Evidence Suggesting That Discontinuous Dosing of ALK Kinase Inhibitors May Prolong Control of ALK+ Tumors

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Abstract

The anaplastic lymphoma kinase (ALK) is chromosomally rearranged in a subset of certain cancers, including 2% to 7% of non–small cell lung cancers (NSCLC) and ~70% of anaplastic large cell lymphomas (ALCL). The ALK kinase inhibitors crizotinib and ceritinib are approved for relapsed ALK+ NSCLC, but acquired resistance to these drugs limits median progression-free survival on average to ~10 months. Kinase domain mutations are detectable in 25% to 37% of resistant NSCLC samples, with activation of bypass signaling pathways detected frequently with or without concurrent ALK mutations. Here we report that, in contrast to NSCLC cells, drug-resistant ALCL cells show no evidence of bypassing ALK by activating alternate signaling pathways. Instead, drug resistance selected in this setting reflects upregulation of ALK itself. Notably, in the absence of crizotinib or ceritinib, we found that increased ALK signaling rapidly arrested or killed cells, allowing a prolonged control of drug-resistant tumors in vivo with the administration of discontinuous rather than continuous regimens of drug dosing. Furthermore, even when drug resistance mutations were detected in the kinase domain, overexpression of the mutant ALK was toxic to tumor cells. We confirmed these findings derived from human ALCL cells in murine pro-B cells that were transformed to cytokine independence by ectopic expression of an activated NPM–ALK fusion oncoprotein. In summary, our results show how ALK activation functions as a double-edged sword for tumor cell viability, with potential therapeutic implications. Cancer Res; 75(14); 2916–27. ©2015 AACR.

Introduction

ALK is a receptor tyrosine kinase expressed in the developing nervous system (1, 2). Chromosomal rearrangements in subsets of several cancers result in constitutive expression and activation of its C-terminal kinase domain, which prolifercally turns on oncogenic signaling pathways, including JAK3/STAT3, MEK/ERK, and PI3K/AKT (3–6). Addiction of tumor cells to ALK activity in laboratory models and promising activity of ALK inhibition in early-phase clinical trials have made it an intensive target for TKI development in recent years. ALK originally was cloned from the recurrent t(2;5)(p23;q35) chromosomal rearrangement found in anaplastic large-cell lymphoma (ALCL), an uncommon tumor derived from mature T cells (7). The resulting NPM–ALK fusion kinase and other less common ALK fusions drive malignant growth in ~70% of ALCL cases. Though identified in ALCL 20 years ago, ALK has only become a target for intensive drug development since 2007, when its presence was discovered in a subset of non–small cell lung cancer (NSCLC). Here, activation is again through chromosomal rearrangement creating an expressed and activated fusion kinase, most commonly EML4-ALK (8, 9).

Such rearrangements are present in 2% to 7% of NSCLC cases and led to a 57% response in phase 1 evaluation of the first-in-class TKI crizotinib in relapsed ALK+ NSCLC patients (10). The drug won accelerated limited FDA approval in 2011 and subsequently promoted longer progression-free survival than chemotherapy as first or second-line treatment for metastatic ALK+ NSCLC (11, 12). The second-generation inhibitor ceritinib (LDK378) was approved recently for crizotinib-resistant ALK+ NSCLC patients based on a 58% response rate in phase 1, including 56% response in patients with prior crizotinib exposure (13), and several other ALK TKIs are under development (14). ALCL, meanwhile, which makes up 2% to 5% of non-Hodgkin lymphoma (NHL), is the most common T-cell NHL in children and the third most common in adults. Although ALK+ ALCL has better response to chemotherapy than other peripheral T-cell lymphomas (15), poor prognosis of relapsed or refractory patients and its predilection for younger populations have prompted clinical investigation of ALK tyrosine kinase inhibition in both adults and children with the disease (16, 17).
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Studies of resistance to crizotinib in NSCLC identify target-dependent mechanisms such as kinase-domain mutations and fusion-ALK copy-number gains in 34% to 46% resistant cases, whereas many cases are resistant for unclear reasons (14, 18, 19). Here, we studied resistance to ALK-kinase inhibition in ALK-ALCL using both crizotinib and ceritinib. In contrast to findings in lung cancer, our study identified no ability of ALCL cells to bypass the driver kinase by activation of alternate pathways. Instead, cells upregulated NPM-ALK expression through genomic amplification and other mechanisms, suggesting a nearly absolute addiction to ALK-kinase activity. Strikingly, however, withdrawal of ALK inhibitor from resistant cells causes rapid growth arrest followed by entry into apoptosis, which promoted regression of tumors in vivo.

