

# Chapter 7

## Chronic Myeloid Leukaemia

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**Abstract** Chronic myeloid leukaemia (CML) was the first leukaemia associated with a unique genetic abnormality, the Philadelphia chromosome. This results from a reciprocal translocation between chromosomes 9 and 22, which generates the *BCR-ABL1* fusion gene encoding a constitutively active tyrosine kinase. The complex intracellular signalling initiated by BCR-ABL1 is responsible for disease development, and targeted tyrosine kinase inhibitors have been the most successful therapeutic advance in CML. In this chapter, we review the implications of

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BCR-ABL1 signalling in CML, how this knowledge revolutionized CML treatment, and discuss approaches to further improving therapeutic response by the targeting of leukaemic stem cells.

**Keywords** Chronic myeloid leukaemia • BCR-ABL1 • Tyrosine kinase inhibitor • Blast crisis • Leukaemic stem cell

## 7.1 Introduction

Chronic myeloid leukaemia (CML) was probably the first form of leukaemia to be independently recognized in 1845 by John H. Bennett, in Scotland, and Rudolf Virchow, in Germany [1]. The discovery of the Philadelphia (Ph) chromosome, in 1960 [2] was the first consistent chromosomal abnormality associated with a specific type of leukaemia, and was not only a breakthrough in cancer biology but also the first important clue to CML pathogenesis. In 1973, Rowley identified the Ph chromosome as a shortened chromosome 22 (22q-), result of a reciprocal t(9;22) (q34.1;q11.2) translocation [3]. In the next decade, the Ph chromosome was shown to carry a unique fusion gene, *BCR-ABL1* [4], the deregulated BCR-ABL1 tyrosine kinase activity was defined as the pathogenetic principle of CML [5], and the first animal models were developed [6]. Ultimately, this knowledge provided the basis for the design of a targeted therapy for CML with the development of ABL1 specific tyrosine kinase inhibitors (TKIs), which selectively inhibit the growth of *BCR-ABL1* positive cells *in vitro* and *in vivo* [7–9].

## 7.2 CML Characteristics and Disease Phases

CML is a clonal myeloproliferative disease originating in a single haematopoietic stem cell (HSC). It represents 15–20 % of the leukaemias in adults and has a relatively low incidence (1–1.5 new cases per 100,000 people per year). However, its prevalence is on the rise due to the significant improvement in its treatment over the past 15 years [10]. In the Western countries, the median age of patients at diagnosis is 55–65 years old, whereas it is significantly lower, averaging 38–41 years, in Asia, Africa, Southern/Eastern Europe and Latin America [11]. The disease affects both sexes, with a slight male preponderance (male:female ratio of 1.3:1).

The only known predisposing factor to CML is high-dose ionizing radiation, as best demonstrated by studies of survivors of the Hiroshima and Nagasaki atomic bomb explosions [12]. Apart from a borderline increased risk of CML in first-degree relatives of patients with myeloproliferative disorders [13], there is no evidence of an inherited disposition or association with chemical exposure.

In its natural history, CML is a tri-phasic disease, predominantly presenting in a chronic phase (CP) averaging around 3–7 years. In most cases of CP CML, the neoplastic expansion involves a leukaemic clone that differentiates into mature granulocytes which function normally, despite being derived from malignant progenitors. The ‘indolent’ phenotype of CP means that some patients are asymptomatic, and the diagnosis is frequently an incidental finding; however, the majority typically present with mild symptoms of fatigue, weight loss and sweats [14, 15]. CP progresses to either the transitional accelerated phase (AP) or transforms directly into blast crisis (BC). When present, the AP precedes BC by 2–15 months [16]. Transformation to BC is characterized by the presence, in the peripheral blood or bone marrow (BM), of 20 % or more blasts, which can be of myeloid (approximately 70 % of cases) or lymphoid (30 %) origin [17]. BC is clinically indistinguishable from acute leukaemia and can present leukocytosis, cytopenia, hepatosplenomegaly, enlarged lymph nodes, and marked refractoriness to treatment which results in a dismal clinical outcome, with a historical median survival of no more than 3–6 months [18]. Even with the advent of TKIs, response of BC to this type of therapy is minimal, and median survival is still only 9 months [19, 20].

Until the emergency of TKIs, the only curative treatment for CML was HSC transplantation, but this was restricted to a minority of patients, due to age restrictions and the need for a histocompatible donor. The prognosis has now substantially improved for most CML patients who respond well to TKIs, a proportion of whom are able to survive indefinitely without evidence of disease.

