

# Targeted therapy in BRAF-mutant melanoma: Advances and challenges (Review)

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**Abstract.** Over half of patients with melanoma exhibit v-Raf murine sarcoma viral oncogene homolog B (BRAF) mutations, which drive hyperactivation of the MAPK pathway and confer high proliferative potential. To target this oncogenic mutation, BRAF inhibitors, as well as MEK inhibitors (targeting the downstream effector of BRAF), have been approved for melanoma therapy. Although these inhibitors initially decrease the tumor burden, nearly all patients eventually develop drug resistance, leading to aggressive disease relapse at both the primary and metastatic sites. Understanding the mechanisms underlying tumor escape from drug lethality is crucial for the development of strategies against melanoma. The present study aimed to summarize the discovery, development and clinical evolution of the BRAF and MEK inhibitors approved for the treatment of melanoma, their notable efficacy in suppressing aggressive melanoma progression and the underlying mechanisms of acquired resistance.

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## 1. Introduction

During embryonic development, melanoblasts, derived from neural crest stem cells (NCSCs), migrate to the epidermis and differentiate into melanocytes. Upon stimulation by ultraviolet radiation or genetic alterations, melanocytes initiate tumorigenesis in the epidermis (1). They invade the dermis by reacquiring NCSC-like characteristics and losing well-differentiated melanocytic phenotypes (1). Mutations in driver gene are key for the carcinogenic transformation of melanocytes. Among these, the v-Raf murine sarcoma viral oncogene homolog B (BRAF) mutation is the most prevalent in melanoma and was first identified in 2002 (2). Somatic mutation screening has shown that BRAF mutations occur in 59% of melanoma (2,3), 44% of papillary thyroid carcinomas (4), 18% of colorectal cancer, 11% of glioma, 9% of sarcoma and 3% of lung cancer cases (2).

As a member of the RAF kinase family (which also includes ARAF and CRAF), BRAF serves a key role in the MAPK signaling pathway, regulating critical cellular processes including proliferation, metastasis, differentiation and survival. Serving as the primary regulator of the RAS/RAF/MAPK kinase (MEK)/ERK signaling cascade, BRAF mediates the activation of downstream targets, MEK and ERK, throughout this pathway (5,6). The kinase activity of the class I mutant BRAF is constitutively activated, leading to hyperstimulation of the MAPK pathway and excessive cell proliferation and metastasis. Class I BRAF mutations typically occur at the V600 residue, with the mutant protein exhibiting high kinase activity even in its monomeric form. Notably, the kinase activity of V600-mutant BRAF is less RAS-dependent than that of non-V600 mutations, similar to that of class II mutant BRAF (5). By contrast with class I mutations, class II BRAF mutations occur at non-V600 sites and result in moderate kinase activity in the dimeric conformation.

Class III BRAF mutations, which also involve non-V600 sites, typically form heterodimers with wild-type RAF and exhibit RAS-dependent, minimal kinase activity (5-7) (Table I). In total, >97% of BRAF mutations are class I mutations. Non-V600 mutations, such as K601, L579, G469, G464, D549, G466, and D287, occur in ~1% of patients with melanoma (5,8). Given the high prevalence of V600-mutant BRAF in patients with melanoma, targeted small-molecule inhibitors of BRAF<sup>V600</sup> have been developed, such as vemurafenib, dabrafenib and encorafenib (6). While BRAF inhibitors are promising in delaying disease progression, the majority of patients with melanoma develop resistance after several treatment cycles, and ~70% of patients succumb to disease progression within 5 years of treatment (9), highlighting the importance of understanding and overcoming the relapse phase in therapeutic resistance.

The present study aimed to review the discovery, development and clinical evolution of BRAF and MEK inhibitors for targeted melanoma therapy (Table II). Tumor-intrinsic resistance mechanisms driven by dynamic phenotypic plasticity and acquired genetic mutations, as well as the potential therapeutic strategies to overcome drug resistance, are also discussed.

## 2. BRAF inhibitor monotherapy

*Vemurafenib, the first BRAF inhibitor approved for clinical trials.* Vemurafenib, known as PLX4032 during preclinical testing, is an analog and optimized derivative of PLX4720 (10), the first selective BRAF<sup>V600E</sup> inhibitor. PLX4720 served as the lead compound and demonstrated high selectivity for BRAF<sup>V600E</sup> over wild-type BRAF and a panel of 70 other kinases (11). Mechanistically, it occupies the interlobe cleft of the BRAF kinase domain and targets the hinge-proximal region to competitively block the ATP-binding site (11). PLX4032 replaced PLX4720 as the first-in-class therapeutic drug in human clinical trials because of its superior pharmacokinetic properties (12). Preclinical evaluation of PLX4032 antitumor activity demonstrated that it suppresses ERK phosphorylation, a downstream target of BRAF, and inhibits cell proliferation by inducing cell cycle arrest and apoptosis in BRAF-mutant melanoma cells (13-15). PLX4032 exhibits the opposite effect in BRAF wild-type melanoma cells. By stimulating CRAF in a RAS-independent manner, it paradoxically activates ERK signaling, thereby promoting cell proliferation and migration (16,17). This may explain PLX4032 selective inhibition of BRAF<sup>V600E</sup>-mutant cells while maintaining minimal toxicity in normal cells. The predominant preclinical results in BRAF-mutant melanoma cells led to the initiation of PLX4032 phase I clinical trials in 2009 to evaluate its safety, pharmacokinetics and pharmacodynamics (18). Similar to most small-molecule inhibitors, PLX4032 shows dose-dependent toxicity in arthralgia, keratoacanthoma/cutaneous squamous cell carcinoma (cSCC) and rash. Notably, 89% of these adverse events are grade 1 or 2, indicating manageable toxicity (10,12). The aforementioned clinical trial established the optimal therapeutic dose of PLX4032 for melanoma therapy through dose-escalation assay, while also providing a critical foundation for subsequent clinical trials and the development of next-generation BRAF inhibitors.

PLX4032 was renamed vemurafenib in 2010 and was approved by the US Food and Drug Administration (FDA) in 2011 as the first-in-class BRAF inhibitor for unresectable or metastatic BRAF<sup>V600E</sup>-mutant melanoma (19). This was primarily supported by the positive results of the phase 3 BRIM-3 trial (trial no. NCT01006980) of vemurafenib in melanoma (20). Despite adverse events consistent with the PLX4032 known safety profile, vemurafenib-treated patients show superior outcomes compared with dacarbazine chemotherapy, with a higher objective response rate (48 vs. 5%) (20) and improved median overall survival (13.6 vs. 9.7 months) (21). Although all patients in the aforementioned study discontinued treatment owing to disease progression, vemurafenib set a benchmark for BRAF inhibitors optimization and transformed the therapeutic landscape for melanoma.

*Dabrafenib is a widely utilized BRAF inhibitor with advanced safety.* Concurrently with the clinical application of vemurafenib, dabrafenib (GSK2118436), a second-generation BRAF inhibitor, was developed. Approved by the FDA in 2013, dabrafenib has become the second BRAF inhibitor for unresectable or metastatic BRAF<sup>V600E</sup>-mutant melanoma, offering an alternative therapeutic option. Similar to vemurafenib, GSK2118436 competitively binds the ATP-binding sites of the BRAF kinase domain (22). Preclinical studies demonstrate that GSK2118436 inhibits ERK and MEK phosphorylation, suppressing cell proliferation through induction of cell cycle arrest (23,24). GSK2118436 was renamed dabrafenib in 2012 and has superior efficacy vs. dacarbazine, with higher objective response rate (50 vs. 6%), improved median progression-free survival (mPFS, 5.1 vs. 2.7 months) and lower progressive disease rate (5 vs. 37%) (25). These preclinical and clinical results collectively supported the FDA 2013 approval of dabrafenib as a BRAF<sup>V600E</sup>-specific inhibitor for targeted melanoma therapy.

