

Review

C-myc Contributes to Malignancy of Lung Cancer: A Potential Anticancer Drug Target

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Abstract. Emerging evidence has provided important information on oncoproteins involved in cancer initiation, progression, metastasis, and resistance to current therapies. C-myc, one of the critical oncoproteins, has been shown to be implicated in enhancing the aggressiveness of many cancers, mainly through its ability to increase cancer cell growth and cellular survival mechanisms. Despite the more precise and earlier detection and the availability of better therapies, lung cancer remains the most dreadful cancer as it causes high mortality rate with relatively poor treatment success. In lung cancer, C-myc is frequently dysregulated and associated with unfavorable patient survival. C-myc plays a role in regulation of lung cancer cell behaviors including growth, resistance, death, and dissemination through the activation of cell cycle driving proteins, an increase in the cellular levels of anti-apoptotic proteins, and the modulation of metabolism. Besides, C-myc has been shown to be important for cancer stem cell (CSC) properties. Taken together, targeting as well as inhibiting C-myc could provide promising means for resolving lung cancer. This review emphasizes on the molecular mechanism by which C-myc influences lung cancer growth, metastasis, drug resistance, and CSC maintenance, and suggests the target proteins that may benefit drug discovery and design.

Although the specific mechanisms are not clear, there is hypothesis that non-lethal genetic alterations as well as multiple gene lesions could render carcinogenesis (1). The

affected genes that associate with cancer can be divided in to several groups. Among them, the proto-oncogenes that acquire active function and tumor suppressor genes that lose their function contribute to the initiation of cancer (2). An oncogene is an altered gene that encodes for a protein that accelerates cell division that warrants uncontrolled tumor growth. In addition, apoptosis resistance as well as immune escape are related to the functions of an oncogene (2-4). Recently, a new concept has been proposed that cancer stem cells (CSCs) playing a key role in carcinogenesis, cancer progression, and poor prognosis require continuously active oncogenes (5). C-myc, which belongs to the myc family, has been shown to regulate carcinogenesis and progression in many cancers (6-9). Besides, recent evidence has pointed its significant role on CSC properties and metastasis of certain cancers including lung cancer (10). C-myc is known to enhance cell survival and growth *via* the induction of its down-stream proteins involved in protein translation, cell cycle drive, apoptosis, and metabolism (11, 12). These effectors of C-myc govern a broad range of cancer cell behaviors and activities, such as cell growth, survival, resistance to chemotherapies, immune surveillance, and metastasis.

As lung cancer is among the most aggressive types of human cancer with a relatively high growth rate and metastatic potential, to understand the role and function of key oncogenes frequently activated in this cancer would lead to better treatment approaches.

Lung Cancer

Lung cancer is a disease in which cells of the lung tissue cannot control their growth, proliferation, and maintenance of their normal function. This causes the development of tumors that compromise a person's ability to breath and reduce quality of life. The uncontrolled cells will invade neighboring tissues, disseminate, and form new metastasized

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tumors throughout the body. Cancer statistics in 2019, showed that lung cancer incidence is slightly decreasing in male but remaining as ever in female due to the changing of smoking behavior.

Generally, lung cancer is classified into 2 types by histology, non-small cell lung cancer (NSCLC) and small cell lung cancer (SCLC). SCLCs are quite rare compared to NSCLCs and account for approximately 15% of all lung cancers, whereas NSCLCs account for about 85% of all lung cancers. SCLCs tend to grow faster than NSCLCs and often metastasize to other organs or lymph nodes, thus they are more responsive to chemotherapy (13). NSCLCs are still being divided into 3 sub-categories, adenocarcinoma, squamous cell carcinoma (SqCC), and large cell carcinoma. The most common type of NSCLC is adenocarcinoma which presents in the outer parts of lung. It has been shown that this subtype occurs with higher frequency in females than in males and develops more frequently in younger age than other subtypes. However, adenocarcinoma can be detected earlier before it starts to metastasize. Squamous-cell carcinoma (epidermoid) accounts for approximately 25-30% of all lung cancers. It initiates from squamous cells in the central parts of the lungs, near bronchi. This subtype is firmly related to cigarette smoking. Large cell (undifferentiated) carcinoma comprises about 10-15% of all lung cancer cases. It can present in any part of the lung but often starts in the central of the lung. It has a tendency to proliferate and metastasize quicker than other subtypes (13).

