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Structural Basis of PML-RARA Oncoprotein Targeting by Arsenic Unravels a Cysteine Rheostat Controlling PML Body Assembly and Function

Pierre Bercier, Qian Qian Wang, Ning Zang, Jie Zhang, Chang Yang, Yassen Maimaitiyiming, Majdouline Abou-Ghali, Caroline Berthier, Chengchen Wu, Michiko Niwa-Kawakita, Thassadite Dirami, Marie-Claude Geoffroy, Omar Ferhi, Samuel Quentin, Shirine Benhenda, Yasumitsu Ogra, Zoher Gueroui, Chun Zhou, Hua Naranmandura, Hugues de Thé, and Valérie Lallemand-Breitenbach.
ABSTRACT

PML nuclear bodies (NB) are disrupted in PML-RARA-driven acute promyelocytic leukemia (APL). Arsenic trioxide (ATO) cures 70% of patients with APL, driving PML-RARA degradation and NB reformation. In non-APL cells, arsenic binding onto PML also amplifies NB formation. Yet, the actual molecular mechanism(s) involved remain(s) elusive. Here, we establish that PML NBs display some features of liquid–liquid phase separation and that ATO induces a gel-like transition. PML B-box-2 structure reveals an alpha helix driving B2 trimerization and positioning a cysteine trio to form an ideal arsenic-binding pocket. Altering either of the latter impedes ATO-driven NB assembly, PML sumoylation, and PML-RARA degradation, mechanistically explaining clinical ATO resistance. This B2 trimer and the C213 trio create an oxidation-sensitive rheostat that controls PML NB assembly dynamics and downstream signaling in both basal state and during stress response. These findings identify the structural basis for arsenic targeting of PML that could pave the way to novel cancer drugs.

SIGNIFICANCE: Arsenic curative effects in APL rely on PML targeting. We report a PML B-box-2 structure that drives trimer assembly, positioning a cysteine trio to form an arsenic-binding pocket, which is disrupted in resistant patients. Identification of this ROS-sensitive triad controlling PML dynamics and functions could yield novel drugs.

INTRODUCTION

Promyelocytic leukemia (PML) protein organizes the formation of stress-sensitive membrane-less organelles (MLO): PML nuclear bodies (NB). PML controls various biological functions, such as apoptosis, senescence, or stem cell self-renewal (1, 2). PML may elicit these functions by scaffolding the spherical shells of NBs, which subsequently act as hubs of posttranslational modifications, in particular sumoylation, for the broad range of proteins trafficking through NB inner cores. PML NBs are disrupted in acute promyelocytic leukemia (APL) driven by the PML-RARA oncogenic fusion protein. PML protein expression and NB formation are also downregulated in many other cancers (3–5). The combination of arsenic trioxide (ATO) and retinoic acid treatments drives APL cure by enforcing PML-RARA degradation and PML NB reassembly, subsequently leading to the activation of a senescence-like program in APL cells (3). ATO, which as single therapy cures 70% of patients with APL (6, 7), directly binds PML-RARA and PML proteins (8, 9). While ATO-driven PML-RARA degradation is biochemically well understood (10), ATO-enforced NB assembly remains understudied. Formation of PML intermolecular disulfide bonds was reported in response to ATO (8) and arsenic was proposed to replace a Zn2+ ion in the RING finger (9). However, ATO effects on NB assembly remain imperfectly understood.

Biogenesis of MLO has been revisited through the prism of liquid–liquid phase separation (LLPS). Biomolecular condensates may arise by multivalent weak interactions between proteins, or proteins and RNAs, which demix from the surrounding media to form spherical structures, maintained as an equilibrium despite dynamic exchange of their components (11, 12). LLPS has been proposed to increase kinetics of biochemical reactions among its constituents and could contribute to disease initiation (13, 14). In leukemia, chimeric transcription factors may condensate through LLPS. Resulting in aberrant 3D chromatin structures and contributing to their aberrant transcriptional activity (15, 16). In vitro, chimeric GFP-polySUMO proteins condense in droplets through LLPS when combined with chimeric proteins containing repetitions of SUMO-interacting motif (SIM; ref. 17). Yet, PML sumoylation is dispensable for PML NB assembly (18, 19) and the contribution of LLPS in PML NB assembly still remains elusive.
In this study, we elucidate the crystal structure of PML B-box 2 (B2) and identify an $\alpha$-helix that mediates B2 trimerization through hydrophobic interactions, controlling PML NB assembly and PML dynamics. This $\alpha$-helix–mediated trimer organizes a triad of free C213 cysteines to which trivalent arsenic covalently docks, switching PML NBs from liquid-like to gel-like bodies. B2 trimerization and C213 are mandatory for PML-mediated function, such as oxidative stress response in vivo, as well as ATO-triggered PML-RARA degradation, uncovering the very first step by which ATO achieves antileukemia cure.

RESULTS

PML NBs Switch from Liquid-like to Gel-like Structures upon ATO

PML NBs are spherical membrane-less organelles forming core-shell structures (Fig. 1A). To determine whether PML assembly in NBs reflects LLPS, we stably expressed GFP-PML in Pml KO mouse embryonic fibroblasts (MEF) s. Scale bar, 1 $\mu$m. B, Time-lapse analysis of PML NB appearance upon GFP-PML WT expression in Pml KO MEFs. The white circle indicates the nucleus. Representative time-lapse of PML NB fusion (left) and quantification of effective viscosity (right). Mean values ± SD of n = 21 fusion events in independent cells from three independent experiments. Scale bar, 1 $\mu$m. D, Quantification of PML NB nucleation, fusion, and fission events over 1 hour. Mean value ± SD of n = 37 cells from five independent experiments. E, FRAP analyses of GFP-PML WT dynamics at NBs in control (Ctrl) or ATO-treated MEFs (1 $\mu$mol/L, 30 minutes). Mean value ± SD. Number of dots assessed Ctrl (n = 36), ATO (n = 28), from at least five independent experiments. WT, wild-type. F, Confocal analysis of PML NBs in GFP-PML WT or GFP-PML-RARA MEFs treated with 1 $\mu$mol/L of ATO for 1 hour. Scale bar, 5 $\mu$m. G, STED analysis demonstrating incomplete PML NB fusion upon ATO in Pml KO MEFs s. Scale bar, 1 $\mu$m. H, Comparison between GFP-PML WT and GFP-PML-RARA dynamics at NBs by FRAP. ATO treatment (1 $\mu$mol/L, 30 minutes) induces a liquid- to gel-like transition of GFP-PML-RARA. Mean value ± SD. Number of dots assessed PML (n = 36), PML-RARA (n = 20), PML-RARA + ATO (n = 37), from at least five independent experiments. RFI, Relative fluorescence intensity.
First, we examined whether PML could demix from the nucleoplasm above a concentration threshold by live-cell imaging following retroviral cell transduction. PML was initially homogeneously distributed in the nucleoplasm, but as GFP-PML expression increased, the first PML NB appeared (Fig. 1B). NBs then became more numerous, while the diffuse fraction remained constant (Supplementary Fig. S1A). Similarly, the number of PML NBs increases with PML transcriptional activation upon IFNα treatment (20, 21). Thus, PML demixes from a diffuse nucleoplasmic fraction into NBs above a concentration threshold. Live-cell imaging revealed that two PML NBs can fuse and relax in a novel single spherical body, supporting liquid-like behavior of PML NBs (Fig. 1C; Supplementary Movie S1). In these experiments, analysis of the relaxation curves and plotting the size of fusing PML NBs as a function of time, allowed extraction of the diffusion coefficient of PML proteins and a NB capillary viscosity in the 10−11 Pas range (Supplementary Fig. S1B; ref. 22), comparable to that of nucleoli or nuclear speckles (23, 24). We then quantified the number of events of GFP-PML nucleation from the diffuse nucleoplasmic fraction, of PML NB fusions or fissions (Fig. 1D). Fusion events occurrence were similar to nucleation ones, maintaining a mean number of 40 PML NBs per nucleus, while fission events were rare. We then assessed the dynamics of PML NB assembly by fluorescence recovery after photobleaching (FRAP). As reported, PML protein dynamically exchanges between the nucleoplasm and NBs, with a half recovery time (t1/2) of 3.2 minutes (Fig. 1E; refs. 8, 25, 26). Taken together, these results establish that PML NBs exhibit some hallmarks of LLP-separated condensates. However, the residence time of PML at NBs is much longer than other MLO nucleators, such as those driving Cajal bodies, speckles, or nucleoli (minutes vs. seconds), indicating higher interaction affinity between PML proteins at NBs. Moreover, 30% of the GFP-PML fluorescence bleached at NBs never recovers (Fig. 1E), implying that two PML fractions coexist at NBs, one exchanging with the surrounding nucleoplasm, the other remaining immobile. Together with the existence of the core-shell structure, this challenges a pure LLPS of PML proteins as a simple model of NB assembly.

