

Recent discoveries in the genetics of melanoma and their therapeutic implications

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Received: 2007.08.31, **Accepted:** 2007.10.18, **Published online first:** 2007.12.03

Abstract

The incidence of cutaneous malignant melanoma, tumors arising from melanocytes, has increased markedly over the past few years in many countries. Although early melanoma is curable through surgical excision, the prognosis of advanced melanoma is very poor, this tumor being resistant to current therapies. Thus there is a need for new therapies to improve the treatment of advanced melanoma. This review provides an overview of recent discoveries in the genetics of melanoma which could offer new therapeutic opportunities.

Key words: melanoma, receptor tyrosine kinase, MAPK pathway, PI3K pathway, cAMP pathway, small molecule inhibitor.

Abbreviations: BAD – Bcl-2 antagonist of cell death, cAMP – cyclic AMP, CSD – chronic sun-induced damage, ERK – extracellular regulated kinase, FTI – farnesyltransferase inhibitor, MAPK – mitogen-activated protein kinase, GGT – geranylgeranyltransferase, HGF – hepatocyte growth factor, LF – lethal factor, NSCLC – non-small-cell lung cancer, MEK – MAPK/ERK kinase, MITF – microphthalmia-associated transcription factor, mTOR – mammalian target of rapamycin, PH – pleckstrin homology, PI3K – phosphatidylinositol 3-kinase, PIP3 – phosphatidylinositol 3,4,5 phosphate, pTyr – phosphotyrosine, PTEN – phosphatase and tensin homologue deleted on chromosome ten, RTK – receptor tyrosine kinase, SCF – stem cell factor, SH2 – src homology 2, VEGF – vascular endothelial growth factor.

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INTRODUCTION

Cutaneous melanoma, a tumor arising from melanocytes, has become a major public health problem in many countries. Episodic exposure of fair-skinned individuals to intense sunlight is thought to be responsible for the steadily increasing worldwide incidence of melanoma over recent decades. Since the mid 1960s, the incidence of melanoma has risen by 3–8% per year among most people of European background. Despite this increase and an overall rise in mortality due to melanoma, the survival rate has improved substantially. Roughly 60% of those diagnosed with melanoma in the 1960s died of the disease, compared with just 11% more recently, an improvement attributed mainly to early detection [66]. However, although early melanoma is curable through surgical excision, the prognosis of advanced melanoma is very poor because it is resistant to most chemotherapeutic agents. Therefore, identifying molecular targets for the diagnosis and treatment of patients is of particular importance and has been the focus of recent melanoma research. At least three sig-

nal-transduction pathways have been implicated in the genesis of melanoma: the mitogen-activated protein kinase (MAPK) pathway, the phosphatidylinositol 3-kinase (PI3K) pathway, and the cyclic AMP (cAMP) pathway (Fig. 1). Their involvement in melanoma development and their therapeutic implications are detailed below.

THE MAPK PATHWAY

The MAPK pathway is activated downstream of most growth factor receptors and is an essential signal-transduction cascade that controls cell survival, growth, differentiation, and transformation [13]. Activation of the MAPK pathway is initiated by receptor tyrosine kinases (RTKs), which are transmembrane cell-surface proteins that contain an N-terminal extracellular ligand-binding domain and a C-terminal intracellular tyrosine kinase domain. Most RTKs dimerize following binding to their ligand, which induces receptor activation and autophosphorylation of tyrosine residues in the RTK

intracellular domain. These phosphorylated tyrosines serve as binding sites for adaptor proteins responsible for the activation of several molecules, including the small GTPase of the Ras family [47]. Ras is the critical link that allows RTKs to signal to the extracellular regulated kinase (ERK). Once activated, Ras recruits the Raf kinase to the plasma membrane, where it becomes activated. Raf phosphorylates and activates a second protein kinase called MAPK/ERK kinase (MEK) which in turn activates ERK. ERK regulates downstream signaling complexes of transcription factors that affect gene expression, rearrangements of the cytoskeleton, and metabolism [67] (Fig. 1). The MAPK pathway regulates melanocyte proliferation downstream of agonists such as basic fibroblast growth factor, epidermal growth factor, hepatocyte growth factor (HGF), and stem cell factor (SCF) [26]. The recent discovery in melanoma of frequent mutations in the MAPK pathway represents a major breakthrough in the genetics of this cancer and brings great hope for its treatment as detailed below.

