

Noncatalytic Bruton's tyrosine kinase activates $PLC\gamma_2$ variants mediating ibrutinib resistance in human chronic lymphocytic leukemia cells

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Treatment of patients with chronic lymphocytic leukemia (CLL) with inhibitors of Bruton's tyrosine kinase (BTK), such as ibrutinib, is limited by primary or secondary resistance to this drug. Examinations of CLL patients with late relapses while on ibrutinib, which inhibits BTK's catalytic activity, revealed several mutations in BTK, most frequently resulting in the C481S substitution, and disclosed many mutations in PLCG2, encoding phospholipase C- γ_2 (PLC γ_2). The PLC γ_2 variants typically do not exhibit constitutive activity in cell-free systems, leading to the suggestion that in intact cells they are hypersensitive to Rac family small GTPases or to the upstream kinases spleen-associated tyrosine kinase (SYK) and Lck/Yes-related novel tyrosine kinase (LYN). The sensitivity of the PLC γ_2 variants to BTK itself has remained unknown. Here, using genetically-modified DT40 B lymphocytes, along with various biochemical assays, including analysis of PLC γ_2 -mediated inositol phosphate formation, inositol phospholipid assessments, fluorescence recovery after photobleaching (FRAP) static laser microscopy, and determination of intracellular calcium $([Ca^{2+}]_i)$, we show that various CLL-specific PLC γ_2 variants such as PLC γ_2 S707Y are hyperresponsive to activated BTK, even in the absence of BTK's catalytic activity and independently of enhanced PLC γ_2 phospholipid substrate supply. At high levels of B-cell receptor (BCR) activation, which may occur in individual CLL patients, catalytically-inactive BTK restored the ability of the BCR to mediate increases in [Ca²⁺], Because catalytically-inactive BTK is insensitive to active-site BTK inhibitors, the mechanism involving the noncatalytic BTK uncovered here may contribute to preexisting reduced sensitivity or even primary resistance of CLL to these drugs.

The two members of the γ subfamily of inositol phospholipid–specific phospholipase C (PLC),⁴ PLC γ_1 and PLC γ_2 , have recently been found to be involved in a number of ostensibly different human disease states (1). These range from rare hereditary diseases caused by, or associated with, germline mutations in the PLCG2 gene, such as complex immunological diseases with an autoinflammatory hallmark (2, 3) and childhood-onset steroid-sensitive nephrotic syndrome (4), to acquired conditions associated with somatic PLCG1 or PLCG2 mutations, such as angiosarcoma and T-cell lymphomas (PLCG1) (5, 6), and endemic Burkitt lymphoma (PLCG2) (7). Point mutations in PLCG2 have also been reported to modify the risk of developing neurodegenerative diseases like Alzheimer's disease (8, 9) and to cause resistance of chronic lymphocytic leukemia (CLL) cells to catalytic-site inhibitors of Bruton's tyrosine kinase (BTK) (10).

BTK is one of the five members of the strongly-conserved Tec family of nonreceptor tyrosine kinases, also including the IL-2–inducible <u>T</u>-cell kinase ITK, TEC proper, RLK, and BMX (11). Although all five Tec variants are expressed in cells of the hematopoietic lineage, BTK and ITK are key regulators of B-cell and T-cell transmembrane signaling, respectively (12). Mutations of the human and mouse *BTK* and *Btk* genes functionally affecting BTK were found to be associated with human

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This article contains Figs. S1–S6 and Table S1.

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⁴ The abbreviations used are: PLC, inositol phospholipid-specific phospholipase C; RAC, Ras-related C3 botulinum toxin substrate; BTK, Bruton's tyrosine kinase; PIP5K, phosphatidylinositol-4-phosphate 5-kinase; BCR, B-cell receptor; [Ca²⁺]_i, intracellular calcium ion concentration; PtdInsP₃, phosphatidylinositol 3,4,5-trisphosphate; PtdInsP₂, phosphatidylinositol 4,5-bisphosphate; CLL, chronic lymphocytic leukemia; WM, Waldenström's macroglobulinemia; FRAP, fluorescence recovery after photobleaching; NFAT, Ca²⁺-regulated nuclear factor of activated T cells; XLA, human X-linked agammaglobulinemia; ANOVA, analysis of variance; CFSE, 5-(and-6)-carboxyfluorescein diacetate succinimidyl ester; SH, Src homology; PH, pleckstrin homology; v-SRC, rous sarcoma virus tyrosine kinase.

X-linked agammaglobulinemia (XLA) and murine X-linked immunodeficiency (11). BTK and the other Tec family members share an overall similar domain organization that closely resembles the organization of the Src family tyrosine kinases, with an SH3-SH2-protein-tyrosine kinase domain tandem at their C termini, but divergent N-terminal regions (11). In B cells, BTK couples antigen-activated B-cell receptors (BCR) to tyrosine phosphorylation of PLC γ_2 at the four canonical tyrosine residues, Tyr-753, Tyr-759, Tyr-1197, and Tyr-1217 (13, 14). The latter modifications activate PLC γ_2 to hydrolyze its substrate phosphatidylinositol 4,5-bisphosphate (PtdInsP₂) to inositol 1,4,5-trisphosphate and diacylglycerol. All three of the latter act as intracellular second messengers (15, 16), which are involved in controlling key functions of both normal and neoplastic B lymphocytes. The activation of PLC γ_2 is greatly facilitated by the adaptor protein BLNK/SLP-65 (17, 18) and requires membrane targeting of BTK via its N-terminal pleckstrin homology domain to phosphatidylinositol 3,4,5-trisphosphate generated from PtdInsP₂ by phosphatidylinositol 3-kinases. For this reason, it can be blocked by the R28C and mimicked by the E41K mutation within its PH domain (19, 20). The K430R mutation of BTK, by replacing a crucial lysine coordinating the α - and β -phosphates of the substrate ATP and being present in this position in all protein kinases (21), renders the BTK protein catalytically inert (22).

Previous experimentation has shown that, during B-cell development, BTK partially acts as an adaptor molecule, independent of its catalytic activity (23), and that the tumor suppressor function of BTK identified in pre-B cells is independent of its catalytic activity (24). Specifically, kinase-inactive BTKK430R completely reconstituted λ usage in BTK-deficient mice and partially corrected the defective modulation of pre-B cell–surface markers, peripheral B-cell survival, and BCR-mediated NF- κ B induction (23). Activation of BTK by pre-BCR stimulation was also shown to be independent of BLNK/SLP-65 (24). These effects have thus far been attributed to the observation that BTK associates with phosphatidylinositol-4-phosphate 5-kinases (PIP5Ks), the enzymes that synthesize the generic substrate of inositol phospholipid–specific phospholipase C, PtdInsP₂ (25).

Irreversible BTK inhibitors such as ibrutinib have demonstrated remarkable activity in a number of B-cell malignancies with approval in CLL, mantle cell lymphoma, marginal zone lymphoma, and Waldenström's macroglobulinemia (26, 27). As a result, ibrutinib is being used with increasing frequency as frontline therapy, beginning to displace chemoimmunotherapy in this setting (28, 29). Currently, the drugs are also being evaluated for the treatment of other diseases, such as other malignancies and various autoimmune and/or inflammatory diseases (30-33). As is the case for other targeted tumor therapies, BTK inhibitor treatment of CLL is limited by either primary or secondary, i.e. acquired drug resistance (10). Thus, whole-exome sequencing of CLL cells causing late relapses revealed (i) C481S and a small number of other mutations in the same and in other positions in BTK and (ii) a higher variety of mutations in PLCG2. To date, some 25 point mutations of one or two adjacent residues are known in PLCG2, some of which cluster in specific regions of the encoded PLC γ_2 protein, such as one of the two SH2 domains and the C2 domain (34-36). Collectively, the *BTK* and *PLCG2* mutations are associated with about 85% of CLL cases with acquired resistance to BTK inhibitors (37).

Although the C481S mutation of *BTK* eliminates covalent binding of some BTK inhibitors, such as ibrutinib, to their target and hence markedly reduces their affinity to their binding site, the mechanism of resistance caused by the other BTK and the *PLCG2* mutations is less clear. PLC γ_2 is immediately downstream of BTK (26) leading to the suggestion that the variant proteins may be constitutively active. However, we have previously found that several PLC γ_2 variant enzymes associated with ibrutinib resistance carrying mutations in various regions are not constitutively active when assayed, even as purified proteins, in a cell-free system employing artificial lipid vesicles as substrate (38, 39). The observation that PLC γ_2 variants are, instead, hypersensitive in intact cells to the Rho GTPase RAC2, as well as the upstream protein-tyrosine kinases SYK and LYN (39, 40), has led us to suggest that the PLCG2 mutations found in BTK inhibitor-resistant cells may cause a rerouting of the transmembrane signals emanating from BCR to converge on and activate PLC γ_2 .

This work was undertaken to study the functional interaction of BTK with PLC γ_2 , WT, and ibrutinib resistance variants in a system reconstituted in intact cells from the two protein constituents. We chose enhanced inositol phosphate formation as a functional readout of a productive interaction between the two, rather than PLC γ_2 phosphorylation, as it is the most relevant functional outcome of stimulated PLC γ_2 in terms of B-cell signaling. Also PLC γ_2 is phosphorylated at many other residues, for instance Tyr-733 or Tyr-1245, in addition to the four canonical sites utilized by activated BTK (41, 42), which may confound results. To our knowledge, this approach has not been reported previously. Here, we report that several PLC γ_2 variants mediating BTK-inhibitor resistance in CLL patients are strikingly hypersensitive to activated and/or membranebound BTK and to BTK variants lacking protein-tyrosine kinase activity. Importantly, we demonstrate that the activity of the PLC γ_2 variants in the context of catalytically-inactive BTK is not contingent on enhanced formation of the PLC substrate PtdInsP₂ via stimulation of PtdInsP kinases, as postulated earlier. Hence, stimulation of PLC γ_2 variants mediating BTK inhibitor resistance can be explained by their hypersensitivity to the noncatalytic actions of BTK. We suggest that this mechanism contributes to the acquired BTK inhibitor resistance observed in CLL patients with PLCG2 mutations and, potentially, to preexisting reduced sensitivity or even primary resistance of clonal populations of CLL cells with hyperactivated BCR.

