Vulnerability of drug-resistant EML4-ALK rearranged lung cancer to transcriptional inhibition

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Abstract

A subset of lung adenocarcinomas is driven by the EML4-ALK translocation. Even though ALK inhibitors in the clinic lead to excellent initial responses, acquired resistance to these inhibitors due to on-target mutations or parallel pathway alterations is a major clinical challenge. Exploring these mechanisms of resistance, we found that EML4-ALK cells parental or resistant to crizotinib, ceritinib or alectinib are remarkably sensitive to inhibition of CDK7/12 with THZ1 and CDK9 with alvocidib or dinaciclib. These compounds robustly induce apoptosis through transcriptional inhibition and downregulation of anti-apoptotic genes. Importantly, alvocidib reduced tumour progression in xenograft mouse models. In summary, our study takes advantage of the transcriptional addiction hypothesis to propose a new treatment strategy for a subset of patients with acquired resistance to first-, second- and third-generation ALK inhibitors.

Keywords ALK/EML4 translocation; ALKi; CDKi; drug resistance; NSCLC

Introduction

In non–small-cell lung cancer (NSCLC), small molecule inhibitors that target mutant kinases have offered unprecedented success in the management of the disease. One of the most successful examples is echinoderm microtubule-like-4-anaplastic lymphoma kinase (EML4-ALK)-mutant lung cancer, which affects 4–5% of lung cancer patients (Gainor et al., 2013). A fusion of ALK with EML4 (Soda et al., 2007) causes the constitutive activation of the ALK kinase domain and subsequent oncogenic signalling, typically through the MAPK, JAK-STAT and PI3K-AKT pathways (Chiarle et al., 2008). To date, the first-generation ALK inhibitor crizotinib, second-generation ALK inhibitors ceritinib, alectinib and brigatinib, and the third-generation ALK inhibitor lorlatinib have been approved by the Food and Drug Administration (FDA) for the treatment of patients with lung cancer harbouring the EML4-ALK translocation. The objective response rate for the ALK inhibitors crizotinib and alectinib in the clinic surpasses 60%, while a median progression-free survival of 34 months has been demonstrated with alectinib (Camidge et al., 2018). However, patients eventually develop disease progression due to drug resistance.

A common mechanism of resistance is represented by mutations in the ALK kinase domain that hinder small molecule binding, such as the G1202R mutation which occurs after alectinib treatment (Gainor et al., 2016). A multitude of parallel pathways’ alterations can also cause resistance to ALK inhibitors, compensating for the lack of EML4-ALK activity. Usually, these are receptor tyrosine kinases (RTKs), such as EGFR, HER3/4 and c-KIT (Lin et al., 2017) but they can also be other oncogenes, such as KRAS (Doebele et al., 2012). Treatment options upon failure of ALK inhibitors are limited and chemotherapy offers only a short-lived benefit to these patients whereas the additive benefit of immunotherapy in this context is still unclear (Pacheco & Camidge, 2019).

In this study, we discovered a cell cycle dysregulation and a vulnerability of EML4-ALK lung cancer cells to the pan-CDK inhibitors alvocidib and dinaciclib, as well as the CDK7/12 inhibitor THZ1. We put forward the idea of testing these inhibitors in the clinic after ALK inhibitors have failed due to the development of acquired resistance.
Results

Pathways dysregulated in crizotinib resistance

To mimic the context of acquired resistance to ALK inhibitors in vitro, we employed cell lines with acquired resistance to crizotinib (Fig 1A and B), ceritinib and alecitinib (Appendix Fig S1A) obtained by long-term exposure to increasing concentrations of the drugs. These cell lines were derived from the parental H3122 cells (Lovly et al, 2011) and STE-1 cells, a patient-derived lung cancer cell line described in (Lovly et al, 2014), both of which carry the EML4-ALK (E13;A20) translocation.

As revealed by Sanger sequencing, all the resistant cells have wild-type ALK kinase domain. Due to the absence of ALK kinase domain mutations, we reasoned that this lack of response to ALK inhibition was a result of alterations in parallel signalling. To identify the driver of crizotinib resistance, we followed a transcriptomic approach and performed RNA-seq of CrizR1 and isogenic parental H3122 cells (Dataset EV1). Through this analysis, we detected an upregulation of the EGFR mRNA that we further validated at the protein level (Appendix Fig S1B). Increased EGFR signalling, through ligand upregulation, gene amplification or point mutation, is to our knowledge the most common ALK-independent mechanism of resistance to ALK inhibitors (Camidge et al, 2014). To investigate whether this was the main driver of resistance, we silenced EGFR by RNAi (Appendix Fig S1C). We asked if this silencing in combination with crizotinib could re-sensitize CrizR1 cells; however, we observed no significant induction of apoptosis (Appendix Fig S1D).

We used HCC-827 EGFR-driven cells as positive control, which indeed became apoptotic upon EGFR silencing. In addition, we detected an upregulation of the TGF-β receptors 1 and 2 (Appendix Fig S1E) and found that inhibition of TGF-β activity with the small molecule inhibitor galunisertib resulted only in a marginal decrease of cell proliferation (Appendix Fig S1F). Ruling out that EGFR/TGF-βR act as drivers of resistance, we searched for more dysregulated oncogenes.

