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G-protein-coupled receptors and melanoma

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Summary

G-protein-coupled receptors (GPCR) are the largest family of receptors with over 500 members. Evaluation of GPCR gene expression in primary human tumors identified over-expression of GPCR in several tumor types. Analysis of cancer samples in different disease stages also suggests that some GPCR may be involved in early tumor progression and others may play a critical role in tumor invasion and metastasis. Currently, >50% of drug targets to various human diseases are based on GPCR. In this review, the relationships between several GPCR and melanoma development and/or progression will be discussed. Finally, the possibility of using one or more of these GPCR as therapeutic targets in melanoma will be summarized.

Keywords

G-protein-coupled-receptors; oncogenes; melanocytes; melanoma

Introduction

The processes of cell growth and cell differentiation are determined by a combination of cellular microenvironmental influences, as well as inter- and intracellular interactions. Included in the many consequences of altered regulation of either cellular growth or differentiation is tumorigenesis. Melanoplasia is a complex disease whose etiology may involve several possible pathways controlling normal melanocytic growth. Cancer research conducted in the past several years has provided convincing evidence that mutations in proto-oncogenes and/or tumor suppressor genes, which control growth and proliferation of normal cells, can give rise to neoplastic transformation. Proto-oncogenes may be activated by a number of mechanisms including mutational changes in the coding region or over-expression caused by genomic amplification or transcriptional up-regulation. For tumor suppressor genes, deletions and/or mutations in both copies are required to abrogate its activity, in most cases.

The occurrence of melanoma in the US is rising rapidly and, on its present course, the lifetime risk will reach one in 75 among Caucasians in the next 5 years (American Cancer Society, Cancer Facts and Figures, 2007). Despite a great deal of clinical and molecular efforts directed towards the treatment and prevention of this disease, the precise genetic lesions leading to melanoma remains to be discovered. The availability of an animal model system that recapitulates the onset and progression of a given human disease is a valuable tool. Normally spontaneous, malignant melanomas are a rare occurrence in rodents. However, melanomas have been induced by carcinogenesis protocols in several mouse model systems (Bradl et al., 1991; Chin et al., 1997; Iwamoto et al., 1991; Kato et al., 1998; Klein-Szanto et al., 1994;

Krimpenfort et al., 2001; Mintz et al., 1993; Noonan et al., 2003; Otsuka et al., 1998; Powell et al., 1999; Takayama et al., 1997). In these model systems, the anomalous expression of a multi-functional cytokine or an oncogene is needed for tumor formation and, in some instances, introduction of an exogenous carcinogen is also required. Furthermore, tumorigenesis in these model systems occurs in a wide variety of tissues in addition to cutaneous melanoma. Nevertheless, these mouse models have been very valuable for the assessment of melanoma susceptibility genes and molecular events leading to the disease (Bardeesy et al., 2000).

G-protein-coupled receptors as oncogenes

G-protein-coupled receptors (GPCR) have a major role in regulating physiological functions, including neurotransmission, hormone and enzyme release from endocrine and exocrine glands, immune responses, cardiac- and smooth-muscle contraction and blood pressure regulation. Their dysfunction contributes to some of the most prevalent human diseases, as reflected by the fact that GPCR represent the target, directly or indirectly, of 50–60% of all current therapeutic agents (Lundstrom, 2006; Pierce et al., 2002; Schlyer and Horuk, 2006).

