

# Mechanisms of action and resistance to all-*trans* retinoic acid (ATRA) and arsenic trioxide (As<sub>2</sub>O<sub>3</sub>) in acute promyelocytic leukemia

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**Abstract** Since the introduction of all-*trans* retinoic acid (ATRA) and arsenic trioxide (As<sub>2</sub>O<sub>3</sub>) for the treatment of acute promyelocytic leukemia (APL), the overall survival rate has improved dramatically. However, relapse/refractory patients showing resistance to ATRA and/or As<sub>2</sub>O<sub>3</sub> are recognized as a clinically significant problem. Genetic mutations resulting in amino acid substitution in the retinoic acid receptor alpha (RAR $\alpha$ ) ligand binding domain (LBD) and the PML-B2 domain of PML-RAR $\alpha$ , respectively, have been reported as molecular mechanisms underlying resistance to ATRA and As<sub>2</sub>O<sub>3</sub>. In the LBD mutation, ATRA binding with LBD is generally impaired, and ligand-dependent co-repressor dissociation and degradation of PML-RAR $\alpha$  by the proteasome pathway, leading to cell differentiation, are inhibited. The PML-B2 mutation interferes with the direct binding of As<sub>2</sub>O<sub>3</sub> with PML-B2, and PML-RAR $\alpha$  SUMOylation with As<sub>2</sub>O<sub>3</sub> followed by multimerization and degradation is impaired. To overcome ATRA resistance, utilization of As<sub>2</sub>O<sub>3</sub> provides a preferable outcome, and recently, a synthetic retinoid Am80, which has a higher binding affinity with PML-RAR $\alpha$  than ATRA, has been tested in the clinical setting. However, no strategy attempted to date has been successful in overcoming As<sub>2</sub>O<sub>3</sub> resistance. Detailed genomic analyses using

patient samples harvested repeatedly may help in predicting the prognosis, selecting the effective targeting drugs, and designing new sophisticated strategies for the treatment of APL.

**Keywords** APL · PML-RAR $\alpha$  · ATRA · Arsenic trioxide (As<sub>2</sub>O<sub>3</sub>) · Drug resistance

## Introduction

Almost two decades ago, the prognosis of acute promyelocytic leukemia (APL) was critically poor due to fatal coagulation disorders at diagnosis [1, 2]. Even with conventional chemotherapy using anthracyclines, more than 70 % of APL patients showed poor prognosis [3, 4]. After introduction of all-*trans* retinoic acid (ATRA) in the clinical setting in combination with conventional chemotherapy, the prognosis of APL has improved dramatically, with the result that more than 85 % of patients now achieve complete remission (CR) and nearly 70 % of patients can be cured [5–8]. Since 1994, the marked effectiveness of As<sub>2</sub>O<sub>3</sub> in APL patients, even in relapsed patients after combination therapy with ATRA, has been confirmed [9–12]. When As<sub>2</sub>O<sub>3</sub> is utilized as a single agent, ~70 % of patients can be cured, whereas nearly 90 % of patients can be cured if As<sub>2</sub>O<sub>3</sub> is utilized in combination with ATRA [13, 14]. Although outcomes of APL treatment with ATRA and/or As<sub>2</sub>O<sub>3</sub> in combination with conventional chemodrugs have improved, relapsed/refractory patients are still observed in the clinical setting and drug resistance to ATRA and As<sub>2</sub>O<sub>3</sub> has been recognized as a critical problem.

