REVIEW ARTICLE

PHARMACOLOGY

Bordea et al: An insight into lung cancer: ALK TKI resistance

An insight into lung cancer: a comprehensive review exploring ALK TKI and mechanisms of resistance

Adela Pătcaș¹, Ana Florica Chiș¹, Claudia Florentina Militaru²,³, Ioana Roxana Bordea⁴*, Ruxandra Rajnoveanu¹, Ovidiu Florin Coza⁵,⁶, Reem Hanna⁷,⁸, Tamaș Tiberiu⁹, Doina Adina Todea¹

¹Department of Medical Sciences, Pneumology, Faculty of Medicine, “Iuliu Hatieganu” University of Medicine and Pharmacy, Cluj Napoca, Romania
²Department of Pharmacology, Toxicology and Clinical Pharmacology, “Iuliu Hatieganu” University of Medicine and Pharmacy, Cluj-Napoca, Romania
³Medisprof Cancer Center, Cluj Napoca, Romania
⁴Department of Oral Rehabilitation, “Iuliu Hatieganu” University of Medicine and Pharmacy, Cluj-Napoca, Romania
⁵Department of Medical Oncology and Radiotherapy, “Iuliu Hatieganu” University of Medicine and Pharmacy, Cluj-Napoca, Romania
⁶Institute of Oncology “Prof.Dr.I.Chiricuta”, Cluj Napoca, Romania
7Department of Surgical Sciences and Integrated Diagnostics, Laser Therapy Centre, University of Genoa, Genoa, Italy

8Department of Oral Surgery, Dental Institute, King’s College Hospital NHS Foundation Trust, London, United Kingdom

9Department of Oral and Maxillofacial Surgery, “Iuliu Hatieganu” University of Medicine and Pharmacy Cluj-Napoca, Cluj Napoca, Romania

#These authors equally contributed

*Corresponding author: Roxana Bordea, Department of Oral Rehabilitation, “Iuliu Hatieganu” University of Medicine and Pharmacy, Cluj-Napoca 400000, Romania

E-mail: roxana.bordea@ymail.com

DOI: https://doi.org/10.17305/bjbms.2021.5859

Submitted: 31 March 2021/Accepted: 05 May 2021
Conflict of interest statement: Authors declare no conflict of interest
Funding: The authors received no financial support for the research and authorship
Licence: © The Author(s) (2021). This work is licensed under a Creative Commons Attribution 4.0 International License
ABSTRACT

Implementation of precision medicine in lung cancer has benefited from intense research in the past years, developing subsequently an improved quality of life and increased overall survival of the patients. Targeted therapy has become one of the most important therapeutic innovations for the non-small cell lung cancer (NSCLC) category with anaplastic lymphoma kinase (ALK) gene rearrangement. The aim of this review is to provide a thorough overview of the main molecules of ALK tyrosine kinase inhibitors (TKI) with their general and particular mechanisms of resistance, the main methods of ALK gene detection, each with advantages and limits and the future perspectives currently under research which try to overcome the mechanisms of resistance. We have used two of the most reliable medical databases EMBASE and PubMed to properly select the latest and the most relevant articles for this topic. Encouraged by the promising results, the clinical practice was enriched by the approval of tyrosine kinase inhibitor molecules, three generations being developed, each one with more powerful agents than the previous ones. Unfortunately, the resistance to TKI eventually occurs and it may be induced by several mechanisms, either known or unknown. Crizotinib was the most intensely studied TKI, becoming the first molecule approved into clinical practice and although four other drugs have been broadly used (alectinib, ceritinib, brigatinib and lorlatinib) it seems that even the most recently developed one remains imperfect due to the resistance mutations that developed. There are two types of resistance generally described for the entire class and for the particular drugs, but half of them remain unknown.

KEYWORDS: NSCLC, anaplastic lymphoma kinase, ALK, tyrosine kinase inhibitors, TKI, resistance mechanisms
INTRODUCTION

Lung cancer has gained a top place in the cancer-related incidence and mortality worldwide. Non-small cell lung cancer which represents almost 80%-85% of the patients is considered a heterogeneous disease, due to the wide spectrum of molecular targets identified which have benefited from personalized therapy in the recent years [1,2]. In order to better select the patients for this type of treatment, a proper method of ALK (anaplastic lymphoma kinase) gene detection must be used according to the diagnosis standards and the main options applied in clinical practice are fluorescence in situ hybridization (FISH), immunohistochemistry (IHC), reverse transcriptase – polymerase chain reaction (RT-PCR), next-generation sequencing (NGS), liquid biopsy and new potential biomarkers such as CTCs (circulating tumour cells), cfDNA (cell-free DNA) and exosomes are being investigated [3]. The therapeutic development in this domain has led to the implementation of three generations of ALK TKI with five molecules approved into clinical practice and two more molecules, such as entrectinib and ensartinib are waiting for clinical approval [4]. The development of the ALK TKI in NSCLC patients, beginning with crizotinib, the first molecule approved and followed by second and third-generation inhibitors (ceritinib, alectinib, brigatinib and lorlatinib) has provided an increased PFS (progression-free survival) and OS (overall survival) in comparison with chemotherapy [5,6]. Unfortunately, despite the initial benefit of ALK TKI, resistance mechanisms have been identified upon progression [7,8]. From the available data, we have discovered that almost half of the mechanisms of resistance remain unknown at this moment, but we have tried to present the recognized mutations and the future perspectives, even though they are under research. In order to properly identify the mechanisms, we have encompassed the main detection methods
implemented into clinical practice or in preclinical data. Besides the particular mutations for each molecule, we have also described the factors which determine secondary mutations for the entire class [9,10]. Regarding the challenges of overcoming resistance, promising results are represented by the combination between ALK and EGFR (epidermal growth factor receptor) TKI, metformin, MYC (avian myelocytomatosis viral oncogene homolog) - inhibitors, HER (human epidermal growth factor receptor) family, mTOR (mammalian target of rapamycin) pathway, anti-angiogenesis factors, etc. Nevertheless, the most awaited results are for the combination between ALK TKI and immunotherapy, which represents the most innovative therapeutic option for non-small cell lung cancer patients [11-14].

