

INSIGHT INTO THE TARGETS AND DRUG DEVELOPMENT AGAINST LUNG CANCER

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INTRODUCTION

Lung cancer is the leading cause of death among men and women, which accounts for 350 deaths per day United States in 2022[1]. It is generally subdivided into a small cell (SCLC) and non-small cell lung cancer (NSCLC) types. The absence of sensitive tests for early diagnosis of lung cancer and ineffective treatment regimens for locally and advanced metastatic disease is the root cause of increased lung cancer prevalence[2, 3].With the broad endeavors for tobacco awareness education, development of imaging, and consolidated treatment modalities, it was observed a 5 year endurance pace of lung cancer improved by 12% (in 1977) to 16% (in 2007) [1]. Although lung cancer is diagnosed at an early stage, then complete resection might help improve 5-year survival by 67%[4]. Thus, we can conclude that early diagnosis of lung cancer disease by sensitive screening test may be used as a crucial strategy to improve the prognosis of affected lung cancer patients and reduce mortality incidence[5]. Smoking causes more than 80% of cancers in the Western world, and advances in smoking cessation have reduced morbidity and mortality. Continuing to smoke, with other risks such as occupational exposure to asbestos and combustible gases, as well as environmental exposure to arsenic and air pollution, remains important in countries where it is created. Cancer is divided into small cell lung cancer (SCLC) and non-small cell lung cancer (NSCLC) based on cell of origin, and these are further divided. According to the 2015 World Health Organization classification, the most common types of lung cancer include adenocarcinoma (adenocarcinoma), squamous cell carcinoma (SCC) and cell carcinoma (SCLC), neuroendocrine carcinomas such as large cell neuroendocrine carcinoma (LCNEC), and carcinoid [6]. Carcinoid tumors are tumors of well-differentiated cells of neuroendocrine cells (Kurczycki cells), whereas small carcinoid tumors also originate from poorly differentiated cells and cause rapid metastasis, poor response to treatment, and poor

prognosis. Squamous and small cell carcinomas are more likely to be associated with moderate and smoking history, especially for men. Adenocarcinomas are more common in women and nonsmokers, adenocarcinomas are of peripheral origin, and the discovery of driver mutations such as epidermal growth factor receptor (EGFR), anaplastic lymphoma kinase (ALK), BRAF and ROS1 is positive. Small molecule inhibitors of receptor tyrosine kinases target these changes in combination with anti-inflammatory agents such as programmed cell death protein 1 (PD-1) and cytotoxic T-lymphocyte-associated protein 4 (CTLA-4) inhibitors. recent years. Modify or add chemotherapy for eligible patients [7].

Screening of Lung Cancer

Several useful screening tools are exploited for early detection of lung cancer patients, including chest X-ray (CXR) or computed tomography (CT) employed with or without sputum sampling, LDCT, circulating DNA and RNA, serum biomarkers, CTC, exosomal microRNA will be reviewed further.

CXR

In the early 1980s, numerous randomized control trials have been performed using plain CXR and sputum cytology at Mayo clinic. In the randomized trial of high-risk patients, 9211 contributors were selected from 10,933, aged over 45 to CXR and sputum cytology assigned as the control group versus repeated CXR and sputum cytology analysis for a span of 6 years. Studies suggest 206 cases were diagnosed with lung cancer, and 160 cases were in the control group with significantly improved screening for early diagnosis and 5- year survival of lung cancer patients. Although statistically, studies do not demonstrate disease-specific mortality

difference among the two studied groups from lung cancer, this remains in the case with the follow-up extended to over 20 years[8–12].

The MSKLP and JHLP is a randomized trial of participants aged more than 40 years was done annually where analysis of CXR in the presence (screening group) or absence (control group) of sputum cytology was checked every four months. In the MSKLP study, 10,040 participants were enrolled, and 144 cases were diagnosed in both groups, but no difference was observed in overall survival, stage distribution, and disease-specific mortality amongst the two groups [8, 9] [13, 14]. In the JHLP study, 10,382 participants and around 194 cases with affected lung cancer were reported in the screening group, whereas 202 were in the control group. Similar to the MSKLP trial, the JHLP study did not show any difference in overall survival or disease-specific mortality amongst the two groups [15–17]. Two studies were done at Johns Hopkins and Memorial Sloan-Kettering cancer centers that involved 10,000 participants each, compared plain CXR in the presence and absence of sputum cytology. In patients who developed lung cancer accomplices with dual screening, nearly 20% were diagnosed by cytology alone (most probably early-stage squamous cell carcinomas). However, there seems to no difference in mortality by adding cytology screening [14, 17].