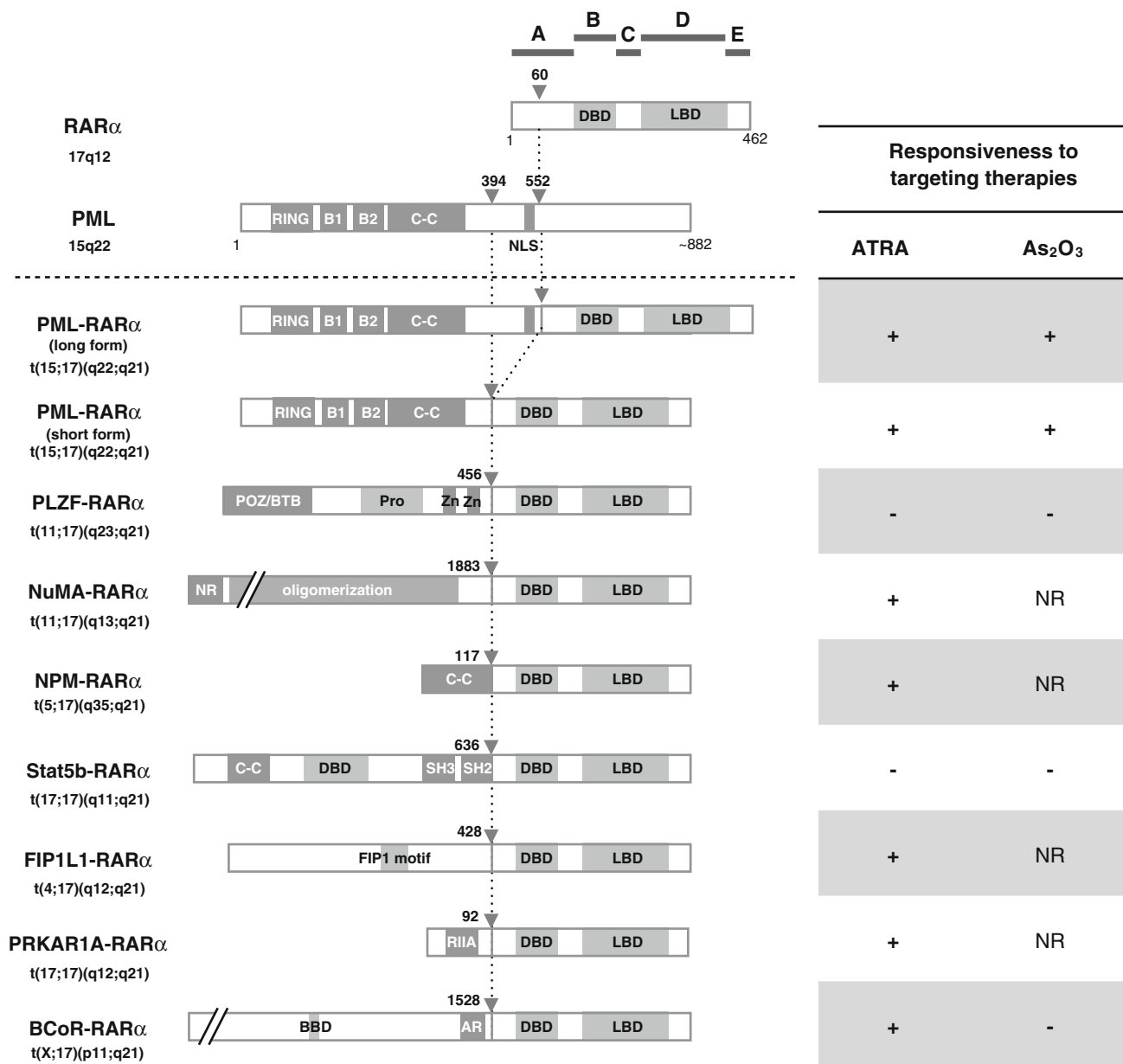
More than 98 % of APL patients carry the t(15;17) translocation, which results in fusions of the retinoic acid

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receptor alpha ( $RAR\alpha$ ) gene with the promyelocytic leukemia (PML) gene,  $PML-RAR\alpha$  (Fig. 1) [15–17]. A very limited number of patients, showing APL phenotype without t(15;17), exhibit a variety of X- $RAR\alpha$  fusions (Fig. 1) [18–25]. Interestingly, some patients expressing X- $RAR\alpha$  show clinical resistance to ATRA and/or

$As_2O_3$ . Previous reports have indicated that both ATRA [26, 27] and  $As_2O_3$  [28–30] have rigorously defined molecular targets, an improved understanding of their molecular mechanisms of action and resistance may be important to further improving clinical outcomes in APL treatment.