## 7.3 Molecular Pathogenesis

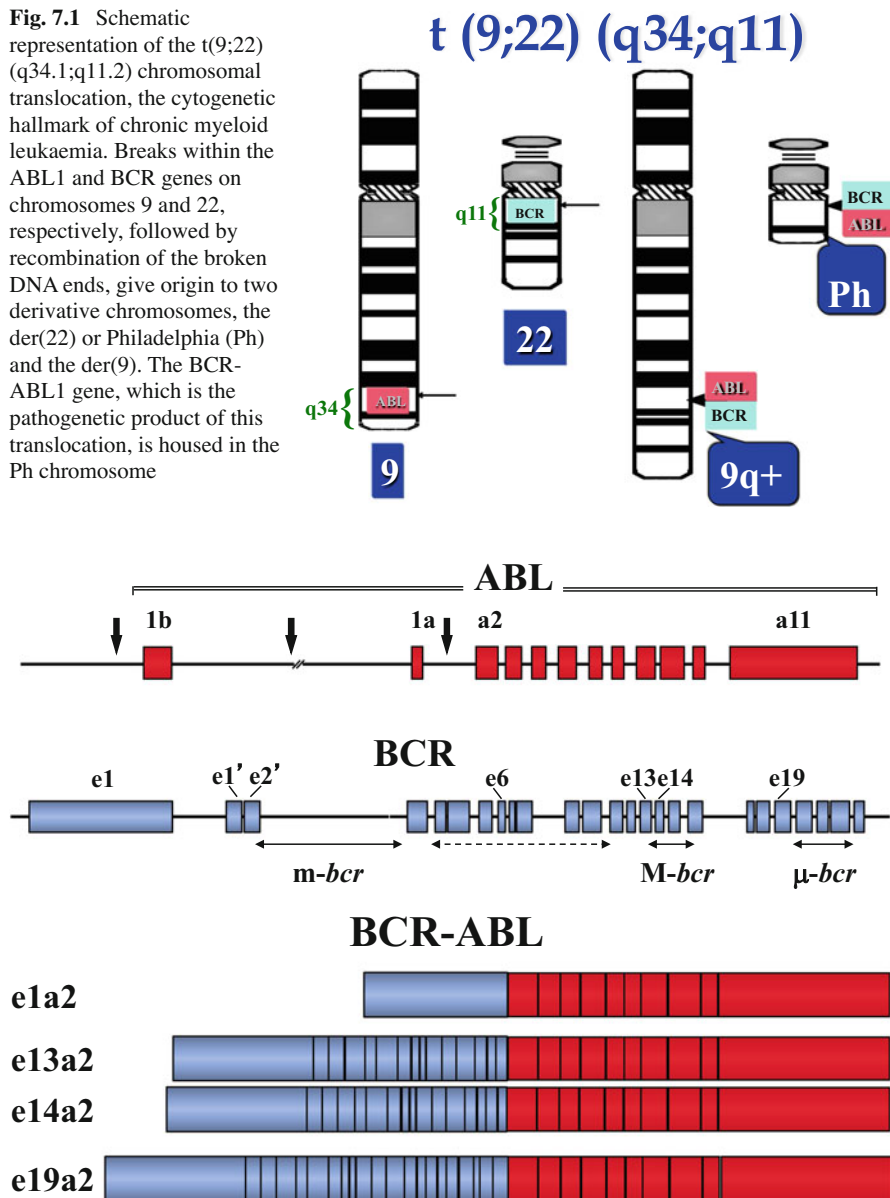
### 7.3.1 *The BCR-ABL1 Gene*

The t(9;22)(q34.1;q11.2) reciprocal translocation gives rise to two pathognomonic fusion genes, *BCR-ABL1* on the der(22) (Ph) chromosome, and *ABL1-BCR*, on the der(9) (Fig. 7.1). Although the latter is transcribed, there is no evidence that it has functional relevance to the disease [21]. Thus, it is the translation of the *BCR-ABL1* gene into an abnormal fusion protein that is responsible for the leukaemic process.

The breakpoints within *ABL1* at 9q34.1 can occur anywhere over a large (>300 kb) area at its 5' end, either upstream of exon 1b, downstream of exon 1a or, more frequently, between the two [22]. Regardless of the exact location of the breakpoint, splicing of the transcript yields an mRNA molecule where *BCR* is fused to *ABL1* exon a2 (Fig. 7.2).

In contrast to *ABL1*, breakpoints within *BCR* localize to one of three breakpoint cluster regions (bcr). In most CML cases and in about one third of Ph + acute lymphoblastic leukaemias (ALL), the break occurs within *BCR* exons 12–16 (previously exons b1–b5), defined as the major bcr (M-bcr) [22]. Due to alternative splicing, the mRNA usually contains the *BCR-ABL1* junctions e13a2 or e14a2

**Fig. 7.1** Schematic representation of the t(9;22) (q34.1;q11.2) chromosomal translocation, the cytogenetic hallmark of chronic myeloid leukaemia. Breaks within the ABL1 and BCR genes on chromosomes 9 and 22, respectively, followed by recombination of the broken DNA ends, give origin to two derivative chromosomes, the der(22) or Philadelphia (Ph) and the der(9). The BCR-ABL1 gene, which is the pathogenic product of this translocation, is housed in the Ph chromosome



**Fig. 7.2** Schematic representation of the ABL1 and the BCR genes disrupted in the t(9;22) (q34.1;q11.2). Exons are represented by *boxes* and introns by connecting *horizontal lines*. Breakpoint regions in ABL1 are illustrated as *vertical arrows*, and in BCR by the three double-headed *horizontal arrows*. The lower half of the figure shows the structure of the various BCR-ABL1 mRNA transcripts which are formed in accordance with the position of the breakpoint in BCR. Breaks in *m-bcr* give origin to BCR-ABL1 mRNA molecules with an e1a2 junction. The breaks in *M-bcr* occur either between exons e13 and e14 or between e14 and e15, generating fusion transcripts with a e13a2 or a e14a2 junction, respectively. Breakpoints in *μ-bcr*, the most 3' cluster region, result in BCR-ABL1 transcripts with an e19a2 junction

(originally b2a2 or b3a2) and is translated into a 210 kDa protein (P210<sup>BCR-ABL</sup>). The majority of Ph + ALL and very rare cases of CML, characterized by prominent monocytosis [23, 24], have breakpoints further upstream between exons e2' and e2, termed the minor bcr (*m-bcr*). The resulting e1a2 mRNA is translated into a 190 kDa protein (P190<sup>BCR-ABL</sup>). A third bcr (*μ-bcr*) is located downstream of exon 19, giving rise to a 230 kDa fusion protein (P230<sup>BCR-ABL</sup>), which is sometimes associated with an uncommon neutrophilic variant of CML [25, 26]. Although all three major BCR-ABL1 fusion proteins induce a CML-like disease in mice, they differ in their ability to induce lymphoid leukaemia [27].

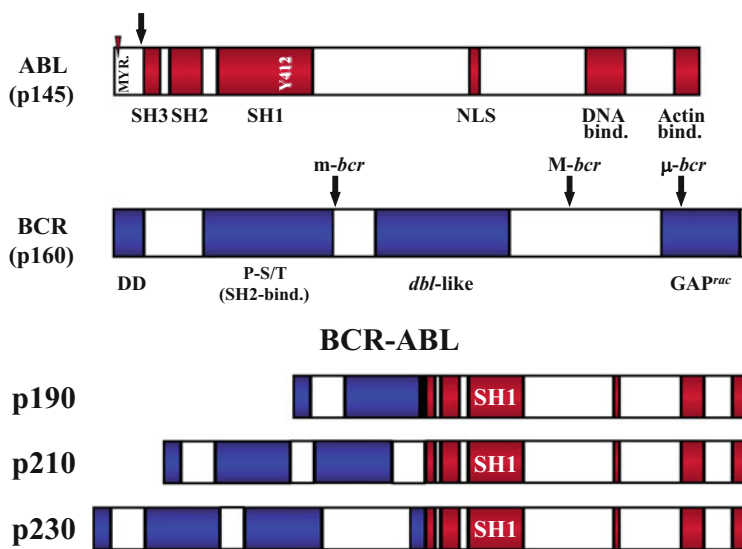
The mechanism by which the Ph chromosome is first formed and the time required for overt disease to appear are unknown. *BCR-ABL1* fusion transcripts can be induced in haematopoietic cells by exposure to ionizing radiation *in vitro* [28]; such induced translocations may not be random events but may depend on the cellular background and the particular genes involved. Translocations between *BCR* and *ABL1* may be favoured by their relative proximity during the interphase of cycling haematopoietic cells [29]. Furthermore, a 76 kb 'duplicon' near *ABL1* and *BCR* has been implicated in the translocation, but this mechanism is purely speculative [30].

