PU.1 downregulation in murine radiation-induced acute myeloid leukaemia (AML): from molecular mechanism to human AML

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Abstract

The transcription factor PU.1, encoded by the murine Sfpi1 gene (SPI1 in humans), is a member of the Ets transcription factor family and plays a vital role in commitment and maturation of the myeloid and lymphoid lineages. Murine studies directly link primary acute myeloid leukaemia (AML) and decreased PU.1 expression in specifically modified strains. Similarly, a radiation-induced chromosome 2 deletion and subsequent Sfpi1 point mutation in the remaining allele lead to murine radiation-induced AML. Consistent with murine data, heterozygous deletion of the SPI1 locus and mutation of the −14 kb SPI1 upstream regulatory element were described previously in human primary AML, although they are rare events. Other mechanisms linked to PU.1 downregulation in human AML include TP53 deletion, FLT3-ITD mutation and the recurrent AML1-ETO [t(8;21)] and PML-RARA [t(15;17)] translocations. This review provides an up-to-date overview on our current understanding of the involvement of PU.1 in the initiation and development of radiation-induced AML, together with recommendations for future murine and human studies.

Introduction

Just over a decade following the discovery of X-rays by Wilhelm Roentgen in 1895, the first cases of leukaemia were suspected in medical radiation workers (1). Over the past 70 years, a variety of epidemiological studies provided support for an increased leukaemia incidence after both high and low dose radiation exposure (radiotherapy and CT-scan, respectively). The continuing epidemiological survey of the Japanese atomic bomb survivors estimates that ~50% of all leukaemia cases observed in survivors exposed to >5 mGy, are associated with radiation exposure. Remarkably, over the last 15 years of this follow-up, acute myeloid leukaemia (AML) became the pre-dominant radiation-associated leukaemia, accounting for ~80% of excess leukaemia cases (2). Although a clear association between radiation exposure and leukaemia development is acknowledged, today, 80 years since two-time Nobel Prize winner Marie Curie died of radiation-induced leukaemia, the underlying mechanisms remain unidentified. Elucidating the cytogenetic and molecular alterations in murine radiation-induced AML (rAML) should provide further insight in the genetic basis of human radiation leukaemogenesis. Here we provide an overview on our current understanding of the involvement of the haematopoietic transcription factor PU.1 in the initiation and development of murine rAML, and seek to further define its involvement in human primary and therapy-related AML (tAML).

Murine modelling of rAML

Since 99% of human protein-coding genes are also present in mice and given the power of murine genetic interventions (including gene knock-in/-down), the use of murine models remains the most representative and ethical option available to study the cytogenetic and molecular mechanisms underlying radiation leukaemogenesis. The CBA mouse strain is regarded...
as the primary model in the study of rAML due to the very low background leukaemia incidence (<1/1000), the reproducible rAML induction in ~20% of mice exposed to a single acute 3 Gy X-irradiation, and the histopathological similarities with human myeloid leukaemia (3). The CBA inbred strain originates from the cross of a Bagg albino female and a DBA male. Three rAML susceptible CBA substrains [CBA/H, MRC Harwell (UK); CBA/Ca, Institute of Animal Genetics (UK); CBA/Cne, ENEA Casaccia Laboratory (Italy)] have been extensively used in the study of radiation leukaemogenesis (4). Beside the CBA strain, three further mouse strains were described previously as moderately susceptible to rAML: the RF, SJL/J, and the C3H/He strains. For the above-mentioned reasons, we will mainly focus on the CBA leukaemogenesis model and its relevance to rAML in humans. 

