

The Antioxidant Enzyme Prdx1 Controls Neuronal Differentiation by Thiol-Redox-Dependent Activation of GDE2

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SUMMARY

The six-transmembrane protein GDE2 controls the onset and progression of spinal motor neuron differentiation through extracellular glycerophosphodiester phosphodiesterase metabolism. Although this process is likely to be tightly regulated, the relevant mechanisms that modulate its activity are unknown. Here we show that the antioxidant scavenger peroxiredoxin1 (Prdx1) interacts with GDE2, and that loss of Prdx1 causes motor neuron deficits analogous to GDE2 ablation. Prdx1 cooperates with GDE2 to drive motor neuron differentiation, and this synergy requires Prdx1 thiol-dependent catalysis. Prdx1 activates GDE2 through reduction of an intramolecular disulfide bond that bridges its intracellular N- and C-terminal domains. GDE2 variants incapable of disulfide bond formation acquire independence from Prdx1 and are potent inducers of motor neuron differentiation. These findings define Prdx1 as a pivotal regulator of GDE2 activity and suggest roles for coupled thiol-redox-dependent cascades in controlling neuronal differentiation in the spinal cord.

INTRODUCTION

The assembly of functional neural circuits depends upon the precisely controlled temporal and spatial differentiation of distinct neuronal subtypes (Jessell, 2000; Kintner, 2002). Deregulated differentiation can lead to severe deficits including the depletion of progenitor pools, imbalances in neuronal diversity and number, and at the other extreme, unchecked proliferation and tumor formation (Bertram, 2000; Kintner, 2002). Although the transcriptional pathways that control the transition between proliferation and differentiation are emerging, the regulatory mechanisms that control this switch are poorly understood (Jessell, 2000).

The differentiation of spinal motor neurons has proved to be a useful paradigm to understand the molecular mechanisms that control neuronal differentiation (Jessell, 2000). Retinoic

acid (RA) signals trigger the differentiation of motor neuron progenitors into postmitotic motor neurons in part by downregulating Olig2, which maintains cells in a motor neuron progenitor state (Mizuguchi et al., 2001; Novitsch et al., 2001, 2003; Lee et al., 2005). Decreased Olig2 expression causes a change in the equilibrium of Olig2 and the proneural protein Ngn2, causing the parallel implementation of neurogenic and motor neuron fate specification programs (Lee et al., 2005). These events correlate with changes in cell-body position along the medial-lateral axis of the spinal cord that accurately reflect the progress of motor neuron differentiation (Jessell, 2000; Hollyday, 2001). Thus, actively cycling Olig2⁺ motor neuron progenitors reside within the ventricular zone (VZ), but after completing their terminal mitosis at the medial margin of the VZ, Olig2⁺ progenitors undergo cell-cycle arrest and migrate laterally into the intermediate zone (IZ) (Figure S1 available online) (Hollyday, 2001). Subsequently, differentiating cells in the IZ downregulate progenitor markers, express postmitotic motor neuron markers such as Islet1 and HB9, and migrate laterally to occupy their final settling positions in the ventral horn (Figure S1) (Jessell, 2000; Hollyday, 2001).

The molecular pathways that link RA signaling pathways to the transcriptional programs that regulate the transition from proliferation to differentiation are beginning to emerge. RA signaling triggers motor neuron differentiation by upregulating GDE2, a six-transmembrane protein containing an extracellular glycerophosphodiester phosphodiesterase (GDPD) domain. GDE2 is necessary and sufficient to drive motor neuron differentiation by coordinately triggering neurogenic and motor neuron fate specification pathways (Nogusa et al., 2004; Rao and Sockanathan, 2005; Yanaka et al., 2007). Single point mutations that negate GDE2 GDPD function fail to induce motor neuron differentiation, revealing GDE2 as a signaling system that drives motor neuron differentiation through extracellular GDPD activity (Zheng et al., 2003; Santelli et al., 2004; Rao and Sockanathan, 2005). GDE2 belongs to a vertebrate-specific family of six-transmembrane GDPD-containing proteins that includes GDE3 and GDE6 (Nogusa et al., 2004; Yanaka et al., 2003; Yanaka, 2007). GDE3 is capable of driving osteoblast differentiation in vitro, suggesting that these proteins are a unique family of signaling molecules that critically regulate differentiation in diverse cellular contexts (Yanaka et al., 2003; Yanaka, 2007).

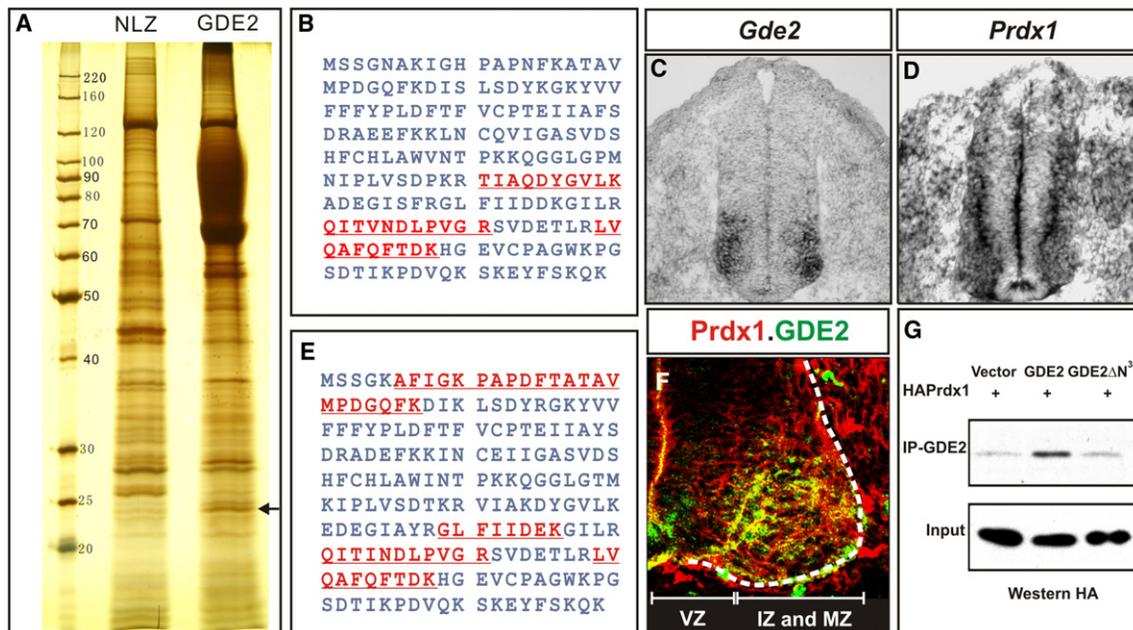


Figure 1. Prdx1 Interacts and Overlaps with GDE2 in the Ventral Spinal Cord

(A) Silver-stained SDS-PAGE gel shows a 23 kDa band (arrow) coimmunoprecipitates with GDE2. NLZ, control plasmid; GDE2, pCAGGS-GDE2NLZ.

(B and E) Tryptic peptides (red) from LC-MS/MS analyses of proteins derived from the 23 kDa band correspond to human (B) and chick Prdx1 (E).

(C, D, and F) In situ hybridization of *Gde2* and *Prdx1* mRNA, and immunohistochemical analyses on transverse sections of St 19–20 chick spinal cords. Prdx1 and GDE2 proteins colocalize in intermediate (IZ) and marginal zone (MZ) cells but not in ventricular zone progenitors (VZ).

(G) Coimmunoprecipitates of transfected HEK293T cells show HA-tagged Prdx1 interacts with the N terminus of GDE2.

Loss of GDE2 leads to deficits in motor neuron production, whereas premature exposure of progenitors to GDE2 GDPD signals precipitates differentiation and the depletion of progenitors (Rao and Sockanathan, 2005). Thus, the precise regulation of GDE2 activity is a critical prerequisite for the normal progression of spinal motor neuron differentiation. However, virtually nothing is known of the mechanisms that control GDE2 function, and how it integrates with cellular regulatory networks. In order to define the mechanisms that regulate GDE2 function, we carried out unbiased proteomic screens to isolate proteins that interact with GDE2. Here, we identify the antioxidant enzyme Prdx1 as an interactor of GDE2 and uncover a developmental role for Prdx1 in regulating neuronal differentiation in the spinal cord. Prdx1 is a 2-cysteine (Cys) thiol reductase that forms a component of cellular antioxidant and thermal stress defense mechanisms through its ability to metabolize H_2O_2 , and its properties as a molecular chaperone (Wood et al., 2003; Rhee et al., 2005; Jang et al., 2004). We show here that Prdx1 is expressed in differentiating progenitors in the developing spinal cord. Ablation of Prdx1 causes deficits in motor neuron differentiation but no changes in the specification or number of $Olig2^+$ progenitors, reminiscent of GDE2 loss of function phenotypes. Prdx1 binds and activates GDE2 by causing the reduction of an intramolecular disulfide bond between the N- and C-terminal domains of GDE2 that normally gates its function. Single point mutants of GDE2 that fail to form the intramolecular disulfide bridge are potent inducers of motor neuron differentiation, and gain independence from Prdx1 regulation. Our findings extend to the

control of spinal interneuron differentiation, implicating thiol redox pathways as key controllers of neuronal differentiation in the spinal cord.