All GPCR share a characteristic core composed of seven-transmembrane α -helices that weave in and out of the membrane (Pierce et al., 2002) allowing them to be regulated by many agonists/antagonists. Activated GPCR typically control cellular physiology by releasing the signaling potential of inactive heterotrimeric G-proteins. These inactive heterotrimers consist of a guanine diphosphate-bound $G\alpha$ subunit, which maintains a high affinity for a $G\beta\gamma$ functional monomer. Upon activation by a cognate ligand or signal, a GPCR catalyzes the exchange of GTP for GDP on the $G\alpha$ subunit resulting in a decreased affinity of $G\alpha$ for $G\beta\gamma$. This alteration causes dissociation of the subunits (Hamm, 1998) or rearrangement of the heterotrimers (Bunemann et al., 2003) allowing $G\alpha$ and $G\beta\gamma$ to interact with and to modulate the activities of a diverse and growing repertoire of effector molecules (Cabrera-Vera et al., 2003). Ultimately, the G-protein-coupling specificity of each receptor determines the nature of its downstream signaling targets (Neves et al., 2002). GPCR have traditionally been linked to many of the functions performed by differentiated, post-mitotic cells. However, GPCR are also expressed in proliferating cells, and contribute to embryogenesis, tissue remodeling and repair, inflammation, angiogenesis, normal cell growth and cancer. Indeed, many potent mitogens such as thrombin, lysophosphatidic acid (LPA), gastrin-releasing peptide (GRP), endothelin and prostaglandins stimulate cell proliferation by acting on their cognate GPCR in various cell types (Dorsam and Gutkind, 2007; Marinissen and Gutkind, 2001; Mills and Moolenaar, 2003; Rozengurt et al., 2002). Furthermore in 1986 the discovery of *MAS*, the first GPCR with oncogenic potential, provided a direct link between cellular transformation and GPCR (Young et al., 1986). Surprisingly, in contrast to most oncogenes identified at that time, *MAS* did not harbor activating mutations. Further work showed that wild-type GPCR can become tumorigenic when exposed to an excess of locally produced or circulating ligands/agonists (Gutkind et al., 1991; Julius et al., 1989) while in other GPCR, mutations in key conserved residues can render GPCR to have transforming activity even in the absence of their ligands (Allen et al., 1991; Pollock et al., 2003a). Currently, aberrant functioning of GPCR pathways have been shown to lead to several important human diseases and a large body of evidence links aberrant G-protein signaling to cancer development and progression. For example, a recent examination of publicly available gene expression data identified a variety of GPCR that are over-expressed in diverse types of cancer tissues (Li et al., 2005). In addition, GPCR have a central role in tumor-induced angiogenesis and tumor metastasis. Many cancers metastasize to specific organs with an incidence much greater than would be expected from the circulatory pattern between the primary tumor site and the secondary organs. Lymph node metastasis is one of the first elements of tumor cell dissemination in most human cancers. Tumor cell migration and metastasis share very similar patterns in movement with leukocytes, which is critically regulated by GPCR and their ligands, particularly G-protein-linked

chemokine receptors and chemokines. Enhanced levels of chemokines have been detected in secondary organs prior to evidence of metastasis. Organ-specific metastasis is likely mediated by aberrant expression of G-protein-linked chemokine receptors in cancer cells concomitant with the release of chemokines from the secondary organs resulting in promoting tumor cell proliferation, migration and neovascularization in tumor tissue (Balkwill, 2004; Ben-Baruch, 2008; Chambers et al., 2002). Taken together these results suggest that tumor cells use several strategies to satisfy their increasing needs for nutrients and oxygen, including the modification of their local environment and switching their gene-expression programs to produce angiogenic factors. Many solid tumors rely on GPCR, such as thrombin, prostaglandin and S1P receptors, as well as CXCR2 and CXCR4 chemokine receptors, to elicit an angiogenic response either by acting on endothelial cells for stromal components directly or through the regulation of the release or activity of other angiogenic mediators such as vascular endothelial growth factor (VEGF) and basic fibroblast growth factor (bFGF), by stromal and immune cells (Richard et al., 2001). Taken together, these results suggest that interfering with these receptors and their downstream targets might provide an opportunity for the development of new, mechanism-based strategies for cancer diagnosis, prevention and treatment.

GPCR and melanoma

Melanocytes arise from the neural crest, the differentiation of which is crucial to vertebrate development. Neural crest cells develop into melanoblasts, the precursors of melanocytes, undergo massive proliferation, and migrate beneath the ectoderm along a dorso-lateral pathway. Similar to melanocyte development, tumorigenesis involves morphogenesis, movement and proliferation. Several recent reports hypothesize that the aggressive metastatic characteristic of melanoma may be attributed to the neural crest origin of melanocytes (Gupta et al., 2005; Kim et al., 2006). Increasing evidence suggests that GPCR are involved in tumorigenesis and metastatic progression of melanoma. The role of some GPCR in melanoma tumor biology including transformation, proliferation, migration, invasion, and angiogenesis are summarized below.

Melanocortin type 1 receptor (MC1R) and melanoma

The melanocortin type 1 receptor (MC1R) is a key determinant of the broad phenotypic diversity in mammals. MC1R preferentially binds to the pro-opiomelanocortin derived peptides α -melanocytes stimulating hormone (α -MSH) and adrenocorticotrophic hormone (ACTH) resulting in the activation and crosstalk of multiple downstream signaling cascades, predominantly in a cAMP-PKA-dependent manner (Newton et al., 2007a,b; Rees, 2003; Roberts et al., 2006, 2007, 2008; Smith et al., 2008). In addition to being an important contributor in the proliferation and differentiation of melanocytes, MC1R has also been implicated in the development and growth of melanoma cells (Cheng et al., 2007; Kadekaro et al., 2003). Abdel-Malek et al. (2000) have demonstrated toxic responses to UV in human melanocytes that carry loss of function mutations in MC1R. On the contrary, melanocytes with functional MC1R can tolerate UV-induced cell death better, which may initial several early events in cell transformation leading to tumor development (Abdel-Malek et al., 1999, 2000; Kadekaro et al., 2005a; Suzuki et al., 1999). In addition, a large number of natural polymorphisms of MC1R have been identified in different populations. Association between hair and skin color phenotypes, melanoma and non-melanoma skin cancers with particular MC1R polymorphisms have been studied by many investigators. Results from these studies have shown that MC1R variants, particularly those variants most strongly associated with red hair color and fair skin (RHC), increase risk of melanoma (Gerstenblith et al., 2007; Kennedy et al., 2001; Matichard et al., 2004; Palmer et al., 2000; Valverde et al., 1996). Epidemiology studies showed correlations between MC1R RHC variants and two commonly mutated genes in melanoma, CDKN2A and BRAF in melanoma patients (Box et al., 2001; Goldstein et al.,