Using the HALLMARK gene collection, we found a significant enrichment in epithelial-to-mesenchymal transition (EMT)-related genes in CrizR1 cells (Fig 1C and D). Given the mesenchymal phenotype of the crizotinib-resistant cell lines (Appendix Fig S2A), we asked whether EMT played a role in these drug-resistant cells. We chose 4 genes known to induce mesenchymal characteristics and confirmed their expression levels via qPCR. AXL, LOX, SNAI2 and VIM were upregulated in the majority of the resistant cell lines (Fig 1E). AXL protein levels were particularly elevated in the CrizR1 and CrizR4 cells and AXL is known to be activated in drug-resistant EML4-ALK cells (Nakamichi et al, 2018). Interestingly, we detected a downregulation of ALK in the same cells, raising the possibility that AXL compensates in part for the reduced EML4-ALK activity. Moreover, AXL inhibition with the small molecule inhibitor bemcentinib (Holland et al, 2010) resulted in the downregulation of LOX, SNAI2 and VIM, indicating that AXL activation is responsible for the induction of these genes and subsequently EMT (Fig 1F). Next, we asked whether AXL upregulation is functional in these cells and in a proliferation assay, bemcentinib halted proliferation in CrizR1 and CrizR4 cells in combination with crizotinib (Fig 1G), suggesting that AXL activation has a functional role in these cells. However, bemcentinib alone or in combination with crizotinib did not induce cell death or senescence (Fig 1H and Appendix Fig S2B), indicating a cytostatic instead of a cytotoxic effect. In summary, we have detected an AXL-mediated induction of resistance to crizotinib. Although AXL inhibitors significantly reduce cell proliferation, they are unable to kill crizotinib-resistant cells.

Dysregulation of cell cycle-related genes in crizotinib-resistant cells

In the RNA-seq data comparing crizotinib-resistant versus crizotinib-sensitive cells, a KEGG pathway analysis by GSEA revealed 9 pathways enriched in dysregulated genes (Dataset EV1 and Fig 2A). Among them, there was a significant enrichment in cell cycle-related genes (Fig 2A and B, Dataset EV2). We were able to confirm by immunoblot the upregulation of multiple cell cycle-related genes in the crizotinib-resistant cells. Notably, CDK1 and CCNB1, as well as CDK6, were upregulated in the majority of the resistant cell lines (Fig 2C). CDK2 was not upregulated, but we found an upregulation...
Figure 1.
of its partner CCNE1. In alectinib-resistant cells, CDK1, CCNB1 and CDK6 were also upregulated (Fig 2D).

With CDK6 being the most strongly upregulated protein, we hypothesized that pharmacological inhibition of CDK6 would reverse the resistance to crizotinib. To this end, we used the specific CDK4/6 inhibitor palbociclib in a proliferation assay and identified a limited sensitization to crizotinib only at high micromolar concentration (Fig EV1A). We reasoned that upregulation of CDK6 on its own might not be sufficient to induce crizotinib resistance. Therefore, we used the CDK inhibitor alvocidib (Flavopiridol), a potent inhibitor of CDK1, CDK2, CDK4, CDK6 and CDK9, with or without crizotinib in a proliferation assay. Although alvocidib did not synergize with crizotinib in CrizR1 cells (Fig 2E and F), we observed a remarkable sensitivity to single-agent alvocidib in both parental and isogenic resistant cells (Fig 2G). In addition to the H3122, which carry the EML4-ALK variant 1, we also tested H2228 cells, which harbour the EML4-ALK v3a/b variant and are primarily more resistant to crizotinib compared with H3122 cells. Alvocidib treatment resulted in comparable inhibition of proliferation (Fig EV1B).

To follow up on this observation, we also tested dinaciclib, a newer, more potent CDK1, CDK2, CDK5 and CDK9 inhibitor (Parry et al, 2010). Both alvocidib and dinaciclib significantly inhibited cell proliferation at low nanomolar concentrations in EML4-ALK cells with acquired resistance to these inhibitors as well as the parental cells (Fig 2H).

We then asked whether CDK1, CDK2 or CDK6 could affect the resistance to crizotinib individually or in synergy. Upon silencing of these CDKs (Fig EV1C) and after a cell cycle profile, it was evident that CDK6 silencing did not affect these cells, while CDK1 silencing (or silencing of all the three CDKs simultaneously) resulted in arrest of the cell cycle in the G2/M phase and an induction of cell death as assessed by DNA content (Fig EV1D and E).

**CDK inhibitors induce apoptosis through transcriptional inhibition**

Considering the efficacy of both alvocidib and dinaciclib in inhibiting the transcriptional CDKs, and the preferential activity against CDK9, we next hypothesized that their pronounced anti-proliferative activity could be in part due to the suppression of transcription. To evaluate the transcriptional hypothesis, we used the CDK7/12 inhibitor THZ1 (Kwiatkowski et al, 2014), since CDK7 is also influencing transcription by phosphorylating the RNA polymerase II (Blagowski, 2004). As with alvocidib, we followed up on the effectiveness of THZ1 as a single agent. All EML4-ALK cells showed a remarkable decrease in cell proliferation upon THZ1 treatment (Fig 3A).