Although dabrafenib monotherapy displays tumor suppression efficacy comparable with vemurafenib in melanoma treatment, it exhibits superior performance in several other aspects. Unlike vemurafenib, which impairs lymphocyte counts (particularly central memory CD4<sup>+</sup> T cell populations) and interferon- $\gamma$ /interleukin-9 cytokine production, dabrafenib shows minimal immunotoxicity (26). Cutaneous toxicity of dabrafenib is lower than that of vemurafenib (skin papilloma, 15 vs. 29; cSCC/keratoacanthoma, 10 vs. 26; photosensitivity, 1 vs. 52%) (27). The markedly decreased dermatological toxicity, combined with the lower immunosuppressive risk of dabrafenib, establishes it as a clinically optimized BRAF inhibitor.

## 3. MEK inhibitor monotherapy

While the development of vemurafenib and dabrafenib has improved outcomes for patients with BRAF-mutant melanoma, long-term therapy has revealed paradoxical activation of the MAPK signaling pathway. Theoretically, the dimerization of RAF family members is key for the activation of their kinase activity and transduction of signals from upstream RAS. Monomeric wild-type BRAF remains inactive due to autoinhibition mediated and maintained by the 14-3-3 protein cradle (28). V600 mutations induce a conformational change

Table I. Categorization of BRAF mutations.

Property	BRAF variant			
	Wild-type	Class I	Class II	Class III
Mutation site	Not applicable	V600	Non-V600 (G464, G469, L597, K601)	Non-V600 (D287, V459, G466, S467)
Kinase activity	Regulated	High	Moderate	Low or inactive
RAS-dependency	Dependence	Independence	Partial dependence	Dependence
Dimerization activation	Yes	No	Yes	Yes
Sensitivity to BRAF inhibitors	Resistance	High sensitivity	Low sensitivity	Resistance

Table II. MAPK inhibitors approved by the US Food and Drug Administration for melanoma therapy.

Drug	Year	Phase	Trial ID	Enrolled	(Refs.)
Vemurafenib	2011	1	NCT00405587	55 patients in the dose-escalation phase; 32 metastatic melanomas with BRAF <sup>V600E</sup> in the extension phase	(10)
		2	NCT00949702	132 stage IV metastatic melanomas with BRAF <sup>V600E</sup>	(170)
		3	NCT01006980	675 unresectable stage IIIC or IV melanomas with BRAF <sup>V600E</sup>	(20)
Dabrafenib (GSK2118436)	2013	1	NCT00880321	156 metastatic melanomas with BRAF <sup>V600E/K</sup> ; 28 non-melanoma solid tumors with BRAF <sup>V600E</sup>	(171)
		2	NCT01153763	92 stage IV metastatic melanomas with BRAF <sup>V600E/K</sup>	(27)
		2	NCT01266967	172 brain-metastatic melanomas with BRAF <sup>V600E/K</sup>	(172)
Trametinib (GSK112021)	2013	3	NCT01227889	250 metastatic melanomas with BRAF <sup>V600E</sup>	(25)
		1	NCT00687622	81 melanomas; 30 NSCLCs; 28 CRCs; 26 PCs; 16UMs	(173)
		2	NCT01037127	97 metastatic melanomas with BRAF <sup>V600E/K/D</sup> previously treated with a BRAF inhibitor or chemotherapy/immunotherapy	(36)
Dabrafenib and trametinib	2014	3	NCT01245062	322 unresectable stage IIIC or IV melanomas with BRAF <sup>V600E/K</sup>	(35)
		1/2	NCT01072175	247 metastatic melanomas with BRAF <sup>V600E/K</sup>	(38)
		2	NCT02039947	125 brain-metastatic melanomas with BRAF <sup>V600D/E/K/R</sup>	(174)
		3	NCT01584648	423 unresectable stage IIIC or IV metastatic melanomas with BRAF <sup>V600E/K</sup> ; compared to dabrafenib monotherapy	(175)
Vemurafenib and cobimetinib	2015	3	NCT01597908	704 metastatic melanomas with BRAF <sup>V600E/K</sup> ; compared with vemurafenib monotherapy	(39)
		1	NCT01682083	870 completely resected, stage III melanomas with BRAF <sup>V600E/K</sup>	(176)
		1	NCT01271803	129 unresectable stage IIIC or IV melanoma with BRAF <sup>V600E/K</sup>	(177)
Encorafenib and binimetinib	2018	2	NCT02230306	101 brain metastatic melanomas with BRAF mutations	(178)
		3	NCT01689519	495 unresectable stage IIIC or IV melanoma with BRAF <sup>V600E/K</sup> ; compared with vemurafenib monotherapy	(45)
		1/2	NCT01543698	126 melanomas or CRCs with BRAF V600 mutations	(179)
		2	NCT05026983	35 melanomas with brain metastases or leptomeningeal disease harboring BRAF V600 mutations	(180)
		3	NCT01909453	577 unresectable or metastatic cutaneous melanomas with BRAF <sup>V600E/K</sup> ; compared with encorafenib or vemurafenib monotherapy	(54)

CRC, colorectal cancer; NSCLC, non-small-cell lung cancer; PC, pancreatic cancer; UM, uveal melanoma.

in the kinase domain of BRAF, stimulating the kinase function of monomeric BRAF and enabling RAS-independent MEK activation (6). Owing to the development of BRAF<sup>V600</sup> selective

inhibitors, abnormal proliferation and metastasis driven by activated BRAF monomers are no longer a notable concern. However, BRAF<sup>V600E</sup> and wild-type RAF form heterodimers to

enhance kinase activity. When BRAF inhibitors bind mutant BRAF, the conformation of the inhibitor-free RAF protomer changes, leading to its release and transactivation, triggering the activation of the MAPK pathway (29-31). This is known as paradoxical activation. To address this, MEK inhibitors are combined with BRAF inhibitors as a dual-targeted therapy for melanoma.

**Trametinib.** Trametinib, originally known as GSK1120212, is the only FDA-approved MEK inhibitor for monotherapy, authorized in 2013 for the treatment of patients with unresectable or metastatic melanoma harboring BRAF<sup>V600E</sup> or BRAF<sup>V600K</sup> mutations. It directly binds unphosphorylated MEK1 and MEK2, maintaining them in an inactive, dephosphorylated state, leading to allosteric inhibition of kinase activity and suppression of cell proliferation and tumor growth (32,33). Notably, trametinib demonstrates a more favorable safety profile than BRAF inhibitors, with fewer severe adverse events, potentially due to its lower therapeutic dosage. Although rash and diarrhea are the most frequent adverse events, trametinib treatment, by contrast with BRAF inhibitors, is not associated with secondary malignancy such as cSCC (34).

In treatment-naïve patients, trametinib demonstrates superior clinical outcomes compared with that with conventional chemotherapy (intravenous dacarbazine or paclitaxel). mPFS and response rate (RR) are improved in the trametinib cohort compared with that in the chemotherapy cohort (mPFS: 4.8 vs. 1.5 months; RR: 22 vs. 8%) (35). Although the RR to trametinib is not as high as that to vemurafenib and dabrafenib, the PFS and overall survival are comparable. Patients pretreated with BRAF inhibitors show minimal response to trametinib (36), implying potential cross-resistance mechanisms between BRAF and MEK inhibitors. Trametinib avoids the toxicities associated with BRAF inhibitors, particularly in cSCC. Thus, combinations of BRAF and MEK inhibitors have emerged as strategies to optimize the therapeutic index through efficacy enhancement and toxicity reduction.