The *BCR-ABL1* gene is expressed in all CML patients, but the reciprocal *ABL1-BCR* gene on the der(9) occurs in only 70 % of cases [21]. Approximately 20 % of CML patients have deletions on the der(9) and have significantly shorter survival than those lacking the deletions [31, 32]. Notably, absence of the *ABL1-BCR* gene, which is always included in the deleted region, does not by itself have the same ominous prognostic implication [33]. Similarly, no prognostic relevance of the der(9) deletions was observed on patients treated with TKIs [34, 35].

The idea that CML may result from a multi-step process was first broached over 30 years ago [36] but there is little evidence of additional abnormalities that precede the t(9;22) translocation. Even so, the presence of *BCR-ABL1* in any haematopoietic cell is not in itself sufficient to cause leukaemia, since *BCR-ABL1* is detectable at low frequency in the blood of many normal individuals [37, 38]. Thus the generation of a *correct BCR-ABL1* in a *multipotent HSC*, possibly under reduced immunological surveillance, is necessary to initiate the clonal expansion that leads to CML. This hypothesis is supported by the production of a CML-like disease in mice transplanted with *BCR-ABL1*-positive stem cells [6, 39, 40]. However, once established, the 'tempo' or aggressiveness of the CP disease varies in different patients and must be influenced by other factors.

### 7.3.2 The *BCR-ABL1* Protein

The BCR-ABL1 oncoprotein includes several important domains of its parental BCR and ABL1 normal counterparts, which endow it of specific biological properties (Fig. 7.3).



**Fig. 7.3** Schematic representation of the normal ABL1 (p145), the normal BCR (p160) and the leukaemia-associated BCR-ABL1 fusion proteins. Note that the variation between the three forms of BCR-ABL1 proteins is due to the different contributions of BCR rather than of ABL1 sequences to the hybrid product. The arrows in BCR indicate the sites of protein fusion arising from *m-bcr* (p190<sup>BCR-ABL</sup>), *M-bcr* (p210<sup>BCR-ABL</sup>) and  $\mu$ -*bcr* (p230<sup>BCR-ABL</sup>) breakpoints. Some special features and regions of these proteins are shown: In the ABL1 protein these are the myristoylation (MYR) site present in the human type 1b protein, the regulatory *src*-homology (SH) regions SH3 and SH2, the SH1 (kinase domain) with its principal site of autophosphorylation (Y412), the nuclear localisation signal (NLS), the DNA- and the actin-binding domains. In the BCR protein these are the dimerization domain (DD), the phospho-serine/threonine (P-S/T)-rich SH2-binding domain, the *dbl*-like and the *GAP<sup>rac</sup>* domains

In ABL1, they include the SRC-homology SH1, SH2 and SH3, a nuclear localisation signal, DNA and actin-binding domains, and in BCR a coiled-coil motif contained in amino acids 1–63 [41], the tyrosine at position 177 [42] and phospho-serine/threonine rich sequences between amino acids 192–242 and 298–413 [43]. The most important feature for its leukaemogenic potential resides in the fact that the tyrosine kinase of the ABL1 protein is constitutively activated by the juxtaposition of BCR. The BCR dimerization domains connect two BCR-ABL1 molecules which then phosphorylate their respective partners on tyrosine residues in the kinase activation loops [41]. The consequent increase of phosphotyrosine residues on BCR-ABL1 itself creates binding sites for the SH2 domains of other proteins. A host of substrates can be tyrosine phosphorylated by BCR-ABL1, the net result of which is deregulated cellular proliferation, decreased adherence of leukaemia cells to the BM stroma, reduced response to apoptotic stimuli, increased genomic instability and increased capacity for self-renewal [44, 45].

Tyrosine phosphatases counterbalance and regulate the effects of tyrosine kinases under physiological conditions. Two tyrosine phosphatases, SYP and PTPN1, have

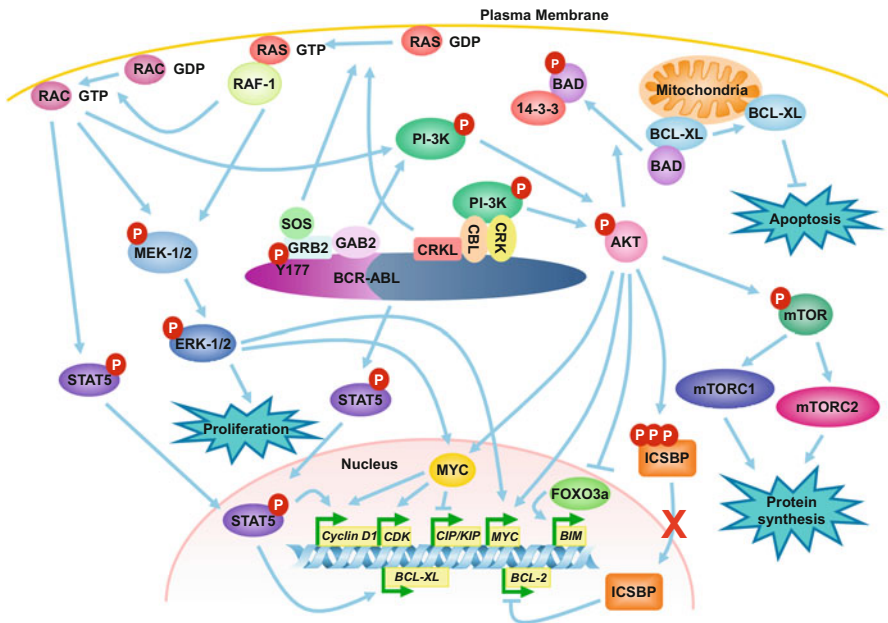
been shown to form complexes with BCR-ABL1, and both appear to dephosphorylate BCR-ABL1 [46, 47]. On the other hand, BCR-ABL1 protects itself from the protein tyrosine phosphatase 1 (PTPN6/SHP1), which can dephosphorylate BCR-ABL1 and induce its proteasomal degradation, by inhibiting the PTPN6/SHP1 activator PP2A [48].

### 7.3.3 Signalling and Disease

#### 7.3.3.1 Proliferation and Survival

BCR-ABL1 shifts the balance towards inhibition of apoptosis while simultaneously providing a proliferative stimulus through multiple signals. These are frequently difficult to separate but mostly involve PI3K/AKT1, JAK/STAT, RAS/RAF/MEK/ERK and MYC pathways (Fig. 7.4).

