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NF- κ B activation in melanoma

Yukiko Ueda¹ and Ann Richmond^{1,2,*}

¹ Department of Cancer Biology, Vanderbilt University School of Medicine, Nashville, TN, USA

² Department of Veterans Affairs, Nashville, TN, USA

Summary

Metastatic melanoma is an aggressive skin cancer that is notoriously resistant to current cancer therapies. In human melanoma, nuclear factor-kappa B (NF- κ B) is upregulated, leading to the deregulation of gene transcription. In this review, we discuss (i) the relationship between gene alteration in melanoma and upregulation of NF- κ B, (ii) mechanisms by which activated NF- κ B switch from pro-apoptotic to anti-apoptotic functions in melanoma and (iii) autocrine mechanisms that promote constitutive activation of NF- κ B in metastatic melanoma.

Keywords

NF- κ B; IKK; melanoma; MAP3K; cytokines; apoptosis

Introduction

Melanoma is a skin cancer that originates in melanocytes, specialized pigment-producing cells found in both the basal layer of the epidermis and in the eye (Hurst et al., 2003). The known environmental risk factor is exposure to ultraviolet light, and the risk is greatly increased in people with fair skin (Bauer and Garbe, 2003; Bliss et al., 1995). Normally, melanocytes synthesize melanin pigments and transfer them to surrounding keratinocytes. The resulting skin pigmentation protects against damage caused by solar ultraviolet radiation (Gilchrest et al., 1999). Melanoma progresses from pigmented lesions called benign nevi, which are then converted to dysplastic nevi (Clark, 1991; Clark et al., 1989; Koh, 1991; Mooi, 1997; Parmiter and Nowell, 1993). Further progression leads to an *in situ* melanoma, which grows laterally and is mostly confined to the epidermis. This stage is known as radial growth phase (RGP) melanoma (Clark, 1991). RGP melanoma can be treated efficiently by surgical dissection, with low risk of relapse or metastasis. However, if left untreated, the melanoma can progress to the vertical growth phase (VGP), which is associated with invasion of the dermis by melanoma cells and the acquisition of metastatic potential (Clark, 1991). Due to the complex nature of the disease, melanoma has proven to be highly resistant to conventional chemotherapy treatment with dacarbazine (DTIC) or its derivative temozolomide (TMZ), which exhibits the best single agent activity with a response rate of only 15–20% (Balch and Cascinelli, 2001; Sondak et al., 2001). Patients at high risk for recurrence are frequently given interferon- α (IFN- α) and/or interleukin-2 (IL-2) as an adjuvant. The effectiveness of this treatment is widely debated, and even its supporters acknowledge that benefits are small and offset by a high level of toxicity (de Gast et al., 2003; Meric et al., 2003; Punt and Eggermont, 2001).

The activation of nuclear factor-kappa B (NF- κ B) has been proposed as an event that promotes melanoma tumor progression (Huang et al., 2000a; Payne and Cornelius, 2002; Richmond,

*Address correspondence to Ann Richmond, e-mail: ann.richmond@vanderbilt.edu.

2002). In human melanoma, a number of NF- κ B-regulated chemokines are constitutively expressed at high levels: CXC ligand 8 (CXCL8 or IL8, interleukin-8; Singh et al., 2005), CXCL1 (Melanoma growth stimulatory activity or MGSA; Richmond et al., 1985), CCL5 (regulated on activation, normal T expressed and secreted, or RANTES; Mrowietz et al., 1999) and CCL2 (monocyte chemoattractant protein-1, or MCP1; Bottazzi et al., 1992). These NF- κ B-regulated chemokines, when transcriptionally activated, are thought to enhance melanoma progression through autocrine and paracrine loops (Payne and Cornelius, 2002; Richmond, 2002; Strieter, 2001). Indeed, overexpression of CXCL8 causes metastatic tumor growth in normal primary melanoma cells (Schaidter et al., 2003; Singh et al., 2005), and is associated with the transition from RGP to VGP in melanoma (Leslie and Bar-Eli, 2005). Antibodies which neutralize CXCL8 inhibit tumor angiogenesis in human melanoma (Huang et al., 2000a, 2002), and melanoma patients responding to chemotherapy exhibited a significant decrease in CXCL8 serum levels (Brennecke et al., 2005). Overexpression of the murine homologue of CXCL1 in *INK4a/ARF*^{-/-} immortalized melanocytes increases melanoma tumor incidence (Yang et al., 2001b) and induces malignancy in squamous cell carcinoma in nude mice (Dong et al., 2001). Furthermore, antibodies that are specific for these ligands or their receptors slow the growth of melanoma tumors in mice (Payne and Cornelius, 2002).

All members of the NF- κ B family [Rel A (p65), Rel B, C-Rel, NF- κ B1 (p50), and NF- κ B2 (p52)] contain a Rel homology domain (RHD) in the N-terminal region that mediates dimerization and DNA binding (Dixit and Mak, 2002; Ghosh and Karin, 2002; Hayden and Ghosh, 2004; Richmond, 2002). Inactivated forms of p65, Rel B, and C-Rel are associated with cytoplasmic I κ B (inhibitor protein of NF- κ B), while p100 (precursor of p52) and p105 (precursor of p50) contain intrinsic inhibitory domains. I κ B proteins are regulated through a mechanism in which they are phosphorylated by the I κ B kinase complex (IKK) and subsequently degraded by the 26S proteasome (Dixit and Mak, 2002; Ghosh and Karin, 2002). p65 is phosphorylated by a number of kinases during the phosphorylation and degradation of I κ Bs, and these events enhance the nuclear translocation of p65 (Naumann and Scheidereit, 1994; Sakurai et al., 1999). Upon stimulation, p100 and p105 are cleaved into active forms p52 and p50 respectively. These post-translational modifications generate active NF- κ B complexes, most importantly the p65/p50 heterodimer, which represents the major activated form of NF- κ B in many cell types (Dixit and Mak, 2002; Ghosh and Karin, 2002; Richmond, 2002).