ATO exposure rapidly increased PML NB-associated fraction at the expense of the diffuse one and PML NB assembly dynamics dramatically dropped, so that almost all PMLs became immobilized (Fig. 1E). Live-cell imaging and super-resolution microscopy showed that PML NBs tend to aggregate without achieving complete fusion, forming PML NB strings, consistent with an increase in their viscoelasticity (Fig. 1F and G; Supplementary Movie S2). Thus, ATO triggers the transition from liquid-like to gel-like PML NBs.

PML fusion to RARA altered its distribution in the nucleus, as GFP-PML-RARA localized into many tiny dots with diameter below 100 nm in Pmleo MEFs (refs. 8, 27; Fig. 1F). The basal dynamics of GFP-PML-RARA at these microdots was increased compared with PML at NBs, with a t1/2 of 1.37 minutes and, importantly, no immobile fraction (Fig. 1H). Yet, here again, ATO treatment drastically decreased PML-RARA exchange rates, closer to the dynamics of PML. Thus, ATO therapy drives the gel-like transition of both PML- or PML-RARA-driven condensates.

PML NB Assembly Requires the B2 Box Domain Rather than Disulfide Bridges

Arsenic atoms may bind sulfhydryl groups, primarily targeting cysteine residues in cells. Within PML, arsenic was proposed either to directly target cysteines of the RING finger, in which arsenic would replace the structuring zinc atom, or B2, another zinc finger domain that contains adjacent cysteines: C212 and C213 (8, 9). We first assessed the role of free cysteines in NB formation by using N-ethyl-maleimide (NEM), which alkylates cysteine residues with a freely accessible -SH group. Pretreatment with NEM blocked both basal PML NB assembly and ATO-enforced PML NB formation (Fig. 2A). Conversely, treatment with ATO precluded subsequent NEM-induced disorganization of PML NBs. Thus, the cysteine(s) required for baseline NB assembly are accessible, not involved in zinc coordination, and likely the same as those targeted by ATO. This does not support the RING finger as being the primary ATO target site.

ATO exposure induces ROS production due to glutathione scavenging and mitochondrial poisoning (28–30). We previously showed that disulfide bonds may link PML monomers, driving their covalent multimerization upon oxidative stress (8). We sought to disentangle the respective contribution of direct arsenic binding or ATO-enhanced disulfide bonds in PML NB assembly. By homology with other TRIpartite Motif (TRIM) proteins, the C213 residue is likely not involved in zinc coordination (31). We thus focused on both C213 and C389, the latter being an oxidation-sensitive residue implicated in oncoprotein targeting (32, 33). PML intermolecular disulfide bonds can be assessed by Western blot analysis in nonreducing conditions, which revealed high molecular weight PML multimers, whose abundance sharply increased upon ATO or H2O2 (Fig. 2B; Supplementary Fig. S1C; ref. 8), but were lost under reducing conditions (Supplementary Fig. S1C and S1D). C389S mutation impaired ATO-induced disulfides, but only modestly affected those induced by H2O2, while C213A decreased PML intermolecular-bound species induced by both ATO and H2O2. The double C213A/C389S mutation completely abrogated the formation of these PML multimers (Fig. 2B).

following PML NB assembly, PML becomes sumoylated (18, 21, 34). ATO-induced gel-like NBs are associated with a massive increase in PML sumoylation (Fig. 2B). Interestingly, PMLC213A mutants were defective for sumoylation, while PMLC389S did not affect basal or ATO-induced SUMO conjugation of PML. We then assessed the localization patterns of wild-type or mutant PML upon these stresses. Surprisingly, in contrast to ATO, H2O2 did not significantly alter the diffuse nuclear fraction of wild-type (WT) PML, nor increase the NB-associated fraction, suggesting that intermolecular disulfides are not responsible for the gel-like transition (Fig. 2C). Critically, C213A or C389S mutations had very different effects on NB formation (Fig. 2C). While defective for ATO-induced disulfide, PMLC389S NBs and diffuse fraction were identical to those of WT PML, including full ATO sensitivity. In contrast, PMLC213A remained mainly diffuse, with a single enlarged body, unaffected by ATO. Taken together, these results indicate that C213 is essential for PML NB assembly, but intermolecular disulfide bonds mediated by C213 or C389 are not, and suggest that C213 may directly contribute to arsenic binding.
Figure 2. PML NB assembly depends on C213 in B2 domain, but not on C389-mediated intermolecular disulfide bonds. A, Confocal analysis of PML NB formation following cysteine alkylation with NEM (10 μmol/L, 1 hour) or ATO (1 μmol/L, 1 hour) used alone or sequentially in GFP-PMLWT MEFs. Scale bar, 5 μm. Ctrl, control. B, Western blot analysis (nonreducing conditions) of PML disulfide bond formation in MEFs expressing HA-PMLWT or PML cysteine mutants, treated or not with ATO (10 μmol/L, 1 hour) or H2O2 (500 μmol/L, 1 hour). Brackets: SUMO-conjugated or intermolecular disulfide-bound PML. Blue arrowheads, intermolecular disulfide-bound PML. Molecular weight (kDa). C, Confocal analysis of PML NBs upon ATO (1 μmol/L, 1 hour) or H2O2 (500 μmol/L, 1 hour) exposure in HA-PMLWT- or cysteine mutant-expressing MEFs. Arrowheads, single NB in HA-PMLC213A-expressing MEFs. Scale bar, 5 μm.
B-box domains are found in TRIM proteins and are often involved in protein–protein interaction (31). We identified a highly conserved short sequence encompassing the adjacent cysteines C212/C213 in all PML-like proteins across evolution (Fig. 3A). Interestingly, this stretch of conserved residues exactly corresponds to the hotspot mutations of PML-RARA or PML in patients with therapy-resistant APL (35–38).

Crystal Structure of PML B2 Box Reveals an α-Helix Exposing C213

B-box domains are found in TRIM proteins and are often involved in protein–protein interaction (31). We identified a highly conserved short sequence encompassing the adjacent cysteines C212/C213 in all PML-like proteins across evolution (Fig. 3A). Interestingly, this stretch of conserved residues exactly corresponds to the hotspot mutations of PML-RARA or PML in patients with therapy-resistant APL (35–38).
Despite numerous attempts, no PML B2 crystal structure has been reported to date. We fused MBP to PML B2 to produce a soluble fusion protein from bacteria and obtain a crystal structure at 2.1 Å resolution (Fig. 3B; Supplementary Fig. S2A). In this structure, the B2 domain adopted a typical B-box–type zinc finger fold, where C3H1 residues coordinated two zinc atoms in a cross-braced conformation and with a conserved β1–β2–α1 arrangement (Fig. 3B and C). Analysis of the crystal packing showed that B2 was sandwiched between two MBP molecules. Indeed, B2 β1 formed an antiparallel β sheet with MBP β8 through main chain hydrogen bonds, while B2 α1 packed against a hydrophobic patch in the neighboring MBPs (Supplementary Fig. S2A–S2C). Structure alignment demonstrated that PML B2 was similar to other TRIM family MBPs (Supplementary Fig. S2A–S2C). Structure alignment involved C212, but importantly, not C213, which was positioned at the edge of the α1-helix pointing out of the overall B2 structure (Fig. 3B and C). Remarkably, this helix corresponds to the evolutionary conserved primary sequence identified above (Fig. 3A; Supplementary Fig. S2D and S2F).