Treatment of the parental, crizotinib-, ceritinib- or alectinib-resistant cells with modest concentrations of alvocidib, dinaciclib or THZ1 led to near-complete inhibition of cell proliferation as assessed by crystal violet staining (Fig 3B). These data suggest that CDK inhibition may target an inherent vulnerability of EML4-ALK lung cancer and should be further tested.

We next questioned whether this pronounced effect observed upon treatment with CDK inhibitors was a result of cell cycle arrest or apoptotic cell death. Alvocidib treatment caused an accumulation of cells in the G2/M phase assessed by DNA content (Fig EV2A). Apoptotic cell death was the main outcome of alvocidib and dinaciclib treatment in all cell lines tested, assessed via PARP cleavage (Fig EV2B) as well as Annexin V+/PI staining (Figs 3C and EV2C). In addition, this induction of apoptosis was not due to toxicity, as normal lung epithelial HBEC cells did not become apoptotic (Fig EV3A). Furthermore, there was selectivity towards EML4-ALK cells, as alvocidib and dinaciclib induced significantly higher levels of apoptosis in CrizR1 and AlerR cells compared with KRASmut A549 cells, KRAS<sup>mut</sup>/EGFR<sup>mut</sup> PC-9 cells or cells isolated from metastatic sites (H1299 and H460) (Figs 4A and EV3B).

To approach the induction of apoptosis in a more unbiased fashion, we treated CrizR1 cells with alvocidib and used an apoptosis array that profiled 43 different proteins (Figs 4B and EV3C). We found an upregulation of critical pro-apoptotic components such as BIM, BID, SMAC and as expected, CASP3 and CASP8. In agreement with a previous study (Ma et al, 2003) after alvocidib or dinaciclib treatment, we observed a downregulation of MCL-1 as well as of the anti-apoptotic protein BIRC5 (Survivin) in all EML4-ALK cells resistant to all ALK inhibitors (Fig 4C).

We then reasoned that all the three inhibitors affect transcriptional regulation and subsequently the mRNA levels of pro- and anti-apoptotic proteins. Alvocidib is known to decrease transcriptional output by inhibiting CDK9 and, consequently, elongation by the RNA Polymerase II (Blagowski, 2004). Indeed, in our system, alvocidib and dinaciclib treatment decreased phosphorylation at the Ser2 repeat of the RNA Pol II (Fig EV3D). To test the specificity of these inhibitors, we used siRNAs for CDK7 and CDK9. Only a modest knockdown of CDK9 was sufficient to induce apoptosis.
Figure 2.
Figure 3.
Effects of alvocidib and THZ1 on transcription initiation and elongation

In order to add confidence to the transcriptional hypothesis, we performed ChIP-seq for RNA polymerase II after treating CrizR1 cells with alvocidib or THZ1. A global overview of RNA pol II peaks suggested that alvocidib treatment dramatically increased occupancy at the transcription start site (TSS), while THZ1 decreased it (Fig 5A). We performed GSEA analysis based on the core enrichment of the mapped peaks and found 6 differentially enriched signatures with alvocidib (Fig 5B) and 11 with THZ1 (Fig 5C). Notably, both drugs induced different RNA pol II occupancy in the TSS of MYC targets. Lastly, we looked at the peaks of the previously examined genes MCL1, Survivin and CCND1 and we also included MYC. From the gene tracks, it was evident that alvocidib treatment resulted in pausing of the RNA pol II at the TSS while reducing the occupancy across the gene bodies, while THZ1 resulted in reduced binding of RNA pol II at the TSS and in the gene bodies (Fig 5D). This is highly concordant with previous findings which suggest that CDK7 mediates the binding of the RNA pol II at the promoters while CDK9 regulates the release and elongation steps (Kwiatkowski et al., 2014). MYC and CCND1 downregulation upon alvocidib or THZ1 treatment was confirmed by qPCR (Fig 5E). Notably, MYC silencing induced upregulation of the pro-apoptotic proteins BIM and significantly increased cell death (Fig 5F and G). Furthermore, MYC indirect inhibition via trame tinib, rapamycin or both significantly induced cell death in CrizR1 cells (Fig 5H). In conclusion, transcriptional inhibition with the described CDK inhibitors offers a new way to induce apoptosis in EML4-ALK lung cancer cells.