2005, 2006, 2007; Landi et al., 2006). Box et al. (2001) reported the increased risk of melanoma of three common MC1R variants with CDKN2A mutation(s). These three MC1R variants have been associated previously with red hair, fair skin and sensitive skin to UV light. Recently, Smith et al. (2008) reported possible mechanisms of enhanced melanoma risk by MC1R variants. They showed induction of three NR4A receptors as one of the immediately downstream transcriptional targets of MC1R in melanocytes. NR4A receptors belong to the nuclear receptor superfamily of transcriptional regulators and a large sub-group of orphan receptors. In addition, they also demonstrated that melanocytes with the homozygous RHC MC1R variants exhibited a decrease in NR4A induction in response to MC1R-agonist. Prior to UV-irradiation, primary human melanocytes were transfected with siRNA to two of the NR4A receptors. As a consequence, the ability to remove UV-induced cyclobutane pyrimidine dimers was reduced in these melanocytes. These results suggest that activation of NR4A receptors by stimulated MC1R play critical roles in protecting melanocytes to UV-induced DNA damage.

Endothelin receptors (EDNR) and melanoma

The endothelin (ET) system is a family of three similar small peptides (ET-1, 2, 3; Inoue et al., 1989; Itoh et al., 1988), two G-protein coupled receptors (EDNRA, EDNRB; Ihara et al., 1992a,b; Ishikawa et al., 1994) and two proteinases (ECE-1, ECE2; Kedzierski and Yanagisawa, 2001). Endothelins and EDNRB have been demonstrated to participate in melanocyte transformation and melanoma progression (Bittner et al., 2000; Lahav, 2005; Lahav et al., 2004; Soufir et al., 2005, 2007; Thirumaran et al., 2006). Expression profiling of human melanoma biopsies and cell lines indicates that EDNRB is over-expressed and therefore associated with an aggressive phenotype and is used as a tumor progression marker (Bittner et al., 2000). Other studies that have supported this notion included UV-induced activation of the ET-1/EDNRB pathway down-regulated by E-cadherin, a suppressor of melanoma cell invasion, resulting in an enhancement of melanoma invasive capability (Hsu et al., 2000; Jamal and Schneider, 2002). When levels of ET-1 were elevated by transfection of exogenous ET-1 into human melanoma cells, an increase in cell growth was detected (Berger et al., 2006). Possible mechanisms that may be contributed by excess ET-1 in the increase of survival of melanocyte and inhibition of UV-induced apoptosis is by activating the phosphatidylinositol 3-kinase (PI3K)-Akt pathway (Kadekaro et al., 2005b).

Blockade of EDNRB by several known antagonists including Bosentan, a dual antagonist for endothelin receptors, BQ788, a specific antagonist of EDNRB, or another antagonist A-192621, increased melanocyte differentiation markers, apoptotic cells and decreased cell growth were detected in in vitro cultured cells and in vivo xenografts in nude mice. In addition, suppression in the accumulation of several key factors in tumor metabolism and tumor progression including HIF-1 α , VEGF, and MMP-2 were also detected (Berger et al., 2006; Kefford et al., 2007; Lahav, 2005; Lahav et al., 1999, 2004). A phase II clinical trial with Bosentan as monotherapy in patients with stage IV metastatic melanoma resulted in stabilization of the disease in six of 32 patients (Kefford et al., 2007).

Wnt/frizzled receptor and melanoma

Signaling through the Wnt pathway begins with Wnt ligands, which are a family of secreted, cysteine-rich peptides that act by binding to their cell surface transmembrane receptors in the frizzled family to initiate the downstream signaling cascades. Three distinct pathways have been identified to participate in Wnt signaling and possible crosstalk between these pathways has been suggested (Polakis, 2000; Weeraratna, 2005). Earlier studies showed that, in developing mouse embryos, the absence of both Wnt1 and Wnt3a resulted in a deficiency in neural crest derived cells, including melanocytes, suggesting that both Wnt1 and Wnt3a are