In the second zinc finger, the zinc was coordinated by C227 instead of the Alphafold-predicted D219 (Fig. 3B; Supplementary Fig. S2D and S2E). Note that C227 is not conserved in TRIM5 or TRIM28 B2 nor are the residues from the conserved α-helix (Supplementary Fig. S2D–S2G). The residues equivalent to PML C227-surrounding sequence in TRIM5 and TRIM28 form a β strand that does not coordinate zinc (Supplementary Figs. S2D, S2F, and S2G). Altogether, we have unraveled the PML B2 structure, highlighting an α-helix that positions outwards the free C213 that is key to NB assembly.

**PML B2 α1-Helix and C213 Drive NB Assembly and Dynamics**

To determine the respective roles of PML B2 zinc fingers and the C213-containing helix in NB assembly, we engineered mutations disrupting zinc coordination (C189S or C212S) or point mutations on the α1-helix (C213S or L218G) and stably expressed these GFP-tagged PML mutants in PmRKO MEFs. All these PML mutants exhibited a sharply increased nuclear diffuse fraction with only one to three unusually large bodies, implying that this α1-helix and C213 play key roles in NB formation (Fig. 4A; Supplementary Fig. S3A).

FRAP analysis showed a slight increase in the GFP-PMLC189S, GFP-PMLC212S, or GFP-PMLC213S body assembly dynamics, with similar immobile fractions when compared with WT PML (Fig. 4B and C; Supplementary Fig. S3B). In contrast, C213S or L218G mutations drastically increased the dynamics of PML NB assembly, with a drop of the half recovery time from 3.2 minutes to 0.6 or 0.8 minutes, respectively. Moreover, we observed a complete recovery of the photobleached C213S and L218G PML proteins at the remaining body, pointing to a fully liquid compartment. Thus, the α1-helix, including C213, dictates PML dynamics and NB assembly. The crystal structure of MBP-PML B2 with C213A and A216V double mutation (A216V being the hotspot mutation driving ATO resistance; refs. 35, 36) was very similar to that of WT B2, with a size exclusion chromatography with multi-angle light scattering (RMSD) of 0.26 Å over 42 Cα atoms (Fig. 4D; Supplementary Fig. S3C). This supports the idea that the effects of these α1-helix mutations on PML NB assembly dynamics were not due to B2 folding alterations, but rather to loss of its biochemical interactions. Overall, while the zinc fingers contribute to the overall domain structure, the conserved α1-helix is crucial for PML NB assembly and dynamics.

**α-Helix Mediated Hydrophobic B2 Trimerization Is Key for NB Dynamics**

TRIM5α B2 was proposed to trimerize through a specific α-helix around a tryptophan core in vitro (39). We thus looked whether PML B2 monomers could self-assemble into a trimer through Alphafold2 molecular modeling (Fig. 5A and B). In the model, the trimer is predicted to be driven by α1-helix–mediated interactions, involving hydrophobic interfaces and in particular, I202, C213, A216, L217, and L218 (Fig. 5A). More specifically, L217 is predicted to play a central role through its two methyl groups, each bridging two other PML B2 monomer through their own L217, as well as with one I202 on β1 (Fig. 5B). Interestingly, L218 could also interact with I202 of another PML B2, further securing this B2 complex (Fig. 5B). Supporting B2 trimerization in vitro size exclusion chromatography with multi-angle light scattering (SEC-MALS) analysis revealed three forms of purified MBP-B2 with molecular weights corresponding to monomer, dimer and, critically, abundant trimer (Fig. 5C).

To interrogate the relevance of this model in cellulo, we generated point mutations of these potentially interfering residues. When analyzed by immunofluorescence, L217G substitution had the most drastic effect, completely blocking PML NB assembly (Fig. 5D, quantification in Supplementary Fig. S3A). GFP-PMLA216V or GFP-PMLC210G localization were diffuse in the majority of cells and formed one or two bodies in the remaining ones. A similar defect in NB assembly was observed with the A216V patient-derived mutation (35–37), consistent with our model predicting a constraint environment due to the short distance between A216 and L217 side chain within the trimer (Fig. 5B and D). In contrast, the A216G mutation had only minor effects, increasing the diffuse PML fraction, consistent with its predicted modest impairment of trimerization. When analyzed in FRAP, PMLC212A, PMLA216V, or PMLC210G, all exhibited highly dynamic exchange with liquid-like behaviors (Fig. 4B; Supplementary Fig. S3B). Conversely, increasing hydrophobicity by substituting leucine to residues with aromatic group at position 218 led to the formation of filaments, on which PML exchange was poorly dynamic (Fig. 5E; Supplementary Fig. S3D and S3E). Thus, the α1-helix–mediated hydrophobic interactions between PML monomers through I202, L217, and L218 regulate PML assembly ranging from large liquid-like bodies to standard PML NBs, up to gel-like PML filaments.

**Arsenic Docks on a C213 Tri-Cysteine Pocket of B2 Trimmers to Drive Gel-Like Transition**

In APL, ATO, and other therapeutic arsenic derivatives provide trivalent arsenic (As(III) oxidation state) at physiologic pH and in vivo. As(III) can form stable complexes with thiol groups through covalent binding to sulfur and may form complex with three glutathiones in solution (30). Critically, the key C213 residues are organized in a triad positioned at the center of the PML B2 helix trimer (Fig. 6A; Supplementary Fig. S4A and S4B), in an enzymatic active center-like configuration. This triad is present
Structural Basis of PML-RARA Targeting by Arsenic

Figure 4. PML B2 α1-helix controls PML assembly and dynamics. A. Representative PML NB formation in MEFs expressing PML B2 mutants in Zn²⁺-coordinating cysteines or α1-helix (underlined in blue) residues. Scale bar, 5 µm. B. FRAP analyses of GFP-PML dynamics at NBs in WT- or mutant-expressing MEFs. Mean value ± SD. RFI, Relative fluorescence intensity. NBs assessed PML\textsuperscript{WT} (n = 36), PML\textsuperscript{C189S} (n = 25), PML\textsuperscript{C212S} (n = 42), PML\textsuperscript{C213A} (n = 24), PML\textsuperscript{C213S} (n = 20), from at least five independent experiments. C, Plot representation of B, with \( t_{1/2} \) (left) and immobile fraction (right) of PML mutants harboring mutations on the α1-helix or zinc finger. Each dot represents an individual NB. Median ± 95% confidence interval, statistical significance by comparison with GFP-PML\textsuperscript{WT}. Kruskal–Wallis test. *** P ≤ 0.001 are displayed. P value for Zn-finger mutants, C189S = 0.0097, C212S = 0.0115, C213S = 0.028. D, Superposition of PML B2 crystal structure (cyan) with that of PML\textsuperscript{C213A/A216V} mutant (orange) demonstrates absence of misfolding.

at the opposite end of the assembled helices compared with the sites of L217 interactions (Figs. 5B and 6A). The C213 residues are separated by 3.2 Å, fitting with an ideal arsenic docking that would lead to an interacting distance of 2.7 Å between arsenic and the sulfur atoms (Fig. 6A; Supplementary Fig. S4A and S4B). We thus hypothesized that ATO could trigger gel-like transition of PML NBs by targeting this triad of C213 residues within the α1-helix or mutants impairing helix-driven trimerization, as well as for C213S, PML nuclear distribution was unaffected by ATO treatment (Fig. 6C). ATO could not drive phase transition of C213S or helix trimer mutant-forming bodies, as supported by FRAP analyses (Fig. 6D; Supplementary Fig. S4E). In contrast, A216G mutation only marginally affected ATO response of PML, as expected from our model (Fig. 6C and D). ReASH, an arsenic derivative that fluoresces when bound to proteins, labeled the

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STO had very similar effects to ATO, decreasing the PML diffuse fraction, turning PML NBs in gel-like string bodies (Fig. 6B; Supplementary Fig. S4C), and subsequently increasing PML sumoylation (Supplementary Fig. S4D; ref. 42).

