

# ROLE OF INTEGRIN SIGNALING IN CELL PROLIFERATION AND SURVIVAL

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Stockholm 2005

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*To Ming and Bilin  
To my parents*

## ABSTRACT

Integrins function as transmembrane cell adhesion receptors for the surrounding extracellular matrix (ECM). Within the tissues, integrins attach the cells to the surrounding ECM and sense the ECM environment by triggering diverse arrays of signaling pathways that are essential for the control of many central cellular functions, including cell proliferation and survival. These cellular processes critically impact tumor development. Therefore, insights into detailed molecular mechanisms of integrin functions will contribute to the understanding of tumor progression, and may thereby provide novel strategies for tumor treatment.

The present study aimed to investigate: (I) the role of integrin signaling in the control of anchorage-dependent cell proliferation, particularly in regulating two cell cycle components; the cyclin-dependent kinase 2 (Cdk2)-inhibitors p21<sup>CIP1</sup> and p27<sup>KIP1</sup>. (II) the role of integrin signaling regulating cell survival, in particular for integrin  $\alpha$ v promotion of melanoma cell survival.

We firstly developed a method for analyzing specific integrin signaling-mediated responses independent of cell spreading by utilizing an agonistic, immobilized anti-integrin monoclonal antibody directed against the fibronectin receptor integrin  $\alpha$ 5 $\beta$ 1. This method was then adopted as a part to examine the role of integrin signaling in the regulation of p21<sup>CIP1</sup> and p27<sup>KIP1</sup>. We showed that integrin ligation led to a rapid degradation of p21<sup>CIP1</sup> and p27<sup>KIP1</sup>, including proteasome-mediated degradation of p21<sup>CIP1</sup> in an ubiquitin-independent manner. Importantly, an integrin-activated small GTPase signaling pathway involving Cdc42 to Rac1 signaling was found to be functionally involved in regulating proteasomal degradation of p21<sup>CIP1</sup>. Our results for the first time revealed that integrin signaling is capable of regulating protein stability and proteasomal degradation. Integrin-mediated proteasomal proteolysis might contribute to anchorage-dependent cell cycle control.

Integrin  $\alpha$ v $\beta$ 3 is a key adhesion receptor for melanoma cell survival and tumor growth in various models. While the tumor suppressor p53 is rarely mutated in malignant melanoma; it is still unclear why wt p53 is rendered non-functional in these tumors. Using a three-dimensional (3D) collagen gel model mimicking the dermal environment of malignant melanoma growth *in vivo*, we found that integrin  $\alpha$ v promoted melanoma cell survival by inactivating p53 and thereby suppressed p53-induced apoptotic cell death. We also found that integrin  $\alpha$ v controls melanoma cell survival in 3D-collagen through a pathway involving p53 regulation of MEK1 signaling. Surprisingly, we also came to the conclusion that integrin  $\alpha$ v induced an unfolded, inactive wt p53 conformation within 3D-collagen. This finding reveals the first example of controlled regulation of wt p53 conformation in tumor cells *in lieu* of mutation, and may contribute to explain lack of need of p53 mutations in malignant melanoma. Thus, our results demonstrate that tumor cells can use an adhesion receptor to sense and respond to the surrounding 3D-environment by regulating the conformational states of a tumor suppressor. Importantly, PRIMA-1<sup>MET</sup>, a small organic compound that can revert a mutant p53 to an active conformation, was also able to reactivate melanoma cell wt p53 conformation, induce apoptosis and suppress melanoma xenograft tumor growth in a wt p53-dependent manner. Therefore, our results point to a novel therapeutic approach against malignant melanoma based on restoration of wt p53 function.

In conclusion, we found an integrin-activated Cdc42 to Rac1 signaling pathway essential for proteasomal degradation of the Cdk2-inhibitor p21<sup>CIP1</sup>. This may provide a novel mechanism in anchorage-dependent cell cycle progression. Furthermore, we found that integrin  $\alpha$ v promotes melanoma cell survival through controlling the conformation, activation and apoptotic function of the tumor suppressor p53. By targeting wt p53 using a small organic compound, our studies also provide proof of principle for a new approach for development of malignant melanoma therapy. Such development is urgently needed given that present therapy is inefficient for metastatic malignant melanoma.

## List of Publications

This thesis is based on the following papers, which will be referred to in the text by their roman numerals:

- I. **Wenjie Bao** and S Strömblad (2002). Use of an immobilized antibody to examine integrin  $\alpha 5\beta 1$  signaling independent of cell spreading. *Biological Procedures Online* 4:81-87.
- II. **Wenjie Bao**, M Thullberg, HQ Zhang, A Onischenko and S Strömblad (2002). Cell attachment to the extracellular matrix induces proteasomal degradation of p21<sup>CIP1</sup> via Cdc42/Rac1 signaling. *Molecular and Cellular Biology* 22:4587-4597.
- III. **Wenjie Bao** and S Strömblad (2004). Integrin  $\alpha v$ -mediated inactivation of p53 controls a MEK1-dependent melanoma cell survival pathway in three-dimensional collagen. *Journal of Cell Biology* 167:745-756.
- IV. **Wenjie Bao**, N Issaeva, M Chen, K Wiman, G Selivanova and S Strömblad. Induction of an inactive wt p53 conformation by integrin  $\alpha v$  points to a potential target for melanoma therapy. Manuscript.