Materials and Methods

Cell lines and reagents

All lines except FL5.12 were purchased from DSMZ, authenticated by STR-fingerprinting (last tested 11/2013) and mycoplasma tested by PlasmoTest kit (Invivogen; REP-PT1). Culture media for Karpas-299, SU-DHL-1, MAC-2A: RPMI 1640, 10% fetal bovine serum (FBS), penicillin/streptomycin (P/S); SUP-M2: RPMI 1640, 10% FBS, P/S; FL5.12 cells (gift of Hans-Guido Wendel, Memorial Sloan Kettering Cancer Center, New York, NY): RPMI 1640, 10% FBS, P/S; ±10% WeHi-3B supernatant and murine IL3 (400 pmol/L; eBioscience).

Antibodies


Inhibitors

Crizotinib (PF-02341066; #S1068) was purchased from Selleck Chemicals. Ceritinib (LDK378) kindly provided by Novartis.

Long insert whole genome sequencing

Long insert whole genome sequencing was carried out as described (20), utilizing genomic DNA extracted using the AllPrep DNA/RNA Mini Kit (Qiagen #80204).

Proliferation assays and imaging

Cells were plated at 100,000/mL on day 0 and counted using Trypan-blue exclusion. Cells were stained with Hoechst (1.5,000; Invitrogen #33342) and imaged using the DeltaVision Core system (Applied Precision) equipped with an Olympus IX71 microscope, a 40× objective (NA 1.35) and a 20× objective (NA 0.70), and a cooled charge-coupled device camera (CoolSNAP HQ2; Photometrics). Images were acquired with softWoRx v1.2 software (Applied Science).

Protein extraction, quantification, and immunoblotting

Cells were seeded at 500,000/mL and incubated as indicated. Proteins were extracted using RIPA (50 mmol/L Tris-HCl pH 8.0, 150 mmol/L NaCl, 1% NP40, 0.5% sodium deoxycholate, and 0.1% SDS), 7× phosphatase inhibitor (Roche #0493159001), Phosphatase Halt (Thermo #78428), and Triton X-100. Proteins were quantified using the BCA Assay (Thermo #23223) with 30 μg loaded per lane for Western blotting. All blots were developed using autoradiography film (GeneMate #F-9023-8×10) after incubation with antibodies indicated above.

Copy-number assays

Genomic DNA was extracted by AllPrep DNA/RNA Mini Kit (Qiagen #80204). Copy-number probes for NPM1 exon 1 (#Hs01219772_cn), NPM1 intron 11 (#Hs046724352_cn), ALK intron 1 (#Hs05853206_cn), ALK intron 23 (#Hs04555433_cn), and TERT (#4401633) were purchased from Life Technologies, and assays were conducted per the manufacturer’s instructions. Copy-number analysis was by Applied Biosystems Prism 7000 Sequence Detection System. Data were normalized to the housekeeping gene (TERT) and analyzed using the 2ΔΔCt method.

qRT-PCR

RNA isolation by RNeasy Mini Kit (Qiagen #74106); cDNA generated by Taqman Reverse Transcriptase Kit (Roche; #N808-0234) on a Bio-Rad T100 Thermal Cycler; qRT-PCR employed an Applied Biosystems Prism 7000 Sequence Detection System with Taqman probes (Life Technologies): NPM-ALK (#Hs03024828_ft), CDKN2A (#Hs00923894_m1), and GAPDH as endogenous control (#Hs02758991_g1). Data were analyzed using the 2−ΔΔCt method.

