

Abnormal activation of the Ras/MAPK signaling pathway in oncogenesis and progression

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Author contributions

Xu H conducted the literature review and prepared the original draft. Ren SM and Wang Y assisted in gathering literature and write the original draft. Zhang TT contributed to the project conception, reviewed and edited the final manuscript. Lu J contributed to project conception and manuscript review, and secured funding.

Competing interests

The authors declare no conflicts of interest.

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Abbreviations

MAPK, Mitogen-Activated Protein Kinase; MEK, mitogen-activated protein/extracellular signal-regulated kinase; ERK, extracellular signal-regulated kinase; GDP, guanosine diphosphate; GTP, guanosine triphosphate; GAPs, GTPase-activating proteins; CDKs, cyclin-dependent kinases; p-ERK, activated ERK; MMP, matrix metalloproteinase.

Citation

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Abstract

The Ras/MAPK signaling cascade plays an essential role in the regulation of cellular processes, including proliferation, differentiation, and survival, serving as a pivotal intracellular communication network. Dysregulation of this pathway, frequently attributable to mutations within Ras genes, has been strongly associated with the development of a spectrum of cancers. This review underscores the pivotal role of the Ras/MAPK pathway in oncogenic transformation and tumor progression, briefing the intricate mechanisms through which the aberrant activation of this pathway leads to unbridled cell proliferation, inhibition of apoptosis, promotion of metastasis, and induction of angiogenesis, thereby providing valuable insights into the pathogenesis of malignancies. It also underscores the significance of the Ras/MAPK pathway as a therapeutic target and discusses the challenges and potential of targeted therapies, including combination treatments and personalized medicine approaches, to overcome resistance and enhance treatment efficacy in cancers driven by pathway dysregulation.

Keywords: Ras; MAPK; oncogenesis; therapeutic targets

Introduction

Tumorigenesis and tumor progression are multifaceted processes encompassing the dysregulation of numerous molecules and signaling cascades. Among the many signal transduction pathways, the mitogen-activated protein kinase (MAPK) signaling axis, an evolutionarily conserved cascade in eukaryotic cells, has garnered significant interest due to its pivotal role in governing cellular proliferation, differentiation, and survival [1–3]. The canonical MAPK signaling pathway typically involves Ras, Raf, mitogen-activated extracellular signal-regulated kinase (MEK), and extracellular signal-regulated kinase (ERK) cascade, also known as Ras/MAPK pathway. Aberrant activation of this pathway is closely linked to the etiology and progression of diverse malignancies, with its deregulation contributing to unchecked proliferation and the promotion of oncogenesis and tumor progression [4]. Hence, elucidating the regulatory mechanisms of the Ras/MAPK pathway is imperative for devising efficacious anti-neoplastic treatment protocols.

Abnormal activation of the Ras/MAPK signaling cascade often stems from regulatory malfunctions at various levels, including overexpression of receptor tyrosine kinases (RTKs), loss of function in GTPase-activating proteins (GAPs), and sustained activation of downstream effectors like MEK and ERK [5, 6]. These alterations not only fuel the proliferation and survival of cancer cells but also play a crucial role in reshaping the tumor microenvironment, promoting angiogenesis, and conferring drug resistance, thereby emerging as significant targets for therapeutic intervention in oncology.

Decades of research have provided an in-depth dissection of the structure and function of the Ras/MAPK signaling pathway. Notably, researchers have identified numerous molecular events associated with oncogenesis, particularly focusing on mutations in Ras or Raf proteins and the activation status of the pathway [7–9]. Concurrently, targeted therapeutic strategies against this pathway are evolving, including small molecule inhibitors and antibody-based drugs. Nonetheless, the diversity of mutations and the intricacy of pathway regulation present considerable challenges for developing effective therapeutic interventions targeting the Ras/MAPK signaling axis.

This article provides a brief overview of the role of the Raf-MAPK pathway in oncogenesis and tumor progression, detailing the

transduction mechanism and implications of abnormal activation within the pathway, as well as evaluating current therapeutic approaches targeting this pathway, aiming to offer new insights and strategies for cancer management by leveraging this in-depth understanding of the regulatory mechanism.

Composition and transduction mechanism of Ras/MAPK signaling pathway

The Ras/MAPK pathway stands out as a quintessential signal transduction cascade that relays signals from upstream extracellular growth factors to a series of downstream effectors within the nucleus, thereby modulating various cellular functions [10, 11]. Activation of the Ras/MAPK pathway commences with the activation of Ras proteins [12]. Activated Ras triggers the recruitment and subsequent activation of Raf kinases, which in turn phosphorylates and activates MEK, propelling it to phosphorylate ERK, and this phosphorylated ERK then translocates to the nucleus to orchestrate gene expression changes and modulate a myriad of transcription factors [13]. This section will delve into the composition of the Ras/MAPK pathway and the mechanisms by which it transduces signals, setting the stage for understanding how dysregulation can contribute to cancer development (Figure 1).