Although the trends in incidence rate of lung cancer have been declining, it remains the highest leading cause of cancer-related death worldwide (14). Overall the 5-year survival of lung cancer is approximately 19%. Interestingly, the 5-year survival of lung cancer localizing inside the lung is as high as 54%, however, after metastasis the survival rate is only less than 4% (14). Unfortunately, more than half of lung cancer cases were found with metastasis at the time of first diagnosis (14). This information led to the development of strategies of metastasis inhibition as well as investigations on mechanisms of cancer cell dissemination. The new insights regarding cancer cell biology have indicated that there is a small cancer cell population inside the tumor that possesses the properties of stem cells (5, 15, 16). Such cancer cells have been termed cancer stem cells or cancer initiating cells as they were believed to be the original seed of cancer (15). Besides, it has been shown that CSCs are the major cells that disseminate and form distant metastases (16).

C-myc Proto-oncogene

The activation of oncoproteins together with the inactivation of tumor suppressor proteins are the generally accepted concept of initiation of human cancers. The myc proto-oncogenes are gene encoding transcription factors, which are

commonly overexpressed in cancer patients and have been intensively investigated as they may be potential targets of cancer treatment (17, 18). Myc associates with the tumorigenesis and tumor maintenance in many human cancers (7, 12, 19). Basically, the myc family proteins comprise L-myc, N-myc and C-myc (6). The structure and their important domains are presented in Figure 1. C-myc is expressed in many kinds of adult tissues while N-myc is found mostly in early developmental stages of neuronal tissues. L-myc is prominently expressed in embryonic brain, kidney and lung tissue (6) but the function of L-myc is not well studied. C-myc exhibits many important functions regarding the regulation of signaling in normal and cancerous cells. C-myc is involved in cell growth, division, differentiation, genome stability, cell survival and death, and angiogenesis (10, 20-23). C-myc functions as a down-stream signal of several growth receptors such as epidermal growth factor receptor (EGFR), transforming growth factor alpha (TGF- α), transforming growth factor beta (TGF- β) receptor, interleukin-6 (IL-6) receptor, Notch receptor, and Frizzled receptor (24). Therefore, C-myc usually responds to growth factors-receptor interaction and contributes to cellular response through its transcriptional activity (25) (Figure 2).

Regarding the mechanism of action, C-myc forms a dimer with Myc - associated factor X (MAX) before binding to E-boxes (CACGTG) in DNA within enhancers and promoters of genes (Figure 2). Its target genes encode for proteins that participate in the regulation of cell growth and proliferation including CDK4, CDC25A, p15, p21, PTMA and E2F1 (12). They are also linked to DNA damage and apoptosis responses as C-myc has been shown to regulate the expression of Bax, Bcl-2 and Mcl-1 (26). In normal cells, overexpression of myc proteins will lead to apoptosis, proliferation arrest, or senescence (11). In addition, the myc protein has been shown to act as a central contributor to the survival and division of cancer cells (8). This myc is recognized as an important therapeutic target as it has been shown to be dysregulated in about 50% of human cancers (27). It is likely that the alteration or dysregulation of myc oncogene contributes to cancer progression and aggressiveness (6-9) and myc has been linked with poor prognosis in several cancers (28). Evidence indicates that myc functions in several steps of carcinogenesis and disease progression including enhancement of cell proliferation, inhibition of apoptosis, and deregulation of differentiation (6-9). It has been widely suggested that C-myc inhibition could be a promising approach for cancer treatment (10, 18, 28, 29). This is supported by many studies indicating that the inactivation or inhibition of C-myc can induce tumor regression by restoration of the normal cell checkpoint mechanisms or induction of proliferation arrest, cellular senescence, and apoptotic mechanisms (8, 30).