Results

PLC γ_2 S707Y can be functionally reconstituted with and is hypersensitive to activation by BTK

To investigate and compare the functional reconstitution of various PLC isozymes with WT BTK and its predominantly membrane-bound and, hence, active variant E41K, WT PLC γ_1 , PLC γ_2 , PLC β_2 , WT, and Δ 44 variant PLC δ_1 , and S707Y variant PLC γ_2 were coexpressed with the two BTK variants in COS-7





Figure 1. Analysis of the functional reconstitution of PLC γ_2 and BTK. A, COS-7 cells were transfected as indicated with 250 ng/well of either empty vector (*Control*) or 150 ng/well of vector encoding either WT PLC $\gamma_1(\gamma_1WT)$, WT PLC $\gamma_2(\gamma_2WT)$, WT PLC $\beta_2(\beta_2WT)$, or WT PLC $\delta_1(\delta_1WT)$, 50 ng/well of vector encoding PLC γ_2 S707Y (γ_2 S707Y) or PLC $\delta_1\Delta$ 44 ($\delta_1\Delta$ 44), and 100 ng/well of vector encoding either WT BTK (*BTKWT*) or a constitutively-active version of BTK (*BTKE*41K). *B*, cells from one well each functionally analyzed in A were washed with 0.2 ml of Dulbecco's PBS and then lysed by addition of 100 μ l of SDS-PAGE sample preparation buffer. Aliquots of the samples were subjected to SDS-PAGE, and immunoblotting was performed using an antibody reactive against the c-Myc epitope present on WT PLC γ_1 , WT PLC γ_2 , PLC γ_2 S707Y, WT PLC δ_1 , and PLC $\delta_1\Delta 44$ (a-d and f-g), antibody reactive against PLC β_2 (e), antibody reactive against BTK (a-g), or antibody reactive against β -actin (a-g). C, COS-7 cells were transfected as indicated with 50 ng/well of vector encoding WT PLC γ_2 ($\gamma_2 WT$) or PLC₂₂S707Y (γ_2 S707Y) and increasing amounts (0-450 ng/well) of vector encoding WT BTK (*BTKWT*) (*left panel*) or BTKE41K (*right panel*). A and \hat{C} , 24 h after transfection, the cells were incubated for 18 h with *myo*-[2-³H]inositol, and inositol phosphate formation was then determined. D, cells from one well each functionally analyzed in C were washed with 0.2 ml of Dulbecco's PBS and then lysed by addition of 100 µl of SDS-PAGE sample preparation buffer. Aliquots of the sample's were subjected to SDS-PAGE, and immunoblotting was performed using an antibody reactive against the c-Myc epitope present on WT PLC γ_2 and PLC_{γ2}S707Y (*a*-*c*), antibody reactive against BTK (*d*-*f*), or antibody reactive against β-actin (*g*-*i*). *E*, COS-7 cells were transfected as indicated with 150 ng/well of vector encoding WT PLC γ₂ (γ₂WT) and 100 ng/well of vector encoding BTKE41K or BTKE41K/C481S. Twenty four hours after transfection, the cells were incubated for 18 h with myo-[2-³H]inositol and either solvent (0.1% (v/v) DMSO) or increasing amounts of ibrutinib (0.1 nm to 10 μm), vecabrutinib (0.1 nm to 10 μM), or acalabrutinib (1 nM to 3 μM). Inositol phosphate formation was then determined. The results were normalized to percent of maximal inositol phosphate formation, which was 10,012, 9747, and 15,178 cpm for ibrutinib, acalabrutinib, and vecabrutinib, respectively. The IC₅₀ values of ibrutinib, acalabrutinib, and vecabrutinib for the inhibition of BTKE41K and BTKE41K/C481S obtained by nonlinear curve fitting are shown above the graph in nm. F, COS-7 cells were transfected as indicated with 1.33 μ g/well of vector encoding WT PLC γ_2 ($\gamma_2 WT$) and 0.66 μ g/well of empty vector (*Control*) or vector encoding BTKWT or BTKC481S. Twenty four hours after transfection, the cells were incubated for 18 h, as indicated with either solvent (0.1% (v/v) DMSO), acalabrutinib (1 μ M), or vecabrutinib (1 µm). Cells were lysed, and immunoblotting was performed as indicated using an antibody reactive against the c-Myc epitope present on WT PLC_{γ2}, antibody reactive against BTK, antibody reactive against β-actin, antibody reactive against phosphorylated tyrosine on PLC_{γ2} at position 759 (pY- $PLC\gamma_{2}$), and antibody reactive against phosphorylated tyrosine on BTK at position 223 (pY-BTK). A, C, E, and F show representative results from three independent experiments each as mean values of three technical replicates.

cells radiolabeled with [³H]inositol for measurement of [³H]inositol phosphate formation (Fig. 1*A*). WT and constitutively-active Δ 44 variants of the evolutionarily divergent PLC isoform PLC δ_1 , carrying a deletion of the autoinhibitory *X*-*Y*

linker (43), were analyzed for comparison. $PLC\delta_1$ is not known to be regulated by heterotrimeric GTP-binding proteins or members of the Tec kinase family and is thus considered to be distinct from a mechanistic point of view. There was little effect

of WT BTK on inositol phosphate formation in the absence of exogenous PLC enzymes and in the presence of any of the WT PLCs. In contrast, in the presence of PLC γ_2 S707Y, WT BTK caused a 4.6-fold increase in inositol phosphate formation. BTKE41K caused a minor increase in inositol phosphate formation in the absence of exogenous PLCs but triggered much more marked increases in the presence of WT PLC γ_1 , PLC γ_2 , PLC β_2 , and, most strikingly, of PLC γ_2 S707Y. Neither WT nor $\Delta 44$ variant PLC δ_1 activity was affected by WT or E41K variant BTK, suggesting that the stimulatory effects observed for the other PLC isozymes were not due to enhanced supply of their common substrate PtdInsP₂. Fig. 1B shows that the differences in inositol phosphate formation observed in Fig. 1A were not explained by differences in protein expression. Note that there was no difference in the expression of WT PLC γ_2 and PLC γ_2 S707Y when directly compared on the same immunoblots (cf. Fig. 3D and Fig. S3).

Fig. 1*C* shows the dependence of WT *versus* S707Y variant PLC γ_2 activity on increasing expression levels of WT *versus* E41K variant BTK after correction of inositol phosphate formation for background activity observed in the absence of exogenous PLC γ enzyme. In contrast to WT PLC γ_2 activity, which was unaffected by WT BTK even at the highest expression level, PLC γ_2 S707Y variant activity was markedly stimulated by WT BTK in a concentration-dependent fashion. Furthermore, increased expression of BTKE41K caused striking increases in the activities of both WT and S707Y variant PLC γ_2 , although the variant was severalfold more sensitive to BTKE41K. The E41K mutation also rendered BTK more potent in activating PLC γ_2 S707Y (*cf.* Fig. 1*C, left versus right panel*). There were no differences in protein expression that would explain the functional differences shown in Fig. 1*C* (*cf.* Fig. 1*D*).

To determine whether the productive interaction between WT PLC γ_2 and BTKE41K (Fig. 1*C*, *right panel*) was contingent on the protein-tyrosine kinase activity of BTKE41K, the effects of BTK protein-tyrosine kinase inhibitors, ibrutinib, acalabrutinib, and vecabrutinib, were investigated (Fig. 1E). In addition, the effect of the BTK C481S mutation was tested by incorporating this mutation into a BTKE41K/C481S compound variant. The C481S mutation is known to cause resistance to the two irreversible covalent BTK inhibitors, ibrutinib and acalabrutib, with limited, if any, impact on vecabrutinib activity, a novel noncovalent and reversible BTK inhibitor (44). Fig. 1E shows that both the E41K single and the E41K/C481S double variants caused a similar \sim 38-fold increase in PLC γ_2 activity. All three drugs showed potent inhibition of PLC γ_2 activity in the E41K single variant cells. However, ibrutinib and acalabrutinib reduced inositol phosphate formation by only 50% in PLC γ_2 and BTKE41K/C481S cells. Estimated IC₅₀ values of these covalent inhibitors were \sim 3530-fold (ibrutinib) and 410-fold (acalabrutinib) higher in cells expressing the BTK C481S acquired resistance mutation than in cells without this mutation. In contrast, this difference was only about 4.8-fold for vecabrutinib, which does not require BTK Cys-481 interaction for activity. We also tested the effects of acalabrutinib and vecabrutinib at a single concentration, 1 μ M, on protein tyrosine phosphorylation of WT PLC γ_2 and either WT BTK or its C481S variant. Fig. 1F shows that acalabrutinib was capable of substantially reducing both the autophosphorylation of WT BTK and the BTK-mediated phosphorylation of PLC γ_2 , but not of BTKC481S and PLC γ_2 , respectively, whereas vecabrutinib was strongly inhibitory in the presence of either WT or C481S variant BTK together with PLC γ_2 . Collectively, the results shown in Fig. 1, *E* and *F*, clearly support the view that activation of WT PLC γ_2 by BTKE41K in the reconstituted systems requires the tyrosine kinase activity of BTK.

$PLC\gamma_2$ S707Y is stimulated by catalytically-inactive BTK independently of tyrosine phosphorylation and increased PtdInsP₂ substrate supply

To interrogate the pharmacology of the BTK-mediated activation of WT and S707Y variant PLC γ_2 , both PLC γ_2 variants were coexpressed with WT or variant BTK to examine the effects of 1 μ M acalabrutinib on inositol phosphate formation (Fig. 2A). Acalabrutinib caused an almost complete loss of the PLC γ_2 activity in BTKE41K cells but, as expected, had a much lower impact in BTKE41K/C481S cells. Surprisingly, acalabrutinib was much less effective in the context of PLC γ_2 S707Yexpressing BTKE41K cells, showing only ~25% inhibition. Acalabrutinib had no activity at all in the PLC γ_2 S707Y-BTKE41K/C481S cells. Several point variants of BTK were coexpressed with PLC γ_2 S707Y to further investigate the functional differences between WT and S707Y variant PLC γ_2 shown in Fig. 2A and to also extend this analysis to WT PLC γ_1 (Fig. 2B). Point mutations of BTK, Y223F, or Y551F, which prevent tyrosine phosphorylation of BTK in cis or in trans by upstream protein kinases, and the covalent inhibitor binding site mutation C481S had only small, if any, effects on the ability of WT BTK to mediate PLC γ_2 S707Y activation. As expected, modulating the plasma membrane interaction through either inhibitory (R28C) or stimulatory (E41K) mutations caused considerable decreases and increases, respectively, in the reconstitutive activity of BTK. For both WT PLC γ_1 and PLC γ_2 , enzyme activation was only observed for the E41K variant of BTK. Most interestingly, however, when BTK protein-tyrosine kinase activity was blocked by the K430R mutation, the BTK-mediated stimulation of PLC γ_2 S707Y was only reduced by ~50%. This result, together with those shown in Fig. 2A, right panel, raised the distinct possibility that PLC γ_2 S707Y is sensitive to activation by BTK even in the absence of its tyrosine kinase activity.