Ras

Ras proteins, a family of small GTPases that include H-Ras, K-Ras, and N-Ras isoforms, serve as key upstream regulators of the Ras/MAPK pathway [14]. Upon binding to receptors on the cellular membrane, Ras proteins receive extracellular signals and transmit these signals by activating downstream effectors, thereby modulating cellular processes such as growth, differentiation, and survival. Ras proteins function as molecular switches in signal transduction, cycling between a GTP-bound active form and a GDP-bound inactive form within the cell. This shift is stringently regulated by guanine nucleotide exchange factors (GEFs) and GAPs: GEFs facilitate the activation of Ras by catalyzing GTP binding, whereas GAPs promote Ras inactivation through the acceleration of GTP hydrolysis.

In normal cells, the activity of Ras proteins is precisely regulated to maintain intracellular homeostasis, however, cancerous mutations in Ras proteins sustain its activation, driving unbridled cell proliferation and invasion, further exacerbating the malignancy of tumor [15, 16].

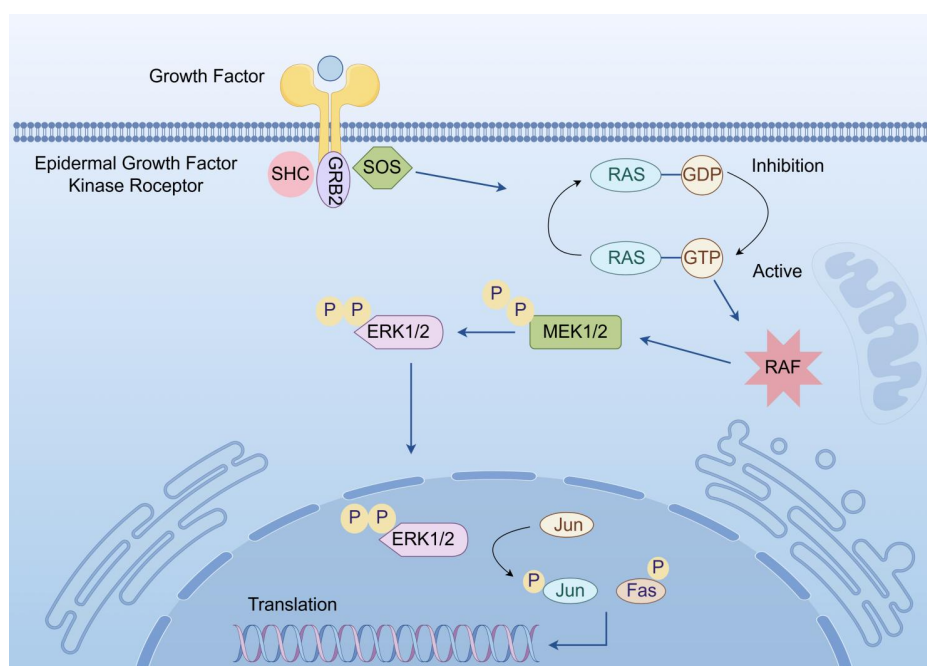


Figure 1 Composition of the Ras/MAPK pathway and the mechanism of its transduction signal

RAS is among the most prevalent genetic mutations in oncology, with a mutation rate of up to 21% across all cancer types, which differ in mutation subtypes, mutation sites, and amino acid substitutions among different cancer types [17]. Among these, *KRAS* mutations are the most prevalent, primarily involving codon 12 with G12D (glycine replaced by aspartic acid) and G12C (glycine replaced by cysteine) substitutions. *KRAS* point mutations are identified in 14.3% of all tumors, with particularly high rates in pancreatic ductal adenocarcinoma (90%), colorectal cancer (CRC) (50%), thyroid cancer (50%), and lung cancer (30%) [18–21]. *NRAS* mutations rank second, primarily observed in melanoma (23%), chronic myelomonocytic leukemia (CMML, 13.1%), and acute myeloid leukemia (AML, 13.6%) among hematological malignancies. *HRAS* mutations are less frequent, with reports of bladder cancer (4.06%) and head and neck squamous cell carcinoma (4.21%). In contrast to *KRAS*, mutations in *NRAS* and *HRAS* are predominantly localized to codon 61 [22, 23]. Such mutations abrogate the normal negative feedback of Ras proteins, leading to their persistent activation of downstream signaling cascades, thus fostering uncontrolled cellular proliferation and invasion, and propelling the initiation and progression of tumors.

