Review

PARP Inhibitors as Therapeutic Options for Tyrosine Kinase-dependent Leukemia: A Review

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Abstract. The idea of utilizing poly-ADP-ribose polymerase inhibitors (PARPi) as therapeutics for cancer has grown in popularity since its original approval for clinical usage in treatment of BRCA DNA repair-associated-mutated ovarian cancer. In this study, we evaluated experimental data regarding in vitro studies utilizing PARPi as a treatment for tyrosine kinase (TK)-dependent leukemia. Studies from 2015 to 2019 were compiled and the ones with most relevant TK pathways and PARP inhibition were analyzed. PARPi showed activity against many leukemia cell lines and samples from patients with primary leukemia, especially when combined with other signaling pathway inhibitor drugs, improving upon the hypothesis that the utilization of PARPi has potential as a new therapeutic approach in treatment of primary leukemia and TK-dependent leukemia.

The term 'leukemia' is used to represent a cohort of hematopoietic malignancies in which a deregulation of the production of mature leukocytes and their precursors is present. Leukemia is one of the most common types of cancer involving pediatric patients in the world, and its distribution may be associated with a wide array of factors such as socioeconomic status and ethnicity (1, 2).

Even though in recent years the treatment of different leukemia subtypes has steadily advanced, there are still many obstacles to overcome. As an example, the occurrence of therapy-related neoplasms is highly associated with exposure to conventional chemotherapy for primary leukemia. Moreover, the development of multidrug resistance in cancer

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cells may occur even after few chemotherapy cycles and is considered to be one of the main challenges in leukemia treatment (3-5).

Conventional oncology therapies with cytotoxic agents still has its limitations and has shown itself to be ineffective when treating many malignancies by causing patients side-effects. Knowing that, it is of the utmost importance in oncology to strive always for innovation in the search for new pathways and targeted molecular therapies to improve prognosis and quality of life for patients with neoplasms (6, 7).

The development of targeted molecular therapies has completely changed the dynamics in the treatment of most neoplasms, being less toxic and more effective alternatives than conventional chemotherapy (8).

Poly-ADP-Ribose Polymerase (PARP) Activity and Clinical Usage

The inhibition of PARP is becoming more popular as a target in the treatment of BRCA1/2 DNA repair-associated (BRCA1/2)-deficient tumors that present defects in the homologous recombination (HR) repair pathway (9).

The PARP family is composed of 17 enzymes with different functions in the cellular matrix, however, PARP1 is primarily the one responsible for DNA damage repair (DDR) activity attributed to these enzymes and, therefore, is the main target in molecular therapies utilizing PARP inhibitors (PARPi) in the treatment of cancer. The mechanism of action of PARP1 is related to its capacity to execute post-translation modifications of proteins through the addition of PARP chains, inducing structural and functional changes in a process called PARylation (10, 11).

PARP1 possesses three zinc-finger domains, two of which are responsible for recognizing and binding the enzyme to DNA (Figure 1A). When genetic damage is identified, PARP1 auto-PARylates and signalizes for the recruitment of other enzymes which initializes the DDR mechanism. Before

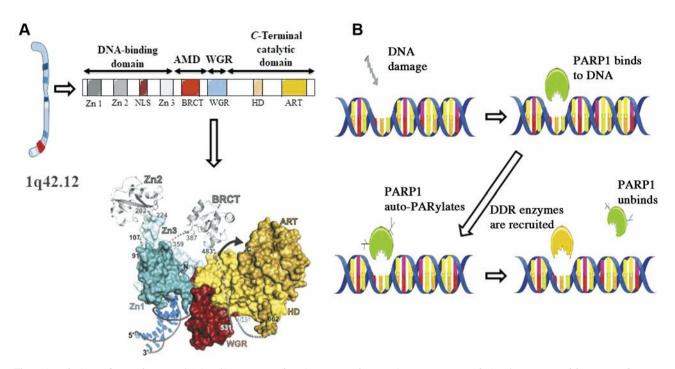


Figure 1. Poly-ADP-ribose polymerase 1 (PARP1) structure and DNA-repair mechanism. A: Representation of PARP1 structure and functioning domains. Zn1: Zinc-finger 1; Zn2: Zinc-finger 2; NLS: nuclear localization signal; Zn3: Zinc-finger 3; AMD: auto-modification domain; BRCT: breast-cancersusceptibility protein carboxy terminus; HD: helical subdomain; ART: ADP-ribosyl transferase subdomain. B. Multifactorial DNA damage generates single-strand breaks which are then recognized by PARP1. After binding, PARP1 auto-PARylates, signaling for the recruitment of proteins involved in the repairing mechanism. PARP1 unbinds from DNA due to charge repulsion and DNA damage-repair (DDR) enzymes initiate the repair.