Although causality is often difficult to determine in melanomas, sun exposure and genetic susceptibility are considered important predisposing factors. On the contrary, *in vitro* and *in vivo* studies have shown that NF- κ B activity is upregulated in dysplastic nevi and lesions of human melanoma when compared with human nevi or melanocytes in normal skin (Dhawan and Richmond, 2002; McNulty et al., 2001, 2004). Inhibition of NF- κ B in highly metastatic melanoma xenografts in nude mice resulted in a decrease in angiogenesis as measured by microvessel density, which correlated with a decrease in the level of CXCL8 expression (Huang et al., 2000b). In this review, we discuss (i) relationships between gene alteration in melanoma and the upregulation of NF- κ B, (ii) mechanisms by which activation of NF- κ B results in a switch from a pro-apoptotic to anti-apoptotic function in melanoma, and (iii) autocrine mechanisms that sustain the constitutive activation of NF- κ B in metastatic melanoma.

Gene mutation in sporadic melanoma and NF- κ B upregulation

Exposure to UV light is known as an inducer of gene mutation in sporadic melanoma (Bauer and Garbe, 2003; Bliss et al., 1995; Clark et al., 1989; Gilchrist et al., 1999). Specific gene mutations reported with high frequency include the 16 kDa cyclin-dependent kinase 4 (CDK4) inhibitor (*p16 INK4a*), the 14 kDa protein derived from the alternative reading frame of INK4 (*p14 INK4/ARF*), *p53*, human neuroblastoma retrovirus-associated sequences (*N-Ras*), *v-Raf*

murine sarcoma viral oncogene homolog B1 (*B-Raf*), and a lipid phosphatase known as phosphatase and tensin homolog (*PTEN*; Table 1).

There is increasing evidence that melanoma progression is mediated through multiple genetic routes. For example, an analysis of 41 melanoma samples revealed an uneven distribution of *B-Raf*, *N-Ras*, *PTEN*, *P53* and *p16 INK4a* mutations, and among the samples, 12 distinct mutational profiles were identified (Daniotti et al., 2004). These gene mutations are thought to coordinately promote the dermatological transitions from normal melanocyte to malignant melanoma as shown in Figures 1 and 2A. In the first section of this review, these gene mutations are reviewed in terms of the upregulation of NF- κ B, as shown in Figure 1.

NF- κ B upregulation and *p16 INK4a* mutation

p16 INK4a regulates not only cell proliferation (Hayward, 2000; Rocco and Sidransky, 2001; Ruas and Peters, 1998; Sharpless and DePinho, 1999), but also the activity of the retinoblastoma (RB) protein family members, which are tumor suppressors and inhibitors of cell proliferation (Castellano and Parmiani, 1999; Soufir et al., 1999). The p16 INK4a/RB pathway is critical to the prevention of melanoma, as p16 INK4a or RB deficiency leads to the overexpression of cyclin D1, enhancement of proliferation, and/or immortalization (Bartkova et al., 1996; Sauter et al., 2002; Utikal et al., 2005).

Wild-type p16 INK4a has been shown to bind to the NF- κ B subunit p65, whereas mutated p16 INK4a exhibits reduced binding (Becker et al., 2005; Wolff and Naumann, 1999). Expression of wild-type p16 INK4a strongly inhibits NF- κ B transcriptional activity (Becker et al., 2005), suggesting that loss of p16 INK4a directly leads to the upregulation of NF- κ B activation (Figure 1).

NF- κ B upregulation and *p14 INK/ARF-P53* mutation

p14 INK4/ARF activates a key tumor suppressor, p53 (Albino et al., 1994; Papp et al., 2003; Sherr, 2001; Straume et al., 2000). Thus, *p14 INK/ARF* loss/inactivating mutation is associated with the reduction or loss of p53 activation (Ghiorzo et al., 2004; Rizos et al., 2001).

The *IKK α* promoter contains a p53 binding site, which inhibits gene transcription (Gu et al., 2004). Therefore, loss of p53 leads to the upregulation of *IKK α* and the activation of NF- κ B. An inhibitor of p53-dependent transcription leads to an increase in UV-induced activation of NF- κ B (Wang et al., 2005). These experimental data suggest that p53 loss/mutation directly leads to the upregulation of NF- κ B (Figure 1).

NF- κ B upregulation and *N-Ras/B-Raf* mutation

The responses of cells to their environment are controlled by conserved signaling mechanisms that transmit signals from the cell surface to the nucleus. The Ras/Raf/mitogen-activating-kinase (MAPK) cascade leads to cell proliferation and the inhibition of cell apoptosis. Ras proteins, small guanine-nucleotide binding proteins that are embedded in the inner surface of the plasma membrane, are inactive in their GDP-bound state and are active in GTP-bound state. Ras proteins are activated by receptor tyrosine kinases or G-protein coupled receptors (Marais and Marshall, 1996; Robinson and Cobb, 1997). Ras-GTP can bind to several effector proteins, including Raf serine/threonine-specific kinases (Marais and Marshall, 1996; Robinson and Cobb, 1997). The *B-Raf* gene undergoes point transversion mutations in the kinase domain (predominantly V600E, where valine is substituted for glutamic acid) at high frequency (Davies et al., 2002), as shown in Table 1. Most cases of *B-Raf* mutations are associated with melanoma and are not commonly associated with other cancers (Brose et al., 2002; Davies et al., 2002). The *B-Raf* mutation is found in early stages of benign nevi (Jackson et al., 2005), and even causes oncogene-induced cell senescence (OIS) through the induction of p16 in

human nevi (Michaloglou et al., 2005). However, as shown in Figure 3A, OIS is overridden when p16 is deleted or mutated in melanoma. When OIS is overridden, the kinase activity of mutated *B-Raf* is 500-fold greater than that of wild type *B-Raf* (Wan et al., 2004). This kinase activation leads to downstream effects such as the constitutive activation of extracellular signal-regulated kinase 1 and 2 (ERK1/2) in various melanoma cell lines and melanoma tumors (Bloethner et al., 2005; Karasarides et al., 2004; Zuidervaart et al., 2005).