#### 4. Combination therapy with BRAF and MEK inhibitors

Despite encouraging initial responses, clinical evidence shows that most patients relapse after responding to BRAF or MEK inhibitor monotherapy. To improve treatment efficiency, prolong response, enhance survival and reduce toxicity, a combination of BRAF and MEK inhibitors has emerged as a promising strategy for patients with melanoma (37).

**Dabrafenib + trametinib.** In 2014, the FDA approved a combination of dabrafenib and trametinib for patients with unresectable or metastatic melanoma carrying BRAF<sup>V600E</sup> or BRAF<sup>V600K</sup> mutations. The combination therapy demonstrates improved outcomes compared with dabrafenib monotherapy, with higher RR (76 vs. 54%), longer mPFS (9.4 vs. 5.8 months) and decreased incidence of skin-related toxicity (7 vs. 19% cSCC) (38). The dabrafenib-trametinib combination outperforms not only dabrafenib alone but also vemurafenib monotherapy, with an mPFS of 11.4 vs. 7.3 months and a RR of 64 vs. 51% (39). Baseline lactate dehydrogenase (LDH) levels influence treatment outcomes of dabrafenib and trametinib combination therapy. Additional baseline prognostic factors

associated with improved clinical outcomes in patients with melanoma include older age, female sex, BRAF<sup>V600E</sup> mutation status and limited disease burden (<3 sites) (40).

Dabrafenib and trametinib combination therapy may be a suboptimal therapeutic choice for patients at risk of fever, given the 50% incidence of drug-induced pyrexia (38,41). These findings highlight the need to develop alternative therapeutic strategies for treating patients with distinct clinical risk profiles. Notably, the combination therapy shows limited efficacy in patients who develop acquired resistance to BRAF inhibitor monotherapy (42). This may be because the resistant cells are no longer dependent on MAPK signaling.

**Vemurafenib + cobimetinib.** The most frequent adverse effects of vemurafenib are cutaneous events, arthralgia, fatigue and photosensitive skin reactions, whereas pyrexia occurs in only 22% of treated patients (20). This favorable febrile profile makes vemurafenib an advantageous BRAF inhibitor option for fever-prone patients. A key therapeutic consideration is identifying the optimal MEK inhibitor partner. Cobimetinib, a selective MEK1 inhibitor developed by Exelixis, is a promising therapeutic candidate. By contrast with trametinib-induced dual inhibition of MEK1 and MEK2, cobimetinib (also known as GDC-0973 or XL518 during the developmental stage) demonstrates highly selective MEK1 inhibition, showing negligible activity against MEK2 and >100 other kinases. Although cobimetinib monotherapy elicits a RR of 50% in patients with melanoma, the FDA has not granted approval for single-agent use in melanoma therapy because of the high risk of serious adverse events, such as gastrointestinal disorder (43).

The recommended cobimetinib regimen employs a 21-day on/7-day off-dose schedule, administered once daily (43). This intermittent dosing minimizes drug accumulation risks, a key consideration given the prolonged half-life of cobimetinib, while maintaining optimal pharmacodynamic synergy with vemurafenib. Compared with vemurafenib monotherapy, the cobimetinib-vemurafenib combination extends both 5-year PFS (14 vs. 10%) and overall survival rate (31 vs. 26%), while enhancing the confirmed objective RR (70 vs. 50%) with comparable toxicity (44-46). Similar to the dabrafenib-trametinib combination regimen, treatment outcomes with the vemurafenib-cobimetinib combination therapy also vary based on baseline LDH levels. Typically, patients with elevated LDH levels have poorer survival outcomes than those with normal LDH levels (47). Based on these findings and supported by positive results, the FDA approved the vemurafenib-cobimetinib combination in 2015 for metastatic or unresectable melanoma harboring BRAF<sup>V600E</sup> or BRAF<sup>V600K</sup> mutation.

**Encorafenib + binimetinib.** Even in the absence of a high risk of pyrexia, the vemurafenib-cobimetinib combination leads to a high incidence of rash (73%), indicating cutaneous toxicity (45). To address this issue, Array BioPharma developed a new BRAF inhibitor, encorafenib, and a new MEK inhibitor, binimetinib. This combination strategy was approved by the FDA in 2018 for the treatment of unresectable or metastatic melanoma with BRAF V600E or V600K mutations (48).

At the 103rd Annual Meeting of the American Association for Cancer Research in 2012, encorafenib (LGX818) was

Table III. Terminal half-life and dosages of US Food and Drug Administration-approved BRAF and MEK inhibitors.

Class	Drug	Terminal half-life	Dosage	(Refs.)
BRAF inhibitors	Dabrafenib	4.0-6.8 h	150 mg twice daily	(181)
	Vemurafenib	57.0 h	960 mg twice daily	(19)
	Encorafenib	2.9-4.4 h	450 mg once daily	(57)
MEK inhibitors	Trametinib	4.0 days	2 mg once daily	(173)
	Cobimetinib	43.6 h	60 mg once daily for 21 days and 7 days off	(43)
	Binimetinib	8.7 h	45 mg twice daily	(52)

introduced as a highly potent RAF inhibitor. It demonstrates selective anti-tumor efficacy in BRAF<sup>V600E</sup>-mutant cells, with no notable activity against wild-type BRAF or 100 other kinases (49,50). Mechanistically, encorafenib downregulates cyclin D1, induces G1-phase cell cycle arrest and promotes senescence in BRAF<sup>V600E</sup>-mutant melanoma cells (51).

Binimetinib, a selective MEK1/2 inhibitor, was originally developed for autoimmune disease but was discontinued in clinical development owing to insufficient efficacy in trials (52). It effectively suppresses pERK levels and inhibits the proliferation of BRAF- and NRAS-mutant cells, including melanoma cells, with a low half-maximal inhibitory concentration of 5 nM (53). As both encorafenib and binimetinib were developed by the same pharmaceutical company, their combination therapy could be systematically evaluated for inherent advantages in terms of drug compatibility and synergistic development.

Compared with encorafenib or vemurafenib monotherapy, the encorafenib-binimetinib combination demonstrates improved clinical outcomes, with higher 5-year PFS rate (23 vs. 19 and 10%, respectively) and RR (64.1 vs. 51.8 and 40.8%, respectively). Moreover, the most common adverse events occurring with dabrafenib-trametinib (pyrexia, 50%) and vemurafenib-cobimetinib (rash, 73%) are decreased by the encorafenib-binimetinib combination (19 and 15%, respectively). While gastrointestinal toxicity and serous retinopathy occur frequently, these toxicities are generally managed through dose interruption or adjustment, as most are grade 1-2 in severity (54,55).

Compared with patients who receive monotherapy, those who receive combination therapy with BRAF and MEK inhibitors typically have better outcomes. Combination of BRAF and MEK inhibitors provides a double assurance to block MAPK signal transduction at the same time, thereby delaying or preventing drug resistance (6). The MAPK pathway is a linear cascade reaction involving BRAF, MEK and ERK. When only BRAF inhibitors are used, tumor cells may bypass BRAF through various mechanisms, such as NRAS mutation, BRAF alternative splicing or CRAF dimerization, thereby reactivating downstream MEK and ERK. Once this occurs, the BRAF inhibitors no longer function. However, the application of MEK inhibitors can prevent MAPK signaling activation by blocking MEK, even when BRAF inhibitors are ineffective.

