



The MYBL2 Mechanism as an Oncogene in Cancers-Current Perspective

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Abstract

Background: The abnormal cell division and replication leads to cancerous cells that eventually cause tumors in humans. This is typically due to the metabolic stress as the ultimate causal factor cancer. Among the therapeutic approaches to cancer, targeted therapy is gaining much ground on energy reprogramming. One such is to modulate the tumor cell division in order to stop the proliferation, inhibit angiogenesis and cell cycle arrest. Among the recent transcription factors, MYB Proto-Oncogene Like 2 (MYBL2) from Myb-related protein B protein is a very promising target. MYBL2 is studied to modulate cell cycle progression and physiological processes such as cell survival and differentiation.

Objective: Despite the number of recent studies with cutting edge evidence based roles played by this oncogene, the exact mechanism induced by this gene is not established. Since modulating cell cycle progression in oncology is imperative for both combined therapies and monotherapies such as immunotherapies, there is a need to harness the mechanisms associated with gene entities. This review summarized the updated MYBL2 studies as an oncogene based on its biological functions and mechanisms on various cancers. Furthermore, the review discussed the known mechanistic characteristics and associated genes known with MYBL2.

Conclusion: In sum, with this systematic screening on papers based on MYBL2 oncogene, no two studies are absolutely uniform with regards to the molecular reactions and biological mechanism. Although, majority of the studies could establish delay cell cycle proliferation as anti-tumorigenesis, the biological pathways are not even cancer specific and thus, the need for comprehensive studies to harness the biological mechanisms.

Keywords: MYBL2; Cell Cycle; Energy Metabolism; Cancers; Disease Mechanisms

Abbreviation

ABRACL: Actin-binding Rho Activating C-Terminal Like; ADT: Androgen-Deprivation Therapy; ACTN4: Alpha-Actinin-4; Akt: Activates Phosphorylated-Protein Kinase B; ALL: Acute Lymphoblastic Leukemia; AML: Acute Myeloid Leukemia; CAF: Cancer Associated Fibroblasts; CDCA3: Cell Division Cycle-Associated Protein 3; ccRCC: Cell Renal Cell Carcinoma; circular RNA: cirRNA; CRC:

Colorectal Cancer; DATS: Diallyl Trisulfide; DREAM: Glioblastoma Multiforme; EC: Endometrial Cancer; ERK: Extracellular Signal-Regulated Kinases; EwS: Ewing sarcoma; FLT3-ITD: FMS-like Tyrosine Kinase-3 Internal Tandem Duplication; FOXM1: Forkhead Box M1; HCC: Hepatocellular Carcinoma; lncRNA: Long Noncoding RNA; MDS: Myelodysplastic Syndromes; MM: Multiple Myeloma; PA: Pancreatic Adenocarcinoma; PDAC: Pancreatic Ductal Adenocarcinoma; PDT: Photodynamic Therapy; PIPNA-AS1: PIPNA

Antisense RNA 1; PTBP1: Polypyrimidine Tract-Binding Protein 1; NCAPH: Non-SMC Condensin I Complex Subunit H; NES: Natural Evolution Signature; PNI: Peri-Neural Invasion; RB-like: E2F and Multi-Vulval Class B; SKCM: Skin Cutaneous Melanoma; TNBC: Triple-Negative Breast Cancer; YAP: Yes-Associated Protein; SS: Synovial Sarcoma; TSCCs: Tongue Squamous Cell Carcinomas; TSS: Transcription Start Site

Introduction

Among the MYB family of transcription factors, MYBL2 is a highly conserved that plays a key role in physiological regulator during the cell cycle progression, survival and differentiation (Martin CM., *et al.* 2015) [1], making diagnostic and prognostic values (Qian X., *et al.* 2023) [2]. The deregulation of MYBL2 biological expression is key for the initiation and the progression in number of cancers tumor microenvironment (TME) (Musa J., *et al.* 2017) [3]. The phosphorylated MYBL2 during late G1 and S phase is facilitated by Cyclin CDK2 and this enhances its transactivation activity (Gautschi O., *et al.* 2018) [4]. This makes it a putative biomarker for anti-CDK2-therapy and the mechanism underpinning is predicted to come from releasing of the nuclear receptor co-repressors N-CoR and SMRT (Musa J., *et al.* 2019) [5]. This maintain MYBL2 in an inhibited state especially when non-phosphorylated. Since MYBL2 overexpression is linked to enhanced transactivation of anti-apoptotic cell, it can diminish cytokine dependence thereby enhancing resistance to apoptosis (Rosa-Ribeiro R., *et al.* 2014) [6]. MYBL2 affects the TME by influencing the cancer associated fibroblasts (CAF), immune infiltration level and expression level of CD4⁺ T cells, CD8⁺ T cells, and immune checkpoint-associated cells (Chen X., *et al.* 2021) [7]. The overexpression of MYBL2 in the tumor tissues was significantly correlated with a higher T classification, peri-neural invasion (PNI) and vital status in pancreatic ductal adenocarcinoma (PDAC) (Liu B., *et al.* 2021) [8].