Raf

As downstream kinases of Ras proteins, the Raf kinase family comprises A-Raf, B-Raf, and C-Raf, three homologous subtypes sharing highly similar structural domains [24]. The C-terminus of Raf contains a kinase-binding domain that would bind to the N-terminus in the absence of RAS-GTP, to maintain the inactive conformation of Raf. Upon activation of Ras by GTP binding, Ras-GTP binds to the kinase-binding domain of Raf, initiating Raf activation. Activation of Raf is a complex process that involves Raf recruitment to the cell membrane, the Ras-Raf complex assembly, phosphorylation and dephosphorylation of multiple regulatory sites on Raf proteins, and dimerization of Raf, including both homo- and heterodimer formation [25]. However, the precise sequence of these events and the detailed mechanisms are still under investigation [26]. Yet, the mechanism of RAF inhibitors (RAFi) has revealed that dimerization is a critical step for Raf kinase activity and the effectiveness of RAFi therapy.

The Raf family is highly conserved in mammals, with mutations implicated in numerous cancers [15]. *CRAF*, the first subtype identified for its potential oncogenic properties, is rarely mutated in human cancers, and early development of *CRAF* inhibitors functions as downstream effectors of RAS to inhibit signal transduction [27]. *BRAF* gene mutations are prevalent in several cancer types, notably in thyroid cancer (45–50.9%), melanoma (36.4%), and CRC (6.5–10.2%). The *BRAF* V600E mutation, substituting valine with glutamic acid, constitutes the majority of oncogenic *BRAF* mutations, representing over 90% of such alterations [28]. Other oncogenic *BRAF* mutations are predominantly located within the activation segment or the Gly-rich loop of the *BRAF* protein. Mutations in *ARAF* are relatively rare in cancer, occasionally observed in lung and melanoma, and may influence the modulation of RAS activity [29]. Hyperactivation of *CRAF* is a frequent hallmark of oncogenic signaling by upstream proteins, including RAS and growth factor receptors, whereas *BRAF* mutation can lead to sustained activation of the Raf/MAPK pathway, promoting tumorigenesis.

MEK

MEK, a pivotal intermediate node in the Ras/MAPK signaling pathway, serves as a bridge connecting upstream RAS and RAF proteins with downstream ERK proteins, thereby executing its biological function [30]. Upon activation, the C-terminal catalytic domain of Raf engages with MEK, phosphorylating two Ser residues in the VIII subdomain of MEK's catalytic domain, which activates MEK. MEK as a rare dual-specificity kinase, phosphorylates specific threonine and tyrosine residues on ERK, leading to a spectrum of biological outcomes such as cell proliferation, differentiation, migration, and survival [31, 32].

Mutations in *MEK1* and *MEK2*, such as Q56P-MEK1, K57N-MEK1,

and D67N-MEK1, have been detected in lung, gastric, and ovarian cancers [33]. These alterations augment the intrinsic activity of MEK, resulting in the persistent activation of ERK, thereby promoting cell proliferation and oncogenic development. Despite the lower mutation frequency of *MEK1/2* compared to *BRAF* and RAS, their position downstream of these commonly mutated genes makes *MEK1/2* a highly promising therapeutic target.

ERK

ERK kinases, predominantly ERK1 and ERK2, are the exclusive downstream effectors of MEK widely distributed in the cytoplasm [34, 35]. Upon MEK activation, it directly interacts with ERKs through its N-terminal domain, specifically phosphorylating the Tyr and Thr residues within the “TEY motif” of ERK, leading to its activation. Activated ERK translocate to the nucleus, modulating the activity of transcription factors to regulate gene expression, influencing the cell cycle, and promoting cell proliferation, differentiation, and apoptosis [36].

ERK1/2 is implicated in diverse physiological processes, including meiosis and mitosis, and is activated by a spectrum of stimuli, such as growth factors, cytokines, and viral agents. Dysregulated ERK activation acts as a signaling intermediary and amplifier in tumor invasion and metastasis, influencing the proliferation and survival of cancer cells by impacting nuclear transcription factors such as AP-1 and NF- κ B. ERK has been observed to be overactive in various human cancers, including oral, melanoma, and breast [37, 38]. Studies have indicated that ERK inhibitors (ERKi) can effectively block the Ras-Raf-MEK-ERK signaling cascade, overcoming resistance induced by upstream *BRAF* and MEK mutations [39–42]. Currently, primary ERK inhibitors such as AZD0364, KO-947, Ulixertinib, and HH2710 are being evaluated in clinical trials for their efficacy.