RESULTS

The Antioxidant Enzyme Prdx1 Interacts with GDE2

To identify molecules that regulate GDE2 function, we carried out unbiased screens for GDE2-interacting proteins using large-scale immunoprecipitation of FLAG-tagged GDE2 containing complexes followed by Liquid Chromatography-Mass Spectrometry/Mass Spectrometry (LC-MS/MS). Extracts derived from embryonic chick spinal cords electroporated with plasmids expressing FLAG-GDE2 were analyzed to identify neural specific GDE2 interactors, and extracts prepared from FLAG-GDE2-transfected HEK293T cells were utilized to identify general interactors of GDE2. LC-MS/MS analyses of component proteins from GDE2 complexes immunoprecipitated from both sources identified Prdx1 as a GDE2-interacting protein (Figures 1A, 1B, and 1E). We confirmed the interaction between Prdx1 and GDE2 by coimmunoprecipitation, using extracts prepared from HEK293T cells transfected with epitope-tagged versions of Prdx1 and GDE2 (Figures 1G and S2). GDE2 mutants lacking the intracellular N-terminal domain (GDE2 ΔN^{38}) failed to interact with Prdx1, indicating that Prdx1 associates with the N-terminal 38 amino acids of GDE2 (Figure 1G). Analyses of Prdx1 mRNA and protein on sections of chick embryonic spinal cord spanning the peak period of motor neuron differentiation show that

Prdx1 is expressed in progenitor cells located in the VZ prior to the onset of GDE2 expression, but overlaps with GDE2 in IZ cells and postmitotic motor neurons in the MZ (Figures 1C, 1D, and 1F).

Prdx1 Is Required for Motor Neuron Differentiation

The coincident expression of *Prdx1* and GDE2 and their ability to associate raise the possibility that *Prdx1*/GDE2 complexes function to control motor neuron differentiation. To determine the consequences of loss of *Prdx1* on spinal motor neuron differentiation, we ablated *Prdx1* expression in vivo. Twenty-one base pair double-stranded RNA oligonucleotides designed against the *Prdx1* coding sequence were electroporated into developing chick spinal cords at Hamburger Hamilton stage (St) 11, prior to the initiation of motor neuron differentiation (Rao et al., 2004). Embryos electroporated with *Prdx1* siRNA showed complete ablation of *Prdx1* mRNA expression and a dramatic reduction in *Prdx1* protein (Figures 2A and 2B).

Immunohistochemical analyses of motor neuron progenitor and postmitotic markers on serial sections of embryos electroporated with *Prdx1* siRNA show that *Prdx1* silencing caused the loss of approximately 50% of *Islet1*⁺ (or *Isl1*⁺), *HB9*⁺, and *Islet2*⁺ (or *Isl2*⁺) motor neurons but did not alter the number of *Olig2*⁺ motor neuron progenitors or the dorsal-ventral patterning of spinal progenitors (Figures 2C–2G and S3). No increase in TUNEL staining was detected, suggesting that the loss of *Prdx1* did not compromise motor neuron survival (Figure S4). This is in contrast with siRNA ablation of *Gde2* and might reflect additional functions for GDE2 in postmitotic motor neurons (Rao and Sockanathan, 2005). The siRNA-dependent silencing of *Prdx1* is specific, as *Prdx1* knockdown could be titrated with differing amounts of *Prdx1* siRNA; unrelated siRNAs did not trigger *Prdx1* silencing; *Prdx1* siRNA did not induce global changes in gene expression; and coelectroporation of constructs expressing human *Prdx1*, which is insensitive to the siRNA, rescued the motor neuron phenotype (Figures S3 and S5). Thus, *Prdx1* is required for the formation of postmitotic motor neurons but not for earlier events in motor neuron progenitor specification, similar to the function of GDE2 (Rao and Sockanathan, 2005).

Aged *Prdx1*-null mice develop hemolytic anemia and acquire multiple malignancies, indicative of a tumor suppressor function for *Prdx1* (Neumann et al., 2003; Egler et al., 2005). To determine whether *Prdx1*^{-/-} animals exhibit deficits in spinal motor neuron development, we analyzed *Prdx1*^{-/-} embryos at E9.5 during the peak period of motor neuron differentiation. *Prdx1*^{-/-} animals do not express *Prdx1* transcripts, consistent with previous studies demonstrating the absence of *Prdx1* protein in these mutants (Figures 3A and 3E) (Neumann et al., 2003; Egler et al., 2005). *Prdx1*^{-/-} mutants revealed similar phenotypes to chick embryos electroporated with *Prdx1* siRNAs. *Prdx1*^{-/-} embryos lost approximately 50% of *Islet1*/*Islet2*⁺ and *HB9*⁺ motor neurons compared with wild-type (WT) littermates, whereas dorsal-ventral patterning events and the numbers of *Olig2*⁺ progenitors were normal (Figures 3B–3D, 3F, 3G, and S3). Toward the end of the cell death phase at E16.5, *Prdx1*-null, and WT embryos had equivalent numbers of motor neurons (data not shown). The incomplete ablation of

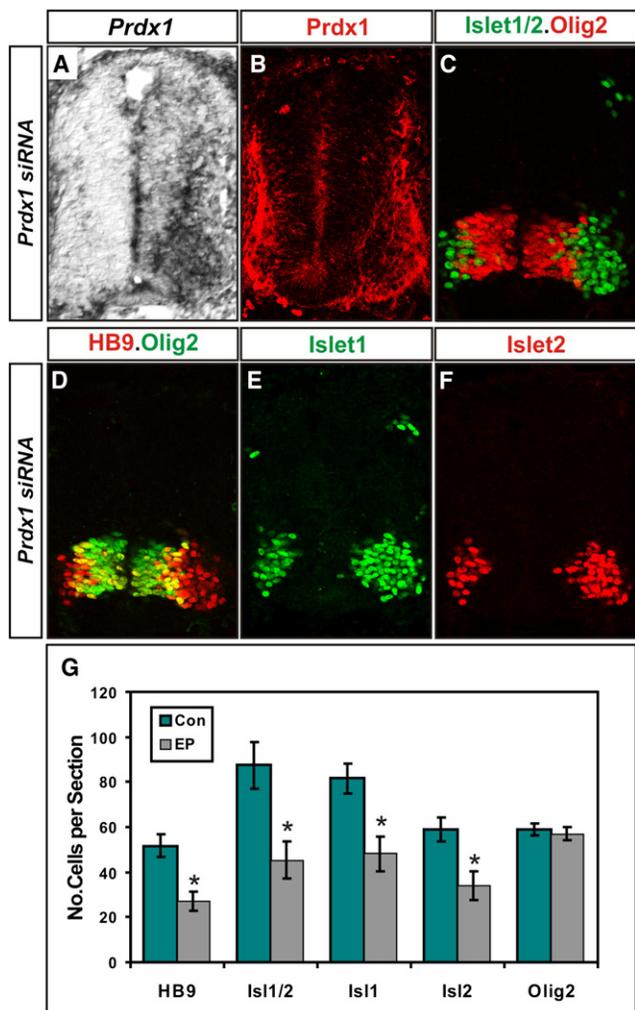


Figure 2. *Prdx1* Is Required for Motor Neuron Generation

(A–F) In situ hybridization (A) and immunohistochemical analyses (B–F) of transverse sections of St 20–21 chick spinal cords electroporated with *Prdx1* siRNAs (left). *HB9*⁺ motor neurons are visualized in red in (D). (G) Graph shows reduction of postmitotic motor neurons on *Prdx1* silencing. Con, nonelectroporated side; EP, electroporated side (mean ± standard error of the mean [SEM]); **HB9*, *p* = 0.000004; *Islet1/2*, *p* = 0.00001; *Isl1*, *p* = 0.00009; *Isl2*, *p* = 0.00008; *Olig2*, *p* = 0.2; paired Student's *t* test, *n* = 6.

motor neurons in *Prdx1*^{-/-} embryos might be a consequence of redundant functions of other *Prdx* proteins that regulate cellular differentiation such as *Prdx2*, which is expressed in the ventral mouse spinal cord and is capable of binding GDE2 or alternatively, redundancy with other known signaling pathways that regulate differentiation in the spinal cord (Figure S6) (Choi et al., 2005).