critical in the growth and the expansion of melanocytes (Ikeya et al., 1997). However, Dunn et al. (2000, 2005) used cell lineage-directed gene targeting approach and showed that, contrary to previous reports, Wnt1 and Wnt3a have distinct roles in promoting the development of neural crest-derived melanocytes. Several studies have demonstrated that the consequences of dysregulation of one or more of the three Wnt signaling pathways are malignant transformation of cells leading to onset of various human cancers, including melanoma (Reya and Clevers, 2005; Weeraratna, 2005). Gene array expression profiling has identified the correlation between Wnt5a and a specific cluster of highly aggressive melanoma samples (Bittner et al., 2000). In addition, transfection of Wnt5a cDNA into less aggressive noninvasive melanoma cells results in increased invasiveness in these recipient cells (Bachmann et al., 2005; Dissanayake et al., 2007; Weeraratna et al., 2002). Constitutive activation of the Wnt signaling pathway can be induced by deregulation of one or more of components in the Wnt signaling pathway including β -catenin, Brn2 and naturally endogenous Wnt inhibitory factor 1 (WIF-1; Rimm et al., 1999; Omholt et al., 2001; Goodall et al., 2004; Lin et al., 2007). In other tumors, the role of Wnt5a is controversial, it is detected to be up-regulated in lung, breast and prostate cancers but down-regulated in pancreatic and urothelial carcinomas, where Wnt5a is considered to act as a tumor suppressor (Crnogorac-Jurcevic et al., 2001; Iozzo et al., 1995; Olson et al., 1997). This is in line with the findings that Wnt5a signals through not only the canonical pathway via stabilization of β -catenin but also different non-canonical pathways (Itoh et al., 2005; Topol et al., 2003). In a panel of benign and malignant melanocytic tumors, expression of both Wnt5a and its receptor frizzled were significantly reduced from benign nevi to melanomas; this is consistent with a tumor suppressor role (Bachmann et al., 2005). How Wnt signaling is involved in melanoma development and progression still remains largely unknown thus requiring further evaluation.

Chemokine receptor (CXCR) and melanoma

The chemokines are divided into four structural types: CXC, CC, C and CX₃C. All chemokines signal via receptors belonging to the seven transmembrane domain family of G protein-coupled receptors (Kakinuma and Hwang, 2006; Murphy et al., 2000; Rot and von Andrian, 2004). Chemokine receptors have been detected in a variety of human cancer cell lines including melanoma cells. In addition to being expressed in melanoma cells, CXCR3 and CXCR4 were shown to be functional in these cells and may contribute to cell proliferation (Robledo et al., 2001). Recent reports suggest that the expression of chemokines and chemokine receptors in melanoma cells may contribute to the ability of these cells to escape tumor surveillance, which may explain preferential patterns of melanoma metastasis to sites such as lymph nodes and lung. In human and murine melanoma cell lines, expression of chemokine receptor has been reported to facilitate site-directed metastases. For example, expression of functional CXCR4 in either B16 mouse melanoma cells or human melanoma cells shows enhanced metastases in lung, liver, lymph nodes and dermal layer of skin (Cardones et al., 2003; Murakami et al., 2002; Scala et al., 2006). Other chemokine receptors including CCR7 and CCR10 have also been linked to lymph node or skin metastases (Forster et al., 2001; Kawada et al., 2004; Murakami et al., 2003, 2004; Simonetti et al., 2006; Takeuchi et al., 2004). Recently, Seidl et al. (2007) reported that expression profiles of chemokine receptors are substantially different in melanocytic lesions and cultured melanoma cell lines. Expression of CXCR6 was detected in primary melanomas and melanoma metastases, but absent in melanoma cell lines and congenital nevi. Only two chemokines receptors, CXCR4 and CCR1, were consistently detected in melanocytic lesions. Moreover, a significant increase in levels of CCR1 was found in melanoma. These investigators suggest that expression profiles of metastatic and adjacent normal tissue likely to share some chemokine receptors at similar expression levels, but only a select few receptors are then up-regulated during tumor progression to metastases (Seidl et al., 2007).