For B2 mutants of zinc finger 1 formation (C212S, C189S), or mutants impairing helix-driven trimerization, as well as for C213S, PML nuclear distribution was unaffected by ATO treatment (Fig. 6C). ATO could not drive phase transition of C213S or helix trimer mutant-forming bodies, as supported by FRAP analyses (Fig. 6D; Supplementary Fig. S4E). In contrast, A216G mutation only marginally affected ATO response of PML, as expected from our model (Fig. 6C and D). ReASH, an arsenic derivative that fluoresces when bound to proteins, labeled the

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**Figure 4.** PML B2 α1-helix controls PML assembly and dynamics. A. Representative PML NB formation in MEFs expressing PML B2 mutants in Zn²⁺-coordinating cysteines or α1-helix (underlined in blue) residues. Scale bar, 5 µm. B. FRAP analyses of GFP-PML dynamics at NBs in WT- or mutant-expressing MEFs. Mean value ± SD. RFI, Relative fluorescence intensity. NBs assessed PML\textsuperscript{WT} (n = 36), PML\textsuperscript{C189S} (n = 25), PML\textsuperscript{C212S} (n = 42), PML\textsuperscript{C213A} (n = 24), PML\textsuperscript{C213S} (n = 20), from at least five independent experiments. C, Plot representation of B, with \( t_{1/2} \) (left) and immobile fraction (right) of PML mutants harboring mutations on the α1-helix or zinc finger. Each dot represents an individual NB. Median ± 95% confidence interval, statistical significance by comparison with GFP-PML\textsuperscript{WT}. Kruskal–Wallis test. *** P ≤ 0.001 are displayed. P value for Zn-finger mutants, C189S = 0.0097, C212S = 0.0115, C213S = 0.028. D, Superposition of PML B2 crystal structure (cyan) with that of PML\textsuperscript{C213A/A216V} mutant (orange) demonstrates absence of misfolding.
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AB C

C213A) and increasing steric hindrance (C213L or C213F) lent binding (Supplementary Fig. S4F). Altogether, our findings washout experiments after removing ATO, suggestive for covariant ATO on PML NBs after 30-minute exposure was not reversed by α on both C213 and n.

While mutations of C213 removing thiol group (C213S or C213A) and increasing steric hindrance (C213L or C213F) all disrupted basal PML NB assembly, replacing C213 by valine unexpectedly fully rescued the basal NB formation and normal dynamics (Fig. 6D and F). These data suggest that the branched methyl groups of three valines can maintain hydrophobic interactions within the center of the B2 trimer, somehow similar to L217 on the other side of the helix. Strikingly, both PML C213V localization and dynamics were insensitive to ATO, implying that the sensor function was lost (Fig. 6C and D). Accordingly, alkylation by NEM, which disrupted WT NBs, had no effect on PML C213V NBs (Figs. 2A and 6G), stressing the unique features of this cysteine residue. Altogether, this suggests that, within the B2 domain, C213 thiol modification controls PML NB assembly dynamics.

Figure 5. PML B2 mediates PML trimerization and is required for biological functions. A, Modeling of a PML B2 trimer: B2 monomers are colored in green, gray, and pink. Exponents refer to affiliation to a specific monomer. B, Close-up view of the PML B2 trimer model depicting hydrophobic interactions between the α1- helices. Residues involved in these hydrophobic interactions are shown in blue, linked by dashed lines. Distance between these key hydrophobic residues are in Å, SEC-MALs analysis showing a mix of monomeric, dimeric, and trimeric PML B2 (left) (ΔRI: differential refractive index, RIU: refractive index unit). The C213A mutant shifts toward monomeric and dimeric states (right). MBP-B2 molecular weight: 46.2 kDa. D, Representative PML NB formation in PML B2 mutants predicted to impair trimerization expressed in MEFs. Scale bar, 5 μm. E, GFP·PML 1218F yields filaments (left). Scale bar, 5 μm. FRAP analysis of the exchange rates of GFP·PML 1218F mutant compared with GFP·PML WT (right). Mean value ± SD. NBs assessed GFP·PML WT (n = 36) and PML 1218F (n = 24), from at least five independent experiments. RFI, Relative fluorescence intensity.

GFP·PML WT shell and triggered gel-like transition of PML NBs, similar to ATO (Fig. 6E; ref. 8). In contrast, the shell of the body formed by PML 218G could not bind ReAsH. Rather, ReAsH accumulated within the NB inner core, an unexpected observation that deserves further studies. Similarly, PML 218G failed to bind ReAsH, stressing the fact that efficient arsenic binding depends on both C213 and α1-helix trimerization. Finally, the effect of ATO on PML NBs after 30-minute exposure was not reversed by washout experiments after removing ATO, suggestive for covariant binding (Supplementary Fig. S4F). Altogether, our findings imply that AsIII requires prior P2 helix trimerization to directly and irreversibly targets C213 and trigger gel-like transition.

While mutations of C213 removing thiol group (C213S or C213A) and increasing steric hindrance (C213L or C213F)...

Figure 6. ATO binding to B2 trimer is responsible for ATO-induced phase transition. A, Modeling of PML B2 trimer around an arsenic atom. The key C213 residues are indicated in blue and the arsenic atom is shown as an orange sphere. The predicted distance between the arsenic atom and C213 represented by the dashed line is around 2.7 Å. B, FRAP analyses of GFP·PML WT dynamics at NBs in untreated cells or cells treated with trivalent metalloid oxides: ATO (1 μmol/L, 30 minutes) or STO (1 μmol/L, 30 minutes). ATO-treated nontransduced cells or PML C213S could not bind ReAsH. Rather, ReAsH accumulated within the NB inner core, an unexpected observation that deserves further studies. Similarly, PML 218G failed to bind ReAsH, stressing the fact that efficient arsenic binding depends on both C213 and α1-helix trimerization. Finally, the effect of ATO on PML NBs after 30-minute exposure was not reversed by washout experiments after removing ATO, suggestive for covariant binding (Supplementary Fig. S4F). Altogether, our findings imply that AsIII requires prior P2 helix trimerization to directly and irreversibly targets C213 and trigger gel-like transition.

While mutations of C213 removing thiol group (C213S or C213A) and increasing steric hindrance (C213L or C213F) all disrupted basal PML NB assembly, replacing C213 by valine unexpectedly fully rescued the basal NB formation and normal dynamics (Fig. 6D and F). These data suggest that the branched methyl groups of three valines can maintain hydrophobic interactions within the center of the B2 trimer, somehow similar to L217 on the other side of the helix. Strikingly, both PML C213V localization and dynamics were insensitive to ATO, implying that the sensor function was lost (Fig. 6C and D). Accordingly, alkylation by NEM, which disrupted WT NBs, had no effect on PML C213V NBs (Figs. 2A and 6G), stressing the unique features of this cysteine residue. Altogether, this suggests that, within the B2 domain, C213 thiol modification controls PML NB assembly dynamics.
Basal PML sumoylation was severely impaired in all mutants predicted to destabilize the B2 trimer and after NB formation (Fig. 6H and I). In contrast, basal PML$^{C213V}$ sumoylation was normal or even enhanced (Fig. 6I), while sumoylation of PML$^{C213S}$ was ATO-insensitive (Fig. 6I; Supplementary Fig. S4G and S4H). As expected, all B2 trimer and other C213 mutants were resistant to ATO-enhanced sumoylation. PML sumoylation of K160 drives partner recruitment (18, 43).

