

A copper binding site within the pathological conformer epitope of mutant SOD1

Ashley I. Bush*

Mental Health Research Institute, The University of Melbourne, Parkville, VIC, Australia *Correspondence: a.bush@mhri.edu.au

A commentary on

Wild-type and mutant SOD1 share an aberrant conformation and a common pathogenic pathway in ALS

by Bosco, D. A., Morfini, G., Karabacak, N. M., Song, Y., Gros-Louis, F., Pasinelli, P., Goolsby, H., Fontaine, B. A., Lemay, N., McKenna-Yasek, D., Frosch, M. P., Agar, J. N., Julien, J. P., Brady, S. T., and Brown, R. H. Jr. (2010). Nat. Neurosci. 13, 1396–1403.

The etiopathogenesis of amyotrophic lateral sclerosis (ALS) remains contentious, but new findings related to mutations of the Cu, Zn-superoxide dismutase (SOD1) gene continue to provide crucial insights. Using a conformation-specific antibody that detects misfolded SOD1 (C4F6), Bosco et al. (2010) recently reported that oxidized wild-type SOD1 and mutant SOD1 share a conformational epitope that is not present in normal wild-type SOD1, but present in a subset of sporadic ALS (SALS) cases. Recombinant, oxidized wild-type SOD1 and wild-type SOD1 immunopurified from SALS tissues inhibited axonal transport in a manner similar to that of familial ALS (FALS)-linked mutant SOD1 (Bosco et al., 2010), indicating that wild-type SOD1 might develop a pathogenic modification even in SALS cases. The authors noted that a specific SOD1 residue, Cys111, was critical for the pathological C4F6 epitope (Bosco et al., 2010). This report carries added significance because it overlaps with recent observations about copper interactions in ALS pathogenesis that implicate the same residue in oxidized SOD1.

Since SOD1 is a major Cu-binding protein, and since Cu can be harmfully prooxidant, considerable research has explored whether aberrant Cu biochemistry could underlie FALS pathogenesis. Indeed, pharmacological and genetic interventions that lower intracellular Cu partly rescue the FALS phenotype in mutant SOD1 transgenic mice (Hottinger et al., 1997; Nagano et al., 1999, 2003; Kiaei et al., 2004; Tokuda et al., 2008). Conversely, overexpression of the Cu-chaperone of SOD1 (CCS), which presents Cu to SOD1, worsens the FALS phenotype in double CCS/mutant SOD1 transgenic mice (Son et al., 2007). On the other hand, the FALS phenotype was not affected by genetic deletion of CCS (CCS knockout mice crossed with mutant SOD1 mice; Subramaniam et al., 2002). Also, active site copper was effectively eliminated from the pathogenic reaction via amino acid substitutions that disrupt copper binding but do not eliminate toxicity, and pathogenic mutant SOD1 mice express normally active and normally metallated dimeric SOD1 (Lelie et al., 2011).

The critical Cys111 of pathogenic SOD1 described by Bosco et al. (2010) may reconcile the evidence implicating Cu with the evidence supporting pathogenic SOD1 instability, by supporting the possibility that ectopic binding of Cu outside the active site could contribute to pathogenesis (Liu et al., 2000). Immobilized Cu affinity chromatography resolves FALS-mutant SOD1 into an abnormal high-affinity fraction, termed SOD1^{HAC} (Watanabe et al., 2007). SOD1^{HAC} was observed for all pathogenic SOD1 mutants whether expressed in yeast, mammalian cell culture, or transgenic mouse spinal cords (Watanabe et al., 2007). SOD1^{HAC} could be generated from wild-type SOD1 by Cys111 oxidation with GSNO or hydrogen peroxide, which induced SOD1 monomerization. Covalent cross-linking of mutant SOD1 prevented such monomerization (Kishigami et al., 2010), consistent with monomerization of SOD1 being necessary for the formation of the adventitial high-affinity Cu-binding site on SOD1^{HAC}. While the precise site is not clear, ectopic Cu binding to SOD1^{HAC} gains redox-activity. (Kishigami et al., 2010).

Mutant SOD1 is more susceptible to intramolecular disulfide reduction (Tiwari and Hayward, 2003). This renders the critical Cys111 vulnerable to modification by GSNO or peroxide that could induce monomerization and SOD1^{HAC} formation, consistent with the hypothesis that SOD1 is dissociated into a potentially toxic SOD1HAC monomer when Cvs111 is targeted by oxidative stress products like GSNO or H₂O₂, an event of increased likelihood in SOD1 mutants. Cys111 modification appears to disrupt the contact of the dimer interface between subunits. The finding that C111S substitution decreased SOD1^{HAC} in mutant SOD1 (Watanabe et al., 2007) supports this contention. A similar cysteinemediated conformational change has been reported for transthyretin, whose mutations cause familial amyloid polyneuropathy. Modification of a cysteine residue in transthyretin was shown to decrease tetramer stability, thereby generating monomer that subsequently formed amyloid (Zhang and Kelly, 2003, 2005). The findings of Bosco et al. (2010), who demonstrated that oxidation of Cys111 mediated the pathogenic properties of SOD1, would be consistent with a similar pathogenic mechanism, and explain why dimeric forms of SOD1 mutants may not be the primary toxic species (Lelie et al., 2011).

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