## Contents

<b>1 ABBREVIATIONS</b> .....	8
<b>2 INTRODUCTION</b> .....	9
2.1 THE EXTRACELLULAR MATRIX .....	9
2.1.1 Extracellular matrix proteins .....	9
2.2 INTEGRIN RECEPTORS .....	10
2.2.1 Integrin structure .....	10
2.2.2 Integrin-mediated cell-matrix adhesions .....	12
2.3 INTEGRIN SIGNALING .....	13
2.3.1 FAK signaling .....	13
2.3.2 The Rho family of small GTPases .....	14
2.3.3 MEK/ERK1/2 signaling .....	15
2.4 INTEGRIN CONTROL OF CELL PROLIFERATION AND SURVIVAL .....	16
2.4.1 Anchorage-dependent G1-cell cycle progression .....	16
2.4.2 Control of G1-cell cycle components by integrin signaling .....	17
2.4.3 Proteasomal proteolysis in cell cycle .....	17
2.4.4 Control of cell survival by integrin signaling .....	18
2.5 MECHANISMS OF CANCER .....	19
2.5.1 The hallmarks of cancer .....	20
2.5.2 Malignant melanoma .....	21
2.5.3 Integrin $\alpha v \beta 3$ in melanoma progression .....	22
2.6 THE TUMOR SUPPRESSOR p53 .....	22
2.6.1 Apoptotic activities of p53 .....	23
2.6.2 p53 post-translational modifications .....	24
2.6.3 Regulation of p53 conformation .....	24
2.7 THREE-DIMENSIONAL CELL CULTURE MODELS .....	27
2.7.1 Characteristics of 3D cell culture environment .....	27
2.7.2 Examples of 3D cell culture models .....	27
<b>3 AIMS OF THE PRESENT INVESTIGATION</b> .....	29
<b>4 RESULTS AND DISCUSSION</b> .....	30
4.1 An immobilized anti-integrin monoclonal antibody developed to examine specific integrin signaling independent of cell spreading (paper I) .....	30
4.2 Integrin ligation activates proteasomal degradation of the Cdk2-inhibitor p21 <sup>CIP1</sup> (papers I and II) .....	30
4.3 Integrin-activated Cdc42/Rac1 signaling pathway controls proteasomal degradation of p21 <sup>CIP1</sup> (paper II) .....	30
4.4 Integrin $\alpha v$ promotes melanoma cell survival by inactivating p53 (paper III) .....	31
4.5 Integrin $\alpha v$ -mediated p53 inactivation controls a MEK1-dependent melanoma cell survival pathway (paper III) .....	32
4.6 Integrin $\alpha v$ induces an unfolded, inactive wt p53 conformation in melanoma cells (paper IV) .....	32
4.7 PRIMA-1 <sup>MET</sup> reactivates wt p53 conformation and its apoptotic function in melanoma cells (paper IV) .....	33
4.8 PRIMA-1 <sup>MET</sup> suppresses melanoma xenograft tumor growth in mice in a wt p53-dependent manner (paper IV) .....	33
4.9 The 3D-collagen gel model for studying integrin signaling-mediated melanoma cell survival (papers III and IV) .....	33
<b>5 CONCLUDING REMARKS</b> .....	35
<b>6 ACKNOWLEDGEMENTS</b> .....	38
<b>7 REFERENCES</b> .....	40

## 1 ABBREVIATIONS

2D	Two-dimensional
3D	Three-dimensional
Apaf1	Apoptosis activating factor 1
ARF	Alternative reading frame (p14 <sup>ARF</sup> in human, p19 <sup>ARF</sup> in mice)
Cdk	Cyclin-dependent kinase
CDKI	Cyclin-dependent kinase inhibitor
CDKN2A	Cyclin-dependent kinase inhibitor 2A (p16 <sup>INK4A</sup> , MTS1)
ECM	Extracellular matrix
ERK	Extracellular signal-regulated kinase
FAK	Focal adhesion kinase
GEF	Guanine nucleotide exchange factor
Mab	Monoclonal antibody
MAPK	Mitogen-activated protein kinase
MEK	MAPK kinase
PI-3K	Phosphatidylinositol 3-OH kinase
PIX	PAK-interactive exchange factor
PRIMA-1	p53 reactivation and induction of massive apoptosis
PUMA	p53-upregulated modulator of apoptosis
Raf	MAPK kinase kinase
RGD	Arginine-Glycine-Aspartate
RGP	Radial growth phase
VGP	Vertical growth phase
wt p53	Wild-type p53
→	Activates
—	Inhibits