TUNEL analysis showed no difference in cell death between *Prdx1*^{-/-} and WT embryos, suggesting that *Prdx1* regulates the differentiation of motor neurons rather than their survival (Figure S4). To explore this possibility in more detail, we compared the frequency of cell-cycle exit between *Prdx1*^{-/-} and WT embryos at the peak period of motor neuron

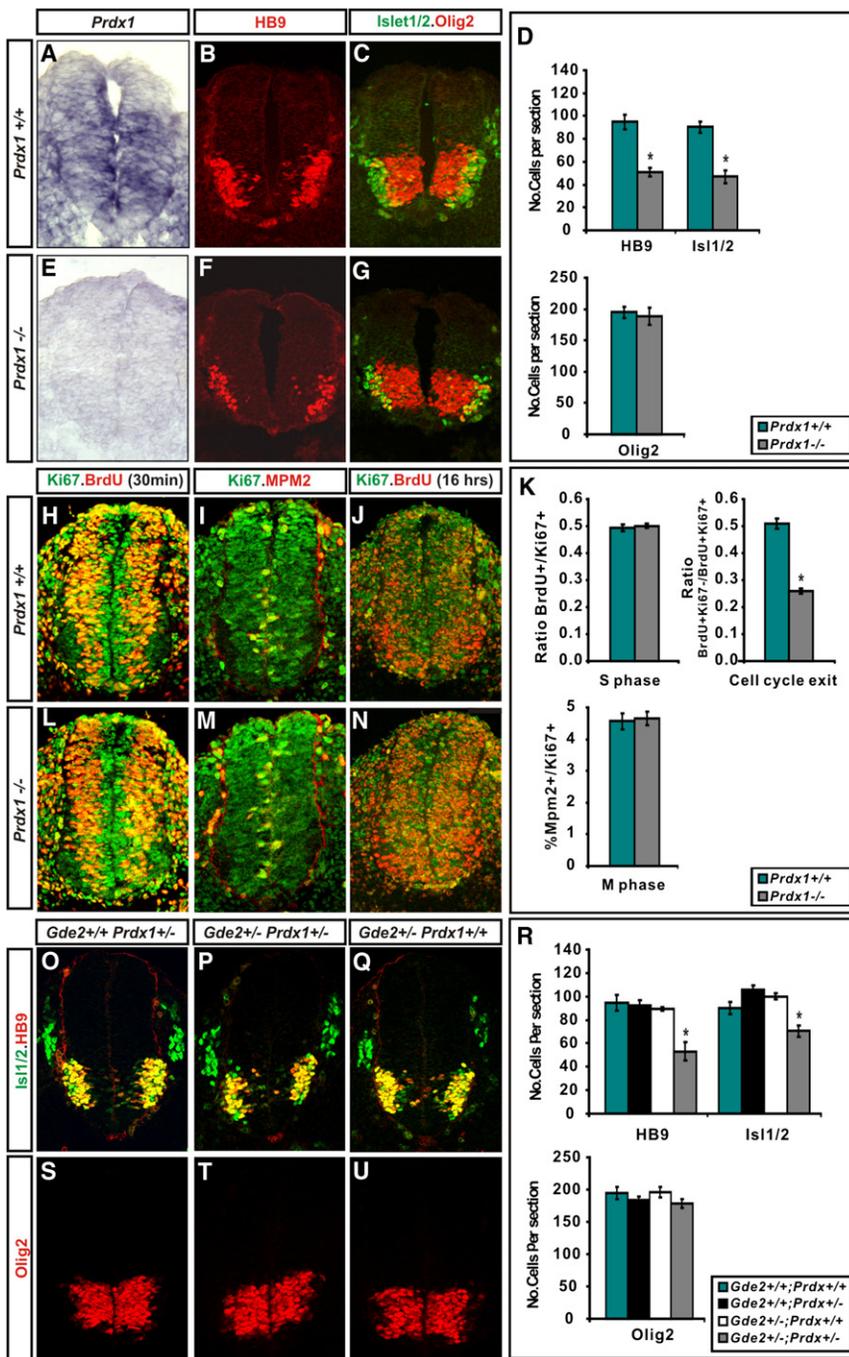


Figure 3. Prdx1^{-/-} Embryos Show Deficits in Motor Neuron Generation

(A–N) In situ hybridization (A and E) and immunohistochemical analyses (B, C, F, G, H–J, and L–N) of transverse sections of mouse E9.5 Prdx1^{+/+} and Prdx1-null spinal cords. In (D), graphs show motor neuron loss in Prdx1 nulls (mean ± SEM). *HB9, p = 0.00054, *Isl1/2, p = 0.0004; Olig2, p = 0.69; two-tailed Student's t test, n = 5. In (K), graphs show deficits in cell-cycle exit in Prdx1 nulls (mean ± SEM). *Cell-cycle exit, p = 0.0002; S phase, p = 0.63; M phase, p = 0.8; two-tailed Student's t test, n = 5. (O–Q and S–U) Immunohistochemical analyses of transverse sections of mouse E9.5 spinal cords. (R) Graphs show motor neuron loss in double heterozygotes for Prdx1 and Gde2 (mean ± SEM). Two-way analysis of variance shows significant interaction between GDE2 and Prdx1; *HB9, p = 0.00783; *Isl1/2, p = 6.54 × 10⁻⁵; Olig2, p = 0.72; n = 5.

peak period of neurogenesis, but not for motor neuron progenitor specification or proliferation.

Prdx1 Synergizes with GDE2 to Drive Spinal Neuron Differentiation

The similarity between the loss of function phenotypes between Prdx1 and GDE2 suggests that they operate within the same pathway to regulate motor neuron differentiation. To test this possibility, we carried out gene dosage experiments by generating mice heterozygous for Gde2 and Prdx1. At the peak of spinal motor neuron differentiation, WT, Prdx1^{+/-} and Gde2^{+/-} animals contain comparable numbers of Olig2⁺ motor neuron progenitors and HB9⁺ and Isl1/2⁺ motor neurons (Figures 3O–3U). In contrast, double-heterozygous Prdx1^{+/-}; Gde2^{+/-} embryos exhibit an approximately 40% and 30% reduction in HB9⁺ and Isl1/2⁺ motor neurons, respectively, while retaining equivalent numbers of Olig2⁺ motor neuron progenitors to controls (Figures 3P, 3T, and 3R). This observation provides strong genetic evidence that

differentiation. We injected pregnant dams with BrdU to label cells in S phase, harvested embryos 16 hr later, and calculated the cell-cycle exit index by analyzing the ratio of nonproliferating to proliferating BrdU⁺ cells in the ventral spinal cord. At E9.5, there was a marked reduction in the cell-cycle exit index of Prdx1^{-/-} embryos compared with WT littermates, but no differences in independent studies of cell-cycle progression at S and M phase (Figures 3H–3N). Thus, Prdx1 is required for the differentiation of postmitotic motor neurons during the

Prdx1 and GDE2 function within the same pathway to control motor neuron differentiation.

To investigate the synergy between Prdx1 and GDE2 in promoting motor neuron differentiation, we performed in vivo gain of function assays using in ovo electroporation of embryonic chick spinal cords. We engineered expression constructs placing an HA-tagged version of Prdx1 under the control of the chick β-actin promoter (pCAGGS-Prdx1) and bicistronic constructs expressing GDE2 (pCAGGS-GDE2IRESnLacZ). As