**Fig. 1** Schematic representation of PML-RAR $\alpha$  and X-RAR $\alpha$  fusion protein confirmed in APL. Chromosomal translocations resulting in the fusion protein are also indicated under the name of fusion protein. Long and short forms of PML-RAR $\alpha$  with or without nuclear localizing signal (NLS) are reported [86]. ATRA and  $As_2O_3$  responsiveness in the clinical setting and/or in vitro analyses is indicated in the right panel. Gray triangles indicate break points of chimeric protein. Numbers indicate the amino acid positions. A to

E functional domains in RAR $\alpha$ , DBD DNA binding domain, LBD ligand binding domain, RING really interesting new gene finger domain, B1 and B2 B-box motifs, C-C coiled-coil domain, POZ/BTB pox virus and zinc finger/BR-C, ttk and bab domain, Pro proline rich domain, Zn zinc finger domain, NR nuclear reassembly, RIIA dimerization domain, BBD BCL6-binding domain, AR ankyrin repeats, + sensitive, - resistant, NR not reported

## Mechanisms of action of molecular targeting drugs to APL cells

### ATRA

Wild-type RAR $\alpha$  is a nuclear hormone receptor that binds to consensus sequence DR5 (five bases spaced between two AGGTCA motifs) in target gene promoters, normally as heterodimer with retinoid X receptor (RXR) [31–33]. Without ligands, ATRA and 9-*cis* retinoic acid, RAR-RXR heterodimer induces transcription repression throughout chromatin remodeling by recruiting transcription co-repressors, such as N-CoR/SMRT large protein complexes, that contain histone deacetylases (HDACs) [27, 34–37] and histone methyltransferases [38–40]. In the presence of ligand ( $\sim 10^{-7}$  M), the co-repressor complexes dissociate from RAR-RXR, and transcriptional de-repression and activation are induced [34–37, 41]. PML-RAR $\alpha$  binds to DR5 of target gene promoters primarily as a homodimer, but also as a heterodimer with RXR [42, 43], and induces transcription repression by recruiting N-CoR/SMRT complexes and polycomb group repressive complex 1 and 2 (PRC1/2) [39, 40], which contain histone methyl transferases, in the absence of ligands [27] (Fig. 1). PML-RAR $\alpha$  can be SUMOylated at K160 of the PML protein to recruit death domain-associated protein (DAXX), resulting in the transcriptional repression of target genes [44]. Even in the presence of physiological concentration of ligand ( $10^{-7}$  M), the co-repressor complex still binds with PML-RAR $\alpha$  and the transcriptional repression cannot be dissolved. In the presence of pharmacological concentration of ATRA ( $10^{-6}$  M), transcription activation can be induced by dissociation of co-repressor complexes from PML-RAR $\alpha$  and proteasome-dependent PML-RAR $\alpha$  degradation [45–47].

### As<sub>2</sub>O<sub>3</sub>

The efficacy of As<sub>2</sub>O<sub>3</sub> on APL cells was first reported by Chen et al. in 1996 [28], who showed the dual effect of apoptosis at relatively high concentrations (0.5–2  $\mu$ M/L) and partial differentiation at low concentrations (0.1–0.5  $\mu$ M/L) in both ATRA-responsive and ATRA-resistant APL cells. As<sub>2</sub>O<sub>3</sub> induces the targeting of nucleoplasmic PML-RAR $\alpha$  with a micro speckled pattern into nuclear bodies with a normal speckled pattern prior to degradation [30, 48–50]. As<sub>2</sub>O<sub>3</sub> induces the formation of reactive oxygen species (ROS) [30], which induce multimerization of PML-RAR $\alpha$  through intermolecular disulphide crosslinks at PML B1-domain (Fig. 2) and PML-RAR $\alpha$  SUMOylation by ubiquitin-conjugating enzyme 9 (UBC9) [30]. A recent report indicated that As<sub>2</sub>O<sub>3</sub> directly binds with PML at the C–C motif in the PML B2-domain, and that PML SUMOylation can be induced by enhancement of UBC9

binding at the PML RING domain [29, 30, 50]. SUMOylated PML recruits RING finger protein 4 (RNF4), which is known as a SUMO-dependent ubiquitin ligase [51], and polyubiquitylated PML-RAR $\alpha$  can be degraded by ubiquitin–proteasome pathway [29, 49, 51].