Alvocidib is effective in vivo

To test the activity of alvocidib in vivo, we first characterized the resistant cells to verify whether they could keep the resistance in the absence of the drugs for up to 6 weeks. CrizR1, CrizR4 and AlecR cells showed marked resistance in the absence of crizotinib for up to 6 weeks (Fig EV4A), although the AlecR cells are primarily more sensitive to the drug compared with the crizotinib-resistant cells. Next, we tested the activity of alvocidib in vivo. As expected, H3122 xenograft mouse models responded to crizotinib and alvocidib (Fig EV4B and C). CrizR1 and CrizR4 xenograft mouse models were resistant to crizotinib while treatment with alvocidib resulted in reduced tumour growth (Figs 6A and B, and EV4D and F). We also noticed a significant decrease in tumour growth in response to alvocidib in mice harbouring alectinib-resistant tumours (Figs 6C and EV4). Alvocidib treatment was generally well tolerated, although weight loss was observed in some of the mice (Appendix Fig S4). Upon sacrificing the mice, we assessed the apoptotic status of these tumours by in situ immunohistochemistry (IHC). The increase in cleaved caspase 3 was evident in CrizR1 and AlecR tumours (Fig 6D), while in CrizR4 tumours the levels of cleaved caspase 3 were marginally significant (Fig EV5A). However, we should note that in the CrizR4 model the absence of drug treatment during the last week before sacrifice complicates this interpretation.

In agreement with in vitro studies, in tumours treated with alvocidib we observed downregulation of the marker of proliferation Ki67 as well of MYC, Survivin and MCL1, and upregulation of BIM and p21(Figs 6E and F, and EV5B and C).

These results raised questions in terms of sequential use of ALK inhibitors. For patients with wild-type ALK who progress on...
Figure 4.
crizotinib or alectinib, the third-generation ALK inhibitor lorlatinib could conceivably be used to more potently inhibit ALK. In a proliferation assay, while H3122 parental cells were very sensitive to lorlatinib, 250 ng/ml actinomycin D for 6 h. RNA was extracted, and the mRNA levels of the induced genes were quantified by RT-qPCR. CDK1: DMSO versus H3122 DMSO P = 0.002, Actinomycin versus DMSO P = 0.003, Alvocidib versus DMSO P = 0.005; CDK2: DMSO versus H3122 DMSO P = 0.0001, Actinomycin versus DMSO P < 0.0001, Alvocidib versus DMSO P = 0.0005, Actinomycin versus DMSO P = 0.0004; CDK9: DMSO versus H3122 DMSO P = 0.0003, Actinomycin versus DMSO P = 0.0002, Alvocidib versus DMSO P = 0.0003; CCNB1: DMSO versus H3122 DMSO P = 0.0004, Actinomycin versus DMSO P = 0.0004, Alvocidib versus DMSO P = 0.0001, dinaciclib versus control P = 0.01, dinaciclib versus control P = 0.01, THZ2 versus control P = 0.0001.

G (Top) Western blot analysis of CrizR1 cells treated with siScrambled or with a pool of 4 different siRNAs targeting Survivin (siBIRC5). (Bottom) Cells were stained with Annexin V/PI and analysed by flow cytometry for Annexin V+ cells 72 h post-transfection. Annexin: early apoptosis P = 0.0003, late apoptosis P = 0.5, alive P < 0.0001.

H The CCLE RNA-seq data set was used and RPMK values were plotted for the Cyclin D1 and Survivin genes, indicating high expression in H3122 cells compared with other LUAD cells.

Data information: Statistical comparisons were performed using a paired, two-tailed Student t-test. Plotted graphs show mean ± SD (n = 3, unless otherwise specified). *P < 0.05, **P < 0.01, ***P < 0.001, N.S. = Not Significant P > 0.05.

Source data are available online for this figure.

Discussion

In this paper, we have found that a global transcriptional dysregulation leads to crizotinib resistance in EML4-ALK cells. Furthermore, we have shown that transcriptional inhibition is highly potent in this context and that the CDK inhibitors Alvocidib, dinaciclib and THZ1 warrant clinical testing in patients with disease progression due to ALK-independent mechanisms of resistance. Specifically, we have shown that downregulation of key cell cycle proteins as well as an upregulation of pro-apoptotic proteins mediate the response to crizotinib.

In our data, even though EGFR overexpression and activation was present in CrizR1 cells, it did not mediate resistance to crizotinib. This is not surprising, given that a case of crizotinib-resistant cells with EGFR amplification that had another main driver of resistance has been reported before (Katayama et al., 2012). TGF-β inhibition had a marginal effect on the proliferation of crizotinib-resistant cells, implying that TGF-β activity acts in part to promote resistance to crizotinib. Furthermore, although AXL inhibition partially reduced cell proliferation it had no effect in inducing programmed cell death in ALK-resistant cells.

Amplification of CDKs or their partner Cyclins has been described to confer a proliferative advantage to tumour cells (Otto & Sincinski, 2017). Recent work in EGFR-mutant lung cancer revealed that amplification of the CCNE1 gene can be found in patients with acquired resistance to EGFR inhibitors (Blakely et al., 2017) and specifically with acquired resistance to osimertinib (Yang et al., 2018). We have demonstrated that cells with acquired resistance to ALK inhibitors present CDKs/Cyclins upregulation. We thereby observed the impressive single-agent activity of CDK inhibitors that cannot be explained by single inhibition of CDK1, CDK2 or CDK6, as evidenced by siRNA experiments. This previously unseen potent activity of CDK inhibitors at concentrations that are easily achievable in the clinic (Shapiro et al., 2001; Stephenson et al., 2014) prompted us to investigate this further.