Once the adapter molecule GRB2 binds to P-Tyr177 on BCR-ABL1, it recruits SOS and constitutively activates RAS, which, in turn, activates MAPK3/ERK1 and MAPK1/ERK2 [42, 49]. Two other adapter molecules, SHC1 and CRKL, can also activate RAS after binding to BCR-ABL1 [50, 51]. Ultimately, activated MAPKs indirectly induce gene transcription and cell proliferation [49, 52].



**Fig. 7.4** Some of the major signalling pathways directly or indirectly regulated by BCR-ABL1 (see text for detailed descriptions)

Signalling from RAS can be relayed via RAC GTPases [53] to activate MAPK8/JNK, which is required for BCR-ABL1 malignant transformation [54]. Accordingly, downregulation of the JNK pathway negative regulator JUNB, by promoter hypermethylation, has been described in CML primary cells [55]. RAC GTPases themselves play an important role in BCR-ABL1 leukaemogenesis, activating STAT5, PI3K and MAPKs pathways [56]. Moreover, concomitant loss of *Rac1* and *Rac2* impaired the development of a myeloproliferative disease and increased survival of mice transplanted with BCR-ABL1-expressing cells [57].

Constitutive phosphorylation of STAT1 and STAT5 has been reported in several *BCR-ABL1* positive cell lines [58] and primary CML cells [59], and seems to be independent of JAK. STAT5 can be directly activated by BCR-ABL1 [60] or indirectly through GRB2/RAS/RAC or HCK [56] to then up-regulate target genes, such as *CCND1* (leading to cell cycle progression) and the anti-apoptotic *BCL2L1/BCL-XL* [61, 62]. Although one study found that BCR-ABL1 induced a CML like disease in *Stat5a/b*<sup>-/-</sup> mice [63], another reported that complete deletion of *Stat5a/b* locus turned mice resistant to BCR-ABL1 transformation [64]. In addition, knock-down of STAT5 in primary CML cells blocks Ph + colony formation [62], and cells expressing a mutant BCR-ABL1 unable to activate STAT5 or wild type BCR-ABL1 with a dominant negative STAT5 are more apoptotic than wild type cells [65]. Altogether, these results support a role for STAT5 in BCR-ABL1 transformation.

BCR-ABL1 forms complexes with PI3K, CBL and the adapters CRK and CRKL [66], in which PI3K, and the downstream AKT1 and mTOR, are constitutively activated [67]. In addition, activation of RAS and the adapter GAB2 by GRB2 cause constitutive activation of PI3K [62]. PI3K exerts its oncogenic effects mainly by activation of mTOR, which forms the mTORC1 and mTORC2 complexes that play important roles in the proliferation and survival of BCR-ABL1-positive cells [49, 68]. PI3K activity is required for BCR-ABL1-mediated leukaemogenesis, since its inhibition impairs BCR-ABL1 transformation of HSCs [49, 67]. PI3K also hyperphosphorylates the transcription factor (TF) IRF8/ICSBP, preventing its DNA binding and reverting its transcriptional repression of the antiapoptotic *BCL2* gene [69].

*AKT1* itself is an oncogene, and is essential for the resistance to apoptosis of BCR-ABL1-positive cells. It phosphorylates BAD, which promotes its sequestration by 14-3-3, and blocks its binding to BCL2 family members, consequently inhibiting apoptosis [70]. AKT1 also blocks apoptosis through phosphorylation of caspases [67], and downregulation of antiapoptotic *BCL2L1/BIM* [49].

Activation of MYC by BCR-ABL1 is dependent on the SH2 domain [71]. In addition, RAS/MAPK and PI3K/AKT1 pathways contribute to inducing *MYC* transcription or promoting MYC stability [67, 72]. Depending on the cellular context, MYC may transduce proliferative or apoptotic signals [67]; however, considering BCR-ABL1-mediated antiapoptotic mechanisms, the apoptotic arm of MYC is most likely inhibited in CML. Proliferation, on the other hand, may be induced by MYC's activation of cyclin and CDK transcription, repression of CIP/KIP family cyclin/CDK inhibitors' expression, and indirect induction of mTORC1 transcription [67].



### 7.3.3.2 Progression to Blast Crisis

CML progression is characterized by the occurrence of non-random chromosomal abnormalities. The most frequent are trisomy 8 (33 %), an additional Ph (30 %), isochromosome 17 (20 %), trisomy 19 (12 %), loss of the Y chromosome (8 % of males), trisomy 21 (7 %) and monosomy 7 (5 %) [73]. Although these changes are used as markers of disease progression, they may not necessarily be causal agents of transformation. Two important mechanisms and phenotypes related to the emergence of BC are addressed below.

#### Block in Differentiation

With progression of CML, the leukaemic clone undergoes differentiation arrest, resulting in a major increase of immature blasts at the expense of the terminally differentiated leucocytes. This differentiation arrest implies pathological interference with differentiation programmes involving the targeted activation/inactivation of tissue-specific genes by TF [74].

Abnormal CTNNB1/ $\beta$ -catenin signalling leads granulocyte-macrophage progenitors to acquire the stem cell-like capacity of unrestricted self-renewal [75]. In addition, interaction between CTNNB1 and BCR-ABL1 increases  $\beta$ -catenin transcriptional activity influencing leukaemic stem cell (LSC) lineage commitment as early as in CP, and loss of CTNNB1 impairs the self-renewal of CML stem-cells [76, 77].

Another mechanism of differentiation arrest is the down-modulation of the TF CEBPA by BCR-ABL1, in BC but not in CP, through regulation of pre- and post-transcriptional mechanisms [78, 79]. CEBPA activates transcription of the *CSFR3/GCSFR* and *IDI1* genes in myeloid cells, and its ectopic expression restores differentiation in BCR-ABL1-transformed cell lines or BC CML primary cells [80–83].

Additional causes of the block in differentiation in BC CML include mutations, translocations or deletions in genes that regulate differentiation and self-renewal of haematopoietic stem and progenitor cells, such as *GATA2* [84, 85], *RUNX1* [86–88], *ASXL1* [79, 87, 89], *IKZF1* [87, 90, 91] and *PAX5* [90, 92].