C-myc protein levels are increased in about 70% in cancer patients but only 15-20% of the patients have a gene

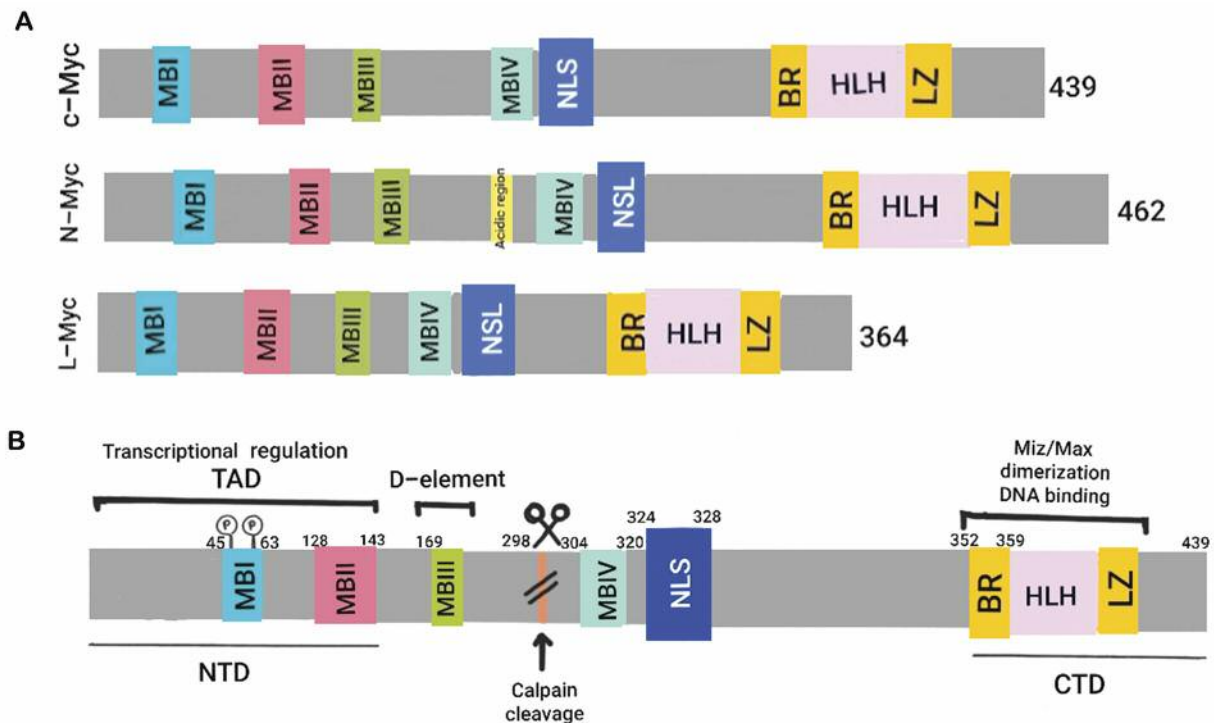


Figure 1. Schematic display of the myc family members (A) and detail of C-myc protein (B). MBI: Myc-box I, MBII: Myc-box II, MBIII: Myc-box III, MBIV: Myc-box IV, NLS: nuclear localization signal, BR: basic region, HLH: helix-loop-helix, LZ: leucine zipper domain, TAD: transactivation domain, NTD: N-terminal domain CTD: C-terminal domain.

amplification. Recently, a meta-analysis has shown that the rate of C-myc amplification in cancers varies from 1-50% with an average of about 15.7% (31). It has been accepted that overexpression of C-myc could be the result of the amplification of the gene, however, the frequency of overexpression of the C-myc protein in cancer tissues is much higher (approximately 2 folds) than C-myc amplification (32).