Protease-activated receptor-1, thrombin receptor (PAR-1) and melanoma

Protease-activated receptor-1, thrombin receptor (PAR-1) is a unique G-coupled protein receptor that belongs to the protease-activated receptor family. Activation of PAR is mediated enzymatically by serine protease through the cleavage of the amino terminal domain. Activated PAR have been implicated in numerous biological process, including inflammation (Asokanathan et al., 2002), coagulation (Ruf et al., 2003), mitogenesis (Madamanchi et al., 2001), and cell proliferation (Darmoul et al., 2003). In addition to its roles in normal vascular regulation and tissue remodeling, PAR-1 also facilitates tumor invasion, angiogenesis, and metastasis by modulating the expression of cell adhesion molecules, matrix-degrading proteases and the secretion of angiogenic factors in several cancers including melanoma (Even-Ram et al., 1998, 2001; Fischer et al., 1995; Nierodzik et al., 1992, 1998; Zain et al., 2000). In stable PAR-1 transfected mouse melanoma cells, activation of PAR-1 was shown to promote synthesis and secretion of functional vascular endothelial growth factor proteins, which are highly effective in eliciting tumor angiogenesis (Yin et al., 2003). Furthermore, B16 mouse melanoma cells, when treated with a specific thrombin inhibitor, argatroban, demonstrated suppressed cell migration and metastasis in vivo (Asanuma et al., 2004). Recent studies demonstrated that PAR-1 expression is altered in melanomas in comparison with dysplastic nevi and primary melanoma. The metastatic potential of some human melanoma cell lines was found to correlate with the expression of PAR-1 (Massi et al., 2005; Tellez and Bar-Eli, 2003; Tellez et al., 2003, 2007). A recent study reported that immunohistochemistry for PAR-1 in a panel of 240 malignant melanoma cases showed that PAR-1 can be used as a supplement to Breslow thickness and ulceration as a prognosis indicators for melanoma. In addition, expression of PAR-1 was the best marker of recurrence risk in the study (Depasquale and Thompson, 2008).

Platelet-activating factor (PAF)–PAF receptor and melanoma

Platelet-activating factor (PAF) is a potent pro-inflammatory phospholipid, which is normally produced when neutrophils, macrophages, lymphocytes, and endothelial cells are stimulated by mediators of inflammation (Prescott et al., 2000; Robert and Hunt, 2001; Zimmerman et al., 2002). In addition to the authentic PAF, several PAF-like oxidized phospholipids are produced as byproducts of oxidative fragmentation of cellular phospholipids. These by-products have nearly identical arrays of biological activities as the authentic PAF and when activated, members of this large family mediate their action through the PAF receptor (PAFR). PAFR is a G-protein-coupled-membrane-spanning molecule that engages in multiple signaling pathways which promote tumor growth, angiogenesis and metastatic progression (Balkwill and Mantovani, 2001; Coussens and Werb, 2002; Deo et al., 2004; Mantovani, 2005; Pikarsky et al., 2004; Prescott et al., 2000; Stafforini et al., 2003; Zimmerman et al., 2002).

Im et al. (1996) were the first group to demonstrate the role PAF in melanoma metastasis. They showed that PAF enhanced lung colonization of inoculated B16F10 mouse melanoma cells (Im et al., 1996). Further studies on the pro-proliferative activity of PAF/PAFR were performed with PAFR-over-expressing transgenic mice. In these transgenics, hyper-proliferative alterations in the epidermis were evident as early as 2 weeks after birth. The hyperplasia in keratinocytes was accompanied by hyper-pigmentation and an increase in the number of dermal melanocytes in the ear and tail, and consequent development of melanocytic tumors late in life (Ishii et al., 1997; Sato et al., 1999).

More recently, expression of PAFR was detected in eight-cultured human melanoma cell lines regardless of their metastatic potential (Melnikova and Bar-Eli, 2007; Melnikova et al., 2006). In addition, this group also showed that PAF/PAFR mediated its pro-invasion activity through induction of expression of matrix metalloproteinase (MMP) 2 and MMP-2 activator,

membrane type 1 MMP by stimulation of two key transcription factors, cAMP-response element binding protein (CREB) and activating transcription factor (ATF-1) in human melanoma cells. Treatment with antagonist of PAFR (PAC4248) abolished melanoma metastases (Melnikova and Bar-Eli, 2007; Melnikova et al., 2006). However, growth of solid tumors derived from colon 26 or Ehrlich cells in PAFR null mice was not altered. In these tumor cell xenografts, in addition to lack of inhibition in tumor cell growth, angiogenesis of these xenografts was not altered; only a decrease in some aspects of inflammation were detected (Ferreira et al., 2007; Ishii and Shimizu, 2000). In view of the discrepancies in results with respect to tumor growth and angiogenesis in the absence of a functional PAFR, perhaps differential mechanisms may mediate genetic manipulation (gene knockout) versus pharmacological reagents (PAFR antagonists). This suggests that PAF/PAFR may exert its effects differently in different types of tumors and tumor microenvironment. Furthermore, in PAFR knockout mice, the possibility remains that the inoculated tumor cells still have the ability to synthesize PAFR and being responsive to PAF either produced by the injected cells or from the PAFR knockout host.