Alvocidib and dinaciclib are known to potently inhibit the transcriptional regulator CDK9 (Parry et al., 2010), while THZ1 inhibits the transcriptional regulators CDK7/12 (Kwiatkowski et al., 2014). CDK7/12 and CDK9 regulate transcription by phosphorylating the RNA polymerase II (Oelgeschläger, 2002). With siRNA experiments, we were able to induce apoptosis by partial CDK9 downregulation. CDK7 knockdown did not lead to apoptosis, but it has been observed before that concurrent inhibition of CDK7/12/13 is required for an effect on transcription (Olson et al., 2019).

While phosphorylation of RNA pol II at the Ser5 and Ser7 sites by CDK7 has been shown to be important for the recruitment of the complex at the TSS (Sampathi et al., 2019), phosphorylation at Ser2 by CDK9 is important for the release and the elongation step...
Figure 5.
Figure 5. Alvocidib or THZ1 treatment is concordant with CDK9 or CDK7 inhibition based on RNA polymerase II ChIP-seq.

A. CrizR1 cells were treated with vehicle control, 200 nM alvocidib or 1.00 nM THZ1 for 6 h, then chromatin was precipitated with an anti-RNA polymerase II antibody and sequenced. Plotted is the average number of peaks per condition.

B, C. GSEA analysis using the HALLMARK gene collection for the differentially enriched peaks around the TSS (±1 kb) with (B) alvocidib or (C) THZ1 treatment. Shown on the right is the plot of the “MYC targets”-enriched signature.

D. Gene tracks of RNA polymerase II occupancy at the MCL1, BIRC5 (Suruvin), CCND1 and MYC genes.

E. qPCR of MYC and CCND1 upon treatment of CrizR1 cells with Alvocidib or THZ1 for 6 h. The graph represents the mean fold change ± SD. MYC: alvocidib versus DMSO P = 0.03, THZ1 versus DMSO P < 0.0001; CCND1: alvocidib versus DMSO P = 0.001, THZ1 versus DMSO P = 0.003.

F. BIM is upregulated upon MYC silencing in CrizR1 cells.

G. Annexin V assay showing the percentage of apoptotic CrizR1 cells upon MYC downregulation using siRNA. Early apoptosis P = 0.002, late apoptosis P = 0.04, alive P = 0.0008.

H. Annexin V assay showing the percentage of apoptotic CrizR1 cells after treatment with trametinib, rapamycin or both. Trametinib: early apoptosis P = 0.002, late apoptosis P = 0.05, alive P = 0.009; rapamycin: early apoptosis P = 0.04, late apoptosis P = 0.8, alive P = 0.003; tram+rapa: early apoptosis P = 0.0001, late apoptosis P = 0.04, alive P = 0.01.

Data information: Statistical comparisons were performed using a paired, two-tailed Student t-test. Plotted graphs show mean ± SD (n = 3, unless otherwise specified). *P < 0.05, **P < 0.01, ***P < 0.001. Source data are available online for this figure.

(Jonkers et al., 2014). Through ChIP-seq, we demonstrated that alvocidib treatment results in RNA Pol II promoter-proximal pausing, while THZ1 treatment decreases the occupancy of PolIII at TSS. These results suggest that in the described cellular context, inhibition of CDK7 and CDK9 has a widespread transcriptional effect leading to downregulation of the transcription factor MYC and its family members along with several other oncogenes, including CCND1 and Survivin.

Our proposed model of action for these compounds is an induction of apoptosis independent of cell cycle arrest since in our data it is clear that cell cycle arrest is minimal compared with apoptotic induction. We posit that there is a p53-independent induction of apoptosis since the parental H3122 cells harbour the E285V inactivating mutation of the TP53 gene (COSMIC project, Sanger Institute and (Russell-Swetek et al., 2008)). Furthermore, we suggest that the downregulation of RNA polymerase II activity promotes the loss of short-lived mRNAs, such as MYC and Survivin (Blagosklonny, 2004) and an upregulation of pro-apoptotic genes followed by initiation of apoptosis and specifically of the mitochondrial apoptotic pathway. Notably, the increase of the pro-apoptotic gene BIM in this context appears to be, at least in part, MYC-dependent.

We confirmed that alvocidib and dinaciclib induced significantly higher levels of apoptosis in crizotinib-resistant cells compared with KRASmut and metastatic NSCLC cell lines or non-transformed epithelial cells. This could explain why, in terms of clinical testing, alvocidib was not effective in a previous clinical trial on advanced metastatic NSCLC (Shapiro et al., 2001). Dinaciclib was shown to be inactive as monotherapy in patients with NSCLC previously treated with erlotinib (Stephenson et al., 2014). However, the ALK mutational status in these patients was not assessed; therefore, the trial did not test the patient cohort that our data would represent, namely patients with EML4-ALK NSCLC. Consistent with the compelling in vitro activity, alvocidib was also active in xenograft models of crizotinib and alectinib resistance, where ALK inhibitors failed. To our knowledge, this is the first time this has been demonstrated in a xenograft mouse model of lung adenocarcinoma.