To further challenge this hypothesis, WT and S707Y variant PLC γ_2 were coexpressed with increasing concentrations of BTKK430R and its membrane-targeted variant BTKE41K/ K430R (Fig. 2*C*, *left panel*). Although the activity of WT PLC γ_2 remained unaffected by the two BTK variants, inositol phosphate formation of the S707Y variant was markedly and concentration-dependently increased. Membrane targeting of even the catalytically incompetent BTK caused an almost 10-fold shift to the left of the concentration-response relationship. The functional effects observed in Fig. 2C were unrelated to changes in PLC γ_2 expression (Fig. 2D). Analysis of protein tyrosine phosphorylation showed that the two BTK variants, K430R and E41K/K430R, similar to their catalytically-competent counterparts, WT and E41K, in the presence of ibrutinib or acalabrutinib were unable to mediate phosphorylation of the PLC_{γ2} residues Tyr-759 or Tyr-1217, *i.e.* known BTK phosphor-





ylation sites, or other PLC γ_2 tyrosine residues (Fig. 2C, right panel, subpanels labeled pY759 and pY1217, and pY, respectively). Importantly, stimulation of PLC γ_2 S707Y, but not WT $PLC\gamma_2$, was not confined to the catalytically-inactive variant K430R and was also observed for another variant devoid of catalytic activity, R525Q (13). This stimulation was even seen for a BTK deletion variant (Δ amino acids 402–659) lacking the protein-tyrosine kinase domain (Fig. 2E). Fig. 2F shows that the effects of BTK variants on WT and variant $PLC\gamma_2$ activity observed in Fig. 2E were not explained by differences in protein expression. We then determined how the differential sensitivity of the variant PLC γ_2 S707Y to the actions of both the catalytic and the noncatalytic functions of BTK translates into the concentration dependence of acalabrutinib-mediated BTK inhibition. It is clear from these results that the inhibitor did not affect the strikingly enhanced inositol phosphate formation in the presence of BTKE41K/K430R and PLC γ_2 S707Y (Fig. 2G). Furthermore, acalabrutinib reduced the activities of the BTKE41K/WT PLC γ_2 and BTKE41K/PLC γ_2 S707Y pairs with very similar, if not identical, IC $_{50}$ values (\sim 20 nM), but did so in a markedly different extent. Although enhanced activity was almost fully abrogated in the presence of WT PLC γ_2 , it was only partially reduced (\sim 23%) in the presence of PLC γ_2 S707Y, most interestingly to a level very similar to the one observed for catalytically-incompetent BTKE41K/K430R and PLC γ_2 S707Y. Notably, this level of activity, which was unaffected by acalabrutinib over the whole range of concentrations, was still ${\sim}14$ -fold higher than that observed in the presence of PLC γ_2 S707Y alone. Therefore, the acalabrutinib resistance of the BTKE41K/ PLC γ_2 S707Y pair is very likely based on the BTK variant exerting tyrosine phosphorylation-independent, stimulatory effects on PLC γ_2 S707Y.

To address the possibility that the stimulatory effect of membrane-targeted, catalytically-inert BTKE41K/K430R on inositol phosphate formation by PLC γ_2 S707Y is due to enhanced supply of the enzyme phospholipid substrate directly, the effects of WT as well as E41K, K430R, and E41K/K430R variant BTK on the abundance of the inositol phospholipids, PtdIns, PtdIns*P*, and PtdIns*P*₂, in COS-7 cells were examined (Fig. 3*A*). No effect of any of the BTK variants on the abundance of these phospholipids was observed. To further examine potential effects of BTK on substrate availability rather than enzyme activity of PLC γ_2 , a close congener of PLC γ_2 S707Y, PLC γ_1 S729Y, which shares enhanced activity in intact cells with its PLC γ_2 counterpart (Fig. 3B), was coexpressed with WT as well as variant BTK and functionally compared with PLC γ_2 S707Y. As shown in Fig. 3C, there was a marked difference between the two PLC γ_2 variants vis à vis BTK, in that PLC γ_1 S729Y largely behaved like WT PLC γ_1 and PLC γ_2 and displayed a functional phenotype very different from that of PLC γ_2 S707Y, which was not due to differences in protein expression (Fig. 3D). These results are difficult, if not impossible, to explain by an effect of BTK on substrate availability to the two PLC γ variants in the reconstituted system. Interestingly, the PLC γ_2 -specific functional phenotype is not restricted to the S707Y variant. Instead, it is also observed for many of the PLC γ_2 variants that have previously been associated with ibrutinib resistance of CLL cells: D334H (catalytic subdomain X), R665W, S707F, and S707P (all C-terminal SH2) domain), L845F (C-terminal half of split PH domain), D993H (catalytic subdomain Y), and M1141R (C2 domain) (34, 45, 46). All listed variants were found to be sensitive to stimulation by catalytically-inert BTK (activity ratios BTKE41K/K430R: BTKE41K \geq 43.5%; Table 1). Notably, the highest activity ratios, maximal sensitivities for catalytically-inactive BTK, with no difference between BTKE41K and BTKE41K/K430R were observed for the PLC γ_2 variants L845F and M1141R. Note that there are no differences in variant PLC γ_2 protein expression in the presence of BTKE41K or BTKE41K/K430R. Therefore, the differences in activity ratios BTKE41K/K430R:BTKE41K analyzed for each row of data sets cannot be explained by differences in PLC γ_2 and/or BTK protein expression (Fig. S4).

Functional phenotype of PLC γ_2 S707Y vis à vis BTK is instigated by mutational preactivation of PLC γ_2

To determine whether the enhanced sensitivity of PLC γ_2 S707Y to catalytically-inert BTK is related to its augmented basal activity in intact cells, PLC γ_2 S707Y was compared with two other variants of PLC γ_2 also showing this property, the phosphomimetic variant PLC γ_2 4E, carrying glutamic acid residues in all four canonical positions of BTK-mediated tyrosine phos-

Figure 2. In contrast to the WT enzyme, the PLC γ_2 S707Y variant is activated by catalytically-inert BTK. A, COS-7 cells were transfected as indicated with 50 ng/well of vector encoding WT PLC γ_2 (γ_2 WT) (*left panel*) or PLC γ_2 S707Y (γ_2 S707Y) (*right panel*) and 150 ng/well of empty vector (ϕ) or vector encoding WT BTK (W7) or the BTK variants C4815, E41K, or E41K/C4815. Twenty four hours after transfection, the cells were incubated for 18 h with myo-[2-3H]inositol and either solvent (0.1% (v/v) DMSO) (–) or 1 μ M acalabrutinib (+) prior to determination of inositol phosphate formation. *B*, COS-7 cells were transfected as indicated with 50 ng/well of vector encoding WT PLC γ_1 (γ_1 WT), WT PLC γ_2 (γ_2 WT), or PLC γ_2 S707Y (γ_2 S707Y) and 150 ng/well of vector encoding WT BTK (WT) or the BTK variants K430R, Y551F, Y223F, R28C, C481S, or E41K. C, left panel, COS-7 cells were transfected as indicated with 50 ng/well of vector encoding WT PLC γ_2 (γ_2 WT) or PLC γ_2 S707Y (γ_2 S707Y) and increasing amounts (0 – 450 ng/well) of vector encoding BTKE41K/K430R or BTKK430R. *Right panel*, COS-7 cells were transfected as indicated with 1.33 μ g/well of vector encoding PLC γ_2 S707Y (γ_2 S707Y) and 0.66 μ g/well of vector encoding WT BTK or BTK harboring the E41K for BTK harbor or K430R mutations. Twenty four hours after transfection, the cells were incubated for 18 h with either solvent (Co.), 1 µm ibrutinib (lbru.), or 1 µm acalabrutinib (*Acal.*). The cells were lysed, and immunoblotting was performed as indicated using an antibody reactive against the c-Myc epitope present on PLC γ_2 S707Y, antibody reactive against BTK, antibody reactive against phosphorylated tyrosine on PLC γ_2 at position 759 (*p*Y⁷⁵⁹), antibody reactive against phosphorylated tyrosine phosphorylated proteins in all species (*p*Y). *D*, cells from one well each functionally analyzed in C were washed with 0.2 ml of Dulbecco's PBS and then lysed by addition of 100 µl of SDS-PAGE sample preparation buffer. Aliquots of the samples were subjected to SDS-PAGE, and immunoblotting was performed using an antibody reactive against the c-Myc epitope present on WT PLC γ_2 and PLC γ_2 S707Y (a-c), antibody reactive against BTK (*d*-*f*), or antibody reactive against β -actin (*g*-*i*). *E*, COS-7 cells were transfected as indicated with 50 ng/well of vector encoding WT PLC γ_2 ($\gamma_2 WT$) or PLC γ_2 S707Y ($\gamma_2 S707Y$) and increasing amounts (0–450 ng/well) of vector encoding BTKE41K/R525Q or BTKE41K/ Δ Kinase (BTKE41K/ Δ Kin). F, cells from one well each functionally analyzed in E were washed with 0.2 ml of Dulbecco's PBS and then lysed by addition of 100 μ l of SDS-PAGE sample preparation buffer. Aliquots of the samples were subjected to SDS-PAGE and immunoblotting was performed using an antibody reactive against the c-Myc epitope present on WT PLC γ_2 and PLC γ_2 S707Y (*a*–*c*), antibody reactive against BTK (*d*–*f*), or antibody reactive against β -actin (*g*–*i*). *G*, COS-7 cells were transfected as indicated with 150 ng/well of vector encoding WT PLC γ_2 (γ_2 WT), 50 ng/well of vector encoding PLC γ_2 S707Y), and 100 ng/well of vector encoding BTKE41K or BTKE41K/K430R. Analysis of inositol phosphate formation and treatment with BTK inhibitor was done as in Fig. 1. A–C, E, and G show representative results from three independent experiments each as mean values of three technical replicates.





Figure 3. Activation of PLC γ_2 **S707Y by catalytically-inert BTK is not mediated by augmented PLC substrate availability.** *A*, COS-7 cells were transfected as indicated with 2 μ g/well of empty vector or 0.5 μ g/well of vector encoding WT BTK (*WT*) or BTK variants K430R, E41K, or E41K/K430R. Twenty four hours after transfection, the cells were incubated for 18 h with *myo*-[2-³H]inositol. Then, the amounts of radioactively labeled PtdIns (*PI*), PtdIns*P* (*PIP*), and PtdIns*P*₂(*PIP*) in the intact COS-7 cells were determined by TLC analysis as described under "Experimental procedures." *Inset*, cells from one well each were lysed and subjected to SDS-PAGE. Subsequent immunoblotting was performed using an antibody reactive against BTK or antibody reactive against *B*-actin. *B*, COS-7 cells were transfected as indicated with 500 ng of empty vector (*Co*.) or increasing amounts (15, 50, 150, or 500 ng) of vector encoding WT PLC γ_1 (γ_1 ,*WT*), PLC γ_2 (γ_2 ,*WT*), or PLC γ_2 (γ_2 ,*ST0TY* (γ_2 ,*S70TY*). *C*, COS-7 cells were transfected as indicated with 50 ng/well of vector sa described in *B*, and 100 ng/well of vector encoding WT BTK (*WT*) or BTK variants K430R, E41K, or E41K/K430R. Analysis of inositol phosphate formation was done as in Fig. 1. *D*, cells from one well each functionally analyzed in *C* were washed with 0.2 ml of Dulbecco's PBS and then lysed by addition of 100 μ l of SDS-PAGE sample preparation buffer. Aliquots of the samples were subjected to SDS-PAGE, and immunoblotting was performed using an antibody reactive against *B*-actin. *A*-*C* show representative results from three independent experiments each as mean values of three technical replicates.

phorylation, Tyr-753, Tyr-759, Tyr-1197, and Tyr-1217, and the N-myr–PLC γ_2 carrying an artificial N-terminal signal for myristoylation. The *inset* of Fig. 4 shows that the two variants caused specific enhancements of inositol phosphate formation in intact cells (PLC γ_2 4F < PLC γ_2 <<< PLC γ_2 4E < N-myr-PLC γ_2 < PLC γ_2 5707Y). Importantly, a very similar, if not identical, order was observed for the sensitivity of the five PLC γ_2 variants to membrane-targeted BTKE41K, both catalyticallycompetent and -incompetent. Hence, preactivation of PLC γ_2 appears to predispose the enzyme to further activation by catalytically-inert BTK.