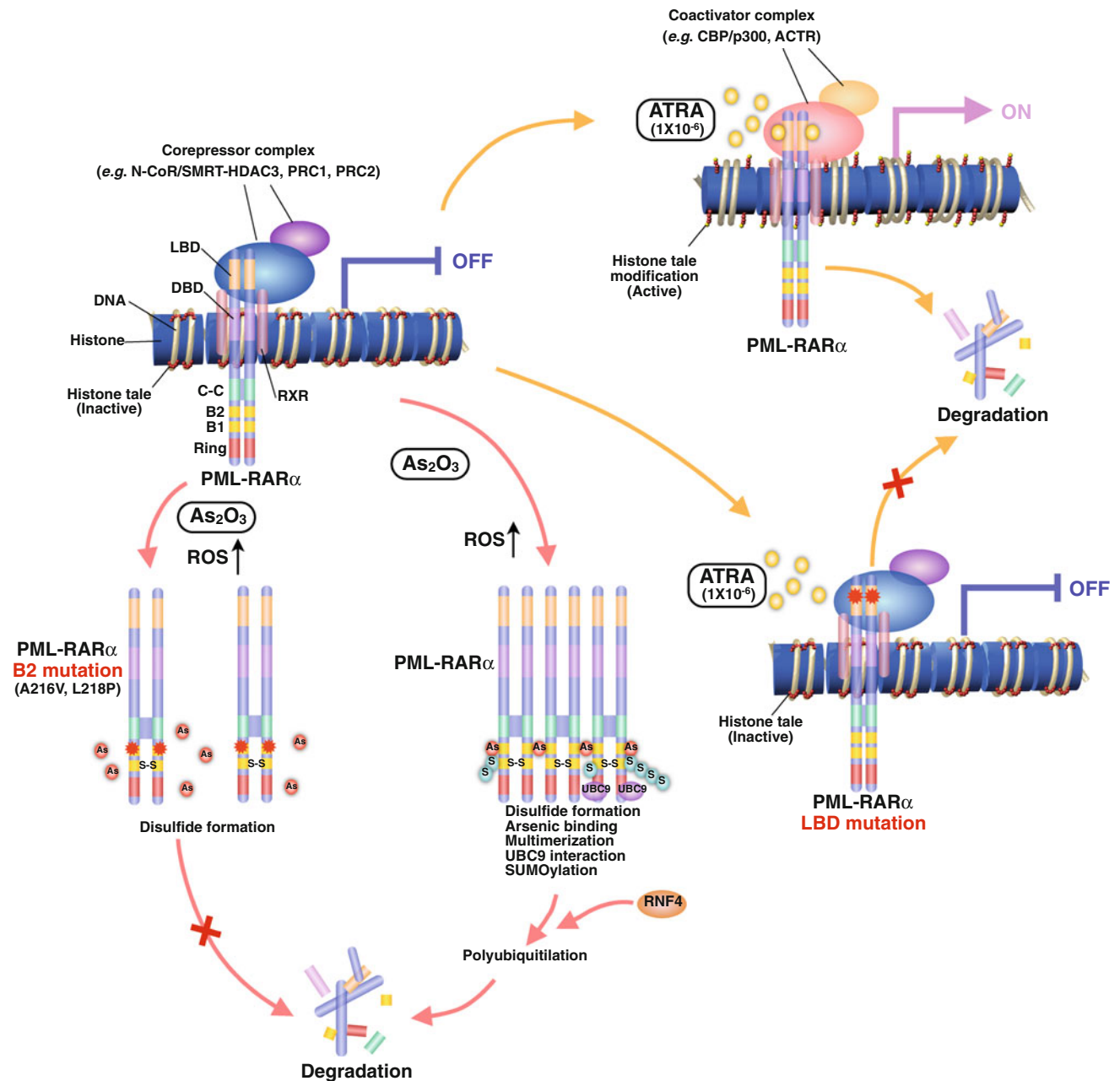
## Molecular mechanisms of drug resistance in APL cells

From the molecular mechanisms of ATRA and As<sub>2</sub>O<sub>3</sub> effectiveness as indicated above, several mechanisms of drug resistance have been speculated [52]. In this section, we outline the molecular mechanisms of resistance that are thought to be significant from the clinical perspective.