Cytogenetic aberrations following X-ray exposure

Twenty-four hours following a single acute exposure to 3 Gy whole-body X-irradiation (the optimal AML induction dose), all CBA/H mice exhibit bone marrow cells carrying chromosome 2 aberrations as assessed by G-banding, at an approximately 2-fold greater frequency in chromosome 2 compared with chromosomes 1 and 3 (5). Conversely, chromosomal aberration frequencies in chromosomes 1, 2 and 3 of non-susceptible mouse strains (such as C57BL/6 and AKR) are statistically identical (6). Over time, an increasing number of mice show clonal expansion of bone marrow cells with chromosome 2 aberrations. After 12–18 months, ~20% of the irradiated mice develop rAML (5). Leukaemic mice present in most cases with hepato-/splenomegaly and myeloblastic infiltration of the bone marrow, liver and spleen (3).

The first experimental murine rAML cases were described in the early 1930s. However, it was not until 1977 that a partial deletion of one chromosome 2 homologue was reported as the primary event in radiation-induced leukaemogenesis (4). Almost 20 years later, the loss of a chromosome 2 homologue (Sfpi1 gene) was postulated (5). Recently, the R235 point mutation was reported as not being the primary event in radiation-induced leukaemogenesis (4). Interestingly, in ~85% of murine rAML cases the remaining Sfpi1 copy exhibits point mutations confined to a single CGG sequence (Table 1; Sfpi1 DNA sequence from the Mouse Genome Informatics (MGI) entry MGI:98282). The amino acid residue arginine 235 (R235) is replaced with cysteine (R235C, 62%), histidine (R235H, 9%), serine (R235S, 8%) or leucine (R235L, 2%). The first cytosine of the CGG sequence is often methylated (10,16). Spontaneous deamination of 5-methylcytosine leads to a C to T transition via uracil formation and the replacement of thymine in one of the two daughter strands during the next replication round. Similarly, the mutation spectrum of 24 human primary AML cases reported mainly transitions, with C to T transition as the most common single nucleotide mutation (19). To be noted, TET2, an important epigenetic regulator, which oxidates 5-methylcytosine, is often found mutated in human primary AML (20). We have recently sequenced exon 5 in a large murine rAML panel (>100 cases). Remarkably, no mutations could be found outside codon 235 (unpublished observations). It is surprising that no additional passenger mutations are captured between the occurrence of the initiating event (chromosome 2 deletion) and the second hit (R235 point mutation), as the latency for murine rAML is over a year.

Recently, the R235 point mutation was reported as not being a major rate limiting step in murine rAML (21). There are data suggesting that this point mutation probably leads to complete abolition of PU.1 activity (22), and that mice carrying a deletion of the other allele might develop AML relatively soon after the mutation is acquired. To verify this observation, it will be important to investigate AML frequency and latency in mice engineered to carry a R235 point mutation (see Future directions). It was also postulated that hemizygosity for one of the numerous genes located in the MDR could facilitate radiation leukaemogenesis (21). For example, the DDB2 gene is present in the MDR and is involved in nucleotide excision repair. Nevertheless, this repair pathway is associated with the resolution of bulky adducts and pyrimidine dimerization, and not with abasic sites and damaged bases which are corrected by the base excision repair pathway, and its role in point mutagenesis has yet to be clarified.