So far, it is not clear how mutant *N-Ras* and/or *B-Raf* activates NF- κ B, although these mutated genes are known to activate ERK 1/2. In human melanoma cell lines with *B-Raf* mutations and constitutively active NF- κ B and ERK, the anti-proliferative and pro-apoptotic reagent curcumin suppresses NF- κ B/IKK activation, but not ERK activation (Siwak et al., 2005). These data suggest that ERK activation is not directly linked to the activation of NF- κ B. However, constitutively active ERK also activates expression of various cytokines such as TNF- α and IL-1 α/β , as well as chemokines, all of which are known activators of NF- κ B (Castelli et al., 1994; Gaggioli et al., 2005). Therefore, mutant *N-Ras* and/or *B-Raf* may indirectly activate NF- κ B through constitutive activation of ERK and the upregulation of inflammatory cytokines (Norris and Baldwin, 1999).

NF- κ B upregulation and *PTEN* loss/mutation

The responses of cells to their environment are also controlled by another conserved signaling module, the phosphatidylinositol (3, 4, 5) kinase (PI3K) cascade. In the PI3K cascade, PI3K binds to an activated tyrosine kinase receptor or G-protein coupled receptor and transfers the gamma phosphate group from ATP to the 3'-OH of phosphatidylinositol (PI) substrates (Vanhaesebroeck et al., 1999). The phosphorylated PI, such as PIP2 or PIP3, in turn recruits adapter kinases to the cell membrane, which subsequently phosphorylates AKT thymoma (AKT; Cooray, 2004). AKT is a serine/threonine kinase that phosphorylates many target proteins (Cooray, 2004; Sliva, 2004). AKT also phosphorylates IKK α at the consensus sequence RXXRXXS/T, leading to the p65 phosphorylation (Li and Stark, 2002; Sizemore et al., 2002). In addition, AKT has been reported to phosphorylate the NF- κ B subunit p65, increasing the binding of the NF- κ B complex to DNA (Koul et al., 2001). Inhibitors of PI3K block endogenous NF- κ B activity in malignant melanoma cells (Dhawan et al., 2002). These results indicate that AKT directly mediates NF- κ B activation.

PTEN is the regulatory molecule in the PI3K/AKT pathway and is known to shut off AKT activation by dephosphorylating phosphatidylinositol-3, 4, 5-triphosphate (PIP3) and blocking AKT membrane localization (Koul et al., 2001). PTEN is often deleted or mutated in melanoma tumors (Table 1), leading to the constitutive activation of AKT as well as NF- κ B in human melanoma (Celebi et al., 2000; Dhawan et al., 2002; Tsao et al., 2003; Zhou et al., 2000).

NF- κ B: molecular switch from pro-apoptotic to anti-apoptotic melanoma

Gene mutations lead to dermatological melanoma progression (Figure 2A), during which NF- κ B is upregulated. NF- κ B is known to coordinate the expression of over 150 genes and contribute to the balance between cell survival and apoptosis (Ivanov et al., 2003; Richmond, 2002). This section discusses how upregulated NF- κ B coordinately regulates these genes and how NF- κ B switches from pro-apoptotic to anti-apoptotic cell stages.

In melanocytes or early stages of melanoma, NF- κ B upregulates three major pro-apoptotic pathways, which leads to caspase activation through (i) tumor necrosis factor receptor-1 (TNFR-1; Baldwin, 1996), (ii) TNF-related apoptosis-inducing ligand receptor 1/2 (TRAILR-1/2; Ravi et al., 2001), and (iii) Fas receptor (FAS-R; Chan et al., 1999; Ivanov and Ronai, 2000; Figure 2B). On the contrary, in late stages of metastatic melanoma, NF- κ B upregulation inhibits these three pro-apoptotic pathways through the upregulation of (i) tumor

necrosis factor receptor-associated factor-1 (TRAF-1) and TRAF-2 (Baldwin, 1996) to inhibit the TNF-R1/caspase-8-mediated pro-apoptotic pathway (Wang et al., 1998), (ii) TRAIL decoy receptor, inhibiting the TRAIL-mediated cell-death pathway (Bernard et al., 2001; Oya et al., 2001; Zhang et al., 2000), and (iii) Fas-associated phosphatase-1 (FAP-1; Sato et al., 1995), which inhibits FAS-R trafficking from cytoplasm to membrane (Ivanov et al., 2006; Figure 2B).

In late-stage melanoma, upregulated NF- κ B also enhances several anti-apoptotic molecules such as inhibitor of apoptosis (IAP; Deveraux et al., 1998), caspase-8 (FLICE) inhibitory protein (FLIP; Micheau et al., 2001) and BclxL genes (Ravi et al., 2001). In addition, NF- κ B upregulates Myc (Kraehn et al., 2001) and the cell cycle regulatory proteins, cyclin D1 and cyclin dependent kinase 2 (CDK2; Guttridge et al., 1999; Hinz et al., 1999), which further contribute to melanoma tumor growth.

Autocrine system for constitutive activation of NF- κ B in melanoma

As discussed above, in malignant melanoma NF- κ B is activated because of the activity of IKK complex-mediated degradation of I κ B family members. I κ B family members include I κ B α , I κ B β , BCL-3, I κ B ϵ , I κ B γ , and the domains inside NF- κ B precursors p100 and p105 (Hatada et al., 1993).