Catalytically-inert BTK causes WT and S707Y variant to differentially interact with the plasma membrane

Next, fluorescence recovery after photobleaching (FRAP) static laser microscopy, employing a fixed-localization Gaussian beam and photon counting to follow fast recoveries (see under "Experimental procedures") (47), was used to investigate the effects of BTKE41K and BTKE41K/K430R on the membrane interaction and diffusion of GFP-tagged WT and S707Y variant PLC γ_2 in intact cells. A significant fraction of PLC γ_2 is cytoplasmic and can therefore recover in FRAP by either lateral

Table 1

Activation of PLC γ_2 by catalytically-inert BTK is not limited to PLC γ_2 S707Y but is also observed for other PLC γ_2 variants mediating ibrutinib resistance in CLL cells

COS-7 cells were transfected as indicated with 150 ng/well vector encoding WT PLC γ_2 (*PLC* γ_2 , *WT*); 50 ng/well vector encoding the PLC γ_2 variants D334H, R665W, S707Y, S707F, L845F, D993H, and M1141R; 15 ng of vector encoding PLC γ_2 S707P; and 100 ng/well of vector encoding BTKWT or BTK variants K430R, E41K, or E41K/K430R. The ratios of the PLC activities determined in the presence of BTKE41K/K430R and BTKE41K are specified in the *right column*. The data depicted in the table show representative results from three independent experiments each as mean values of three technical replicates.

ВТК	Inositol phosphate formation					Ratio (E41K/K430R:
	Control	WT	K430R	E41K	E41K/K430R	E41K)
	срт					%
$PLC\gamma_2WT$	67	86	67	2358	121	5.2
$PLC\gamma_2D334H$	40	1097	236	10089	4390	43.5
$PLC\gamma_2R665W$	42	374	138	4420	1956	44.3
$PLC\gamma_{2}S707Y$	231	1998	713	17442	8132	46.6
$PLC\gamma_{2}S707F$	464	2561	1488	20150	11215	55.7
$PLC\gamma_2S707P$	728	2991	2563	17734	11584	65.3
PLC _{y2} L845F	219	1660	455	8937	9668	108.2
PLCγ ₂ D993H	702	3604	1888	10808	7892	73.0
$PLC\gamma_2M1141R$	1966	5858	5395	14268	14187	99.4



Figure 4. Preactivation of PLC γ_2 **sensitizes the enzyme to further activation by catalytically-inert BTK.** COS-7 cells were transfected as indicated with 50 ng/well of vector encoding WT PLC γ_2 ($\gamma_2 WT$), PLC $\gamma_2 4Y \rightarrow F$ ($\gamma_2 4F$), PLC $\gamma_2 4Y \rightarrow E$ ($\gamma_2 4E$), PLC $\gamma_2 N$ -myr ($\gamma_2 N$ -myr) (*left panel*), or PLC $\gamma_2 S707Y$ ($\gamma_2 S707Y$) (*right panel*) and 100 ng/well of vector encoding WT BTK (*WT*) or BTK variants K430R, E41K, or E41K/K430R. *Inset*, COS-7 cells were transfected as indicated with 500 ng/well of vector to examine the influence of the PLC γ_2 mutations on basal inositol phosphate formation in intact transfected cells. Analysis of inositol phosphate formation was done as in Fig. 1. The *graph* shows representative results from three independent experiments as mean values of three technical replicates.

diffusion along the membrane surface or by exchange between membrane-associated and cytoplasmic populations. To evaluate the relative contribution of lateral diffusion and exchange (where the faster process contributes more), we previously developed the FRAP beam-size test (48, 49). This method is based on performing the FRAP experiment using two different laser beam sizes; if the fluorescence recovery is by exchange, the characteristic recovery time (τ) reflects the chemical relaxation time, which is independent of the beam size (48). Under such conditions, the ratio between the τ values measured with the two beam sizes generated in the current experiments by the two objectives equals 1 ($\tau(\times 40)/\tau(\times 63) = 1$). For lateral diffusion, τ is the characteristic diffusion time τ_D , which is proportional to the area bleached by the beam ($\tau_D = \omega^2/4D$, where ω is the Gaussian radius of the beam, and D is the lateral diffusion coefficient). The results obtained with WT PLC γ_2 (Fig. 5) are in line with recovery by lateral diffusion, because the $\tau(\times 40)/\tau(\times 63)$ ratio (Fig. 5C, *leftmost bar*) is not significantly different from 2.28, which is the ratio between the beam sizes generated with these two objectives. However, the *D* value calculated from the FRAP studies, 3.1 μ m²/s, is much faster than the *D* value of a lipid probe DiIC₁₆(3) (1,1'-dihexadecyl-3,3,3',3'-tetramethylindocarbocyanine perchlorate) in the plasma membrane of the same cells (1 μ m²/s) (50). This suggests that PLC γ_2 membrane interactions are characterized by "gliding" along the inner membrane surface (i.e. it dissociates from the membrane but re-associates before it can diffuse away into the cytoplasm). The current results are similar to our earlier FRAP measurements of WT PLC γ_2 with the smaller beam size (×63) (49), but we find a somewhat slower recovery with the beam generated by the $\times 40$ objective. Slower recovery suggests stronger interactions with the membrane (because free GFP in the cytosol recovers at a rate faster by at least an order of magnitude). This difference may reflect a higher level of RAC activity in the current measurements, because overexpression of constitutively-active RAC2 increased to a similar level the τ (×40) of WT PLC γ_2 (49). The effects of coexpressing BTKE41K or BTKE41K/K430R on the membrane interactions of WT PLC γ_2 –GFP are depicted in Fig. 5B, left panel. Both BTK variants induced increases in the τ (×40) values of WT PLC γ_2 -GFP and in the τ (×63) values; here, the effect of BTKE41K/K430R was weaker. Most importantly, neither of the BTK variants significantly affected the $\tau(\times 40)/\tau(\times 63)$ ratio of WT PLC γ_2 -GFP (Fig. 5C, *left*), which remained only insignificantly different from the beam-size ratio





Figure 5. BTK mediates subdiffusion of PLC γ_2 S707Y but not of WT PLC γ_2 . COS-7 cells were transfected with a vector encoding PLC γ_2 -GFP (γ_2WT) or PLC₇₂S707Y-GFP (y₂S707Y) together with either empty vector or a vector encoding BTKE41K or BTKE41K/K430R. FRAP studies were conducted 24-26 h post-transfection at 22 °C. A, typical FRAP curves obtained using ×63 (smaller beam size) or ×40 (larger beam size) objectives. The time segments showing pre-bleach fluorescence intensity, the bleach point, and post-bleach recovery are indicated by arrows. Solid lines show the best fit of a nonlinear regression analysis (102), with the resulting τ and mobile fraction (R_{cl} values. B and C, FRAP beam-size analysis. Bars are means \pm S.D. of multiple measurements. The τ data depicted in B are also used to calculate the τ ratios shown in C. The number of measurements for each condition was as follows: (i) PLC γ_2 , ×63 objective, n = 28; (ii) ×40 objective, n = 62; (iii) PLC γ_2 with BTKE41K, ×63, n = 24; (iv) ×40, n = 22; (v) PLC γ_2 with BTKE41K/K430R, ×63, n = 27; (vi) ×40, n = 29; (vii) PLC γ_2 S707Y–GFP, ×63, n = 30; (viii) ×40, n = 80; (ix) PLC γ_2 S707Y–GFP with BTKE41K, ×63, n = 63; (x) ×40, n = 58; (xi) PLC γ_2 S707Y–GFP with BTKE41K/K430R, \times 63, n = 58; and (xii) \times 40, n = 51. The studies employed \times 40 and \times 63 objectives, whose beam size measurements (n = 59) yielded a $\omega^2(\times 40)/\omega^2(\times 63)$ ratio of 2.28 \pm 0.15. Thus, a similar $\tau(\times 40)/\tau(\times 63)$ ratio is expected for FRAP by lateral diffusion. A τ ratio of 1 is expected for recovery by exchange (48). The R_f values were high in all cases (0.98–1.00) and are given in Table S1. B displays the τ values, and C displays the τ (×40)/ τ (×63) ratios. B, asterisks indicate significant differences between the sample without BTK and the samples with the two BTK variants; the comparison was done separately for the τ (×63) values and the τ (×40) values, comparing the same PLC γ_2 -GFP protein without BTK and with one of the BTK variants (*n.s.*, not significant; **, $p < 5 \times 10^{-3}$; ***, $p < 10^{-5}$; ****, $p < 10^{-10}$; one-way ANOVA and Bonferroni post hoc test). *C*, bootstrap analysis (see under "Experimental variants". (*n.s.*, not significant; **, $p < 5 \times 10^{-3}$; ****, $p < 10^{-5}$; ****, $p < 10^{-10}$; one-way ANOVA and Bonferroni post hoc test). *C*, bootstrap analysis (see under "Experimental variants". procedures"; 1000 bootstrap resampling values for both τ and beam-size values) shows that the τ ratio of PLC γ_2 (WT or the S707Y variant) in the absence of BTK fits FRAP by lateral diffusion. In the presence of BTK (either E41K or E41K/K430R), the τ ratio of PLC γ_2 S707Y, but not of WT PLC γ_2 , becomes significantly higher than the 2.28 beam size ratio (*, p < 0.05; ****, $p < 10^{-20}$; bootstrap analysis and Student's two-tailed t test). The source data for the FRAP studies containing statistics (B and C) are provided in Table S1.