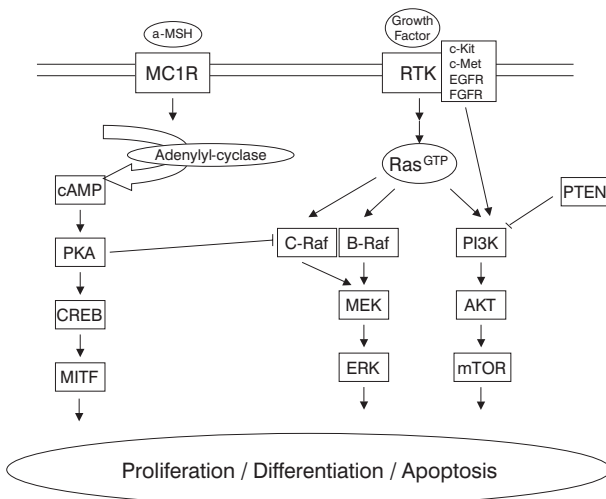


Fig. 1. Description of the three signal transduction pathways which have been implicated in melanocyte proliferation, differentiation, and apoptosis and in melanoma genesis: the cAMP pathway (left), MAPK pathway (center), and PI3K pathway (right). Explanations: MC1R – melanocortin 1 receptor, α-MSH – α melanocyte-stimulating hormone, CREB – cAMP-responsive element binding protein, EGF – epidermal growth factor, PKA – protein kinase A, MITF – microphthalmia-associated transcription factor, RTK – receptor tyrosine kinase, ERK – extracellular regulated kinase.

Receptor tyrosine kinases

c-Kit. The c-Kit RTK is the receptor for SCF and is centrally involved in the development of multiple cell lineages, including melanocytes. Insight into the roles of this receptor and its cognate ligand has been greatly facilitated by the large series of naturally occurring mutations in the murine genes that encode these molecules, the dominant white spotting (W) and steel (Sl) loci, respectively. Thus, mice with loss-of-function in either the W or

Sl loci exhibit white spotting, highlighting the importance of c-Kit in melanocyte development [31]. c-Kit is a type III RTK characterized by the presence of five immunoglobulin-like domains in its extracellular portion. SCF binds to the second and third immunoglobulin domains, while the fourth domain plays a role in receptor dimerization [56]. Binding of SCF to c-Kit induces receptor dimerization and the autophosphorylation of specific tyrosine residues. These phosphorylation events create docking sites for specific Src homology 2 (SH2) domain-containing proteins which, in turn, control various intracellular signaling pathways. Recruitment of particular targets is mediated by the ability of their SH2 domains to recognize specific phosphotyrosine (pTyr)-containing motifs on the activated receptor. Numerous signaling molecules have been identified as binding partners for specific pTyr residues on activated c-Kit, including the p85 subunit of PI3K (by means of tyrosine 721), phospholipase C (by means of tyrosine 730), and the Grb2 and Grb7 adapter proteins (by means of tyrosine residues 703 and 936). Additionally, signaling molecules, including Src family kinases and the protein tyrosine phosphatases Shp-1 and Shp-2, have been shown to associate with a dual tyrosine motif in the juxtamembrane region of c-Kit (tyrosine residues 568 and 570) [36].

Until recently, data suggested that c-Kit might act as a tumor suppressor gene in melanoma. Indeed, c-Kit is expressed in melanocytes, benign melanocytic nevi, and *in situ* malignant melanoma, but it tends to be reduced or lost with tumor progression to invasive and metastatic melanoma [49]. Furthermore, c-Kit expression is lost in most melanoma cell lines [35]. However, a subset of melanoma has been found to maintain c-Kit overexpression, even in metastatic lesions, and the activated c-Kit mutations have recently been identified in 2–3% of melanoma cases [9]. The majority of c-Kit mutations are present in exons 11, 13 17, and 18 of the c-Kit gene, K642E and L576P being the most frequent. The biological significance of these mutations in melanoma remains unclear as it was recently shown that constitutive signaling from an active c-Kit mutant found in gastrointestinal stromal tumors (D814Y) did not stimulate melanocyte proliferation or induce their transformation [2]. Whether K642E and L576P are oncogenic in melanocytes remains to be demonstrated. This is particularly important as a c-Kit inhibitor is available in the clinic and could benefit a subset of melanoma patients (Table 1). Imatinib mesylate is an oral tyrosine kinase inhibitor that targets bcr-Abl, c-Kit, and platelet-derived growth factor receptor α and β, leading to remarkable clinical responses in several cancers, such as gastrointestinal stromal tumors [59] and myeloid leukemia [70]. Unfortunately, clinical trials in melanoma patients did not show promising responses. Indeed, different phase II trials were undertaken, but no clinical responses were noted among those patients. Tumor biopsies were obtained from patients who received imatinib treatment and cell lines were established from these tumors. *Ex vivo* imatinib treatment of the cell lines showed no anti-

