Diffuse large B-cell lymphoma (DLBCL) remains incurable in nearly 30% of patients, who do not achieve durable remission with current first-line immunochemotherapeutic approaches. It is now clear that a major barrier to improved outcome is the remarkable heterogeneity of this disease, which makes the generic nontargeted R-CHOP regimen (rituximab plus cyclophosphamide, doxorubicin, vincristine, and prednisone) only partially effective. Of the two molecular subtypes recognized in the updated World Health Organization classification, the activated B-cell–like (ABC)-DLBCL is characterized by a less favorable prognosis (1). Further heterogeneity was revealed by the analysis of the DLBCL coding genome, which led to the discovery of distinct genetic clusters defined by the cooccurrence of specific genetic alterations underlying the involvement of distinct oncogenic survival pathways (1, 2). In this context, ABC-DLBCL is highly enriched in three subtypes—including MCD (or the partially overlapping C5 cluster), defined by recurrent MYD88-L265P and CD79B gene mutations; BN2 (or cluster 1), defined by BCL6 translocations and NOTCH2 mutations; and the rare N1 (NOTCH1) group—with MCD cases displaying inferior clinical outcome (1, 2). Precision medicine approaches tailored to subtype-specific tumor addictions are being developed to further our ability to cure these patients.

A hallmark of ABC-DLBCL, and particularly of the MCD subtype, is the presence of mutations targeting the B-cell receptor (BCR)–driven NF-κB signaling pathway, including the genes encoding for the BCR subunits CD79α/β, the CARD11 component of the signalosome complex, the negative regulator TNFAIP3, and the MYD88 scaffolding protein, which relays signals from TLR9 to the NF-κB transcription complex (Fig. 1). These mutations maintain a “chronically active” form of BCR signaling that culminates in the constitutive activation of NF-κB, thereby promoting cell proliferation and survival (3). The critical importance of BCR signaling in the pathogenesis and viability of ABC-DLBCL cells was revealed by functional genomic screens and by the selective toxicity of drugs targeting this pathway to ABC- but not germinal center B-cell–like (GCB)-DLBCL models (3).

Following on these insights, the first phase I/II clinical trial for relapse/refractory (r/r) DLBCL treated with the small-molecule irreversible inhibitor of Bruton tyrosine kinase (BTK) ibrutinib has shown significant clinical activity in patients with ABC-DLBCL, including exceptional responses in tumors that belong to the MCD subtype (4). High response rates were also seen in primary central nervous system lymphoma, which shares a similar genetic profile (3). However, median progression-free survival was short, and most patients experienced rapid disease progression. Signal transduction through the BCR also plays a critical role in other B-cell malignancies such as chronic lymphocytic leukemia (CLL) and mantle cell lymphoma (MCL), where its activity is sustained by a variety of tyrosine kinases in addition to BTK. Consistently, treatments that selectively target the BCR have revolutionized the clinical approach to CLL, where ibrutinib is highly effective, and are among the preferred standards of care for patients with r/r MCL. Nonetheless, ibrutinib as a single agent does not eradicate the malignant B-cell clone due to emerging drug resistance and/or recurrence upon drug discontinuation (5). To reduce side effects and overcome resistance, a new generation of irreversible or reversible BTK inhibitors (BTKi) is being developed, and promising results were recently reported in DLBCL with acalabrutinib monotherapy, a second-generation covalent BTKi with enhanced kinase selectivity and possibly lower toxicity (6). The best-characterized mechanism of ibrutinib resistance (IR), particularly in the context of CLL progression after initial response, is represented by genetic mutations affecting components of the BCR pathway. These comprise amino acid substitutions of the cysteine 481 in BTK, which prevent the covalent binding of ibrutinib, or gain-of-function mutations in its downstream substrate PLCγ2 (7). However, a...
The enhanced biochemical interaction between RAC2 and B transcription complex (Fig. 1).