Accordingly, PML$^{C213V}$ efficiently recruited partner proteins, such as Sp100 (Fig. 6J) and the RNF4 SUMO-dependent ubiquitin ligase (Supplementary Fig. S4I), while PML$^{C213S}$ did not. As expected, in contrast to PML, ATO did not further promote recruitment of partners into C213V bodies (Fig. 6J). Accordingly, all B2 mutants were resistant to ATO-induced SUMO-triggered degradation (Fig. 6I; Supplementary Fig. S4H). Thus, C213-mediated trimerization controls PML sumoylation and partner recruitment.

PML NBs couple oxidative stress to control of partner sumoylation through recruitment of UBC9 (18, 21). We questioned whether impeding α1-helix-mediated B2 trimerization would affect partner biochemical modifications. We generated a Pml$^{-/-}$ mESC line (corresponding to L218G in human PML, forming liquid-like bodies), stably expressed His$_{6}$SUMO2 and we purified SUMO2 conjugates before or after ATO exposure. As we previously described (21), ATO enhanced global sumoylation, as well as that of endogenous mouse PML (pPML) and KAP1 (Fig. 6K). None of these were observed in Pml$^{L222G}$ mESCs (Fig. 6K; Supplementary Fig. S4J). Thus, α1 helix-mediated B2 trimerization is required for the biochemical function of PML NBs to promote partner sumoylation.

**C213 Mediates PML-RARA ATO Sensitivity**

We then assessed the role of PML C213 residue in the context of the oncogenic PML-RARA protein, by transducing hematopoietic progenitors [hematopoietic stem and progenitor cells (HSPC)] and MEFs with WT or C213 mutant PML-RARA. We first examined the distribution of human PML-RARA and endogenous mouse PML proteins by immunofluorescence. As previously reported (27, 44), PML-RARA WT exhibited a microspotted pattern where it recruited endogenous mPML. In contrast, PML-RARA$^{C213S}$ was diffuse in the nucleus, consistent with C213 role in PML-RARA self-assembly, but endogenous mPML NB formation was unaffected in both MEFs (Fig. 7A) and HSPCs (Supplementary Fig. S5A). PML-RARA$^{C213V}$ formed numerous small microdots and also disrupted endogenous mPML localization, similar to PML-RARA WT. Thus, C213 controls the efficiency of homo- and hetero-interactions between PML-RARA and Pml within microspeckles. In ATO-treated primary progenitors or MEFs, PML-RARA and mPML progressively reassembled into NBs (Fig. 7A; Supplementary Fig. S5A). In sharp contrast, PML-RARA$^{C213S}$ did not respond to ATO, while endogenous mPML aggregated into fewer NBs (Fig. 7A; Supplementary Fig. S5A).

Finally, PML-RARA$^{C213V}$-expressing cells had a mixed phenotype, with ATO-aggregated endogenous mPML NBs, particularly in progenitors that express high levels of mPML proteins, but with unresponsive PML-RARA micro-speckles. We then examined the effects of ATO on PML-RARA sumoylation/degradation (45). In the context of the oncogenic protein, C213S precluded basal PML-RARA sumoylation, while PML-RARA WT or PML-RARA$^{C213V}$ were both efficiently sumoylated in the basal state (Fig. 7B). Importantly, the two C213 mutants were completely resistant to ATO-triggered hyper-sumoylation and degradation (Fig. 7B quantification in Supplementary Fig. S5B), explaining the remaining PML-RARA$^{C213V}$ microspeckles (Fig. 7A; Supplementary Fig. S5A). In FRAP analyses performed either in Pml$^{WT}$ (Supplementary Fig. S5C and S5D) or Pml$^{KO}$ MEFs (Fig. 7C), GFP-PML-RARA$^{C213V}$ exhibited a reduced basal assembly dynamics compared with that PML-RARA microdots. This mutation blocked ATO-driven gel-like transition, consistent with PML-RARA$^{C213V}$ inability to bind arsenic. Altogether, these data demonstrate the key role of C213 in ATO-targeted effects on PML and PML-RARA. Interestingly, dynamics of GFP-PML-RARA were distinct in Pml$^{WT}$ or Pml$^{KO}$ background (Fig. 7C; Supplementary Fig. S5C), supporting the idea that PML reduces PML-RARA assembly dynamics and could contribute to its ATO sensitivity.

**B2 Trimer and C213 Control Oxidative Stress Responses**

The role of PML is likely much broader than just being an arsenic binder and PML was repeatedly linked to oxidative stress control (46–49). To question any contribution of the C213 triad in oxidative stress sensing, we compared the effects of ROS on PML NB assembly dynamics in Pml$^{WT}$ and Pml$^{C213V}$, expressing MEFs. Depending on the dose, H$_{2}$O$_{2}$ increased or decreased PML dynamics assessed by FRAP (Fig. 7D). Remarkably, PML$^{C213V}$ was completely insensitive to H$_{2}$O$_{2}$ (Fig. 7E), suggesting that C213 modification by ROS regulates NB dynamics and could play an important role in oxidative stress sensing.
Structural Basis of PML-RARA Targeting by Arsenic

**A**

<table>
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<tr>
<th></th>
<th>PML-RARA&lt;sup&gt;WT&lt;/sup&gt;</th>
<th>PML-RARA&lt;sup&gt;C213S&lt;/sup&gt;</th>
<th>PML-RARA&lt;sup&gt;C213V&lt;/sup&gt;</th>
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<tr>
<td>ATO (6 h)</td>
<td>-</td>
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**B**

PML-RARA:

- WT
- C213S
- C213V

**C**

![Graph](chart.png)

**D**

WT

**E**

C213V

**F**

**G**

C213SC 213V

**H**

Ctrl (A220V vs. WT)

**I**

WT

**J**

α-Helix mutants

Normal NBs

ATO-treated NBs

Liquid-like NBs

Gel-like NBs

B2 trimer interaction strength

**K**

Ctrl (A220V vs. WT)

**L**

Ctrl (KO vs. WT)

**M**

Ctrl (KO vs. WT)

**N**

Ctrl (A220V vs. WT)

**O**

Ctrl (A220V vs. WT)

**P**

Ctrl (A220V vs. WT)

**Q**

Ctrl (A220V vs. WT)

**R**

Ctrl (A220V vs. WT)

**S**

Ctrl (A220V vs. WT)

**T**

Ctrl (A220V vs. WT)

**U**

Ctrl (A220V vs. WT)

**V**

Ctrl (A220V vs. WT)

**W**

Ctrl (A220V vs. WT)

**X**

Ctrl (A220V vs. WT)

**Y**

Ctrl (A220V vs. WT)

**Z**

Ctrl (A220V vs. WT)
PML is involved in oxidative stress responses (50, 51), notably in hepatocytes (46). To explore any role of B2 trimerization, we engineered a PmlA220V knock-in mice (corresponding to the A216V hotspot mutation in the human sequence). Similar to PmlA220 mice, these animals did not exhibit obvious phenotypes and were fertile. As for stably expressed PmlA216V mutant in MEFs (Fig. 5D), rare mPMLA220V NBs were observed in hepatocytes and the mutant protein did not undergo detectable sumoylation (Supplementary Fig. S5E). Hepatocytes from PmlA220V or PmlKO animal exhibited an increased number of γH2AX foci (Fig. 7F), which could reflect basal oxidative stress (46) or defects in DNA repair (52). Transcriptomic studies and gene-set enrichment analysis (GSEA) analyses comparing basal gene expression in the livers of PmlA220V and WT animals revealed major differences (including stress signatures, Fig. 7G), many of which were shared with PmlKO animals (Supplementary Fig. SSF). Thus, B2 trimer formation has important consequences in physiologic conditions.