Table 1. Targets and selected drugs for melanoma therapy

Main targets	Inhibitors	Other known targets
c-Kit	Imatinib SU11248 (sunitinib)	Bcr-Abl, PDGFR α/β VEGFR, PDGFR α/β
c-Met	SU11274 PHA-665752	Unknown Unknown
Ras	Tipifarnib (Zanestra) SCH66336	Farnesylated proteins Farnesylated proteins
Raf	Sorafenib (BAY-439006) CHIR-265 PLX720	VEGFR2, PDGFR β VEGFR, PDGFR α/β Unknown
MEK	CI-1040 (PD184352) ARRY-142886 (AZD6244) PD0325901 Lethal factor	Unknown Unknown Unknown Unknown
mTOR	Rapamycin CCI779 (temsirolimus) RAD-001 (everolimus) AP-23573 (deforolimus)	Unknown Unknown Unknown Unknown

PDGFR – platelet-derived growth factor receptor, VEGFR – vascular endothelial growth factor receptor.

-proliferative effect [68]. The lack of efficacy of imatinib in those clinical trials can be explained by the fact that no mutations were found in any of the analyzed c-Kit sequences. A clinical phase II trials with imatinib is currently in process in patients affected by acral or mucosal melanoma, which often carry a c-Kit mutation.

c-Met. c-Met is an RTK that has been found mutated in several human cancers, including sporadic papillary renal carcinoma, gastric and liver cancer, small-cell and non-small-cell lung cancer (NSCLC), and metastases of head and neck squamous cell carcinoma, and it is known to stimulate the invasive growth of cancer cells and increase their metastatic potential [6]. The natural ligand for c-Met is HGF, which is also known as “scatter factor”. HGF is a multifunctional cytokine acting as a mitogen and morphogen for many epithelial cells. Recent studies by Herlyn’s group have shown that most melanoma cells, but not normal melanocytes, produce HGF, which can induce sustained activation of its receptor, the MAPK and the PI3K pathways [38]. Hence an autocrine HGF/c-Met signaling loop may be involved in the development of melanoma. In transgenic mice ubiquitously expressing HGF, hyperpigmentation of the skin is observed and melanocytes are located within the dermis and epidermis, whereas mouse melanocytes are normally located in the hair follicle [51]. Moreover, melanoma arose spontaneously, but could also be UV induced in these transgenic animals [50]. It is therefore suggested that c-Met autocrine activation induces the development of malignant melanoma and the acquisition of the metastatic phenotype. Recently, a mutation in exon 13 in the juxtamembrane domain (N948S) of c-Met was found in three melanoma cell lines. Also, a mutation of c-Met was discovered (R988C) in exon 14 in the juxtamembrane domain in 1 out of 14 melanoma tumors. This mutation has also been

seen in NSCLC and small-cell lung cancer tumors, but this is the first report of a mutation in c-Met in human melanoma tumors [54]. Whether these c-Met mutants are oncogenic in melanocytes remains to be demonstrated, but therapy targeting c-Met could be suitable for melanoma treatment.

