The Evolutionarily Conserved Tre2/Bub2/Cdc16 (TBC), Lysin Motif (LysM), Domain Catalytic (TLDc) Domain Is Neuroprotective against Oxidative Stress*

Received for publication, August 13, 2015, and in revised form, December 1, 2015 Published, JBC Papers in Press, December 14, 2015, DOI 10.1074/jbc.M115.685222

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Oxidative stress is a pathological feature of many neurological disorders; therefore, utilizing proteins that are protective against such cellular insults is a potentially valuable therapeutic approach. Oxidation resistance 1 (OXR1) has been shown previously to be critical for oxidative stress resistance in neuronal cells; deletion of this gene causes neurodegeneration in mice, yet conversely, overexpression of OXR1 is protective in mice and mouse models of amyotrophic lateral sclerosis. However, the molecular mechanisms involved are unclear. OXR1 contains the Tre2/Bub2/Cdc16 (TBC), lysin motif (LysM), domain catalytic (TLDc) domain, a motif present in a family of proteins including TBC1 domain family member 24 (TBC1D24), a protein mutated in a range of disorders characterized by seizures, hearing loss, and neurodegeneration. The TLDc domain is highly conserved across species, although the structure-function relationship is unknown. To understand the role of this domain in the stress response, we carried out systematic analysis of all mammalian TLDc domain-containing proteins, investigating their expression and neuroprotective properties in parallel. In addition, we performed a detailed structural and functional study of this domain in which we identified key residues required for its activity. Finally, we present a new mouse insertional mutant of Oxr1, confirming that specific disruption of the TLDc domain in vivo is sufficient to cause neurodegeneration. Our data demonstrate that the integrity of the TLDc domain is essential for conferring neuroprotection, an important step in understanding the functional significance of all TLDc domain-containing proteins in the cellular stress response and disease.

This work was supported by a United Kingdom Medical Research Council Programme grant (to K. E. D.) and funding from the European Research Council under the European Union’s Seventh Framework Programme (FP7/2007–2013)/ERC Grant 311394 (to P. L. O.). The authors declare that they have no conflicts of interest with the contents of this article.

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The abbreviations used are: ROS, reactive oxygen species; TBC, Tre2/Bub2/Cdc16; AS, alternative start.

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control of GTP-binding protein ADP-riboisolation factor 6 (ARF6) activation (21, 29) as well as vesicle recycling in neurons (30, 31). Taken together, these data suggest that OXR1 and TBC1D24 are important for normal brain function. NCOA7 is also expressed in the brain (32), although nothing is known regarding its transcriptional role in the nervous system. To assist these studies, the three-dimensional structure of the TLDc domain has been solved (17). Nevertheless, due in part to the lack of structural similarity to known protein folds, it remains unclear whether other TLDc proteins possess similar functional properties and how the TLDc domain contributes to essential cellular processes; indeed, there is no evidence that the TLDc domain imparts catalytic properties as originally predicted (18).

To, therefore, understand the functional significance of this domain, we carried out a structural-functional study of all mammalian TLDc proteins, demonstrating that they share a common protective role in neurons and identifying critical residues in the domain. Our data provide valuable new insight into the function of TLDc domain-containing proteins in the neuronal stress response.

**Experimental Procedures**

*In Situ Hybridization*—Regions representing all isoforms of Oxr1 (2723–3139 bp of NCBI accession number NM_130885), Ncoa7 (2650–3284 bp of NM_172945), Tbc1d24 (2705–3558 bp of NM_001163847), Kiaa1609 (1337–1959 bp of NM_028883), and Tbc1d24 (1337–1959 bp of NM_001163847), and Kiaa1609 have been described previously (8). For Ncoa7, Tbc1d24, and Kiaa1609 knockdown experiments, shRNA constructs were purchased from Sigma (NM_172945.5–2897s1c1, NM_173186.2–1208s1c1, and NM_028883.2–256s1c1, respectively). Site-directed mutagenesis was used to introduce the various mutations into the pcDNA3 constructs above as per the manufacturer’s protocol (Agilent Technologies) and confirmed by sequencing.

*Cell Culture, Transfection, and Treatment*—Neuronal N2a cells were cultured in DMEM supplemented with glutamax (Gibco), 1% penicillin-streptomycin (Gibco), and 10% fetal calf serum (Gibco). Cells were transfected with either FuGENE 6 (Promega) for 48 h (for shRNA experiments and overexpression for lipid peroxidation and S-nitrosylation assays) or Magnetofection (OZBiosciences) for 24 h (for all other overexpression experiments) as per the manufacturers’ protocol. Cells were treated with arsenite (50 μM for 5 h to quantify ROS, 50 μM for 4 h lipid peroxidation and S-nitrosylated assays, or 150 μM for 4 h to quantify cell death) in water or with water-only as a control. To visualize pyknotic nuclei, cells were fixed with 4% paraformaldehyde for 10 min at room temperature, washed with PBS twice, blocked with blocking buffer (5% goat serum, 0.5% Triton X-100) for 1 h at room temperature, and mounted in DAPI medium (Vectorlabs). Cells were visualized using a fluorescent microscope (Leica), and those with typical condensed and fragmented nuclei were counted as pyknotic cells. Anti-HA immunostaining was carried out as previously described (15).