To date, the FDA has approved three combined targeted therapeutic approaches: Dabrafenib + trametinib, vemurafenib + cobimetinib and encorafenib + binimetinib. The timelines for FDA-approved BRAF and MEK inhibitors are

shown in Fig. 1. The doses and terminal half-lives are listed in Table III. Typically, the terminal half-life of an inhibitor is negatively associated with its administrated frequency. However, although vemurafenib has a terminal half-life of 57 h, it is administrated twice daily, whereas encorafenib, with a half-life of only 2.9-4.4 h, is dosed once daily. This is attributed to the non-linear pharmacokinetics and narrow therapeutic index of vemurafenib. Although the terminal half-life of encorafenib is short, its active metabolite, LHY746, has an extended half-life of up to 83 h (56). To the best of our knowledge, there is no study directly comparing the efficacy of these three strategies. However, these differences may be understood by examining the RR and mPFS. The latter two combination regimens are slightly, but not significantly, more effective than the former and all combination options exhibit notable improvements over single-agent therapy. Overall, the most recently approved combination therapy, encorafenib + binimetinib, is the most effective option for melanoma in terms of antitumor efficacy (Table IV). Notably, encorafenib exhibits a longer dissociation half-life (>30 h) than dabrafenib (2 h) and vemurafenib (0.5 h) (57), meaning that once bound to mutant BRAF proteins, encorafenib inhibits tumor proliferation for an extended period, thus showing a durable inhibitory effect. Paradoxical ERK activation is a notable concern associated with BRAF inhibitor administration. Encorafenib shows a higher paradox index (the time in which anti-tumor activity is exerted without ERK activation) than that of dabrafenib and vemurafenib (50 vs. 10 and 5.5, respectively), indicating it is less likely to activate ERK while exerting its antitumor effect (58). Due to its longer dissociation half-life and greater paradox index, the combination of encorafenib and binimetinib exhibits better tolerability and antitumor efficacy than the other two strategies. When considering adverse events, the encorafenib-binimetinib combination is associated with a high risk of diarrhea and vomiting, which limits its use in patients with sensitive gastrointestinal systems (54). For patients prone to fever, dabrafenib-trametinib is not the preferred choice (39). In such cases, vemurafenib and cobimetinib combination therapy may serve as alternatives.

### 5. Challenges in melanoma targeted therapy

MAPK inhibitor (MAPKi) therapy, particularly the combination of BRAF and MEK inhibitors, shows promise in delaying disease progression in melanoma. However, nearly all patients who initially respond to treatment develop drug insensitivity, leading to relapse not only at the primary lesion but also at

Table IV. 5-year follow-up of phase 3 clinical trials of BRAF and MEK inhibitors combination therapy for unresectable or metastatic melanomas with BRAF<sup>V600E/K</sup>.

Therapy	Overall survival		Progression-free survival		(Refs.)
	Median, months	Rate, %	Median, months	Rate, %	
D	20.2	21	5.8	3	(182)
D + T	25.0	28	9.4	13	
V	17.4	26	7.2	10	(47)
V + C	22.5	31	12.6	14	
E	23.5	35	9.6	19	(183)
E + B	33.6	35	14.9	23	

D, dabrafenib; V, vemurafenib; E, encorafenib; T, trametinib; C, cobimetinib; B, binimetinib; AEs, adverse event.

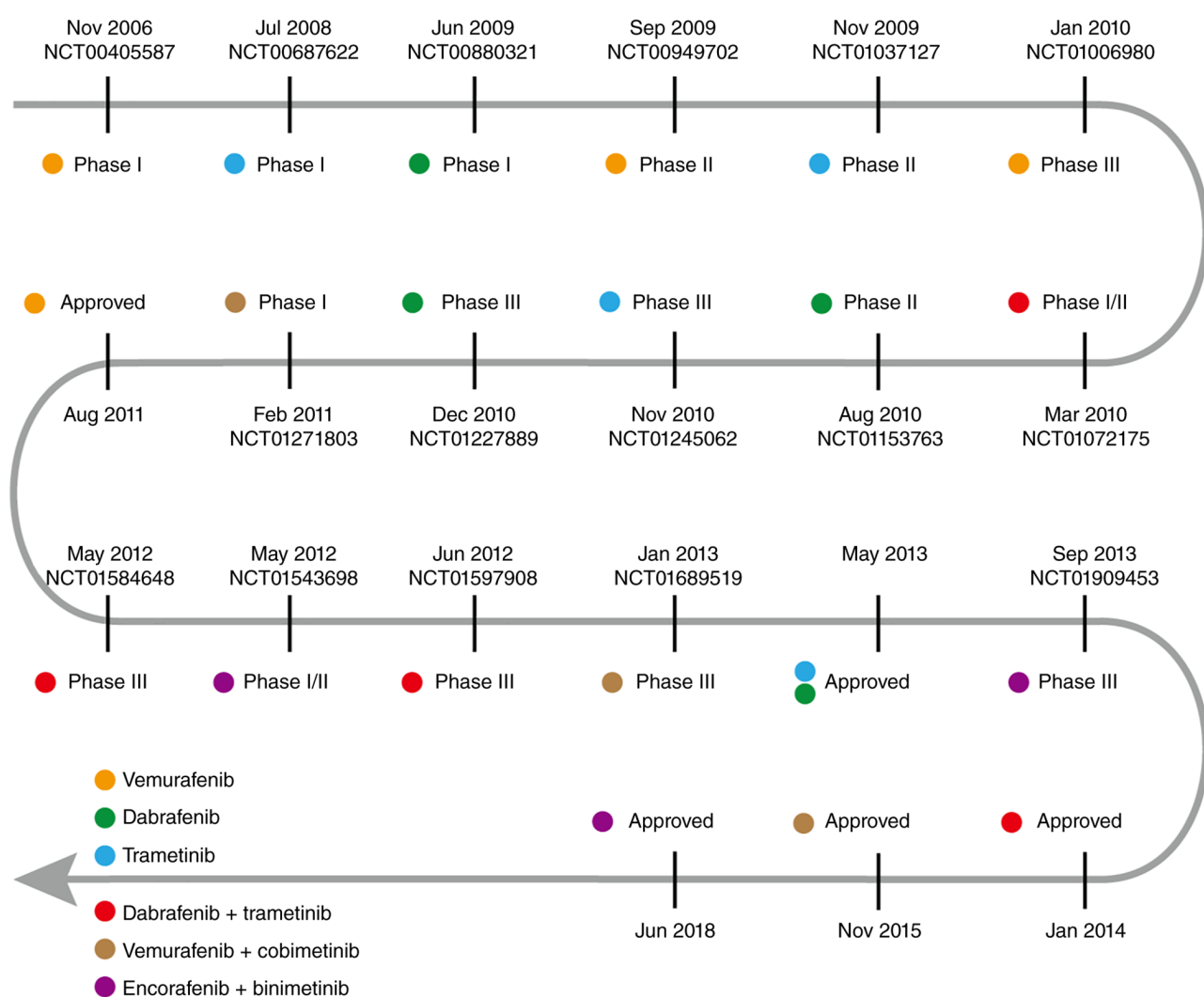


Figure 1. Timeline of clinical trials and US Food and Drug Administration approval for BRAF and MEK inhibitors in melanoma therapy. Dates indicate the study start dates. All data were sourced from ClinicalTrials.gov (clinicaltrials.gov).