As shown in Figure 3, the classical NF- κ B activation pathway (Ghosh and Karin, 2002) includes an activated IKK complex composed of two kinase subunits, IKK α and IKK β , and a regulatory subunit IKK γ . In this pathway, IKK β is necessary and sufficient to phosphorylate I κ B molecules, which are bound to p65-containing homo- and heterodimers (Figure 3). Mice with p65-null mutation are lethal in the embryonic developmental stage, causing liver degeneration via TNF- α signaling (Beg et al., 1995). The lethality caused by p65-null mutation was suppressed by crossing the p65 null mice onto a TNF α -null background (Alcamo et al., 2001; Beg and Baltimore, 1996; Doi et al., 1999). p50 null mice are not embryonic lethal, but exhibit decreased immunoglobulin production and abnormal immunoglobulin responses (Campbell et al., 2000; Sha et al., 1995).

There is an alternative NF- κ B activation pathway (Ghosh and Karin, 2002) that contains the activated IKK α homodimer complex (Figure 3). In this pathway, IKK α binds to the p100/RelB complex, then phosphorylates and processes p100, producing the active p52/RelB heterodimer (Figure 3). Rel B binds to p100, but does not homodimerize or heterodimerize with p65 (Ryseck et al., 1992). p52⁻ null mice exhibit defects in their peripheral B-cell population, humoral response, as well as splenic architecture (Caamano et al., 1998; Franzoso et al., 1998). Rel B-null mice exhibit decreased NF- κ B activity in the thymus and spleen, and increased inflammatory infiltration into multiple organs. Rel B is critical to the coordinated activation of genes, which determine lineage commitment in the immune system (Burkly et al., 1995; Weih et al., 1995). This alternative pathway is activated by a LT β R family-mediated cascade, as shown in Figure 3.

In general, these previous data indicate that p65-containing NF- κ B complexes in the classical pathway are crucial to protection from apoptosis, whereas RelB/p52 dimerization in the alternative pathway is responsible for lymphoid organogenesis (Figure 3). Following the degradation of I κ B molecules or domains, the released and activated NF- κ B complexes are free to translocate into the nucleus and bind to the consensus enhancer sequence (Parry and Mackman, 1994) on the promoters of various target genes. We also observed this sequence in the promoter enhancer region of NF- κ B-regulated chemokine genes *CXCL1*, *CXCL2*, *CXCL5*, *CXCL6*, and *CXCL8*. In the following five cascades, we discuss the mechanism of IKK activation with the NF- κ B autocrine activation loop in melanoma.

Chemokines/GPCR/GIP cascade for autocrine NF- κ B activation

As reviewed above, a number of NF- κ B-regulated chemokines such as CXCL8 (Singh et al., 2005), CXCL1 (Richmond et al., 1985), CCL5 (Mrowietz et al., 1999) and CCL2 are overexpressed in melanoma (Bottazzi et al., 1992). Chemokines and their receptors direct cell movement and gene expression signaling in melanoma. These chemokines are divided into the α (CXC), β (CC), γ (C), and δ (CXXXXC) subclasses according to the configuration of the first two cysteine residues on their N-termini (Premack and Schall, 1996), which bind to G-protein coupled receptors (GPCR). The GPCRs then activate heterotrimeric G-proteins, which dissociate from the receptors and initiate second messenger signaling (Ganju et al., 1998; Hamm, 1998). GPCRs also interact with many other proteins, designated GPCR interacting proteins (GIP), most commonly through consensus domains located on their intracellular carboxyl terminal domains (Bockaert et al., 2004). For example, β -arrestin, a common GIP, binds to most GPCRs, regulating the receptor function (Sun et al., 2002). The activation of some GPCR/ β -arrestin complexes mediates new signals via activation of MAP kinases such as c-Jun N-terminal kinase 3 (JNK3), extracellular-signal-regulated kinase 1/2 (ERK1/2), and p38 MAP kinase (McDonald and Lefkowitz, 2001; Shenoy and Lefkowitz, 2003; Tilton et al., 2000).

Human melanoma lesions are known to overexpress GPCRs that play a role in these chemokine-mediated signaling pathways (Luan et al., 1997; Muller et al., 2001; Payne and Cornelius, 2002; Robledo et al., 2001; Wiley et al., 2001). The constitutive expression of CXCL-8 receptors (CXCR1 and CXCR2) leads to a IL-8-mediated metastatic phenotype in human malignant melanoma cells (Varney et al., 2003). Synthesis of the autocrine CXCL-8 also leads to a CXCL-8-dependent proliferation and angiogenesis in a subgroup of human melanomas (Bobrovnikova-Marjon et al., 2004; Leslie and Bar-Eli, 2005; Singh et al., 1999). The expression of CXCL-1 also further activates NF- κ B through the sensitization of GPCRs (Richmond, 2002; Yang et al., 2001b). NF- κ B is also activated by CXCL1 through the MEKK1 and p38 MAPK pathway (Wang and Richmond, 2001). Melanoma cells exposed to CCL27 undergo rapid activation of AKT and exhibit resistance to cell death induced by melanoma antigen-specific cytotoxic T cells, or by Fas-mediated apoptosis (Murakami et al., 2003, 2004).

These data suggest that GPCR signaling mediates melanoma tumor progression through an autocrine system, which is mediated by the activation of PI3K/AKT as well as MAPK cascades (Figure 3).

EGF/EGFR/Ras cascade for autocrine NF- κ B activation

The binding of epidermal growth factor (EGF) to its receptor leads to the activation of NF- κ Bs, DNA binding to the consensus sequences, and an increase in NF- κ B-dependent gene transcription (Haussler et al., 2005). The inhibition of NF- κ B causes a reduction in EGF-induced cyclin D1 promoter activity (Haussler et al., 2005). These recent experimental data indicate that, in melanoma, EGF receptor (EGFR) mediates Ras/AKT/MEKK3 and NF- κ B activation through autocrine loops. Indeed, a combination of specific inhibitors for PI3K/AKT and MAPK kinase kinase (MAPK3)/ERK induces high levels of apoptosis in melanomas (Ivanov and Hei, 2005).