*Purified Cortical Cell Cultures*—Cortical cells from wild-type P1 pups were prepared and cultured as previously described (37). Briefly, cortices were dissected in cold Hanks’ balanced salt solution (Gibco), and meninges and hippocampi were removed and trypsinized for 15 min at 37 °C. Trypsin was inactivated using trypsin inhibitor (Life Technologies) for 5 min, and cortices were triturated and purified on an OptiPrep gradient following Brewer and Torricelli (37). Cells were plated in culture medium (Neurobasal phenol-free, 5% FCS, 2% B27, 0.5

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**TABLE 1**

*List of primers used for qRT-PCR*

| Primer           | Sequence | 5’–3’ |
|------------------|----------|-------|
| Gapdh F          | AGAACATCATTCTGCTATCC |       |
| Gapdh R          | CACGTTGGGTTGAGCAACAA |       |
| Oxr1FL F         | CGTCTGAGCTGACAGGTTTT |       |
| Oxr1FL R         | ATGCGCTACATTGAGTCG  |       |
| Oxr1 C F         | CCTAAATACACCTTCTGAGTCG |       |
| Oxr1 C R         | TTGTGCTGAGAAGATTCAGG |       |
| Ncoa7 FL F       | TCTGCTATCCTGCTAGTG  |       |
| Ncoa7 FL R       | GCTCTGTGATCTCCTGAG  |       |
| Ncoa7 B F        | GCCCTCCGCTTTTTGATAGG |       |
| Ncoa7 B R        | CTGCTGGGCTTCTTGAATAGG |       |
| Tbc1d24 F        | TTATGCCGCTAGAGAAGCA |       |
| Tbc1d24 R        | AGGAGTACAGCCAGAAAATG |       |
| Kiaa1609 F       | CACCTGCTGAGGTTACAGAG |       |
| Kiaa1609 R       | CCCCCTGCATCCCCTATTAC |       |
| C20orf118 F      | TTCCTCACGCGGAGGAGGC |       |
| C20orf118 R      | CTGGCTCAGTCTGCTGAG  |       |

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*In Silico Analysis*—Alignments were produced using T-Coffee (34) using default parameters and refined manually. Protein alignments are presented using Belvu (35) with a coloring scheme indicating the average BLOSUM62 scores (which are correlated with amino acid conservation) of each alignment column: red (>3.5), purple (between 3.5 and 2), and light yellow (between 2 and 0.5). Sequences were named with their Uniprot identifiers. The corresponding secondary structures were acquired from the zebrafish Oxr2-TLDc domain structure (PDB ID 4ACJ) (17). The NCOA7-B structural model was created using Modeler (36) based on the zebrafish Oxr2-TLDc domain structure (PDB ID 4ACJ) (17). The NCOA7-B-TLDc domain model is presented using PyMOL. The amino acid evolutionary conservation was based on alignment BLOSUM62 scores.

*Constructs and Mutagenesis*—Full-length cDNAs representing mouse Ncoa7, Tbc1d24, Kiaa1609, and C20orf118 (accession numbers as above) and short isoform Ncoa7-B were cloned into a pcDNA3 vector with an HA tag in-frame at the C-terminus. Oxr1-FL and Oxr1-C have been described previously (8). For Ncoa7, Tbc1d24, and Kiaa1609 knockdown experiments, shRNA constructs were purchased from Sigma (NM_172945.5–2897s1c1, NM_173186.2–1208s1c1, and NM_028883.2–256s1c1, respectively). Site-directed mutagenesis was used to introduce the various mutations into the pcDNA3 constructs above as per the manufacturer’s protocol (Agilent Technologies) and confirmed by sequencing.
Dihydroethidium Assay—Cells were cultured in 96-well plates as described above. Cells were treated for 4 h with arsenite (50 μM) or vehicle supplemented with dihydroethidium (Sigma) diluted in culture medium (15 μM). After experimental treatment, cells were washed twice in PBS, wells were filled with 100 μL PBS, and the fluorescence was immediately measured on a Fluostar Omega (BMG Labtech) plate reader at an excitation wavelength of 430 nm and an emission wavelength of 590 nm.