### RAR $\alpha$ fusion proteins in APL

In very limited cases with APL phenotype, RAR $\alpha$  translocations with X-genes other than PML (PLZF [18], NuMA [19], NPM [20], STAT5b [21, 53], FIP1L1 [22], PRKARIA [23, 24], and BCOR [25]) resulting in the production of X-RAR $\alpha$  fusion protein have been reported (Fig. 1). PML-RAR $\alpha$  forms mainly homodimers, and it has been reported that homodimerization of PML-RAR $\alpha$  is critical for the pathogenesis of APL [42, 43]. Sternsdorf et al. [54] indicated that forced homodimerization of RAR $\alpha$  induces ALP-like leukemia in a mouse model, indicating that the dimerization domain of the fusion protein may be critical to the induction of leukemogenesis by X-RAR $\alpha$ . In fact, homodimerization through specific domains (coiled-coil; PML-, NPM-, and STAT5b-, POZ/BTB; PLZF-, RIIA; PRKARIA-, and so on) has been confirmed in all X-RAR $\alpha$  proteins. Interestingly, in PML-, PRKARIA- [24], and BCOR-RAR $\alpha$  [25], heterodimerization with RXR is also important for transformation and/or RARE binding.

Since those chimeric proteins all hold RAR $\alpha$  DNA binding domain (DBD) and ligand binding domain (LBD), ATRA responsiveness is speculated in all cases. However, ATRA resistance has been confirmed clinically in cases showing PLZF-RAR $\alpha$  [18, 34, 41] and STAT5b-RAR $\alpha$  [21, 53, 55] fusions. One explanation for ATRA resistance is that the N-CoR/SMRT-corepressor complex interacts with PLZF, even in the presence of pharmacological concentration of ATRA, such that transcriptional de-repression cannot occur at RAR $\alpha$  target gene promoters [34, 41]. The molecular mechanisms of ATRA resistance in STAT5b-RAR $\alpha$ -expressing cells has not been fully explicated. Wild-type Stat5b is localized in cytoplasm, but STAT5b-RAR $\alpha$  aberrantly localizes in nucleus [21]. STAT5b is a component of the janus kinase (JAK)-STAT signaling pathway, and phosphorylation of STAT5b by JAK causes homodimerization and translocation into the nucleus, where it acts as a transcription factor [56]. Aberrant transcription



**Fig. 2** Molecular mechanisms of action and resistance to ATRA and  $As_2O_3$  in APL cells. PML-RAR $\alpha$  are found mainly as homodimers through the C–C domain of PML, and partially as heterodimers with RXR. PML-RAR $\alpha$  binds with target gene promoter in the absence of ligand, and recruits co-repressor complexes, such as N-CoR/SMRT complexes containing histone deacetylases (e.g. HDAC3) [34–37, 41] and PRC1/2 complex containing histone methyltransferases (e.g. EZH2) [39] to repress the gene expression. Histone tail deacetylation and/or methylation are related to transcription repression. In the presence of pharmacological concentration ( $1 \times 10^6 \mu\text{M}$ ) of ligand (ATRA), co-repressor complexes are dissociated from RAR $\alpha$ , while co-activator complexes containing histone acetyltransferases (e.g. p300/CBP) are recruited, and transcription activation occurs. In the

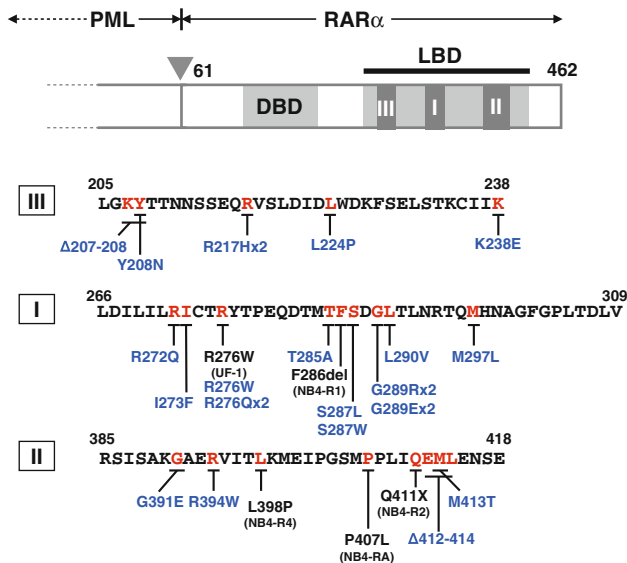
cases of PML-RAR $\alpha$  with LBD mutations, ligand binding with LBD is interfered and co-repressor dissociation does not occur in the presence of pharmacological concentrations of ATRA. In the presence of  $As_2O_3$ , the formation of reactive oxygen species (ROS) is induced, and PML intermolecular disulfide crosslinks through B1 domain, that induce multimerization, and SUMOylation of PML by ubiquitin-conjugating enzyme 9 (UBC9) occur.  $As_2O_3$  directly bind with PML-B2 domain and enhancing UBC9 binding and SUMOylation of PML. SUMOylated PML recruits RING finger protein 4 (RNF4), and is polyubiquitylated by RNF4, and proteasome-dependent degradation occurs. If PML-RAR $\alpha$  has PML-B2 mutation, direct binding of  $As_2O_3$  with PML is impaired, and polyubiquitylation and degradation are perturbed