κ and the downstream NF-κB complex. The My−T−BCR supercomplex (MYD88–TLR9–BCR) is also indicated. In sensitive cells, BTK inhibition by ibrutinib blocks proliferation and survival (left). The mechanism of epigenetic ibrutinib resistance described by Shaffer and colleagues is illustrated in the middle, where increased amounts of RAC2 and enhanced RAC2–PLCγ2 interaction substitute for BTK in rewiring BCR signaling to downstream NF-κB. This phenotypic shift is driven by TCF4-dependent enhancer activation of critical target genes (only RAC2 and TLR9 shown). On the right, genetic mutations blocking the covalent binding of ibrutinib to BTK or activating PLCγ2 (red thunderbolts) lead to irreversible ibrutinib resistance. BTK, Bruton tyrosine kinase; RAC2, RAC2 inhibitor.

Figure 1. Modes of ibrutinib resistance in ABC/MCD-DLBCL. Simplified schematic of the chronic active BCR signaling pathway leading to constitutive NF-κB activation in ABC-DLBCL of the MCD genetic subgroup. Positive and negative pathway regulators commonly targeted by genetic mutations are color-coded in orange (CD79α/β and CARD11, TNFAIP3, and MYD88). A double oval is used to illustrate the downstream activation of the NF-κB complex. The My−T−BCR supercomplex (MYD88–TLR9–BCR) is also indicated. In sensitive cells, BTK inhibition by ibrutinib blocks proliferation and survival (left). The mechanism of epigenetic ibrutinib resistance described by Shaffer and colleagues is illustrated in the middle, where increased amounts of RAC2 and enhanced RAC2–PLCγ2 interaction substitute for BTK in rewiring BCR signaling to downstream NF-κB. This phenotypic shift is driven by TCF4-dependent enhancer activation of critical target genes (only RAC2 and TLR9 shown). On the right, genetic mutations blocking the covalent binding of ibrutinib to BTK or activating PLCγ2 (red thunderbolts) lead to irreversible ibrutinib resistance. BTK, Bruton tyrosine kinase; RAC2, RAC2 inhibitor.

simple genetic mechanism causing resistance is questioned by several observations suggesting that the mutations may not be the initial drivers, including their timing and the subclonal heterogeneity of resistant disease (7). Notably, a persistent or progressively expanding CLL clone that lacks detectable BTK/PLCG2 mutations or carries them at less than 10% variant allele frequency could be detected in nearly as many as 50% of patients in stable remission on ibrutinib (8). In DLBCL, data are limited, but monitoring of circulating tumor DNA in three patients receiving ibrutinib monotherapy revealed the appearance of likely independent resistance mutations in BTK with distinct clonal dynamics after prolonged treatment (9). Together, these data raise the possibility that clones resistant to therapy may exist for prolonged periods of time under treatment, before the mutation appears and prior to final clonal expansion.

In this issue of Blood Cancer Discovery, Shaffer and colleagues set out to address these issues by integrating elegant functional genomic and proteomic tools in several ABC-DLBCL cell lines that were induced to develop resistance via exposure to low ibrutinib concentrations (10). Of note, the resulting resistant populations often lacked the typical genetic mutations associated with resistance to the drug; instead, they rewired their BCR signaling pathway by substituting BTK with the small GTPase RAC2 in activating PLCγ2 and the downstream NF-κB transcription complex (Fig. 1). The enhanced biochemical interaction between RAC2 and PLCγ2 was sustained in part by a TCF4-dependent transcriptional shift, and could be efficiently targeted by the small-molecule RAC1/2-specific inhibitors NSC-23766 and EHT1864, both in vitro and in preclinical mouse models. These findings offer a promising new therapeutic approach to overcome IR and to potentially improve the clinical outcome of several common B-cell malignancies dependent on active BCR signaling.