Low Dose CT Screening

CT is more effective than CXR as it offers a more detailed image of the chest and is more helpful in diagnosing cancer. Although, it is mostly accepted that the radiation dose of LDCT, which is approximately 1000 times greater than CXR, is too high to assist the early diagnosis of lung cancer to exceed radiation exposure danger. Hence, until CT was approved at lower radiation doses, there was a reestablished appetite for lung cancer screening. LDCT generally has 22% of effective radiation dose when compared to standard CT. LDCT screening reflects the risk of

radiation prompting cancer, which was recently estimated by a Milan study that screened 4 per 10,000 patients with a radiation dose of follow up PET CTs for patients with a positive LDCT scan (carrying high radiation doses). Adjusting this risk against the advantages of screening, the authors related to this study suggested that LDCT can be viewed as safe. However, alternative protocols have been suggested to reduce the usage of PET CTs in the screening tool to mitigate the risks of radiation exposure.

Selecting the Target Population

Screening of lung cancer needs to target those who are likely to at high risk of lung cancer. As such, screening of never smokers was found to be ineffective.

Bronchoscopy

Bronchoscopy is the widely used diagnostic tool, firstly performed by Gustav Killian of Freiburg, Germany, in 1887[18], employing endobronchial ultrasound (nodal staging of the lung cancer) [19, 20]. Bronchoscopy is commonly used for indicating tissue sampling and determining the degree of lung cancer [21]. Several diagnostic accessories can be introduced by the working channel of the flexible bronchoscope. These accessories include brushes, biopsy forceps, needles, and an immense role in diagnosing and staging lung cancers. Their combined effect has significantly improved in obtaining pulmonary biopsies, specifically of ever-smaller lesions. Computed tomography (CT) has emerged as the current cornerstones of imaging techniques [22]. Autofluorescence bronchoscopy (AFB) profited by perceiving that the emission spectrum of the bronchial mucosa under blue light fluctuates when dysplastic or carcinomatous lesions develop[23, 24].

Liquid Biopsies

Liquid biopsies or blood-borne biomarkers is gaining much attention for monitoring the advanced stage lung cancers. Liquid biopsies include circulating proteins, circulating nucleic acid, or circulating tumor cells (CTCs). The limitation lies in its sensitivity and specificity for the early diagnosis of lung cancer[25].

Circulating miRNAs in Lung Cancer Diagnosis

MicroRNAs (miRNAs) are important regulators of gene expression, acting through transcriptional repression or degradation of mRNA targets. Changes in miRNA expression have been implicated in the pathogenesis of many cancers [26]. An example of this includes let7 miRNA, which is downregulated in most lung cancer tissues and upregulated in suppressed lung cancer cell lines [27]. Studies have shown that exosomes produced by cancer cells [28] increase the long-term guidance time and prepare them for metastatic disease, which is a good scientific discipline. The power of miRNA profiling has been fully exploited to improve the performance of lung cancer diagnosis. Boeri *et al.* [29] tested miRNA expression in plasma of patients in LDCT lung examination to differentiate miRNAs before lung cancer development and prognosis [30] for identifying differentially expressed miRNAs before the development and diagnosis of lung cancer. The inclusion of miRNAs in early diagnosis appears to be a promising NSCLC diagnostic tool, but it is now important to establish a well-established, independent tool and there is good research to prove it is worth using.

Antibodies in lung cancer detection

It is well-known that the hereditary distortion included within the handle of carcinogenesis leads to distinctive expressions of ‘self-antigens’ either by unseemly expression of tissue-specific proteins (neo-antigens) the items of non-synonymous quality mutations[31]. These tumor

antigens are found to be at the interface among the resistant framework and creating cancers, emerging through the dangerous prepare [32], thus offers the likelihood of abuse as an early discovery biomarkers. The affiliation between the resistant framework and cancer is by and large complex, and the writing centers on the parts of cytotoxic T cells [33]. In any case, it has long been anticipated that the humoral safe framework may be dysregulated, coming about in autoantibodies that can be related with biomarker revelation [34]. Several investigations uncover the affiliation of antibodies with the occurrence of lung cancer. The primary was p53 antibodies, which exist in around 12% of lung cancer patients [35].]. Certainly, the capacity that those may need to hold ended up underscored by utilizing the rise of p53 antibodies some time recently radiologically self evident lung cancers [36] related with lung cancer, which may constrain its utility in huge screening programs.