In brief, the Ras/MAPK signaling pathway orchestrates a series of phosphorylation events, amplifying initial signals to elicit an appropriate cellular response. Under normal conditions, this process is stringently regulated to preserve cellular homeostasis. In cancer, however, this balance is perturbed, resulting in pathological outcomes. Gaining insight into the regulatory mechanisms of this pathway is essential for devising targeted therapies to restore cellular equilibrium and curb tumorigenesis.

Implication of Ras/MAPK pathway in oncogenesis and progression

Aberrant activation of the Ras/MAPK signaling pathway can drive tumorigenesis by promoting cellular proliferation, survival, invasion, and metastasis through multiple mechanisms. Approximately one-third of cancers exhibit abnormal activation of the Ras/MAPK signaling pathway, particularly *KRAS* mutations in pancreatic, CRC, and lung cancers, as well as *BRAF* mutations in melanoma and hypermutated CRCs [43, 44]. Notably, despite RAS being recognized as an proto-oncogene, a single RAS mutant alone is insufficient to trigger cancer; instead, the combination of mutant RAS with hyperactivated downstream effectors in the MAPK pathway is more likely to contribute to cancer progression [45]. This section will dissect how the dysregulation of this pathway contributes to the hallmarks of cancer, including uncontrolled cell proliferation, inhibition of apoptosis, the acquisition of invasive properties, and tumor angiogenesis.

Cell proliferation

A hallmark of cancerization is uncontrolled cell proliferation, characterized by disruptions in cell cycle regulation, hyperactivation of growth factor signaling, and resistance to apoptosis [46]. Mutations in Ras genes are a major driving force behind the initiation and progression of various cancers, typically identifiable in the early phases of oncogenesis (Figure 2). Such mutations confer Ras proteins with insensitivity to GAPs, perpetuating their active state and triggering stimuli-free, unrestrained signal transduction, resulting in unchecked cell growth and proliferation. Extensive experimental data

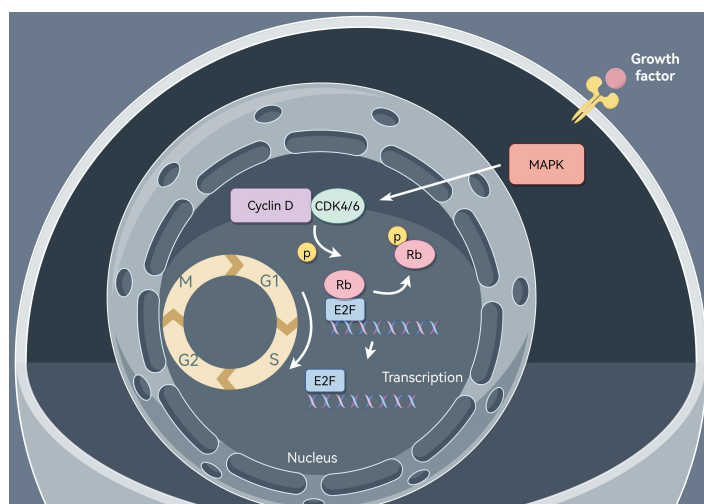


Figure 2 Regulation of Ras/MAPK signaling pathway on tumor cell cycle

demonstrated that the Raf-MEK-ERK signaling cascade, triggered by the activation of Ras proteins, is one of the primary pathways in tumorigenesis, promoting a variety of cellular processes, including cell proliferation and survival [47–49]. Activated ERK, for instance, can stimulate transcription factors such as Fos and Jun to form AP-1 complexes, or bind to specific DNA sequences adjacent to genes such as Myc, thereby initiating the transcription of these genes and further activating other gene expressions [50].

Ultimately, the activation of these signaling pathways results in increased Cyclin D expression, which forms complexes with cyclin-dependent kinases (CDKs) such as CDK4 and CDK6, driving the cell from the G1 phase into the S phase to initiate DNA replication, thereby facilitating cell cycle progression [51]. In short, the seamless progression of the cell cycle is essential for cell proliferation, which is crucially stimulated by the Ras/MAPK pathway.