The two-hit model of rAML involves a first irreversible mutational hit (interstitial deletion of one Sfpi1 gene on chromosome 2) creating intermediate cells that have a growth advantage but which are not fully malignant. Subsequently, intermediate cells acquire a second mutational hit (point mutation in the remaining Sfpi1 copy), resulting in the formation of a malignant cell which undergoes further clonal expansion and eventually develops into cancer (23). This two-hit model is supported by the finding that Sfpi1 mutations are only observed in rAMLs with a partially deleted chromosome 2 homologue (9,10). Whereas 87% of (CBA/H × SJL) F1 rAMLs (i.e. 2 rAML-susceptible genomes) harbour Sfpi1 point mutations (16), only 67% of (CBA/H × C57BL) F1 rAMLs (i.e. one rAML-susceptible genome [CBA/H] and one rAML-resistant genome [C57BL]) harbour this point mutation (18). This percentage decreases even further when backcrossing...
(CBA/H × C57BL/6) F1 mice to C57BL (11%). Intriguingly, none of these 11% Sfpi1 point-mutated rAMLs exhibited the most common C to T transition (17). The type of R235 point mutation appears to differentially affect PU.1 mRNA levels in rAML cell lines. Whereas mRNA levels in R235S AMLs are similar to those observed in normal bone marrow, mRNA levels are 4-fold higher in R235C AMLs. Interestingly, PU.1 mRNA levels did not correspond to protein levels (no detectable protein levels in R235C and R235H AMLs). This discrepancy might be explained by a greater stability of the R235S protein, a differential regulation of mRNA translation, or be related to protein phosphorylation as serine 235 has been identified as a strong novel candidate phosphorylation site (24). Furthermore, the mutations were assessed as being deleterious to protein function by a range of bioinformatics approaches. In contrast, several PU.1 target genes (including Flt3, GATA-1 and c-Jun) were downregulated, irrespective of the type of R235 mutation (24). While the fact that these are single base substitutions suggests that they are of spontaneous origin (13), it remains unknown at what time after irradiation these point mutations occur.

**Target cells for rAML development**

Little is currently known about the characteristics of the 'cell at risk' in radiation leukaemogenesis and it remains unknown whether the mutations leading to the generation of leukaemic stem cells occur in haematopoietic stem cells (HSCs) or progenitor cells. Adult HSCs reside primarily in the G0 phase of the cell cycle (25). Haematopoietic reconstitution following radiation exposure requires the release of the surviving HSCs from their quiescent state into G1. Approximately 60% of surviving HSCs actively cycle for >10 months, with the number of cell divisions per surviving HSC reported 10 times as high compared with unexposed mice (26). Upon entry in G1, DNA damage is primarily repaired by error-prone non-homologous end-joining, potentially promoting the formation of de novo mutations following DNA damage (25). Similarly, the enhanced replicative stress contributes to premature HSC ageing and induction of HSC premature senescence in a reactive oxygen species-dependent manner (27), hereby decreasing their DNA repair capacity and rendering them more prone to spontaneous mutations. This hypothesis is further supported by the finding of a common myeloid progenitor (CMP)-like leukaemic stem cell (Lin−Sca-1−c-Kit−CD34+) in a murine rAML model where it was postulated that, amid continuous cycling to reconstitute the CMP population, chromosome 2 deleted HSCs acquired additional aberrations, including point mutations of the remaining Sfpi1 allele (28).

The increased mutation rate with age might also play a role in the acquisition of secondary point mutations, hereby explaining the relatively long latency between exposure and rAML presentation (10). In addition, PU.1 directly regulates the HSC cell cycle machinery by inhibition of cell cycle activators and induction of cell cycle inhibitors: loss of PU.1 autoregulation dysregulated the balanced cell cycle regulation, leading to excessive proliferation (29), thereby increasing the acquisition of point mutations, and eventually resulting in either exhaustion of the HSC pool or leukaemia.

Recent advances in genetic engineering of mouse models allow tracking of cytogenetic alterations in living cells, from the time of irradiation and throughout tumour ontogenesis. In 2005, the Nutt laboratory generated a Sfpi1GFP reporter strain containing an internal ribosome entry site GFP cassette adjacent to the Sfpi1 gene within the radiation-induced MDR (30). Therefore, GFP fluorescence levels decrease (CBA/H Sfpi1GFP/GFP) or disappear (CBA/H Sfpi1ΔC2) following a radiation-induced chromosome 2 deletion, allowing this leukaemia initiating event to be detected by flow cytometry in live leukaemic cells (31). Using fluorescent in situ hybridisation, we previously demonstrated that partial chromosome 2 deletions are present in the HSC-enriched LSK subpopulation, but are not observed in the more differentiated lineage-negative cells (32).