During cell proliferation, *E2F1* and its target gene *MYBL2* contributes to the repression of Arachidonate 5-lipoxygenase, which is also known as 5-LO, ALOX5, 5-LOX or 5-lipoxygenase. This is an enzyme of non-heme iron coded by human gene *ALOX5* gene from a family lipoxygenase. The enzymes is able to transform essential fatty acids substrates to leukotrienes in addition to other biologically active products thus, making it a target for pharmaceutical intervention (Rosa-Ribeiro R., *et al.* 2014) [9]. B-MYB promotes the chemoresistance to OXA via regulating the *CCAT1/*

DNMT1/SOCS3 axis and oxaliplatin-resistant (Liu F., *et al.* 2023) [10] in CRC (Chen G., *et al.* 2022) [11] and contributes to tamoxifen resistance in breast cancer (Li X., *et al.* 2020) [12]. MYBL2 overexpression with poor patient outcome are significantly correlated in numerous cancer entities (Mullen DJ., *et al.* 2020) [13]. In addition, it contributes to lagging anaphase chromosomes that can initiate aneuploidy in tumors (Pfister K., *et al.* 2018) [14]. MYBL2 is associated with natural evolution signature (NES) in regulating brain development (Wu L., *et al.* 2022) [15] and contribute to the evolution of glioblastoma multiform (GBM) (Jiang L., *et al.* 2020, Liu Y., *et al.* 2020) [16,17]. Among the studied types of cancer associated with MYBL2 oncogene are; Ewing sarcoma (EwS) (Prexler C., *et al.* 2022) [18], hepatocellular carcinoma prognostic (Wang Y., *et al.* 2023) [19], skin cutaneous melanoma (SKCM) (Huang CH., *et al.* 2022) [20], lung adenocarcinoma (Liu C., *et al.* 2017) [21], cell renal cell carcinoma (ccRCC), childhood acute lymphoblastic leukemia (ALL) (de Smith AJ., *et al.* 2018) [22], colorectal cancer (CRC) (Hao S., *et al.* 2019) [23], triple-negative breast cancer (TNBC) (Fiscon G., *et al.* 2021) [24] and TNBC-specific CRC transcription factors (Shi W., *et al.* 2023) [25], gall bladder cancer (Liang HB., *et al.* 2017) [26], basal cell carcinoma (Chae YK., *et al.* 2016) [27] and endometrial cancer (EC) (Le L., *et al.* 2021) [28]. From previous studies, MYBL2 knockdown slows cell proliferation in addition to the expression of G2/M genes with reduced amount of cells in the G2/M phase thus, serving as anti-tumor (Rosa-Ribeiro R., *et al.* 2014) [29]. MYBL2 is an oncogene that participates in carcinogenesis through its role in cell proliferation through cycle regulation, apoptosis, and cell differentiation. To this day, MYBL2's exact function is not known, and conflicting mechanisms of action have been published. Moreover, there is no review with an updated biological functions and mechanisms on MYBL2 on various cancers. To this end, this review gives a summary of the known mechanistic characteristics and associated genes known with MYBL2.