regulation of STAT5b target genes in addition to RAR $\alpha$  target genes by STAT5b-RAR $\alpha$  may be related to ATRA resistance.

On the other hand, As<sub>2</sub>O<sub>3</sub> resistance in clinical setting was observed in patients expressing PLZF- [57, 58], STAT5b- [55], and BCoR-RAR $\alpha$  [25]. The As<sub>2</sub>O<sub>3</sub>-binding C–C motif is confirmed in PML-B2 domain, and As<sub>2</sub>O<sub>3</sub> binding is critical for the multimerization followed by PML-RAR $\alpha$  degradation [29, 30, 42]. Lack of As<sub>2</sub>O<sub>3</sub> binding sites in X-RAR $\alpha$  protein may be one explanation of loss of As<sub>2</sub>O<sub>3</sub> responsiveness. However, no direct effect of As<sub>2</sub>O<sub>3</sub> on RAR $\alpha$  has been reported.

### Mechanisms of resistance to ATRA

A number of mechanisms have been proposed to explain ATRA resistance in APL patients expressing PML-RAR $\alpha$ , such as amino acid substitution in RAR $\alpha$  LBD domain by genetic mutations, increased catabolism of ATRA, presence of cytoplasmic retinoic acid binding protein (CRABP), and abnormal ATRA delivery to the cell nucleus. Only genetic mutations on the RAR $\alpha$  LBD domain in PML-RAR $\alpha$  have been confirmed as an ATRA-resistant mechanism, from both clinical observations and in vitro molecular analyses [59–66]. Genetic mutations (missense, nonsense, and deletions) on RAR $\alpha$  LBD domain



**Fig. 3** Genetic mutations resulting in amino acid substitution in PML-RAR $\alpha$  LBD confirmed in clinically ATRA-resistant patients and ATRA-resistant cell lines. Mutations are confirmed in 3 cluster regions (zones I to III) in RAR $\alpha$ -LBD [66]. Red letters indicate amino acids substituted in specific patients and/or cells. Amino acid substitutions and deletions in ATRA-resistant patients are indicated in blue letters. Substitution in ATRA-resistant cell lines indicated in black. Names of cell lines are indicated in brackets. The position of the mutation is described with reference to normal amino acid sequence of RAR $\alpha$ 1 [31]