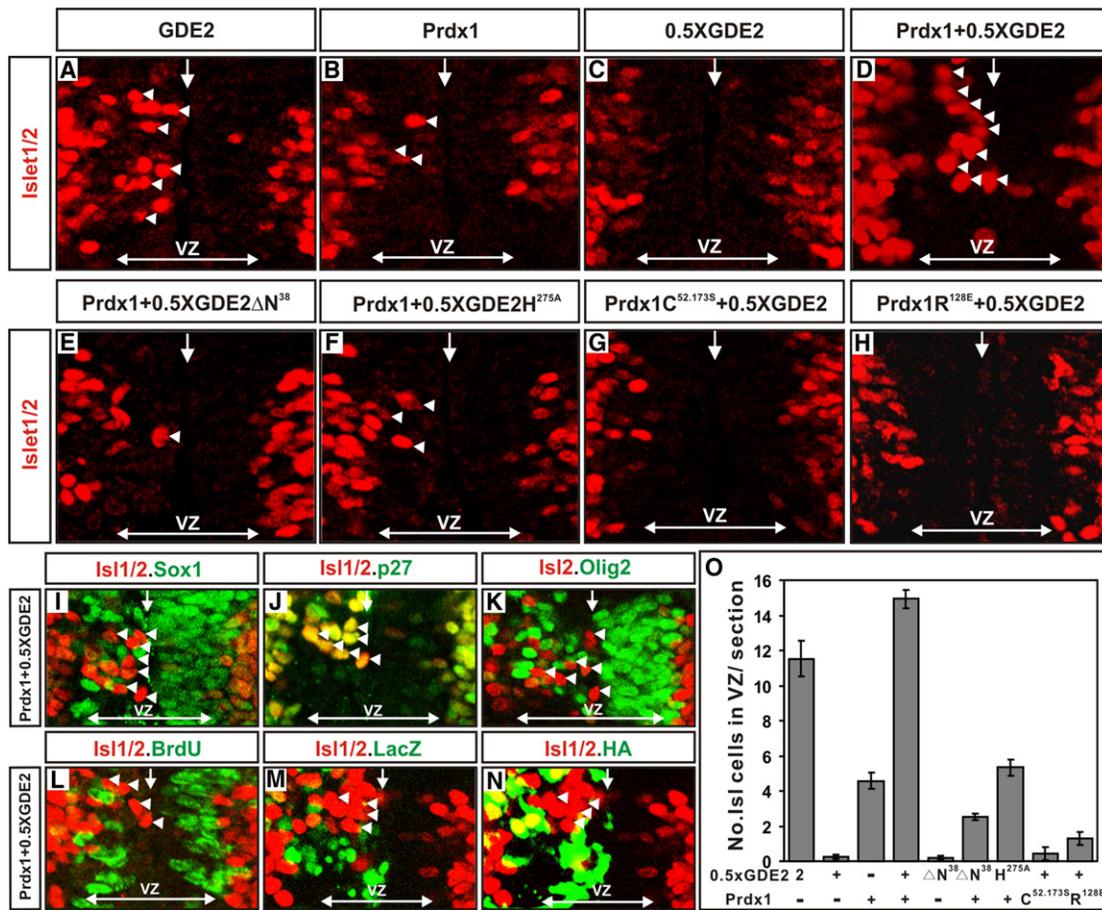


Figure 4. Prdx1/GDE2 Complexes Drive Motor Neuron Differentiation In Vivo

(A–N) Immunohistochemical analyses of transverse sections of ventral St 19–20 chick spinal cords electroporated (left) with GDE2 and Prdx1. Arrowheads mark terminally differentiated neurons in the ventricular zone (VZ). The VZ was defined by BrdU pulse labeling to mark S-phase cells at lateral margins. Midline: vertical arrow, VZ: horizontal arrow. (M) and (N) show the same section stained with HA and LacZ to detect Prdx1 and GDE2, respectively.

(O) Graph quantifying ectopic motor neurons in the VZ of electroporated embryos (mean ± SEM; n = 5–10). Prdx1 overexpression weakly induces ectopic motor neurons, presumably through interactions with GDE2-related proteins in VZ cells such as GDE6 (S.S., unpublished data).

described previously, overexpression of GDE2 in cycling progenitors caused many cells to differentiate into postmitotic motor neurons prematurely; in contrast, overexpression of Prdx1 induced very few Islet1/2⁺ motor neurons (Figures 4A, 4B, and 4O) (Rao and Sockanathan, 2005). To determine whether Prdx1 and GDE2 cooperate to induce motor neuron differentiation, we coexpressed Prdx1 and a suboptimal amount of GDE2 in the spinal cord that normally does not give rise to motor neurons (0.5 X GDE2; Figures 4C and 4O). Coelectroporation of Prdx1 and GDE2 generated many ectopic Islet1/2⁺ motor neurons in the VZ in numbers that exceeded that of Islet1/2⁺ cells induced when optimal amounts of GDE2 alone are electroporated (Figures 4A, 4D, and 4O). The ectopic Islet1/2⁺ motor neurons bore the hallmarks of motor neurons generated by GDE2 activity: they had downregulated progenitor markers such as Sox1 and Olig2, they had exited the cell cycle as assessed by the lack of BrdU incorporation, and they expressed the postmitotic marker p27 and the motor neuron markers Islet2 and HB9 (Figures 4I–4L and data not shown) (Rao and Sockana-

than, 2005). Furthermore, 30% of the ectopic motor neurons did not express Prdx1 or GDE2, consistent with the ability of GDE2 to promote non-cell-autonomous motor neuron differentiation (Figures 4M and 4N) (Rao and Sockanathan, 2005). Thus, Prdx1 synergizes with GDE2 to promote motor neuron differentiation in vivo. Prdx2 can similarly cooperate with GDE2 to drive motor neuron differentiation, consistent with redundant functions for 2-Cys Prdx proteins in controlling GDE2-dependent motor neuron differentiation (Figure S6).

Strikingly, coexpression of Prdx1 and GDE2 in the dorsal spinal cord led to a similar induction of p27 and concomitant downregulation of Sox1 in VZ progenitors (Figures 5A–5D). Further, these medially located postmitotic cells expressed appropriate postmitotic interneuron markers specific to their dorsal-ventral position, suggesting that Prdx1 and GDE2 cooperate to promote the differentiation of diverse interneuron subtypes (Figures 5E–5I). This observation is consistent with the dorsal expression of Prdx1 in IZ cells, and the dorsal expansion of GDE2 expression, which coincides with the temporal

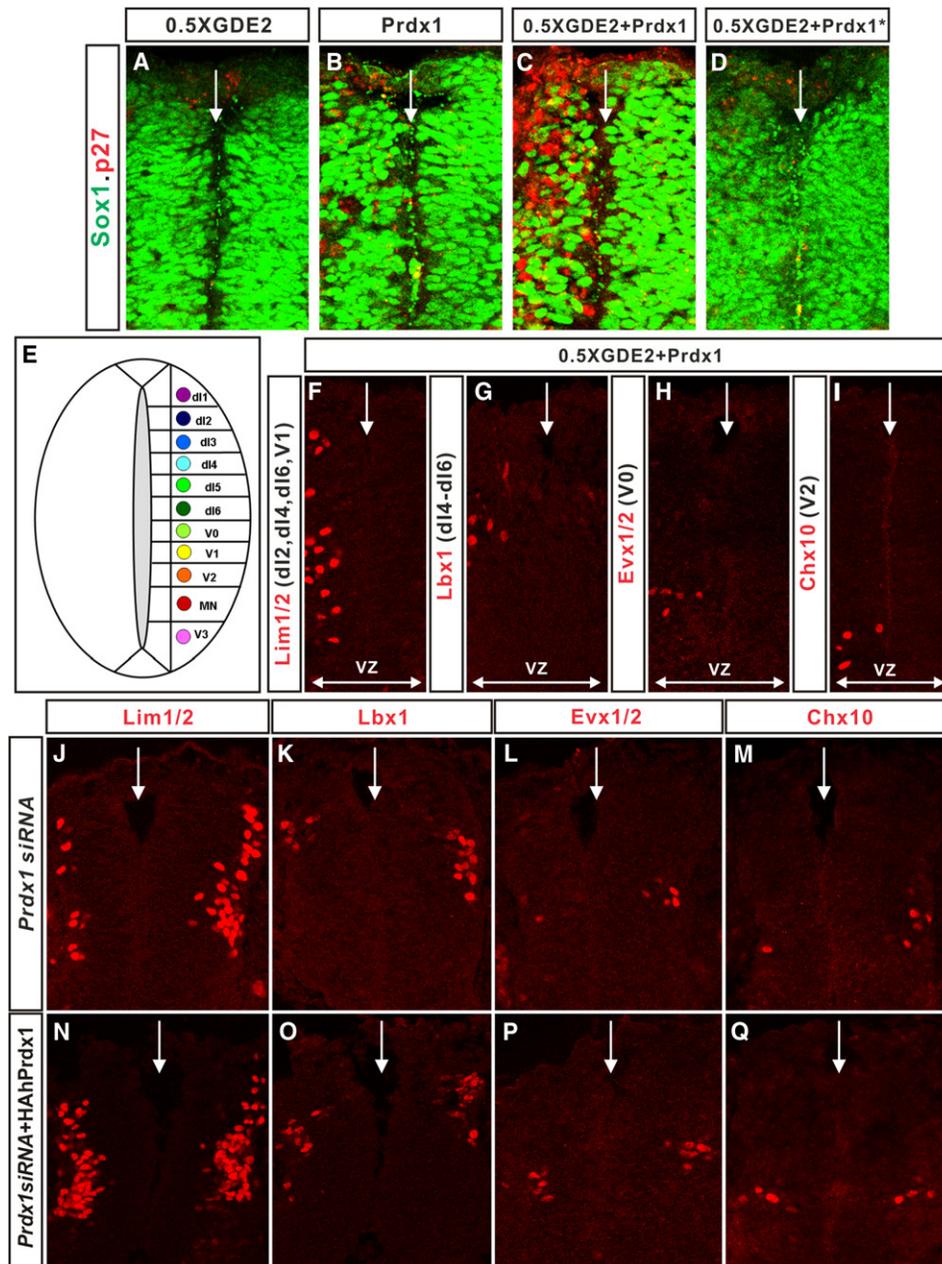


Figure 5. GDE2 and Prdx1 Regulate Spinal Interneuron Differentiation

(A–D and F–Q) Immunohistochemical analysis of transverse sections of St 20–21 dorsal chick spinal cords, electroporated on the left. Arrows mark the midline. VZ, ventricular zone; double-headed arrows, VZ extent; Prdx1*, Prdx1C^{52.173.S}.

(E) Schematic of the spinal cord showing the location of dorsal (dl1–6) and ventral (V0–V3) interneurons in relation to motor neurons (MN).

(F–I) Prdx1 and GDE2 overexpression induces multiple interneuron subtypes in spinal progenitors (defined by their molecular gene expression profiles; Helms and Johnson, 2003) within their respective dorsal-ventral domains.

(J–M) Ablation of *Prdx1* by electroporation of siRNA reduces the number of dorsal and ventral spinal interneurons.

(N–Q) Spinal interneuron populations are rescued by electroporation of human Prdx1, which is insensitive to the electroporated *Prdx1* siRNA.

profile of spinal neurogenesis. In support of this model, ablation of *Prdx1* expression by siRNA caused a loss of dl2–d6 dorsal interneurons and ventral interneuron subclasses, suggesting general roles for GDE2 and Prdx1 in controlling neuronal differentiation in the spinal cord (Figures 5J–5Q).