DDR initiation, PARP1 unbinds from the DNA due to accumulation of negative charges from the PARP chains and the PARylation process is reverted, returning PARP1 to its original conformation (Figure 1B) (12-14).

PARPi in treatment of neoplasms represents the first ever clinical application of the synthetic lethality concept, which describes cell death when a series of intrinsic and extrinsic cell factors are activated through pharmacological manipulation (15). PARP1 is responsible for signalizing the repair of singlestrand breaks in DNA, therefore, its inhibition induces escalation of these injuries and conversion into double-strand breaks. Tumors which are deficient in HR mechanism, such as BRCA1/2-deficient tumors, are unable to effectively repair double-strand breaks and are induced to undergo apoptosis when treated with PARPi as a consequence (16, 17).

Another means through which PARPi exerts cytotoxicity is by forming insoluble PARP–DNA complexes, in a process known as PARP trapping. When PARP binds to DNA and is unable to be released, the DDR mechanisms are unable to bind and act on that sequence, impairing DNA repair and inducing genetic damage. Some PARPi agents are more efficient than others in binding PARP to DNA, and some even induce PARP release; this difference in their activity has no direct correlation with their capability of inhibiting PARylation itself (18-20). The current usage of PARPi in clinical practice is still restricted to treatment of solid tumors and most indications for their use revolve around treatment of BRCA-mutated tumors (21). However, a series of recent experimental and clinical studies demonstrated that PARPi may also be useful when treating a great variety of leukemia subtypes and related diseases that may present other mutation categories, without damage to the DDR mechanism. Even though experimental evidence attests the efficacy of these drugs, their antitumor mechanism has not been fully elucidated in many of the leukemia subtypes in which they are active (22).

Tyrosine Kinases and Carcinogenesis

TKs are a large protein family that is involved in a variety of cellular signaling pathways and other survival and replication mechanism in a way that grants them a major role in the carcinogenesis of many tumor type (Figure 2). Approximately 100 TKs have been characterized in the human genome and are divided into receptor TKs, these being proteins with transmembrane domains, and nonreceptor TKs, characterized as being cytoplasmic or nuclear proteins (23-25).

The first TK inhibitor (TKI) to be approved as a therapeutic in neoplasms was designated for the treatment of chronic

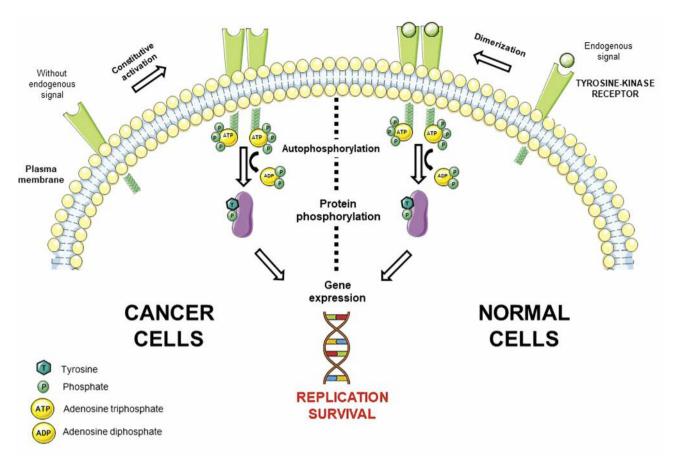


Figure 2. Tyrosine-kinase signaling pathway. Tyrosine-kinase mutations may induce constitutive activation or overexpression in cancer cells, leading to signaling pathways deregulation and malignant cells replication and survival.

myeloid leukemia (CML) due to the high frequency of expression of the chimeric TK breakpoint cluster region -Abelson murine leukemia (*BCR–ABL*) in this subtype. Currently, the roles of many TKs in carcinogenesis have been well characterized for other leukemia subtypes and are used as targets of inhibition for the treatment of neoplasms. The development of TKIs astoundingly changed the prognosis of patients suffering from TK-dependent leukemia by drastically increasing the rates of cure and overall survival (25-27).