We then subjected WT, PmlA220V, and PmlKO animals to CCl4, a classic trigger of oxidative stress, ultimately resulting in fibrotic scars, which are limited by senescence activation (53). We first examined acute response by performing transcriptomic studies of livers 18 hours postinjection. Remarkably, differentially regulated pathways compared with WT animals were virtually identical between PmlA220V and PmlKO ones (Fig. 7H), highlighting defects in multiple pathways, including p53, E2F, G2M checkpoint, fatty acid, hypoxia, IFNs, Myc, TNFα, or TGFB. They are functionally related to processes regulated by PML, such as apoptosis and senescence, cell growth, metabolism, oxidative stress response, as well as inflammatory processes (1, 2, 50). When we examined liver fibrosis after 5 weeks of treatment, increased fibrosis was noted upon Picosiris red staining in PmlA220V and PmlKO animals when compared with WT animals (Fig. 7I), as expected from impaired P53 activation and senescence (53).

Altogether our findings support that B2 helix–positioned C213 triads act as rheostats controlling PML NB assembly dynamics, liquid- to gel-like properties, and sumoylation, depending on C213 oxidation states (Fig. 7J). This rheostat controls physiologic functions of PML for basal homeostasis and stress adaptation. As(III) highjacks this sensor, turning reversible interactions into high-affinity ones, ultimately driving PML-RARA sumoylation/degradation and yielding APL cure.

**DISCUSSION**

In this study, based on the first determination of PML B2-box crystal structure, we unravel the PML/arsenic interplay on a cysteine trio within a B2 trimer, driving a polymerization-like process of PML NB assembly.

Despite repeated claims, there was little available experimental evidence that PML undergoes phase separation. Here, we show that PML can demix from the nucleoplasm, forming bodies as a result of a dynamic process of PML exchange between condense and diffuse fractions, with viscosity similar to other LLPS-driven NBs. PML NB biogenesis and LLPS were proposed to rely on SUMOs and SUMO-interacting motifs (17, 54). Yet, PML mutants on sumoylation sites can nevertheless demix into few bodies, underscoring the dispensable nature of sumoylation for PML condensation (18, 19). Our FRAP data unravels that the typical PML NB assembly dynamics is the result of complex PML self-interactions requiring B2 trimers rather than a simple multi-SUMO/SIM–driven LLPS. PML crystal structure and B2 trimer model resembles that of TRIM5α (39), with PML-specific tunable central cysteine residues that set PML NB assembly dynamics. Liquid-like bodies are defective for PML and partner sumoylation, while ATO-induced gel-like condensates promote both of them. This interplay thus unravels tight links between NB biochemical activity and B2-controlled PML NB dynamics.

Arsenic may bind three adjacent cysteines on the same polypeptide (55, 56). Here, arsenic binding is achieved through a trio of C213 residues from distinct B2 polypeptides, locking a polymeric-like PML complex and driving gel-like transition. *In vivo*, interfering with C213 positioning, with the mouse equivalent of the A216V mutation, induced basal and stress-responsive transcriptional changes similar to those observed in PmlKO cells (47). These included defects in p53, E2F, fatty acid metabolism, hypoxia, Myc, TNFα, or TGFB (Fig. 7H), many of which are directly implicated in oxidative stress response and altered in cancers. Thus, in physiologic conditions, the oxidation status of the sulfur atoms of C213 trio could be the rheostat of NB biogenesis, accounting for their oxidative stress sensitivity (46, 48, 51). The biochemical nature of oxidation status changes in the C213 triad remains to be investigated. Distinct from C213, C389-mediated oxidation or disulfide formation may be involved in other functions (33), such as ROS buffering within NBs (21).

ATO-driven APL remission requires PML-RARA degradation and subsequent PML NB formation (3, 57). PML-RARAC213S lost the ability to form microspeckles and delocalize endogenous mouse PML. In this setting, mPML localization was normal and remained fully ATO sensitive. A similar situation may be observed during clinical resistance observed in patients with PML-RARA B2-mutated APL (36, 37). Thus, although ATO-induced NB restoration is required in murine APL models (57), it may be insufficient on its own to initiate response, without concomitant degradation of PML-RARA and the resulting clearance of master genes promoters (58).

Identification of the 3D catalytic-like site controlling NB assembly could allow the design of novel arsenic-like molecules to enhance or impede NB formation. These could be of high value for PML NB–targeted therapies (59), or conversely, in cancers where PML is an important survival factor (60, 61). Overall, our results elucidate the long-standing question of ATO targeting of PML (62, 63) and unravel novel basic regulatory mechanisms that are likely to be important in other physiopathologic settings.

**METHODS**

**Sequence Analysis, Cloning, and Constructs**

Human PML B2 amino acid sequence was extracted from the NCBI databank (NP_150241.2) and compared with the following sequences: *Macaca mulatta* (NP_001035899.1), *Mus musculus* (NP_835188.2), *Molossus molossus* (XP_036113734.1), *Gallus gallus* (XP_004943755.1), *Chrysemys picta bellii* (XP_042705708.1). Amino acid conservation was assessed using the ClustalW2 software (64).
PML mutations were performed in pMSCVpuro-HA-PMLIII or pMSCVpuro-GFP-PMLIII using the Q5 site-directed mutagenesis kit (NEB, catalog no. E0554S) according to the manufacturer’s protocol and controlled by sequencing (Eurofins Genomics). PML-RARA was cloned into pMSCVpuro (SfiI/AgeI) from pMSCVpuro-GFP-PMLIII and pMSCV-PML-RARA-neo. PML-RARA B2 mutants were generated using AvrII/SfiI restriction fragments from pMSCVpuro-PMLIII mutants. Restriction enzymes and T4 DNA ligase were purchased from NEB. Additional primer sequences used for site-directed mutagenesis can be found in Supplementary Table S1.

**Cell Culture and Cell Treatments**

All reagents and cell sources are indicated in Supplementary Tables S2 and S3. Large T-transformed Pmlko MEF cells (our laboratory; ref. 46), HEK293T (Platinum-E from Catherine Lavau, Durham, NC), and HeLa cell lines were maintained in DMEM (Thermo Fisher Scientific, catalog no. 41966029) supplemented with 10% FCS, 50 U/mL penicillin/streptomycin (Thermo Fisher Scientific, catalog no. 10378016), 2 mmol/L glutamine (Thermo Fisher Scientific, catalog no. 25030024), at 37°C with 5% CO2. Pmlko MEFs were originally obtained from P. Navarro (Pasteur Institute, Paris, France) and cultured in the same culture medium as MEFs, supplemented with 1% nonessential amino acid (Thermo Fisher Scientific, catalog no. 11400050), 1% Glutamax (Thermo Fisher Scientific, catalog no. 35050-038), 1,000 U/mL of recombinant Leukemia Inhibitory Factor (LIF, Sigma-Aldrich, catalog no. ESG1107) and 0.1% β-mercaptoethanol (Merck, catalog no. M6250) on gelatin-coated plates. HSPC isolation, culture, and transformation with PML-RARA were performed as described previously (65). Pmlko MEFs were transduced using retroviruses produced by Platinum-E packaging cells, after transfection with Effectene reagent (Qiagen, catalog no. 301425) with pMSCVpuro-HA-PMLIII or pMSCVpuro-GFP-PMLIII WT or mutants. transduction with vectors produced by Platinum-E packaging cells, after transfection with Effectene reagent (Qiagen, catalog no. 301425) with pMSCVpuro-HA-PMLIII or pMSCVpuro-GFP-PMLIII WT or mutants. Immunolabeling and Microscopy Analysis

Cells were fixed with 10% formalin (Sigma-Aldrich, catalog no. HTS01128) for 15 minutes and permeabilized in PBS 0.5% Triton X-100 (Sigma-Aldrich, catalog no. T9284) for 15 minutes. Incubation with antibodies was performed in PBS 0.5% Triton X-100 for 1 hour. Primary antibodies: anti-GFP (1/1,000, Roche, catalog no. 11814460001), anti-HA (1/1,000, Covance, catalog no. MMS-101R-1000), anti-Actin (1/1,000, Sigma-Aldrich, catalog no. A2066), homemade anti-hPML. Secondary antibodies from Jackson Immuno-Research: anti-mouse-HRP (1/5,000, catalog no. 115-035-056), or anti-Rabbit-HRP (1/5,000, catalog no. 111-035-045). Proteins were detected using SuperSignal West Dura or Femto (Thermo Fisher Scientific, catalog nos. 34076 and 34096), using Vilber Fusion-Fx (Vilber). To avoid nonspecific signals, membranes were not reprobed.