Targeted selection and sequencing of the expressed NPM1–ALK translocation locus

CDNA was synthesized from 100 ng total RNA using the Nugen Ovation RNA-Seq System v2. Presence of NPM–ALK confirmed by PCR giving a 429bp product (Kapa Biosystem’s HiFi Ready-mix; #KK1006) using previously published primers flanking the breakpoint (21). NPM1–ALK fusion cDNA was then amplified using the Qiagen Long Range PCR Kit (#206401) and custom primers (F1: GTCCGGCTTCTCTTCTACTT, R1: TTGGCA CAAAAACAAACGTG) flanking the breakpoint, encompassing 391 bp of NPM1 and 1804 bp of ALK DNA. Size selection and purification of the PCR product using Bio-Rad’s Freeze ‘N’ Squeeze DNA gel extraction spin columns (#4106139) followed by Beckman Coulter Agencourt AMPure XP Bead purification (#A63880). A total of 50 ng of each PCR product was fragmented to 300bp using the Covaris E210 sonicator, and libraries were constructed using Kapa Biosystems’ Hyper Kit (#KK8504) following the manufacturer’s protocol. Libraries
were equimolarly pooled and sequenced on the Illumina MiSeq for paired 84bp reads using Illumina's MiSeq Reagent Kit v3 (#MS-102-3001). FASTQ files generated from the Illumina MiSeq were aligned against build 37 of the human reference genome using the Burrows-Wheeler Alignment (BWA) tool (22). Following alignment, .sam files were used to create .bam (sequence alignment map) files, which were used to create binary sequence (.bam) files using SAMtools (23). PCR duplicates were flagged for removal using Picard (http://picard.sourceforge.net), and base quality scores were recalibrated using Genome Analysis Toolkit (GATK; ref. 24). Comparisons within each cell line family were performed to identify point mutations and small indels using three somatic callers, including Searat (25), MuTect (26), and Strelka (27) as well as Sanger sequencing.

Transfections, infections, and selection

Phoenix packaging cells were seeded at 700,000 cells/mL for 16 hours, to which, a cocktail of DMEM, X-treme GENE 9 DNA Transfections, infections, and selectioning Seurat (25), MuTect (26), and Strelka (27) as well as Sanger within each cell line family were performed to identify point mutations and small indels using three somatic callers, including Searat (25), MuTect (26), and Strelka (27) as well as Sanger sequencing.

Xenograft experiments

All mouse experiments were approved by the University of Arizona Animal Care and Use Committee (protocol no. 12-377). Mice were maintained under specific pathogen-free conditions, and food and water were provided ad libitum.

In vivo dependence

Severe combined immunodeficiency (SCID) mice were injected with 2 × 10⁶ K299-CR1000 cells in 1:1 Matrigel and sterile saline in a total volume of 100 μL subcutaneously into the lower flank. These mice were divided immediately to two groups for treatment with ceritinib or vehicle by oral gavage. Ceritinib was formulated freshly before each dosing as a solution in 0.5% MC (methylcellulose)/0.5% Tween 80 as described (28). Because of the requirement for ALK inhibition for K299-CR1000 cells in vitro, dosing began on the day of flank injections 2 hours before hand and continued daily.

Up-front intermittent versus continuous dosing

SCID mice were injected with 2 × 10⁶ Karpas-299 parental cells as above. After tumors reached ~500 mm³, the mice were split into seven cohorts (n = 3) and were treated continuously with vehicle, continuously with ceritinib (at either 33.33 or 50 mg/kg) or intermittently with the same concentrations of ceritinib using a ‘4 weeks on, 2 weeks off’ schedule.