However, malignant cells are easily mutated and the selective pressure exerted by treatment with TKIs usually results in emergence of resistant tumors, especially in relapsed leukemias. The mechanism involving resistance may vary depending on the drugs used and the leukemia subtype being treated with strategies to overcome resistance mostly consisting of increases in TKI dosage or utilization of second generation TKIs. Both strategies represent more risks to the patients, due to the increased drug toxicity, and will not necessarily provide a longer overall survival (28–31).

New Therapeutic Strategies

The development of alternative therapeutic approaches is extremely necessary in the goal of tackling the inevitable cases of resistance originated from the selective pressure of conventional and targeted therapies (32).

Even though some mechanisms remain to be elucidated, the utilization of PARPi has been shown to be a promising therapeutic strategy in the treatment of many leukemia subtypes (22). It is also important to note that some PARPi may have off-target effects beyond inhibition of PARylation and PARP trapping and may interfere directly with kinase activity pathways (33). In this review, we aimed to evaluate experimental data in the literature regarding *in vitro* studies utilizing PARPi as a treatment for TK-dependent leukemia.

Table I comprises a number of relevant studies from 2015 to 2019 reporting *in vitro* PARPi activity against leukemia cell lines and in samples of patients with different leukemia subtypes.

Leukemia	Genetic mutation	PARPi	Synergy	Mechanism	Cell lines	Reference
AML	RUNX1–ETO; cKIT; CBFB–MYH11	Olaparib	Avapritinib	Synthetic lethality by HR down-regulation	Kasumi-1; patient samples from primary AML	Nieborowska- Skorska <i>et al.</i> , 2019 (34)
MDS/CMML and AML	ASXL1; FLT3–ITD; JAK2; RUNX1	Talazoparib	APE1 inhibitor III; decitabine	-	Bone marrow samples	Kohl <i>et al.</i> , 2019 (35)
and T-ALL	LMO2	Olaparib	Doxorubicin	Synthetic lethality by DSB-induction in HR-deficient cells	VAL; OCI-LY8; OCI-LY19; DOHH2; MOLT16; MOLT4	Parvin <i>et al.</i> , 2019 (36)
CML	BCR-ABL	Talazoparib	Chloroquine	Inhibition of Talazoparib-induced autophagy	Peripheral blood from pediatric patients with CML	Liu <i>et al.</i> , 2019 (37)
CML	BCR-ABL	Perezone	-	Apoptosis through PARP1 inhibition and redox alterations	K562	Hernández- Rodríguez <i>et al.</i> 2019 (38)
MPN	JAK2 ^{V617F} ; CALR	Veliparib	Busulfan	Double-strand DNA breaks	SET2; HEL; HL-60; K562; patient blood samples	Patel <i>et al.</i> , 2019 (39)
AML	RUNX1–ETO	Olaparib	BMS; daunorubicin	PARylation, HR and NHEJ deregulation	KG1α; Kasumi-1	Li <i>et al.</i> , 2019 (40)
AML	NPM1; FLT3–ITD; CEBPA; DNMT3A; IDH1; IDH2	Talazoparib	NL101	Impairment of cell cycle and apoptosis induction	Samples from patients with AML; MV4-11; MOLM-13; HL-60; Kasumi-1	Li <i>et al.</i> , 2018 (41)
CML	BCR-ABL1	Olaparib; talazoparib	5F02; imatinib	Accumulation of DSB	Samples from patients with CML	Nieborowska- Skorska <i>et al.</i> , 2019 (42)
CML	BCR-ABL1	Talazoparib	Imatinib	Accumulation of DSB	Samples from patients with CML	Podszywalow- Bartnicka <i>et al.</i> 2019 (43)
AML	FLT3–ITD	Olaparib; talazoparib	Quizartinib; gilteritinib; crenolanib	Accumulation of DSB and cell death induction	Patient samples from primary AML; MV-4-11; HL-60; REH; BaF3	Maifrede <i>et al.</i> , 2018 (44)
AML	NPM1mutA; FLT3–ITD	Olaparib	-	Up-regulation of death receptors	Samples from patients with AML	Faraoni <i>et al.</i> , 2018 (45)
AML	IDH1/2 ^{MUT}	Olaparib; talazoparib	Daunorubicin	Down-regulation of AML level	Samples from patients with AML	Molenaar <i>et al</i> . 2018 (46)
AML	MLL-AF9	Olaparib	5-Azacytidine; decitabine; doxorubicin	Increased DNA damage, cell-cycle arrest and increase in apoptosis	MML-AF9 murine leukemia cells; MOLM13	Zhao and So, 2017 (47)
AML and ALL	MLL; FLT3; NPM1; DNMT3A; TP53; FTV6; PUNV1	Olaparib	AZD1775	Impairment of HR, increase in DNA damage and apoptosis	Jurkat; Molm13; MV4-11; REH; OCI-AML3; 32D	Garcia <i>et al.</i> , 2017 (48)
CML, AML and ALL	TP53; ETV6–RUNX1 TCF3–HLF	Olaparib; veliparib	-	Impairment of HR and accumulation of DSB	MOLT3; Jurkat; NALM6; REH; RS4-11; Raji; Daudi; BV137; K562; MEG-01; KG-01; NB4; HL-60; ML-1; THP-1; U-937; Kasumi-1; CMK; HAL-01; YCUB-2; AR230	Piao <i>et al.</i> , 2017 (49)