previously non-tumor sites. Therefore, a challenge for melanoma-targeted therapy is the development of drug resistance. Currently, several resistance mechanisms have been identified: Tumor heterogeneity and plasticity enable melanoma cells to rapidly rewire phenotypic plasticity and adapt to therapeutic

stress (59); epigenetic reprogramming renders tumor cells less sensitive to drug treatment through histone modification, chromatin remodeling and metabolic rewiring (60) and genetic mutations provide melanoma cells with additional survival signaling pathways (9). Phenotypic switching and epigenetic

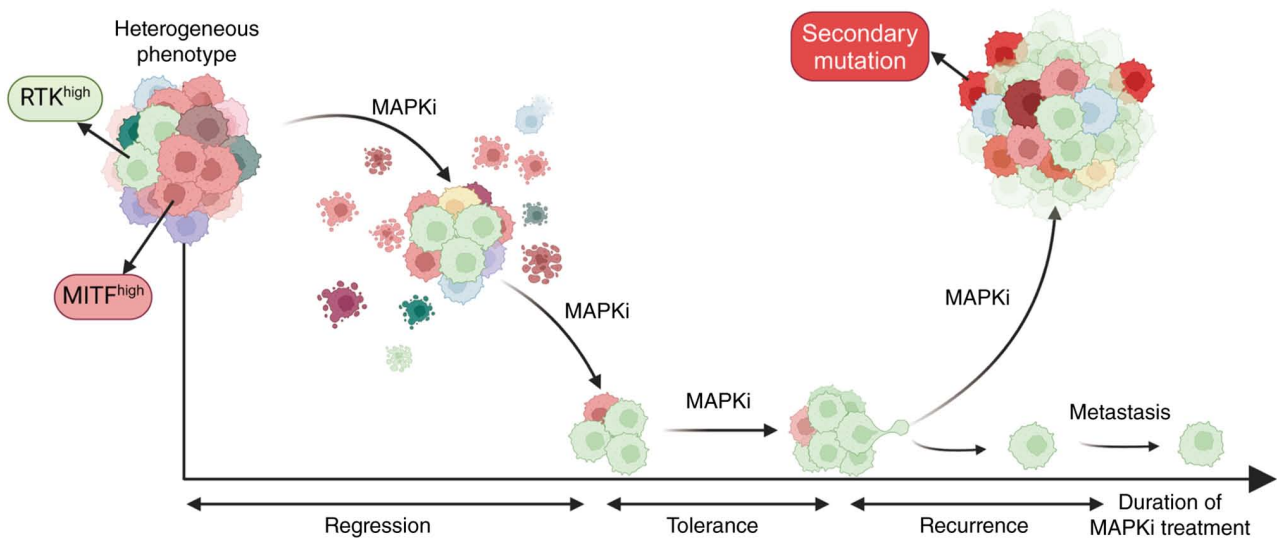


Figure 2. Acquisition of drug resistance in melanoma. Melanoma is highly heterogenous and exhibits phenotypic plasticity, enabling phenotypic switching in response to MAPKi treatment. In the early-treatment phase, MAPKi-mediated induction of cell death preferentially targets MITF-high melanoma populations, leading to tumor shrinkage within a short timeframe. Cells expressing high levels of RTKs, such as AXL receptor tyrosine kinase and nerve growth factor receptor, are intrinsically resistant to MAPKi and survive drug-induced cell death. The duration of this drug-tolerant phase varies and dormant cells typically suppress proliferative signals to evade immune surveillance. Through epigenetic reprogramming, residual tumor cells acquire an invasive phenotype, facilitating dissemination to distant organs, or a dedifferentiated phenotype, enabling them to evade continuous drug pressure until they develop secondary mutations (64,71,169). i, inhibitor; MITF, microphthalmia-associated transcription factor; RTK, receptor tyrosine kinase.

reprogramming are adaptive responses of melanoma cells to drug pressure. A subset of cells rapidly shifts their phenotype to survive MAPKi treatment-induced apoptosis, which is accompanied by epigenetic remodeling. As these changes do not involve alterations at the DNA level, they are reversible (61). During long-term treatment, melanoma genomes become unstable owing to metabolic changes, such as increased reactive oxygen species (ROS) levels. Once genetic mutations are acquired, tumor cells enter a rapid proliferation phase; changes at this stage are irreversible (62). Resistant melanoma is essentially heterogenous. Phenotypic switching, epigenetic reprogramming and genetic mutation can occur simultaneously and coexist in distinct tumor cell subpopulations.

**Heterogeneity and phenotype plasticity.** Microphthalmia-associated transcription factor (MITF), the master transcriptional regulator of melanocytes, drives the phenotypic switch of melanoma cells between proliferative and invasive states (63). MITF expression exhibits a dynamic bell-shaped distribution, with both high and low levels linked to therapeutic resistance. Melanoma cells with high MITF expression exhibit enhanced proliferative capacity and differentiation, as evidenced by the upregulation of cell cycle-associated and anti-apoptotic genes. This phenotype decreases dependence on the MAPK pathway for survival, thereby conferring intrinsic tolerance to MAPKi (64). By contrast, melanoma cells with low MITF levels exhibit a more invasive and stem cell-like phenotype, enhancing their adaptability to evade therapeutic pressure (64). During the initial treatment response, melanoma cells with high basal MITF levels are MAPKi-sensitive and undergo rapid cell death, whereas those with low basal MITF levels exhibit intrinsic resistance that counteracts MAPKi-induced cytotoxicity (65). However, MITF expression is significantly increased following MAPKi treatment (66-68).

This reflects the dynamic fluctuations in MITF expression, wherein residual cells may transiently upregulate MITF expression as a survival mechanism under therapeutic stress. As treatment progresses to the minimal residual disease (MRD) phase, stem cell-like cells with an invasive phenotype become the most abundant population in residual tumors. These cells are characterized by a high expression of receptor tyrosine kinases (RTKs), including AXL receptor tyrosine kinase (AXL) (69), nerve growth factor receptor (NGFR) (70), epidermal growth factor receptor (EGFR) (71), and platelet-derived growth factor receptor  $\beta$  (PDGFRB) (72), as well as the transcriptional factor SOX9. Simultaneously, the expression of MITF and its upstream regulator SOX10 decreases (71). At this stage, a subset of the residual surviving cells remains dormant, exhibiting minimal proliferation marker Ki67 activity. Another subset undergoes transcriptional reprogramming to acquire a mesenchymal phenotype that facilitates its dissemination to distant organs (73). The increase in RTKs during the MRD stage provides alternative survival pathways, allowing melanoma cells to bypass dependency on the MAPK signals. Consequently, cells with low MITF and high RTK expression exhibit resistance to MAPKi treatment, ultimately driving relapse (65,69,74) (Fig. 2).