In malignant cancers, an increase in C-myc expression has been linked to malignant phenotypes. Recent studies have indicated that amplification of the C-myc gene is observed in many cancer cell lines including human colon cancer cells and SCLC cells. C-myc oncoprotein has been shown to be overexpressed in about 50-100% of breast cancers (32, 33), in about 50-75% of NSCLC cases (34-36, 37) and also to be critical for the pathogenesis of NSCLC (10). In NSCLC, overexpression of Myc has been shown to be associated with mutated *PHACTR3* and *E2F4* genes (38).

C-myc and Drug Resistance

Drug resistance is the main problem in cancer therapy and has been found to mostly correlate with amplification and overexpression of the c-Myc oncogene (39-41). A study has shown that C-myc is an effective therapeutic target for

overcoming drug resistance in acute myeloid leukemia (AML) (42). C-myc expression levels have not only been associated with aggressive phenotypes in many cancers (43), but also with chemotherapy resistance in several cancers, such as melanoma, ovarian cancer, hepatocellular carcinoma, and lung cancer (10, 44, 45). The mechanism through which C-myc contributes to drug resistance may involve increased expression of genes that promote cell survival, genomic instability, and blockage of apoptosis (10, 46).

Drug resistance has been recognized as a long important concern regarding lung cancer therapy. The rate of chemotherapeutic resistance in lung cancer is relatively high (47). Although the targeted therapy, including epidermal growth factor receptor-tyrosine kinase inhibitors (EGFR-TKIs), has been shown to improve the clinical outcome and recommended as a first choice for lung cancer with EGFR mutations (48, 49), the platinum-based drugs as well as other chemotherapeutic agents remain the standard of care for other patients with advanced disease (50). One important platinum-based compound is cisplatin [cis-DDP, cis-diamminedichloroplatinum (II)], which is widely prescribed for the treatment of many human cancers with a high curative effect on lung cancer (51). However, in the process of NSCLC treatment with chemotherapy, cancer frequently