Table I. Continued

Leukemia	Genetic mutation	PARPi	Synergy	Mechanism	Cell lines	Reference
AML	FLT3–ITD	Veliparib; talazoparib	Decitabine; 5-azacytidine	Increase in PARP trapping and DSB accumulation	Patient samples from primary AML; MV411; MOLM13; MOLM-14; KASUMI	Muvarak <i>et al.</i> , 2016 (50)
CML and ALL	BCR–ABL TP53	P10	SAHA	Accumulation of DSB, cell-cycle arrest and induced apoptosis	K562; MOLT4; Nalm6; REH	Hegde <i>et al.</i> , 2016 (51)
MPN	JAK2 ^{V617F} ; BRCA1; CHEK2; RAD50	Veliparib; olaparib	-	Synthetic lethality by HR pathway dysfunction	Samples from patients with diverse MPN	Pratz <i>et al.</i> , 2017 (52)
AML	RUNX1–ETO; PML–RARa; MLL–AF9	Olaparib; veliparib	LiCl	Synthetic lethality by HR pathway dysfunction	Human primary AML cells; NB4-LR2; THP1; Kasumi-1; GP2; NIH3T3	Esposito <i>et al.</i> , 2015 (53)
ATLL	p53	PJ-34	-	Cell-cycle arrest, accumulation of DSB and reactivation of p53 pathways	Patient-derived ATLL cells; MT-4; MT-2; C8166; C91PL; MT-1; ATL-7; ED-40515(-); ALT-25; ATL-43T; KOB; ATL-55T	Bai <i>et al.</i> , 2015 (54)
AML and ALL	NPM1; TP53	Rucaparib	5FU	Increase in DNA damage and induction of apoptosis	OCI-AML2; RPMI-8402	Falzacappa et al., 2015 (55)
AML	FLT3; NPM1	Olaparib	-	Increase in DNA damage	Patient samples from primary AML; HL-60; U937; NB4; HL-60R; OCI-AML2; OCI-AML3	Faraoni <i>et al.</i> , 2015 (56)

Table I. Continued

ALL: Acute lymphocytic leukemia; AML: acutemyeloid leukemia; ATALL: adult T-cell leukemia/lymphoma; CML: chronic myeloid leukemia; CMML: chronic myelomonocytic leukemia; DLBCL: diffuse large B-cell lymphoma; DSB: double-strand break; HR: homologous recombination; MDS: myelodysplastic syndrome; MPN: myeloproliferative neoplasm; NHEJ: non-homologous end joining; PARP1: poly-ADP-ribose polymerase; TALL: T-cell acute lymphoblastic leukemia.

PARPi Studies

Most studies that were found in the literature, reported the effects of combined therapy utilizing one of the inhibitors already used in clinical practice for treatment of solid tumors, alongside inhibitors of other cellular pathways and some TKIs (34-37, 39-44, 46-48, 50, 51, 53, 55). The most commonly described leukemia subtype was acute myeloid leukemia (AML) harboring mutations such as Runt-related transcription factor1–eight twenty-one (*RUNX1–ETO*) and fms-like tyrosine kinase 3-internal tandem duplication (*FLT3–ITD*) (34, 35, 40, 41, 44, 45, 48, 50, 53, 56).

While *RUNX1–ETO* AML cells displayed increased sensitivity to treatment with olaparib, when accompanied by *cKIT* mutation, these cell lines tended to lose this sensitivity

(34, 53). *RUNX1* is a well-known transcription factor involved in normal hematopoiesis and its mutation into *RUNX1–ETO* causes deficiency in BRCA1/2 status and deregulation of normal DDR pathways, conferring sensitivity to PARPi. However, *cKIT* mutations have experimentally been shown to restore tumor HR capacity, conferring increased resistance to treatment with PARPi that would benefit from synthetic lethality. This resistance was shown to be overcomed when using a combination treatment with *cKIT*_{MUT} inhibitors (34, 53, 57, 58).