throughout (2.28). This suggests that the mechanism of the FRAP remains by gliding, albeit with somewhat enhanced interactions with the membrane, as suggested by the larger τ values. We then compared the membrane interactions of PLC γ_2 S707Y–GFP with those of the WT enzyme (Fig. 5*B*, *right panel*). The FRAP results for this variant in the absence of BTK resembled those obtained for WT PLC γ_2 –GFP, suggesting recovery by gliding lateral diffusion. However, expression of BTKE41K or BTKE41K/K430R had a markedly different effect than in the case of WT PLC γ_2 . Here, only the $\tau(\times 40)$ values of PLC γ_2 S707Y–GFP became larger (slower recovery kinetics), resulting in a highly-significant deviation of the $\tau(\times 40)/\tau(\times 63)$ ratio from the 2.28 beam-size ratio expected for recovery by

lateral diffusion (Fig. 5*C*, *right panel*). The τ ratio dramatically increased, to 3.6–3.8, suggesting that the recovery becomes slower than expected for lateral diffusion with increasing distances. Such a phenomenon, termed subdiffusion or hop diffusion, may arise due to sensing of membrane heterogeneity by the diffusing molecule, which may reflect phase separation, potentially assisted by the cytoskeleton (51, 52). This indicates that the interactions of the variant PLC γ_2 S707Y with membrane heterogeneities, which give rise to the anomalous diffusion, are enhanced by BTK to a much higher degree than those of WT PLC γ_2 . Of note, BTKE41K and BTKE41K/K430R had a similar effect, indicating that the effect on PLC γ_2 S707Y–GFP arises due to



Figure 6. Stimulation via RAC2 augments the responsiveness of the PLC γ_2 enzyme to catalytically-inert BTK. *A*, COS-7 cells were transfected as indicated with 50 ng/well of vector encoding WT PLC γ_2 (γ_2WT), PLC γ_2 S707Y (γ_2 S707Y), and PLC γ_2 S707Y containing a Phe \rightarrow Gln mutation at position 897, providing resistance toward RAC2 stimulation (*F*897Q) and 100 ng/well of vector encoding WT PLC γ_2 (γ_2WT) and BTK (*W*T) or BTK variants K430R, E41K, or E41K/K430R. *B*, *lower panel*, COS-7 cells were transfected as indicated with 50 ng/well of vector encoding WT PLC γ_2 (γ_2WT) and BTKE41K/K430R or 25 ng/well of vector encoding WT PLC γ_2 (γ_2WT) and BTKE41K/K430R or 25 ng/well of vector encoding PLC γ_2 S707Y (γ_2 S707Y) or increasing amounts (0–100 ng/well) of vector encoding RAC2G12V. *Upper panel*, COS-7 cells were transfected as indicated with 50 ng/well of vector encoding RAC2G12V. Upper panel, COS-7 cells were transfected as indicated by nonlinear curve fitting are shown *above the graphs* in ng/well. *C*, cells from one well each functionally analyzed in *B* were washed with 0.2 ml of Dulbecco's PBS and then lysed by addition of 100 μ l of SDS-PAGE sample preparation buffer. Aliquots of the samples were subjected to SDS-PAGE, and immunoblotting was performed using an antibody reactive against the c-Myc epitope (a-b) present on WT PLC γ_2 and PLC γ_2 S707Y, antibody reactive against BTK (c-d), antibody reactive against BAC2G12V or increasing amounts (0–350 ng/well) of vector encoding BTKE41K/K430R. Analysis of inositol phosphate formation was done as in Fig. 1. *A*, *B*, and *D* show representative results from three independent experiments each as mean values of three technical replicates.

interactions of BTK with the enzyme, but it does not require BTK tyrosine kinase activity.

Activated RAC2 allows catalytically-inert BTK to activate WT $PLC\gamma_2$

The previous demonstration that PLC γ_2 variants mediating ibrutinib resistance in CLL, PLC γ_2 R665W, and PLC γ_2 L845F are hypersensitive to activated RAC endogenously present in COS-7 cells (38) prompted us to determine the contribution of RAC to the effects of catalytically-competent and -incompetent BTK on PLC γ_2 S707Y. Fig. 6A shows that blocking the functional interaction of PLC γ_2 S707Y with activated RAC in variant PLC γ_2 -F897Q caused conspicuous losses of inositol phosphate formation, which were particularly striking for the catalyticallyinert BTK variants K430R (~85%) and E41K/K430R (~58%). Because the F897Q mutation, located in the C-terminal half of the split PH domain of PLC γ_2 , is known to neither affect the overall three-dimensional structure of the PH domain nor the catalytic activity of PLC γ_2 in vitro (49, 53, 54), these results indicate that activated RAC may facilitate BTK-mediated PLC γ_2 stimulation, in particular through the noncatalytic functions of BTK. Fig. 6B shows that the cellular abundance of exogenous, activated RAC2G12 exerts impressive effects on the activation of both WT and S707Y variant PLC γ_2 by catalytically-inert BTKE41K/K430R. Thus, PLC γ_2 S707Y not only shows higher activity in the presence of RAC2G12V and catalyticallyinactive BTKE41K/K430R, but also reveals a higher sensitivity to RAC2G12V in the presence of the latter. The basal activities of the constitutively-active PLC variants PLC $\gamma_2\Delta$ SH (lacking the complete autoinhibitory SH2-SH2-SH3 tandem (55)) and PLC $\delta_1 \Delta 44$ are shown in Fig. 6B, top panel, to demonstrate that the plateau observed for PLC γ_2 S707Y in the presence of BTKE41K/K430R at high RAC2G12V levels is not limited due to exhaustion of the enzyme substrate PtdInsP₂. Increasing concentrations of RAC2G12V had no effect on the expression of PLC γ_2 and BTKE41K/K430R (Fig. 6C).





Time (s)

Figure 7. Ability of catalytically-inert BTK to mediate intracellular Ca²⁺ mobilization depends on the level of BCR stimulation. A, DT40 cells (1.5 × 10⁶) were lysed as described under "Experimental procedures," and aliquots of the samples were subjected to SDS-PAGE, and immunoblotting was performed using an antibody reactive against both human and chicken BTK, antibody reactive against human and chicken PLC γ_2 , or antibody reactive against β -actin. One *empty lane* was present between each of the four lanes from the same immunoblot with the same length of exposure time. These lanes were removed by splicing. The positions of the splice sites are indicated by *gray dotted lines* and *arrowheads*. *B*, WT DT40 cells ($BTK^{+/+}$), DT40 BTK^{-/-}), and DT40 BTK^{-/-} cells expressing either human WT ($BTK^{-/-} + BTKWT$) or human K430R BTK ($BTK^{-/-} + BTKK430R$) were loaded with Indo-1-AM. After pre-warming to 37 °C, the cells were applied to the fluorescence analyzer and treated with anti-IgM followed by ionomycin as described under "Experimental procedures." C, DT40 cells expressing either human WT ($BTK^{-/-} + BTKWT$) or human K430R BTK ($BTK^{-/-} + BTKK430R$) were either left unstained (BTK^{-} BTK⁻ +BTKWT) or stained with CFSE (BTK-/ $^-$ + BTKK430R). After mixing the two populations at a 1:1 ratio, the cells were incubated for 1 h at 37 °C in the presence of either solvent (0.1% (v/v) of DMSO, Co.), or 1 μM ibrutinib (*lbr.*), or acalabrutinib (*Aca.*) followed by washout. Afterward, cells were incubated with indo-1-AM, and the changes in [Ca²⁺], were analyzed as described above. The individual points shown in B and C correspond to the times in full seconds versus the medians of all fluorescence ratios representing [Ca²⁺], following their correction for basal fluorescence intensity in the absence of anti-IgM and normalization according to the maximal values reached after addition of 2 μ M ionomycin. In PLC $\gamma_2^{-/-}$ DT40 cells expressing WT PLC γ_2 , type M4 anti-IgM causes BCR-mediated increases of [Ca²⁺], at EC₅₀ values between 30 and 50 ng/ml (49). Hence, there were no substantial changes in the [Ca²⁺], responses in BTK^{-/-} cells expressing WT BTK when the concentration of anti-IgM was increased to values higher than 30 ng/ml. Specifically, the values were 32.6, 42.9, 35.9, and 28.0% of the maximal Ca²⁺ concentrations upon addition of ionomycin following the addition of anti-IgM at concentrations of 30, 100, and 300 ng/ml and 1 µg/ml, respectively, in B), and 28.5, 18.0, 32.8, and 45.4% following the addition of anti-IgM at concentrations of 30 and 100 ng/ml and of 1 and 10 μ g/ml, respectively, in C).

Strikingly, however, RAC2G12V appeared to unmask a conspicuous sensitivity of WT PLC γ_2 to stimulation by the tyrosine phosphorylation–independent functions of BTK. This strikingly permissive effect of RAC is substantiated by the results shown in Fig. 6*D*, demonstrating insensitivity of PLC γ_2 to BTKE41K/K430R in the absence of RAC2G12V, but with an ~25-fold stimulation of inositol phosphate formation in its presence. The latter results indicate that coactivation of BTK and RAC by upstream regulators may render even WT PLC γ_2 sensitive to the noncatalytic functions of BTK and, by extension, render WT BTK and WT PLC γ_2 at least partially resistant to active-site inhibitors of BTK.

The ability of catalytically-inert BTK to mediate BCR-dependent Ca²⁺ mobilization in intact DT40 B-lymphoma cells is conditional on the degree of BCR stimulation

To investigate the functional significance of the catalytic functions of BTK, the WT enzyme and its catalytically-inactive variant BTKK430R were stably expressed in BTK-deficient DT40 B-lymphoma cells. Fig. 7*A* shows that $BTK^{-/-}$ cells lack immunoreactive BTK protein and that the two reconstituted cells lines, $BTK^{-/-} + BTKWT$ and $BTK^{-/-} + BTKK430R$, express BTK at levels very similar, if not identical, to each other and to unmodified DT40 $BTK^{+/+}$ cells. Fig. 7, *B* and *C*, shows the changes of intracellular free Ca²⁺ in response to increasing concentrations of anti-IgM, as determined by flow cytometry

followed by statistical analysis of the results to allow for direct, quantitative comparison between the different experimental conditions. The most-right panel of Fig. 7B shows how the maximal Ca^{2+} concentration in response to 2 μ M ionomycin was used to correct the traces shown in the other panels for differences in fluorescent dye loading. The corrected traces were then normalized to the maximal Ca²⁺ concentrations observed in BTK^{-/-} + BTKWT cells (100%). Fig. 7*B* shows that there was little, if any, effect of anti-IgM in $BTK^{-/-} + BTKK430R$ cells compared with $BTK^{-/-}$ cells upon addition of anti-IgM at the lowest concentration, 30 ng/ml. Raising the concentration of anti-IgM over 100 and 300 ng/ml to 1000 ng/ml led to a gradual, distinct increase in the ability of the receptor ligand to increase free Ca^{2+} . In addition, there was a progressive loss of the differences in the lag time of the Ca²⁺ responses from about \sim 35 s at 100 ng/ml anti-IgM and \sim 20 s at 300 ng/ml, such that there were only relatively minor differences in the kinetics of the Ca²⁺ responses at 1000 ng/ml anti-IgM between the two genetically-modified cell lines and unmodified BTK^{+/+} cells, both in terms of the lag time and the maximal Ca²⁺ concentrations. The results show that the ability of catalytically-inert BTK to mediate BCR-mediated increases in intracellular Ca²⁺ is conditional on the concentration of the BCR ligand, anti-IgM, ranging from no to very sizable responses between 30 and 1000 ng/ml of anti-IgM.