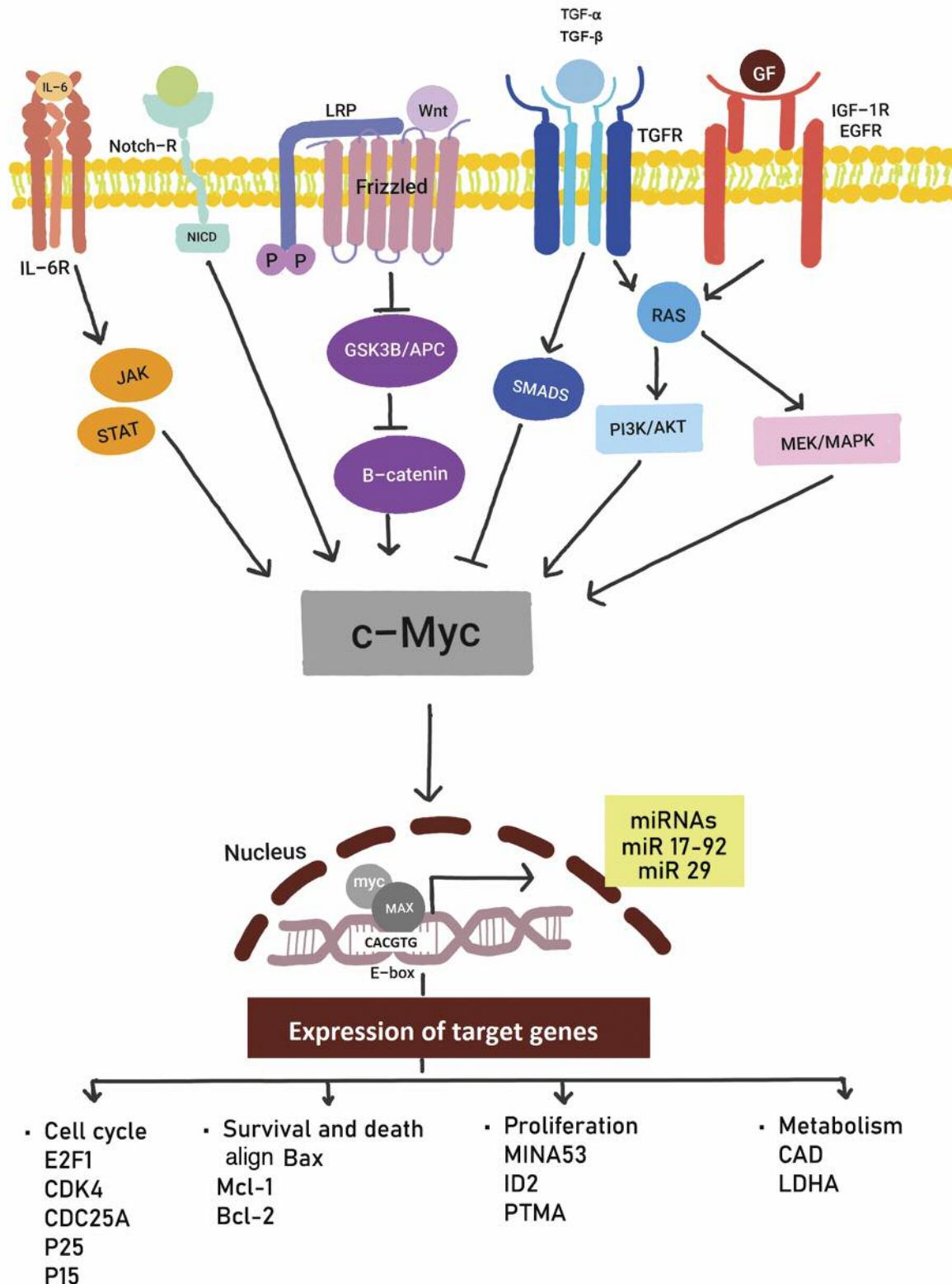


Figure 2. *C-myc* can be regulated by several mechanisms, such as JAK/STAT, Wnt/ β catenin signaling, Notch signaling and Ras/PI3K/AKT/GSK-3 pathways which increase *C-myc* levels. *Myc* will form a dimer with the Myc-associated factor X (MAX) before binding to E-box (CACGTG) within enhancers and promoters of genes. As an important transcription factor, *c-myc* controls the expression of many genes that affect numerous cellular activities such as cell cycle progression, proliferation, metabolism, survival and death.

develops primary or acquired resistance to the therapy (52). Therefore, better understanding of the molecular basis of drug resistance in this cancer is important for improving DDP-based chemotherapy and overcoming cancer resistance.

Interestingly, a study has shown that C-myc may associate with cisplatin resistance in lung cancer as niclosamide could enhance cisplatin-mediated apoptosis in cisplatin-resistant cells by attenuating C-myc (53). Cisplatin induces apoptosis of cancer cells *via* a mechanism involving formation of DNA adducts and DNA damage (54, 55). DNA damage mediates p53-dependent increase and decrease in pro-apoptotic and anti-apoptotic members of the Bcl-2 family of proteins, respectively. However, over activated C-myc acts as an inducer of anti-apoptotic proteins including Mcl-1 and Bcl-2 that can sufficiently block cisplatin-mediated death (56). Besides, an interesting study has suggested that the C-myc-mediated drug resistance can be acquired after the cancer cells receive cisplatin (57). It has been shown, in head and neck squamous cell carcinoma, that prior cisplatin treatment could induce resistance to palbociclib *via* a mechanism involving C-myc up-regulation. The results and the underlying mechanism were confirmed by evidence indicating that co-treatment with palbociclib and the C-myc inhibitor JQ1 resulted in a synergistic anti-growth effect (58). Also, studies have shown that c-Myc is an effective therapeutic target for overcoming drug resistance in acute myeloid leukemia (AML) (42).