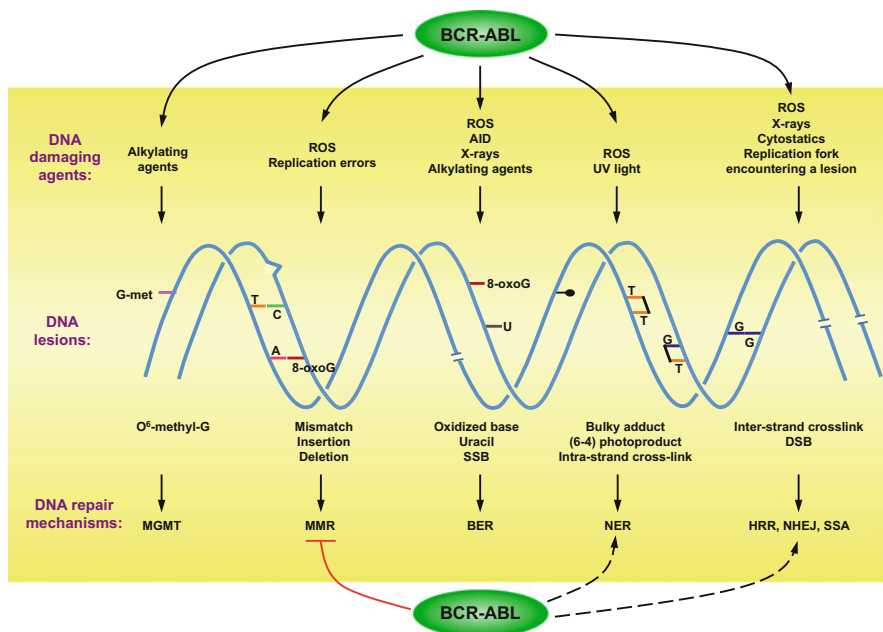
#### Genomic Instability

BCR-ABL1-transformed cell lines and CD34+ primary CML cells produce 2–6 times more ROS than the normal controls [93]. ROS can damage the DNA generating oxidized bases and double strand breaks (DSB). Accordingly, CD34+ CML cells accumulate three to eight times more oxidized bases and DSBs than normal cells [93]. At the same time, they display defective mismatch repair; stimulate DSBs repair but with low fidelity, through homologous recombination repair (HRR), non-homologous end-joining (NHEJ), and single strand annealing (SSA) repair mechanisms; and induce mutagenic nucleotide excision repair (NER), all of which

exacerbate genomic instability and contribute to disease progression (Fig. 7.5). The mechanisms of altered DNA repair in CML are addressed below.

ATR is a DNA damage ‘sensor’ that controls cell cycle check points. BCR-ABL1 was reported to translocate to the nucleus, following exposure to genotoxic agents, where it bound and inhibited ATR and CHEK1, allowing inappropriate DNA replication [95, 96]. In a contradictory study, however, ATR signalling was stimulated in BCR-ABL1-positive cells in response to genotoxic agents [97]. This result was further corroborated by recent findings that BCR-ABL1 inhibition reduces CHEK1 activation and cell cycle arrest in G2/M phase, and induces apoptosis in cells exposed to genotoxic agents [98]. Therefore, ATR signalling might contribute to chemotherapeutics resistance in CML.

The tumour suppressor BRCA1 is another ‘sensor’ that detects DNA damage and mediates cell cycle check points and HRR [99]. BRCA1 is virtually undetectable in CML cells and *BCR-ABL1*-transformed cell lines [100] and this absence contributes to the genomic instability observed in BCR-ABL1 cells [101]. To overcome BRCA1 deficiency, HRR occurs through the alternative RAD52-RAD51 pathway [102, 103].



**Fig. 7.5** BCR-ABL1 enhances DNA damage and deregulates DNA repair, the two main components of genomic instability. BCR-ABL1 positive cells accumulate more DNA lesions induced by endogenous and exogenous DNA genotoxic agents and, in parallel, activates cellular pathways which favour unfaithful DNA repair mechanisms. The overarching consequence of the two processes is the generation of improperly repaired DNA molecules containing point-mutations, insertions or deletions in genes which, once inappropriately expressed and/or activated, lead to the transformation into blast crisis (Figure modified from [94])

Both HRR and NHEJ promote less faithful ROS-induced DSB repair in *BCR-ABL1-transformed* cells [104]. Downregulation of PRKDC/DNA-PKcs, LIG4/DNA ligase IV and DCLRE1C/Artemis, and upregulation of LIG3/DNA ligase III $\alpha$ , WRN nuclease and RBBP8/CtIP in BCR-ABL1-positive cells may be responsible for the alternative error-prone NHEJ pathway observed in CML [105–108]. HRR, in turn, is abnormally stimulated to the detriment of its fidelity in CML due to BCR-ABL1-mediated overexpression and activation of RAD51, which promotes erroneous HRR when overstimulated [109–111]. Incorrect DNA repair can be prevented by mismatch repair, but BCR-ABL1 inhibits this process by abrogating heterodimerization of the mismatch repair proteins MLH1 and PMS2 [112]. SSA is a rare and unfaithful mechanism of DSB repair and BCR-ABL1 stimulates SSA activity in a dose-dependent manner and through up-regulation of *RBBP8/CtIP* [108, 113].

NER activity status in CML is controversial. In initial reports, BCR-ABL1 was found to interfere with NER proteins reducing NER activity [114, 115]. It was later suggested that P210<sup>BCR-ABL</sup> induced NER in myeloid but repressed it in lymphoid cell lines [116]. However, more recent findings reported no difference in NER activity between lymphoid and myeloid CML cell lines, and a BCR-ABL1 kinase-dependent increase in NER activity in CML cell lines [117].

Expression of BCR-ABL1 is also associated with upregulation of DNA polymerase  $\beta$  [118, 119], an enzyme involved in HRR, NER and base excision repair (BER) [120–122]. Due to its low-fidelity DNA repair, it might be expected that DNA polymerase  $\beta$  overexpression contributes to CML genomic instability. Accumulation of point mutations in CML might also result from BCR-ABL1 inhibition of UNG, the most active glycosylase during BER, in both CML primary and *BCR-ABL1-transformed* cells [123].

## 7.4 Targeted Therapy

The knowledge on BCR-ABL1 structure and function that accumulated over the past 30 years set up the scene for the design of ‘molecularly targeted’ therapy for CML. Since the tyrosine kinase activity of BCR-ABL1 is essential for disease development, it was the most attractive target for designer therapy, although not the only one approached [124–132]. Undoubtedly, the advent of TKIs, which block or prevent BCR-ABL1 oncogenic signalling, has been so far the most exciting and successful therapeutic advance in CML.

### 7.4.1 First Generation TKI: Imatinib

Imatinib mesilate (IM) is a small chemical compound which competes with ATP for binding to its pocket in the BCR-ABL1 kinase domain (KD), thus blocking the BCR-ABL1 oncogenic signal [45]. IM inhibits the kinase activity of all ABL1- and

ARG-containing proteins, the PDGFR family and the KIT receptor [133–135]. Such inhibition results in transcriptional modulation of various genes involved in the control of cell cycle, cell adhesion and cytoskeletal organization, leading the Ph + cell to an apoptotic death [44]. In addition, IM inhibits growth of CML primary cells and cell lines *in vitro* and *in vivo* [7, 8, 136].