ctDNA in lung cancer detection

DNA is thought to enter the plasma passively through cell death (apoptosis or necrosis) or its release from living cells. In cancer patients, some cell-free DNA originates from the tumor and produces fragmented tumor DNA (ctDNA) [36]. The efficacy of ctDNA in lung cancer has been confirmed in NSCLC studies, where mutations have been identified and a library has been created to identify mutations associated with NSCLC. In the validation cohorts of healthy controls and NSCLC patients, sensitivity and specificity reached approximately 85% and 96%, respectively. ctDNA is detectable in all advanced NSCLC cases, but only in 50% of early cases [37]. Total ctDNA was confirmed by sequencing the human telomerase (hTERT) gene. Connectivity levels were higher in NSCLC patients compared to gender/age/smoking matched controls using this method [38]. Recent advances in ctDNA therapy in personalized ctDNA assays based on biopsy-derived genomic landscapes to monitor patient response and hopefully

prevent treatment and tumor development [39]. Mutations such as p53 can be used in lung cancer; but they are also seen in non-cancer smokers. [40]. In addition, new evidence is emerging of genetic mosaicism in healthy tissues, including mutations in genes that play an important role in cancer [41]. While candidate gene analysis using droplet digital PCR-based techniques is better understood, overall genetic variation will provide more insight into the presence of tumor cancer due to the need for next-generation sequencing.

Circulating tumor cells in lung cancer detection

As cancer grows and progresses, cell subpopulations change their phenotype and become motile, invade surrounding tissue and invade blood vessels through multiple layers such as epithelial-mesenchymal transition [42], angiogenic mimicry [43], and cell cooperation [44]. These so-called CTCs are often heterogeneous and are assumed to have many cells responsible for distant metastasis [45]. In the field of cancer, this hypothesis is confirmed by the fact that CTCs produced from SCLC patients are tumorigenic in mice and produce responsive transplants. Treatment has been observed in primary patients [46]. There are many strategies for detecting CTCs [47], and in summary they have an important role in making quantitative and positive biomarkers of cancer. With the help of various CTC detection techniques, it seems that early detection can benefit. Extraction of tumor cells by size (ISET) detected CTCs prior to treatment in approximately 50% of NSCLC patients, compared with 39% in cell line studies. The combination of the two methods resulted in an improvement in 69% of patients [48]. Another study used a ligand-PCR method to quantify CTCs. After immunodepletion of leukocytes and erythrocytes, cells were labeled with oligonucleotide conjugated folate receptor ligand (FOLR1), allowing quantification by real-time PCR. This method was able to detect CTCs in 8 out of 10 stage I/II NSCLC patients, with an overall sensitivity of approximately 82% for the diagnosis of

stage I-IV NSCLC patients [49]. A problem with the use of CTC analysis is the low frequency of CTC in advanced patients compared to the large number of blood cells in the sample. CTC heterogeneity has confounding marker-dependent capture, and not all CTCs are larger than blood cells, causing confusion based on size-based methods. In addition, any CTC enrichment step suffers from cell loss. Newer techniques, including high-throughput single-cell analysis platforms, are better for early detection because all cells in the sample can be easily analyzed using variable markers exchange, and cells can be physically viewed and stored for individual analysis [50].

Sputum analysis

Preliminary findings of lung cancer diagnosis by sputum cytology are not satisfactory. However, there has been interest in studying mucus with cell counting and new molecular techniques. An example of this is the UK multicenter Lung SEARCH study, in which COPD patients were randomly assigned or not assigned to annual sputum cytology/cell count. Patients with positive cytology/cell count included chest CT and AFB [51]. MicroRNAs in sputum were also measured for early detection. A study in squamous cell carcinoma of the lung showed that a panel of three miRNAs (eg, mir-205, mir-210, and mir-708) had a diagnostic sensitivity and specificity of approximately 72% in differentiating squamous patients, respectively. cell carcinoma and 95% from controls. There is also interest in linking DNA mutations with sputum samples for early detection of cancer [52]. Interestingly, a retrospective study correlating sputum samples prior to histological diagnosis of lung adenocarcinoma found that approximately 5 of 11 patients with KRAS-positive tumors had sputum KRAS changes between 1 month and 4 years prior to clinical examination [53].