A notable and perhaps unexpected finding of this study is the predominant lack of genetic mechanisms that could account for IR at the population level, even after 1 year in culture. In fact, although mutations in BTK and PLCγ2 could be occasionally detected when individual clones were isolated from the IR population, they never became dominant (their variant allele frequencies remaining consistently below 10%). Moreover, no other resistance mutations or genetic alterations affecting the BCR, NF-κB, and/or other known pathways that could sustain ABC-DLBCL survival could be identified by whole-exome sequencing analysis of multiple IR pools. Instead, the resistance phenotype (pools or independent clones) was associated with alterations in gene expression, including increased levels of the transcription factor TCF4, which could be reverted by its genetic depletion or by treatment with the histone deacetylase inhibitor givinostat, alone or in combination with the DNA methyltransferase inhibitor 5-azacytidine (5-AZA). Importantly, the combination had little to no effect on the ibrutinib sensitivity of genetically mutated IR clones, strongly supporting the involvement of an epigenetic mechanism. Thus, the results herein support a prominent
role for nonmutational retuning of BCR signaling in the escape of ABC-DLBCL cells under the selective pressure of ibrutinib treatment. This mode of resistance could sustain the persistence of a polyclonal population while providing a reservoir for the acquisition of later genetic events, such as BTK and PLCγ2 mutations. In further support of this model, a sophisticated genetic barcode experiment that allowed monitoring of the dynamics of expansion of single cells from the starting population showed a pattern incompatible with the outgrowth of a rare genetic alteration for the vast majority of cells surviving treatment for up to 5 weeks. Together, these data suggest that epigenetic changes may be the initial mechanism by which ABC-DLBCL cells adapt to ibrutinib treatment (“persistent cells”) before the occurrence of genetic events irreversibly locks the resistant phenotype and allows its clonal expansion.

The transcriptional signature shared by persistent and resistant cells was significantly enriched in “BCR signaling” genes, including the small GTPase RAC2. In normal B cells, RAC2 contributes to PLCγ2-mediated calcium mobilization downstream of BCR engagement. Shaffer and colleagues observed that, in IR cells, the increased abundance of RAC2 downstream of BCR engagement. Although these patients carried subclonal mutations, the very low fraction of variant alleles (<15%) was unlikely to explain this protein interaction, which was detected in virtually all tumor cells. Together, these findings reinforce the clinical significance of the TCF4–RAC2–PLCγ2 axis, and suggest its validity as a general mechanism of IR that could also be implicated in CLL and possibly MCL.

An important question that remains is whether targeting epigenetic resistance will prevent the development of genetic resistance. While the answer to this question awaits further studies, the authors observed that cells with genetic IR mutations, and, to a lesser extent, parental ABC-DLBCL cells also displayed some response to EHT1864 in culture. Moreover, EHT1864 decreased PLCγ2 activity in one clone with a PLCγ2 mutation, indicating that RAC2 regulates PLCγ2 in genetic IR as well. In line with this model, treatment with EHT1864, while ineffective alone, augmented the ability of ibrutinib to control the growth of sensitive parental ABC-DLBCL xenografts.

Finally, the study by Shaffer and colleagues has several implications for both the development of new predictive biomarkers of epigenetic IR and rationally designed clinical trials that maximize the targeting of BCR signaling using new dosing strategies and drug combinations.

The linear quantitative relationship between RAC2–PLCγ2 interactions and IR, revealed by proximity ligation assays in both DLBCL models with nongenetic resistance and IR CLL patient samples, could have important clinical applications and should be exploited as a potential biomarker for patient stratification and treatment decisions.

From a therapeutic perspective, the identification of RAC2 and other altered dependencies in IR ABC-DLBCL (e.g., BCL2, BRD4, or AKT) as promising new targets provides the foundation for the development of more effective regimens combining ibrutinib with drugs modulating the activities of these proteins, either sequentially or in combination. In this regard, one interesting observation of the present work is that, analogous to cell pools with genetic resistance, the epigenetic IR phenotype was remarkably stable when cells were rechallenged with ibrutinib after short-term drug withdrawal. However, this was not the case in cultures that were exposed to ibrutinib for only 1 week. Thus, one may speculate that future clinical trials involving ibrutinib may benefit from the use of intermittent dosing schedules in which BTK inhibition could be combined with standard R-CHOP chemotherapy or with drugs targeting the acquired addictions of RAC2–PLCγ2 resistant cells. Such an approach may also contribute to reducing the toxicity associated with continuous ibrutinib treatment.