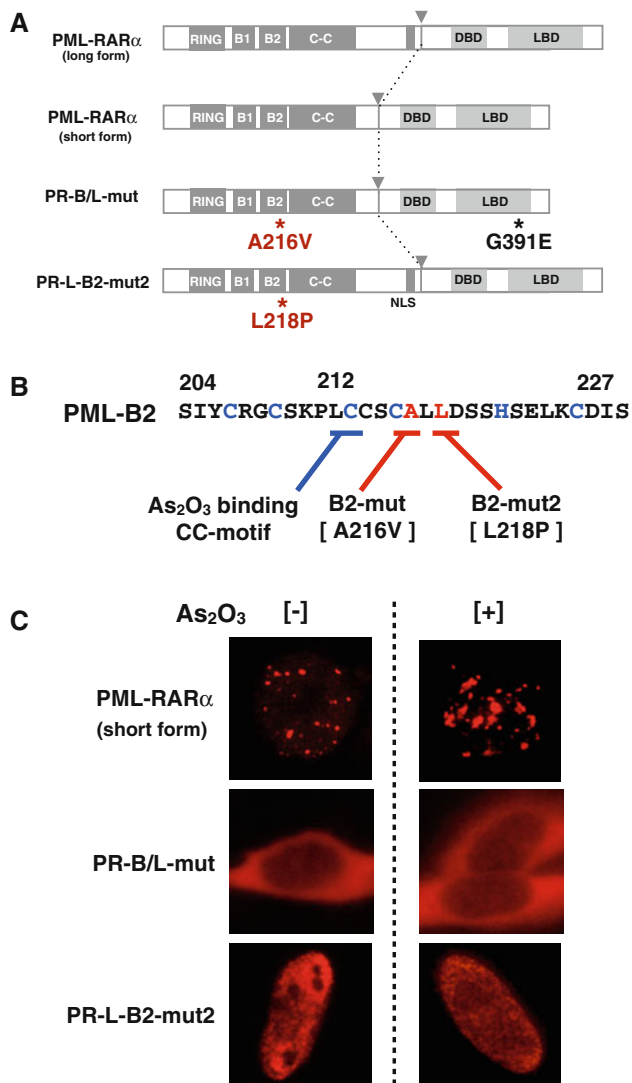
have been confirmed in ATRA-resistant patients and APL cell lines, which grow despite pharmacological concentrations of ATRA, as summarized in Fig. 3. These mutations accumulate in the three subregions (zones I, II, and III in Fig. 3) of the LBD domain [66]. Gallagher et al. [66] reported that PML-RAR $\alpha$  LBD mutation was confirmed in 18 of 45 (40 %) relapse patients treated with ATRA/chemotherapy. In vitro analyses using ATRA-resistant NB4 cells (NB4-R1, -R2 [67], -R4 [60], and -RA [61]) and mutated-PML-RAR $\alpha$  expressing Cos-1 cells [65] indicated that ATRA binding affinity with mutated PML-RAR $\alpha$  was generally lower than that with PML-RAR $\alpha$  without mutations, due to conformational changes in LBD. Furthermore, ligand-dependent N-CoR/SMRT co-repressor release and co-activator recruitment (e.g. ACTR histone acetyltransferase), which are critical for the transcriptional activation of genes with RARE sites and morphological cell differentiation, was impaired under the therapeutic dose of ATRA [60, 65, 67].

To overcome ATRA resistance, a number of therapeutics has been tested in vitro and in vivo. Several clinical reports indicated that As<sub>2</sub>O<sub>3</sub> rescue most of relapsed/refractory patients treated with ATRA/chemotherapy [9–12, 68]. Am80, a synthetic retinoid that shows higher binding affinity with PML-RAR $\alpha$  than ATRA, is utilized in the clinical setting [69–71]. Am80 is approximately 10 times more potent than ATRA as an in vitro inducer of differentiation in NB-4 and HL60 cells, and is chemically more stable than ATRA [72, 73]. Histone deacetylase (HDAC) inhibitors [74], such as sodium butyrate (NaF), valproic acid (VPA), and trichostatin A (TSA), have been utilized with ATRA and are expected to transcriptionally activate PML-RAR $\alpha$  target genes to inhibit co-repressors complexes that contain HDACs [75–77]. Another approach to overcoming the resistance uses other molecular targeting therapeutics, such as gemtuzumab ozogamicin (GO), an anti-CD33 monoclonal antibody linked with calicheamicins [78, 79].

### Molecular mechanisms of resistance to As<sub>2</sub>O<sub>3</sub>

Even for relapsed/refractory patients following treatment with ATRA/chemotherapy, As<sub>2</sub>O<sub>3</sub> therapy is highly effective, with a complete remission rate of more than 80 % [80–82]. Although the CR rate is high even in relapsed patients, resistance to As<sub>2</sub>O<sub>3</sub> treatment has been recognized as a clinically critical problem. Information on As<sub>2</sub>O<sub>3</sub> resistance remains limited compared with that on ATRA resistance.