In a phase I trial, IM showed little toxicity but proved to be highly effective [137]. The 8-year follow-up of the phase III IRIS trial reported an overall free survival rate (excluding discontinuation of therapy) of 85 % for CP CML patients under IM as first-line therapy, with 86 % of major molecular responses (MMR) [138]. In contrast, most of the responses of patients in BC are short-lived with very low (12–17 %) cytogenetic responses and median survival of 6.5–10 months [20].

#### 7.4.1.1 Resistance to IM

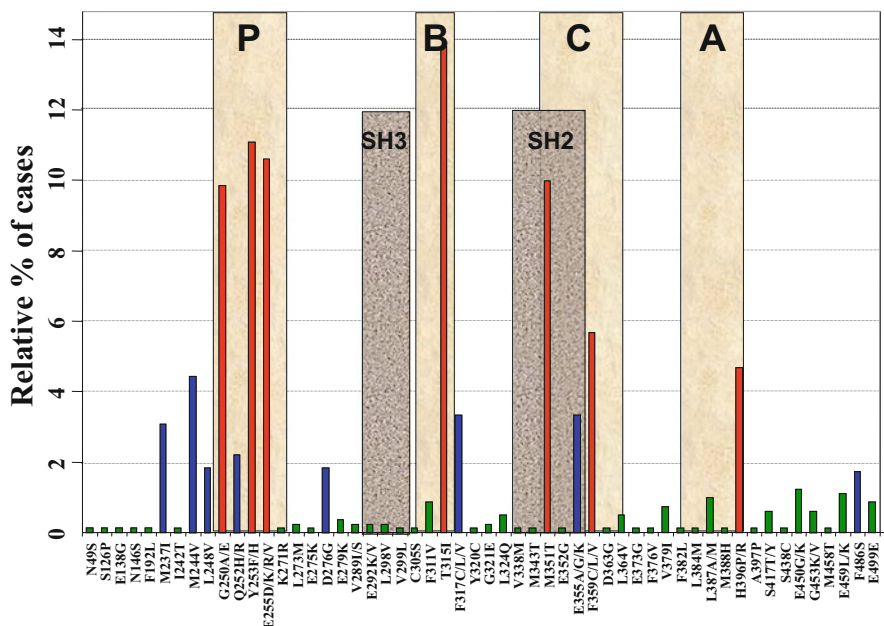
While the efficacy of IM is unquestioned, resistance to TKIs became a pressing challenge in CML treatment. The persistence of minimal residual disease and, more worryingly, the development of refractoriness to single drug therapy, have dampened the initial enthusiasm. At the 8-year follow-up on the IRIS study, only 55 % of patients remained on IM therapy, and in 16 % of those who discontinued this was due to unsatisfactory therapeutic outcome [138]. Other studies have reported even higher resistance rates, varying from 12 to 50 % [19].

The definition of resistance can be based on its time of onset as primary resistance, i.e., failure to achieve a significant cytogenetic response, and secondary or acquired resistance, i.e., progressive reappearance of the leukaemic clone after an initial response to the drug. In addition, resistance can also be classified as BCR-ABL1-dependent and -independent. The first group encompasses the emergence of leukaemic clones with mutations in the BCR-ABL1 KD [139], overexpression of the BCR-ABL1 protein [140, 141] and amplification of the BCR-ABL1 oncogene [142, 143]. The mechanisms of BCR-ABL1-independent resistance include mostly defects in drug transport in and out of the leukaemic cells, and activation of oncogenic pathways downstream of BCR-ABL1 [144].

The most common mechanism for acquired IM resistance is through the development of point mutations in the ABL1 KD of BCR-ABL1 [144]. These mutations are not induced by the drug but, rather, confer resistance to rare populations of progenitors which are selected due to their capacity to survive and expand in the presence of the drug.

Mutations can be broadly categorized into four groups: (i) those which directly impair IM binding; (ii) those within the ATP binding site; (iii) those within the activation loop; and (iv) those within the catalytic domain (Fig. 7.6).

The substitution of isoleucine for threonine at position 315 of ABL1, or T315I, reduces the affinity for the drug by preventing the formation of a hydrogen bond between T315 and the secondary amino group of IM, and by sterically preventing the binding of IM [143]. Another amino acid that makes contact with IM is phenylalanine 317, and its mutation to leucine (F317L) also leads to resistance.



**Fig. 7.6** Incidence of reported mutations within the kinase domain by percentage of total. The seven most frequent mutations are depicted in *red* and the following eight in *blue*; mutations shown in *green* have been reported in less than 2 % of clinical resistance cases. Specific regions of the kinase domain are indicated as P-loop or ATP binding site (P), imatinib binding site (B), catalytic domain (C) and activation loop (A). Also shown as SH2 and SH3 are the contact regions with SH2 and SH3 domain-containing proteins (Data based on [145, 146])

The ATP-binding loop (or P-loop) domain spans amino acids 248–256 [147]. Mutations in this domain are the most common and modify the flexibility of the P-loop destabilizing the conformation required for IM binding [148]. The most frequent of such mutations are substitutions at G250, Q252, Y253 and E255. An additional feature of clinical relevance is that IM-treated patients who harbour P-loop mutations have a worse prognosis than those with non-P-loop mutations [149–152].

The activation loop of the ABL1 kinase begins at amino acid 381 and can adopt a closed (inactive) or an open (active) conformation. IM forces ABL1 into the inactive conformation and is incapable of binding to the active one [153]. Mutations in the activation loop may disturb the energetic balance required to stabilize the closed conformation of the loop and, thus, favour the open conformation resulting in IM resistance [148].

Finally, some substitutions cluster in the catalytic domain (amino acids 350–363), a region that has a close topologic relation to the base of the activation loop. Therefore, mutations in this region can also influence IM binding [148].

The degree of IM resistance varies between mutations and is predicted to affect prognosis and response to treatment. Thus far, more than 100 different point mutations leading to a substitution of approximately 50 amino acids in the ABL1 KD have been identified in patients resistant to IM and this number is likely to increase with more sensitive methods of detection [154].

## 7.4.2 Second and Third Generation TKIs

### 7.4.2.1 Dasatinib

Dasatinib is a dual SRC/ABL1 kinase inhibitor that also binds to the ATP-binding site, but extends in the opposite direction from IM. It binds the inactive and active conformation of the ABL1 KD, has a greater affinity to this domain, and is more potent than IM [155]. In clinical trials, dasatinib showed significantly higher MMR and overall survival rates than IM for CP CML patients [156, 157]. CML patients in advanced phase also showed improved complete cytogenetic response (CCyR) rates under dasatinib; however, those are still low, at 32 % [158].