Author’s Disclosures

No disclosures were reported.

Published first September 22, 2021.

REFERENCES

1. Young RM, Phelan JD, Shaffer AL 3rd, Wright GW, Huang DW. Taming the heterogeneity of aggressive lymphomas for precision therapy. Annu Rev Cancer Biol 2019;3:429–55.
2. Chapuy B, Stewart C, Dunford AJ, Kim J, Kamburov A, Redd RA, et al. Molecular subtypes of diffuse large B cell lymphoma are associated with distinct pathogenic mechanisms and outcomes. Nat Med 2018;24:679–90.
3. Young RM, Phelan JD, Wilson WH, Staudt LM. Pathogenic B-cell receptor signaling in lymphoid malignancies: new insights to improve treatment. Immunol Rev 2019;291:190–213.
4. Wilson WH, Young RM, Schmitz R, Yang Y, Pittaluga S, Wright G, et al. Targeting B cell receptor signaling with ibrutinib in diffuse large B cell lymphoma. Nat Med 2015;21:922–6.
5. Woyach JA, Furman RR, Liu TM, Ozer HG, Zapatka M, Ruppert AS, et al. Resistance mechanisms for the Bruton’s tyrosine kinase inhibitor ibrutinib. N Engl J Med 2014;370:2286–94.
6. Strati P, de Vos S, Ruan J, Maddocks KJ, Flowers CR, Rule S, et al. Acalabrutinib for treatment of diffuse large B-cell lymphoma: results from a phase 1b study. Haematologica 2021 Jul 8 [Epub ahead of print].
7. Burger JA, Landau DA, Taylor-Weiner A, Bozic I, Zhang H, Sarosiek K, et al. Clonal evolution in patients with chronic lymphocytic leukaemia developing resistance to BTK inhibition. Nat Commun 2016; 7:11589.
8. Quinquenel A, Fornecker LM, Letestu R, Ysebaert L, Fleury C, Lazarian G, et al. Prevalence of BTK and PLCG2 mutations in a real-life CLL cohort still on ibrutinib after 3 years: a FILO group study. Blood 2019;134:641–4.
9. Scherer F, Kurtz DM, Newman AM, Stehr H, Craig AFM, Esfahani MS, et al. Distinct biological subtypes and patterns of genome evolution in lymphoma revealed by circulating tumor DNA. Sci Transl Med 2016;8:364ra155.
10. Shaffer AL 3rd, Phelan JD, Wang JQ, Huang D, Wright GW, Kasbekar M, et al. Overcoming acquired epigenetic resistance to BTK inhibitors. Blood Cancer Discov 2021;2:630–47.
Epigenetic Rewiring of BCR Signaling as a Novel Mechanism of Ibrutinib Resistance in ABC-DLBCL

Laura Pasqualucci

_Blood Cancer Discov_ 2021;2:555-558. Published OnlineFirst September 22, 2021.

Updated version  Access the most recent version of this article at: doi: 10.1158/2643-3230.BCD-21-0131

Cited articles  This article cites 9 articles, 3 of which you can access for free at: http://bloodcancerdiscov.aacrjournals.org/content/2/6/555.full#ref-list-1

E-mail alerts  Sign up to receive free email-alerts related to this article or journal.

Reprints and Subscriptions  To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubs@aacr.org.

Permissions  To request permission to re-use all or part of this article, use this link http://bloodcancerdiscov.aacrjournals.org/content/2/6/555. Click on "Request Permissions" which will take you to the Copyright Clearance Center's (CCC) Rightslink site.