Statistical analysis

Two-tailed Student t test was carried out for all expression data using the GraphPad t test calculator and verified using the SPSS Statistics software from IBM, with P < 0.05 considered statistically significant with a 95% confidence interval. Apoptosis data were calculated using the Mann–Whitney test in GraphPad where P = 0.05 was considered statistically significant with a 95% confidence interval.

Results

TKI resistance and dependence are invariably coselected in ALK⁺ ALCL

NPM–ALK-driven ALCL cell lines Karpas-299, SU-DHL-1, and SUP-M2 were highly sensitive to crizotinib and ceritinib, with the latter drug having 3 to 5× greater potency (Fig. 1A; Supplementary Table S1). We selected for resistance to both inhibitors independently through serial plating in increasing drug concentrations (Supplementary Fig. S1A). Cells derived from Karpas-299 able to grow in 1,000 nmol/L crizotinib (hereafter K299-CR1000) strikingly when washed out of ALK inhibitor and reassessed for drug sensitivity showed viability stimulation by both inhibitors (Fig. 1B). Stimulation was an on-target effect, indicated by the stimulation at lower concentration by the more potent inhibitor. All resistant clones emerging from selections demonstrated similar findings [Fig. 1C, lines named for parent, drug used in selection (L for ceritinib/LDK378), and top nanomolar concentration]. When washed out of inhibitor and plated in drug-free media, resistant cells halted growth, suggesting ALK inhibition had become a requirement for viability (Fig. 1D–F). Plated without ALK inhibitor, resistant lines appeared shrunken and involuted, consistent with onset of apoptosis, while those in either ALK inhibitor appeared viable similar to parent cells growing without drug (Fig. 1F; Supplementary Fig. S1B). Flow cytometry confirmed entry into apoptosis by resistant cells plated in drug-free media, in contrast to those maintained in either ALK inhibitor (Fig. 1G). ALK⁺ ALCL cells therefore reliably develop ALK-inhibitor dependence at the same time they develop resistance, suggesting selection for a process with paradoxical effects on viability.

NPM–ALK upregulation drives both resistance and dependence

To investigate the resistant-dependent phenotype, we performed long-insert whole-genome sequencing (LI-WGS; ref. 20) of the Karpas-299 parent line and the K299-CR1000 subclone. Mapping of reads against the reference genome (hg19) showed amplification in the subclone of the portions of the NPM and ALK loci that are translocated to form NPM–ALK (Fig. 2A). Copy-number assays demonstrated gain consistent with genomic amplification specifically of the fusion locus but not the uninvolved portions of either gene (Fig. 2B). This generated more than 50-fold increased expression of NPM–ALK mRNA [Fig. 2C]. The additional resistant-dependen subclones also had increased expression relative to their corresponding parent lines [Fig. 2D], ranging from 1.5× for SUP-LR150 to 12.0× for K299-LR150. Of these, only K299-LR150 had clear evidence of NPM–ALK copy-number gain (Supplementary Fig. S2), demonstrating increased expression results also from other mechanisms. NPM–ALK protein levels also were elevated in subclones [Fig. 2E]. This is seen at NPM–
Figure 1.
TKI resistance dependence in ALK+ ALCL. A, initial sensitivities to ALK inhibition (see also Supplementary Figure S1 for timelines acquired resistance). B and C, stimulation of viability by both ALK inhibitors in cells with acquired resistance. D and E, proliferation of parent and subclonal cells seeded at 10^5/mL in media with DMSO, crizotinib, or ceritinib. F, Hoechst-stained cells from D on Day 4 (scale bars, 15 μm). G, combined early/late apoptotic cells from D to E at day 4 by flow cytometry. Means of technical quadruplicates (A–C) or independent triplicates (D, E, G) ±SEM. *P = 0.05 (Mann–Whitney).
ALK’s full-length position (80 kDa) and at a prominent high molecular weight aggregate band known to result from elevated NPM–ALK protein levels (29). Activating ALK autophosphorylation, highly drug sensitive in parent lines, was drug resistant in subclones during TKI exposure. STAT3 activation previously was shown to be required for ALK-mediated lymphomagenesis (30). In addition, the gene-expression signature of clinical cases is most similar to that of a STAT3 survival signature (31). We found all resistant subclones preserved STAT3 phosphorylation during ALK inhibitor exposure in marked contrast to the drug-sensitive parent lines (Fig. 2E). Subclones withdrawn from drug showed increase in ALK and STAT3 phosphorylation but, interestingly, slight but noticeable decline in total STAT3, suggesting feedback repression of STAT3 expression. In sum, increased ALK expression drives resistance associated with preserved STAT3 activation but leads to increased ALK signaling when drug is withdrawn. This combined with the rescue of cell viability by ALK inhibition (Fig. 1) supports a conclusion that ALK overdose is the reason for growth arrest and apoptosis upon inhibitor withdrawal.