MATERIALS AND METHODS
In the present review we have tried to encompass the most relevant and accurate available data from the literature regarding ALK TKI mechanisms of resistance in NSCLC patients. Our working hypothesis is based on describing the mechanisms of resistance for each molecule approved, presenting the advantages and disadvantages of the main detection methods currently used in clinical practice and describing the future possibilities identified or still under research, in order to provide therapeutic benefit. Our process of selection included two of the most reliable databases in the medical field, EMBASE and PubMed, under specified criteria such as 10-years filter, English language and Human species following PRISMA (A Preferred Reporting Items for Systematic Review and Meta-analysis) statement as mentioned in Figure 1, but the final article selection remained subjective [15].
RESULTS

The role of ALK gene rearrangement in NSCLC

ALK gene has an incidence of 3%–7% in patients with NSCLC and although more than 27 variants of ALK fusion proteins have been discovered, the most common partner is EML 4 (echinoderm microtubule - associated protein-like 4) [16,17]. The EML4-ALK fusion gene results from the paracentric inversion of chromosome 2 with at least 15 variants identified, variant 1 (v1) involving exon 13 being the most common, followed by the variant 3a/b (v3a/b) affecting exon 6 and variant 2 involving exon 20 [18,19]. This category of patients with ALK rearrangement has the following clinicopathological characteristics: young age at diagnosis (a median of 50 years old), women gender, non-smokers/light smokers, histology of adenocarcinoma with particular morphologic patterns such as and cribriform and solid signet ring, expression of thyroid transcription factor 1 (TTF-1), tendency to metastasize in pleura or pericardium, frequently with more metastatic sites than other molecular types and predominant central nervous system (CNS) metastases [20-22].

Identifying the main mechanisms of resistance to ALK TKI

Despite the major therapeutic improvement of ALK TKI in NSCLC, disease progression after initial benefit has been described due to the development of resistance mechanisms with clinically progressive disease and a variable range of aggressiveness [23-25]. The mechanisms of resistance can be divided into ”de novo” or acquired depending on the timeline of occurrence and according to the involvement of ALK are classified into ALK-dependent or ALK - independent mechanisms [26,27]. Regarding the ALK dependency, ALK- dependent “on-target” tumours are driven by ALK signalling, while ALK “off-target”
means that the driver mutation and the tumour cells are based on a different mechanism such as by-pass signaling pathways activation, drug efflux mechanisms or histological transition (such as small cell transformation)[28,29]. Secondary resistance can be divided into dominant (ALK intra-kinase domain mutation, increased copy number gain of ALK gene) and non-dominant such as tumour heterogeneity, bypass signalling pathways activation like the epidermal growth factor receptor (EGFR), Kirsten rat sarcoma viral oncogene homologue (KRAS), v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homologue (KIT), met proto- oncogene (MET) and insulin-like growth factor 1 receptor (IGF-1R) as presented in Figure 2 [30,31]. Studies have shown that multiple mechanisms of resistance can occur simultaneously by the identification of epithelial–to- mesenchymal transition (EMT) in ALK kinase domain mutations [31,32]. Also, the presence of TP53 (tumour protein 53) mutations in ALK-rearranged NSCLC defines a category with instability of the chromosomes, conferring a prognostic role and determines pathogenic aberrations which can co-occur [32-34]. Clinical data suggests that the baseline level of TP53 is correlated with worse progression-free survival, a shorter overall survival and a more aggressive disease [35-37]. Also, other genes involved with low frequency were identified such as: BRAF, FGFR2, MET, NRAS and PIK3CA [38,39]. Most of the secondary resistance mutations from ALK tyrosine-kinase domain currently are mainly point mutations such as: the gatekeeper mutation L1196M, G1269A, G1202R [40,41]. Although in non-small cell lung cancer patients personalized therapy was developed using not only using ALK gene, but also EGFR as molecular target, the mechanisms of resistance between these two genes are completely distinct due to different tumour biology including genomic instability and different oncogenic dependency. Also, the TKI implemented have contrasting properties determined by the binding modalities and inhibiting potency of the molecules [42,43]. Among the by-pass
signalling mechanisms which confer resistance to ALK inhibition, the human epidermal growth factor receptor family activation is one the most important identified [43,44]. The identification of EGFR in post-crizotinib resistance, even in the absence of mutations, suggests the activation of this pathway by the paracrine stimuli, such as NRG-1 (neuregulin 1) [44,45].