The shift of melanoma cells from a melanocytic/proliferative phenotype to a dedifferentiated/invasive phenotype in response to therapeutic pressure is typically considered one of the reasons for acquiring drug resistance. The switch between these two phenotypes is not saltatory, which means there is an intermediate state to mediate the transition. An increasing number of studies have demonstrated an intermediate state that can transition to an alternative state depending on micro-environmental factors (71,75,76). For example, treating cells with TGF $\beta$  and TNF $\alpha$  induces a shift from a melanocytic or intermediate to mesenchymal phenotype, leading to enhanced

migratory and invasive capabilities, as well as resistance to subsequent therapy (75). Tsoi *et al* (71) proposed a comprehensive two-dimensional trajectory model to describe the temporal changes in melanocyte dedifferentiation during therapy. In brief, starting from a well-differentiated melanocytic state, melanoma cells transition to a transitory state following BRAF inhibitor treatment and adopt an NCSC-like phenotype within 11-21 days. Notably, the transitory state exhibits hybrid characteristics of both the melanocytic and NCSC-like states. Over the next 60-90 days, the cells further shift to an undifferentiated state, which displays high dissemination similar to that by mesenchymal cells and increased NF- $\kappa$ B signaling. The inherent heterogeneity of melanoma facilitates phenotypic plasticity, allowing dynamic transitions between four broadly defined states: A melanocytic, differentiated, pigmented and proliferative state; a transitory, intermediate and starved-like state; a NCSC-like invasive state; and an undifferentiated, mesenchymal-like state. Melanomas are highly heterogeneous. Beyond therapy-induced resistant cells, a subset of pre-existing subtypes exhibits intrinsic resistance to drug treatment, characterized by increased RTKs, including EGFR and AXL (77).

*Epigenetic reprogramming.* Epigenetic mechanisms associated with melanoma resistance induced by targeted therapy include histone modification, chromatin remodeling and metabolic rewiring.

The mechanisms by which histone modifications and chromatin remodeling influence therapeutic resistance typically involve the regulation of gene transcriptional (60). BRAF inhibitors induce the switch from suppressive histone H3K27 methylation (H3K27me<sub>3</sub>) to active acetylation (H3K27ac) by downregulating the methyltransferase EZH2. The H3K27 methyl-to-acetyl shift increases PGC1 $\alpha$  expression, leading to a change in oxidative metabolism that confers resistance to BRAF inhibitors. Blocking this switch re-sensitizes melanoma cells to therapy (78). Similarly, the methyltransferase SETDB1/2 (79) and demethylase KDM5B/JARID1B (80) are associated with transcriptional suppression in MAPKi-treated melanoma cells.

Under physiological conditions, melanoma cells preferentially use glycolysis rather than oxidative phosphorylation (OXPHOS) to acquire energy for accelerated proliferation (81). However, to adapt to the therapeutic pressure of MAPKi treatment, melanoma cells switch their metabolic patterns through PGC1 $\alpha$  by increasing OXPHOS, fatty acid oxidation (FAO) and glutamine metabolism, while decreasing glycolysis (82). This metabolic reprogramming enables melanoma cells to maintain their energy balance and suppress apoptosis under MAPKi inhibition, thereby conferring resistance to targeted therapy. U2AF homology motif kinase 1 (UHMK1), a RNA processing kinase that is key for the transport and translation of metabolism-associated proteins, is involved in metabolic reprogramming induced by targeted therapy (83). UHMK1 activation reduces cell death and induces resistance to MAPKi therapy by regulating mitochondrial metabolism (83). Moreover, melanoma cells increase FAO through carnitine palmitoyltransferase 1A under MAPKi treatment to survive therapeutic pressure (84). The surviving cells with elevated FAO levels contribute to melanoma resistance.

*Acquired mutations.* The approach of reversing the undifferentiated melanoma cells and epigenetic reprogramming allows MAPKi to regain efficacy owing to the reversible and transient nature of non-genetic switching. Once melanoma cells acquire additional driver gene mutations, they become independent of MAPK signaling, rendering MAPKi ineffective. There are three notable mechanisms underlying MAPKi resistance: BRAF alterations that reactivate the MAPK pathway; non-BRAF alterations that also reactivate the MAPK pathway and activation of alternative survival pathways.

FDA-approved MAPK inhibitors typically target BRAF V600E or V600K mutations but are ineffective against other BRAF mutations outside the V600 position. Therefore, patients with non-V600 BRAF mutations typically exhibit resistance to MAPKi therapy. Whole-exome sequencing reveals that patients with BRAF<sup>V600E</sup> mutations who progress on MAPKi treatment acquire secondary BRAF mutations at L514V (85) or L505H (86,87). Mutations at these sites, located in the kinase domain, confer continuous activation of BRAF kinase activity, mimicking the V600E mutation (88). Reactivation of BRAF kinase caused by non-V600 mutations leads to continuous activation of the MAPK pathway, independent of BRAF<sup>V600</sup>. Therefore, MAPK inhibitors that specifically target the V600 site of BRAF are no longer effective. BRAF amplification also drives melanoma drug resistance to MAPKi, as supported by whole-exome sequencing, which reveals a BRAF<sup>V600E</sup> copy-number gain in 20% of patients with melanoma resistant to MAPKi treatment (89,90). However, high-dose BRAF inhibitors reverse this resistance by downregulating pERK levels due to the saturated state of ERK reactivation (89). Alternative splicing of BRAF<sup>V600E</sup> is another cause of drug resistance to MAPKi (91,92). MAPKi-resistant melanoma cells acquire a truncated BRAF<sup>V600E</sup> protein through mRNA splicing, which lacks the Ras-binding domain. The truncated BRAF<sup>V600E</sup> shows increased dimerization compared with the full-length version; thus, MAPKi is not sufficient to block the activation of downstream ERK signaling (93). Up to 30% of patients with melanoma resistant to MAPKi treatment have an alternative BRAF<sup>V600E</sup> mRNA isoform, including isoforms lacking exons 4-8, 3-9, 1-9 and 2-11 (94). Although rare, the formation of BRAF fusions (95), such as the ArfGAP with GTPase domain, ankyrin repeat and PH domain 3/BRAF fusion gene (96) and switching between the three RAF isoforms (97), are associated with the acquisition of drug tolerance. BRAF fusions typically involve the rearrangement of the 3' portion of the BRAF gene, which encodes the kinase domain, behind the 5' portion of another gene. This rearrangement results in constitutive activation of BRAF due to the loss of the 5' portion of the BRAF gene, which encodes the autoinhibitory domain (98). The fusion of BRAF with other genes is observed not only in MAPKi-resistant melanomas harboring BRAF mutations but also in EGFR tyrosine kinase inhibitor-resistant lung cancer with EGFR mutations, as evidenced by fusions involving acylglycerol kinase (AGK/BRAF) or praja ring finger ubiquitin ligase 2/BRAF (99). Such fusions are also found in FGFR inhibitor-resistant gastric cancer, as demonstrated by fusions with jumonji C domain-containing histone demethylase 1 homolog D/BRAF (100). Moreover, an AGK/BRAF fusion mutation has been reported in immunotherapy-resistant advanced acral melanoma (101). These findings highlight

the key role of BRAF rearrangements in drug resistance. In the mechanisms associated with RAF switching, melanoma cells rewire signaling pathways by using ARAF and CRAF under chronic BRAF inhibition to reactivate MAPK signaling, although the underlying mechanisms remain poorly understood (97).

In addition to BRAF alterations, mutations in other genes involved in MAPK signaling activate the MAPK pathway, enabling melanoma cells to evade suppression by BRAFi, such as NRAS mutations at Q61K (72), Q61R (102), G13R and P185S (91), MEK2 mutations at F57C (91), Q60P (90,103) and C125S (104) and MEK1 mutations at Q56P and P124L (105). The aforementioned mutations in NRAS result in its constitutive activation, which reactivates the MAPK pathway by inducing the dimerization of BRAF and CRAF. The kinase function of this RAF dimer is not affected by BRAF inhibitors that target only monomeric BRAF (31). Normally, MEK is activated by its upstream regulator, BRAF. However, MEK mutations induce conformational changes that render MEK activation independent of BRAF. Consequently, the MAPK pathway evades the inhibitory effects of MAPK inhibitors and remains active (106).