In conclusion, we have reinforced the idea that the appearance of a known oncogene as mutated or over-activated does not necessarily mean that this oncogene is the main driver of drug resistance. We have shown multiple alterations that concurrently occur in the resistance to ALK inhibitors. This complicates the diagnostic setting and suggests that testing for individual ALK-independent mechanisms of resistance in the clinic could be inefficient. We can therefore envision that a more efficient way to address off-target TKI resistance is either with rational upfront combinations that aim to prevent it altogether (Hrustanovic et al., 2015; Rusan et al., 2018), or using a drug with universal activity able to dampen parallel oncogenic pathways simultaneously.

Figure 6. Alvocidib reduces tumour growth in vivo.

A. Tumour growth of in vivo xenografts of H3122 CrizR1 cell lines in response to crizotinib or alvocidib and correspondent tumour weights (P.O. control n = 5; I.P. control n = 4; crizotinib n = 8 and alvocidib n = 6). Tumour weights, crizotinib P = 0.44, alvocidib P = 0.03.

B. Tumour growth of in vivo xenografts of Ste-1 AlectR cell lines in response to alvocidib and correspondent tumour weights (I.P. control n = 6; alvocidib n = 4). Tumour weights alvocidib P = 0.004.

C. Number of cleaved caspase-3-positive nuclei in alvocidib treated tumours compared with controls.

D. Ki67 and p21 staining of CrizR1 xenograft tumours. Scale bar = 200 μm. Quantitative analysis of IHC staining is presented on the right. Ki67 P = 0.0004; p21 P = 0.02.

E. qPCR of Survivin (P = 0.0009), MCL-1 (P = 0.04), MYC (P = 0.007) and BIM (P = 0.03) in Ste-1 AlectR cells xenografts treated with alvocidib (Control n = 6; alvocidib n = 4).

F. Proliferation assay of H3122 parental and isogenic drug-resistant cell lines, treated with DMSO, 100 nM lorlatinib, 200 nM alvocidib or 50 nM dinaciclib for 72 h (n = 4).

G. Growth curve of CrizR1 xenograft tumours in response to lorlatinib (Control n = 7; lorlatinib n = 7).

H. Model suggesting the clinical sequencing of CDK inhibitors post-ALK inhibition failure as a potential alternative to chemotherapy.

Data information: Statistical comparisons were performed using a paired, two-tailed Student t-test. Plotted graphs show mean ± SD. *P < 0.05, **P < 0.01, ***P < 0.001, N.S. = Not Significant P > 0.05.
Figure 6.
Materials and Methods

Aptoptic assay

Annexin V/PI
Cells were trypsinized and processed with a TACS® Annexin V/PI kit (Trevigen) according to the manufacturer’s instructions. Samples were then run through a Novocyte flow cytometer (ACEA biosciences) and quantified for Annexin V+ cells. Spectral overlap was compensated with unstained and single stained controls. Plots were gated to exclude cell debris and cell doublets.

Senescence assay
Cellular senescence was detected measuring the activity of the β-Galactosidase (β-Gal) using CellEvent Senescence Green Detection kit (Invitrogen). 2,000 cells/well were plated in Nunc 96-well optical plates. At 72 h after treatments, cells were washed with PBS, fixed by adding 100 μl/well of fixation solution for 10 min and then washed again with 100 μl of 1% BSA in PBS. Next, 100 μl/well of the pre-warmed working solution, containing the fluorescence-based β-gal substrate, were added to each well and incubated for 2 h at 37°C. Cells were washed three times with PBS and, finally, fluorescence by β-gal-cleaved substrate was measured at 488 nm with M5 SpectraMax plate reader.

Cell culture
HEK293T cells were maintained in DMEM with 1 g/l glucose (Gibco) + 10% fetal bovine serum (Gibco). HBEc cells were maintained in Airway Epithelial Cell Basal Medium (ATCC) combined with a Bronchial Epithelial Cell Growth kit (ATCC). All the other cell lines were maintained in RPMI-1640 (Gibco) + 10% fetal bovine serum (Gibco).

HEK293T and A549 cells were a kind gift from Dr. John Brog-nard. H1299 cells were a kind gift from Prof. Angeliki Malliri. HBEc, H2228 and H460 cells were purchased from ATCC. The following cell sources have been described before: H3122 (Lovly et al., 2011), STE-1 (Lovly et al., 2014), PC-9 and isogenic cell lines (Meador et al., 2015), H1975 and isogenic cell lines (Meador et al., 2015). H3122 and STE-1 parental cells were STR-profiled upon receipt and found to be free of contamination with another line. All cell lines were routinely monitored for mycoplasma contamination using an in-house Core Facility service.

Drug-resistant cell lines

Full information for drug-resistant cells can be found in Fig 1A. Briefly, the parental cell lines were exposed to a low concentration of the primary inhibitor until cells could proliferate fully in the presence of it. Then cells were split and exposed to 20% higher concentration. The process was repeated until the corresponding cell lines were resistant to > 500 nM of the primary inhibitor and were then maintained by adding drug after every passage.