Recently, we reported two cases showing clinical As<sub>2</sub>O<sub>3</sub> resistance after treatment with ATRA/chemotherapy, which exhibited missense mutations leading to substitution of amino acids in the PML-B2 domain in PML-RAR $\alpha$  [50, 68, 83]. One patient with the M3 variant, expressing PML-



**Fig. 4** Genetic mutations resulting in amino acid substitution in PML-B2 domain confirmed in clinically  $As_2O_3$  resistant APL patients. **a** Schematic representation of PML-RAR $\alpha$  chimeric protein with B2-domain mutation. One patient held PML-B2 mutation (A216V) and RAR $\alpha$ -LBD mutation (G391E) on short form PML-RAR $\alpha$  (PR-B/L-mut), and another patient held PML-B2 mutation (L218P) on long form PML-RAR $\alpha$  [68]. **b**  $As_2O_3$  direct binding dicysteine motif (C212/C213) [29, 30] and mutated positions in  $As_2O_3$ -resistant patients (C216 and L218) occur quite close to each other. **c** Flag-tagged PML-RAR $\alpha$  short form, PR-B/L-mut, and PR-B2-mut2 were over expressed in HeLa cells with or without  $As_2O_3$ . Over expressed PML were detected by immunofluorescence staining using anti-Flag antibody. When using PML-RAR $\alpha$  short form without  $As_2O_3$ , PML body was confirmed in the microspeckled pattern in cytoplasm. After incubation with  $As_2O_3$ , PML bodies showed macro granular patterns. When using PR-B/L-mut or PR-B2-mut2, the PML body showed diffuse pattern in cytoplasm or nucleus. No difference was seen with/without  $As_2O_3$

RAR $\alpha$  short form without nuclear localizing signal (NLS) [84], showed ATRA and  $As_2O_3$  resistance at his terminal stage. Significant clonal expansion of PML-RAR $\alpha$  mutant leading to A216V (PML-B2 domain mutation) and G391E

(RAR $\alpha$ -LBD mutation) was confirmed in leukemia cells harvested at the terminal stage (Fig. 4a, b). In vitro analysis using wild-type and mutant PML-RAR $\alpha$  (PR-B/L-mut)-expressing HeLa and HL60 cells indicated that PML-RAR $\alpha$  (short form) localized in cytoplasm as micro speckled pattern without  $As_2O_3$ , and as a macro granular pattern after adding  $As_2O_3$  (Fig. 4c; PML-RAR $\alpha$ ). In contrast, PR-B/L-mut localized in cytoplasm with diffuse pattern without  $As_2O_3$ , and no change was confirmed in the presence of  $As_2O_3$  (Fig. 4c; PR-B/L-mut). Another case carried an L218P mutation, also in the PML-B2 domain (PR-B2-mut2), in PML-RAR $\alpha$  long form with NLS. PML-RAR $\alpha$  long form localized in nucleus, while PR-B2-mut2 was diffusely localized in the nucleus. No change was confirmed with or without  $As_2O_3$  (Fig. 4c; PR-B2-mut2). Further in vitro analysis using PML-RAR $\alpha$  overexpressed HeLa cells indicated that SUMOylation of PR-B/L-mut and PR-B2-mut2 after  $As_2O_3$  treatment was strictly impaired. Recent reports have indicated that direct  $As_2O_3$  binding to PML-B2 domain is critical for the serial reaction including SUMOylation, multimerization, and degradation [29, 30]. Jeanne et al. conclude that dicysteine C212/C213 in PML-B2 domain may be the direct  $As_2O_3$  binding motif. From these results, genetic mutations identified in  $As_2O_3$ -resistant patients resulting in A216V and L218P may contribute to  $As_2O_3$  resistance through impairment of direct  $As_2O_3$  binding to PML-RAR $\alpha$  due to conformational changes in  $As_2O_3$  binding sites. Further accumulation of patients for genetic analyses is required for confirming the clinical significance of PML-B2 domain mutations in  $As_2O_3$  resistance.

## Conclusion

Although the overall survival of APL has been significantly prolonged since the introduction of ATRA and  $As_2O_3$ , relapse/refractory disease due to ATRA and/or  $As_2O_3$  resistance remains a serious clinical problem. Additional genetic mutations in PML-RAR $\alpha$  and another gene, such as FLT3-ITD or TP53 [66, 85], may contribute to disease progression and drug resistance in APL. Detailed genomic analyses using clinical samples harvested repeatedly from patients may help for predicting prognosis, selecting effective targeting drugs, understanding molecular backgrounds, and designing sophisticated new therapeutic strategies.

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