Several therapies targeting the HGF/c-Met signaling pathway are being developed. One therapeutic strategy is to develop antagonism of ligand-receptor interaction. NK4, composed of the N-terminal hairpin and four subsequent kringle domains of HGF, acts as the competitive antagonist for HGF and angiogenesis inhibitor. In experimental models of distinct types of cancers, NK4 protein administration or NK4 gene therapy inhibited tumor invasion, metastasis, and angiogenesis-dependent tumor growth [33]. Recently, five different humanized monoclonal antibodies that bound to and neutralized human HGF were generated and characterized. Antibodies with subnanomolar affinities for HGF blocked binding of human HGF to c-Met and inhibited HGF-mediated c-Met phosphorylation, cell proliferation, survival, and invasion [5]. Recent successes in the treatment of chronic myeloid leukemia, gastrointestinal stromal tumors, and other cancers using RTK inhibitors strongly support the potential efficacy of this therapeutic strategy in targeting c-Met (Table 1). SU11274 and PHA665752 are two selective synthetic inhibitors of c-Met ATP binding which block HGF-stimulated activities in cultured cells and tumorigenicity in well-characterized c-Met driven xenograft models [53]. Clinical trials are now underway.

Ras GTPase

Ras proteins are small G-proteins embedded on the inner surface of the plasma membrane through post-

-translational processing. Ras acts as a molecular switch that is "on" when bound to GTP and "off" when bound to GDP. Following binding of cytokines, growth factors or mitogens to their appropriate receptors, the protein complex Shc/Grb2/SOS is recruited to the receptor. Upon stimulation by Shc/Grb2/SOS, the inactive Ras exchanges GDP for GTP, undergoes a conformational change and becomes active [57]. The signaling responses induced by Ras activation are highly varied, owing largely to the myriad effector molecules that bind Ras in its GTP-bound state, such as the Raf kinase family, PI3K, RalGDS, and phospholipase C ϵ [42]. There are three closely related Ras proteins, H-, K-, and N-Ras. Mutations in codons 12, 13, or 61 of one of the three Ras genes convert these genes into active oncogenes. This results in the Ras proteins remaining predominantly bound to GTP compared with the wild-type and losing the ability to be deregulated. Around 20% of melanomas harbor oncogenic mutations in the Ras genes, most mutations being located in codon 61 of N-Ras (Q61R or Q61K) [9]. Ras has several effectors that may contribute to the oncogenic property of mutated Ras. However, the existence in melanoma of frequent mutations in B-Raf, an effector of Ras, suggests that the Ras/Raf/MEK/ERK pathway is the predominant effector of Ras in melanoma [12].

The presence of mutations in Ras or upstream of Ras, in RTK, makes Ras a good therapeutic target for melanoma treatment. However, the only clinical agents used to date that affect Ras activity are the farnesyltransferase inhibitors (FTIs; Table 1). These agents impair the post-translational modification of the Ras proteins and prevent their membrane localization, which is required for signaling activity [27]. Several strategies have been developed to inhibit the farnesylation of Ras, the most common being the design of compounds that mimic the carboxy-terminal CAAX motif of Ras and compete for binding to farnesyltransferase. Another strategy has been to make compounds that compete with the farnesyl pyrophosphate group. A large number of highly effective FTIs have been identified, mostly through high-throughput screening of compound libraries [29]. Farnesylation is clearly not a process that is limited to the Ras proteins; this class of agents is therefore surely limited by lack of specificity. Nonetheless, in preclinical models and in limited correlative studies in clinical trials, there is evidence that Ras activity is impaired by FTIs. Indeed, a phase II study was undertaken to evaluate the activity and tolerability of the FTI tipifarnib (Zarnestra) as well as its ability to inhibit protein farnesylation and oncogenic pathways in patients with relapsed multiple myeloma. Results show that tipifarnib can induce disease stabilization and can inhibit farnesylation [3]. Data from a limited number of patients (4/34) of this phase II study show that treatment with tipifarnib affected the main oncogenic and tumor survival pathways differently. The data show that tipifarnib inhibited phospho-signal transducer and activator of transcription-3 levels in all four patients. However,

this inhibition did not correlate with clinical activity, since two of the four patients progressed. Similarly, the effects on phosphorylated ERK1/2 levels also did not correlate. In contrast, tipifarnib treatment inhibited the phosphorylated Akt levels in the two patients who stabilized, but not in the patients who progressed [3]. In conclusion, the significance of this observation could not be determined due to the limited number of samples. Another phase II study was undertaken in patients with metastatic pancreatic adenocarcinoma, but no antitumor activity was measured [7].