Metabotropic glutamate receptor 1 (GRM1) and melanoma

Metabotropic glutamate receptors (mGluRs) are members of the G protein-coupled receptor (GPCR) super-family (Hermans and Challiss, 2001; Pin and Duvoisin, 1995). mGluRs have been shown to play important roles in the mammalian central nervous system, such as learning and memory, neuronal development, and neurodegeneration (Dhami and Ferguson, 2006; Riedel et al., 2003). The natural ligand for mGluRs is glutamate, the predominant excitatory neurotransmitter of the central nervous system and is involved in several central neuronal functions. Glutamate exerts its modulatory effects on neuronal excitability and synaptic transmission by interacting with a family of glutamate receptors. In addition to metabotropic glutamate receptors, there are also the ionotropic glutamate receptors, which include the ligand-gated cation channels NMDA (*N*-methyl-*D*-aspartic acid), AMPA (α -amino-3-hydroxy-5-methyl-sioxazole-4-propionate) and kainate receptors. Eight distinct mammalian mGluRs have been identified and divided into three subgroups based on sequence homology, intracellular signal transduction pathways and pharmacological properties (Dhami and Ferguson, 2006; Pin and Duvoisin, 1995). Group I mGluRs include GRM1 and GRM5 (To conform to the format of nomenclatures for mouse and human, 'Grm1' and 'GRM1' refers to mouse and human respectively. In some cases, both may be interchangeable.), they are positively coupled to G_q/q11 proteins. Activation of GRM1/GRM5 stimulates polyphosphoinositide hydrolysis via the formation of inositol 1, 4, 5- triphosphate (IP₃) and diacylglycerol (DAG). These second messengers, in turn, stimulate intracellular calcium release and activate protein kinase C (PKC; Aramori and Nakanishi, 1992; De Blasi et al., 2001; Francesconi and Duvoisin, 1998). Thus, these mGluRs can trigger signaling cascades and modulate the activity of ion and ligand-gated channels through functional coupling with transduction pathways such as phospholipase C, adenylyl cyclase, phospholipase A₂, phospholipase D (PLD), tyrosine kinases, extracellular signal-regulated protein kinases and mitogene-activated protein kinase kinase (Aramori and Nakanishi, 1992; Bertrand et al., 2002; Bruno et al., 1999; Busca and Ballotti, 2000; Busca et al., 2000; Choe and Wang, 2002; Ferraguti et al., 1999; Francesconi and Duvoisin, 1998; Iacovelli et al., 2003; Kingston et al., 1998, ¹⁹⁹⁹; Littman et al., 1995; Marin and Chen, 2004; Ohashi et al., 2002; Skinner et al., 2001; Thandi et al., 2002; Valenti et al., 2002). Results obtained from biochemical studies on Group I mGluRs in heterologous cellular systems showed them to be very similar to the metabotropic receptors observed in brain slices (cortex, hippocampus, etc.) and primary neuronal cultures (Conn and Pin, 1997; Pin and Duvoisin, 1995), confirming the functionality of mGluRs in heterologous cells. Although GRM1 and GRM5 are highly homologous, they have distinct levels of expression and tasks in the central nervous system (Battaglia et al., 2001; Bordi and Ugolini, 1999; Pisani et al., 1997; Valenti et al., 2002). In addition to the central nervous system, differences in tissue distribution and

functions have been reported for GRM1 and GRM5 (Battaglia et al., 2001; Frati et al., 2000; Storto et al., 2000). GRM5, but not GRM1, is found in melanocytes and hepatocytes where it is involved in cell death and inappropriate stimulation and in development of anoxic damage, respectively (Frati et al., 2000; Storto et al., 2000). Atkinson et al. (2006) reported that activation of second messengers in GRM1 is very sensitive to agonist concentration, in contrast, GRM5 mediated activation of second messengers was insensitive to the concentration of agonist. In addition, our laboratory has demonstrated previously that melanoma development in our transgenic models is independent of Grm5 (Marin et al., 2005). We showed that aberrant expression of Grm1 in melanocytes was sufficient to drive melanomagenesis in Grm5 null mice (Marin et al., 2005).

Depending on the cell type of a heterologous system, GRM1 has been shown to have the ability to couple to multiple second messenger systems IP3, DAG and cAMP in the presence of GRM1 agonists (Aramori and Nakanishi, 1992; Francesconi and Duvoisin, 1998). Signaling cascades mediated by GRM1 have been extensively studied in the central nervous system, as well as in heterologous cells transfected with exogenous cDNA of GRM1. In heterologous systems, GRM1 can activate extracellular-signal regulated kinases (ERK1/2) upon stimulation with its natural ligand, glutamate, or other agonists (Ferraguti et al., 1999; Thandi et al., 2002). It is well known that the Ras-Raf-MEK-ERK module of the MAPK signaling cascade partially controls cell proliferation; alterations in the balance of the MAPK signals could contribute to loss of cellular growth control (Cohen et al., 2002; Kolch, 2000; Mercer and Pritchard, 2003; Peyssonnaud and Eychene, 2001). Normally, cells require extracellular mitogenic signals to proliferate through this cascade; however, several lines of evidence indicate that the MAPK pathway is constitutively stimulated in human melanomas. For example, activating BRAF mutation (V600E) has been identified in a large percentage of biopsies from human malignant melanoma and nevi and is thought to involve in the constitutive activities of MAPK. This indicates that BRAF activation is an early and critical step in the initiation of melanocytic neoplasia (Calipel et al., 2003; Davies et al., 2002; Karasarides et al., 2004; Kumar et al., 2003; Laud et al., 2003; Pollock et al., 2003b; Uribe et al., 2003; Wan et al., 2004). This idea is further supported by results from additional studies in which activated ERK was inhibited via RNAi of mutated BRAF led to a decrease in tumor cell growth (Hingorani et al., 2003; Karasarides et al., 2004; Satyamoorthy et al., 2003). Also, an inhibitor of the MEK kinase, CI1040 (Sebolt-Leopold et al., 1999), when administered orally, was successful in inhibiting the establishment and maintenance of metastatic melanoma (Collisson et al., 2003). These results provide strong evidence that the Ras-RAF-MEK-ERK pathway plays a critical role in melanocytic tumorigenesis.