Lipid Peroxidation Assay—N2a cells were transfected for 48 h and treated with 50 μM arsenite for 4 h before the levels of lipid peroxidation were quantified using a lipid peroxidation assay as per the manufacturer’s protocol (Abcam). Briefly, one confluent 63-cm² dish was used per condition, and cells were washed with cold PBS, homogenized by sonication in the lysis buffer provided, and clarified by centrifugation. Three volumes of thiobarbituric acid were added to the samples and incubated for 1 h at 95 °C. Samples containing a known concentration of malondialdehyde were processed in parallel and used to generate a standard curve. Samples were transferred to a transparent 96-well plate, and absorbance was read in duplicate at 532 nm on a Fluostar Omega (BMG Labtech) plate reader.

S-Nitosylated Protein Assay—N2a cells were transfected for 48 h on coverslips and treated with 50 μM arsenite for 4 h, and the levels of S-nitrosylated proteins were assayed by using a S-NO protein detection kit (Cayman). Cells were fixed with 4% paraformaldehyde for 20 min at room temperature and subsequently washed and blocked using buffers provided following the manufacturer’s protocol. Cells were incubated with reducing and labeling reagents for 1 h at room temperature followed by incubation for an additional hour with fluorescein detection reagent. Cells were observed by fluorescence microscopy (Leica). All images were captured using Axiosview software. The signal intensity of each cell was measured using ImageJ software and expressed as the mean gray value divided by the surface of the cell. Approximately 40 cells were assessed per condition.

Tissue Staining—Terminal deoxynucleotidyltransferase dUTP nick end labeling (TUNEL) staining was carried out on fresh frozen brain sections as recommended by the manufacturer (In situ cell death kit, Roche Applied Science). For quantification, four 12 μm sections at 60 μm intervals across the midline of the cerebellum were counted for TUNEL-positive cells per replicate. β-Galactosidase staining was also carried out on fresh frozen brain sections as previously described (38).

Western Blotting—Protein extracts were prepared from cells using standard radioimmunoprecipitation assay buffer, and protein levels were quantified using BCA assays (Millipore). Proteins were run on pre-cast NuPAGE Bis-Tris gels (Life Technologies) and transferred as per the manufacturer’s protocol. Primary antibodies used were as follows: Ncoa7 (Abcam ab103993), Oxr1 (antiserum as previously described (8)), Tbc1d24 (Santa Cruz), Kiaa1609 (Biorbyt), and β-actin (Abcam).

Animals—All experiments were conducted in adherence to the guidelines set forth by the UK Home Office regulations and with the approval of the University of Oxford Ethical Review Panel. The Oxr1 “knock-out first” allele (Oxr1tm1a(EUCOMM)Wtsi) was generated as part of the International Knock-out Mouse Consortium (IKMC) program (IKMC project 84243). Briefly, a L1L2_Bact_P cassette was inserted after exon 12 of Oxr1, composed of a splice acceptor site and lacZ followed by neomycin under control of the human β-actin promoter (see Fig. 6 and Ref. 39). Thus the lacZ reporter is designed to be under the control of the native promoter of Oxr1-FL and Oxr1-C. Intercrossing of mice heterozygous for the tm1a allele was used to generate homozygous animals, thus maintaining the line on a C57BL/6N background.

Results

TLDc Domain-containing Genes Show Distinct Tissue Distribution Patterns—To compare systematically the expression pattern of all the TLDc domain-encoding genes in parallel, we quantified their mRNA levels in a range of organs from wild-type mice. For Oxr1 and Ncoa7 we assayed the full-length transcripts (Oxr1-FL and Ncoa7-FL) in addition to the shortest known isoforms that almost exclusively contain the TLDc domain, Oxr1-C (9, 15) and Ncoa7-B (40) (equivalent to human NCOA7-AS) (41) (Fig. 1A). We showed that Oxr1-FL, Oxr1-C, Ncoa7-FL, and Tbc1d24 are the most highly expressed TLDc genes in the central nervous system (Fig. 1B). In addition, both Ncoa7 isoforms tested are more highly expressed in the kidney, liver, lung, and spleen than other TLDc genes, suggesting that Ncoa7 has a specific function in these peripheral organs (Fig. 1B). Interestingly, the relative expression of Ncoa7-FL and Oxr1-FL is significantly higher than their corresponding short isoforms in several tissues, supporting the notion that these specific isoforms are differentially or independently regulated (Fig. 1B). We next used in situ hybridization to determine the anatomical localization of the TLDc domain-encoding genes during development at embryonic day (E) 14.5 using riboprobes spanning exons common to all known isoforms. These data show that Oxr1 and Ncoa7 are expressed throughout the developing embryo, whereas Tbc1d24 expression is more localized to the brain, spinal cord, and liver (Fig. 1C). Kiaa1609 and C20orf118 were, however, virtually undetectable at this developmental time point (Fig. 1C). Lastly, we investigated the localization of the TLDc-encoding genes in the adult brain, and we showed that Ncoa7, Oxr1, and Tbc1d24 are expressed in all major structural regions, particularly in the cortex, hippocampus, and cerebellum, with Ncoa7 expression enriched in Purkinje cells as opposed to the cerebellar granule cell layer for Oxr1 and Tbc1d24 (Fig. 1C). In agreement with our qRT-PCR data, Kiaa1609 is expressed at a generally low level, although expression in the hippocampus is apparent (Fig. 1C).
Ncoa7-B or Oxr1-C under arsenite treatment, a well-characterized oxidative stress inducer. Interestingly, we found that expression of every TLDc domain-containing protein significantly reduced the proportion of dying neurons as compared with cells transfected with an empty control vector (Fig. 2A). All TLDc proteins reduced the proportion of cell death by at least half, and Ncoa7-B appeared to be the most potent neuroprotective protein in this assay, reducing cell death by up to 85% compared with control cells (Fig. 2A). There was no difference in the levels of cell death between untreated cells expressing the TLDc constructs or the control vector, confirming that overexpressing these proteins was not toxic to the cells (data not shown).