Although H-Ras is exclusively modified by farnesyltransferase, K-Ras and, to a lesser extent, N-Ras can also be modified by geranylgeranyltransferase (GGT) [74]. GGT of K-Ras and N-Ras becomes important only when farnesylation is blocked. As the vast majority of Ras mutations in human tumors are in K-Ras, followed by N-Ras, with very few in H-Ras, it is likely that inhibition of mutant Ras farnesylation is not responsible for any antitumor effects of FTIs. Attempting to inhibit the function of K-Ras and N-Ras by using FTIs and GGT inhibitors together has failed because of the very high toxicity associated with the combination. However, combination studies with FTIs and chemotherapy in N-Ras-mutated melanoma cells seem justified by preclinical data. Indeed, preclinical studies showed that FTI (SCH66336) inhibits farnesyl transferase, leads to morphological changes in melanoma cells associated with actin stress fiber formation, and inhibits the growth of melanoma cells. They also showed that SCH66336 induced a concentration- and time-dependent increase in apoptosis, cell cycle arrest and, finally, increased melanoma sensitivity to cisplatin [61]. Clinical trials associating FTI and other inhibitors in melanoma patients are now underway.

Raf serine/threonine kinase

Raf proteins are serine/threonine kinases that play a pivotal role in the MAPK pathway. The Raf kinase family is composed of three members: A-Raf, B-Raf, and C-Raf (also termed Raf-1), that share a common architecture with three conserved regions: two (CR1 and CR2) in the N terminus and the third (CR3), which encodes the kinase domain, in the C terminus [71]. Raf proteins are subject to complex regulation, which is reflected by the presence of numerous phosphorylation sites that are distributed throughout the proteins. Some of the sites are conserved in all three isoforms, which indicates common mechanisms of regulation, but others are not conserved, which shows that these proteins can be independently regulated [17]. Raf proteins are recruited to the plasma membrane by direct binding to activated Ras and are activated through many steps, including lipid binding, binding to other proteins, conformational changes, and phosphorylation. Raf positively regulates MEK1 and 2 by phosphorylating serine residues in the catalytic domain. All three Raf family members are able to activate MEK, but different bio-

chemical potencies have been observed (B-Raf>C-Raf>A-Raf). Downstream MEK targets are ERK1 and 2 serine threonine kinases, which can directly regulate many transcription factors, including Ets-1, c-Jun, and c-Myc [48]. The most commonly mutated component of the MAPK pathway in melanoma is B-Raf, which is mutated in 50–70% of cutaneous melanoma [12]. The most common mutation is found within the kinase domain of B-Raf, with a single substitution (T to A) of glutamate for valine at codon 600 (V600E) being responsible for 80% of observed mutations [23]. V600E-B-Raf stimulates constitutive ERK signaling, driving proliferation and survival and providing essential tumor growth [28, 30]. V600E-B-Raf also contributes to neo-angiogenesis by stimulating autocrine vascular endothelial growth factor (VEGF) secretion [58].

Because activating mutations in B-Raf allows the kinase to remain constitutively active irrespective of upstream Ras activity, Ras is an unattractive target in B-Raf mutant melanoma (Table 1). Sorafenib (BAY 43-9006) is an agent with B-Raf inhibitory activity that has reached clinical trials [73]. This agent was selected for clinical development before B-Raf was identified as an oncogene relevant to melanoma and is most potent against C-Raf. Nonetheless, the homology in the ATP binding sites of the Raf kinases provides for potent cross-reactivity against B-Raf. Although sorafenib was found to be a potent inhibitor of VEGF receptors later in its clinical development, its activity against B-Raf remains the focus of interest in the context of melanoma. In melanoma cell lines, sorafenib induces cell-cycle arrest and apoptosis and was able to elicit a significant retardation in the growth of human melanoma tumor xenografts, even if the animals were not cured [30]. In clinical trials, sorafenib as a single-agent has been associated with few objective responses and only a modest degree of tumor stabilization [18, 19]. However, phase I/II trials combining sorafenib with chemotherapy has been undertaken and combination with dacarbazine and carboplatin/paclitaxel showed promising efficacy and acceptable tolerability [21]. It remains to be determined in appropriately controlled trials in patients with melanoma whether combination therapies with sorafenib show superior efficacy to chemotherapy alone and whether this effect is mediated through inhibition of the Raf kinase pathway rather than inhibition of angiogenesis [52].