Characterization of resistant cell lines

The capacity of the cells to maintain resistance to crizotinib and alectinib was assessed over a period of 6 weeks. Briefly, resistant cell lines (CrizR1, CrizR4 and AlecR) were split to generate a subline of cells cultured in the absence of drug (−drug), in parallel to the original resistant cell line cultured in the presence of the drug (+drug). Cell viability was assessed every week until 6 weeks upon treatment with crizotinib (1 μM) or alectinib (500 nM) for 72 h.

Cell cycle analysis
After the corresponding treatment, cells were fixed in 70% ethanol and stained with an FxCycle™ PI/RNase Staining Solution (Molecular Probes). Cell cycle plots were generated in a Novocity instrument using the device’s software.

Compounds used

Crizotinib, ceritinib, alectinib, erlotinib, osimertinib, palbociclib, alvocidib, dinaciclib, THZ1, galunisertib and trametinib for in vitro experiments were all purchased from Selleck. Lorlatinib was purchased from MedChemExpress. Bemcentinib (R428) was purchased from Axon. Rapamycin was purchased from Caymen Chemical. Actinomycin D was purchased from Sigma. Alvocidib, dinaciclib, crizotinib, lorlatinib and THZ1 for in vivo studies were purchased from MedChemExpress whereas alectinib was purchased from Selleck.

Computational analyses

GSEA
Gene set enrichment analysis was performed by ranking the gene sets after differential expression analysis of RNA-seq data. The cut-off for the final list of genes was $P_{adj} < 0.05$ and log2foldchange $>1$ or $<-1$. The.rnk files were loaded to the supplied desktop GSEA v2.0 software (Subramanian et al, 2005). The analysis parameters were based on 1,000 permutations and a minimum of 15 genes per identified set. The individual gene set collections used are described in the text or figure legends.

Heatmap

Heatmap was generated using the R Package pHeatmap based on Euclidean distance clustering.

Crystal violet staining

Cells were treated in 6-well plates, fixed for 20 min in 3.7% paraformaldehyde and then stained for 20 min in a 0.05% crystal violet solution (Sigma).

In vivo xenograft studies
Female athymic nude mice or NOD-SCID mice from Charles River were used at 6-8 weeks old. After acclimatization, mice were injected with 2 million H3122 cells in 50% matrigel, or 2 million CrizR1 cells in 50% matrigel, 2.5 million CrizR4 cells or 5 million AlecR cells in 50% matrigel (Corning). When tumours reached between 100 and 200 mm³, mice were randomized in different groups.

H3122/CrizR1 experiment: 10 ml/kg vehicle control by oral gavage daily (n = 5), 50 mg/kg crizotinib by oral gavage daily
(n = 8), 10 ml/kg vehicle control by I.P. injection 3× a week (n = 5), 10 mg/kg alvocidib by I.P. injection 3× a week (n = 8). In the H3122 experiment, the tumour size of the control group and the gavage group were combined in the graph to facilitate comparison with crizotinib. For the CrizR1 experiment, measurements shown are 3 days before sacrifice.

CrizR4 experiment: Initially, mice were randomized to receive 10 ml/kg vehicle control (n = 8) or 10 mg/kg alvocidib (n = 8), by I.P. injection, daily for 3 weeks. In the crizotinib group, mice were treated with 10 ml/kg vehicle control or 50 mg/kg crizotinib daily, by oral gavage.

AlecR experiment: Initially, mice were randomized to receive 10 ml/kg vehicle control by I.P. injection 3×/week (n = 7), 10 mg/kg alvocidib by I.P. injection 3×/week (n = 7). After 3 weeks of consecutive treatment, a 1 week on/1 week off pattern was adopted for the alvocidib/I.P. control group.

CrizR1 experiment with lorlatinib treatment: 10 ml/kg vehicle control by oral gavage daily (n = 8), 5 mg/kg lorlatinib by oral gavage daily (n = 8).

Tumours were measured with a digital calliper, and volumes were calculated using the formula \[ \text{volume} = (\text{width})^2 \times \text{length}/2. \] In all the experiments, mice that showed weight loss > 20% of body weight or with tumours that reached a size of 1,500 mm³ or that developed tumour ulceration/bleeding were sacrificed and discounted from the graphs from that point onwards. In all experiments, mice in the control group that did not develop tumours bigger than 300 mm³ by the end of the study were discounted. Crizotinib and alvocidib were dissolved in 5% DMSO, 40% PEG300 and 55% sterile PBS, and the same mix was used as vehicle control. Crizotinib and alvocidib were administered by oral gavage daily (n = 8).

**IHC**

Tumours in formalin were embedded in paraffin blocks, and different slices were obtained. Slides were incubated with an anti-cleaved caspase-3 antibody (Cell Signaling #9661) at 1/100 dilution and anti-Ki67 (Cell Signaling #12206) at 1/100 dilution. For the H3122 experiment, the tumour size of the control group and the gavage group were combined in the graph to facilitate comparison with crizotinib. For the CrizR1 experiment, measurements shown are 3 days before sacrifice.

**Quantification**

One section per tumour was imaged at 20×, and the number of stain-positive cells was quantified in 5 random fields (one field contains approximately 1,600 cells). The mean number of positive cells was then plotted.