Members of the human EGFR family are expressed in cultured human melanocytes, and several combinations of heterodimers exhibit the differential responses to the ligand TGF- α in migration and proliferation (Gordon-Thomson et al., 2005). This indicates a molecular switch function for the EGFR family in melanoma growth (Gordon-Thomson et al., 2005). In this subsection, EGFR family-mediated signaling is specifically discussed, because among the

large number of the growth factor receptors, EGFR upregulation is commonly reported in relation to melanoma progression.

The human EGFR family contains HER1 (receptor for EGF), HER2 (orphan receptor), HER3, and HER4 (receptors for hereglin; Coussens et al., 1985; Plowman et al., 1993; Ullrich et al., 1984). The binding of ligands to the cysteine-rich ectodomains of receptors results in the formation of homodimeric and heterodimeric complexes, which is rapidly followed by the activation of the cytoplasmic receptor tyrosine kinase (RTK; Riese and Stern, 1998). The activation of the intrinsic RTK auto-phosphorylates C-terminal tyrosine residues, which in turn recruit signaling molecules (Alroy and Yarden, 1997). The activated RTK is known to bind SH2 domain-containing proteins such as Shc and Grb2, leading to the activation of Ras/MAPK (Segatto et al., 1993), PLC γ (phospholipase γ ; Fazioli et al., 1991), and PI3K (Medzhitov et al., 1998) pathways.

So far, we have discussed NF- κ B as a downstream target of signaling pathways initiated via EGFR in melanoma. In Ras inducible transgenic mice, the activation of Ras leads to the upregulation of the EGF family, and the mice exhibited enhanced melanoma progression (Bardeesy et al., 2005). This indicates that an autocrine loop of EGFR signaling cascade contributes to melanoma progression (Bardeesy et al., 2005). However, the *EGF* promoter does not have an NF- κ B binding element within -300 and +1 of the promoter. On the other hand, *EGFR (HER1)* (reference accession no. NM_005228) does contain the NF- κ B-binding consensus sequence GGGAACGCC at position -275 (TFSEARCH <http://www.cbrc.jp>), similarly *HER2* (NM_004448) contains GGGAGTTGCC at position -79, and *HER4* (NM_005235) contains GGGATCTCTG at position -51. These sequences exceed the 85% threshold in relation to the NF- κ B consensus sequence in M00054. In contrast, the *HER3* (NM_004448) promoter does not contain an NF κ B binding site. Though the NF- κ B binding site in the *EGFR (HER1)* promoter at position -275 is distant from the TATA box, the proximal location of the NF- κ B binding sites in *HER2* and *HER4* promoters suggest possible functions as enhancer regions for core transcription factor binding sites. HER2 is an orphan receptor which homo- or heterodimerizes with other EGF receptors and transduces signaling to downstream cascades. Therefore, the upregulation of NF- κ B possibly upregulates EGFRs, especially HER2 and HER4, to mediate an EGFR autocrine activation system (Figure 3). Indeed, constitutively active HER2 can activate NF- κ B and induce resistance to apoptotic stimuli by TNF- α in NIH3T3 cells (Makino et al., 2004).

IL-1/IL-1R/IRAC cascade for constitutive NF- κ B activation

Toll receptors are known to sense the invasion of microorganisms with pathogen-associated microbial patterns (PAMPs) among many species (Belvin and Anderson, 1996). Toll-like receptor (TLR) in human also recognize many PAMPs including LPS, double stranded RNA (dsRNA), non-methylated CpG DNA, and flagellum in innate immune system (Liew et al., 2005). Both TLR and interleukin-1 receptor (IL-1R), designated TIR for these two receptors, contain a highly homologous intracellular domain (TIR domain; Suzuki et al., 2002). Upon the activation of PAMPs or IL-1 family, the TIR domain recruits MyD88 protein, followed by serine/threonine kinase, interleukin-1 receptor associated kinase (IRAK; O'Neill et al., 2003). The activated IRAK binds to TNF-receptor-associated factor 6 (TRAF-6; Jiang et al., 2002). TRAF-6 deficient cells exhibit a complete loss of NF- κ B DNA binding induced by IL-1R, which indicates that the activation of TRAF-6 upregulates NF- κ B (Lomaga et al., 1999). TRAF-6 possesses an E3 ubiquitin ligase activity, which modifies protein function in K63-linked ubiquitination without leading to the degradation, and this modification activates a member of the MAP3K including TGF-beta-activated kinase 1 (TAK1; Jiang et al., 2002). The activated TAK-1 phosphorylates and activates both IKK α and IKK β , leading to NF- κ B activation (Jiang et al., 2002). When melanoma cells constitutively expressing TLR-4 are

treated with LPS, CXCL8 is overexpressed, suggesting that NF- κ B is activated through the TIR domain-mediated signaling in melanoma to stimulate CXCL8 transcription (Molteni et al., in press).

Hiscott et al. reported that the promoter of the *IL-1 β* gene contains an NF- κ B consensus sequence, GGGAAAATCC, at the -300-nt position (Hiscott et al., 1993). However, the other TIR-mediated signaling molecules listed in this review do not have the NF- κ B binding consensus sequence within -300 and +1. We therefore deduced that the autocrine NF- κ B activation loop does not function in this pathway. The TIR-mediated NF- κ B activation pathway can respond with varied and unexpected PAMP stimulation, including processed dsDNAs accompanied by sudden infection with viral or bacterial pathogens. In this pathway, NF- κ B activation is transient, allowing return to the homeostatic regulated state.