Dasatinib requires fewer contact points with ABL1 residues; therefore, it is active against several IM-associated mutations. The T315I and F317L mutations, however, lead to the least favourable responses [159–162]. Due to a direct interaction between F317 and dasatinib, several amino acid substitutions in this position result in dasatinib-resistant mutants, such as F317L, F317V, F317I, and F317S [150, 163]. In a phase III study of dasatinib in CP CML patients, development of mutations T315I, F317L, V299L, and, rarely, E255K correlated with loss of response [19].

### 7.4.2.2 Nilotinib

Nilotinib was designed as a chemical modification of IM and is 10–50 times more potent [164]. It also inhibits the activity of ARG, KIT, and PDGFRA and PDGFRB, but not SRC kinase. CP patients treated with nilotinib showed higher CCyR, MMR and overall survival rates, and lower transformation events than those under IM [19, 165, 166]. Moreover, in trials for patients with advanced CML, nilotinib treatment also resulted in higher CCyR rates than IM [19].

Similar to dasatinib, nilotinib inhibits the *in vitro* proliferation of most of the clinically relevant BCR-ABL1 mutants, except for the T315I [167–170]. Likewise, the degree of sensitivity/resistance to nilotinib also varies for individual mutants. Accordingly, the mutations T315I, E255K/V, F359C/V, and Y253H have shown association with lack of CCyR to nilotinib, followed by disease progression [170].

### 7.4.2.3 Bosutinib

Bosutinib is a potent second generation TKI that, like dasatinib, also has SRC inhibitory activity. In a phase III trial it showed higher MMR rates, and lower disease progression than IM [171]. Bosutinib also induces CCyR, albeit at a low rate (23 %), in patients resistant to IM or to either nilotinib or dasatinib [172]. At present, bosutinib is registered in many countries as a second- or third-line therapeutic agent.

### 7.4.2.4 Ponatinib

Ponatinib is a third generation TKI rationally designed to inhibit the T315I mutation, whilst still keeping activity against the unmutated and the majority of other BCR-ABL1 mutants. It also inhibits VEGFA, FGF, KIT and SRC kinases [173]. In a clinical trial of patients resistant or intolerant to nilotinib or dasatinib, or with the T315I mutation, ponatinib treatment caused CCyR and MMR in 46 % and 34 % of CP patients, respectively [174]. Moreover, 24 % of AP patients achieved CCyR and 16 % MMR, while only 18 % of BC patients experienced CCyR. Ponatinib's toxicity profile, however, can be a major drawback, since 5 % of patients suffered pancreatitis, and there was a significant association between ponatinib treatment and cardiovascular, cerebrovascular, and peripheral vascular events [174]. As a consequence, its indication is currently restricted to patients with a T315I mutation or for whom no other TKI is indicated.

### 7.4.2.5 Rebastinib

Rebastinib (or DCC-2036) is a switch pocket TKI rationally designed to induce an inactive conformation on BCR-ABL1. It retains full activity against the majority of BCR-ABL1 mutations, including T315I, but five P-loop mutants, G250E, Q252H, Y253H and E255K/V, in addition to F359I, have shown resistance to it [175, 176]. Preliminary results from a phase I trial (NCT00827138; [www.clinicaltrials.gov](http://www.clinicaltrials.gov)) suggest it has anti-leukaemic activity in patients intolerant/refractory to other TKIs or positive for T315I [177], but a Phase II trial is not presently planned.

## 7.5 LSC as a Therapeutic Target in CML

Despite the success of TKI treatment, the persistence of minimal residual disease or the recurrence of disease upon cessation of therapy in most patients with undetectable BCR-ABL1, indicate that LSC persist even when response to treatment is optimal [178, 179].

Although primitive CML cells were shown to stop proliferating and enter a reversible cell cycle arrest upon IM treatment, they are resistant to TKI-induced

apoptosis both *in vitro* and *in vivo*, even when BCR-ABL1 signalling is effectively inhibited [180–188]. These results suggest that the LSCs are capable of surviving independently of BCR-ABL1.

It has been suggested that the LSC quiescent state was responsible for their resistance to IM. In fact, stimulating quiescent LSCs to enter the cell cycle with CSF3/G-CSF reduces the overall non-cycling cell population *in vitro* [189, 190]; however, in clinical practice, this does not impact on disease outcome [191]. Accordingly, even the cycling primitive CML cells resist apoptosis due to BCR-ABL1 inhibition [187]. Therefore, LSCs capacity to survive BCR-ABL1 inhibition may be mediated by their ability to escape apoptosis and/or to self-renew, or by interactions with the BM stroma [192]. Indeed, the resistance of primitive LSC is not confined to apoptosis induced by TKI but apparently extends to multiple pro-apoptotic agents, such as cytosine arabinoside and arsenic trioxide [183].

From the self-renewal aspect the Wnt/CTNNB1 and Hedgehog (Hh) pathways are altered in CML and are potential targets [193, 194]. For instance, knockout or pharmacological inhibition of either CTNNB1 or SMO in combination with TKI efficiently reduces LSC numbers *in vivo* and delays disease relapse [195, 196]. These data support the hypothesis that targeting self-renewal is effective to eradicate LSCs and is the basis of ongoing clinical trials with inhibitors of these pathways (NCT01606579, NCT01357655, NCT01218477, NCT01456676; [www.clinicaltrials.gov](http://www.clinicaltrials.gov)).

It has been proposed that sequestration of LSCs in the BM niche induces the phenotype of environment-mediated drug resistance (EMDR) [197]. The mechanisms so far identified for EMDR include interaction of  $\beta 1$  integrins and CD44 with fibronectin on BM stromal cells, degradation of BCL2L1/BIM due to  $\beta 1$  integrin-mediated cell adhesion, activation of AKT1 through integrin-linked kinase, activation of JAK/STAT and HIF1A pathways, increase in STAT3 phosphorylation and subsequent expression of anti-apoptotic proteins, and interactions of CXCR4 in CML cells with extra cellular-matrix components and BM stromal cells [197, 198]. Special focus on CXCR4 as a possible drug target in CML has produced contradictory results with two studies showing that combination of CXCR4 antagonists with TKIs reduced leukaemia burden on CML mouse models [199, 200], while a third showed that combination of plerixafor with dasatinib had no advantage over dasatinib alone [201].

On a different approach, a farnesyltransferase inhibitor, BMS-214662, was found to selectively kill quiescent and dividing CML stem/progenitor cells *in vitro*, and its effect was enhanced when combined with either TKIs or a MEK inhibitor, PD184352, making it a promising agent for clinical development [202, 203].