In our laboratory, we have generated a transgenic mouse line that displays spontaneous melanoma. These transgenic mice were the classical example of insertional mutagenesis. The transgene, Clone B DNA – a small fragment of genomic sequence that was isolated by our laboratory was able to commit a variety of cells in culture to undergo adipocyte differentiation (Chen et al., 1989; Colon-Teicher et al., 1993). There were five independent founder mice, each possessing a different transgene-integration site. The expected phenotype was obesity, but all the mice were of normal weight. After eight months, raised melanotic lesions were detected in one of the transgenic founders (TG-3), and were confirmed as melanomas by histological means. Subsequent progeny homozygous at the transgene integration/host deleted region showed pigmented lesions as early as one month of age with 100% penetrance. These lesions progressed to overt tumors and invaded nearby tissues as the mice grew to adulthood. Mice heterozygous at the same region showed identical tumor phenotypes and progression as the homozygous mice but at later ages. Animals of the other four transgenic lines remained normal even past 2 years of age (Chen et al., 1996; Zhu et al., 1998).

From genome mapping studies on the TG-3 mouse line, we were able to determine that approximately 70kb of the host sequences on chromosome 10 had been deleted by insertion of the transgene. This region of mouse chromosome 10 is syntenic to human chromosome 6q. A large number of human non-familial malignant melanomas display rearrangements in this same region of chromosome 6 (Thompson et al., 1995; Trent et al., 1990). We identified the deleted 70kb host region to be part of intron 3 of the gene encoding metabotropic glutamate receptor 1 (Grm1). To undeniably demonstrate that Grm1 has a direct etiological role in melanoma development in our model system and to distinguish between causes and consequences of ectopic expression of Grm1 in tumor tissues, we generated a new transgenic line with wild-type mouse Grm1 cDNA under a melanocyte-specific promoter, Dct (dopachrome tautomerase). Pigmented tumors developed in the founder and subsequent progeny of this new transgenic line (line E; Pollock et al., 2003a). These results unequivocally demonstrated that the introduction of Grm1 alone was sufficient to induce melanoma development in vivo.

Identification of aberrant Grm1 expression in melanocytes being the causative agent in melanoma development in TG-3/E directed us to extend our studies to the human form of the disease. Initially, we demonstrated GRM1 expression in seven of 19 melanoma biopsies and 12 of 18 human melanoma cell lines (Pollock et al., 2003a). To date, we have tested over 120 human melanoma biopsies and 25 human melanoma cell lines, and found approximately 40% of these samples express GRM1 at levels of both RNA and protein (Namkoong et al., 2007). Recently we also investigated GRM1 expression in a custom-designed tissue array with duplicated cores made from 38 melanoma and 15 normal skin biopsies. Positive GRM1 expression was detected in 39.5% (15/38) of melanoma samples while none of the 15 normal skin biopsies showed GRM1 expression. In addition, a meeting report by Funusaka et al. (2006) showed GRM1 expression in 80% (49/61) of melanoma tissue samples consisting of superficial spreading, nodular, lentigo maligna, acral lentiginous and metastatic melanomas. GRM1 expression was detected in 33% (6/18) of common, blue and Spitz nevi. Positive GRM1 was observed in 75% (6/8) human melanoma cell lines and 50% (2/4) of nevus lines while none of normal melanocytes was positive. These additional data strongly suggest that a better understanding on the regulation of GRM1 expression in melanocytes at the molecular level contribute to the design of more effective treatment of this disease.