CHIR-265, a molecule with B-Raf and VEGF inhibitory activity, is in phase I clinical trial in melanoma patients [39]. Preclinical experiments show that CHIR-265 induces tumor regression in melanoma tumor xenografts that express V600E-B-Raf. Significant and sustained inhibition of downstream pathway biomarkers (phospho-MEK, phospho-ERK, and cyclin D1) was associated with this tumor response, whereas sorafenib caused tumor stasis and no detectable inhibition of Ras/Raf/MEK/ERK pathway biomarkers.

PLX720 is a novel inhibitor of oncogenic B-Raf which shows specificity toward the V600E-B-Raf mutant

[20]. PLX720 induces inhibition of proliferation in A375 melanoma cells *ex vivo* and inhibition of tumor growth can be measured in an A375 tumor xenograft model. The inhibition of proliferation correlates with the inhibition of the MAPK pathway. Clinical trials in patients harboring the V600E-B-Raf mutant are underway.

MEK serine/threonine kinase

Although MEK has never been found mutated in melanoma, it is the immediate and sole downstream target of Raf and therefore an appealing therapeutic target in melanoma with mutations in the MAPK pathway. Due to the prevalence of mutations in the MAPK pathway in human cancers in general, many MEK inhibitors are in clinical development and could benefit melanoma therapy (Table 1).

The highly specific MEK inhibitor CI-1040 inhibits *ex vivo* proliferation, soft agar colony formation, and matrigel invasion of V600E-B-Raf mutant human melanoma cells. Moreover, administration of CI-1040 to mice bearing A375MR-Luc xenograft prevents the formation of pulmonary metastases and causes regression of established metastases [8]. CI-1040 reached phase II clinical trials, but its development was stopped due to insufficient efficacy [55].

ARRY-142886 (AZD6244) is a second-generation and ATP-noncompetitive inhibitor of MEK which has shown better efficacy than CI-1040 in preclinical models and is currently in early clinical development. It has been recently shown that ARRY-142886 was able to inhibit cellular growth and induce apoptosis of several lines containing B-Raf and Ras mutations. Moreover, ARRY-142886 demonstrated its efficacy against pancreatic BxPC3 xenograft model and human colon carcinoma tumors [75]. This compound is currently being investigated in clinical studies.

PD0325901 is a derivative of CI 1040 that has improved oral bioavailability and induces a longer duration of target suppression. Preclinical studies showed that PD0325901 completely suppressed the growth of V600E-B-Raf mutant xenografts [62]. Phase I trials were performed in patients with breast, colon NSCLC, or melanoma. According to the analysis performed on serial biopsies, PD0325901 treatment shows more than 80% ERK inhibition. However, despite target inhibition, it appears that as a single agent, PD0325901 is not sufficient to induce tumor regression and stabilization [41]. The combination of MEK inhibition with chemotherapy seems justified, but remains to be clinically investigated.

Lethal factor (LF), one of the three proteins of the anthrax toxin of *Bacillus anthracis*, inhibits MAPK signaling by proteolytically cleaving MEK 1 and 2. Preclinical studies show that LF induces regression of human melanoma xenografts [1, 32]. These studies should pave the way for melanoma clinical trials using LF.

It is important to note that B-Raf-mutated melanoma cell lines were recently shown to be more sensitive to

MEK inhibition than Ras-mutated cell lines *ex vivo*. Moreover, pharmacological MEK inhibition completely inhibited tumor growth in B-Raf mutant xenografts, whereas Ras mutant tumors were only partially inhibited [62]. These data suggest that MEK inhibitors may provide a therapeutic strategy for B-Raf, but not Ras mutant melanoma. We have recently shown that Ras-mutated melanoma cell lines switch their signaling from B-Raf to C-Raf [16]. This finding has important therapeutic implications because it suggests that both B-Raf and C-Raf are valid targets in melanoma, but this depends on whether B-Raf or Ras are mutated in the tumor.