Prdx1/GDE2 Properties Necessary for Motor Neuron Induction

We utilized the synergistic gain of function assay to define the basis of the cooperativity between GDE2 and Prdx1. To determine whether physical interaction between GDE2 and Prdx1 is

required for premature motor neuron induction, we coelectroporated expression constructs for Prdx1 and GDE2 Δ N³⁸ into chick spinal cords. GDE2 Δ N³⁸ lacks the Prdx1 interaction domain and is expressed and transported to the membrane at similar levels as GDE2 (Figures 1 and S7). Coexpression of GDE2 Δ N³⁸ and Prdx1 failed to induce ectopic Islet1/2⁺ motor neurons in the VZ, suggesting that Prdx1 functions in a complex with GDE2 to regulate motor neuron differentiation (Figures 4E and 4O). Both GDE2 and Prdx1 contain catalytic domains that are essential for their functions. Mutation of a histidine residue to alanine within the GDE2 GDPD domain severely impairs its ability to drive motor neuron differentiation (GDE2H^{275A}), whereas mutation of the reactive Cys (Prdx1C^{52.173S}) or an arginine residue located near the Prdx1 active site (Prdx1R^{128E}) abolishes Prdx1 catalytic activity (Jang et al., 2004; Zheng et al., 2003; Rao and Sockanathan, 2005; Montemartini et al., 1999; Flohe et al., 2002). Coimmunoprecipitation assays show that GDE2H^{275A}, Prdx1C^{52.173S}, and Prdx1R^{128E} retain their ability to form complexes with WT Prdx1 and GDE2, respectively (Figure S8). GDE2H^{275A} did not synergize with Prdx1 to promote premature motor neuron differentiation, whereas coexpression of Prdx1C^{52.173S} or Prdx1R^{128E} with GDE2 in chick spinal cords did not induce ectopic Islet1/2⁺ motor neurons in the VZ (Figures 4F–4H and 4O). These observations confirm that GDE2 GDPD activity is required for GDE2/Prdx1 complexes to promote motor neuron differentiation. Moreover, they reveal that Prdx1 catalytic activity is required for the ability of GDE2 to regulate motor neuron differentiation, and further argue against a molecular chaperone function for Prdx1 in this context, because Prdx1C^{52.173S} mutants retain effective chaperone activity in the absence of elevated H₂O₂ (Jang et al., 2004).

Prdx1 Reduces an Intramolecular Disulfide Bond within GDE2

How does Prdx1 catalytic activity regulate GDE2 function? The yeast Gpx3 and TSA peroxiredoxins can induce disulfide bond formation in the redox-response transcription factor Yap1 under conditions of oxidative stress, whereas the bacterial peroxiredoxin AhpC has *in vitro* disulfide reductase activity (Delaunay et al., 2002; Ritz et al., 2001). To evaluate whether Prdx1 is capable of modifying GDE2 disulfide bond formation, we compared the presence of free thiol groups in GDE2 in the absence or presence of Prdx1 using 4-acetamido-4'-maleimidylstilbene-2,2'-disulfonic acid (AMS), a thiol-conjugating reagent that decreases the electrophoretic mobility of bound proteins by 0.5 kDa/free thiol (Sevier et al., 2007). Western blot analyses of deglycosylated surface biotinylated GDE2 in HEK293T cells showed a decrease in GDE2 mobility in the presence of AMS, indicating that GDE2 at the cell surface normally contains free thiols (Figure 6A). When Prdx1 is coexpressed with GDE2, there was a small but reproducible shift in the mobility of GDE2 by AMS modification consistent with an increase of free thiol groups (Figure 6A). The Prdx1-dependent decrease in GDE2 mobility requires Prdx1 redox activity because the catalytically inactive Prdx1C^{52.173S} mutant fails to alter GDE2 migration (Figure 6A).

GDE2 contains three closely spaced Cys residues within its intracellular N-terminal region (C15, C18, C25) and one Cys within its C-terminal domain (C576) (Figure 6B). To identify

the Cys residues reduced by Prdx1, we mutated the C15 and C18 residues (GDE2C^{15.18S}), and the C25 and C576 residues (GDE2C^{25.576S}) of GDE2 to serine. Both GDE2C^{15.18S} and GDE2C^{25.576S} retained the ability to bind Prdx1 and are expressed at the membrane at equivalent levels (Figures S7 and S9). Coexpression of Prdx1 and GDE2C^{15.18S} in HEK293T cells caused a shift in GDE2 mobility by AMS modification, similar to that observed when Prdx1 and WT GDE2 are cotransfected (Figure 6A). Because C25 and C576 are the only intracellular thiol groups available in GDE2C^{15.18S}, this result suggests that Prdx1 causes the reduction of a disulfide bond normally formed between the C25 and C576 residues of GDE2. Consistent with this observation, Prdx1 did not alter the mobility of GDE2C^{25.576S} modified by AMS (Figure 6A).

To investigate the effect of Prdx1 on GDE2 further, we utilized biochemical assays adapted to detect the presence of disulfide bonds in GDE2 in transfected HEK293T cells (Leichert and Jakob, 2004). Free thiol groups in GDE2 were blocked by N-ethylmaleimide (NEM) prior to the stepwise addition of Tris (2-carboxyethyl) phosphine (TCEP) and N-(6-(biotinamido)hexyl)-3'-(2'-pyridyl)di-thio)propionamide (biotin-HPDP), which respectively causes the reduction of disulfide bonds and the modification of resultant free thiols by biotin. Western blotting of immunoprecipitated GDE2 shows that in the absence of TCEP, GDE2 was not labeled by biotin, demonstrating effective blockade of free thiols in GDE2 (Figure 6C). Addition of TCEP resulted in biotinylated GDE2, consistent with the reduction and labeling of endogenous disulfide bonds in GDE2 (Figure 6C, GFP). However, coexpression of Prdx1 with GDE2, but not the redox-inactive Prdx1C^{52.173S} mutant, decreased the amount of biotinylated GDE2, suggesting that Prdx1 catalytic activity causes reduction of disulfide bonds within GDE2 (Figure 6C). Analysis of GDE2 Cys mutants showed that although a similar reduction of biotinylated GDE2C^{15.18S} was observed in the presence of Prdx1, no changes in biotin labeling of GDE2C^{25.576S} were detected (Figure 6C), consistent with our AMS data and the model that Prdx1 can cause reduction of the C25-C576 disulfide bond in GDE2.

The C25-C576 disulfide bridge is unusual given the reducing environment of the cell; thus, we utilized LC-MS/MS to confirm that C25 and C576 participate in disulfide bond formation in transfected HEK293T cells. Free thiol groups were blocked by NEM prior to reduction by DTT and subsequent thiol modification by iodoacetamide (IAM). LC-MS/MS analysis revealed that C576 was labeled by NEM and IAM, suggesting that C576 participates in disulfide bond formation and that this disulfide bond is dynamic (Figure 6E and S10). To examine if Prdx1 leads to the reduction of GDE2 disulfide bonds utilizing C576, we compared the relative signal intensities of GDE2 peptides containing C576 NEM and C576 IAM by LC-MS/MS in the absence and presence of Prdx1. In the absence of Prdx1, the relative intensities of both peptides were approximately similar. GDE2 and Prdx1 coexpression led to a 5- to 6-fold increase of C576 NEM labeling compared with C576 IAM, suggesting that Prdx1 shifts the equilibrium of C576 to a reduced state (Figure 6E). In addition, LC-MS/MS analysis showed that C25 can be labeled by IAM (data not shown). These collective observations are consistent with our AMS and biotin labeling experiments, and support the model that Prdx1 catalytic activity causes reduction