We showed in a previous study that knockdown of Oxr1 led to increased neuronal sensitivity to oxidative stress in vitro (8); thus we investigated whether similar effects would be observed for other TLDc proteins. We were able to knock down Ncoa7, Tbc1d24, and Kiaa1609 in N2a cells using shRNAs by 64, 54, and 64% at the RNA level, respectively (Fig. 2B), and ~50% at the protein level (Fig. 2C). Treatment of these cells with arsenite led to a small but non-significant increase in cell death compared with those transfected with a control scramble shRNA vector (Fig. 2D). To compare these findings with Oxr1, we knocked down this gene by as much as 82% of the normal RNA level using increasing concentrations of transfected shRNA (Fig. 2E) and showed a corresponding 80% decrease at the protein level (Fig. 2F). Interestingly, only at the 82% mRNA knockdown level was there a significant increase in cell death under the same oxidative stress conditions (Fig. 2G). These data suggest that reducing the expression levels of TLDc genes to around two-thirds that of their normal level is not sufficient to elicit a change in oxidative stress sensitivity.

It has also been suggested that the levels of OXR1 can be induced as part of the oxidative stress response (9); hence, we next determined whether other TLDc proteins share the same properties by quantifying their mRNA levels in purified primary cortical neurons treated with arsenite. Ncoa7-FL and Oxr1-C were induced significantly by this treatment, whereas

![FIGURE 1. The TLDc members have specific expression patterns in various organs in embryonic and adult wild-type mice.](image-url)
the levels of the other TLDc genes remained unchanged (Fig. 2H), suggesting that Ncoa7-FL and Oxr1-C are more likely to participate in the oxidative stress response under arsenite treatment.

To provide some mechanistic insight into how overexpression of TLDc proteins could be neuroprotective, we tested whether it might occur by reducing the oxidative stress level in cells. Thus we quantified the level of ROS using the fluorescent dye dihydroethidium in N2a cells transfected with each of the wild-type TLDc constructs and then treated with arsenite. We showed that overexpression of Oxr1-FL, Oxr1-C, and Ncoa7-B significantly decreased the level of cellular oxidative stress, whereas the other TLDc proteins caused only a small reduction without reaching significance (Fig. 2I). Taken together, our data show that all of the TLDc domain-containing proteins can be neuroprotective, yet Ncoa7-FL, Tbc1d24, Kiaa1609, and C20Orf118 were unable to reduce the level of oxidative stress in treated cells. Therefore, our results indicate that the TLDc domain can elicit some of its functional effects alone, yet the context of this domain among the additional protein motifs in each protein may influence these properties.

The TLDc Domain Contains Highly Conserved Residues Required for Its Neuroprotective Function—Next, we investigated how the neuroprotective function of the TLDc proteins may be driven by the conserved TLDc domain. Initially, we performed a protein alignment of this region using sequences from humans to yeast (Schizosaccharomyces pombe) to assist in the identification of the most conserved amino acids and structural features (Fig. 3). These analyses predicted 4 α-helices and 10 β-strands and identified ~10 residue positions within the domain that were highly conserved in all species analyzed (Fig. 3). We hypothesized that these particular residues would be...
essential for the function of this domain and used an alanine-scanning approach, mutating six of the most conserved amino acids of Ncoa7-B, to investigate the functional consequences. We chose to focus on Ncoa7-B as it is almost entirely composed of the TLDc domain (40), it is expressed from an independent promoter in mammalian cells (41), and it represented the most potent neuroprotective TLDc domain-containing protein we tested in neurons (Fig. 2A).