**PU.1 and haematopoietic cell fate**

Beyond its role as a tumour suppressor, PU.1 plays a vital role in commitment and maturation of the lymphoid and myeloid lineages. Analysis of Sfpi1ΔGFP reporter mouse strains has revealed a dynamic regulation of PU.1 expression in adult haematopoietic cell lineages. All HSCs and common lymphoid progenitors express high levels of PU.1, with expression being reduced to a characteristic low level in early B-cell development. In contrast, two distinct PU.1 expressing subpopulations were identified within the CMPs. PU.1<sup>high</sup> CMPs were characterised as precursors of granulocyte/macrophage progenitors (GMPs), while the PU.1<sup>low</sup> CMPs were reported immediate precursors of the megakaryocyte/erythrocyte progenitors, confirming the hypothesis that downregulated PU.1 expression in CMPs restricts

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**Table 1. Frequency of Sfpi1 R235 point mutations in murine rAML**

<table>
<thead>
<tr>
<th>Genetic background</th>
<th>rAML-susceptible genomes</th>
<th>Radiation quality</th>
<th>Dose (Gy)</th>
<th>WT R235 CCG</th>
<th>R235C TGC</th>
<th>R235H CAC</th>
<th>R235L CTC</th>
<th>R235S AGC</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>CBA/H</td>
<td>2</td>
<td>X-ray</td>
<td>3 Gy</td>
<td>17% (1/6)</td>
<td>nd</td>
<td>nd</td>
<td>nd</td>
<td>15% (4/27)</td>
<td>(15)</td>
</tr>
<tr>
<td>C3H/He</td>
<td>2</td>
<td>X-ray</td>
<td>3 Gy</td>
<td>19% (5/27)</td>
<td>67% (18/27)</td>
<td>0</td>
<td>0</td>
<td>15% (4/27)</td>
<td>(9)</td>
</tr>
<tr>
<td>(CBA/H × SJL) F1</td>
<td>2</td>
<td>γ-ray</td>
<td>3 Gy</td>
<td>22% (4/18)</td>
<td>50% (9/18)</td>
<td>11% (2/18)</td>
<td>0</td>
<td>17% (3/18)</td>
<td></td>
</tr>
<tr>
<td>CBA/CaJ</td>
<td>2</td>
<td>γ-ray</td>
<td>2 Gy</td>
<td>13% (5/39)</td>
<td>54% (21/39)</td>
<td>18% (7/39)</td>
<td>5% (2/39)</td>
<td>3% (1/39)</td>
<td>(16)</td>
</tr>
<tr>
<td>CBA/H</td>
<td>2</td>
<td>neutron</td>
<td>0.4 Gy</td>
<td>0</td>
<td>100% (7/7)</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>(10)</td>
</tr>
<tr>
<td>(CBA/H × C57BL/6)</td>
<td>1.5</td>
<td>X-ray</td>
<td>3 Gy</td>
<td>14% (4/29)</td>
<td>66% (19/29)</td>
<td>7% (2/29)</td>
<td>3% (1/29)</td>
<td>10% (3/29)</td>
<td>(17)</td>
</tr>
<tr>
<td>(CBA/H × C57BL/6)</td>
<td>1</td>
<td>X-ray</td>
<td>3 Gy</td>
<td>33% (15/45)</td>
<td>49% (22/45)</td>
<td>2% (1/45)</td>
<td>0</td>
<td>16% (7/45)</td>
<td>(18)</td>
</tr>
<tr>
<td>(C3H/He × C57BL)</td>
<td>1</td>
<td>X-ray</td>
<td>3 Gy</td>
<td>89% (17/19)</td>
<td>0</td>
<td>0</td>
<td>11% (2/19)</td>
<td>(17)</td>
<td></td>
</tr>
</tbody>
</table>

nd, not determined.
their differentiation to the erythroid and megakaryocytic lineages (30). Small changes in PU.1 expression are also proposed to impact on cell fate decisions of the GMP through alterations in the PU.1 to CEBPA ratio: relatively high PU.1 commits GMPs towards a monocyte/macrophage fate, while increased CEBPA results in commitment towards granulocytes (33). Similarly, lymphomyeloid progenitors lengthen their cell cycle to allow PU.1 to accumulate to higher levels, which is functionally important for macrophage differentiation (34).