Because the actions of catalytically-inert BTKK430R are insensitive to catalytic site BTK inhibitors like ibrutinib or acalabrutinib (see above), the relative inhibitory effect of these drugs was tested as a function of the degree of BCR activation by anti-IgM. Fig. 7C, most left panel, shows that ibrutinib $(1 \ \mu M)$ caused an \sim 67% decrease in the maximum Ca²⁺ response in cells expressing WT BTK at the lowest anti-IgM concentration, 30 ng/ml, very close to the Ca²⁺ concentrations observed for cells expressing BTKK430R. In addition, there was a slight inhibitory effect of the drug in the latter cells, presumably due to the known off-target effects of ibrutinib (56). Therefore, acalabrutinib, with less off-target effects than ibrutinib (56), was used. It is evident from the comparison shown in Fig. 7C that, at increasing anti-IgM concentrations, not only was there a gradual increase in the ability of catalytically-inert BTK to reconstitute BCR-mediated Ca²⁺ increases, as before, but that, at the same time, there was a quantitative loss to BTK catalytic site inhibition, down to only ${\sim}25\%$ in the presence of the maximal anti-IgM concentration tested, 10 μ g/ml. In addition, less inhibition at high-ligand concentrations also coincided with a continuous loss of the lag time of the Ca^{2+} response in BTK^{-/-} + BTKWT cells in the absence versus presence of the BTK inhibitor. In other words, both the inhibitory efficacy and the kinetic effects on $[Ca^{2+}]_i$ of BTK catalytic site inhibitors were found to be both conditional on and inversely related to the degree of BCR stimulation.

Discussion

Although the molecular basis of clinical resistance to BTK inhibitors, such as ibrutinib and acalabrutinib, caused by mutations at position Cys-481 of BTK are relatively clear, the mechanism of resistance caused by the other *BTK* and the *PLCG2* mutations is less understood. Although *PLCG2* mutations have

been suggested to constitute, as a whole, gain-of-function mutations (40, 45, 57), we have previously found that several PLC γ_2 variant enzymes carrying mutations in various regions are not constitutively active when assayed in cell-free systems (38, 39). The observation that these PLC γ_2 variants are, instead, hypersensitive in intact cells to the Rho GTPase RAC2 led us to suggest that the *PLCG2* mutations found in BTK inhibitor-resistant CLL cells may cause a rerouting of the transmembrane signals emanating from BCR and converging on as well as activating PLC γ_2 (38, 39). In addition, Liu *et al.* (40) showed that PLC γ_2 R665W is sensitive to activation by the proximal tyrosine kinases SYK and LYN even in BTK-deficient chicken DT40 B cells. Even in the presence of BTK, PLC γ_2 R665W appeared to be resistant to ibrutinib in this system.

Here, we have established a reconstituted system allowing us to monitor the functional interaction of WT and variant forms of BTK and PLC γ_2 in intact cells, placing special emphasis on a comparison between WT PLC γ_2 and variants known to mediate clinical BTK inhibitor resistance in CLL patients. Although BTK has long been known to mediate protein tyrosine phosphorylation of PLC γ_2 following coexpression in cells or cellfree preparations devoid of BLNK (58–60), information on the structural and functional requirements of this interaction to occur and result in enhanced PLC γ_2 enzyme activity is limited. This is presumably due to the known requirement of the adaptor protein BLNK to observe BCR-mediated, BTK-dependent activation of PLC γ_2 in B cells (61), together with the known difficulties to functionally reconstitute all three components outside the B cells context.

Our findings reveal that functional interaction of BTK and PLC γ_2 in a non-B-cell environment is conditional on the introduction of mutations into the two coding regions and on the level of protein expression. Thus, although there was no productive interaction between the two WT components even at the highest expression level of BTK, mutational alteration of either PLC γ_2 (S707Y) or BTK (E41K), or both, caused profound increases in PLC γ_2 activity. The results obtained on WT PLC γ_2 are consistent with the view that one of the roles of BLNK is to provide membrane targeting to PLC γ_2 to make it more susceptible to BTK-mediated protein tyrosine phosphorylation. In fact, a membrane-targeted variant of PLC γ_2 was sensitive to BCR stimulation even in the absence of BLNK (62, 63). According to this view, membrane targeting of BTK, such as introduced by the E41K mutation, would serve the same purpose. Extrapolating this concept to the altered functional properties of PLC γ_2 S707Y, which is highly sensitive to stimulation by even WT BTK, could indicate that this PLC γ_2 variant may also be different from the WT enzyme in its membrane interaction.

The marked sensitivity of the functional BTKE41K– PLC γ_2 WT interaction to BTK inhibitors of all three generations shows that the protein kinase activity of BTKE41K is an important determinant of this interaction; phosphoblot analysis shows that PLC γ_2 is a likely substrate of this activity. However, comparison of PLC γ_2 WT and PLC γ_2 S707Y revealed, unexpectedly, a fundamentally different dependence on protein tyrosine phosphorylation of the two PLC γ_2 isoforms. Thus, the catalytically-inactive forms of BTKE41K and even BTKWT were clearly capable of causing marked activation of



PLC γ_2 S707Y, but not of PLC γ_2 WT, in the absence of apparent protein tyrosine phosphorylation of the PLC γ_2 variant. Importantly, this activity was also observed for another known catalytically-inactive variant of BTK, BTKE41K/R525Q (13), and even by a deletion variant of BTK lacking its catalytic domain.

In the absence of alternative regulatory pathways between BTK and PLC γ_2 , as is the case in the cell system employed here for transient functional reconstitution, activation of PLC γ_2 , both WT and the various point variants analyzed herein, are, on first approximation, expected to be similarly sensitive to inhibition by active-site inhibitors of BTK. However, as shown in Fig. 2, A and G, they are not. PLC γ_2 S707Y was inhibited by acalabrutinib only to the extent of its activity that depended on the kinase activity of BTKE41K, whereas the remaining activity, which results from BTK catalysis-independent functions, was completely acalabrutinib-resistant. This drug-resistant portion may even be higher for other PLC γ_2 point variants with a higher BTK E41K/K430R:E41K ratio, such as the variants L845F or M1141R (Table 1). This mechanism provides an explanation, at least in part, for active-site BTK inhibitor resistance in tumor cells expressing PLCG2 point variants, without a requirement for constitutively-enhanced intrinsic activity, which is consistent with previous studies of the R665W and S707Y PLC γ_2 variant proteins in vitro (38, 39).

Preactivation of PLC γ_2 , regardless whether by phosphomimetic mutations or by membrane targeting at its N terminus (64), rendered the variants hypersensitive to activation by both catalytically-active and -inactive BTK (cf. Fig. 4). This effect was particularly striking for the variant carrying the myristoylation tag of Rous sarcoma virus v-SRC at its N terminus, PLC γ_2 Nmyr, which had a functional phenotype vis à vis BTK, WT, and variants, very similar to PLC γ_2 S707Y. Importantly, PLC γ_1 phosphorylation and Ca²⁺ release were previously promoted in Xenopus laevis egg extracts by lipid rafts prepared from COS-7 cells expressing the Xenopus SRC protein, suggesting that COS-7 cells contain lipid raft microdomain structures and that SRC kinase is targeted to these structures (65, 66). Hence, the N-terminal SRC-derived myristoylation tag was likely to promote lipid raft targeting of PLC γ_2 N-myr to COS-7 cell lipid rafts. Membrane-targeting tags of lipid raft-associated proteins FcyRIII (62, 67, 68) or the Src family member LYN (63) have previously been attached to PLC γ_2 and found to render BCR-mediated stimulation of PLC γ_2 in DT40 cells independent of the adaptor protein BLNK. The similarity of the functional phenotypes vis à vis BTK, WT, as well as variants, between PLC γ_2 N-myr and PLC γ_2 S707Y (*cf.* Fig. 4) and the hop diffusion in the membrane detected by FRAP for PLC γ_2 S707Y in the presence of BTKE41K or BTKE41K/K430R (cf. Fig. 5), suggests that the latter protein functionally resembles a lipid raft-associated protein, possibly with acquired BLNK independence of activation by BTK. With regard to the FRAP results, an "anchored membrane-protein picket model" has been proposed by Fujiwara et al. (51), in which transmembrane proteins referred to as "pickets" are anchored to the membrane skeleton to act as posts along the membrane skeleton fence. The anchored protein pickets, observed in all examined cell types, including COS cells, were suggested to act as effective diffusion barriers due to steric hindrance as well as circumferential slowing (packing and frictional) effects even for phospholipids in the outer leaf of the membrane. According to this model, the longrange lateral diffusion of diffusible molecules in compartmentalized membranes is largely limited by their hop rate across the compartment boundaries. Importantly, compartmentalization of the cell membrane has also been suggested to occur for glycosylphosphatidylinositol-linked proteins and to be involved in modulating the size and lifetime of lipid rafts. Collectively, the results suggest that the point mutation S707Y promotes association with compartmentalized plasma membrane subdomains, possibly with lipid rafts. The importance of the latter for BCR-mediated signal transduction in B cells has previously been emphasized (69–72).

We have shown earlier that RAC, by physically interacting with the split PH domain of PLC γ_2 , amplifies BCR-induced Ca²⁺ signaling and markedly increases the sensitivity of B cells to BCR ligation, BCR-mediated Ca²⁺ release from intracellular stores, Ca²⁺ entry from the extracellular compartment, and nuclear translocation of the Ca²⁺-regulated nuclear factor of activated T cells (49). We also showed that various PLC γ_2 variants are strikingly hypersensitive to activation by RAC2, such that even WT RAC2 suffices to activate the variant enzymes upon its introduction into intact cells (38, 39). These findings are highly consistent with the cooperative interaction between RAC2 and BTK as stimulators of PLC γ_2 shown here, in particular with the striking permissive effect of activated RAC on the ability of catalytically-inert BTKE41K/K430R to activate even WT PLC γ_2 (cf. Fig. 6, B and D). This result may indicate an "unleashing", via VAV and RAC, of even WT PLC γ_2 activity by the catalysis-independent functions of BTK. This effect could act in cis, i.e. within the BCR signal transduction pathway in a positive feed-forward regulatory loop, or in trans, via BCR coreceptors or integrins also capable of activating RAC (38), both enhancing BCR-mediated PLC γ_2 activation. In either case, the sensitivity of BCR-mediated inositol phosphate formation to catalytic site-targeted inhibitors of BTK would be dependent on the relative penetrance of the pathways mediated by BTK independently of its protein kinase activity in the various physiological and pathophysiological environments of either normal or leukemic B cells. Of note, both VAV and RAC have been shown to localize to lipid rafts in B cells (70, 73).

An important extracellular variable encountered by B cells in different tissue environments is the abundance of the BCR antigen stimulus and, hence, the degree of BCR activation. The result shown herein indicate that this degree takes a profound influence on both the kinetics of the $[Ca^{2+}]_i$ response and on the portion that may be contributed by the protein-tyrosine kinase–independent functions of BTK, which are resistant to catalytic site-targeted BTK inhibitors. Remarkably, in DT40 cells, this portion increased considerably when the concentration of anti-IgM was increased over the range of concentrations commonly used in the functional analysis of these cells.