MYBL2 mechanisms in tumor proliferation

MYBL2 is studied for deregulation of the dimerization partner in a number of cancers. This RB-like, E2F and multi-vulval class B (DREAM) complex assembly is a protein complex that regulates the expression of cell cycle-dependent gene. For instace, through Wnt/ β -catenin signaling pathway, cell division cycle 20 (CDC20) and MYBL2 inhibit apoptosis (Vera O., *et al.* 2021) [30]. Among the mechanism studied with MYBL2 includes, single nucleotide polymorphisms 20q13 gene coding region amplification and micro

RNAs regulations changes (Deng Q., *et al.* 2021) [31]. For instance, the uncoupling MYBL2 expression observed with negative transcriptional regulation, due to p53 mutation or the transformation by HPV16 E7 oncogene will enable MYBL2 to progressively bind to MuvB and forkhead box M1 (FOXM1) OV oncogenes. Specifically, FOXM1 plays a role in the control of cell proliferation and DNA break repairs as part of DNA damage checkpoint response (Qin WS *et al.* 2017) [32]. MYBL2-FOXM1 complex knockdown reduces the CHK1i-induced DNA replication stress. This prevention of premature mitosis during late S phase is positively correlated with resistance to CHK1 (Branigan TB., *et al.* 2021) [33]. In addition, MYBL2 interacts with FOXM1 to co-regulate the transcription of cell division cycle-associated protein 3 (CDCA3). Furthermore, MYBL2/FOXM1 and CDCA3 activates Wnt/ β -catenin signaling in bladder cancer (Liu W., *et al.* 2022) [34]. FoxM1 expression can be reduced with MTDH knockdown to inhibit the expression of MYBL2 and further reduce tumor proliferation, the cell migration and invasion as seen in glioma cells (Fu J., *et al.* 2022) [35]. B-Myb overexpression activates phosphorylated-protein kinase B (Akt) and extracellular signal-regulated kinases (ERK) signaling pathways in NSCLC (Jin Y., *et al.* 2017) [36].

In MYBL2-dependent manner, oncogene yes-associated protein (YAP) can support cell proliferation (Wei T., *et al.* 2019) [37]. For

instance, the YAP -dependent MYB family is studied with postnatal cardiomyocytes (Wang J., *et al.* 2019) [38]. YAP-mediated entry into mitosis is facilitated by MMB subunit B-MYB (Nientiedt M., *et al.* 2021) [39]. Overexpression of MYBL2 facilitates castration-resistant growth and metastatic capacity in androgen-dependent cells by promoting YAP1 transcriptional activity. It facilitates this via modulating the activity of the Rho GTPases RhoA and LATS1 kinase (Li Q., *et al.* 2021) [40]. Another MYBL2 adaptation to androgen deprivation is seen with prostate gland (Li ZB., *et al.* 2020) [41]. Lower MYBL2 levels enhance LNCaP and LAPC4 sensitivity to androgen deprivation and taxanes in prostate cancer (Yoshikawa Y., *et al.* 2022) [42]. B-MYB family is a tumor-promoting gene via suppressing IGFBP3 (Prexler C., *et al.* 2022) [43]. The DNA repair genes to some extent rely on the MYBL2 axis for regulation as in Wnt/ β -catenin/MYBL2 axis (Huang CH., *et al.* 2022) [44]. Moreover, MYBL2 and A3B in B-Myb-A3B signaling contributes to cytosine-to-thymine (C-to-T) DNA mutation. Since this signaling can be attenuated with EGF receptor with afatinib, inhibiting EGF receptor seems a targeted therapy (Chou WC., *et al.* 2017) [45]. In synovial sarcoma (SS), MYBL2 contributes to diallyl trisulfide (DATS)-induced increased intracellular reactive oxygen species (ROS) and G2/M cell cycle arrest (Xia SL., *et al.* 2021) [46] (Figure 1).