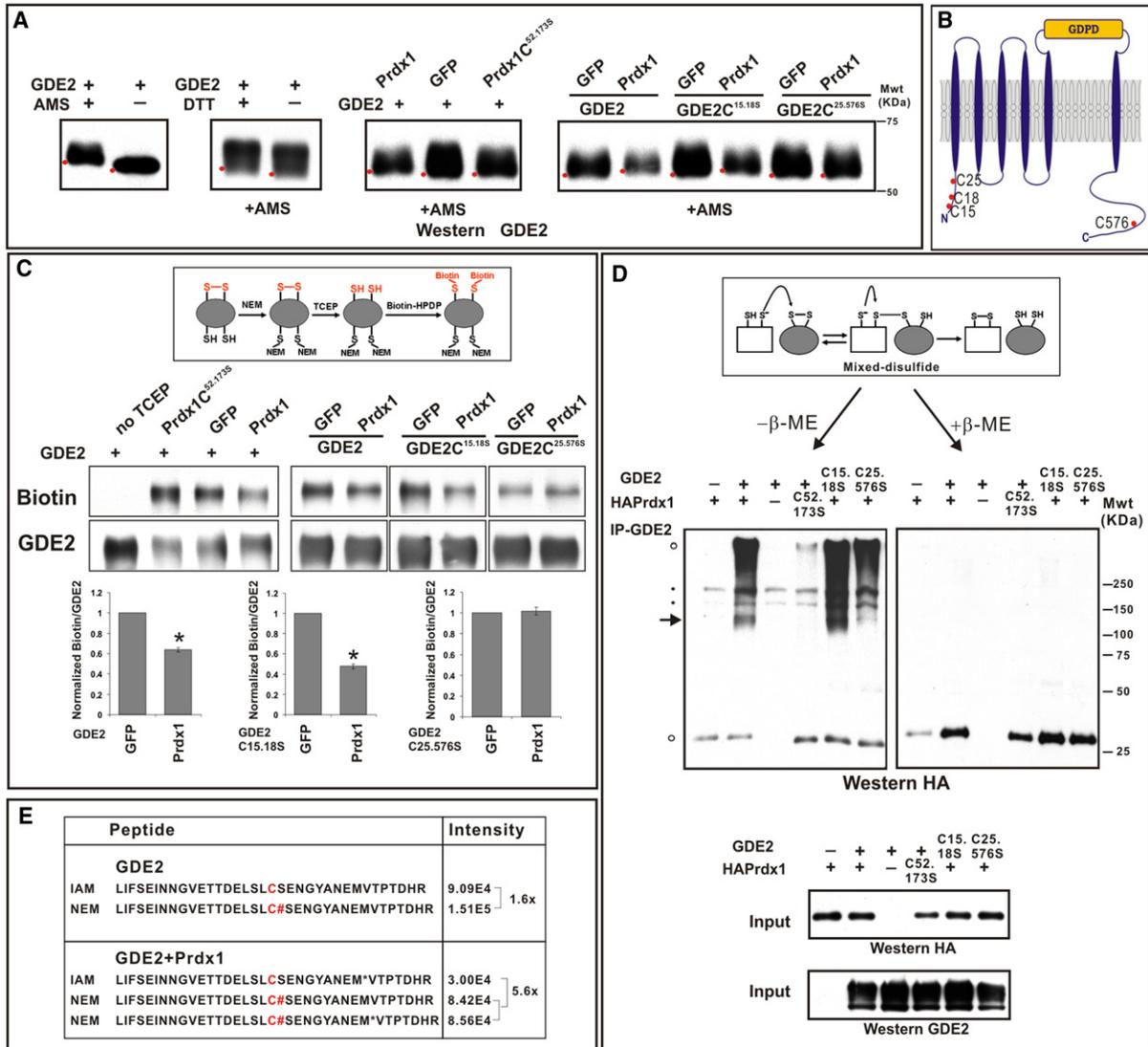


Figure 6. Prdx1 Reduces an Intracellular Disulfide Bridge in GDE2

(A) Western blots of AMS-modified surface biotinylated GDE2 in transfected HEK293T cells. Red dots mark horizontal position of the bands. Similar results were obtained with total protein. Addition of DTT caused further shifts in GDE2 mobility consistent with the presence of additional disulfide bonds in GDE2. MS analysis reveals that C15 and C18 can form a disulfide bond that is insensitive to Prdx1 activity (data not shown).

(B) Schematic of intracellular cysteines in GDE2. Other cysteines are not marked.

(C) Western blots of immunoprecipitated GDE2 detecting biotinylated GDE2 compared with GDE2. Graphs quantify the amount of biotinylated GDE2 normalized to total GDE2, mean \pm SEM, GDE2 + GFP values are normalized to 1, GDE2 + Prdx1 * $p = 6.4 \times 10^{-18}$, GDE2C^{15,18S} + Prdx1 * $p = 2.05 \times 10^{-13}$, GDE2C^{25,576S} + Prdx1 $p = 0.27$; $n = 7$ assays; one sample Student's t test.

(D) Nonreducing gels of GDE2 coimmunoprecipitates from transfected HEK293T cells with or without β -mercaptoethanol (β -ME). Arrow represents 120–130 kDa mixed-disulfide Prdx1/glycosylated GDE2 intermediate. Black circles represent nonspecific bands; open circles, higher order Prdx1-containing oligomers, Prdx1 monomers. The band comigrating with the Prdx1 monomer in lane 1 is not specific and forms a minor component when Prdx1 complexes interacting with GDE2 are reduced by β -ME.

(E) Relative signal intensities of GDE2 C-terminal peptides containing C576 labeled with IAM (C; oxidized thiol) or NEM (C#; free thiol) in the absence or presence of Prdx1. Ratio = NEM/IAM.

of an intramolecular disulfide bond formed between C25 and C576 of GDE2.

Prdx1 and GDE2 Form a Disulfide Intermediate

If Prdx1 directly reduces a disulfide bond formed between C25 and C576 in GDE2, then GDE2 and Prdx1 should form a transient

mixed-disulfide intermediate during the transfer reaction (Sevier and Kaiser, 2002). To address this question, we coimmunoprecipitated GDE2 containing complexes from extracts prepared from HEK293T cells transfected with Prdx1 and GDE2. Analysis of Prdx1 redox state in transfected extracts shows that Prdx1 exists in reduced and oxidized forms (Figure S8). Western blots

show that forms of Prdx1 associated with GDE2 include reduced monomers, high-molecular-weight complexes and a band of approximately 120–130 kDa that corresponds to the predicted molecular weight of a GDE2/Prdx1 complex (open circles, arrow, Figure 6D). Addition of β -mercaptoethanol abolished formation of the 120–130 kDa complex, suggesting that its assembly utilizes disulfide bonds (Figure 6D). Coexpression of GDE2 and Prdx1^{C52.173S}, or GDE2^{C25.576S} and Prdx1, failed to form the 120–130 kDa complex, though Prdx1^{C52.173S} and GDE2^{C25.576S} retain their abilities to bind GDE2 and Prdx1, respectively (Figures 6D, S8, and S9). In contrast, GDE2^{C15.18S}, which preserves the capacity to form an intracellular disulfide bond between C25 and C576, can form the 120–130 kDa complex (Figure 6D). These observations suggest that the 120–130 kDa complex is a mixed-disulfide Prdx1-GDE2 intermediate, and that the cysteines responsible for Prdx1 redox activity, and the C25 or C576 residue in GDE2, participate in its formation.

GDE2^{C25.576S} Is a Potent Inducer of Differentiation that Is Independent of Prdx1

Our developmental and biochemical studies are consistent with the model that Prdx1 directly activates GDE2 by reducing an intracellular C25-C576 disulfide bond that bridges the N- and C-terminal domains of GDE2. If so, then GDE2^{C25.576S}, which cannot form the disulfide bridge, should be more effective than GDE2 in promoting motor neuron differentiation. In addition, GDE2^{C25.576S} should no longer cooperate with Prdx1 to induce ectopic motor neurons in the VZ. To evaluate the activity of GDE2^{C25.576S}, we compared the ability of GDE2^{C25.576S} and GDE2 to induce ectopic Islet2⁺ motor neurons in the VZ of embryonic chick spinal cords, using suboptimal amounts of GDE2 that normally fail to elicit premature motor neuron differentiation (Figures 4C, 4O, 7A, 7C, 7G, and 7H). In contrast to GDE2, electroporation of suboptimal amounts of pCAGGS-GDE2^{C25.576S} effectively induced the differentiation of Islet2⁺ motor neurons in VZ progenitors (Figure 7C). Variants of GDE2 that contained a single point mutation converting the C25 or C576 residue to serine (GDE2^{C25S}, GDE2^{C576S}) were similarly effective (Figures 7D, 7E, 7G, and 7H). However, expression of GDE2^{C15.18S}, which retains the ability to form the C25-C576 disulfide bridge, showed similar activity as GDE2 in promoting motor neuron differentiation under these conditions (Figure 7B, 7G, and 7H). Surface biotinylation and expression studies in transfected HEK293T cells showed that GDE2, GDE2^{C25.576S}, GDE2^{C25S}, GDE2^{C576S}, and GDE2^{C15.18S} are expressed at similar levels on the cell membrane (Figure S7). These findings extend to the differentiation of dorsal and ventral spinal interneurons, and thus collectively imply that reduction of the C25-C576 disulfide bond between the N- and C-terminal domains of GDE2 increases the efficacy of GDE2 to promote neuronal differentiation, suggesting that the C25-C576 bridge normally gates GDE2 function (Figures 7I–7P).

To test whether GDE2 mutants that fail to form the C25-C576 bridge cooperate with Prdx1 to promote motor neuron differentiation, we electroporated suboptimal amounts of pCAGGS-GDE2^{C25S} into embryonic chick spinal cords, and compared the ability of GDE2^{C25S} to induce ectopic motor neurons in the absence or presence of Prdx1. GDE2^{C25S} is capable of binding

Prdx1 and effectively induced Islet2⁺ motor neurons in the VZ (Figures 7E, 7G, 7H, and S9). However, Prdx1 failed to potentiate the ability of GDE2^{C25S} to induce ectopic motor neurons, suggesting that GDE2^{C25S} does not require Prdx1 activity to drive motor neuron differentiation (Figures 7F, 7G, and 7H). This finding suggests that the major function of Prdx1 in the context of the Prdx1/GDE2 complex is to reduce the C25-C576 disulfide bridge that normally gates the ability of GDE2 to drive motor neuron differentiation.