TNFR cascade for constitutive NF- κ B activation

As discussed previously in NF- κ B: molecular switch from pro-apoptotic to anti-apoptotic melanoma, TNFR-mediated signaling regulates both cell death and survival. Upon TNF- α stimulation, the TNFR is known to recruit two proteins which have opposite biological effects, TNFR-associated death domain associated protein (TRADD) and TRAF-2 (Hsu et al., 1996; Rothe et al., 1995). TRADD binds to and activates caspase-8, leading to cell apoptosis (Bender et al., 2005; Hsu et al., 1996). On the contrary, TRADD also binds to TRAF-2, which leads to NF- κ B activation and inhibition of TRADD-induced cell apoptosis (Rothe et al., 1995). TRAF2 is subsequently modified by ubiquitination because of the release of a ubiquitination inhibitor, which directly leads to IKK activation (Reiley et al., 2005). Activated TRAF-2 also interacts with MAPK3, which leads to the activation of the IKK complex (Yang et al., 2001a). These IKK activation pathways, mediated by TRAF-2, are illustrated in Figure 3.

These data indicate that homeostasis between proapoptotic and anti-apoptotic pathways are maintained via TNFR-mediated signaling. However, upregulation of TRAF-2 and NF- κ B emphasize the pro-apoptotic pathway. Elevated TRAF-2 expression has been observed in various human tumors, including melanomas (Devergne et al., 1996; Murray et al., 2001; Zapata et al., 2000). The promoter of *TRAF2* contains an NF- κ B binding site GGAATTTCC at the -63 position (TFSEARCH <http://www.cbrc.jp>). The upregulation of NF- κ B and TRAF-2 seems to mediate an autocrine activation loop that promotes the progression of melanoma.

LT β family/LT β R family/TRAFs cascade for constitutive NF- κ B activation

Lymphotoxin- β receptor (LT β R) and CD40, members of the tumor necrosis factor receptor family, play essential roles in the embryonic development and organization of secondary lymphoid tissues (Caamano et al., 1998; Davies et al., 2005; Franzoso et al., 1998; Kuai et al., 2003). Upon ligand activation by lymphotoxin β (LT β) or LIGHT, LT β R recruits TRAF2, TRAF3 and cIAP1 (Kuai et al., 2003). This action leads to the activation of NF- κ B and c-Jun N-terminal kinase MAP kinase (JNK), and eventually to cell death (Kuai et al., 2003). The activation of CD40 with its ligand CD40L leads to the receptor interaction with TRAF2 and TRAF6, and exhibits the upregulation of NF- κ B, JNK, and p38 MAPK (Davies et al., 2005). These data suggest that the LT β R family activates the classical NF- κ B activation pathway (Figure 3). Conversely, the activation of the LT β R family also activates the NF- κ B inducing kinase (NIK), a member of the MAP3K family (Malinin et al., 1997; Song et al., 1997) via a specific sequence motif located in the N-terminal region of NIK, which directly phosphorylates and activates IKK α homodimers, leading to the activation of the p52/RelB complex (Senftleben et al., 2001; Xiao et al., 2001). There is increasing evidence that the upstream activator of NIK is receptor-bound TRAF3, not TRAF-2/6 (Takaori-Kondo et al., 2000; Wu et al., 2006), indicating that the alternative NF- κ B activation pathway is activated by the TRAF-3-mediated pathway (Figure 3). There is also evidence that NIK is participating in the classical pathway

as well as an alternative pathway for NF- κ B activation. CHUK, a NIK associating protein, specifically activates NF- κ B in IL-1- or TNF- α -mediated pathways through its association with I κ B, leading to the ubiquitination and proteasome-mediated degradation of I κ B (Regnier et al., 1997). NIK binds to and activates IKK α with a specific sequence motif in the alternative pathway (Senftleben et al., 2001; Xiao et al., 2001). NIK is also proposed to participate in the classical pathway by binding to IKK complex, where IKK α oligomerizes with IKK β and IKK γ (Woronicz et al., 1997), which suggests that NIK possibly activates the IKK α/β complex in the classical pathway. NIK activity, therefore, is indicated as playing a pivotal role in translating the signal from extracellular stimuli to the classical or alternative NF- κ B activation pathways (Figure 3).

Conclusion

It has become clear that the upregulation of NF- κ B is associated with melanoma tumor progression. During melanoma progression, the upregulation of NF- κ B further amplifies in the autocrine loop through the EGFR-mediated pathway as well as through GPCR-, TIR-, TNFR-, LT β R-mediated pathways. The autocrine loops deregulate the balance between cell death and survival. In this review, the possible mechanism of cross-talk between classical and alternative NF- κ B activation pathways also is discussed. The regulatory molecules NIK and TRAF2/6 are pivotal in connecting these NF- κ B activation pathways. In melanoma, it is important to examine NF- κ B activation as a potential therapeutic target in the future. NF- κ B activity may provide a double-edged sword for the modulation of cell proliferation and cell death in melanoma.