PI3K PATHWAY

Type I PI3K is another effector of Ras. Activated PI3K converts phosphatidylinositol 4,5 phosphate into phosphatidylinositol 3,4,5 phosphate (PIP3), which regulates the activity and localization of a number of target proteins including those that contain pleckstrin homology (PH) domains [22] (Fig. 1). One such PH domain-containing protein regulated by lipids is the serine/threonine kinase Akt (also called protein kinase B). Targets for Akt include kinases, glycogen-synthase kinase 3, p70S6 kinase, transcription factors, FKHR, and cAMP-response element-binding protein, as well as proteins associated with apoptosis, caspase 9 and Bcl-2 antagonist of cell death (BAD) [43]. This pathway is negatively regulated by the phosphatase and tensin homologue deleted on chromosome 10 (PTEN) and SH2 domain-containing inositol phosphatase 1 and 2 which remove the phosphates from PIP3 [11]. PTEN is a protein and lipid phosphatase that inhibits Akt activation by PI3K [60]. Loss of heterozygosity in the region of chromosome 10q, which harbors the PTEN locus, was demonstrated in 30–50% of melanomas and somatic mutations of the PTEN gene were detected in 10% of melanomas [4, 25]. Furthermore, constitutive activation of Akt3, the predominant Akt isoform in melanoma, was recently reported in more than 60% of melanomas [63], emphasizing the importance of the PI3K pathway activation in melanoma development. The expression of phosphorylated and therefore active Akt protein increases dramatically with melanoma invasion and metastasis and is inversely correlated with patient survival [10]. Increased Akt activity prolongs cell survival through the inactivation of the BAD protein. In model systems, suppression of Akt3, a member of the Akt family, reduces the survival of melanoma cells and the growth of human melanoma implanted in immunodeficient nude mice [63]. Therefore, the PI3K is a good therapeutic target for melanoma treatment. Given that restoration of PTEN is more technically challenging than pharmacological inhibition of components of the PI3K pathway, current efforts are aimed at identifying inhibitory compounds for PI3K, Akt, and mammalian target of rapamycin (mTOR), a downstream target of

Akt. The lack of PI3K and Akt inhibitors for clinical use has turned attention to mTOR, for which numerous inhibitors are in clinical development (Table 1). mTOR is a member of the family of protein kinases termed PI3K-related kinase, which are involved in many regulatory cellular functions, such as protein translation, cell cycle progression, and cellular proliferation [45]. Aberrations in the upstream regulators of the PI3K pathway leads to alterations in mTOR regulation activity.

Rapamycin is an inhibitor of mTOR with poor aqueous solubility and chemical stability, which precluded its clinical development as an anti-cancer agent. Recently, a series of rapamycin analogs with improved aqueous solubility and stability have been synthesized and evaluated, such as CCI-779 (temsirolimus), RAD-001 (everolimus), and AP-23573. CCI-779, a soluble ester analog of rapamycin, was selected for development as an anti-cancer agent based on its prominent antitumor profile and pharmaceutical and toxicological characteristics in preclinical studies [15]. Preclinical studies suggest that sensitivity to mTOR inhibitors may correlate with activation of the PI3K pathway or with aberrant expressions of cell-cycle regulatory or anti-apoptotic proteins. CCI-779 has demonstrated activity against melanoma in preclinical models and shown clinical benefit in patients with breast and renal carcinoma. However, a phase II clinical trial with CCI-779 resulted in only one objective response among 33 melanoma patients and early closure of the study [44]. The lack of single-agent antitumor efficacy does not preclude a chemotherapy-enhancing effect, which is suggested by preclinical studies. Indeed, preclinical studies show that CCI-779 has the potential to increase the chemotherapeutic efficacy of dacarbazine in human melanoma xenografts [65]. The combination of CCI-779 with cisplatin has shown promising results in a human melanoma xenograph model in severe combined immunodeficient mice injected with three melanoma cell lines (518A2, Mel-JUSO, or 607B). Four of six tumors of the 518A2 cell line were completely eradicated and the two others were reduced by 97% by CCI-779. Combination of both treatments also had a significant antitumor effect in the tumors of Mel-JUSO and 607B [64].