**RNA isolation**

RNA was isolated using TRIzol® Reagent (Ambion), according to the manufacturer’s protocol.

**RNA profiling**

**RNA-sequencing**

*Poly-A*: Poly-A libraries were prepared with a SureSelect PolyA kit (Agilent). RNA-seq reads were quality checked and aligned to the human genome assembly (GRCh37/hg19). Differential expression (DE) was evaluated using the DESeq2 package.

**ChIP-seq**

CrizR1 cells (100 × 10⁶ per condition) were treated with DMSO, 200 nM alvocidib or 100 nM THZ1 for 6 h. Then, chromatin was isolated according to the published protocol (Nelson et al, 2006) using 10 μg of total RNA polymerase II antibody (Diagenode, #C15200004). Then, purified chromatin was used as input to generate PCR-amplified libraries using the Diagenode Microplex kit according to the manufacturer’s instructions. The library was sequenced on a Nextseq500 instrument (Illumina) using paired-end sequencing at a sequencing depth of 60–80 million reads per sample. Afterwards, the quality of the sequenced reads was assessed by the FastQC (Babraham Institute 2010)/fastq-screen (Babraham Institute 2011) output supplied by the CRUK computational biology facility. Reads were filtered using Trimomatic v0.36 ( Bolger et al , 2014), to remove any remaining adapter sequences, poor quality 5’ ends of reads or reads shorter than 35 nucleotides. Reads were then mapped to the human genome (UCSC GRCh38/hg38 analysis set) using Bowtie2 v2.3.0 (Langmead & Salzberg, 2012). Mapped reads were filtered to retain concordant read pairs with a mapping quality of at least 30, using samtools v1.9 ( Li et al , 2009 The Sequence Alignment/Map format and SAMtools). The peaks were called by the use of MACS2 v2.1.2 (Zhang et al, 2008) with the default parameters. Only binding regions with a Qvalue of < 0.05 were considered. Differential binding analysis was performed using diffReps v1.55.6 (Shen et al, 2013) using the midpoint coordinate of the filtered mapped paired-reads, with fragment size set to 0. RnaChipIntegrator https://github.com/fls-bioinformatics-core/RNAChipintegrator was used to identify the closest gene within 100 K of each peak; the distance being calculated between the closest edge of the summit region and the TSS of each gene.

**RT-qPCR**

Total RNA was extracted using TRIzol. For gene-specific qPCR, 200 ng of total RNA were used as input with the Verso cDNA synthesis kit (Thermo Fisher Scientific) according to the manufacturer’s protocol. Then, 1 μl cDNA from each reaction was amplified with the FS Universal SYBR Green Master Rox master mix (Roche). The reaction was run on a LightCycler 96 instrument (Roche) and normalized for relative expression using either ACTB (β-actin)or GAPDH as housekeeping genes. All the primers used were custom-designed and can be found in Table EV1.

**Proliferation assay**

3,000–5,000 cells were plated in 96-well plates and cell proliferation was assessed by adding 20 μl/well of the CellTiter 96® Aqueous Non-Radioactive Cell Proliferation reagent (Promega). Absorbance was recorded at 490 nm using a SpectraMax plate reader. Absorbance was normalized to the control and was fitted using a nonlinear regression curve (Prism 7, GraphPad).

**Statistical analysis**

All statistics and graphs were generated using Prism 7 (GraphPad). Plotted graphs show mean ± SD from 3 biological replicates for all
For RNA-seq analysis, the resulting P-values were adjusted using the Benjamini and Hochberg approach. Genes with an adjusted P-value determined to be $P < 0.05$ (FDR $< 0.05$) by DESeq2 and that had a fold change value $\geq 2$ ($\log_2$ fold change $\geq 0.55$) between two groups were considered to be differentially expressed.

**Western blotting**

Protein extracts were isolated using a RIPA buffer (Sigma Aldrich) and quantified with the use of the BCA-pierce assay (Thermo Fisher). 30–50 µg of proteins were combined with a Novex™ Tris-Glycine SDS Sample Buffer (Invitrogen) and NuPAGE™ Sample Reducing Agent (10×) (Invitrogen). Samples were then heated at 70°C for 10 min. Afterwards, samples were loaded to either 4–12% or 3–8% NuPage gels (Invitrogen) and run with NuPAGE™ MOPS SDS or NuPAGE™ Tris-Acetate SDS Running Buffer (Invitrogen). Proteins were then transferred to a PVDF membrane (Immobilon) and blocked in 5% non-fat dry milk. Membranes were then incubated O/N at 4°C with the indicated antibodies. Membranes were then incubated with secondary HRP-conjugated antibodies (Amersham) and developed using a WesternBright ECL Spray (Advansta). Chemiluminescence was recorded in a Bio-Rad Chemidoc instrument. The antibodies used can be found in Table EV1. For the apoptotic array, the assay was performed according to the manufacturer’s instructions (Abcam).

**Data availability**

The data sets produced in this study are available in the following databases: RNA-seq data: Array Express repository E-MTAB-8590 (https://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-8590); Chip-Seq data: Array Express repository E-MTAB-8380 (https://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-8380).

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