We first confirmed that all Ncoa7-B mutants could be expressed efficiently in N2a cells and that the mutations did not
We then predicted the consequences of mutating these four specific amino acids on the structure of the TLDc domain of Ncoa7-B using the published zebrafish three-dimensional structure (17) (Fig. 3). We predicted that Gly-93 is likely to be required to maintain the position of α-helices 3 and 4 (42) (Fig. 4C). This suggests that the structural integrity of the superficial helix may be important for function of the TLDc domain. Glu-216 is one of the most evolutionarily conserved positions in the TLDc domain, and structural predictions suggest that a hydrogen bond between the carboxylate group of Glu-216 and the amide group of Ser-60 maintains the position of the N-terminal domain (17).

FIGURE 3. The TLDc domain is highly conserved across species. Alignment of 48 TLDc domain-containing proteins. Colors corresponds to the amino acid conservation of each alignment column: red (highly conserved), purple (mildly conserved), and light yellow (poorly conserved based on BLOSUM62 scores). Residues mutated in this study are labeled according to reference protein sequences for human NCOA7-B (FL) (magenta), and the zebrafish OXR2-TLDc sequence (PDB ID 4ACJ, purple) (17). The limits of the protein sequences included in the alignment are indicated by flanking residue positions. Protein sequences are shown by name or by Uniprot identifier. Secondary structure annotation (in blue) is derived from the zebrafish OXR2-TLDc domain (17). α-Helices (H) and β-strands (S) are indicated by cylinders and arrows, respectively. Species abbreviations: 9CHLO, Bathycoccus prasinos; ACYPI, Acrithosiphon pismum (pea aphid); AEDAE, Aedes aegypti (yellow fever mosquito); ARATH, Arabidopsis thaliana; ASCSU, Ascaris suum (pig roundworm); ASHGO, Ashbya gossypii; CAEL, C. elegans; CALMI, Callorhinchus milii (ghost shark); CHLAE, Chlamydomonas reinhardtii; CHLVA, Chlorella variabilis; CIOW, Ciona intestinalis; DANRE, Danio rerio (zebrafish); DAPPU, Daphnia pulex (water flea); DROME, Drosophila melanogaster (fruit fly); HUMAN, Homo sapiens; MONBE, Monosiga brevicollis (choanoflagellate); MONDO, Monodelphis domestica (opossum); MOUSE, Mus musculus; NASVI, Nasonia vitripennis (wasp); NECAM, Necator americanus (human hookworm); NEMVE, Nematoscelis vectensis (starlet sea anemone); SCHPO, S. pombe; SOLLC, Solanum lycopersicum (tomato); SOYBN, Glycine max (soybean); TRIAD, Trichoplax adhaerens; YARI, Yarrowia lipolytica; YEAST, Saccharomyces cerevisiae.

FIGURE 4. The TLDc domain reduces levels of oxidative stress in neurons. A, N2a cells were transfected with HA-tagged Ncoa7-B wild-type or mutant followed by HA staining to visualize Ncoa7-B localization. All mutants were expressed, and their localization was similar to the cytoplasmic localization of Ncoa7-B wild type. Scale bar: 100 μm. B, cell death was quantified by counting the number of pyknotic nuclei of N2a cells transfected with wild-type or mutant Ncoa7-B under oxidative stress and treated with 150 μM arsenite for 4 h. Cell death was compared with levels in cells transfected with control vector (*, p < 0.05; ***, p < 0.001) or with Ncoa7-B WT (±, p < 0.05; #, p < 0.01). Data are represented as the mean ± S.E. using one-way ANOVA with Dunnett’s multiple comparison test. C, the NCOA7-B mutants were mapped onto the zebrafish OXR2-TLDc domain structure (PDB ID 4ACJ) (17) with mutated residues labeled in red, side chains as sticks, and glycines as balls. The ribbon color indicates amino acid evolutionary conservation: red (highly conserved), purple (mildly conserved), and light yellow (low conservation).
region of the TLDc domain (Fig. 4C). Because this particular position seemed likely to influence an important structural feature of the TLDc domain, we extended the alanine scanning to examine the same glutamic acid in Oxr1 using the oxidative stress assay; in both Oxr1-FL (E773A) and Oxr1-C (E293A). The Oxr1-C mutation led to an approximate 2-fold increase in the proportion of cell death compared with wild-type Oxr1-C, suggesting that altering this amino acid was functionally disruptive, as observed for Ncoa7-B. What was more striking, however, was the same mutation in Oxr1-FL almost completely abolished the protective activity of the protein (Fig. 5A), further illustrating how the context of the TLDc domain within a larger protein structure may impart different functional properties.