The proximal promoter of Sfpi1 contains, beside Oct-1, Sp1 and GATA-1 binding sites, binding sites for PU.1, suggesting autoregulation of its expression (35). Additional regulation is under control of a conserved distal regulatory enhancer (upstream regulatory element, URE) located −14kb from the transcriptional start site (36). Targeted deletion of the URE in mice (Sfpi1−/+−) reduced the PU.1 expression to ~20% of the wild-type level, leading to impaired maturation of myeloid progenitors (37). Molecular analysis of the URE revealed binding sites for various transcription factors influencing other contexts, since PU.1 overexpression inhibits erythroid lineage maturation, eventually resulting in erythroleukaemia (51).

**Gene regulation by PU.1**

Recent studies have identified tens of thousands of PU.1 binding sites in bone marrow derived macrophages. Most of the sites are located in introns and distant intergenic regions, and possess chromatin signatures of enhancers. PU.1 also binds to 80% of promoters associated with actively transcribed genes. Ectopic binding of PU.1 in those studies has an instructive role in nucleosome remodelling, changing chromatin marks and establishing functional enhancers (45,46). In this sense, PU.1 is considered to have a ‘pioneer’ role in establishing competence for genes to be regulated, in a positive or negative fashion, depending on the cross-talk with other transcription factors and co-factors. Prominent among the many known PU.1-regulated genes, are those encoding cytokine receptors and integrins (47,48).

PU.1 has long been recognized as a dose-dependent regulator of haematopoietic cell fate determination, however surprisingly few dose dependent target genes have been reported to date. Examples of dose-sensitive genes include Flt3, whose expression is reduced in Sfpi1−/− progenitors (49), and Sfpi1lac/lac and Sfpi1NINNI mice that show a dose-dependent suppression of various T-cell and natural killer cell genes in interleukin-3 dependent myeloid cell lines (42). A direct comparison of gene expression in adult HSCs derived from Sfpi1−/+− and Sfpi1−/− (generated from a PU.1 conditional knockout strain (22)) mice would greatly add to our understanding of how PU.1 functions in a dose-dependent manner.

**PU.1 and myeloid leukaemia**

In keeping with the role of PU.1 as a suppressor of rAML, Sfpi1−/+− mice or those resulting from the conditional deletion of the DNA binding Ets domain (exon 5) develop AML (22,37). For both models, ~95% of the mice develop AML in 8 months, a significant shortening compared with the 12–18 months latency period following radiation exposure. Leukaemia is observed even earlier (within 3 months) in (PU.1−/+×p53−/−) F1 mice, only expressing 10% of wild-type PU.1 levels. The highly aggressive AML phenotype is attributed to further upregulation of MYB and miR-155 upon p53 loss, resulting in additional downregulation of PU.1 (50). These data clearly indicate that the transcription factor PU.1 acts as a tumour suppressor. However, Sfpi1 can also act as an oncogene in other contexts, since PU.1 overexpression inhibits erythroid lineage maturation, eventually resulting in erythroleukaemia (51).