We also performed both Sanger and targeted deep sequencing of the NPM–ALK fusion locus (Supplementary Table S2). Neither K299-CR1000 nor K299-LR150 cells developed any second-site kinase-domain mutations. Resistance in these lines therefore was driven purely by increased NPM–ALK levels. The same may be true of DHL1-CR500, which acquired only R1192P, a germline predisposition allele for neuroblastoma with no known role in TKI resistance (32). Intriguingly, both SUP-CR500 and SUP-LR150

Figure 2. NPM–ALK upregulation drives resistance dependence. A, LI-WGS reads indicate NPM–ALK amplification in resistant-dependent subclone. B, copy-number assay confirms gain specifically of the fusion kinase-encoding regions of NPM and ALK (see also Supplementary Fig. S2 for additional resistant cells). C and D, increased NPM–ALK mRNA expression in subclones. E, immunoblotting with and without crizotinib in parent and subclones. Means of technical triplicates (B–D) ± SEM. *P < 0.01; **P < 0.05; NS, nonsignificant, P ≥ 0.05 (t test).
developed mutations with known roles in TKI resistance (respectively I1171S, seen only by Sanger sequencing, and F1174L, seen by both targeted and Sanger sequencing; Supplementary Table S2; refs. 33–36). The fact that these lines also developed ALK upregulation leading to TKI dependence to avoid signaling overdose further illustrates the intense pressure for these systems to acquire target-dependent resistance. Moreover, a treatment strategy designed to exploit ALK overdose such as discontinuous dosing may be at least temporarily successful even when drug-specific kinase-domain mutations also have begun to arise.

ALK overdose also impairs the fitness of cytokine-dependent pro-B cells
To replicate resistance-dependence in an independent system, we employed the FL5.12 line, murine pro-B cells that rapidly cease proliferating and undergo apoptosis without IL3 (37). We created NPM–ALK-dependent FL5.12 lines through retroviral introduction of NPM–ALK with GFP coexpression followed by IL3 withdrawal. We hypothesized simultaneous IL3 withdrawal and ALK-inhibitor exposure would require progressively higher NPM–ALK levels to permit survival in the presence of drug. Figure 3A shows representative percentage GFP enrichment in one of three replicate experiments 4 days after IL3 withdrawal and incubation in 0, 10, 20, 50, 150, or 500 nmol/L ceritinib. Confirming NPM–ALK dependence, cells withdrawn in the two highest concentrations always died, whereas the others proliferated only as 100% GFP+ lines. In addition, cells infected with empty vector invariably perished after IL3 withdrawal (not shown). Flow-cytometry analysis showed progressively brighter GFP coexpression in the transformed cells selected and maintained in higher ceritinib concentrations (Fig. 3B), and qPCR confirmed increased NPM–ALK mRNA (Fig. 3C). By immunoblot, we observed progressively higher NPM–ALK total protein and phosphorylation, showing again selection for increased ALK expression and activity to permit survival of NPM–ALK-dependent cells during TKI exposure (Fig. 3D).
We then washed cells selected and maintained in 50 nmol/L ceritinib out of drug, plated them in drug-free media, and compared their proliferation with the same cells maintained in drug. The cells deprived of drug had significantly reduced proliferation (Fig. 3E). Therefore, an independent system confirmed both selection for increased NPM–ALK expression to mediate TKI resistance and the negative impact on cell fitness of this increased expression in TKI absence.