C-myc Regulates Epithelial-mesenchymal Transition (EMT) and Cancer Stem Cells

Epithelial-mesenchymal transition (EMT) has been reported to be an important process that closely relates with tumor metastasis and chemoresistance. EMT involves a cellular change from epithelial phenotypes toward more motile phenotypes with higher ability to migrate and invade the surrounding tissues (59, 60). Cancer cells change not only their morphology to spindle shape, but they also modify the molecular signaling as demonstrated by alterations in several protein markers such as decrease of E-cadherin and occludin, and induction of N-cadherin, Snail, Slug, Zeb, Twist, and vimentin (61). The EMT process can be driven by many cellular signals including epidermal growth factor receptor, transforming growth factor (TGF), fibroblast growth factor, and hepatocyte growth factor (HGF), Notch, and Wnt/ β -catenin pathways (62). It is well accepted that EMT is critical for promoting primary tumor cells to disseminate (63). Besides, it has been suggested that EMT involves the generation of stem-like cancer cells with augmented ability of self-renewal and tumorigenicity (59). Regarding C-myc and EMT regulation, Wolfer and Ramaswamy have reported that the expression of C-myc directly regulates cell migration, invasion, and EMT (64). The amplification of C-myc gene occurs in up to 20%-30% of human cancers, especially in breast cancers (65). In addition, it has been demonstrated, in

human breast cancer cells, that overexpression of C-myc could induce EMT (66). The mechanism by which C-myc mediates EMT involves the extracellular signal-regulated kinase (ERK)-dependent GSK-3 β inactivation and snail activation (66).

The new concept of cancer initiation states that cancer is generated from mutated and dysregulated normal stem or progenitor cells (67). Within the tumor, there is a distinguished hierarchy of heterogeneous cell populations where cancer stem cells (CSC) are on the apex (68). CSC maintain the unique properties of self-renewal and differentiation of their parental normal stem cells (69). CSCs have been discovered in many cancers including lung cancer and were linked to carcinogenesis, tumor growth and maintenance, chemotherapeutic failure, metastasis, and cancer relapse (10, 70, 71). The role of CSCs in lung cancer has been widely described. Importantly, it has suggested that lung cancer relapse and dissemination is caused by the activity of CSCs and their niches that are not sufficiently affected during therapies (63, 72). Indeed, a number of studies have reported that CSCs are a strong chemoresistant population (72, 73). It has been suggested that targeting these CSCs could be an effective strategy to treat lung cancer with reduced disease relapse (74). In particular, Notch, Wnt/ β -catenin, and Hedgehog signals have been widely shown to be critical for CSC properties and maintenance (75). As C-myc is involved in the cellular response to Notch and Wnt/ β -catenin activation, C-myc was prohibit the maintenance and function of CSCs. Activation of β -catenin signaling by the interaction of Wnt to Frizzled receptor resulted in increased levels of cellular β -catenin. β -catenin then translocate to the nucleus, where it functions as a transcription factor for C-myc (10, 76). Thus, there is a direct association between C-myc and β -catenin. The role of Wnt/ β -catenin signaling on CSC has been widely described (77). Besides, Wnt/ β -catenin has been shown to cross talk with several CSC-related pathways including Hedgehog, Notch, and TGF β /BMP. Wnt/ β -catenin has been shown to be critical for CSC survival in many cancers such as lung, breast, ovary, gastric, pancreatic, and colorectal cancers (77, 78). Likewise, C-myc has been shown to be important for the maintenance of CSC properties and chemoresistance of colon cancer stem cells (79). Besides, current studies have pointed out that the contribution of this protein to drug resistance may involve its regulatory role on cancer stem cells (CSCs) (10).