Finally, we assessed mutations in the TLDc domain relevant to epilepsy by testing a Tbc1d24 A515V mutant (equivalent to human A509V) (21) as well as a truncation mutant (Cys156X) to mirror a TBC1D24 frameshift mutation that results in the loss of the TLDc domain (22). Oxidative stress response assays demonstrated that the A515V mutation caused a small but non-significant reduction in cell death compared with a control vector, suggesting that disrupting the disease-associated alanine residue may not have a major influence on the neuroprotective properties of TBC1D24 (Fig. 5B). However, the level of neuroprotection provided by the C156X mutant was as low as that of the control vector or the Oxr1-FL E773A construct (Fig. 5B), suggesting that mutating the highly conserved C-terminal glutamic acid can be as detrimental to the neuroprotective properties of a TLDc protein as losing the entire TLDc domain.

To relate these findings to oxidative stress levels, we went on to measure ROS levels in N2a cells expressing each of the mutant constructs (Fig. 5C). These data suggest that there is some correlation between the levels of ROS and how functionally disruptive the mutations were in the cell survival assay (Fig. 5C). For example, expressing the helix-associated mutants (G93A) did not significantly reduce cell death or ROS, and the same outcome was observed for the Oxr1-FL E773A mutant (Fig. 5C). Conversely, the least destabilizing mutation in Ncoa7-B, G123A, resulted in significantly lower ROS levels, equivalent to cells expressing wild-type Ncoa7-B (Fig. 5C). Taken together, these data show that conserved amino acids at key structural positions in the TLDc domain are required to maintain its functional properties in oxidative stress resistance.

Lipid peroxidation and protein S-nitrosylation are the two main consequences of increased cellular ROS, and these processes have been implicated in triggering neurodegeneration (2). Thus, we first assessed whether overexpression of TLDc proteins would reduce the level of lipid peroxidation in asenite-treated N2a cells. No differences in peroxidation were observed between cells transfected with either the empty control vector or any of the wild-type TLDc constructs (Fig. 5D). Interestingly, cells overexpressing a mutant version of Oxr1-C (E293A) shown to be functionally disruptive (Fig. 5A) caused a significant increase in peroxidation compared with those transfected with the wild-type Oxr1-C vector (Fig. 5D). None of the other mutants affected the global levels of lipid peroxidation in transfected cells however.

We also quantified the level of protein S-nitrosylation under the same oxidative stress conditions. Protein S-nitrosylation levels were significantly decreased in cells overexpressing wild-type Ncoa7-B but not those transfected with Oxr1-C, Oxr1-FL, or Tbc1d24 (Fig. 6A). Importantly, mutations in Ncoa7-B that we have demonstrated are essential for the neuroprotective
properties of the protein (for example, G93A and E216A; Fig. 4B), significantly increased the level of protein S-nitrosylation compared with cells transfected with wild-type Ncoa7-B (Fig. 6, A and B). Furthermore, cells overexpressing mutants of other TLDc proteins (Oxr1-FL E773A, Oxr1-C E293A, and Tbc1d24 A515V) showed significantly higher levels of protein S-nitrosylation than those transfected with the corresponding wild-type protein (Fig. 6A). These data suggest that TLDc proteins can modulate protein S-nitrosylation levels to protect neurons against oxidative stress.

Disruption of the TLDc Domain in Oxr1 Causes Neurodegeneration in Vivo—We showed previously that a mouse deletion mutant (bella) lacking all isoforms of Oxr1 and of the neighboring gene Abra displays ataxia from postnatal day (P) 20 and progressive apoptotic cell death in the cerebellar granule cell layer before death at approximately P26 (8). However, we wanted to specifically examine the disruption of the TLDc domain in the context of an in vivo mammalian system. Therefore, a new mouse mutant was generated in which the TLDc domain-coding exons shared by both Oxr1-FL and Oxr1-C were mutated by insertion of a LacZ reporter downstream of a splice acceptor site (Fig. 7A) (39). In this model any Oxr1 isoforms containing the TLDc domain will be truncated, losing the final 101 C-terminal amino acids. Homozygous mice carrying two copies of the mutant Oxr1 allele (Oxr1tm1a/tm1a) were generated from heterozygous animals, and β-galactosidase staining of the brain at P18 (Fig. 7B) demonstrated an expression pattern almost identical to the Oxr1 in situ hybridization profile (Fig. 1C), as expected. In addition, we confirmed that expression of Oxr1-FL and Oxr1-C transcripts upstream of the inser- tion were present in the brain of Oxr1tm1a/tm1a animals (data not shown). Importantly, Oxr1tm1a/tm1a mutants displayed progressive cerebellar degeneration and ataxia to the same degree as the original homozygous Oxr1 deletion mutants and over an identical timescale (Fig. 7, C and D). These data confirm that the TLDc domain is essential for Oxr1 function in vivo.