DISCUSSION

The antioxidant scavenger Prdx1 plays critical roles in the defense of oxidative and thermal stress by its diverse abilities to respectively metabolize H₂O₂ and act as a molecular chaperone (Wood et al., 2003; Rhee et al., 2005; Jang et al., 2004). Using spinal motor neuron differentiation as a model system, we have uncovered a previously uncharacterized developmental role for Prdx1 in controlling neuronal differentiation. Our study suggests a model where the overlap of Prdx1 and GDE2 expression in cells neighboring VZ progenitors permits the association of Prdx1 with GDE2 (Figure 7Q). GDE2 is normally inactive due to the presence of an intramolecular disulfide bond that links its intracellular N- and C-terminal domains. However, once complexed with GDE2, Prdx1 catalytic activity leads to reduction of the GDE2 C25-C576 disulfide bond and activation of GDE2, triggering motor neuron differentiation through extracellular GDE2 GDPD metabolism (Figure 7Q). These findings uncover critical roles for thiol-redox-dependent mechanisms in activating GDE2 signaling, and identify peroxiredoxins as pivotal regulators of neuronal differentiation in the spinal cord.

Several lines of evidence suggest the intriguing possibility that the requirement for Prdx1 in motor neuron differentiation stems from a previously uncharacterized enzymatic function that is distinct from its molecular chaperone or H₂O₂ metabolic activities. First, Prdx1 mutants that retain effective molecular chaperone activity but are catalytically inactive do not synergize with GDE2 to drive premature motor neuron differentiation in VZ progenitors. Second, loss of Prdx1 causes a deficit of postmitotic motor neurons in the absence of cell death. This observation is consistent with a role for Prdx1 in regulating motor neuron differentiation, and argues against the possibility that motor neuron survival is compromised through increased ROS levels stemming from loss of Prdx1 scavenger function. Third, our data suggest that Prdx1 activates GDE2 through thiol reductase mechanisms that might not utilize H₂O₂ as a substrate, because thiol modifications that utilize H₂O₂ metabolism are consistent with oxidation rather than reduction. Although our data do not rule out the formal possibility that Cys25 and Cys576 form sulfenic acids rather than a disulfide bond, this appears unlikely because sulfenic acids are considered very unstable and do not form when in close proximity to other Cys residues (Paget and Buttner, 2003). Our study thus poses a potential role for Prdx1 in directly regulating the activity of target proteins through disulfide bond reduction. In support of the dual enzymatic capabilities of peroxiredoxins, bacterial AhpC, a typical 2-Cys peroxiredoxin like Prdx1, exhibits disulfide reductase activity *in vitro*, and can function as a biologically active disulfide reductase by the

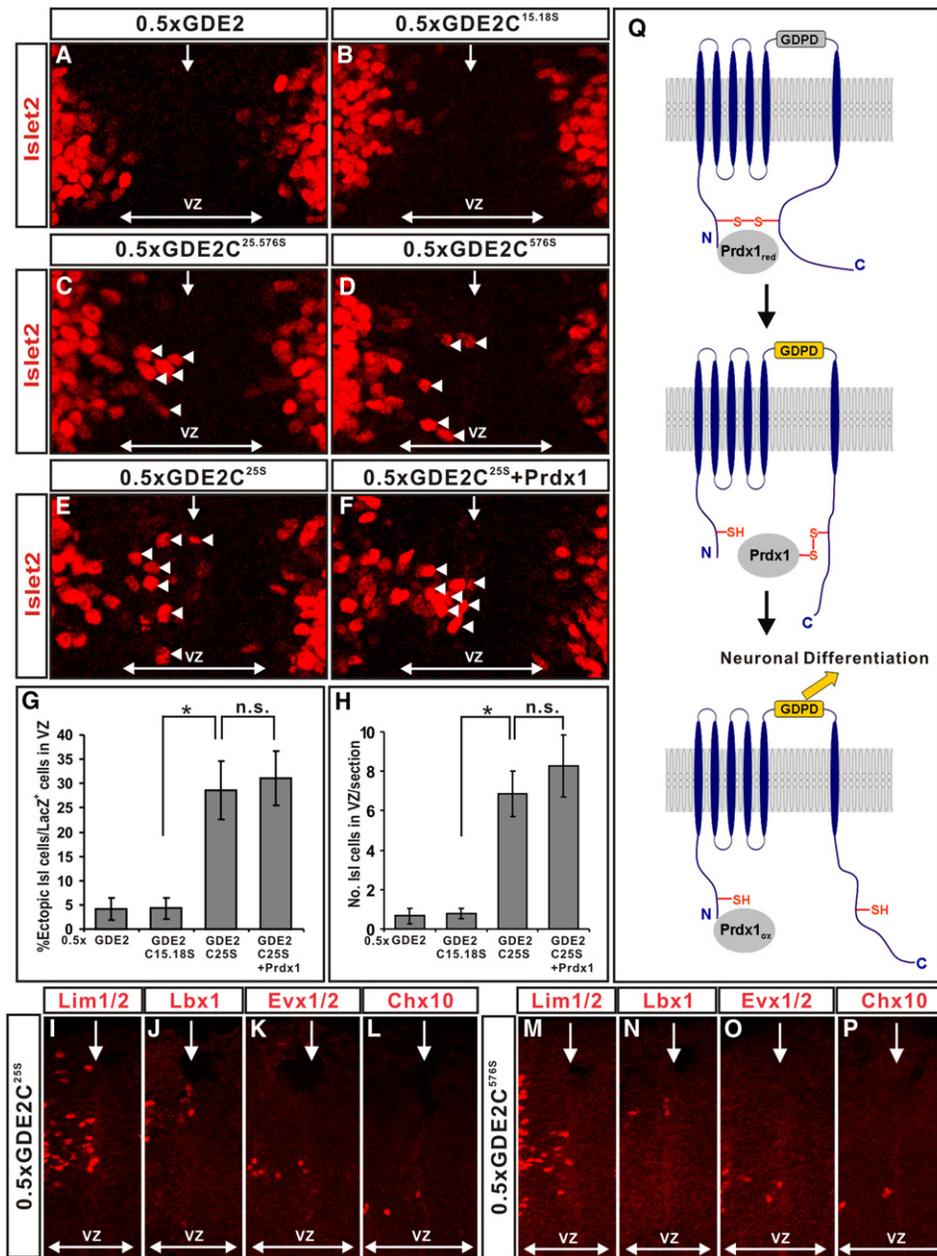


Figure 7. GDE2 Variants Incapable of Forming the N-C Disulfide Bridge Are More Active and Lose Prdx1 Synergy

(A–F) Immunohistochemical analyses of ventral and dorsal (I–P) St 19–20 electroporated chick spinal cords (left). Arrowheads mark Islet2⁺ motor neurons in the ventricular zone (VZ). Vertical arrow, midline; horizontal arrow, VZ.

(G and H) Graphs quantifying the percentage of ectopic motor neurons relative to the number of transfected cells (LacZ) (G) and the number of ectopic motor neurons (H) in the VZ (mean ± SEM; * = p < 0.001, two-tailed Student's t test, n = 7–10; n.s., p > 0.5).

(Q) Model for Prdx1 regulation of GDE2-dependent neuronal differentiation. Reduced forms of Prdx1 bind to the N-terminus intracellular domain of GDE2. The redox active Cys of Prdx1 forms a mixed-disulfide intermediate with GDE2. Here, C576 of GDE2 participates in a direct thiol-disulfide exchange, but C25 might be utilized instead. Reduction of the GDE2 C25–C576 disulfide bond by Prdx1 activates GDE2, promoting differentiation via extracellular GDPD activity. Prdx1 is oxidized during the reaction. The reduced form of Prdx1 might be a transient component of GDE2/Prdx1 complexes.

addition of a single amino acid (Ritz et al., 2001). Nevertheless, confirmation of the possible disulfide reductase activity of Prdx1 awaits further investigation.

Actively cycling progenitors are inherently responsive to GDE2 GDPD differentiation signals and can undergo terminal differen-

tiation if prematurely exposed to GDE2 activity (Rao and Sockanathan, 2005). Thus, the precise regulation of GDE2 activity is crucial to limit the exposure of GDPD differentiation signals to only those progenitors that are poised to undergo differentiation (Rao and Sockanathan, 2005). Our study suggests that this is

accomplished in part by the coexpression of Prdx1 and GDE2 in IZ cells throughout the spinal cord, which restricts the formation of active Prdx1/GDE2 complexes and the subsequent production of GDPD differentiation signals to progenitors at the lateral margin of the VZ. Other strategies to ensure a restricted zone of GDPD-dependent signaling likely include mechanisms to downregulate GDE2 activity. This could occur through the targeted degradation of active, reduced disulfide forms of GDE2 through endocytic pathways; however, our surface biotinylation studies argue against this scenario because WT and hyperactive forms of GDE2 are present at equivalent amounts on the cell membrane. An alternative mechanism to downregulate GDE2 activity is to regenerate the GDE2 C25-C576 disulfide bridge through thiol oxidation. This mechanism poses that the C25-C576 disulfide bridge functions as a reversible thiol-dependent switch to control GDE2 function, and invokes the existence of thiol oxidative proteins that negatively regulate GDE2 function.