Cell Regulation and Possible Strategies for Targeting C-myc

C-myc is a 62 kDa protein functioning as a powerful transcription factor regulating several key cellular behaviors including growth, differentiation, and apoptosis. As a transcription factor, C-myc exerts its regulatory roles *via* the promotion of the expression of a significant number of genes (33).

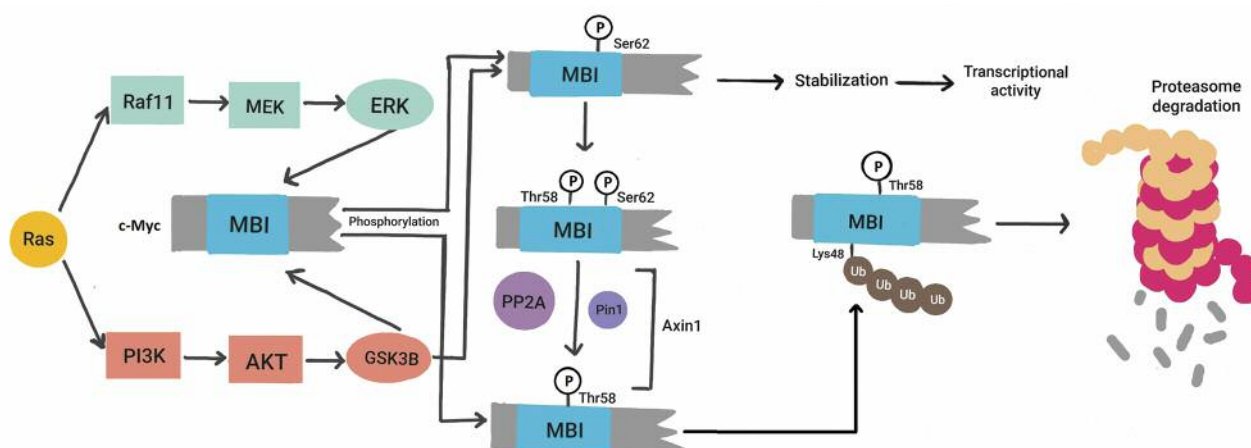


Figure 3. Kinase cascades in the regulation of C-myc stability and ubiquitin-proteasomal degradation. Myc is stabilized upon phosphorylation at serine 62 (S62) and Threonine 58 (T58) on MBI by ERK and GSK-3 β , respectively. Phosphorylation at S62 (p-S62) promotes the stability of c-Myc while p-T58 is recognized as a target for E3 ligase for degradation. In addition, the S62 phosphorylation can be dephosphorylated by PP2A.

In order to function as transcription factor, the C-myc protein consists of several regions including a non-specific DNA binding region, a nuclear target sequence, a transcriptional activation region, a basic region, a helix-loop-helix (HLH) and a leucine zipper region. C-myc dimerizes with max resulting in the myc/max heterodimer complex that binds to the target DNA sequence or E-BOX (sequence 5'-CANNTG-3') to regulate transcriptional activation of genes involved in cell proliferation, cell cycle regulation, and apoptosis (80, 81). The Myc-Max complex also mediates gene suppression by regulating the transcription of target genes through the binding with Miz-1 (Myc-interacting zinc-finger protein1). In free form, Miz-1 interacts with initiator elements (INR) in the promoters of genes and activates their transcription. Interaction with Myc converts the Miz-1 from activator to repressor that may involve in the decrease of tumor suppressor genes. C-myc also regulates miRNA networks by stimulating miR-17-92 to occlude and suppress dozens of miRs, including Let-7, which affects insulin signaling, miR-23a/b, and glutaminase expression and miR-34a, which regulates lactate dehydrogenase (LDHA) expression (82, 83). The miR-17 cluster contains miRNAs that target PTEN, thereby activating AKT, as well as those that target pro-apoptotic BimL or transcription factor E2F1. miRNAs downstream of C-myc have also been associated with EMT and angiogenesis.