Despite the development of TKI resistance mechanisms previously described, targeted therapy is considered the main therapeutic approach in ALK-rearranged NSCLC and literature data reports a median survival time of approximately 4 years in metastatic patients, significantly higher in comparison with chemotherapy [46,47].

Exploring ALK TKI and their particularities

The therapeutic implementation of the ALK TKI agents generates a clinical controversy based on the appropriate use, which should be guided by the potency and the CNS (central nervous system) penetration, a frequent site of metastasis in patients with ALK rearrangement [48-51]. The main studies which have led to the approval of these molecules are summarized in Table 1. Another two molecules, ensartinib and entrectinib have been discovered and are currently into clinical trials, but currently they have not gained FDA approval. Ensartinib is a potent ALK inhibitor with high CNS penetration and potential synergistic activity with the mTOR inhibitor rapamycin. Entrectinib is a new generation inhibitor of multiple targets, such as NTRK1 (neurotrophic tyrosine kinase, receptor type 1), NTRK2 (neurotrophic tyrosine kinase, receptor type 2), NTRK3 (neurotrophic tyrosine kinase, receptor type 3), ROS1 (ROS proto-oncogene 1) and ALK which has been approved in NRK and ROS1 positive NSCLC [52-54]. Among the mechanisms of resistance, there are several point mutations identified for each molecule, which may be common in the same TKI
generation or particularly, as it will be detailed in the following paragraphs and mentioned in Figure 3 [55-58]. Studies have shown that the development of ALK resistance mutations can be induced by the use of multiple sequential lines of TKI [58-60]. After exposure to crizotinib, ALK gene copy number gain has been observed but it was not considered to have a clinical impact and therefore was not reported as resistance mechanism after more potent ALK TKI[61]. After developing resistance to second-generations ALK TKI, literature data has proven that half of the mutations are acquired, out of which G1202R is the most frequent [62,63]. The concept of progressive multistep genetic complexity was implemented due to the identification of two or more mutations in patients who benefited from ALK TKI molecules of first and second generation[64].

Crizotinib is an oral TKI inhibitor of the first generation TKI with recommended oral dose is of 250 mg twice daily in a 28-days cycle until disease progression or no longer tolerated by the patient and its metabolism involves the CYP3A 4/5 mechanisms, The most common side effects include: hepatotoxicity, interstitial lung disease (pneumonitis), prolongation of QT interval, bradycardia, visual toxicity (including visual loss) and gastrointestinal affection, which require either dose reduction or permanent interruption [65]. Ceritinib is a second-generation ALK TKI with a therapeutic dose of 450 mg orally once daily with a mainly hepatic metabolism through the enzyme complex CYP3A. Apart from the common adverse effects mentioned for the first-generation TKI, subsequently to the treatment with Ceritinib the following toxicities have been identified: hyperglycemia, pancreatitis and embryo-fetal toxicity [66]. Alectinib is recommended in a twice-daily dose of 600 mg and its particular side effects include renal impairment, severe myalgia and creatine phosphokinase (CPK) elevation [67]. Brigatinib is approved with a dose of 90 mg once daily for the first 7 days of the treatment, increasing afterwards at 180 mg once daily. It presents the common side effects
of the entire class but also hypertension [68]. Lorlatinib is a third-generation TKI that is metabolized mainly by CYP3A4 and UGT1A4 pathways recommended in a dose of 100 mg once daily. The adverse effects of this class are different from the previous described and include central nervous system side effects (such as seizures, hallucinations, changes in cognitive function), hyperlipidaemia and atrioventricular block [69].