At first glance, these findings may appear to contradict earlier seminal findings, such as the almost complete loss of the reconstitutive activity of catalytically-inert BTK variant R525Q in BTK^{-/-} DT40 cells (K⁻/*btk*⁻), which was tested in response to type M4 anti-IgM at a nominal concentration of 2 μ g/ml (13). Although it seems possible, as pointed out earlier (74), that

the R525Q mutation used by Takata and Kurosaki (13) affects the catalytic capacity of the BTK kinase differently, the three kinase-inactive BTK variants analyzed herein, including the variant R525Q and even lacking the kinase domain, behaved very similarly in our experiments (cf. Fig. 2E). Notably, however, unlike Lys-430, Arg-525 is not conserved in the protein kinase superfamily and is already absent in this position in most of the human Src subfamily members, including LYN. Finally, in our hands, the anti-IgM concentration response of DT40 cells is sensitive to freezing and storage of the cells and, possibly, storage of the ligand at 4 °C, as well as somewhat variable with the particular batch of the ligand. For example, freshly-transfected cells that had not been frozen as such were used with freshlyprepared ligand in Fig. 7B. In Fig. 7C, the anti IgM-mediated $[Ca^{2+}]_i$ increases were already reduced, *e.g.* at 1 μ g/ml anti-IgM, after one freeze-thaw cycle. Therefore, it seems possible that the observations in Fig. 7C did in fact correspond to lessresponsive cells and/or a less potent anti-IgM preparation. In vivo analysis of genetically-modified mice and experiments performed ex vivo on cultured cells from these animals have previously shown that the catalytically-inactive BTK variant K430R could either fully, only partially, only modestly, or not at all fulfill the functions of WT BTK, depending on the particular function tested (23, 24). These results have previously been explained by the finding, in primary and A20 cultured B cells, that BTK, regardless of its catalytic capabilities, associates with PIP5Ks, the enzymes that synthesize $PtdInsP_2$ (25, 75). The findings were taken by the authors (25) to suggest that both forms of BTK act as shuttles to bring PIP5Ks to the plasma membrane and specifically to lipid rafts to enhance the availability of PtdIns P_2 as a substrate for both PI3 kinases and PLC γ_2 with subsequently enhanced membrane targeting of BTK (via its PH domain) and inositol phosphate formation, respectively. Although such a mechanism(s) appears persuasive, it is important to note that increased formation of $PtdInsP_2$ by protein kinase-deficient BTK has not been shown in Saito et al. (25), neither in anti-IgM-stimulated DT40 cells nor in PIP5Kβoverexpressing A20 cells. In addition, the observation herein that a number of PLCG2 point mutations associated with ibrutinib resistance of CLL cells cause markedly enhanced inositol phosphate formation in transfected cells (cf. Table 1), arguing strongly against a shortage of substrate $PtdInsP_2$ at the site of catalysis. Furthermore, even activated BTKE41K did not alter the activity of WT or mutationally preactivated $PLC\delta_1$ in the experimental system utilized here (cf. Fig. 1A). There was also no change in the levels of the major inositol phospholipids in response to expression of various variant forms of BTK, including those capable of stimulating PLC γ_2 S707Y (cf. Fig. 3A). Finally, and perhaps most convincingly, there was a striking PLC isozyme specificity of the stimulatory effect of catalytically-inactive BTK, even within the PLC γ subfamily, where PLC γ_1 S729Y, the direct structural and functional counterpart of PLC γ_2 S707Y (39), did not show activation by BTKE41K/ K430R (*cf.* Fig. 3*C*). Note that both PLC γ_1 and PLC δ_1 associate with lipid raft membrane microdomains (76, 77), and should, as such, be similarly if not equally sensitive, as compared with PLC γ_2 , to an enhanced availability of the PtdIns P_2 substrate.

mediated mediated (ml antispossible d to lessration. In nents perhave prek variant , or not at particular usly been d B cells, iates with 75). The that both pelasma the availmd PLC γ_2 BTK (via pectively.

binding receptor to a second messenger-generating enzyme such as PLC γ_2 , catalytic site-targeted BTK inhibitors can be categorized as variably effective, either irreversible (e.g. ibrutinib and acalabrutinib) or reversible (e.g. vecabrutinib) allosteric inhibitors: allosteric because they act at a site distinct from the (orthosteric) receptor-ligand-binding site. Based on the results presented herein, we suggest that inhibition by ibrutinib and acalabrutinib is only fully expressed at low degrees of BCR activation where only the catalysis-dependent effects of BTK are in effect. At high degrees of BCR activation, more and more of the catalysis-independent BTK functions come into effect, such that the BTK inhibitors acquire the properties of only partiallyeffective inhibitors. Whether or not the remaining relative inhibition suffices to block specific (patho)biologic functions of BCR depends on the "functional reserve" of the particular B-cell response distal to the increase in $[Ca^{2+}]_i$. In other transmembrane-signaling systems, such as those relying on enhanced intracellular formation of cAMP, this term refers to the fact that many receptor agonists are more powerful than they need to be, in that maximal responses of cellular functions are elicited at submaximal, in some cases only minimal degrees of receptor activation or second messenger generation (78, 79). For example, it is well-known that in adipocytes stimulated by lipolytic hormones the levels of cAMP are far in excess of those required for maximal lipolytic rates, even in the presence of inhibitors (80-82). This large "overshoot" of second messenger is also observed, e.g. in the heart and in adrenocortical cells, in many other biological systems with no direct correlation of second messenger concentration with the metabolic or physiological process under investigation (83, 84). Under these conditions, both orthosteric and allosteric inhibitors need to be capable of blocking a substantial portion, if not a great majority, or even all agonist effects to be efficacious (85, 86). Thus, as long as the BCR operates under a functional reserve arrangement in a given

Tomlinson *et al.* (74) showed earlier that an inducible form of kinase-inactive BTK, in contrast to its kinase-active counter-

part, was unable to induce an increase in $[Ca^{2+}]_i$ in BTK-defi-

cient DT40 cells on its own. However, in the context of BCR

activation by 2 µg/ml anti-IgM, there was virtually no differ-

ence in the kinetics of $[Ca^{2+}]_i$ between BTK^{-/-} cells expressing

kinase-active *versus* -inactive BTK. Hence, BCR-mediated activation of $PLC\gamma_2$ via kinase-inactive BTK involves an additional

mechanism. In the context of the results shown here (cf. Fig. 6,

A-D), it is likely that RAC activated by the BCR, e.g. via VAV,

permits the implementation of such a mechanism. We previ-

ously noted major losses of the proportion of singly analyzed

DT40 cells carrying the RAC-resistant PLC γ_2 variant F897Q in



B cell, the changes in BTK inhibitor efficacy shown herein (*cf.* Fig. 7*C*) may take profound effects on and limit their therapeutic efficiency in cells expressing both WT BTK and WT PLC γ_2 , in particular at high degrees of BCR activation, as determined by high affinity and/or high abundance of the antigen.

In CLL cells, BCR activation may occur through engagement of the receptor by (auto)antigens (87, 88) or in a cell-autonomous way by BCR recognition of conserved epitopes within specific regions of the Ig heavy and light chains (89, 90). Either way, there are substantial differences in the degrees of this activation among samples of different patients, which in turn translates (at least in part) to the clinical heterogeneity of the disease (90, 91). Importantly, BTK inhibitor treatment of CLL has been reported to be limited by primary drug resistance in 13-30% (10). Partial efficacy of the drugs caused by the activation of PLC γ_2 through catalysis-independent mechanisms of BTK provides a potential mechanism of this therapeutic problem. Novel drugs capable of interfering with the protein-protein interaction(s) of BTK with PLC γ_2 may provide a way to address this treatment drawback in the future. Finally, clinical heterogeneity, referred to as "leaky" or "mild" phenotype in the less affected patients, is also known in XLA, even in patients from single pedigrees. It has previously been difficult or even impossible to establish a clear genotype-phenotype relationship for this disease caused by a large number of distinct mutations in BTK (RRID:SCR_013101). In some cases, these mutations either abrogate the catalytic functions of BTK (92) or cause a loss of its catalytic domain (93). We suggest that the noncatalytic functions of the variant BTK enzymes, possibly triggered in a sibling-specific fashion by high BCR activation, may contribute to this heterogeneity.

Experimental procedures

Materials

The rabbit polyclonal antibody 3872 reactive against human and chicken PLC γ_2 , the rabbit polyclonal antibody 3871 reactive against human PLC γ_2 phosphorylated at tyrosine 1217, the rabbit polyclonal antibody 3874 reactive against human PLC γ_2 phosphorylated at tyrosine 759, and the rabbit polyclonal antibody 5082 reactive against human BTK phosphorylated at tyrosine 223 were obtained from Cell Signaling Technology. The rabbit polyclonal antiserum reactive against human RAC2 (sc-96), the mouse mAb reactive against human BTK (sc-81735), and the mouse mAb (PY99) reactive against phosphotyrosinecontaining proteins (sc-7020) were purchased from Santa Cruz Biotechnology. The rabbit polyclonal antibody reactive against human and chicken BTK (F52632) was obtained from NSJ Bioreagents. CFSE (eBioscienceTM, 65-0850-84) and Indo-1-AM (I1223) were obtained from Thermo Fisher Scientific. Mouse anti-chicken IgM (clone M-4) was obtained from Southern Biotech. The BTK inhibitors ibrutinib (PCI-32765) and acalabrutinib (ACP-196) were obtained from Selleckchem. The BTK inhibitor vecabrutinib (SNS-062) was kindly provided by Sunesis. The sources of other reagents have been described in Ref. 39, 94. BTK-deficient DT40 cells were kindly provided by J. Wienands, Institute of Cellular and Molecular Immunology, University of Göttingen.

Construction of vectors

The 4E variant (Y753E, Y759E, Y1197E, and Y1217E) of $PLC\gamma_2$ was generated according to the 4F variant. The cDNA encoding PLC γ_2 N-myr was generated by N-terminal insertion of the first 15 amino acids from Rous sarcoma virus SRC (MGSSKSKPKDPSQRR) (95) and a small linker (PGIQ) providing a BamHI site into PLC γ_2 -pcDNA3.1(+). BTK Δ kinase, lacking amino acids 402-659, was generated with help of in vitro mutagenesis by insertion of a stop codon (TAG) right in front of the kinase domain. The primer sequences and PCR protocols are available from the authors upon request. The cDNAs of *n*-FLAG epitope-tagged human BTK and its point variants R28C, E41K, Y223F, and K430R were provided by C. Brunner, Department of Otorhinolaryngology, Head and Neck Surgery, Ulm University Medical Center. The BTK variant Y551F was generated by O.-O. Wolz from the Department of Immunology, University of Tübingen. The generation of all other cDNAs has been detailed in Refs. 43, 49, 96.