The promoter of the *MYC* gene could be activated by a number of pathways such as Wnt/ β -catenin, Jak/STAT, RAS/RAF/MAPK, transforming growth factor- β (TGF- β), and NF- κ B (84, 85). Such cellular pathways have been shown to be dysregulated in cancers, which consequently, are characterized by myc over-expression (18, 24, 27, 29). C-myc

requires post-translational modifications for controlling its stability and degradation. As C-myc mRNA and protein are relatively short lived (approximately 30 min), the protein function depends on its cellular levels (80). One important regulatory modification of C-myc is phosphorylation. The protein could be phosphorylated at multiple sites. C-myc phosphorylation by protein kinase CK-2 at the C-terminal PEST domain (amino acids 240-262 and amino acids 342-439) could enhance the stability of myc (86). Also, it has been suggested that the stabilization of C-myc in many cancers is associated with increased cell proliferation (87, 88). It is noteworthy that CK-2-mediated phosphorylation of the myc dimerization partner max affects DNA binding of myc-max heterodimer (89, 90). Thus, the kinase activity of CK-2 has been suggested to regulate myc levels as well as its transcription factor function. Likewise, phosphorylation of myc at Thr-58 and Ser-62 is critical for myc degradation (91). Phosphorylation at Ser-62 is a prerequisite for Thr-58 phosphorylation. Ser-62 could be phosphorylated by several kinases including mitogen-activated protein kinase (MAPK), cyclin-dependent kinase 1 (CDK1), and c-JUN N-terminal kinase (JNK) (92-97). Interestingly, Ras signaling that is frequently found to be overactivated in lung cancer has been suggested to enhance myc phosphorylation at Ser-62 (95, 96) (Figure 3). Ras also induces the activation of PI3K/Akt that phosphorylates GSK3 and subsequently results in C-myc stabilization (81, 98). After phosphorylation at Ser-62, GSK3 could phosphorylate Thr-58 of the protein (24). These two sites of phosphorylation of C-myc target the protein for degradation by the ubiquitin-proteasomal degradation (Figure 3). The ubiquitin-proteasomal degradation of C-myc protein has been shown to be a critical process that affects C-myc

function. As C-myc is expressed at low levels, the degradation process of the protein is the factor that regulates its function (81, 98).

A study has demonstrated that suppression of C-myc promotes Fas-mediated apoptosis (99). Another study has shown that degradation of C-myc can affect topoisomerase's function in DNA repair, leading to various types of cancer cells to apoptosis (100). Moreover, decrease in C-myc activity was demonstrated to sensitize cancer cells response to vinca alkaloids treatment (101). In addition, C-myc transcription activities have been shown to strengthen cancer aggressiveness by amplifying survival signaling, inducing EMT, increasing metastasis potentials, as well as enhancing CSC signals. Together with the fact that C-myc is a key regulator of survival and growth of cancer, these results have suggested the C-myc protein as a potential molecular target for cancer treatments. There are several strategies for targeting myc in cancer treatment such as inhibition of the expression of myc protein by disrupting up-stream signals including Wnt/ β -catenin, Jak/STAT, RAS/RAF/MAPK, TGF- β , and NF- κ B, as well as inhibition of the dimerization between myc and max, and by inducing myc degradation by the ubiquitin-proteasome system (18). The down-regulation of C-myc in cancer cells could promisingly decrease the ability of cells to grow and metastasize, therefore, improving survival and clinical outcome of current therapeutics.

Conflicts of Interest

The Authors declare that they have no conflict of interest regarding this study.

Authors' Contributions

P.C. conceived of the review, wrote the manuscript, and analyzed results of literature research. N.S., and N.N. conducted the review of the literature. All authors discussed the contents and contributed to the final manuscript.

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