**Describing mechanisms of resistance in the first, second and third generation of ALK TKI**

Crizotinib was the first oral TKI molecule approved in 2011 by the FDA for metastatic NSCLC patients with ALK mutation but almost a third of the patients had developed primary or secondary resistance within 1–2 years [71]. Crizotinib was first implemented to inhibit the c-MET pathway but has also proved important activity against ALK and ROS1 gene [72]. Also, due to the promising results obtained from the clinical trials, crizotinib was approved in November 2013 with the indication of a second therapeutic option for patients with ALK mutation and progressive disease after platinum doublet treatment. About half of the patients developed metastasis in the central nervous system, considered the main or the exclusive site of disease progression, because crizotinib has a decreased capacity to cross the blood-brain barrier [73]. One of the most frequent mutations identified in crizotinib resistance patients was L1196M gatekeeper mutation, analogous to EGFR T790M, which alters the gatekeeper residue at the bottom of the ATP-binding pocket and subsequently inhibits the binding with TKI. In addition, it has been discovered that patients who harbour L1196M mutation tend to have a shorter PFS (progression-free survival) [74]. The G1202R solvent front mutation has been identified in patients treated with first-generation ALK - TKI and determines the alteration of the binding activity of crizotinib [75,76]. Literature data has identified that the most common mutations in crizotinib-resistant patients are the following: L1152R, C1156Y,
F1174C, L1196M, D1203N, C1156Y and G1269A as well as EGFR activation working as the bypass pathway [77,78]. Other mechanisms of resistance to crizotinib have been identified: ALK gene amplification and copy number gain, new mutations such as 1151Tins and point mutation S1206Y in the solvent front of the kinase domain [79,80]. Intrinsic factors like the concomitant KRAS (Kirsten rat sarcoma 2 viral oncogene homolog) mutations, MYC amplification and the Bim deletion polymorphism could determine primary resistance to Crizotinib [80,81]. In the acquired resistance, increased ErbB signalling through phosphorylation has been involved as well as the activation of the IGFR-1R pathway, EMT and autophagy. The extended research in this domain has determined the identification of new mutation genes, such as CSMD3, CDKN2, MAGI1, CREBBP, DOT1L, PBX1 and PRKDC [82,83]. Potential mechanisms of resistance to crizotinib are represented by the activation of EGFR through the overexpression of the cKIT gene determined by its linkage to stem cell factor (SCF) [83]. Activation of the PI3K/AKT/mTOR pathway has also been recognized as a resistance mechanism to crizotinib, possibly through increased autophagy of the ALK receptor. Synergy of crizotinib and a mTOR inhibitor in terms of inhibitory activity has been demonstrated in a cell line [84]. Therefore, due to the identification of crizotinib resistance, further ALK TKI molecules of second and third - generation have been implemented for daily therapeutic approach [85].

Ceritinib was the initial ALK TKI molecule of the second-generation class approved to overcome resistance to crizotinib [86]. In 2014, Ceritinib was indicated ALK-positive patients with disease progression on or intolerance to crizotinib and in 2017 was indicated as first-line therapeutic setting. The mechanism of action is represented by the inhibition of the autophosphorylation of ALK gene and the molecular targets include IGF-1 R, InsR and ROS1 and has an activity of 20 times higher against crizotinib - resistant tumour cell lines [87].
Ceritinib inhibits the most common ALK mutations, such as L1196 M, G1269A, I1171T and S1206Y, which determine resistance to crizotinib [86,87]. In patients who progressed during ceritinib treatment, secondary mutations were detected such as G1202R, F1174 C/L, C1156Y, G1202del, L1196M. The F1174L mutation which can be resistant to ceritinib, but sensitive to alectinib and the I1171 mutation sensitive to ceritinib, but resistant to alectinib has been discovered [88]. In addition, the F1174C/D1203N compound mutations found in patients treated with crizotinib and ceritinib have conferred resistance to these molecules and also to alectinib, brigatinib, and lorlatinib [89]. A combination between a MEK inhibitor and ALK TKI was developed due to ceritinib resistance identified by the MEK activating mutation (MAP2K1-K57N) [90,91].

Alectinib is a molecule from the second generation, which has proved antitumor effect on NSCLC patients with ALK rearrangement who have benefited previously from crizotinib which was approved in December 2015 and subsequently in November 2017 was indicated as first-line setting of patients with advanced ALK-positive NSCLC [92]. Due to its chemical structure it has proved efficient for patients with crizotinib-resistant ALK mutations such as L1196M, F1174L C1156Y, G1269A, 1151Tins, and L1152R but not G1202R [91]. Potential mechanisms of resistance to alectinib include the activation of EGFR signalling pathway, increased activation of IGF1R, HER3 overexpression and P2Y receptors (P2Y1 and P2Y2) which increase the levels of activated protein kinase C (PKC) [93]. At the relapse, among the acquired resistance mutations, G1202R, I1171T/S and V1180L and L1196M were identified [94]. Another mechanism involved in the acquired resistance to alectinib was activation of the hepatocyte growth factor (HGF)/MET signalling pathway [95]. Recent studies have shown that in vitro inhibition of Src and MET restored the sensitivity to alectinib in patient-derived cell lines which have turned resistant to alectinib by the co-activation of this two
mechanisms [96]. A potential resistance mechanism common for alectinib and crizotinib can be represented by the activation of HER3 pathway and overexpression of NRG1. [97]. Also, human neuromedin U (NMU) gene is identified as a potential candidate which confers alectinib resistance in NSCLC patients, according to the recent studies [98,99].

Brigatinib is a potent molecule from the second-generation of ALK TKI with approval in 2017 for the indication of advanced NSCLC with ALK rearrangement with progressive disease on or intolerance to crizotinib. Furthermore, in 2020 it was approved as first-line treatment for ALK-positive metastatic NSCLC patients [100-102]. Brigatinib also inhibits ROS1 fusions and EGFR mutation (L858R) and has a remarkable activity on the central nervous system [102,103]. According to the clinical data, brigatinib is active against all the 17 known resistance mutations to the ALK gene, including G1202R and L1196M [104,105]. Among the mechanisms of resistance to brigatinib, gene mutations such as D1203, S1206, E1210K + S1206C, E1210K + D1203N have been identified [106]. The molecular structure of brigatinib, which may lead to resistance development, is also influenced by the L1196M, G1269A, F1174L and R1275Q mutations [107,108]. Also, it has been discovered that the mutation G1202R occurs after previous exposure to ceritinib, alectinib andbrigatinib, meaning that lorlatinib is the only efficient therapeutic agent [108,109].