Exhaled breath analysis

As a non-invasive and easily accessible model for the patient, the exhaled breath holds promise for emergency diagnosis. In respiratory medicine, NICE currently recommends exhaled nitric oxide for the diagnosis of asthma [54]. There are also some interesting studies using exhaled breath to diagnose lung cancer. Perhaps the most interesting is training dogs to distinguish between breast and lung cancer patients by checking for the presence of volatile organic compounds (VOCs) in breath samples collected for cotton wool soaked with silicone oil coated polypropylene. In a double-blind validation cohort, the specificity and sensitivity were both 99% [55]. However, a recent study with a similar design and sample size had a sensitivity of approximately 71% and a specificity of approximately 93% for the diagnosis of the lung cancer condition [56]. Ion mobility spectrometry provides a highly sensitive method for detecting volatile compounds in exhaled breath. Study of cancer patients was easily distinguished from the control group - Cyranose 320 contains a black carbon polymer that changes resistance to VOC adsorption. Comparison of health versus cancer patients produced "small" cancer in education with sensitivity and specificity of 71% and 92%, respectively, in an independent validation cohort [57].

Treatment of lung cancer

Research into the molecular and cellular biology of cancer has uncovered a picture of the pathways and molecules that gradually lead to the development of cells into an entire lung cancer. These studies involve the identification of genetic and "epigenetic" changes in specific molecules that lead to activation of signaling pathways important in carcinogenesis. Some of these "changes" include so-called "oncogenes" and "pain suppressor genes." In the search for "therapeutic targets", "special attention" is required to identify single or multiple genes required for both the "malignant" phenotype and the "survival" of "cancer" cells. These are "generally"

considered as “oncogene addictions” [58]. In lung cancer, commonly activated oncogenes may include MYC, KRAS, MET, CCND1, EGFR/HER1/ERBB1, HER2/ERBB2, EML4-ALK fusion, CDK4, and BCL-2 [59]. These targeted treatments yield longer progression-free survival, high response rates, and prolonged overall survival than the traditional cytotoxic chemotherapies[60–62].

EGFR pathway inhibitors

Some clinicopathological features were associated with frequency and gene amplification of EGFR mutations, including adenocarcinoma histology, female, non-smoker history, and East Asian people. This signature has been shown to have a probability of more than 50% mutation in the EGFR TK domain[63]. While a proportion of NSCLC patients with EGFR mutations may not respond to TKIs, the 'second' TK mutation (ie, T790M) is associated with resistance [64, 65]. Although "EGFR mutant patients" appear to "significantly" respond to "EGFR TKI", "protein" overexpression and EGFR amplification are associated with "survival" after "EGFR TKI" treatment because "Akt" is required for this to occur [66, 67]. Both erlotinib and gefitinib have been tested in "randomized studies" in combination with "cytotoxic chemotherapy" as "first-line" therapy for "metastatic" NSCLC. These studies did not find a "survival benefit" from adding the agent to treatment, although a "retrospective analysis" concluded that "patients who do not smoke may benefit from chemotherapy [68, 69]. Cetuximab ("humanized monoclonal antibody") binds to the "extracellular" domain of EGFR and has been "examined in NSCLC." In addition, cetuximab is "investigated" in combination with "chemoradiotherapy" for "III" NSCLC [70] and in combination with "chemotherapy" in "neoadjuvant therapy" for non-small "resectable" IB-III A level lung cancer [71]. In addition, other drugs targeting the EGFR pathway in clinical

trials include lapatinib (for EGFR and HER2), panitumumab (for EGFR) and HK-272 (for EGFR). and for HER 2) [72].

Angiogenesis inhibitors

Angiogenesis (growth of new blood vessels from existing blood vessels) is essential for tumor growth to provide adequate oxygen and nutrients for tissue proliferation for targeted angiogenesis for cancer therapy [73, 74]. VEGF (vascular endothelial growth factor) is a growth factor that primarily follows "angiogenesis" in "normal" and "neoplastic" cells [75]. The "VEGF" family consists of approximately "six growth factors" (VEGF-A, "VEGF-B", "VEGF-C", "VEGF-D", "VEGF-E" and "placental growth factor" [PlGF]).) and "three receptors" (VEGFR-1)[72] including {Flt-1}, VEGFR-2 [KDR/Flk-1] and VEGFR-3 [Flt-4]). The "VEGF/VEGFR" pathway has often been found to be dysregulated in "cancer" [76], and "VEGF" overexpression is associated with "proliferation" and "poor prognosis" in NSCLC [77–79]. Several "drugs" have been developed and are "currently" being investigated to target the "VEGF/VEGFR" signaling pathway [77–79]. "VEGF" and "VEGFR" are the "best" antibodies studied against "monoclonal" antibodies to TKIs [72].