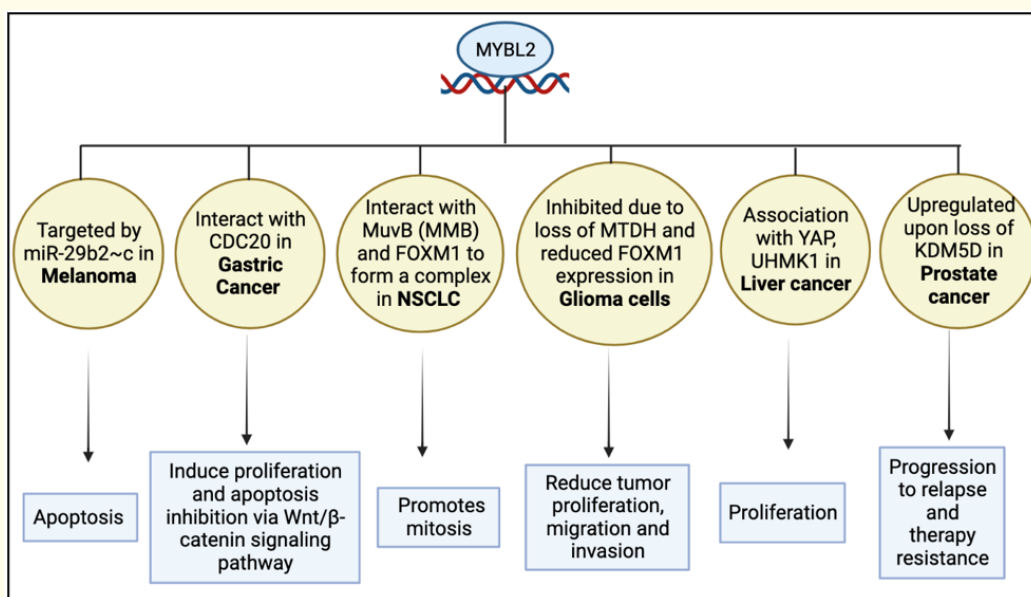


Figure 1: The mechanisms of transcription factor MYBL2 implication in tumor proliferation across various cancer.

MYBL2 associated genes in cancer

With ChIP-seq data, ASCL1 colocalized on Ras/ErbB signaling gene locus, ZEB1 and HEB are key genes to regulate MYBL2 tumorigenesis mechanisms (Zhong F., *et al.* 2022) [47]. The role of MYBL2 in tumorigenesis are seen with inferior DFS in basal breast cancer (Johnson RH., *et al.* 2015) [48], regulating purine synthesis via regulating IMPDH1 (Zhao JZ., *et al.* 2022) [49] and binding to the protective variant, A allele of rs1024176 in breast cancer (Chou WC., *et al.* 2020) [50]. Induction of proinflammatory cytokines such as IFN- γ , IL-1 β and IL-6, IL-8, IL-10 and TGF- β of RPSAP52 overexpression is modulated by MYBL2 in TSSCs proliferation (Wu X., *et al.* 2021) [51]. MYBL2 can be directly bound to the promoter of RRM2 gene and promote its transcription during S-phase together with TAF15 and MuvB components in CRC (Liu Q., *et al.* 2021) [52]. MYBL2 is a crucial regulator of DSB repair and *iMYBL2* expression levels predict cellular response to identify patients with defects in DNA repair. It can transcriptionally activate Actin-binding Rho activating C-terminal like (ABRACL) and can reverse the effects of ABRACL knockdown on cell malignant biological functions (Li J and Chen H., *et al.* 2022) [53]. Upregulating the MYBL2-mTOR axis enables MALAT1 to initiate tumorigenesis (Mu X., *et al.* 2022) [54]. Moreover, MYBL2 directly binds to the transcription start site (TSS) of Non-SMC Condensin I Complex Subunit H (NCAPH) gene in lung adenocarcinoma (LUAD) (Xiong YC., *et al.* 2020) [55]. MYBL2 transcriptional factor is promoted by nuclear translocation of hnRNPD, which is facilitated by PFDN2 in gastric cancer (Fan X., *et al.* 2021) [56]. The directly transactivating of B-Myb and E2F2 to induce malignant phenotypes in CC reveal the molecular mutual collaboration (Geng GJ., *et al.* 2018) [57].

Micro RNA as MYBL2 inhibitor

In apoptosis based therapies, the role of miRNAs as tumor inhibitor is crucial (Lee YJ., *et al.* 2017) [58]. miR-361-3p targets circ-MYBL2 directly and reverse the effects of si-circ-MYBL2 of tumor progression (Mao Y and Wang C., *et al.* 2021) [59]. For instance, with G2 arrest, ginkgetin is studied to regulate bMyb via modulating miR-34a (Bayley R., *et al.* 2020) [60]. Moreover, miR-30b-5p inhibits the progression of tumor via targeting MYBL2 expression in medulloblastoma (MB) (Xu C., *et al.* 2020) [61]. MYBL2 is targeted by miR-143-3p and regulates breast cancer cell proliferation and apoptosis (Chen J and Chen X 2018) [62]. miR-221/222- MYB family-TIMP2 axis regulatory role for breast cancer metastatic is established (Gorbatenko A., *et al.* 2019) [63]. One specific miRNA common with MYBL2 is miR-18a (Luengo-Gil G., *et al.* 2019) [64].