**Live-Cell Imaging and Analysis of PML NBs**

All live-cell analyses were performed using glass-bottom culture dishes (IBIDI, catalog no. 81156). For the analysis of NB formation, Pmlko MEFs were transduced with the culture supernatant of Platinum-E cells transfected two days prior with a pMSCVpuro-GFP-PMLIII vector. Anti-vasopressin-vasotocin (1 mL) in Media was added on top of the supernatant (IBIDI, catalog no. Indoor). The acquisition was performed on an Axio Observer video-microscope (Carl Zeiss Micro-Imaging) equipped with a thermostatic chamber (37°C, 5% CO2). Laser power and exposure time were set at minimum levels to avoid phototoxicity. Acquisitions were performed every 15 minutes. PML NB formation was tracked in the same cells during the entire experiment. The quantification of PML NB nucleation/fusion/fission events was performed on Pmlko MEFs stably expressing GFP-PMLIII on a spinning disk confocal microscope (Nikon Eclipse Ti, Nikon) equipped with a CoolSNAP HQ2 high-sensitivity camera (Photometrics) and a
thermostatic chamber (37°C, 5% CO₂). Cells were imaged during 2 hours every 30 seconds. Quantification was performed using the FIJI software on maximum Z projections of n = 37 cells from four independent experiments. The magnitude of the effective viscosity of the PML NBs was estimated by quantifying the time required for two NBs to relax in a spherical structure during a fusion event, as described before (66). The relaxation time during a fusion event was quantified by measuring the long axis of the two condensates from the beginning of the fusion and was plotted as a function of time for n = 21 NBs from three independent experiments. By computing the fusion time as a function of the diameter of the resulting PML bodies (Supplementary Fig. S1B) and by assuming that surface tension drives the fusion process whereas viscosity tends to impede it, we determined that PML bodies have an effective viscosity of about 10³ Pa·s. Analysis of PML NB distribution was performed on confocal images of fixed cells using the FIJI software.

Analysis by FRAP
FRAP was performed on PmlKO MEFs stably expressing GFP-PML-III, GFP-PML-RARA, or the indicated B2 mutants. One-micron regions of interest (ROI) were used for GFP-PMLIII–expressing cells and 2-μm ROI were used for GFP-PML-RARA. Acquisitions were performed every 10 seconds using a spinning disk confocal microscope (Nikon Eclipse Ti, Nikon) equipped with a CoolSnap HQ2 high-sensitivity camera (Photometrics) and a thermostatic chamber (37°C, 5% CO₂) with a +60° oil-immersion objective. Three images were taken before photobleaching, 15 iterations were used to bleach the ROI, and fluorescence recovery was followed every 10 seconds for 15 to 30 minutes. On the graphs, only the data points prebleaching, immediately after bleaching, and every 2.5 minutes are shown. Fluorescence recovery was analyzed using the FIJI software. For each studied nucleus, the relative fluorescent intensity (RFI) was calculated as previously described using an ImageJ plugin (67). Background correction was applied at every time point and a double exponential (37°C, 5% CO₂) with a +60° oil-immersion objective. Three images were taken before photobleaching, 15 iterations were used to bleach the ROI, and fluorescence recovery was followed every 10 seconds for 15 to 30 minutes. On the graphs, only the data points prebleaching, immediately after bleaching, and every 2.5 minutes are shown. Fluorescence recovery was analyzed using the FIJI software. For each studied nucleus, the relative fluorescent intensity (RFI) was calculated as previously described using an ImageJ plugin (67). Background correction was applied at every time point and a double exponential was performed to account for global sample bleaching. We assessed that PML recovery was independent of the size of the bleached area by testing several sizes of photobleached areas, showing that interactions between PML proteins at the shell have a predominant role over free diffusion. Then every RFI curve was fitted to an y = A*[(1-exp(-B/t)) model where y is the fluorescence intensity, A the plateau of the intensity (mobile fraction), B the time in seconds, and t the half-recovery time (t₁/₂).

Protein Expression and Purification from Bacteria
Escherichia coli Rosetta (DE3) cells (Novagen) were transformed with a pRSFDest-1 vector (Novagen) containing the DNA sequence of human PML B2 domain fused to an MBP tag. IPTG (0.2 mmol/L) was added into the culture to induce expression of the recombinant proteins at 18°C for 16 hours. Bacteria were harvested by centrifugation (5,000 rpm, 8 minutes), resuspended in a buffer containing 20 mmol/L Tris-HCl pH 8.0, 300 mmol/L NaCl, 5% glycerol, 0.3 mmol/L TCEP, 1 mmol/L phenylmethylsulfonylfluoride and lysed using a cell disruptor (JNBIO). The lysate was loaded onto a preequilibrated amylose resin column (NEB). The column was first washed with 5 column volume of lysis buffer and MBP-B2 protein was eluted with a buffer containing 20 mmol/L Tris-HCl pH 8.0, 300 mmol/L NaCl, 5% glycerol, 0.3 mmol/L TCEP, 10 mmol/L maltose. Proteins were concentrated to 20 mg/mL and purified on a Superdex 200 increase gel filtration column (Cytiva; 20 mmol/L Tris- HCl pH 8.0, 200 mmol/L NaCl, 0.3 mmol/L TCEP). Purified MBP-B2 was concentrated to 15 mg/mL for crystallization.

Crystallization and Structure Determination
Crystals of WT MBP-B2 were grown with 24-well plates using the hanging drop vapor diffusion method by mixing 1.2 μL protein (15 mg/mL) with 1.2 μL crystallization buffer containing 100 mmol/L MES pH 6.5, 250 mmol/L potassium acetate, 22% (w/v) PEG 3350. Crystals grew to full size after incubation at 16°C for 1 week. MBP-B2 C213A and A216V-mutant proteins were crystallized in the same conditions. Before X-ray diffraction, crystals were cryoprotected with the reservoir solution supplemented with 25% glycerol and were flash-cooled into liquid nitrogen. Diffraction data were collected at Beamline station BL19U1 of Shanghai Synchrotron Radiation Facility (SSRF, Shanghai, China), integrated and scaled using XDS and the CCP4 program Pointless and Aimless (68–70). The structure of MBP-B2 was determined by molecular replacement using the MBP structure from PDB 1ANF as an initial searching model with Phaser (71). The structural model was built using Coot (72) and refined using PHENIX (73). The structure of MBP-B2 C213A and A216V was determined using WT MBP-B2 structure as the initial search model. Figures were generated using PyMOL (The PyMOL Molecular Graphics System, Version 2.0 Schrödinger, LLC). The statistics of the data collection and refinement are shown in Supplementary Table S4. The B2 trimer model was generated with Alphafold 2 (74). Relevant crystallographic data collection and refinement statistics are provided in Supplementary Table S4. Experimentally determined 3D structures can be found from the Protein Data Bank (PDB ID: 8JZP and 8JZ5).

SEC-MALS Analysis
SEC-MALS were performed using a Superdex 200 increase column (Cytiva) combined with multi-angle laser light scattering using a Wyatt HELEOS-II 18-angle photometer coupled to a Wyatt Optilab rEX differential refractometer (Wyatt Technology Corp.). Experiments were carried out at room temperature with a protein concentration of 2.0 mg/mL and a flow rate of 0.5 mL/minute in 20 mmol/L Tris-HCl pH 8.0, 200 mmol/L NaCl, 0.3 mmol/L TCEP. The data were analyzed using the ASTRA 6.1 software (Wyatt). The molecular mass was determined across the protein elution peak.