cAMP PATHWAY AND MITF

Microphthalmia-associated transcription factor (MITF) is a member of the basic helix-loop-helix leucine zipper transcription factors conserved in essentially all vertebrate species [40]. The M-MITF isoform is considered as a master regulator of differentiation of the melanocyte lineage and is induced through the cAMP pathway. M-MITF transcription is stimulated by hormones such as α melanocyte stimulating hormone, which binds to the melanocortin 1 receptor, and stimulates cAMP production. cAMP activates the serine/thre-

online kinase protein kinase A which phosphorylates the cAMP responsive element binding protein transcription factors which, in turn, stimulate the M-MITF promoter (Fig. 1) [37]. MITF is located in the center of multiple signaling pathways which control differentiation, morphology, proliferation, and survival of the various cells of the melanocyte lineage: melanoblasts, melanocytes, and melanoma. MITF plays a major role in melanoblast differentiation by inducing the key enzyme of melanogenesis, tyrosinase, and its secondary enzymes Tyrp1 and Dct. MITF regulates the morphology and migration of melanocytes, particularly by regulating cytoskeleton organization and cell-cell adhesion [69]. MITF also regulates the transcription of the melanocyte-specific genes silver homologue and melan-A, whose immunohistochemical detection points to the diagnosis of melanoma [14]. Recently, amplification of MITF was identified in 10% of primary cutaneous melanoma cases and 21% of metastatic tumors, but not in nevi [24]. MITF amplification is more prevalent in metastatic disease and correlated with decreased overall patient survival. The cell lines that harbored MITF amplifications also contained B-Raf mutations and p16 inactivation. Ectopic MITF expression in conjunction with the ^{V600E}B-Raf mutant transformed primary human melanocytes, showing that MITF can function as a melanoma oncogene [24]. How MITF acts as an oncogene is not clear, but it may be linked to the transcriptional regulation of the c-MET proto-oncogene. It has been shown that MITF directly regulates the c-MET promoter and is essential for the homeostatic upregulation of c-MET expression following activation of the receptor by its ligand, HGF [46]. c-MET is highly expressed in human melanoma and has been linked to the metastatic potential of melanomas (see above). It was also observed that MITF regulates c-MET expression in primary melanocytes and that the ability of HGF to stimulate invasive growth of melanocytes and melanoma cells in culture was abolished upon suppression of endogenous MITF [46]. MITF may also contribute to melanocyte transformation through its ability to regulate apoptosis [34]. It was recently shown that reduction of MITF activity sensitizes melanoma cells to chemotherapeutic agents, suggesting that targeting MITF in combination with B-Raf or cyclin-dependent kinase inhibitors may offer a rational therapeutic avenue into melanoma [24]. However, others have also demonstrated that MITF is an antiproliferative factor in melanoma that is downregulated by B-Raf signaling and that this is a crucial event for the progression of melanomas harboring oncogenic B-Raf [72]. The therapeutic potential of MITF awaits further studies.

CONCLUSION

The future of melanoma therapy relies on tailored targeted therapies that are likely to result from the significant progress in understanding the molecular mechanisms leading to melanoma. It has become evident that

the response to targeted therapies will depend on which type of genetic alteration is responsible for the dysregulation. Recent melanoma genetic studies allow classification of melanoma into four subtypes: melanoma occurring on the skin without signs of chronic sun-induced damage (non-CSD melanoma), on sun-protected skin such as the palms, soles, or subungual sites (acral melanoma), on mucosal membranes (mucosal melanoma), and on the skin showing evidence of chronic sun-induced damage (CSD melanoma). Signaling pathways are activated differently according to the melanoma subtype. Indeed, although B-Raf mutations are highly prevalent in non-CSD melanoma (59%), they are significantly less frequent in acral and mucosal melanoma and are uncommon in CSD melanoma. However, N-Ras mutations hit approximately 20% of melanomas in all four subtypes. c-Kit mutations are more frequent in acral (36%), mucosal (39%), and CSD melanoma (28%), but absent in non-SCD melanoma. Recent discoveries in melanoma genetics raise expectations for the rational design of more effective anti-melanoma therapies (Table 1). However, it is evident that it will be necessary to vary the single pharmacological approaches to inhibit one pathway and to combine inhibitors of different pathways with classical as well as new chemotherapeutic agents.

Acknowledgment: We thank Dr. Kirsten Dumaz for proof-reading the manuscript. Work in our laboratory is funded by the Institut National de la Santé et de la Recherche Médicale (INSERM), Paris XII University, Société Française de Dermatologie, Société de Recherche Dermatologique, and the Association pour la Recherche sur le Cancer (ARC).

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