Ensartinib is a novel ALK TKI molecule of the second-generation with improved action on central nervous system metastasis and is a potential option for first-line setting according to the preclinical data [110]. Compared to the other ALK TKI, ensartinib is active against the following mutations: G1123S, L1198F, F1174, C1156Y, L1196M, S1206R, T1151, but less potent against G1202R and G1269A [111]. Upon progressive disease, two mutations have been identified: E1210K and S1206F. Apart from the ALK inhibition, ensartinib is also active
against MET, Axl, ABL, EPHA2, LTK (Leukocyte Receptor Tyrosine Kinase), ROS1 and SLK (STE20 like kinase) [112].

Entrectinib is another second-generation ALK inhibitor candidate, which is able to penetrate the blood–brain barrier exhibiting therefore consistent intracranial activity under clinical research. In addition, apart from the ALK inhibition, entrectinib is also active against TRKA (Tropomyosin receptor kinase A), TRKB (Tropomyosin receptor kinase B), TRKC (Tropomyosin receptor kinase C) and ROS1. The results of the clinical data are awaited, in order to conclude the efficacy of this molecule in ALK TKI setting [113].

Lorlatinib is a molecule of the third-generation approved in 2018 by the FDA in the first-line setting for metastatic NSCLC patients and ALK rearrangement with progressive disease on Crizotinib and other ALK inhibitors [114,115]. Due to its activity, it targets mutations, which determine resistance to the other ALK TKI including G1202R solvent-form mutation, and facilitates CNS penetration, subsequently determining an increased survival rate [116]. After analysing the post-progression samples, the literature data suggests that half of the patients developed compound mutations such as: ALK-G1202R/L1196M, ALK-E1210K/D1203N/G1269A, ALK-I1171N/L1198F [117]. Although it proves efficacy against C1156Y gene, resistant to Crizotinib or Ceritinib, a potential mechanism of resistance is conferred by the co-occurrence of L1198Fmutation [118,119]. More clinical data are awaited because the previous mentioned mutations narrow the therapeutic options, therefore this molecule is under active research.
The main methods of detecting ALK rearrangement and mechanisms of resistance in NSCLC

In order to provide the best therapeutic option, ALK gene rearrangement identification is essential. Several mechanisms of detection have been implemented, each with their advantages and limits, as described in Table 2. Fluorescence in situ hybridization (FISH) testing with the ALK break apart probe kit was the mandatory diagnosis test due to its use as a companion diagnostic tool in the clinical trials of crizotinib [120]. Although it has been considered the gold standard because it provides very good specificity, can be performed in small biopsy sample and it is used to validate and compare other ALK detection methods, FISH has disadvantages such as: signal instability, expensiveness, difficulty in scoring, the long turnaround time and the need for specific fluorescence microscopy and particular expertise to validate the results. Also, FISH can only determine if there is a break in the ALK locus but does not have the ability to distinguish between the ALK fusion partners [121]. A modified FISH assay with filtration enrichment, FA-FISH (filter-adapted FISH) was implemented in order to identify ALK rearrangements on the circulating tumour cells (CTC) but specific technological requirements are necessary for both CTC isolation and analysis, but due to the precise results obtained it may become a non-invasive predictive biomarker [122].