Alternative pathways involved in proliferation and survival protect melanoma cells from MAPKi-induced cell death, independent of the MAPK pathway. These pathways enable melanoma cells to escape therapeutic pressure and promote the survival and proliferation of residual cells, leading to relapse. Numerous studies have illustrated the involvement of the PI3K/AKT/mTOR (92,107-109) and Rho-kinase (ROCK)-mediated pathway (110,111) and p21-activated kinase signaling (112-115) in melanoma resistance to targeted therapy.

## 6. Therapeutic strategies to overcome acquired MAPKi resistance

After acquiring resistance to MAPKi, tumors no longer respond to MAPKi treatment and may progress aggressively within a short time. Several strategies have been developed to address.

*Strategies based on phenotype switching.* Guiding intermediate cells towards the melanocytic state rather than the undifferentiated state may be a strategy for overcoming therapy resistance. The corepressor for element 1-silencing transcription factor (CoREST) has been identified as a promising therapeutic target to achieve. Mechanistically, CoREST drives melanoma cell plasticity by decreasing dual-specificity phosphatase levels (116). Treatment of BRAF inhibitor-resistant cell lines with the CoREST inhibitor corin not only enriches the intermediate cell population but also re-establishes BRAF inhibitor responsiveness (116). Proactive intervention during the MRD phase before relapse is optimal for prolonging the treatment response until the complete tumor disappears. However, selective targeting and elimination of dedifferentiated resistant cells at the recurrence stage are viable secondary strategies. For example, dedifferentiated melanoma cells are sensitive to ferroptosis. Consequently, erastin, a small-molecule ferroptosis inducer, has been proposed as a combination therapy with MAPKi to counteract dedifferentiation-mediated resistance (71,117).

*Strategies based on genetic mutation.* Once melanoma cells acquire additional mutations, it is impossible to re-sensitize them to MAPKi treatment. The available strategies either inhibit the newly activated pathways or induce cell death in the resistant cells. For example, combining MAPKi with inhibitors targeting activated pathways, such as LY294002 (a PI3K inhibitor) (118) and blebbistatin (a ROCK inhibitor) (110), is sufficient to delay tumor relapse. Next-generation sequencing is commonly used to identify new mutations that arise during MAPKi therapy. Another agent targeting newly acquired mutations can be administered following tumor progression. Although combining infigratinib (an FGFR inhibitor), capmatinib (a MET inhibitor), bupailisib (a PI3K inhibitor) or ribociclib (a CDK4/6 inhibitor) with encorafenib and binimetinib is insufficient for patients with progressive disease following encorafenib and binimetinib treatment (119), the use of niraparib, a poly (ADP-ribose) polymerase inhibitor targeting genes involved in the homologous recombination pathway, and uprosertib, an Akt inhibitor to block Akt1/2/3, are promising for patients with melanoma who progress on MAPKi therapy (120,121). Furthermore, numerous mutant genes that contribute to MAPKi resistance in melanoma encode client proteins of heat shock protein 90 (HSP90). The HSP90 inhibitor XL888 can overcome acquired MAPKi resistance in melanoma (122). Although a phase 1 clinical trial of XL888 combined with vemurafenib and cobimetinib in patients with melanoma harboring BRAF<sup>V600E/K</sup> mutations show non-negligible toxicity (123), the improved clinical outcomes facilitate further optimization of XL888 dosing strategies.

*Strategies based on activation of immune system.* Immune checkpoint inhibitors have also been used following MAPKi therapy in patients with melanoma who develop resistance to MAPKi. Ascierto *et al* (124) found that treating patients with metastatic BRAF<sup>V600</sup>-mutant melanoma with encorafenib + binimetinib until disease progression, followed by ipilimumab-nivolumab combination therapy, results in slightly improved outcomes, as evidenced by a 29% 4-year total PFS. Similar outcomes are also observed in patients treated with dabrafenib + trametinib until disease progression, followed by nivolumab + ipilimumab therapy, with a 51.5% 2-year overall survival and a 29.6% objective RR (125). Notable, while patients who receive immunotherapy after progression on MAPKi therapy show extended survival, their outcomes are not as favorable as those of patients who receive first-line immunotherapy until disease progression followed by MAPKi therapy (125).

Preclinical studies have demonstrated that macrophages may be involved in the paradoxical activation of MAPK pathways, leading to resistance (126,127). Consequently, the inhibitors LY3022855 [blocking the RTK colony stimulating factor 1 receptor (CSF-1R) expressed on macrophages) or MCS110 (targeting CSF-1, the ligand of CSF-1R) have been evaluated in combination with vemurafenib and cobimetinib in patients with metastatic melanoma harboring mutant BRAF<sup>V600</sup> (128,129). Although the phase I clinical trial was discontinued owing to strategic drug development considerations, the 20% RR in this small melanoma cohort supports the potential feasibility of these two drugs, although further optimization may be necessary.

Additionally, Samarkina *et al* (130) found that the androgen receptor (AR) is increased in BRAF inhibitor-resistant melanoma; thus, inhibiting AR activity with AZD3514 overcomes BRAF inhibitor resistance by promoting CD8<sup>+</sup> T cell infiltration. Although AZD3514 has only been evaluated in patients with castration-resistant prostate cancer (131,132), its low toxicity in humans and potent anti-tumor efficacy against MAPKi-resistant melanoma suggest potential for melanoma therapy.

*Strategies based on metabolic reprogramming.* One hallmark of MAPKi-resistant melanoma is increased metabolic reprogramming (81,133). Therefore, inhibitors targeting metabolic shifting are promising for re-sensitizing melanoma resistant to MAPKi. For example, IACS-010759, a mitochondrial oxidative phosphorylation complex I inhibitor, suppresses the growth of MAPKi-resistant BRAF-mutant melanoma by disrupting the tricarboxylic acid cycle and glycolysis (134). FK866 and GMX1778, inhibitors that decrease nicotinamide adenine dinucleotide levels, extend survival in mice bearing MAPKi-resistant melanoma (135). Inhibitors targeting glutamine (136,137) and FAO (84) suppress the proliferation and metastasis of MAPKi-resistant melanoma. Additionally, MAPKi-resistant melanoma cells show elevated ROS levels. Vorinostat, a histone deacetylase inhibitor, exceeds the tolerable ROS threshold in these cells, triggering lethal ROS accumulation and selective toxicity, which kills the resistant cells. Vorinostat has no cytotoxic effects on normal cells because the low basal ROS levels in these cells prevent the drug from inducing a lethal dose of ROS (138). Although most of these metabolism-associated inhibitors remain in preclinical studies, the aforementioned results support their further clinical investigation for melanoma therapy.