In our mouse model system, we have shown that cell lines derived from mouse tumors and tumor biopsies were wild type for both NRAS/BRAF at the most common mutation sites (codon 600 for BRAF and codons 12, 13 and 61 for NRAS). Furthermore, we also demonstrated that the aberrantly expressed Grm1 is functional in these mouse cell lines; they responded to stimulation or suppression by agonist or antagonist of Grm1 (also dNmutants or siRNA), while Grm5-antagonist had no effect on Grm1-mediated ERK1/2 activation (Marin et al., 2006). In addition, we also showed that Grm1-mediated ERK1/2 activation in these mouse tumor derived cells was mediated by PKC ϵ (Marin et al., 2006). On the basis of these results, we concluded that in some melanomas, activated mutations in BRAF are needed to stimulate MAPK signaling, however, in our system, activated BRAF/NRAS mutations are not required for stimulation of ERKs. Rather the aberrant expression of Grm1 in the mouse tumor-derived cells, upon stimulation by Grm1 ligand/agonist, is sufficient to bring about MAPK activation leading to deregulated cellular proliferation and tumor formation.

Similar experiments were performed with three types of human melanoma cell lines with respect to NRAS and BRAF genotypes. Human melanoma cell lines that were either wild type for both BRAF/NRAS (C8161) or carry the common NRAS Q61R mutation (WM239A) were responsive to stimuli/inhibitors of GRM1 in MAPK signaling cascades as we showed earlier in the mouse system (Namkoong et al., 2007). UACC903, a human melanoma cell line with the activating BRAF mutation (V600E) as predicted, already has a constitutively active MAPK;

no further modulation can be mediated by GRM1 agonist or competitive antagonist (J. Namkoong, unpublished results). However, follow-up studies on UACC903 with GRM1-non-competitive antagonist or an inhibitor of glutamate release showed these cells to be responsive to these GRM1 inhibitors (J. Namkoong, unpublished results). These results suggested that activated GRM1 in human melanoma cells mediated its signals in part through the MAPK cascade, one of the major cell proliferation pathways. Additional supporting evidence that GRM1 is critical in regulating melanoma cell growth was demonstrated by several means. We showed that in the presence of a non-competitive GRM1 antagonist, BAY 36-7620, dominant negative GRM1 mutants, or an inhibitor of glutamate release, Riluzole, melanoma cells were accumulated in the subG1 phase of the cell cycle indicative of apoptotic cells, which was confirmed by the appearance of cleaved PARP [poly (ADP-ribose) polymerase] (Namkoong et al., 2007). Recently another group also reported that another antagonist of GRM1 inhibit the in vitro growth of two human melanoma cell lines (Haas et al., 2007). Taken together, these results suggest that non-competitive antagonists of GRM1 or an inhibitor of glutamate release may be used alone and/or with possible synergistic effects of chemotherapy will likely enhance the existing therapies of melanomas.

Conclusion

Surgical excision of early stages of melanoma remains the most successful treatment for this deadly disease. Once it has progressed to the metastatic stage, it does not respond effectively to current therapeutic means. Onset of melanoma can be contributed by both genetic and epigenetic means. Despite much efforts directed towards understanding this disease, a great deal remains unknown and requires further investigation. Our laboratory has been concentrating on malignant melanoma development using animal models. Our working hypothesis is that the ectopic expression of an otherwise normal neuronal protein (Grm1) in an unnatural cellular environment (melanocytes) triggers pathways leading to changes in the transcription of genes involved in regulation of cell growth and ultimately tumor formation. We have shown that human melanoma cell lines release excess extracellular glutamate and propose that in GRM1-positive human melanoma cells the presence of excess glutamate creates an autocrine loop that promotes cell growth. Very similar circumstances have been suggested previously for the high autocrine activity of hepatocyte-growth factor/scatter factor (the ligand) and its receptor (receptor tyrosine kinase, Met; Otsuka et al., 1998). Complementary data supporting the notion that excess extracellular glutamate in melanoma cells may provide an autocrine loop and enhance cell proliferation includes observations reported by others that antagonists of metabotropic and ionotropic glutamate receptors possess growth suppressive activity towards several types of tumors (Haas et al., 2007; Namkoong et al., 2007; Rzeski et al., 2001; Takano et al., 2001). Finally several investigators put forth an intriguing link between neuro-degenerative diseases and melanoma despite limited empirical evidence. On the basis of the multicenter studies in Australia and the USA, the incidence of melanoma among patients with ALS or Parkinson's disease is approximately 2–3 times higher than that of the general population (Baade et al., 2007; Freedman et al., 2005; Inzelberg and Jankovic, 2007). This observation is found to be in accordance with earlier reports that elevated levels of extracellular glutamate have been detected in a large number of human disorders including glioma, multiple sclerosis, Alzheimer, Parkinson, ALS (Corona et al., 2007; Jacob et al., 2007; Sarchielli et al., 2007; Takano et al., 2001; Ye and Sontheimer, 1999) suggest that the common root of melanoma and Parkinson/ALS may be glutamate. These results put forward the importance of glutamate signaling through metabotropic and ionotropic glutamate receptors and imply the possibility of a new target for therapy including suppression of GRM1 mediated glutamate signaling cascades (Namkoong et al., 2007; Nicoletti et al., 2007).

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