

Myotonic dystrophy associated expanded CUG repeat muscleblind positive ribonuclear foci are not toxic to *Drosophila*

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Myotonic dystrophy type 1 is an autosomal dominant disorder associated with the expansion of a CTG repeat in the 3' untranslated region (UTR) of the DMPK gene. Recent data suggest that pathogenesis is predominantly mediated by a gain of function of the mutant transcript. In patients, these expanded CUG repeat-containing transcripts are sequestered into ribonuclear foci that also contain the muscleblind-like proteins. To provide further insights into muscleblind function and the pathogenesis of myotonic dystrophy, we generated *Drosophila* incorporating CTG repeats in the 3'-UTR of a reporter gene. As in patients, expanded CUG repeats form discrete ribonuclear foci in *Drosophila*

being related only to the number of the transcribed, but not translated, CTG/CCTG repeats. Secondly, mice expressing expanded CUG repeats in the 3'-UTR of an unrelated transgene develop myotonia and a DM-like myopathy (5).

Downstream pathways in DM are linked to splicing defects in a number of genes. Most convincingly, missplicing of the *chloride channel subunit 1 (CLC1)* and *insulin receptor* transcrip- tional promoters underlie the observed myotonia (6) and insulin intolerance (7). The pathways that link the splicing defects to the primary CTG expansion are not completely understood but appear to involve a cluster of proteins that can bind CUG repeats: the CUG-BP1 and ETR-3-like factor (CELF) and the muscleblind-like (MBNL) proteins (8). Both clusters of proteins are regulators of alternative splicing in an agonistic effect on a subset of alternatively spliced genes. Consistent with a direct role for CUG-BP1 in DM pathways, DM splicing defects are mirrored in normal cells over-expressing CUG-BP1 and nuclear levels of CUG-BP1 are increased in DM patient cells (9). Similarly, consistent with a direct role for the MBNL in DM pathways, mice lacking *Mbnl1* develop myopathy and myotonia and splicing defects in the *Clc1* transcrip- tion (10).

Precisely how the CELF and MBNL proteins function are performed in patient cells is not completely understood, but it is a matter to be related to the observation that expanded CUG repeat RNA is trapped in discrete foci in the nuclei of patient cells (11). Although the ribonuclear foci do not contain CUG-BP1 (12), the MBNL proteins bind to CUG RNA and co-localize with the ribonuclear foci, supporting a role for MBNL in the pathogenic process (13,14). Nevertheless, mice homozygous null for *Mbnl1* are born healthy and do not present with the congenital form of DM. Thus, they remain nuclear and have MBNL protein concentrations in the patient pathways and, importantly, the hereditary expanded CUG repeat RNA or ribonuclear foci are inherently non-toxic and have a direct toxic effect on and above the regulation of alternative splicing. A more general toxic effect of expanded CUG repeat RNA might be mediated by the sequestration of transcrip- tion factors, as has been recently proposed (15), and investigated for high- resolution polyglutamine expansion (16).

The rate of progression underlying fundamental mechanisms in DM is restricted by the complexity of analyzing patient samples, the inherent limitation of cell culture models and the relative difficulty of generating additional mouse models. Significantly, a number of simple repeat disorders have been effectively modelled in *Drosophila*, providing critical new insights into the molecular pathways of the disease process (17-20). We have, therefore, created a *Drosophila* model of DM and provided insights into muscleblind function by expressing CTGgl

High magnification cell. In the image, (CUG)₁₆₂-polyoma gene
RNA is also detected in the nuclei of all larval and adult

muscle, despite the presence of muscleblind protein and GFP in the eye.

In humans, MBNL1 is distributed throughout the cytoplasm and nucleus in hindbrain muscle cells but is recruited to the ribonuclear foci in DM patient cells (13). This localization is replicated in *Drosophila* hindbrain larvae (Fig. 3A), both in wild-type and (CTG)₁₁ adult, muscleblind is a clearly localized in nuclear foci in the absence of expanded repeat RNA (Fig. 3B). This suggests that either muscleblind in larval localization is developmentally controlled by other protein or that developmentally regulated muscleblind isoforms differ in their localization. For different *muscleblind* mRNA isoforms have been identified in *Drosophila*: *mbl-A*

with DAPI, but they were not observed in the nucleolus. They therefore shared the interchromatin space with the splicing and mRNA export machinery. The relative location of ribonuclear foci and molecular marker of spliceosome and exosome were analyzed. No colocalization was observed (Fig. 7A). The relative location of the pre-exosome assembly indicated to determine whether the pre-intron present in the ribonuclear foci contain miRNA-folded pre-intron and are targeted for degradation, and again no colocalization was observed (Fig. 7A).

These observations were cell line specific for dealing with nuclear RNA in adenine-uracil RNA editing (25). In vertebrate cells, it is known that editing is followed by a mechanism of nuclear mRNA processing, PSF and p54^{nrb} (26). Although the CUG repeat RNA should be immune to such editing, the hairpin structure may nonetheless interfere with protein in this pathway, so the relative location of ribonuclear foci and non-A, the *Drosophila* PSF/p54^{nrb} or homolog, were analyzed (Fig. 7B). Colocalization of these elements is a very good, indicating that non-A and expanded repeat RNA occupy the same nuclear region and probably interact, directly or indirectly, *in vivo*. To determine whether expanded CUG containing transcripts were edited by the non-A pathway, RT-PCR amplified transcripts were cloned and sequenced from (CTG)₁₆₂ expressing *in vivo*. RNA editing and reverse transcription were performed using adenine-uracil in the cDNA

Figure 7. Relative localization of ribonuclear foci and nuclear markers.

To gain further insight into the organization of ribonuclear foci, their spatial position in the nucleolus was analyzed. Ribonuclear foci occupied nuclear region lightly stained

arrange in DM1 patients. Indeed, it has been shown that additional sequence elements within the *DMPK* 3'-UTR modify the effect of the expanded CUG repeat on mRNA stability (31). Nonetheless, the DM2 mutation (3) and the CUG repeat expansion in transgenic mice (5) demonstrate that an expanded repeat can in the absence of additional *DMPK* sequence efficiently mediate DM pathogenesis in mammalian cells.

In (CTG)₁₆₂ *Drosophila* expressing the transgene, large ribonuclear foci were observed only in salivary gland, larval muscle cells and a subset of adult muscle. Thus, ribonuclear foci formation is not an obligatory manifestation of expressing large expanded CUG repeat arrangements. The hairpin structure of RNA molecules (12) are normally blocked from entering the nucleus, and have been previously proposed (32). The data therefore indicate

been expanded CUG repeat RNA and nuclear matrix. We propose that in normal cells, some MBNL1 is associated with

After blocking for 30 min in 5% normal serum (from the

polyglutamine protein formation, nuclear inclusions, and cerebellar degeneration in *Drosophila*. *Cell*, **93**