Discussion

Here we present the first systematic functional investigation of the TLDc family of proteins performed in parallel. We demonstrate that each protein has the ability to protect neuronal cells from oxidative stress and that conserved residues and secondary structures within the TLDc domain are required for these important functional properties.

Since the original description of OXR1, it has been hypothesized that this protein plays an important role in oxidative stress resistance (7, 9). Evidence has since been accumulating that this protein is involved in a number of key stress response pathways that can be influenced by manipulating its expression (8, 10, 11, 13, 15, 43). Indeed, the importance of OXR1 and related TLDc domain-containing genes has been emphasized by the discovery that their disruption or deletion can result in a reduced lifespan in Caenorhabditis elegans (13), Anopheles gambiae (11), Drosophila (30), and mice (8) or cause a range of inherited human neurological disorders (20–22, 26, 44–46). Conversely, overexpression of TLDc proteins has been shown to increase life expectancy both in normal and disease-associated systems, for example in Drosophila (43) and mouse (14). Therefore, we focused this study on the TLDc domain as the significance of this highly conserved region has not been studied in a comparative manner to date.

We provide the first systematic expression data of TLDc domain-containing genes in embryonic and adult tissues, including Kliaa1609 and C20orf118, which have not been studied previously in mammalian systems. These data emphasized that each gene displays a distinct expression profile, although there are tissues and cell types where their expression is likely to overlap. It is also noteworthy that both the shortest TLDc domain-containing isoforms of Oxr1 and Ncoa7 are differentially expressed in certain tissues compared with the corresponding full-length genes; this is likely to be a reflection of their distinct promoters and potentially different functional requirements. For example, a shift in the splicing profile of human NCOA7, favoring NCOA7-AS (Ncoa7-B in mouse) over NCOA7-FL, is observed in macrophages stimulated with lipopolysaccharide, which models an immune insult (47). In addition, NCOA7-AS specifically is induced in interferon-β-treated peripheral blood mononuclear cells from healthy participants or patients with the autoimmune disease multiple sclerosis (41). There are several examples where independently regulated isoforms of a gene are functionally distinct, for instance only one particular variant of insulin-like growth factor 1 (Igf1) is beneficial in an in vivo model of ALS (48, 49) or is
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As deletion of Oxr1 causes decreased oxidative stress resistance in neuronal cells (8), we tested whether the same effect would be observed for Ncoa7, Tbc1d24, and Kiaa1609 and found that a 54 – 64% knockdown of these genes did not significantly increase sensitivity to oxidative stress. However, we demonstrated that an 82% knockdown of Oxr1 is sufficient to render cells more susceptible to oxidative stress-induced degeneration. This is consistent with previous studies in cortical neurons lacking Oxr1 (8). Moreover, we have shown previously that mice heterozygous for the bella Oxr1 deletion, thus with only a partial reduction of Oxr1 levels, were phenotypically normal (8). Taken together, this suggests there is a threshold level of TLDc gene expression below which other cellular mechanisms, or even other TLDc proteins, cannot compensate.

Interestingly, the deregulation of the TLDc family has been demonstrated in several disease states, including an increase in OXR1 protein expression in end-stage ALS spinal cord biopsies (8) and a reduction in OXR1 in the posterior cingulate cortex of patients with Parkinson disease (51). In addition, levels of NCOA7 are reported to correlate with the clinical outcome of neuroblastomas (52). Thus, it appears that tight regulation of the TLDc domain-containing genes is a key feature of their neuroprotective properties; whether deregulation occurs at critical pre-symptomatic stages of disease warrants further investigation.

Our data suggest that the TLDc domain alone is able to confer oxidative resistance properties to all the TLDc members. This is in part corroborated by the observation that the shortest isoforms expressed in human and mouse, Oxr1-C and Ncoa7-B, are also functional in our assays despite containing almost exclusively the TLDc domain (8). A previous attempt to map
the region of full-length OXR1 that confers oxidative stress resistance utilized a spontaneous mutagenesis assay in a DNA repair-deficient strain of *E. coli* (16). Human OXR1 deletion mutants were assessed, revealing that a particular exon of OXR1 (upstream of the TLDc domain, equivalent to exon 8; Fig. 7) encoded the anti-oxidant function. This apparent discrepancy with our current study could be explained by an organism-specific mode of action, although this is unlikely as human OXR1 has been shown to rescue a *S. cerevisiae* OXR1 mutant phenotype, suggesting that there is functional conservation between species (9). The observations may, therefore, be due to the different methods used to assess oxidative stress resistance or that the two distinct regions or isoforms of OXR1 act via independent antioxidant mechanisms (16). For example, it has been proposed that the TLDc domain-containing proteins can influence the expression of key oxygen free-radical scavengers that, in turn, reduce the levels of ROS in the cell. Indeed, there is evidence that Oxr1 can modulate the expression of catalase (11), heme oxygenase (10), and glutathione peroxidase (8, 10, 11), potentially via a p21/NRF2-dependent pathway (10). Localization of OXR1 in the nucleus has also been described (53); however, which regions of the protein could directly or indirectly influence the transcription of these genes is still unknown.