Bevacizumab (Avastin), a monoclonal antibody [80, 81] generally binds to all subtypes of VEGF-A and has been studied in clinical trials. A recent study has shown that "the addition of bevacizumab to paclitaxel and carboplatin" confers a significant "survival" benefit in the "first-line" treatment of patients with painless NSCLC[81], thus, "bevacizumab" has recently been approved for "non-cancerous brain tumors". VEGFR TKI are small molecules that preferentially bind to the ATP pocket of the VEGFR intracellular domain of tyrosine kinases (TKs), thereby inhibiting the downstream pathway. These compounds are usually associated with other receptor TK's such as EGFR and c-KIT. One of the inhibitors developed, ZD6474 (Zactima), is an oral

"dual kinase inhibitor" responsible for targeting "VEGFR-2" and "EGFR" to "reduce". Combining "ZD6474" as "secondary therapy" with "docetaxel" as "secondary therapy" in patients with advanced NSCLC compared with "docetaxel" alone in a "random" "phase II" study [82] may improve a "growth-free survival" study [83], and a phase III has been initiated for authorization[72].

PI3K/Akt/PTEN pathway inhibitors

PI3Ks are important regulators of many "cellular" processes, including "cell growth", "cell proliferation", "apoptosis" and "cytoskeleton" rearrangement. In many cancer patients, the "PI3K" pathway is actively activated by a "series of events" including activation of the "upstream" receptor "TKs" (such as "PDGFR" and "EGFR") [84]. Akt is the essential downstream effector of PI3Ks and is constitutively stimulated in NSCLCs [85]. Transformation encoding the 'catalytic' subunit Expression of the 'PTEN' protein 'Like to inhibit' PI3K/Akt 'Or lost' in 'approximately 4%' of 'NSCLC' tumors [86, 87], the pathway of a 'other' mechanism is activated (PI3K inhibitor) showed that the drug improved the sensitivity of NSCLC cells to radiotherapy and chemotherapy, and phase I studies of these drugs have been completed [85]. Many inhibitors have been developed against the "mammalian" target (mTOR) of rapamycin, the "downstream" target of "PI3K" signaling. These may include rapamycin and its analogues, temsirolimus (CCI-779), AP23573 and everolimus (RAD001) [88]. These agents have shown promising anti-tumour activity in early clinical studies [72].

RAS/RAF/MEK/ERK pathway inhibitors

The "RAS" family of proto-oncogenes, HRAS, "KRAS" and "NRAS", are "plasma membrane-associated" G "proteins" and are key regulators of "signaling" involved in the differentiation and

survival growth and proliferation of "normal" cells [89]. The RAS/RAF/MEK pathway is activated in lung cancer by activating KRAS mutations (as at codon 12) that occur in approximately 20% of lung cancers, primarily adenocarcinomas [90]. Although the "specific functions" of "HRAS", "NRAS" and "KRAS" have not been determined, "KRAS" mutations are responsible for approximately 90% of "RAS" mutations in "cancer". KRAS "mutations" have been found in "cancers" caused by "smokers" and "associated with poor survival" [91]. In addition, "KRAS and EGFR" mutations appear to be synergistic in lung cancer [92], and "KRAS" mutations are associated with "primary resistance" to "EGFR" TKI therapy [93]. A number of drugs have been developed that "express different components of the RAS pathway" and are currently in "clinical" trials [89]. One of these, the "farnesyl transferase inhibitors" (FTIs), is one of the most studied drugs, while the two "orally bioavailable FTIs", tipifarnib and lonafarib, have been compared in "studies in combination with cytotoxic therapy for lung cancer" [94].