## 7. Conclusion

With the development of MAPK inhibitors, the American Cancer Society predicts that the mortality of patients with melanoma will decrease (139). The immune system helps patients combat progressive disease. In addition to BRAF and MEK inhibitors, the FDA has approved the use of immune checkpoint inhibitors in sequence with MAPKi to enhance antitumor efficacy (6). Generally, immunotherapy shows superior long-term outcomes compared with targeted therapy in patients with treatment-naïve BRAF<sup>V600</sup>-mutant metastatic melanoma, as supported by a higher 2-year overall survival rate (71.8 vs. 51.5%) and longer PFS (11.8 vs. 8.5 months) (125). In addition, induction with MAPKi (encorafenib + binimetinib) for 12 weeks, followed by immune checkpoint inhibitors (ipilimumab + nivolumab), exhibits antitumor efficacy comparable to that of immunotherapy alone (140). The sequence of targeted therapy and immunotherapy affects patient outcomes; however, the effects of the sequence on anti-tumor outcomes vary between patients with different conditions (141,142). The efficiency of three strategies based on the sequencing of targeted therapy and immunotherapy have been evaluated in patients with untreated, metastatic BRAF<sup>V600</sup>-mutant melanoma (143). The strategies included A (targeted therapy with encorafenib + binimetinib first until disease progression, followed by immunotherapy with ipilimumab + nivolumab),

B (immunotherapy until disease progression, followed by targeted therapy) and C (targeted therapy for 8 weeks, followed by immunotherapy until disease progression, followed by targeted therapy). Immunotherapy followed by targeted therapy is the preferred treatment approach for patients with melanoma with stable disease. This is supported by better 5-year outcomes: Total PFS rates for strategies A, B, and C are 27, 50 and 50%, respectively, and the overall survival rates are 45, 52 and 57%, respectively (125,144). Biomarker analyses performed on baseline tumor tissues using next-generation sequencing have demonstrated that patients with higher serum IFN- $\gamma$  levels, tumor mutation burden and LDH levels typically show poor overall survival and PFS (124,144).

Different sequences of targeted therapy and immunotherapy in patients with stable disease lead to differences in antitumor efficacy, which are mainly dependent on changes in the tumor immune microenvironment. Targeted therapy following immunotherapy triggers an immunostimulatory environment, as indicated by the increased infiltration of CD8<sup>+</sup> T effector memory cells and CD8<sup>+</sup> stem-like progenitor T cells, which are necessary for generating tumor-killing effector cells to maintain a long-term immune response (145). However, the reverse sequence (immunotherapy following targeted therapy) shows limited changes in the tumor immune microenvironment (145). Although immunotherapy shows better long-term outcomes, targeted therapy exhibits a superior objective RR compared with immunotherapy (72 vs. 51%) (146), demonstrating that targeted therapy as a first-line therapy is suitable for rapidly decreasing tumor burden, especially in patients with aggressive diseases, such as those with brain metastases or organ dysfunction (147). In general, the sequence of targeted therapy and immunotherapy depends on treatment goal. If there is an urgent need to eliminate large tumor lesions, it is better to administer targeted therapy first, followed by immunotherapy. However, immunotherapy is preferably used as a first-line treatment to achieve more durable efficacy. Notably, targeted therapy and immunotherapies partially share resistance mechanisms. This cross-resistance is attributed to a lack of functional dendritic cells, which results in an immunosuppressive tumor microenvironment characterized by a non-effective T cell response (148).

In addition to the sequential application of targeted therapy and immunotherapy, triplet combination therapy with BRAF, MEK and PD-1 inhibitors has been clinically evaluated for its anti-tumor efficacy in patients with BRAF<sup>V600</sup>-mutant melanoma. Patients receiving triplet therapy consistently exhibit better outcomes than those receiving targeted therapy alone, not only when they are treatment-naïve (149,150), but also following progression to immunotherapy or targeted therapy (151). However, triplet combination therapy is not used as a first-line clinical strategy for patients with melanoma owing to severe adverse events, including diarrhea, fever, rash and elevated liver transaminase, which are caused by increased toxicity (152). Therefore, the triplet regimens combining targeted therapy with immunotherapy are under clinical investigation.

Although the therapeutic methods differ, the underlying mechanisms by which tumor cells acquire resistance to targeted therapy and immunotherapy are similar. Phenotypic switching from a melanocytic to an undifferentiated state

has been observed in immunotherapy-resistant melanoma cells (153,154). This highlights the plasticity of melanoma cells in response to drug treatment. However, epigenetic reprogramming in immune cells contribute to impaired anti-tumor function, affecting macrophage polarization, dendritic cell maturation and T cell infiltration, ultimately leading to immunotherapy resistance (155). Although challenges remain, such as the difficulty in completely eliminating tumor cells and preventing recurrence, advances in targeted therapy and immunotherapy offer hope for patients with melanoma. Therapeutic strategies for patients with melanoma are no longer limited to single-agent approaches,  $\geq 2$  treatment methods are typically combined for clinical treatment. For example, neoadjuvant concurrent therapy with immunotherapy drugs and MAPKi achieves 80.0-86.7% pathological response (156,157) and 71% 2-year event-free survival (158). Similarly, a combination of encorafenib, binimetinib and pembrolizumab has 65% overall response in patients with unresectable advanced or metastatic BRAF<sup>V600E/K</sup>-mutant melanoma (159). Moreover, phenformin, an inhibitor that blocks the mitochondrial electron transport chain to suppress oxidative phosphorylation, has been introduced in combination with dabrafenib and trametinib to enhance the anti-tumor efficacy of MAPKi (160,161). MAPKis exhibit limited efficacy in patients with melanoma with brain metastases owing to poor blood-brain barrier (BBB) penetration. Ren *et al* (162) developed PF-07284890 (ARRY-461), a novel BRAF<sup>V600E</sup> inhibitor with high BBB permeability and notable tumor suppression, in a BRAF<sup>V600E</sup> melanoma xenograft mouse model. Currently, ARRY-461 is being evaluated in a phase 1 clinical trial (trial no. NCT04543188).

Identification of a universal biomarker would be beneficial to predict responses to combination therapy with BRAF and MEK inhibitors in most patients with melanoma. These biomarkers do not exist. However, several promising biomarkers have emerged. BRAF<sup>V600</sup> mutation levels, or the variant allele frequency (VAF) of BRAF<sup>V600</sup>, which indicates the proportion of mutant alleles to total alleles, is a potential marker for reflecting clinical outcomes and response to melanoma-targeted therapy (163). Specifically, patients with metastatic melanoma with BRAF<sup>V600</sup>-VAF >45% show shorter median PFS (10 months) and overall survival (26 months) than those with BRAF<sup>V600</sup>-VAF <45% (13 and 29 months, respectively) (164). Tumors with high BRAF<sup>V600</sup>-VAF are typically associated with strong heterogeneity, invasion and a high dependence on the MAPK signaling pathway for proliferation and survival, leading to poor patient outcomes and high risk of recurrence. Circulating tumor DNA (ctDNA) from liquid biopsy is another biomarker for predicting the treatment response and prognosis of patients with melanoma, with the advantages of being dynamic, non-invasive and real-time (165). ctDNA directly reflects the therapeutic effects during treatment. Elevated ctDNA levels indicate progressive disease with high accuracy (166). In patients with resected BRAF<sup>V600</sup>-mutant melanoma treated with dabrafenib and trametinib combination therapy, the presence of ctDNA in plasma samples is associated with worse median recurrence-free (16.59 vs. 68.11 months) and overall survival (40.31 months vs. not reached) compared with patients without detectable ctDNA (167). Even when not used to predict whether patients will respond to therapy, LDH

is a strong prognostic biomarker. High baseline LDH levels are typically associated with poor outcomes (47,168). Therefore, appropriate therapeutic strategies may be selected based on the levels of BRAF<sup>V600</sup>-VAF, plasma ctDNA and baseline LDH before treatment.

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Not applicable.

### Authors' contributions

LZ and LT conceived the study. LZ wrote the manuscript. DS, JF and LT revised the manuscript. All authors have read and approved the final manuscript. Data authentication is not applicable.

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### Competing interests

The authors declare that they have no competing interests.

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