Immunohistochemistry has excellent sensitivity, with the advantage of being less expensive, following a simplified and rapid method than FISH with the utility as a screening test for diagnosis of NSCLC patients with ALK rearrangement, but it has poor sensitivity and it cannot identify the ALK fusion partner [123]. RT-PCR (Reverse transcription polymerase chain reaction) and NGS (next generation sequencing) technologies allow the analysis of ALK gene rearrangement and its fusion partner. RT-PCR uses specific primers for identified
ALK fusion partners, but a disadvantage is that several tests should be performed prior to identification of the ALK fusion partner variant and the unknown molecules could not be detected [124]. Also, high-quality samples are needed which can determine either false-negative or positive results. RT-PCR was commonly used with screening purpose because of the high sensitivity and the applicability to biofluids, but it requires assay optimization for each new fusion partner and high-quality RNA (ribonucleic acid) [125]. NGS has the ability of identifying ALK mutations, copy number gain and provide identification of numerous oncogenic mutations at the same time in one assay with high sensitivity and reproducibility. Currently, NGS has proved able to detect ALK fusion genes by sequencing the intron between exons 19 and 20, where they usually occur, but confirmation is required in order to gain approval for clinical application [126]. Tumour tissue samples used for the previous described testing methods are obtained from bronchoscopy or percutaneous lung biopsy and present several limitations including: the invasiveness acquisition, which may determine complications or may be insufficient and the tumour heterogeneity. In order to properly identify the mechanisms of resistance, liquid biopsy is considered of great significance due to its potential of detection against tumour heterogeneity and reflects the general particularities of the tumour. Its advantages include a less invasive procedure, which has a simple mechanism of interpretation providing real-time results, and can be repeated at need. [101,102]. Circulating tumour cells (CTC), circulating tumour DNA (ctDNA) and exosomes in body fluids are the main biomarkers which determine real-time resistance and can guide the follow-up treatment. The percentage of mutated CTCs, microRNAs and proteins reflects the resistance mechanism developed by the activation of oncogenic drivers [124,125]. An important discovery was the detection of L1196M gene mutation on circulating tumour cells at an early stage in patients who developed crizotinib secondary resistance [127]. Despite the
low concentration in peripheral blood, CTC are ideal for detection, analysis and overcoming tumour heterogeneity due to their distinct origin from the solid tumour or cancer sites. Circulating tumour DNA is defined as tumour tissue-specific DNA fragment released in the blood stream and its level is correlated with tumour progression, being the most frequent biomarker used in ALK - positive NSCLC resistance monitoring [123,124]. Studies have concluded that ctDNA NGS represents a non-invasive method of detecting targetable alterations and characterizing resistance mechanisms upon TKI progression [128]. Several detecting methods of TKI resistance are currently under research, such as exosome miRNA (micro ribonucleic acid) because the concentration of exosomes in peripheral blood is greater than CTCs and it can also be identified in other body fluids, besides serum and plasma [125,126]. In contrast, circulating ALK RNA analysis has proved low sensitivity due to the low blood stability [127]. A common method to detect resistance is the evaluation of tumor tissue before and after exposure to TKI by sequencing analysis. Also, upon progression, an attempt to provide tissue sample or liquid biopsy is indicated [101,125]. On the other hand, studies reveal that plasma monitoring in ALK - rearranged NSCLC is feasible and could avoid re-biopsy from the tissue and monitoring plasmatic mutation levels could be used as a response parameter [128,129].

DISCUSSION

The actual research in this domain explores the options of overcoming TKI resistance by providing future therapeutic directions. Preclinical studies have identified that inhibitors against HSP90 (heat shock protein 90), the molecular protein responsible for ALK fusion stability, such as 17-AAG, 17-DMAG and ganetespib have antitumor efficacy. Furthermore, HSP90 inhibitors have proved superiority against wild type EML4-ALK mutation, L1196M and F1174L gene mutations [130]. Ganetespib, which is also active on ROS1
rearrangements and RET kinases, has been evaluated individually and in combination with Crizotinib and other ALK TKI to overcome crizotinib resistance in vitro and in vivo [131]. Literature data suggests the use of ALK-TKI ceritinib and the EGFR-TKI afatinib for patients who have acquired ALK TKI resistance through EGFR pathway activation, because afatinib restored the sensitivity of H3122-CER cells and subsequently increased apoptosis and the antitumor activity [124,132]. Studies have identified that crizotinib is active not only against ALK, but also against MET, AXL and MST1R (Macrophage Stimulating 1 Protein Receptor) genes and it may target other TKI which are potential drivers of resistance to ALK inhibition in H3122 cells [133]. Another therapeutic option under research is represented by Metformin, an oral antidiabetic drug which reverses resistance to crizotinib through the inhibition of the IGF-1R signalling pathway [124,131]. At patients with crizotinib resistance, EMT is associated with decreased expression of miR-200c and increased expression of ZEB1 (Zinc Finger E-Box Binding Homeobox 1), therefore it determines cross-resistance to new-generation ALK inhibitors alectinib, ceritinib, and lorlatinib. Also, in patients with coexistence of resistance mutations and EMT, pretreatment with histone deacetylase (HDAC) inhibitor quisinostat has proved efficacy [126,134]. ALK and vascular endothelial growth factor receptor (VEGF-R) share reciprocal downstream signalling, therefore simultaneous inhibition of ALK gene and VEGFR by the linkage between alectinib with afatinib can provide overcoming of ALK resistance [135]. Another combination therapy undergoing preclinical studies is between alectinib and bevacizumab in patients with NSCLC and ALK rearrangement which have central nervous system involvement with at least targetable lesion, because bevacizumab reshares tumour vasculature and subsequently adjusts the systemic and intracranial drug activity [127,135]. In the recent studies, MYC proto-oncogene amplification has been associated with developing primary resistance to
crizotinib, therefore a combination of MYC-directed inhibition treatment such as CDK4/6 inhibitors may provide an alternative option. In NSCLC patients with ALK rearrangement and TP-53 mutation, MYC overexpression determined a potential MYC-dependent resistance mechanism [136,137]. For patients with crizotinib resistance due to the presence of C1156Y mutation, methionine residue (M-1199) may represent a targetable approach [138]. In vitro studies have developed a structural similarity of Alectinib (JH-VIII-157-02) which is active against many resistance mutations, including G1202R and has important CNS activity [139]. Another study concluded that activated HER family signalling and mediated EGFR activation by amphiregulin protein are mechanisms which determine resistance to ALK inhibitors, suggesting that the resistance mechanism is potentially reversible [124,138]. Another potential mechanism of resistance to ALK inhibition is represented by the P2Y purinergic receptors, which co-stimulate and activate the EGFR/MAPK signaling pathway and increase the activation signal through the PKC (protein kinase C) activation [20]. In addition, IGF-1R has a synergistic effect on ALK signalling, due to its protein IRS-1 (Insulin receptor substrate 1) which inhibits the IGFR1/IRS1 pathway and increases the sensibility of the tumor cells to ALK targeting [29]. Preclinical data exhibit the synergistic effect of saracatinib (a dual Src and Bcr-Abl inhibitor) on ALK inhibition through its mechanism of phosphorylation which determines resistance when SRC kinase is upregulated. Actually, the mechanism of phosphorylation of SRC substrates was expanded after both first and second generation TKI [139,140]. Regarding the molecular changes, a tumor suppressor gene NF2 (neurofibromin 2), which activates the bypass signaling of PI3K-AKT-mTOR pathway was identified in mutant forms at the progression with crizotinib and determined a sensibilization at the inhibitory effect of mTOR, providing possible clinical implications [117]. Another option for overcoming ALK-TKI resistance is represented by the YAP (Yes-associated
protein), a downstream effector of the Hippo pathway, due to its overexpression, which inhibits the therapeutic response to alectinib, as suggested by the preclinical data [141,142].