It has also been hypothesized that the unique first coding exon of Ncoa7-B (NCOA7-AS in human) contains amino acid signatures of an aldo/keto reductase-like domain that could be responsible for the anti-oxidant properties of this short isoform (41). However, this hypothesis was based on a limited amino acid sequence alignment, whereas the entire aldo/keto reductase-like domain is predicted to be >300 amino acids long (54). Thus, we believe it is unlikely that the 25 amino acids of the Ncoa7-AS first exon could constitute or confer a functional enzymatic domain on its own.

Our own structural modeling combined with functional assays has highlighted for the first time the significance of certain highly conserved amino acids in the TLDc domain and how the context of this domain in the entire protein is critical. For example, mutating a conserved glycine residue (Gly-93 in Ncoa7-B; Figs. 3 and 4B) between α-helices 3 and 4 is highly detrimental to the oxidative stress resistance function of the domain (Fig. 3). Examining this position in more detail, the main chain torsion angles Φ and ψ (Ramachandran angles) at this position are 102° and 179° (55); only a glycine residue is sufficiently flexible to accommodate these torsion angles, and therefore, the G93A mutation will likely compromise the correct placement of α-helices 3 and 4 during folding. We also focused on a C-terminal glutamic acid (Glu-216 in Ncoa7-B; Figs. 3 and Fig. 4C), as it is not only highly conserved in all TLDc proteins but it was also predicted to interact with a serine residue (Ser-60) bringing the N-terminal region of the TLDc domain into close proximity. We predict that the N-terminal region is the most flexible of the entire domain; therefore, it is likely that a mutation of this key glutamic acid residue would reduce the stability of the N-terminal region and displace one of the α-helices (HI, Fig. 4C). Indeed, mutations at this position were detrimental to the protective properties of the short isoforms of both Oxr1 and Ncoa7 but resulted in a surprising, almost complete loss-of-function in the full-length Oxr1-FL isoform. This suggests that allosteric interactions between the TLDc and other accompanying domains in this family of proteins may be significant.

Consistent with this hypothesis, compound heterozygous mutations in TBC1D24, one in the TBC domain and another in the TLDc domain, cause familial infantile myoclonic epilepsy (FIME), whereas the parents carrying either one of these mutations are phenotypically normal (21). Thus the TLDc mutation in this context must be deleterious as it is unable to compensate for the other mutant allele in the TBC domain. Previous cellular studies revealed that this TLDc mutation (A509V) did not influence the binding of TBC1D24 to ARF6; however, it was striking that the same epileptogenic TLDc amino acid change completely reverted the ARF6-dependent neurite outgrowth phenotype associated with TBC1D24 overexpression (21). Thus these data support the notion that the TLDc domain is essential for the normal function of TBC1D24. Moreover, we have shown here that the TLDc domain of Tbc1d24 can also elicit protection against oxidative stress and that mutations truncating Tbc1d24, as described in the most severe neurological conditions associated with this gene (22), abolishes this property.

In this study we focused on the protective properties of the TLDc family in neuronal cells; however, it has become apparent that TLDc proteins may also play an important role in infection and immunity (12, 14, 41, 56). For example, these proteins may protect against ROS that are generated as part of the normal immune response to infection (12). Furthermore, the therapeutic use of Oxr1 has also been tested successfully in a model of diabetic retinopathy (53) and in kidneys of a nephritis mouse model using Oxr1-overexpressing mesenchymal stem cells (57). Taken together, these data demonstrate that Oxr1 possesses an important and evolutionarily conserved protective function that could be exploited therapeutically in the future. In summary, our study provides important new functional insight into a family of proteins that contain the highly conserved TLDc domain and its vital role in oxidative stress protection and in a range of human neurological disorders.

**Author Contributions**—M. J. F. performed and analyzed the experiments shown in Figs. 1, 2, 4, 5, and 6. P. L. O. performed and analyzed the experiments shown in Figs. 1 and 7. L. S.-P. analyzed and compiled the evolutionary and structural data in Figs. 3 and 4. K. X. L. performed the experiments shown in Fig. 7. M. J. F., K. E. D., and P. L. O. designed the experiments and wrote the paper. All authors reviewed the results and approved the final version of the manuscript.

**Acknowledgments**—We thank Alan Bradley and the International Knock-out Mouse Consortium for generation of the Oxr1 mutant mouse. We are also grateful to Ben Edwards and Arran Babbs for technical assistance and Chris Ponting for critical reading of the manuscript.

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