{c-fos}, the real-time data represent one IP with quadruplicate real-time PCR.}
\end{figure}
in vivo ChIP results indicate that USF resides on the FMR1 promoter in lymphoblastoid cells however it does not regulate the FMR1 promoter through the E-box (18). USF has also been shown to work through initiator (Inr) elements that surround the transcription start site (33). However, mutation of an Inr element in FMR1 did not affect promoter activity in reporter assays (16). The recognition site for USF and its function at FMR1 remain to be elucidated. Our data suggest that USF is not acting in the [-C24]300 bp upstream of the transcription start site and no incriminating in vivo footprints were identified up to [-C24]600 bp upstream of the start site, although there is a perfect consensus E-box at [-C24]800 bp from the transcription start (12,13). If bound by USF, perhaps this site plays a role in maintaining chromatin structure of FMR1 on the endogenous locus and hence, its role, as determined using a minimal promoter fragment on reporter plasmids and through in vitro assays, has not been appreciated. Consistent with this idea, USF has recently been implicated in recruiting histone acetyltransferase activity at genomic regions suggesting that these proteins could play a similar role at FMR1 (34).

The best studied functions for NRF-1 and NRF-2, however, are in controlling transcription of nuclear-encoded mitochondrial-related genes, notably the major transcription factor Tfam, as well as mitochondrial transcription specificity factors (20,39). It is not clear what separates or potentially links NRF-1 and NRF-2 mediated regulation of mitochondrial-related genes and those involved in RNA metabolism, or other functions.

An important question is the inducibility of FMR1 promoter function. Despite the suggestion made several years ago that FMR1 may be cAMP-inducible, we are not aware of any
reports that have tested this hypothesis on the endogenous FMR1 gene. Phosphorylation of CREB was originally thought to be specific and sufficient for the cAMP-induction of genes. Recent work, however, shows that genes can be bound by

Figure 6. NRF-2 is a regulator of FMR1 transcription in vivo. (A) HeLa cells were transfected with wild-type or NRF-2 site mutant pFMR1-luc reporter plasmids. Values for the FMR1 promoter were normalized to a CMV transfection control reporter. Data plotted are the average of six independent transfections ±1 standard deviation. The wild-type reporter was arbitrarily set to 100%. (B) Immunoprecipitation using an anti-NRF-2 antibody or nonspecific IgG (N.S.) was performed on chromatin from normal and fragile X cells. Real-time PCR was carried out on triplicate IPs to quantify the binding of NRF-2 to the Tfam and FMR1 promoters; error bars represent ±1 standard deviation.

Figure 7. Stimulation of the human FMR1 promoter in Drosophila SL2 cells. (A) pFMR1-luc reporter plasmid was co-transfected into SL2 cells with an empty vector or vectors expressing NRF-1 (pACTIN-FL-NRF-1), or NRF-2 (both A5CAP-hGABPα and A5CAP-hGABPβ) or both NRF-1 and NRF-2. Firefly luciferase values are normalized to a Renilla luciferase control. The fold-changes are shown above each bar in relation to the sample representing pFMR1-luc alone which was set to 1x. Each bar represents the average of three transfections and error bars represent ±1 standard deviation, except for NRF-2 for which the average of two transfections was plotted. (B) pFMR1-luc, or pFMR1-luc with the NRF-2 or E-box/CRE sites mutated, were co-transfected with vectors expressing human ATF-1 (A5CAP-hATF1), or NRF-2 (both A5CAP-hGABPα and A5CAP-hGABPβ) or both ATF-1 and NRF-2. The fold-changes are shown above each bar, in relation to their appropriate controls and are plotted in relative light units (RLU) on the vertical axis. Bars represent the averages of at least three transfections. Error bars for all samples represent ±1 standard deviation.
P-CREB regardless of cAMP-inducibility (40). Indeed, we have shown that even though FMR1 is bound by P-CREB/ATF as well as by CBP/p300, it is not cAMP-inducible. An important step in CREB/ATF function is the recruitment of CBP/p300 to P-CREB (41). Sp1, NRF-1 and NRF-2, may also play a role in recruiting CBP/p300 suggesting that these HATs may be recruited to FMR1 through their interactions with multiple transcription factors (42–47).

Interestingly, the overlapping E-box and CRE elements in the FMR1 promoter are almost identical to the E-box/CREs site in the human c-fos promoter with a one base pair difference in the E-box: CCCTGACGT versus FMR1’s: CACGTGACGT. However, we have shown that there are many differences between the two genes and their regulation by CRE-binding proteins. The co-existence of a TATA box and a CRE within a promoter has been shown to correlate with cAMP-responsiveness (48). The absence of a canonical TATA box from the FMR1 promoter may partly explain its non-responsiveness to cAMP. In this regard, FMR1 has many characteristics of a housekeeping gene, including the lack of a TATA box, a high GC content and its regulation by factors such as NRF-1, NRF-2 and Sp1 (49,50). The prior characteristics of a housekeeping gene, including the lack of cAMP responsiveness to cAMP-2 (54,55). Perhaps not responsive to cAMP, or to depolarization which is known that, at some level, FMR1 is recruited to signaling sites (14).

FMRP has been implicated in synaptic plasticity suggesting that, at some level, FMR1 expression may be responsive to neuronal signals (51–53). However, FMR1 transcription was not responsive to CAMP, or to depolarization which is known to activate NRF-2 (54,55). Perhaps FMR1 does not need to be induced at the transcriptional level in adult neurons since post-translational changes modulate FMRP in response to certain stimuli (56–58). For example, FMR1 mRNA and FMRP rapidly localize in dendrites in response to treatment with KCl and FMRP is quickly translated within 5 min of mGlur stimulation of neurons (56,57). Even though these stimuli activate CREB, it would take longer to make FMRP through a transcriptional induction pathway than to directly increase FMRP levels by post-transcriptional processes (59,60). Hence, mobilization of pre-existing FMR1 mRNA and protein, along with rapid local translation may be more important for the neuronal functions of FMRP than new mRNA synthesis. In support of this model, FMRP levels increase in cortical neurons following stimulation by light exposure, but mRNA levels do not change (58). A complete description of the regulatory landscape of the FMR1 promoter will facilitate the examination of the intrinsic developmental and external neuronal signaling mechanisms by which regulation of FMR1 is achieved.

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