Apoptosis inhibition

In cancer cells, the Ras/MAPK signaling pathway dually promotes cell proliferation and inhibits apoptosis under specific conditions, modulating an array of apoptosis-related proteins to influence cellular survival and demise (Figure 3). The modulation of apoptosis by the Ras/MAPK pathway is highly intricate. It has been confirmed that blocking the Ras/Raf/MEK/ERK cascade can activate the expression of PARP and Caspase-3, thereby inducing apoptosis [52]. Moreover, ERK1/2, acting as upstream regulatory kinases, can activate NF- κ B, which then regulates the expression of anti-apoptotic genes Bcl-2 and Bcl-xL, while concurrently reducing the phosphorylation levels of the pro-apoptotic protein Bad, promoting the degradation of Bad, Bax, and Bim [53, 54]. The activated ERK1/2 signaling pathway can also preserve mitochondrial function, inhibiting the release of cytochrome C from mitochondria that would otherwise trigger the caspase cascade, further dampening downstream effector molecules, and consequently reducing cell apoptosis [55]. These studies collectively underscore the pivotal role of the Ras/Raf/MEK/ERK signaling pathway in the induction of apoptosis.

Metastasis and invasion

Tumor metastasis, as a major contributor to cancer-related mortality, involves the Ras/MAPK signaling pathway, which plays a crucial role in tumor cell migration and invasion by regulating the gene expressions associated with cell migration (Figure 4) [56]. For one thing, the Ras/MAPK signaling pathway facilitates cell migration by modulating the expression and activity of integrins, enhancing cell adhesion to the extracellular matrix [57]. For another, activated ERK (p-ERK) fosters the degradation of the extracellular matrix by enhancing the expression of MMP-2 and MMP-9, members of the calcium-dependent matrix metalloproteinases (MMPs) that are involved in tissue remodeling and extracellular matrix degradation,

facilitating the invasion of cancer cells through the basement membrane, thus enabling them to enter the circulatory or lymphatic systems and initiate distant metastasis [58]. The natural product Bruceine A has recently been proven to inhibit the proliferation, migration, and invasion of triple-negative breast cancer, correlating with the downregulation of MMP-2/9 proteins and the suppression of the ERK signaling pathway [59].

Furthermore, ERK activation enhances actomyosin contractility and cell motility, inducing master regulators of the epithelial-mesenchymal transition (EMT) to bolster cell migration capabilities [60]. Studies have shown that in a xenograft mouse model of CRC, ERK2 activation mediates liver metastasis [61]. ERK1 and ERK2 with an 84% sequence homology, are recognized for their overlapping roles, yet recent findings underscore the unique function of ERK2 in mediating EMT in breast and colon cancers, suggesting that inhibiting the ERK pathway could curtail the promotional effects of HGF and similar extracellular signals on cell motility, potentially suppressing tumor invasion and metastasis [62–64]. Additionally, oncogenic *KRAS* effectors were reported to be capable of activating CREB1 for physical interactions with mutant p53, thus hyperactivating multiple prometastatic transcriptional networks, contributing to pancreatic ductal adenocarcinoma [65]. Pharmacologic CREB1 inhibition can disrupt cooperation between oncogenic *KRAS* and mutant p53 to mitigate metastasis, offering a new strategy to dampen pancreatic ductal adenocarcinoma.

Tumor angiogenesis

Angiogenesis refers to the process of forming new blood vessels from pre-existing vascular systems, typically induced by hypoxia, inflammation, or tumor growth [66–68]. This process is crucial for tumor growth and metastasis, as tumor cells require the supply of adequate oxygen and nutrients provided by neovasculature. VEGF is a highly specific angiogenic factor that stimulates blood vessel formation within the body. Studies have shown that the Ras/MAPK pathway acts as a promoter of angiogenesis, capable of activating transcription factors to boost VEGF gene transcription and upregulate VEGF expression in tumor cells, thus fostering the development of new blood vessels (Figure 5) [69]. The Ras/MAPK pathway can also suppress the expression of thrombospondin-1 (TSP-1), a negative regulator of angiogenesis with anti-angiogenic properties. By inhibiting TSP-1 gene expression, activated Ras promotes angiogenesis, thereby facilitating tumor growth, invasion, and metastasis [70].