Cells return NPM–ALK to basal levels to permit growth without ALK inhibition

To identify factors permitting resistant-dependent cells to resume growth without ALK inhibition, we attempted to derive lines with this phenotype in vitro. Invariably, plating resistant cells at <10^6/mL without ALK inhibitor resulted in complete death of the culture plate (data not shown). At concentrations ≥10^5/mL, however, we eventually isolated clones from resistant-dependent

Figure 4.

Proliferation with TKIs requires return of ALK to baseline. A, resensitized (RS) cell viability in response to ALK inhibition, with original parent lines for comparison. B and C, RS proliferation (B) and apoptosis (C) on day 4 after seeding at 10^5/mL in media containing DMSO, crizotinib, or ceritinib. D and E, LI-WGS (D) and qPCR copy-number assays (E) show no amplification of NPM–ALK in K299 RS subclones. F, mRNA expression relative to original parent. See also Supplementary Fig. S3 (for protein analysis). Means of technical quadruplicates (A) or technical triplicates (B, C, E, and F) ± SEM.
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Karpas-299 parent line (Fig. 5E). Consistent with resensitization, ceritinib resumption halted the growth of tumors in all three mice, with two experiencing tumor reduction over the next 22 days when the experiment ended (Fig. 5B). The third tumor began growing again after 12 days despite the ongoing ceritinib therapy. These results show proof of principle that discontinuous dosing in vivo can take cells through full cycles of ALK TKI dependence and sensitivity and can prolong tumor control in host animals bearing tumors with resistance driven by ALK overexpression. Up-front comparison of intermittent versus continuous in SCID mice engrafted with parental Karpas-299 xenografts did not generate relapses in any group at effective treatment doses (Supplementary Fig. S5), however, showing a need to interrogate ALK expression in resistant tumors before attempting discontinuous dosing (see Discussion).

Discussion

ALK-kinase inhibition is an important novel treatment modality for the subset of NSCLC cases containing ALK rearrangements, but median progression-free survival has ranged from 7 to 10 months during treatment with crizotinib or ceritinib (10, 13, 38). Target-independent resistance is common, as target-dependent mechanisms such second-site kinase-domain mutations are detectable in fewer than half of resistant samples and even then activation of alternate signaling may also be present (14, 18, 19). The small number of ALK–ALCL patients treated to date with ALK TKIs has not permitted determination of typical progression-free survival, and resistant clinical samples are not yet available for assessment (16, 17). In this study, we have attempted to predict resistance pathways using laboratory-based selections, an approach that has identified clinically relevant reasons for targeted drug failure in numerous cancer types (39–42).