CRISPR/Cas9 Knock-In mESCs and His Pulldown
PmlKO cells were generated as described previously (21). To generate PmlL222G mESCs, gRNA targeting mouse Pml (5′-GGTTGTGACATTGGCT GTG-3′ and 5′-GCAGCTGGACTTTCTGGTCT-3′) and recombinant Cas9 protein were synthesized from IDT to form Alt-R CRISPR/Cas9 ribonucleoprotein. mESCs were transiently transfected with Alt-R CRISPR/Cas9 ribonucleoprotein by using Amaxa mouse ES cell Nucleaseptor kit (Lonza, catalog no. VPH-1001) and program number A-013 from the nuclease 2b device (Lonza). After three days, 200 mESCs were spread on 150-mm cell culture dishes and cultured until forming visible colonies. After isolation and expansion, the DNA was extracted from these clones and genotyping was performed using PCR primers: 5′-GGTTGTGACATTGGCT GTG-3′ and 5′-GCAGCTGGACTTTCTGGTCT-3′. Products were sequenced with primer: 5′-ATCTCTTGTACCTGTGCTGG-3′ (Eurofins Genomics). mESCs were transduced using viral particles produced by Platinum-E cells, as described above, after transfection with MSCV-ires-GFP constructs expressing Hiss₃₃-HA-SUMO2. Hiss₃₃-HA-SUMO2 conjugates were purified using NiNTA agarose beads (Qiagen, catalog no. L30210) using Guanidium denaturing lysis as described before (21).

Mouse Model Generation
PmlL222G mice were generated by CRISPR/Cas9 genome editing, performed on BALB/cByJ mice using the electroporation method (75). Briefly, 3- to 4-week-old BALB/cByJ females were superovulated using CARD HyperOva (Cosmo bio, #KYD-010-EX) and human chorionic gonadotropin, Sigma; #CG-10) and then mated with males (8–20 weeks) to get zygotes. crRNA, tracrRNA, ssDNA, and Cas9 nucleases were purchased from IDT and electroporated (NEPA21, Sonidal) to introduce Pml point mutation encoding A220V substitution.
using Pml target site: 5′-gtgctggagtgtgctgtaagg-3′ and ssDNA donor sequence: 5′-GAACGCTGCTGCGCGACGGCTGTG-3′. Genotyping was performed using PCR primers: 5′-GGTGTTGACAGTCGTGGTCG-3′ and 5′-GACGCTGGACTTCTTC. 

**In Vivo Oxidative Stress Induction Models**

For the transcriptomic study, an early oxidative stress model was used. A female mice cohort (8–10 weeks) were treated with one intraperitoneal (i.p.) injections of 20% carbon tetrachloride CCl 4 (Sigma, catalog no. 289116) diluted in mineral oil (Sigma, catalog no. M8410) or one intraperitoneal injection of mineral oil (2.5 μL/g, n = 5 for each group). Mice were sacrificed 18 hours after injections and livers were dissected as follows: left median lobes were stored in RNAlater solution (Invitrogen, catalog no. AM7021) before RNA extraction, right median lobes were frozen in tissue freezing medium (Leica Biosystems, catalog no. 14020108926), right lobes were frozen in liquid nitrogen for protein extraction, and left lobes were fixed in AFA fixative solution (VWR, catalog no. 11656713) for 24 hours and embedded in paraffin for histology staining.

To study a model of longer oxidative stress induction, liver fibrosis was triggered on a female cohort by using 5 weeks treatment of 20% CCl 4, two intraperitoneal injections per week (n = 7 CCl 4-treated, n = 3 oil-treated). Mice were sacrificed 48 hours after the last injection, and livers were dissected as follows: right median lobes were stored in RNA later solution (Invitrogen, catalog no. AM7021) before RNA extraction, right median lobes were frozen in tissue freezing medium (Leica Biosystems, catalog no. 14020108926), right lobes were frozen in liquid nitrogen for protein extraction, and left lobes were fixed in AFA fixative solution, embedded in paraffin. The protocol was approved and performed in accordance with animal welfare and ethical guidelines (accreditation number B75–10–08).

**Picrosirius Red Staining and Fibrosis Quantification**

To assess the liver fibrosis, paraffin-embedded tissue sections (6 μm) were deparaffinized, rehydrated, and stained during 1 hour in a 0.1% Picrosirius Red homemade solution: Direct80 (Sigma; catalog no. 365348) diluted in an aqueous solution saturated in picric acid. The stained liver sections were washed in acidified water, dehydrated in several ethanol baths, cleared in SubX (Leica Biosystems, catalog no. 3803670E), and mounted with a permanent mounting medium. Each stained slide was scanned using the Zeiss Axioscan 7 (Carl Zeiss Micro-Imaging). The red collagen fibers stained by Picrosirius Red were measured using an open source software, QuPath (76).

**RNA Extraction and GeneChip Analysis**

Total RNA was extracted using TRIzol (Life Technologies) according to the manufacturer’s protocol. Triplicate samples were generated for each genotype, from 3 Pml KO, 3 Pml WT, and 3 PmlA220V mice. MTa1.0 Affymetrix Protocol was performed as follows: RNA quantification and quality control was performed using the HT RNA Reagent Kit (Perkin Elmer, catalog no. CLS960010), the DNA SKRNA/CZEx LabChip (Perkin Elmer, catalog no. 760435), and the Caliper LabChip Microfluidics System (Perkin Elmer, catalog no. GX1133NN0432). One-hundred nanograms of total RNA was amplified, labeled, and fragmented using GeneChip Plus Reagent Kit (Thermo Fisher Scientific, catalog no. 902314). Each sample was hybridized onto GeneChip Mouse Transcriptome Array 1.0 (Thermo Fisher Scientific, catalog no. 902514), washed, and stained using the GeneChip Hybridization, Wash, and Stain Kit (Thermo Fisher Scientific, catalog no. 900720) and the Affymetrix Fluidics Station 450 (Thermo Fisher Scientific, catalog no. 60110150). Array scanning was performed with the Affymetrix GeneChip Scanner 3000 7G (Thermo Fisher Scientific, catalog no. 54714280), using the Command Console software (Thermo Fisher Scientific) and then analyzed using the Affymetrix rma-sketch routine [Transcriptome Analysis Console (TAC) software v.4.0.1, Thermo Fisher Scientific]. Raw microarray data (CEL files) were corrected for background, log2-transformed, and normalized using the standard method RMA (robust multivariable average) implemented in the oligo package (77). Quantile normalization was then applied to mitigate the effects of technical variables using Limma package (78) and probe sets were annotated using mta10transcriptcluster.db package. A linear model fitted in Limma package was performed to identify differential gene expression between PmlKO versus PmlWT or PmlKO versus PmlWT in basal conditions and after 18 hours of CCl 4 treatment. Differentially expressed genes were identified on the basis of the FDR <0.05 and filtered with a fold change absolute value >2. GSEA were then performed to identify significant hallmark gene sets using the fgsea and misgdb packages.

**Statistical Analysis**

Statistical tests performed with GraphPad prism are indicated in the figure legends. Kruskal–Wallis test was used to determine the P value and look for significant changes in PML dynamics at NBs in PmlKO fibroblasts stably expressing GFP-PML. All data are expressed as mean ± SD of technical or biological replicates as indicated. For all graphs, *P < 0.05, **P < 0.01, and ***P < 0.001.

**Data Availability Statement**

Experimentally determined 3D structures can be found from the Protein Data Bank (PDB ID: 8J2D and 8J25). Sources for reagents and cells are indicated in Supplementary Tables S2 and S3. Primary transcriptomic data are accessible on ArrayExpress (accession ID: E-MTAB-13183). The data generated in this study are available upon request from the corresponding authors.

**Authors’ Disclosures**

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**Authors’ Contributions**

Attention to the nuances of arsenic(III) complexation and stability in biological systems.

30. Han MJ, Hao J, Christodoulatos C, Korfiatis GP, Wan LJ, Meng X. Direct evidence of arsenic(III)-carbonate complexes obtained using...