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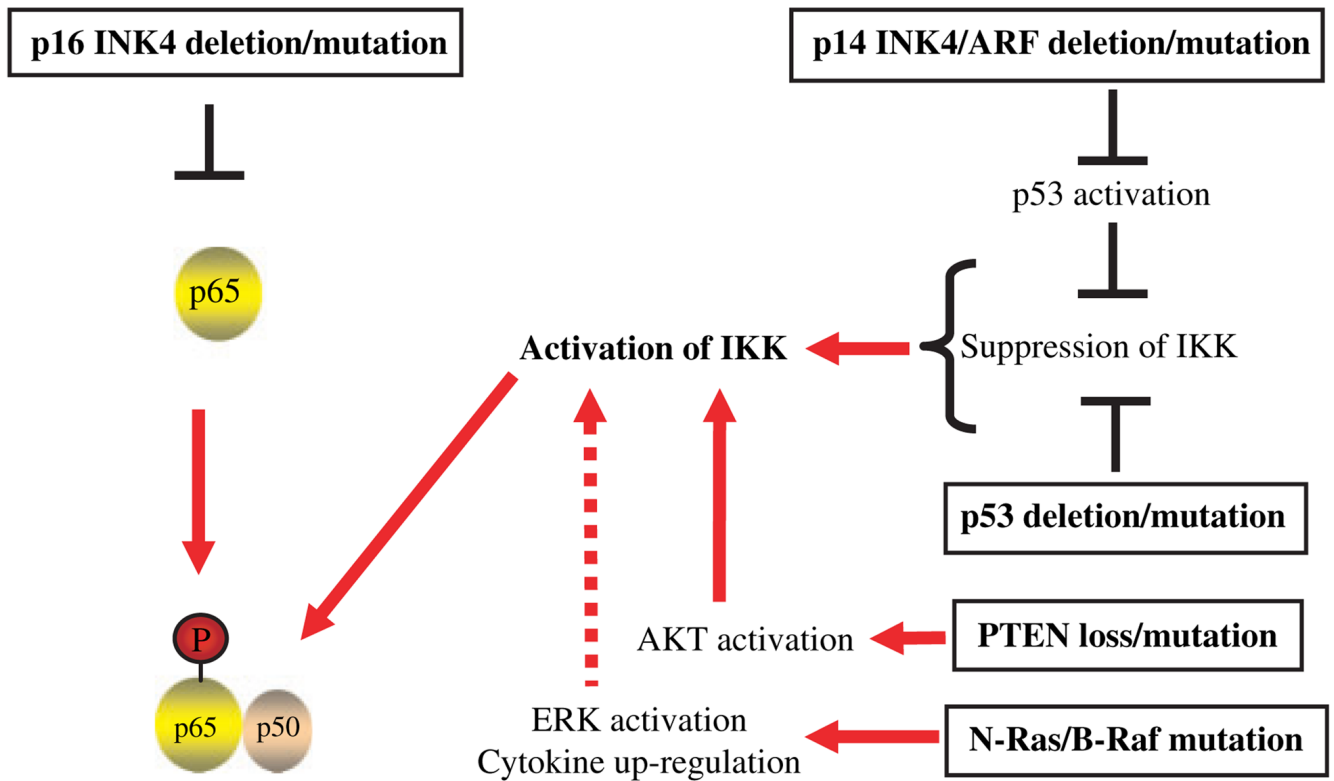
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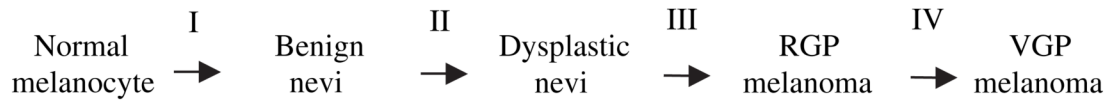
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Phosphorylation of p65
Up-regulation of NF-κB

Figure 1. Gene mutations in sporadic melanoma and NF-κB upregulation. Gene mutations with high frequency in melanoma are listed in Table 1. These mutations directly/indirectly induce NF-κB upregulation. Red arrow (→) indicates direct positive regulation and dotted red arrow indicates indirect positive regulation. The black colored symbol (⊥) indicates negative regulation. This diagram is based on the following articles: Becker et al. (2005);Castelli et al. (1994);Celebi et al. (2000);Cooray (2004);Dhawan et al. (2002);Gu et al. (2004);Ikenoue et al. (2003,2004);Karasarides et al. (2004);Kim and Lee (2005);Koul et al. (2001);Li and Sarkar (2002);Tsao et al. (2003);Wang et al. (2005);Wolff and Naumann (1999);Zhou et al. (2000).

A Progression from a normal melanocyte to a malignant melanoma



- I. Stresses such as UV possibly induce gene mutation, as listed in Table 1.
- II. Loss of p16 possibly overrides senescence.
- III. Telomerase is activated, leading to ALT (alternative lengthening of telomeres).
- IV. Mutated genes are activated, which promote proliferation.
The mechanism of apoptosis is suppressed.

B NF- κ B activation module as molecular switch during melanoma progression

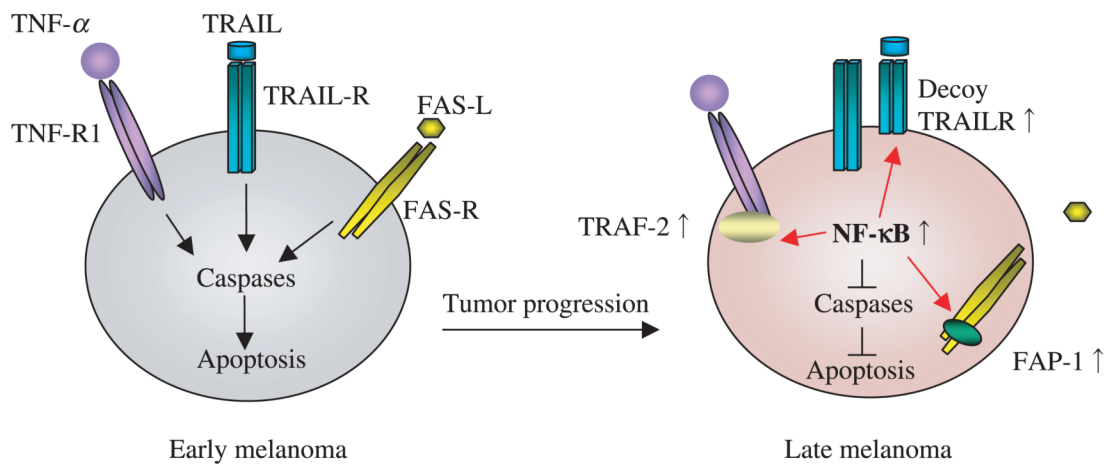


Figure 2.