In regards to *FLT3–ITD* mutation, experimental data have shown low sensitivity to PARPi treatment as a monotherapy, while it was efficient when combined with *FLT3–ITD* inhibitors (44). This lack of sensitivity may be attributed to the capacity of *FLT3–ITD* mutation in restoring cellular HR activity through increased expression of DNA-binding protein 51 (RAD51) (59-61). Garcia *et al.* also demonstrated that inhibition of other kinase pathways, such as WEE1-like protein kinase (WEE1), impaired HR in *FLT3–ITD*-mutated AML cells and synergized with PARPi treatment (48).

Studies analyzing cohorts of samples from patients with AML have demonstrated that high PARP1 expression in AML cells is related both to increased *FLT3-ITD* mutation rate (41), as well as reduced sensitivity to PARPi (56), indicating that the overexpression of PARP1 might be a potential predictive marker to the resistance to PARPi treatment in AML mediated by *FLT3-ITD* mutation, however further investigation is required on this topic. AML cell lines expressing no *FLT3-ITD* or relevant levels of PARP1 are still capable of resisting PARPi treatment through other mechanisms, such as the aforementioned overexpression of RAD51 (56).

Another TK found to have an important role in hematological malignancies is Janus kinase 2 (*JAK2*) harboring the point mutation V617F, which is often expressed in myeloproliferative neoplasms. Contrasting data found in the literature make it still unclear if $JAK2^{V617F}$ cells are indeed sensitive or not to treatment with PARPi, more specifically to veliparib (39, 52). In a similar mechanism to that of *FLT3-ITD*, *JAK2^{V617F}* mutation is known to increase RAD51 expression and up-regulate HR activity, which would, in theory, reduce *JAK2^{V617F}* cell sensitivity to PARPi treatment (60).

One of the most common leukemia subtypes associated with TK dependence is CML as a result of its high BCR– ABL1 expression. Even though TKI development has greatly improved prognosis of patients with CML, cases of primary and secondary resistance are still reported in clinical practice and represent a major obstacle in treatment (62, 63). *BCR– ABL* mutations are known to deregulate cellular signaling pathways, down-regulating BRCA1 protein expression and consequentially inhibiting HR activity (64, 65).

In accordance with the concept of synthetic lethality, the utilization of different PARPi was able to inhibit growth of CML BCR-ABL cells in vitro mainly through increase in genomic instability and consequent apoptosis. This inhibitory activity was shown to be even more relevant when combined with different synergistic drugs (37, 38, 42). Liu et al. demonstrated that the utilization of chloroquine potentiated the activity of talazoparib in samples from patients with CML by inhibiting talazoparib-induced autophagy which may play a cytoprotective role in tumor cells (37). Moreover, Nieborowska-Skorska et al. demonstrated that a combination of NAD-like PARPi, such as olaparib and talazoparib, and non-NAD-like PARPi, as well as combination with the commonly used TKI imatinib, may potentiate NAD-like PARPi inhibitory activity against cell in samples from patients with CML (42).

In the above mentioned studies, as well as those described in Table I, the cytotoxicity of PARPi has been shown for different leukemia subtypes *in vitro*, especially when combined with other drugs capable of deregulating cellular signaling pathways and DDR mechanisms, reinforcing its capability for selectively killing malignant cells through synthetic lethality (66), and improving upon the hypothesis that their use has the potential to improve prognosis of many patients afflicted by TK-dependent leukemia.

Conclusion

The highly significant experimental data support the utilization of PARPi as a potential new therapeutic approach in the treatment of primary leukemia and TK-dependent leukemia through a series of different mechanisms, such as synthetic lethality, PARP trapping and synergy with other signaling pathway inhibitors. The confirmation of this evidence in clinical trials is needed in order to further improve upon this hypothesis.

Conflicts of Interest

The Authors declare no conflicts of interest regarding this study.

Authors' Contributions

Machado CB and Moreira-Nunes CA designed the study; Machado CB, Silva EL and Moreira-Nunes CA prepared the figures; Machado CB, Silva EL, Moraes-Filho MO, Moraes MEA and Moreira-Nunes CA wrote the article; Machado CB and Moreira-Nunes CA revised the final version. All Authors read and approved the final article.

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