Such redox-dependent recycling mechanisms are also likely to apply to Prdx1. Prdx1-dependent activation of GDE2 should result in the oxidation of the Prdx1 reactive Cys and inactivation of Prdx1 catalytic activity. Consistent with this model, coexpression of Prdx1 and GDE2 increases the amount of oxidized Prdx1 (Figure S8). This implies that the progression of neuronal differentiation relies upon the effective recycling of Prdx1 to active reduced forms. Obvious candidates for reactivating Prdx1 include members of the Trx family of proteins, which are known electron donors for Prdx1 (Rhee et al., 2005; Arnér and Holmgren, 2006). The need to recycle Prdx1 and downregulate GDE2 activity thus predicts that a cascade of coupled thiol-redox-dependent pathways plays a central role in regulating the onset and progression of motor neuron differentiation in the spinal cord.

Our studies suggest that GDE2/Prdx1 complexes are not limited to controlling motor neuron differentiation, but that they also regulate the differentiation of dorsal and ventral spinal interneurons. Our findings thus have potential implications for understanding general mechanisms that govern the transition between cellular proliferation and differentiation. In the developing spinal cord, progenitor proliferation is controlled by canonical Wnt signaling pathways (Megason and McMahon, 2002; Zechner et al., 2003). A recent report reveals that nucleoredoxin, a Trx family member, inhibits proliferation by negatively regulating β -catenin-mediated Wnt signaling through interactions with Dishevelled (Funato et al., 2006). This observation, taken together with our study, suggests the compelling possibility that Trx-Prdx-coupled pathways form a thiol-redox-dependent cascade that triggers the onset of neuronal differentiation in the spinal cord. Trx proteins might have dual roles in inhibiting Wnt-dependent progenitor proliferation and ensuring the availability of reduced forms of Prdx proteins, which in turn, activate key modulators of differentiation such as GDE2. Trx and Prdxs are widely expressed, whereas GDE2 and its family members are expressed in other regions of the central nervous system and nonneural tissues such as the heart, lung, gut, and bone (Rhee et al., 2005; Yanaka et al., 2003; Rao and Sockanathan, 2005). The conservation of the N- and C-terminal Cys residues in GDE3 and GDE6, together with the coincident distribution of Trx, 2-Cys Prdxs and six-transmembrane GDPD proteins in varied

cell types, suggests that coupled thiol-redox regulation of GDPD signaling might constitute a key mechanism for regulating cellular differentiation in diverse cellular contexts.

EXPERIMENTAL PROCEDURES

Immunoprecipitation and LC-MS/MS

N-terminal FLAG-tagged GDE2 or control vector was transfected into HEK293T cells or electroporated into approximately 150–200 St 13 embryonic chick spinal cords. Cell extracts and spinal cord lysates were harvested 24 hr later and immunoprecipitated by anti-FLAG M2 Affinity gel (Sigma). Protein complexes were resolved by SDS-PAGE, silver stained, and GDE2-specific bands were excised and subjected to LC-MS/MS (Taplin Biological Mass Spectrometry Facility, Harvard Medical School).

In Situ Hybridization and Immunofluorescence

In situ hybridization and immunostaining analyses were performed as previously described (Rao and Sockanathan, 2005). Details of antibodies are provided in the Supplemental Experimental Procedures. TUNEL analysis was performed using the ApopTag fluorescein in situ apoptosis detection kit (Chemicon S7110). Confocal micrographs were captured on a Zeiss LSM 5 PASCAL microscope.

Loss- and Gain-of-Function Experiments

Chick embryos were electroporated with siRNA (Rao et al., 2004) and analyzed 40 hr later at St19–21. Then 10–20 sections from each of six embryos with at least 80% loss of *Prdx1* mRNA expression were scored. *Gde2*^{+/−} animals were generated by standard procedures involving targeted recombination of the *Gde2* locus in ES cells. Disruption of the *Gde2* allele in animals was confirmed by Southern blotting, polymerase chain reaction (PCR), and immunohistochemistry. For *Gde2*^{+/−} and *Prdx1*-null mutant analyses, 15–20 sections from five embryos were counted.

For gain-of-function experiments, electroporated embryos were BrdU labeled to define the lateral extent of the VZ (Rao and Sockanathan, 2005). Images of 10–20 sections per embryo (n = 5–10 embryos) were scored. Sections were chosen to ensure equivalent electroporation efficiency by LacZ (GDE2) and HA (Prdx1) staining. All mutant and deletion constructs were generated by site-directed (QuikChange Kit, Stratagene) or PCR-based mutagenesis.

Cell-Cycle Analysis

Pregnant dams were injected with BrdU (100 mg/kg body weight) 30 min and 16 hr prior to embryo harvest for calculation of S-phase and cell-cycle exit indices, respectively. S-phase: BrdU⁺/Ki67⁺ cells where Ki67 marks all cycling cells; cell-cycle exit: BrdU⁺, Ki67[−]/BrdU⁺, Ki67⁺; mitotic index: Mpm2⁺/Ki67⁺, where Mpm2 marks cells in mitosis (Chenn and Walsh, 2002).

Biochemical Experiments

Coimmunoprecipitation studies using FLAG-GDE2 and HA- or myc-Prdx1 transfected in HEK293 cells were performed with GammaBind G Sepharose beads (Amersham). Western blotting was performed using HA-HRP (F7, 1:10,000, Santa Cruz) or polyclonal GDE2 antibodies (1:200,000).

GDE2 oxidation states were analyzed by redox western blots on surface biotinylated GDE2 protein in transfected HEK293T cells. Transfected cells were washed with cold phosphate-buffered saline (PBS) and biotinylated with sulfo-NHS-SS-Biotin (Pierce) (1 mg/ml) at 4°C for 30 min. Cells were treated with 10% (w/v) TCA (4°C, 30 min), and proteins were centrifuged and washed with 100% acetone. Protein precipitates were suspended in 80 mM Tris-HCl (pH 6.8), 2% SDS, 6 M urea, 1 mM PMSF with 20 mM AMS (Molecular probes), and the samples adjusted to neutral pH with 1 M Tris-HCl (pH 7.5). AMS labeling was done on ice (15 min), at 37°C (20 min), and boiled for 2 min, and samples were immunoprecipitated by immobilized monomeric avidin (Pierce). Eluted proteins were deglycosylated with 25 U/ μ l PNGase F (New England Biolabs) before resolving by nonreducing SDS-PAGE. GDE2 was detected by western blotting using GDE2 antibodies.

To detect disulfide bonds, transfected cells were washed with cold PBS supplemented with 10 mM NEM (Sigma), lysed in 10 mM Tris (pH 7.0), 150 mM NaCl, 1% NP-40, 0.1% SDS with 40 mM NEM and proteinase inhibitors at 4°C for 30 min, and centrifuged. Supernatants were acetone precipitated at -20°C, washed with 70% acetone, resolubilized in HENS buffer (250 mM HEPES [pH 7.7], 1 mM EDTA, 1% SDS) with 5 mM TCEP, and incubated for 1 hr to reduce disulfide bonds. The reaction was quenched with acetone, and proteins were precipitated and washed as above. Pellets were resolubilized in HENS with 0.5 mM biotin-HPDP (Pierce). Biotin labeling was carried out at room temperature for 90 min, the reaction quenched by acetone precipitation, and the pellet resolubilized in 25 mM HEPES (pH 7.7), 0.1 mM EDTA, 0.75% SDS and diluted with 6 volumes of 1% Triton in TBS. GDE2 was immunoprecipitated using anti-FLAG M2 Affinity gel and western blots were probed with antibodies against biotin (1:10,000, Sigma) and GDE2. GDE2 protein was similarly labeled for LC-MS/MS; however, 10 mM DTT was used instead of TCEP and 40 mM IAM was used instead of biotin-HPDP. GDE2 was immunoprecipitated by anti-FLAG M2 Affinity gel, resolved by SDS-PAGE and stained with Coomassie blue. Cysteines were identified by LC-MS/MS (Taplin Biological Mass Spectrometry Facility).

Trapping of mixed disulfides between GDE2 and Prdx1 was performed by standard immunoprecipitation with anti-FLAG M2 Affinity gel except that 100 mM of the thiol-alkylating agent maleimide was present in all solutions to block free thiol groups and prevent thiol-disulfide exchange or thiol oxidation (Burgoyne et al., 2007). Protein complexes were eluted by nonreducing sample buffer and divided into two equal fractions, one of which was reduced with 10% β -ME before analysis by SDS-PAGE. Prdx1 and Prdx1-GDE2 disulfide intermediates were detected by western blotting using rabbit anti-HA antibodies (1:200, Y11, Santa Cruz).

SUPPLEMENTAL DATA

Supplemental Data include Supplemental Experimental Procedures and ten figures and can be found with this article online at [http://www.cell.com/supplemental/S0092-8674\(09\)00789-2](http://www.cell.com/supplemental/S0092-8674(09)00789-2).

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