Tumor suppressor gene therapy

The p53 tumor suppressor is a chief cellular gatekeeper that becomes activated by multiple stress signals particularly oncogenes, DNA damage, and hypoxia, resulting in the expression of downstream genes that participate in cell-cycle arrest, aiding in DNA repair mechanism or initiation of apoptosis. p53 is commonly inactivated through mutation in lung cancer of around 50% of NSCLCs and 90% of SCLCs [95, 96]. Reactivation of p53 function by p53 mutants or loss of p53 in cancer cells leads to apoptosis of tumor cells [97], and therefore these findings have led to the improvement of pharmacological methods of reactivating p53. Studies have shown that gene therapy from gene replacement studies of p53 gene therapy using retroviral p53 expression vectors is safe and feasible, but vaccine evidence is

weak, especially in patients with non-small cell lung cancer. [98]. FUS1 is a newly discovered cancer gene located on chromosome 3p21, and is a region that is usually deleted in lung cancer. Loss or absence of post mutation of FUS1 protein and exogenous overexpression of FUS1 in most SCLC and NSCLC has been found in most SCLC and NSCLC protein causes inhibition of tumor cell proliferation and apoptosis [99, 100]. In addition, experiments are awaited to check the therapeutic effect of these gene therapies in lung cancer [72].

Histone Deacetylase Inhibition

Hypermethylation of the promoter region of the tumor suppressor gene demonstrates the epigenetic effect of gene silencing that plays an important role in tumor initiation and development [101] and therefore represents the preferred target. Histone deacetylases (HDACs) facilitate modification of histones by limiting access to DNA by transcription factors and repress transcription of genes involved in cell proliferation. HDAC inhibitors can restore silent genes and exert antiproliferative effects by controlling the expression of tumor cells. Many HDAC inhibitors are in clinical trials in cancer, including suberoylanilide hydroxamic acid (SAHA), depsipeptide and valproic acid [72].

Proteasome inhibitors

The ubiquitin-proteasome system plays a role in protein homeostasis by controlling the cell cycle, DNA transcription and degradation of proteins involved in healing, angiogenesis and apoptosis [72]. The proteasome inhibitor bortezomib (Velcade) has demonstrated cytotoxic activity as a single agent or in combination with therapy in clinical studies in cancer cell lines [102]. In addition, the randomized phase II trial of bortezomib alone and bortezomib in combination with docetaxel was valid, and the clear performance of the two treatments was

similar to the secondary treatment in NSCLC [103]. More research on cancer is anticipated with bortezomib along with chemotherapy [72].

Insulin Growth Factor Pathway Inhibition

The insulin-like growth factor (IGF) pathway contributes to the growth and differentiation of bone and cartilage. It usually has two receptors (insulin receptor (IR) and insulin-like growth factor 1 receptor (IGF-1R)) and usually three ligands (IGF-1, IGF-2 and insulin) [104]. The insulin-like growth factor 1 receptor, a receptor tyrosine kinase, forms homodimers and heterodimers mainly with HER2 and IR. Like HER2, IGF-1R does not appear in a mutated form in cancer. Activation of ligand binding leads to activation of several signaling pathways, including the RAS/RAK/MEK and PI3K/AKT/mTOR pathways. Most (up to 70%) overexpression of IGF-1R in NSCLC is evidence of dysregulation of IGF signaling in lung cancer [105, 106], where strong signaling leads to drug resistance and ultimately tumor growth [107]. In addition, regulation of IGF-1 is frequently associated with lung cancer risk [108][109]. A phase III study (ADVIGO 1016) investigating the combination of carboplatin, figitumab, and paclitaxel as first-line therapy in patients with advanced NSCLC was also terminated due to lack of efficacy and efficacy [110].

Enhancing apoptosis

Cancer cells have the ability to escape apoptosis. Bcl-2, overexpressed in 75%-95% of SCLC and 10%-35% of NSCLC, shows anti-apoptotic action[90] and preclinical data demonstrated that sodium oblimersen is an oligonucleotide that targets Bcl-2 and confers resistance to significant cytotoxic chemotherapy, radiotherapy and monoclonal antibodies. A randomized phase II study of Oblimersen combined with chemotherapy in NSCLC and SCLC is ongoing

[111]. Potential small molecule inhibitors of the antiapoptotic proteins Bcl-XL, Bcl-2 and Bcl-w have been further developed (ABT-737) and have again shown efficacy as single agents in both SCLC and NSCLC [112].

Heat Shock Protein Inhibition

Heat shock proteins are molecular chaperones often involved in signal transduction and stability, post-translational folding, activation and maturation of many other proteins essential for the cell cycle. In addition, they are oncogenic chaperones and inhibition of HSP90 (well-known HSP proteins) leads to disruption of oncogenes such as BCR-ABL, HER2 and BRAF, inhibiting many oncogenic transduction pathways [113]. Geldanamycin is an HSP90 inhibitor and several 17-amino acid derivatives have been developed, such as 17-AAG, SNX-5422, ganetespib, and retamycin [114].