Overall, mutations within the Ras/MAPK signaling cascade are pivotal in instigating oncogenic processes, including enhanced cell proliferation, impeded apoptosis, and the facilitation of metastasis and angiogenesis. The dysregulation of Ras/MAPK pathway is a pervasive

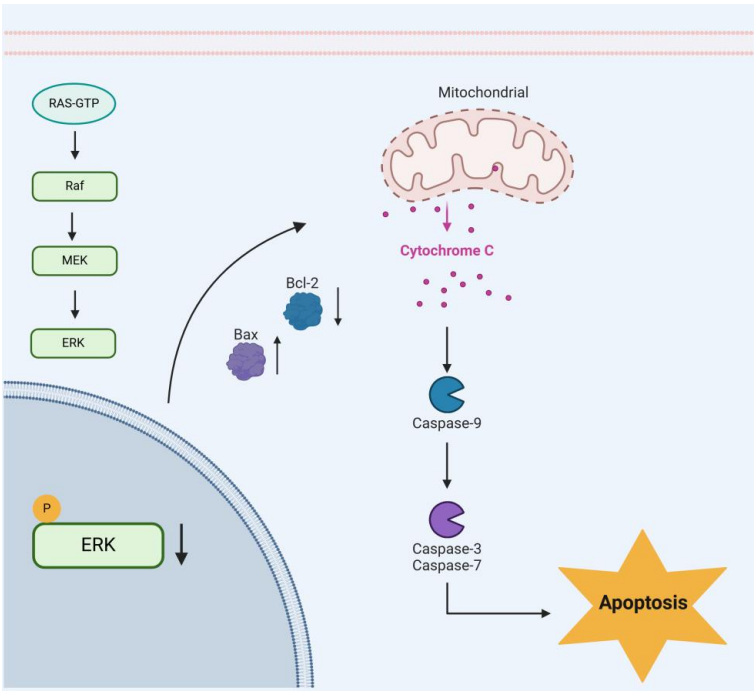


Figure 3 The Ras/MAPK signaling pathway is involved in tumor cell apoptosis

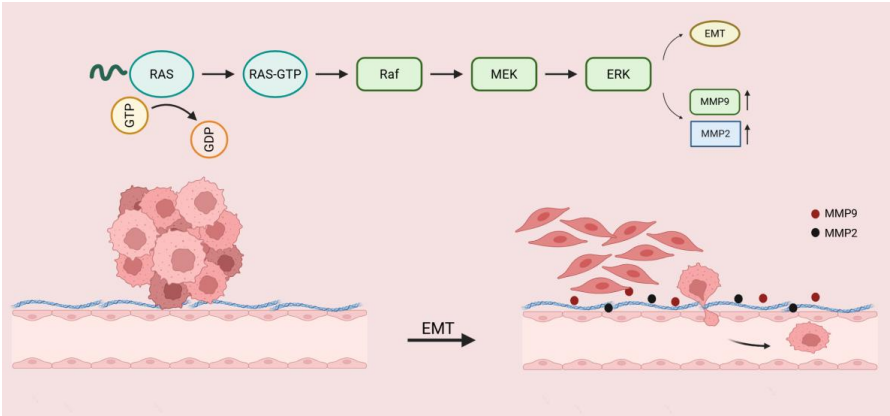


Figure 4 The Ras/MAPK signaling pathway is involved in tumor cell migration

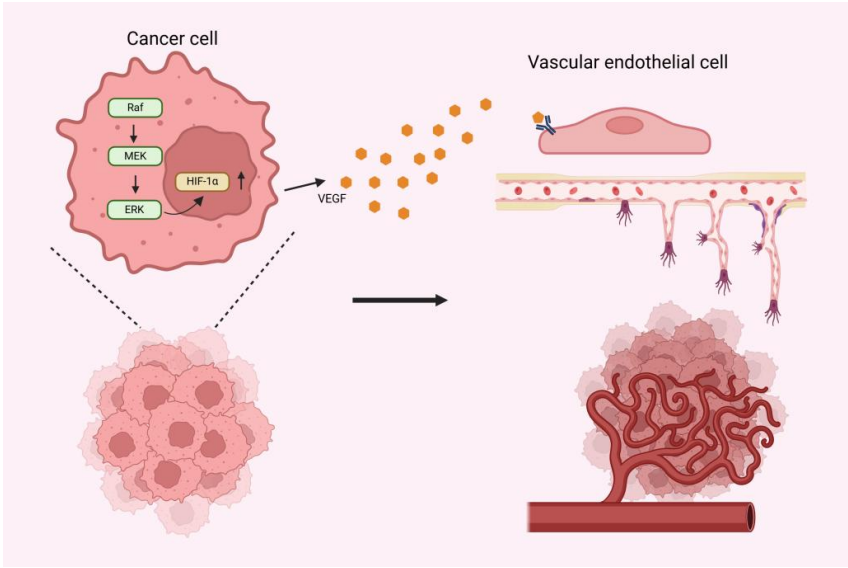


Figure 5 Effect of Ras/MAPK on tumor angiogenesis

feature across various malignances, highlighting its significance as a therapeutic target. Understanding these mechanisms is crucial for developing effective cancer treatments.