Several phase I and II studies are currently studying the potential benefit and tolerability of the combination between ALK TKI and immune checkpoint inhibitors in lung cancer, such as ceritinib with nivolumab, alectinib with cobimetinib, lorlatinib with crizotinib and binimetinib, ceritinib with trametinib, alectinib with cobimetinib, brigatinib with binimetinib and the results are highly awaited [143,144]. Research data has revealed that the expression of PD-L1 is five times higher in patients with ALK gene rearrangement, therefore promising results could highlight the efficacy of anti PD-1/PD-L1 antibodies in this category of patients. Silibinin treatment inhibited the upregulation of the programmed death ligand 1(PD-L1) and EMT regulators in crizotinib - resistance cells, suggesting a potential improvement of ALK TKI resistant NSCLC patients with silibinin - based drugs [145]. Also, combination therapies such as inhibitors of ALK and MAPK signaling pathways, ceritinib + CDK4/6 inhibitor, ceritinib + mTOR inhibitor, alectinib + anti-angiogenesis inhibitor, have potential mechanisms of overcoming resistance [143,144,145,146].

CONCLUSION

We consider that identifying and overcoming mechanisms of resistance to ALK- rearranged TKI represents a promising research domain, which still requires continuous efforts in order to discover the remaining questions. In our opinion, this topic represents one of the most challenging of the oncological research with unmet clinical needs so far.
REFERENCES


65. https://www.accessdata.fda.gov/drugsatfda_docs/label/2012/202570s002lbl.pdf


68. https://www.accessdata.fda.gov/drugsatfda_docs/label/2020/208772s008lbl.pdf


128. Friedlaender A, Banna G, Patel S, Adeo A. Diagnosis and treatment of ALK aberrations
in metastatic NSCLC. Curr Treat Options Oncol 2019; 20:79.

129. Wynes MW, Sholl LM, Dietel M, Schuuring E, Tsao MS, Yatabe Y et al. An
international interpretation study using the ALK IHC antibody D5F3 and a sensitive
detection kit demonstrates high concordance between ALK IHC and ALK FISH and between

inhibition of the molecular chaperone Hsp90 overcomes ALK inhibitor resistance in non-

sequencing analysis of ALK kinase domain identifies resistance mutations in relapsed

EGFR Bypass Signal-Induced Acquired Resistance to ALK Tyrosine Kinase Inhibitors in

133. Bordi P, Tiseo M, Rofi E, Petrini I, Restante G, Danesi R et al. Detection of ALK and
KRAS Mutations in Circulating Tumor DNA of Patients With Advanced ALK- Positive
NSCLC With Disease Progression During Crizotinib Treatment. Clin Lung Cancer 2017;
6:692-697.


**Figure 1.** Description of the literature identification process (PRISMA flowchart) [15]
**Figure 2.** Describing the most common mechanisms of resistance to ALK TKI divided into dominant and non-dominant category

**Table 1.** A summary description of the main studies and results of the ALK TKI in patients with ALK positive NSCLC; mPFS= median progression-free survival, ORR= overall response rate, mDor= median duration of response, BOR= best overall response rate [70]