Telomerase inhibitor

Several studies show that telomerase is upregulated in cancer and that telomerase inhibitors have the ability to turn cancer and make cancer more. Telomeres are repetitive sequences at the ends of mammalian chromosomes that help prevent the degradation and loss of many important genes[115]. With each division of the cell, the telomere gradually shortens, thereby limiting the lifespan of the somatic cell. The shortening of telomeres and the ensuing cell death can be overcome by telomerase, which helps stabilize the telomere length by adding DNA sequences to the telomere end of chromosomes. Human telomerase has two main components: the functional telomerase RNA (hTR, also known as TERC) component and the telomerase reverse transcriptase (hTERT) catalytic subunit. Telomerase activation is thought to play an important role in the immortalization of cells, an early stage of cancer.

Telomerase is ubiquitous in human tumors, whereas telomerase activity is reduced or absent in normal tissues. Although telomerase is silent in normal cells, it is activated in about 80% of NSCLC and about 100% of SCLC. Therefore, telomerase represents a promising treatment against lung cancer, and many drugs targeting telomerase have been developed. GRN163L is a novel telomerase antagonist targeting the RNA template region of Htr. Preclinical data have demonstrated that GRN163L hinders in vivo xenograft tumor growth of lung cancer cells and anchorage-independent growth [116], and phase I studies with this agent is in process. Recently treatments targeting telomerase are in development, which includes gene therapy (telomerase oncolytic virus therapy), reverse transcriptase inhibitors, and immunotherapy (vaccines) [115].

Other cancer stem cell-targeted approaches

In addition to important survival and self-renewal mechanisms, recent guidelines on glioblastoma state that people with cancer become resistant to effective radiation therapy. A good way to avoid cancer stem cells versus cytotoxic therapy is to pharmacologically inhibit checkpoint kinases, thereby helping to control the cell cycle to allow DNA repair (e.g. Chk1, Txc2 [117]). Other studies have demonstrated the possibility of using soluble substances such as bone morphogenetic protein as therapeutic targets to induce stem cell differentiation [118]. Approaches to treat specific CSC populations include selection of targets using CSC assays, sensitivity of CSC to different clinical and therapeutic models, inhibition of signaling pathways important to CSC such as Wnt, Hh, and Notch signaling pathways; and telomerase inhibition. Inhibition of the Hh pathway was evaluated with cyclopamine, a natural inhibitor of SMO, leading to the development of a synthetic oral inhibitor with observed activity against basal cell

carcinoma [119]. Inhibition in the Notch signalling pathway was potentially demonstrated with γ -secretase inhibitors [59].

CONCLUSION

Despite the advanced technology, cancer mortality incidence including that of lung cancer has not yet declined. Enormous resources have been employed globally for developing a preventive, diagnostic, and therapeutic approach for lung cancer. Relapse and metastasis of malignant cells in patients are the demerits that occur after traditional cancer therapies, such as surgery, radiation, or chemotherapy. Drug development with robust and viable lead candidates remains challenging for scientists, which involves an array of transition from screening trials to a drug candidate, which entails expertise and experience. Natural products and their derivatives have been well recognized for many years as a source of promising therapeutic agents and structural diversity. Heterocyclic compounds are the privileged scaffolds that have emerged as a promising agent for designing and developing drugs. They can serve as useful tools to alter the polarity, lipophilicity, and hydrogen-bonding capacity of molecules, resulting in improved pharmacological, physicochemical, pharmacokinetic, and toxicological properties of drug candidates for lung cancer. The synthetic cyclic compounds employed as anticancer drugs imitate natural ligands and substrates to disturb the obscure balance in cells. Molecular hybridization is an innovative and attractive approach that provides a platform for the designing and developing novel drug prototypes with improved pharmacokinetics and pharmacodynamics activity. Currently used anticancer drugs targeting DNA or RNA activity mostly rely on their inhibition against synthesis, transcription factors, and enzymes. The majority of these anticancer drugs display a lack of selectivity and participate in drug resistance, limiting the efficacy of

anticancer drugs. However, novel therapeutic strategies are being developed to overcome these complications, which may discover novel anticancer drugs with low toxicity and resistance.

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