Progress and challenges in anti-tumor research targeting the Ras/MAPK signaling pathway

The widespread dysregulation of the Ras/MAPK signaling pathway across multiple cancer types has spurred significant research into targeted therapeutics. Current treatment approaches are directed either at the mutated Ras proteins themselves or at their downstream effectors. Nonetheless, the propensity for resistance with single-agent therapies underscores the importance of combination drug regimens in pharmaceutical development.

Targeting Ras mutant

RAS inhibitors suppress the activity of Ras protein either by locking its GDP-bound state or covalently binding to the GTP-bound state of RAS. Although Ras proteins were once considered “undruggable” due to the absence of allosteric inhibitor binding pockets and their high affinity for GTP, recent research has surmounted these challenges, especially with significant progress in the development of *KRAS* inhibitors [71–73]. These inhibitors can occupy the newly discovered “Switch-II pocket” on *KRAS* G12C, locking the *KRAS* G12C protein in its GDP-bound inactive state and thereby inhibiting downstream signaling. Sotorasib and adagrasib, as the first approved *KRAS* G12C inhibitors, offer new hope for the treatment of tumors with RAS mutations.

Targeting downstream effectors of Ras

Beyond direct RAS targeting, efforts are underway to develop inhibitors against RAS downstream effectors. RAF kinases, the immediate downstream targets of RAS, have inhibitors like Vemurafenib and Dabrafenib that have been approved for treating melanoma with *BRAF* V600 mutations [74, 75]. However, the application of these drugs in RAS-mutant tumors is constrained, as they may intensify MAPK pathway activation. Next-generation RAF inhibitors, particularly type II RAF inhibitors that target RAF dimers, have demonstrated therapeutic efficacy against RAS-mutant tumors, offering novel strategies for clinical treatment [76]. Advancements in MEK inhibitor research have led to the approval of multiple MEK

inhibitors for market use, with further candidates in various stages of clinical investigation [77]. While ERK, being the exclusive substrate of MEK, lacks approved inhibitors, small molecule compounds targeting ERK1/2 are under assessment in preclinical and clinical studies for cancer treatment [42, 78].

Drug resistance and combination therapy

Tumor resistance to Ras/MAPK pathway inhibitors represents a considerable challenge, potentially attributable to negative feedback mechanisms, sustained activation of upstream receptors, emergence of new mutations at drug-binding sites, redundant activation within the MAPK pathway, and engagement of parallel pathways like PI3K/AKT/mTOR [79]. These resistance mechanisms curtail the effectiveness of monotherapy, thereby driving the exploration of combination therapy strategies to augment therapeutic efficacy.

The essence of combination therapy strategies lies in targeting multiple nodes within the Ras/MAPK pathway simultaneously, as well as integrating immunotherapy and inhibiting parallel pathways. For instance, co-targeting both upstream and downstream nodes of the Ras/MAPK pathway can reduce signal escape, while the integration of immunotherapy may activate the innate immune system to attack tumor cells. Research has demonstrated that MEK inhibitors, such as trametinib and cobimetinib, yield synergistic effects when combined with RAF inhibitors in oncological therapy, an good example is the The Fast Track designation for the combination therapy granted by the U.S. FDA On December 11, 2023, which combines RAF dimer inhibitor naporafenib with MEK inhibitor trametinib for the treatment of adult patients with *NRAS*-mutated unresectable or metastatic melanoma [80, 81]. Additionally, an increase in autophagy activity is observed in numerous RAFi-resistant cells, potentially aiding cancer cells in circumventing RAFi. Consequently, the concurrent targeting of RAF and autophagy genes may constitute a novel and potent therapeutic approach for treating *BRAF* and *KRAS*-mutated cancers.

To date, a variety of drugs targeting the Ras/MAPK signaling pathway have been successfully approved and commercialized (Table 1), with numerous candidates in preclinical or clinical studies. Despite the challenges inherent in therapeutic strategies aimed at the Ras/MAPK signaling pathway, including the emergence of tumor resistance and the intricacies of signal transduction networks, future research promises a field replete with both opportunities and challenges.