Generation of stably-transfected DT40 cell clones, DT40 cell culture, and preparation of DT40 cell lysates

This was essentially done as described in Ref. 49. Proteomic analysis of whole-cell extract proteins, fractionated by SDS-PAGE, was used to verify the expression of WT and K430R variant BTK in the respective cell clones as described previously (97). MS/MS spectra were correlated with the UniProt chicken database complemented with the sequences of human WT and K430R variant BTK. Carbamidomethylated cysteine was considered as a fixed modification along with oxidation of methionine, and acetylated protein N termini as variable modifications. False discovery rates were set on both peptide and protein levels to 0.01.

Calcium flux measurements

Cells were suspended at a density of 10⁷ cells/ml in FACS buffer (143 mM NaCl, 6 mM KCl, 1 mM MgSO₄, 20 mM HEPES/ NaOH, pH 7.4, 1 mM CaCl₂, 5.6 mM glucose) and incubated for 45 min at 37 °C and 10% CO₂ with 5 μM Indo-1-AM. The calcium measurements were performed on a BD FACS CelestaTM. In brief, 10⁶ cells per sample in 0.5 ml of FACS buffer were pre-warmed at 37 °C for 10 min. Next, baseline was measured for 2 min before addition of the ligand anti-chicken IgM. After an additional 4 min, 2 μ M ionomycin (I0634, Sigma) was added to the samples to obtain the maximal Ca^{2+} flux. Cells were kept at 37 °C during the measurements. The fluorescence ratio of Indo-1 violet (Ca²⁺-bound) to Indo-1 blue (Ca²⁺-free) was measured by using FACSDivaTM software (BD Biosciences). In some cases, two cell populations were analyzed simultaneously by staining half of the cells for 10 min at 37 °C and 10% CO₂ with 20 nm CFSE (98), followed by washing of the cells (10^7 cells/ml) with 10 volumes of PBS. For BTK inhibitor treatment, unstained and CFSE-labeled DT40 cells were treated for 1 h at 37 °C with continuous shaking at a density of 10⁷ cells/ml with 1 μ M inhibitor or solvent in RPMI 1640 medium containing supplements. The inhibitor was washed out before adding the Ca²⁺ indicator. For data evaluation, the experimental results contained in FCS files generated by the FACSDiva $^{\rm TM}$ software (BD Biosciences) were imported into the FlowPy Python tool



(RRID:SCR_018195) and then transferred to Excel spread sheets. Following binning of the time attributes of the individual data points to integers (full seconds), the data of one experiment were assembled into a matrix M such that the first row listed the time attributes and the columns j in rows i + 1 tabulated the fluorescence ratios. The resulting matrices were typically made up of about 540 columns and up to about 1650 rows. In experiments analyzing two cell populations at the same time, DT40 cells expressing WT BTK (unstained) and DT40 cells expressing BTKK430R (stained) (Fig. 7C), the matrix was fractionated into two parts, M1 and M2, according to the fluorescence intensities determined for intracellular CFSE. The individual points shown in Fig. 7, B and C, correspond to the times in full seconds versus the medians of all fluorescence ratios representing $[Ca^{2+}]_i$, following their correction for basal fluorescence intensity in the absence of anti-IgM and normalization according to the maximal values reached after addition of 2 μ M ionomycin. Between serial measurements, the latter values were normalized to 100%. Nonlinear least-squares curve fitting of selected portions of the data to equations of either one-phase exponential association, two-exponential association and decay, or log-normal distributions was done using GraphPad Prism[®], versions 8.2.1 or 4.03, to determine the values corresponding to the maximal [Ca²⁺], concentrations for normalization to allow for quantitative comparison between experiments.

Cell culture and transfection of COS-7 cells, extraction, and analysis of inositol phospholipids

This was done as described previously (38, 39, 53, 55, 99).

Radiolabeling of inositol phospholipids and analysis of inositol phosphate formation

Twenty four hours after transfection, COS-7 cells were washed once with 0.3 ml/well of Dulbecco's PBS (PAA Laboratories) and then incubated for 18 h in 0.2 ml/well DMEM-containing supplements, as described previously (38), supplemented with 2.5 μCi/ml myo-[2-³H]inositol (NET1156005MC, PerkinElmer Life Sciences), and 10 mM LiCl. The cells were then washed once with 0.2 ml/well Dulbecco's PBS and lysed by addition of 0.2 ml/well 10 mM ice-cold formic acid. The analysis of inositol phosphate formation was performed as described previously (53) except that 15 ml of scintillation fluid Quicksafe A from Zinsser Analytic was used. To examine BTK inhibition via ibrutinib, acalabrutinib, or vecabrutinib, COS-7 cells were radiolabeled for 18 h in 0.2 ml/well DMEM-containing supplements as described previously (38), supplemented with 2.5 μCi/ml myo-[2-³H]inositol, 10 mM LiCl, 0.1% v/v DMSO (D2650, Sigma) or the respective BTK inhibitor.

Phosphoblot analysis

COS-7 cells were seeded into 6-well plates and transfected. After an additional medium change, the cells were incubated for a further 18 h at 37 °C and 10% CO₂. The medium was removed, and the cells were washed with 0.5 ml of ice-cold TBS and then lysed by addition of 250 μ l of phospholysis buffer (25 mM Tris-HCl, 100 mM NaCl, 1 mM EDTA, 0.5% (v/v) NP40, 0.2% (v/v) Triton X-100, 5% (v/v) glycerol, pH 7.5) supplemented with protease inhibitors (1 mM phenylmethylsulfonyl

fluoride, 10 μ M leupeptin, 2 μ M pepstatin A, 2 μ g/ml soybean trypsin inhibitor, 1 μ g/ml aprotinin, and 3 mM benzamidine) and phosphatase inhibitors (2 mM sodium orthovanadate, 9.5 mM sodium fluoride, 10 mM β -glycerophosphate, and 10 mM tetrasodium pyrophosphate). After lysis, 250 μ l of 2× SDS-PAGE sample preparation buffer were added, and aliquots of the samples were subjected to SDS-PAGE followed by immunoblotting.

FRAP experiments

FRAP studies (100, 101) were conducted as described earlier (49), using a fixed-localization Gaussian laser beam focused to a very small spot on the membrane for both bleaching and monitoring, continuously measuring the fluorescence intensity at the spot by photon counting (47). This method gives a much better time resolution (down to a few milliseconds) than FRAP of larger regions-of-interest in a confocal microscope, which employs nonsynchronous stepwise bleaching and monitoring, which take significantly longer (47). The improved time resolution is critical in the case of fast recovery contributed by exchange and/or gliding, as is the case in this study. The experiments were performed 24-26 h post-transfection on COS-7 cells transfected with PLC γ_2 -GFP derivatives. All experiments were conducted at 22 °C, in Hanks' balanced salt solution supplemented with 20 mM HEPES/NaOH, pH 7.2. The monitoring argon ion laser beam (488 nm, 1.2 microwatts; Innova 70C, Coherent) was focused through the microscope (AxioImager.D1, Carl Zeiss MicroImaging) to a Gaussian spot with a radius $\omega = 0.77 \pm 0.03 \,\mu\text{m}$ (×63/1.4 NA oil-immersion objective) or 1.17 \pm 0.05 μ m (\times 40/1.2 NA water immersion objective). Experiments were conducted with each beam size (beam size analysis is described in Refs. 48, 49). The ratio between the illuminated areas ($\omega^2(\times 40)/\omega^2(\times 63)$) was 2.28 ± 0.15 (*n* = 59; S.D. calculated using bootstrap analysis as described below). After a brief measurement at the monitoring intensity, a 5-milliwatt pulse $(4-6 \text{ or } 10-20 \text{ ms} \text{ for the } \times 63 \text{ and } \times 40 \text{ xobjectives},$ respectively) bleached 50-70% of the fluorescence in the illuminated spot. Fluorescence recovery was followed by the monitoring beam. The apparent characteristic fluorescence recovery time (τ) and the mobile fraction (R_f) were derived from the FRAP curves by nonlinear regression analysis, fitting to a lateral diffusion process with a single τ value (102). The significance of differences between sets of τ values measured with the same beam size was evaluated by one-way ANOVA and Bonferroni post hoc test. To compare the $\tau(\times 40)/\tau(\times 63)$ ratio of a given PLC γ_2 variant with the $\omega^2(\times 40)/\omega^2(\times 63)$ beam-size ratio (comparing a single pair of data sets), statistical significance was evaluated by two-tailed Student's t test using bootstrap analysis with 1000 bootstrap samples (103), which is preferable for comparison between ratios, as described by us previously (104).

Miscellaneous

SDS-PAGE and immunoblotting were performed according to standard protocols using antibodies reactive against the c-Myc epitope for WT and variant PLC γ_1 , PLC γ_2 , and PLC δ_1 or antibodies reactive against BTK, PLC β_2 , RAC2, and β -actin. Immunoreactive proteins were visualized using the Pierce ECL Western blotting detection system (catalog 32106, Thermo



Fisher Scientific). Samples to be analyzed by Western blotting were taken, quasi as a fourth replicate, from the same plate as and immediately adjacent to the samples taken in triplicate for functional analysis. Using this protocol and paying meticulous attention to experimental detail, we were able to demonstrate for all results obtained in transiently-transfected COS-7 cells throughout this work that the differences observed in inositol phosphate formation were not explained by or related to differences in the respective protein expression (cf. Figs. 1, B and D, 2, D and F, 3D, and 6C and Figs. S1–S6). All experiments were performed at least three times. Similar results and identical trends were obtained each time. Data from representative experiments are shown as mean values of triplicate determinations. In the experiments shown in Figs. 1C, 2, A-C and E, 3C, 4, and 6A and Table 1, background inositol phosphate formation in response to PLC and/or BTK expression was determined in parallel on cells transfected with empty vector and subtracted from the corresponding values, with appropriate consideration of error propagation for differences and quotients to determine the standard deviations of means (S.D.) of triplicate determinations (105). Although the S.D. values of these technical replicates are not shown in Figs. 1, A, C, and E, 2, A–C, E, and G, 3, A-C, 4, and 6, A, B, and D, and Table 1, their relationships to the corresponding means were calculated in aggregate for all mean values shown in these representations (n = 500) and found to be distributed with a median of 9.93%, with 95% confidence limits of 8.97% and 10.93%. In the experiments displayed in Figs. 1, *C* and *E*, 2, *C*, *E*, and *G*, 6, *B* and *D*, and 7, *B* and *C*, the data were fitted by nonlinear least-squares curve fitting using all replicate values to three- or four-parameter dose-response equations using GraphPad Prism®, version 4.03. In certain cases, the global curve-fitting procedure contained in Prism was used to determine whether the best-fit values of selected parameters differed between data sets. The simpler model was selected unless the extra sum of squares *F*-test had a *p* value of less than 0.05.

Data availability

All data are contained within the manuscript. Raw data as well as computer subroutines used for data processing and equations used to calculate propagation of experimental errors are available on request from Peter Gierschik (peter.gierschik@uni-ulm.de).

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