Recent reports have also focused on manipulating the PP2A tumour suppressor activity to target LSCs. PP2A reactivation had been shown to effectively kill CML lines and primary cells from BC and both TKI-sensitive and -resistant patients [48, 204, 205]. Recently, the same group demonstrated that reactivating PP2A can eradicate quiescent LSCs, but not normal HSCs, through inhibition of the BCR-ABL1-JAK2-CTNNB1 signalling axis [206].

Other potential molecular targets in the CML LSC are listed on Table 7.1.



**Table 7.1** Potential molecular targets on CML stem cells

Gene	Function	Effect on CML LSCs	Targeting agent <sup>a</sup>	Ref
<i>ALOX5</i>	Arachidonate 5-lipoxygenase	Activates CTNNB1, GATA1 and ZFPM1, therefore regulates LSC self-renewal and differentiation	5-LO inhibitor: Zileuton	[207]
<i>BCL2 family</i>	Anti-apoptotic	Promotes cell survival	Sabutoclax, ABT-737, omacetaxine	[208–210]
<i>BCL6</i>	Transcription factor (repressor)	Proto-oncogene, downstream target of FOXO3. Represses TP53 and CDKN2A/ARF and is essential for colony formation and leukaemia initiation	RI-BPI	[211]
<i>BLK</i>	SRC family tyrosine kinase	Tumour suppressor, induces CDKN1B/p27, inhibits LSC proliferation and delays CML development		[212]
<i>CD27</i>	TNF-receptor superfamily member	Promotes CML progression by inducing expression of Wnt target genes followed by proliferation and differentiation of LSCs	mAb against ligand CD70	[213]
<i>CD44</i>	Cell-surface glycoprotein, involved in adhesion and migration	Promotes homing and engraftment of LSCs	mAb	[214]
<i>PTGS2/COX2</i>	Cyclooxygenase-2, promotes prostaglandin biosynthesis	Stabilizes CTNNB1 through prostaglandin E2 synthesis. Treatment of a CML mouse model with indomethacin reduced CTNNB1 expression and LSC numbers	Indomethacin	[196, 215]
<i>FOXO3</i>	Transcription factor	Key role in maintenance of LSCs by inhibiting apoptosis and promoting self-renewal		[216]
<i>LGALS3/GAL3</i>	Galectin family of carbohydrate binding proteins member	Activates AKT1 and MAPK, enhances clonogenic proliferation and homing of CML cells to the BM, and inhibits apoptosis		[217]
<i>GSK3B</i>	Serine-threonine kinase	Negative regulator of CTNNB1 and Hh pathway	SB216763 (inhibitor)	[218]
<i>HIF1A</i>	Transcription factor (activator), regulates hypoxia response	Essential for self-renewal of HSC and LSC; represses CDKN2A/INK4A (p16) and CDKN2A/ARF (p19)		[219, 220]
<i>HSP90AA1/ HSP90</i>	Molecular chaperone	Stabilizes BCR-ABL1	Relaspimycin (PI-504)	[221]

(continued)

Table 7.1 (continued)

Gene	Function	Effect on CML LSCs	Targeting agent <sup>a</sup>	Ref
<i>JAK2</i>	Tyrosine kinase	Interacts with BCR-ABL1 through the adapter AHI1 in primitive CML progenitors	SAR302503, TG101209, ruxolitinib	[222]
<i>MKNK1/MNK</i>	Ser/Thr protein kinase family	Activates CTNNB1	CGP57380 (inhibitor)	[223]
<i>MSR1</i>	Macrophage scavenger receptor implicated in macrophage-associated processes	Suppresses LSC proliferation and CML development		[224]
<i>PML</i>	Transcription factor member of the tripartite motif (TRIM) family	Tumour suppressor, controls apoptosis, proliferation and senescence; represses mTOR. Essential for maintaining LSC quiescence	Arsenic trioxide	[225]
<i>PP2A</i>	Protein phosphatase 2A, Ser/Thr phosphatase	Inactivates JAK2 and CTNNB1, and thus hinders LSC survival and self-renewal	FTY720, OP449	[205, 206]
<i>PTEN</i>	Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase, dephosphorylates phosphoinositide substrates	Tumour suppressor in CML by reducing LSC number and function and consequently delaying CML development		[226]
<i>RAD52</i>	Recombinase, participates in HRR DSB repair	Promotes survival by repairing DSBs by an alternative HRR pathway in LSCs, which are BRCA-deficient	Peptide aptamer	[103]
<i>SCD</i>	Stearoyl-CoA desaturase	Involved in fatty acid biosynthesis. Tumour suppressor in LSCs with no effect in HSCs; regulates PTEN, TP53 and BCL2	Rosiglitazone (PPAR $\gamma$ agonist)	[227]
<i>SELP</i> ( <i>P-selectin</i> )	Granule membrane protein, calcium-dependent receptor	Mediates cell-cell adhesion, is essential for haematopoiesis and its inhibition induces LSC self-renewal		[228–230]
<i>SETBP1</i>	SET nuclear oncogene protein binding	Cooperates with BCR-ABL1 conferring self-renewal capability to committed myeloid progenitors transforming them into LSCs in BC		[231]

<i>SIRT1</i>	NAD(+)-dependent histone/protein deacetylase	Promotes cell survival under different types of stress	Resveratrol, sirtinol, nicotinamide, tenovin-6	[232, 233]
<i>SMO</i>	Smoothed, frizzled class receptor, part of the hedgehog pathway	Represses NUMB, thus supports maintenance of CML LSC	SMO inhibitors: Cyclopamine, vismodegib, PF-04449913, BMS-833923, LDE-225, LEQ506, TAK-441	[193, 234–236]
<i>TGFBI</i>	Member of the TGFB family of cytokines	Suppresses AKT1 inhibition of FOXO3	LY364947 (inhibitor)	[216]

<sup>a</sup>Clinical drug or experimental compound/biological agent

## 7.6 Conclusion

The knowledge about the biology of CML increased exponentially since the Ph chromosome was first described. Even though this knowledge has led to the development of TKIs, which revolutionized CML treatment, there are still challenges to be overcome. Progression to BC, due to either primary failure to respond to a TKI or ‘acquired’ resistance, is still a major problem, since this aggressive disease stage is refractory to all types of available therapy. In addition, persistence of minimal residual disease in the majority of patients means they will have to continue under TKI therapy indefinitely. This raises two main problems, i.e., the risk that these patients develop resistance, which can then cause progression to BC, and the financial burden to families and/or Government’s medical systems, which will have to provide lifelong expensive treatment for those patients. Therefore, there is still much to be investigated and learned about this apparently benign leukaemia before we can achieve the final goal of a cure for the great majority of patients.

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