Table 1 Overview of approved drugs targeting Ras/MAPK pathway

General name	Trade name	First approval	Targets/biomarkers	Indications
Vemurafenib [82]	Zelboraf	2011	BRAF	<i>BRAF</i> -mutated metastatic melanoma
Dabrafenib [83]	Tafinlar®	2013	BRAF	Unresectable or metastatic melanoma in patients with the <i>BRAF</i> ^{V600E} mutation
Trametinib [84]	–	2013	MEK1/2	Unresectable or metastatic malignant melanoma with <i>BRAF</i> ^{V600E} or ^{V600K} mutations
Cobimetinib [74]	Cotellic®	2015	MEK	Unresectable or metastatic <i>BRAF</i> ^{V600} mutation-positive melanoma
Selumetinib [85]	Koselugo®	2017	MEK1/2	Adjuvant treatment for thyroid cancer, neurofibromatosis type 1 (NF1)
Binimetinib [86]	Mektovi®	2018	MEK	Unresectable or metastatic melanoma with a <i>BRAF</i> ^{V600E} or ^{V600K} mutation
Encorafenib [86]	Braftov™	2018	BRAF	Unresectable or metastatic melanoma with a <i>BRAF</i> ^{V600E} or ^{V600K} mutation
Sotorasib [87]	Lumakras™	2021	RAS	Non-small cell lung cancer (NSCLC) and CRC with <i>KRAS</i> mutations
Tunlametinib [88]	Keluping®	2024	MEK1/2	Solid tumors with <i>RAS</i> and <i>RAF</i> mutations, including melanoma, NSCLC, CRC and NF1 plexiform neurofibromas
Adagrasib [89]	KRAZATI™	2023	KRAS G12C	NSCLC and CRC harboring <i>KRAS</i> G12C oncogenic driver mutation

Perspective and Conclusion

The Ras/MAPK signaling pathway, with its intricate network of kinases and transcription factors, stands at the forefront of oncogenic research due to its pivotal role in tumorigenesis and cancer progression. Dysregulation of this pathway has been implicated in a multitude of cancers, positioning it a promising target for therapeutic intervention.

The advent of therapies specifically targeting the Ras/MAPK pathway has yielded promising results in both preclinical and clinical studies [90–93]. Nonetheless, the intricate nature of the pathway, coupled with the multiplicity of signaling mechanisms, has presented considerable hurdles in the development and application of effective treatments. For instance, the engagement of alternative pathways can lead to resistance against MEK or ERK inhibitors [94, 95]. In light of this, multi-target intervention strategies that simultaneously disrupts various nodes within the pathway may be crucial for achieving robust tumor suppression. Considering the complexity of resistance mechanisms and the intricate interactions within signaling pathways, combination therapy has emerged as a feasible alternative. Research is ongoing to evaluate the synergistic effects of combining MEK inhibitors with other targeted therapeutics, including PI3K inhibitors and immunotherapies, aiming to overcome drug resistance mechanism and enhance treatment efficacy [96–98]. This multi-targeted therapeutic approach is designed to engage multiple key nodes within the Ras/MAPK pathway, leveraging the synergistic action of disparate mechanisms to potentiate treatment outcomes and diminish the incidence of resistance. Moreover, this multifaceted approach may attenuate the adverse effects associated with single-agent therapies, potentially elevating patient quality of life.

Moreover, the rise of personalized medicine has ushered in an era where treatment is tailored to the molecular profile of an individual's tumor [99, 100]. Given the site-specific nature of oncogenic mutations in key components of the Ras/MAPK signaling pathway, such as RAS, RAF, and MEK, genomic sequencing to pinpoint these mutations is essential for the precision development of targeted therapeutics, thereby optimizing treatment efficacy and minimizing unwanted adverse effects. Inhibitors specifically targeting the *KRAS* G12C mutation, such as sotorasib and adagrasib, as well as those targeting the *BRAF* V600E mutation, such as encorafenib, have exhibited therapeutic efficacy in clinical trials for tumors harboring these specific mutations [101–103]. The advancement of these targeted inhibitors offers novel therapeutic avenues for patients with such mutations, signifying a substantial advancement in treatment strategies. The etiology and progression of tumors are intricate and dynamic processes, with malignancy levels leading to significant disparities in tumor biomarkers. Consequently, the precise detection of biomarkers is crucial for devising personalized treatment plans. In addition to chemotherapy, it is imperative to consider a range of therapeutic modalities, including radiotherapy and surgical resection, tailored to the specific conditions of each patient, in order to maximize patients' outcomes.

In conclusion, the Ras/MAPK signaling pathway is a critical mediator of cellular processes that, when dysregulated, contributes significantly to cancer development and progression. An in-depth investigation of the Ras/MAPK signaling pathway not only offers novel insights into the molecular mechanisms underlying tumorigenesis but also provides a scientific rationale for the development of innovative therapeutic strategies and pharmaceuticals. Future research endeavors should delve into the mechanisms of these pathway constituents across diverse tumors and explore how to surmount therapeutic challenges through combinatorial treatments and personalized medicine approaches.

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