**Relationship between murine rAML and human (t)AML**

rAML arises following exposure to chemo- and/or radiotherapy with an average latency period of 5 years, and is more frequently accompanied by unbalanced cytogenetic abnormalities compared with primary AML (75% versus 51%, respectively). The cytogenetic abnormalities 5q−/−5 and 7q−/−7 are often overrepresented in tAML. Among patients with a normal karyotype, a similar incidence of molecular abnormalities is observed in both primary AML and tAML (52). A Danish TAML study predominantly observed FLT3 mutations in patients who previously received radiotherapy and in those patients with a normal karyotype (53). The most common aberrations were chromosome 5 and 7 deletions (50–60% of TAMLs), followed by FLT3-ITD and TP53 point mutations in 20% of TAMLs. Interestingly, the genetic defects 5q−/−5 and 7q−/−7 were positively associated with TP53 and AML1 point mutations, respectively (53). It is important to note that a comparison with murine rAML data is difficult as neither study distinguishes between TAML patients who received radiation therapy alone, chemotherapy alone or a combination of both. To overcome this limitation, we are currently analysing historical samples of TAML patients who received radiation therapy alone and which should provide a better understanding of human TAML development following radiation therapy. Similarly, FISH analysis of Japanese AML patients revealed that those patients heavily exposed (>1 Gy to the bone marrow) during the Hiroshima atomic bombings had a higher incidence of chromosomes 5, 7, 13 and 20 deletions, compared with non-exposed Japanese AML patients (54).

Recently, we reported the presence of FLT3-ITD mutations in murine rAML (3/30 rAMLs) (15). Remarkably, they were only found in rAML with an intact chromosome 2 and no Sfpi1 point mutation, suggesting the involvement of FLT3-ITD and Sfpi1 are mutually exclusive and which is in agreement with published data from the Danish TAML study (53). The observed murine FLT3-ITD mutations were similar to those seen in human primary AMLs (10–30bp insertion into the tyrosine-rich juxta membrane domain). Trisomy 8 is also observed in human primary and TAML (chromosome 8 is homologous to the murine chromosome 15). Half of the AML cases observed in PU.1−/+− mice (4/7 AMLs) gained a chromosome 15 copy (37). The smallest region gained
contains the proto-oncogene c-Myc. Interestingly, c-Myc expression was significantly elevated in PU.1-knockdown mice with AML (37). Similarly, c-Myc expression levels were significantly elevated in murine rAMLs with a partial chromosome 2 deletion, compared with rAMLs with an intact chromosome 2 (9).

Consistent with murine data, heterozygous mutations and deletions of the SPI1 locus (the human analogue of Sfpi1) have been described in human primary AML, although it is a rare event (55). Heterozygous SPI1 mutations were reported in 7% of a Japanese AML study (9/126 AMLs, with half of the cases comprising point mutations and the other half deletions). Mutated SPI1 led to a reduced function of the transcription factor and the median survival of patients with SPI1 mutations was significantly shorter than patients without SPI1 mutations. These mutations were predominantly found in undifferentiated and in (myeloid) monocytic leukaemia subtypes, which is in line with the physiological role of PU.1. Interestingly, they were not observed in leukaemic patients harbouring the chromosome translocations most commonly observed in primary AML, such as AML1-ETO and PML-RARA (55). In contrast with the results of the Japanese AML study, investigations of North-American and European cohorts reported SPI1 mutations in <1% of primary AML patients (56).

Four primary AML patients presented with a mutated NF-κB binding site in the URE of SPI1 (38), thereby suppressing PU.1 mRNA expression. Another primary AML case harboured a deletion spanning at least 40 kb of the SPI1 locus, including the URE region but no CEBPA, FLT3, and NPM1 mutations were detected. The PU.1 mRNA level was significantly lower compared with other AML-M2 patients and 10 times lower compared with unsorted bone marrow cells obtained from healthy individuals (56). Such minor deletions would escape detection by conventional sequencing techniques and may therefore further clarify the conflicting reports on the presence of SPI1 mutations in human primary AML patients. As the mutations in the PU.1 DNA binding domain observed from human primary AML (55) do not correspond to the residues mutated in murine rAML (16), it was speculated that SPI1 point mutations might be more often associated with tAML. However a small human tAML study (24 AML patients who had received therapy for a prior malignancy) did not report any SPI1 mutations in the coding, untranslated or promotor regions (18). To the authors’ knowledge, there are no studies reporting on SPI1 mutations in tAML patients who received radiation therapy alone.