NF- κ B as a molecular switch in melanoma. (A) Model of progression from a normal melanocyte to a malignant melanoma. Adapted from Clark's model (Clark, 1991; Clark et al., 1989) with other reviews (Bennett, 2003; Gray-Schopfer et al., 2005). Oncogene-induced senescence (OIS) and/or ALT-induced senescence are overridden by various gene mutations such as those in p16 and p53. (B) NF- κ B activation module as molecular switch during melanoma progression. In late melanoma stage, NF- κ B is activated and inhibits cell apoptosis (see detail in text). This model is modified from Ivanov et al. (2003) with other articles (Baldwin, 1996; Chan et al., 1999; Ivanov et al., 2003, 2006; Oya et al., 2001; Ravi et al., 2001; Sato et al., 1995; Zhang et al., 2000).

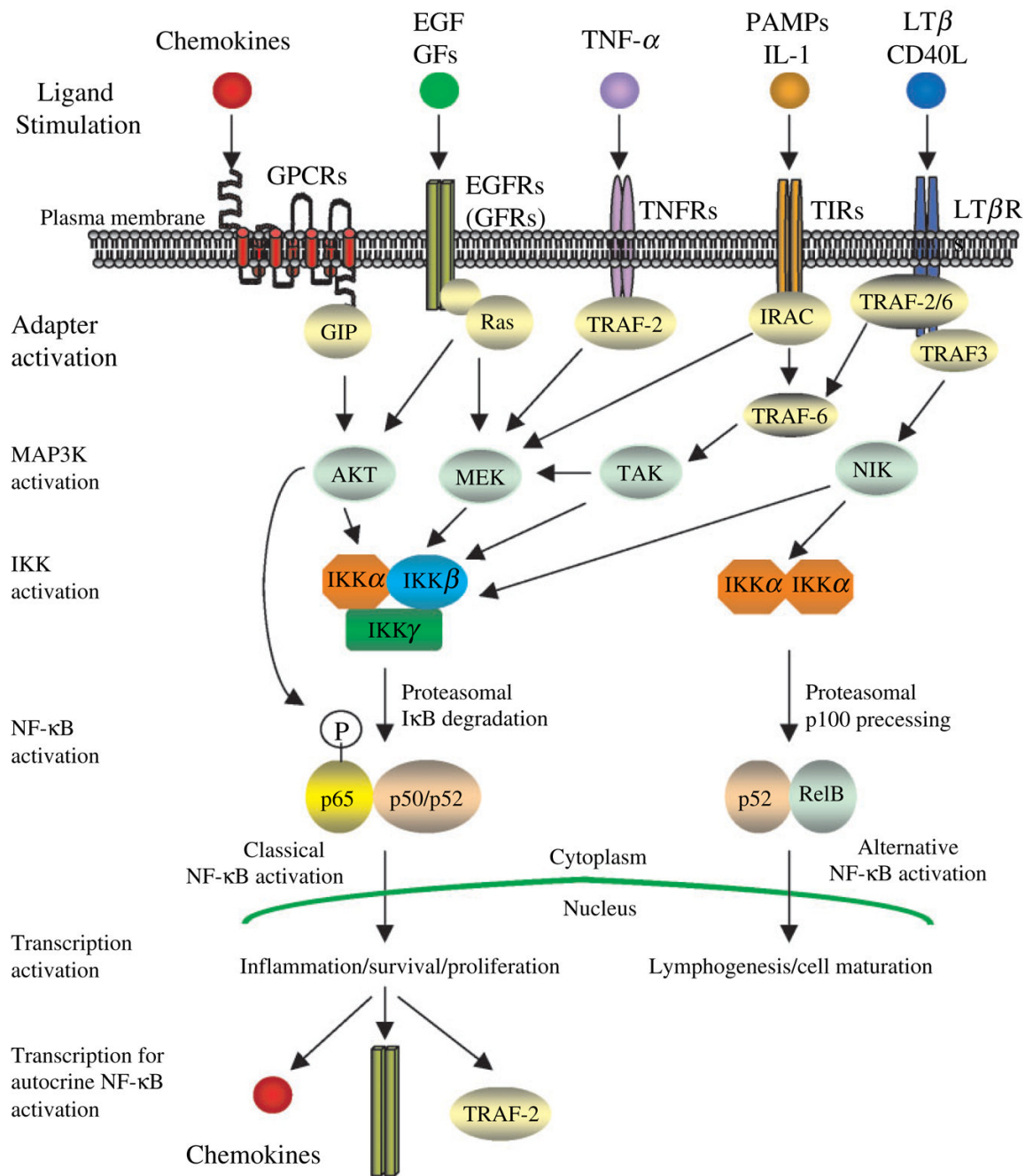


Figure 3. Model for autocrine system by upregulated NF-κB in melanoma. This figure illustrates the autocrine system for constitutive activation of NF-κB in melanoma as detailed in Autocrine system for constitutive activation of NF-κB in melanoma of this review.

Table 1

Genetic mutations recorded in sporadic melanoma gene mutations including loss or alteration of nucleotides with high frequency in melanoma are listed

Pathway	Gene mutation (frequency %)	Reference
p16 INK	<i>p16INK</i> loss/mutation (8–35)	Begg et al. (2005); Berwick et al. (2004); Puig et al. (2005)
	<i>p14 INK/ARF</i> loss/mutation (20–40)	Ghiorzo et al. (2004); Rizos et al. (2001)
p53	<i>p53</i> loss/mutation (10)	Albino et al. (1994); Papp et al. (2003); Sherr (2001); Straume et al. (2000)
MAPK	<i>N-Ras</i> mutation (15–30)	Borner et al. (1999)
	<i>B-Raf</i> mutation (26–70)	Davies et al. (2002); Kumar et al. (2003); Yazdi et al. (2003)
PI3K	<i>PTEN</i> deletion (10–15)	Celebi et al. (2000); Tsao et al. (2003); Wu et al. (2003); Zhou et al. (2000)

The mutation frequencies were documented by Gray-Schopfer et al. (2005).