Our results suggest a much stronger addiction to ALK signaling in ALCL than observed in NSCLC. Multiple-independent selections performed with both crizotinib and ceritinib resulted in upregulation of NPM–ALK to permit survival in the presence of inhibitor, and there was no clear evidence of alternate signaling able to bypass it. Even re-selection of cells already selected for resistance once, but which lost resistance in order to avoid the toxic effects of ALK overdose, again generated ALK upregulation (Supplementary Fig. S4). All resistant lines preserved ALK activation in the presence of inhibitor, though preservation was stronger in some than in others (K299 subclones vs. the others in Fig. 2E), whereas STAT3 activation was strongly preserved in all. It is therefore possible additional mechanisms preserving STAT3 activation arose in some cases, though this was not observed after lines were reselected for ability to grow without inhibitor. Either way, we find the effect of ALK signaling intensity on cell survival exists as an inverted U-shaped curve, which we represent schematically in Fig. 6. NPM–ALK overexpression associated with genomic amplification in the case of resistant clones derived from Karpas-299 and without amplification in other clones. The consistent results with Karpas-299 suggest this line might have a subpopulation with NPM–ALK amplification at baseline. Such population is then most able to upregulate expression from a tolerable prosurvival baseline to the levels necessary to overcome high concentrations of inhibitor. Even in the resistant NPM–ALK-amplified K299-CR1000 clone, however, a subpopulation without the amplification appears to persist, because it reemerges...
Figure 5.
ALK resistance dependence in vivo. A, mean tumor burden of mice injected with $10^6$ K299-CR1000 cells and treated with vehicle or ceritinib ($n = 5$ per group). B, individual tumor burden of tumor-bearing mice following ceritinib discontinuation and subsequent resumption. C-F, viability assays (C), proliferation (D), copy-number (E), and mRNA expression (F) using cells taken from mice 1 and 3 before resumption of ceritinib show the RS phenotype. Cells from mouse 2 were not successfully cultured. Means of technical quadruplicates (C) or independent triplicates (D) or technical triplicates (E and F) ± SEM.
CAS9-mediated chromosomal breaks can generate ALK signaling dosage. The possibility is that the amplification states of lost viability, ending in death withdrawal of TKI from resistant cells with ALK upregulation drives cells into prolonged tumor control as the other edge of the sword comes off therapy and subsequently experience regression should be fully interrogated since no relapses were observed, evaluation of ALK inhibition would then provide a new way of prolonging tumor control as the other edge of the sword comes into play.

**Disclosure of Potential Conflicts of Interest**

S.D. Purvada has received speakers bureau honoraria from Seattle Genetics and is a consultant/advisory board member for Pharmacyclics. No potential conflicts of interest were disclosed by the other authors.

**Authors’ Contributions**

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**Figure 6.**

Schematic of ALK dosage and cell viability. A narrow range of ALK activity promotes cell viability. Addition of TKI to ALK-addicted parent cells or withdrawal of TKI from resistant cells with ALK upregulation drives cells into dynamic states of lost viability, ending in death—but for opposite reasons of ALK signaling dosage.

Evaluation of up-front intermittent dosing and discontinuous dosing in the setting of acquired resistance when such a system becomes available are justified by our findings. It also will permit studies of the mechanisms of ALK-overdose toxicity and of non-amplification-driven NPM–ALK overexpression in a physiologically accurate immunocompetent model system.

Important questions raised by our data include those of broader applicability. In lung cancer, EML4–ALK copy-number gain and increased expression are reported in association with crizotinib resistance (18, 19). There are recent case reports of ALK+ NSCLC patients who became refractory to crizotinib obtaining secondary responses upon re-challenge after a period off the drug (45, 46). Both patients, however, received chemotherapy upon initial crizotinib discontinuation, so we do not know if ALK overdose was present or might have led to spontaneous regressions if they had been observed without therapy. Another case series found continuing crizotinib treatment despite progression led to higher performance status than discontinuation (47), but no study has addressed the question of whether therapy interruption may benefit some patients based on the particular resistance mechanism(s) present in their tumors. In other cancers with known or potential ALK activation, evaluation of ALK inhibition is at early stages with results largely unreported. We encourage careful evaluation for changes in ALK signaling dosage during ALK inhibitor therapy in ongoing and planned trials. Patients who come off therapy and subsequently experience regression should be assessed for the potential role of ALK overdose in these findings.

In sum, ALK activity can exist as a double-edged sword for cancer cells. Those tumors that are most addicted to its activities for continued proliferation correspondingly are most prone to select for higher expression to bypass its inhibition. Interruption of inhibition would then provide a new way of prolonging tumor control as the other edge of the sword comes into play.

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