Although SPI1 seems only infrequently mutated in human primary and tAML, several reports have highlighted downregulated SPI1 gene/PU.1 mRNA expression in primary AML patients. Approximately half of primary AML patients (9/20 AMLs) had lower SPI1 gene expression, compared with SPI1 expression in HSCs from healthy donors (57). Similarly, a Czech primary AML study reported decreased PU.1 mRNA levels in the majority of AML patients (27/36 AMLs) (50), which corresponds with our previous finding of decreased PU.1 mRNA levels in murine rAMLs with a wild-type SPI1 allele (31). Interestingly, TP53 deletions were only observed in human primary AMLs with low PU.1 levels, and concomitantly with elevated MYB and miR-155 levels, directly linking TP53 inactivation and a dysregulated MYB/miR-155/PU.1 pathway in human AML (50). Transduction of human primary AML blasts with a lentivector encoding PU.1 increased the myelomonocytic marker expression and decreased proliferation rates together with increasing apoptosis, changes characteristic of restored differentiation in these myeloid leukaemia blasts (58). Similarly, all trans retinoic acid therapy leads to in vivo differentiation of acute promyelocytic leukaemia blasts through increased PU.1 activity (59), resulting in complete remission in almost all leukaemic patients. Various other mechanisms seem involved in PU.1 downregulation in human primary AML (Figure 1). Firstly, the formation of fusion proteins

![Figure 1](https://academic.oup.com/carcin/article-abstract/36/4/413/300623)
following chromosome translocations, including AML1-ETO in t(8;21) (61,62) and PML-RARA in t(15;17) (62,63), confers reduced PU.1 expression. Similarly, internal tandem duplications in the FLT3 receptor tyrosine kinase suppress the PU.1 expression and function (62,64). Finally, with four of the top eight genes found mutated in human primary AML being epigenetic regulators, epigenetic silencing is most likely involved as well (20). This hypothesis is further supported by the findings that miR-155, a known regulator of PU.1 mRNA, is overexpressed in bone marrow samples of some primary AML subtypes (65), and that in high-risk myelodysplastic patients PU.1 downregulation is associated with DNA methylation of the PU.1 URE (66).

Future directions and conclusion

To begin to define how PU.1 functions as a tumour suppressor in rAML, we have recently generated a Sfpi1 point mutation mouse model. The Sfpi1 point mutation (Sfpi1pm) comprises a C to T substitution in the PU.1 DNA binding domain (R235) and is the most common base transition observed in murine rAML. Preliminary results show that Sfpi1pm mice die during late gestation, indicating the importance of the DNA binding domain in PU.1 functioning (unpublished observations). In-depth analysis is on-going to investigate the impact of this point mutation on haematopoiesis and (radiation) leukaemogenesis. It will be of great interest to see if the presence of the point mutation alters the AML frequency and latency. At the same time, we have developed a mouse model in which the radiation-induced chromosome 2 deletion and concomitant PU.1 loss can be detected early after exposure in live haematopoietic progenitor cells (i.e. knock-in of the mCherry reporter gene in the MDR). Both mouse models should help to characterise the cells at risk and to elucidate the molecular mechanisms underlying radiation leukaemogenesis, and assess how applicable they are to human primary and tAML. Furthermore, gene expression analysis in pre-leukaemic and AML populations of PU.1 knock-down models would aid deciphering the specific changes leading to leukaemia. Consequently, analysis of global PU.1 DNA binding via ChIP-sequencing in normal haematopoietic progenitors and AML cells in murine, and most importantly patient material, would further clarify the impact of reduced PU.1 activity on target gene regulation.

Overall, although PU.1 is rarely directly mutated in human primary and tAML, it appears to be commonly downregulated through a series of indirect mechanisms. The identification of biomarkers for PU.1 downregulation would greatly aid our understanding of how this event facilitates leukaemogenesis. Therefore, we suggest that, in future studies, the levels of PU.1 expression in human primary and tAML are carefully monitored.

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