<table>
<thead>
<tr>
<th>ALK generation</th>
<th>TKI</th>
<th>Drug name</th>
<th>Summary study description</th>
<th>Results</th>
</tr>
</thead>
<tbody>
<tr>
<td>First generation</td>
<td>Crizotinib</td>
<td>PROFILE 1001</td>
<td>Phase I single-arm trial; 149 patients (2008-2011)</td>
<td>ORR= 61%</td>
</tr>
<tr>
<td></td>
<td></td>
<td>PROFILE 1005</td>
<td>Phase II single-arm trial; 1069 patients (2010-2014)</td>
<td>ORR=59.8%</td>
</tr>
<tr>
<td></td>
<td></td>
<td>PROFILE 1014</td>
<td>Open-label phase III trial; 343 patients (2011-2016)</td>
<td>mPFS=8.1 months</td>
</tr>
<tr>
<td></td>
<td></td>
<td>PROFILE 1007</td>
<td>Open-label phase III trial; 347 patients (2009-2016)</td>
<td>mDor=45.6 weeks, ORR=74%, mPFS=10.9 months</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>ORR=75%</td>
</tr>
<tr>
<td>Generation</td>
<td>Drug Name</td>
<td>Study/Phase</td>
<td>Patients</td>
<td>Duration</td>
</tr>
<tr>
<td>------------</td>
<td>-----------</td>
<td>-------------</td>
<td>----------</td>
<td>----------</td>
</tr>
<tr>
<td>Second</td>
<td>Ceritinib (LDK378)</td>
<td>ASCEND-2</td>
<td>Phase II single arm open-label trial; 140 patients (2012-2016)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>ASCEND-5</td>
<td>Open-label randomised controlled phase III trial; 231 patients (2013-2015)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>ASCEND-4</td>
<td>Open-label randomised controlled phase III trial; 376 patients (2013-2015)</td>
<td></td>
</tr>
<tr>
<td>Second</td>
<td>Alectinib (CH5424802/RO5424802)</td>
<td>J-ALEX</td>
<td>Open-label randomised phase III trial; 207 patients (2013-2015)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>ALEX</td>
<td>Open-label multicentre randomised phase III trial; 303 patients (2014-2017)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>ALESIA</td>
<td>Open-label multicentre randomised phase III trial; 187 participants (2016-2019)</td>
<td></td>
</tr>
<tr>
<td>Second</td>
<td>Brigatinib (AP26113)</td>
<td>NCT01449461</td>
<td>Single arm open-label phase I/II trial; 137 patients (2011-2014)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>NCT02094573</td>
<td>Single arm open-label phase I/II trial; 222 patients (2014-2016)</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>ALTA-1 L</td>
<td>Open-label multicentre phase III trial; 275 patients (2016-2020)</td>
<td></td>
</tr>
<tr>
<td>Third</td>
<td>Ensartinib (X-396)</td>
<td>eXalt3</td>
<td>Open-label randomised phase III multicenter trial; 290 participants (2016-2021)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Lorlatinib (PF-06463922)</td>
<td>NCT01970865</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Figure 3. The most common ALK-dependent resistance mutations associated with therapeutic resistance to ALK TKI. Each generation of ALK TKI is presented in the scheme with the approved drug and the main point mutations associated with resistance and different colors were used in order to highlight these point mutations.
Table 2. The main methods used to identify ALK mutation and mechanism of resistance described according to their main advantages and limitations

<table>
<thead>
<tr>
<th>Method of detection</th>
<th>Advantages</th>
<th>Limitations</th>
</tr>
</thead>
<tbody>
<tr>
<td>FISH (gold standard)</td>
<td>ALK break locus identification&lt;br&gt;High specificity&lt;br&gt;Automated&lt;br&gt;Small biopsy samples can be used</td>
<td>Expensive&lt;br&gt;Specific expertise and equipment requirement&lt;br&gt;ALK fusion partners lack of detection</td>
</tr>
<tr>
<td>FA-FISH</td>
<td>ALK rearrangement identification on CTCs</td>
<td>Sensitivity of the filtration system&lt;br&gt;Precise technological requirements</td>
</tr>
<tr>
<td>IHC</td>
<td>High sensitivity&lt;br&gt;Faster&lt;br&gt;Cheaper&lt;br&gt;Small biopsy samples can be used&lt;br&gt;Screening test utility</td>
<td>ALK fusion partners lack of detection&lt;br&gt;Moderate specificity</td>
</tr>
<tr>
<td>RT-PCR</td>
<td>ALK rearrangement + fusion partners identification&lt;br&gt;High sensitivity&lt;br&gt;Biofluids samples can be used</td>
<td>Unknown ALK fusion partners lack of detection&lt;br&gt;High-quality RNA requirement</td>
</tr>
<tr>
<td>NGS</td>
<td>ALK mutation + copy number gain detection&lt;br&gt;Simultaneous multiple oncogenic mutations tested</td>
<td>Complex data analysis and interpretation&lt;br&gt;Expensive&lt;br&gt;Duration of result validation</td>
</tr>
<tr>
<td>Liquid biopsy</td>
<td>Minimally invasive&lt;br&gt;Repeatability</td>
<td>High costs&lt;br&gt;Need for standardization</td>
</tr>
<tr>
<td>Real time results</td>
<td>Technical requirements</td>
<td></td>
</tr>
<tr>
<td>-------------------</td>
<td>------------------------</td>
<td></td>
</tr>
</tbody>
</table>