miR-30a inhibits androgen-independent prostate cancer by targeting MYBL2 (Li X., *et al.* 2020) [65]. Moreover, with upregulating MYBL2, long noncoding RNA (LncRNA) LINC01139 can promote tumor progression through competitively binding to miR-30 family (Pattschull G., *et al.* 2019) [66]. In addition, miR-30a overexpression increases cell apoptosis, induce cell cycle arrest and attenuate expression levels of MYBL2 (Druz A., *et al.* 2013) [67].

In regulating cell cycle signaling via miR-30c-2-3p/MYBL2 axis, a tumorigenesis role in LUAD is studied with LINC00346 (He Q., *et al.* 2023) [68]. MYBL2 interacts with a loop of LncRNA LOXL1 antisense RNA 1 (LOXL1-AS1) promoter to give LOXL1-AS1/miR-423-5p/MYBL2, indicating a positive feedback. MYBL2 knockdown could counteract miR-423-5p repression-mediated enhancement on the progression of LOXL1-AS1 downregulated cells in LUAD (Li W., *et al.* 2019) [69]. MYBL2 activated LncRNA PTPNA antisense RNA 1 (PTPNA-AS1) plays an oncogenic role in triple-negative breast cancer (TNBC) via upregulating SIK2 in breast cancer (Liu B., *et al.* 2021) [70]. Another miR-29 target transcription factor is MAFG. This and MYBL2 are partially associated with miR-29b2~c expression attenuation thereby leading to melanoma (Xu Q., *et al.* 2021) [71].

MM-associated circular RNA (Circ-MYBL2)

circ-MYBL2 can suppress the effects of miR-28 on tumor proliferation and induce apoptosis (Druz A., *et al.* 2013) [72]. In addition, circ-MYBL2 affects the phosphorylation level of its linear isoform, in which it facilitates the binding of Cyclin F to MYBL2, dampening MYBL2 phosphorylation and activation in multiple myeloma (MM) (Yu S., *et al.* 2020) [73]. Moreover, circMYBL2 activates FMS-like tyrosine kinase-3 Internal tandem duplication (FLT3-ITD)-dependent signaling pathways. It enhances the translational efficiency of FLT3 kinase via increasing the binding of polypyrimidine tract-binding protein 1 (PTBP1) to FLT3 messenger RNA (Sun YM., *et al.* 2019) [74]. circ-MYBL2 overexpression increases miR-92b expression while reducing mature miR-92b level. Therefore, circ-MYBL2 inhibits cell proliferation and suppresses the effect of miR-92b in gastric cancer (Luo R. 2022) [75]. MYBL2 is among the frequent miR-29a-downregulated target genes (Dey S., *et al.* 2020) [76]. An instance is the synergistically downregulation of miR-19a via methylation to suppress tumor proliferation in pancreatic adenocarcinoma (PA) (Qian X., *et al.* 2023) [77]. In addition, MYBL2/Ser241 can arrest leukemia at prometaphase (Morita K., *et al.* 2020) [78]. Since MYBL2 binds to OPA3, a promoter region,

and catalyze transcription, *MYBL2* knockdown will seize aerobic glycolysis in hepatocellular carcinoma (HCC) (Liu M., *et al.* 2019) [79]. Alpha-actinin-4 (ACTN4) and *MYBL2* association in tumor progression requires further studies (Gründl M., *et al.* 2020) [80].

Conclusion

In a more specific approach to cancer research, in addition to immunotherapy, radiotherapy and chemotherapy, energy metabolism is fundamental. Among the genes and proteins that influence the energy metabolism of tumor mechanism is *MYBL2*. This gene enhances cell cycle progression for tumor evasion and dominating the immune cells via TME. This review could establish *MYBL2* as cell cycle modulator, survival and the differentiation. Based on its biological functions and mechanisms, no two study are seen with a uniform pathway. Although, majority of the studies could establish delay cell cycle proliferation as anti-tumorigenesis, the biological pathways are not even cancer specific and thus, the need for comprehensive studies to harness the biological mechanisms. Moreover, tobacco (Nicotine), liquor, carcinogens as in the packed food additives etc. needs can hold key to the cellular mechanism.

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