## 2 INTRODUCTION

Normal tissue cells continuously communicate with their surrounding environment (Geiger and Bershadsky, 2002). One of the important environmental factors is the extracellular matrix (ECM) that can interact with the integral membrane adhesion receptors, integrins, and activate a variety of signaling pathways leading to control of various cellular functions, including cell attachment, spreading, migration, invasion, differentiation, proliferation and survival. These cellular functions profoundly influence many physiological and pathophysiological processes, including embryonic development, tissue regeneration, wound repair, inflammation, angiogenesis and tumor progression.

### 2.1 THE EXTRACELLULAR MATRIX

The ECM is a highly organized, insoluble meshwork of macromolecules made up of three major components: fibrous elements (e.g. collagens, elastin and reticulin), adhesive glycoproteins (e.g. fibronectin, vitronectin, laminin), and space filling molecules (e.g. glycosaminoglycans covalently linked to proteins in the form of proteoglycans). The ECM constitutes the connective tissues of the body, including for example the different ECM types basement membrane, interstitial stroma and elastic connective tissue. The ECM is secreted, assembled and remodelled by the cells within or in contact with the ECM, and the ECM then surrounds and organizes the cells by providing a structural scaffold. The ECM is a key environmental factor that can exchange information with cells through cell surface receptors such as integrins, and contribute to the control of diverse cellular functions, including cell proliferation and survival (Bissell and Radisky, 2001).

#### 2.1.1 Extracellular matrix proteins

Collagens are a family of fibrous glycoproteins composed of three collagen polypeptide chains, called  $\alpha$  chains. Each  $\alpha$  chain contains the repetitive motif Glycine-X-Y, in which X and Y can be any amino acid. The three  $\alpha$  chains are warped around one another to fold into a rope-like, triple stranded helix (Gordon and Olsen, 1990; van der Rest and Garrone, 1991). Slightly varied collagen chains assemble and generate distinct types of collagens that either further polymerize to form collagen fibrils or promote network-formation with other ECM proteins. The collagens type I, II, III, V and XI are able to form fibers and are thereby referred to as fibrillar collagen (or fibril-forming collagens), which are the most abundant components of interstitial connective tissues as well as in elastic connective tissues like the dermis, and in ligaments, cartilage and bone (Kadler, 1994.). Collagens type IV, VI, VIII, X and XVIII are network-forming collagens, and these are the most abundant constituent of basement membranes (Knupp and Squire, 2003). The network-forming collagens can self-assemble and organize into a lattice-network within the lamina densa of the basement membrane.

Fibronectin is a large nonfibrous glycoprotein. The fibronectin monomer is built up by three types of repeating modules (type I, II and III) that allow fibronectin to bind to various molecules, including collagen, heparin, fibrin, glycosaminoglycans, fibronectin itself as well as integrin and syndecan cell adhesion receptors (Hynes, 1990). Fibronectin exists in insoluble multimeric fibrils in the ECM. Fibronectin not only plays a role in organizing the matrix, but also functions as an adhesive protein that helps cell to attach. In contrast to collagen assembly, the polymerization of fibronectin is driven by the cells (Schwarzbauer and Sechler, 1999).

The triplet sequence arginine-glycine-aspartate (RGD) motif is found in many ECM proteins, including in fibronectin, collagen, vitronectin, osteoponin and thrombospondin. This triplet sequence can be recognized by certain integrins, including integrin  $\alpha\beta3$  (Ruoslahti, 1996). Therefore, peptides containing an RGD motif can be used to block the integrin to ECM interactions (Ruoslahti and

Pierschbacher, 1986). In collagen, the present RGD motifs are normally cryptic and inaccessible. Under denatured conditions, however, the RGD-motif of type I collagen is exposed (Davis, 1992). Melanoma cell adhesion to denatured collagen type I was found to use integrin  $\alpha v \beta 3$  to recognize the collagen RGD motif (Davis, 1992). In a 3D-collagen model, melanoma cells were found to be able to degrade collagen type I leading to the exposure of cryptic integrin  $\alpha v \beta 3$ -binding sequence (Montgomery et al., 1994).

## 2.2 INTEGRIN RECEPTORS

Integrins are principle cell adhesion receptors that mediate cell to ECM interactions. Integrins are a large family of heterodimeric transmembrane adhesion receptors, consisting of non-covalently bound  $\alpha$  and  $\beta$  subunits (Hynes, 1992). In mammalian cells, the 18  $\alpha$  and eight  $\beta$  subunits combine in a restricted manner to form 24 distinct integrins with differing but overlapping ligand binding and functional properties (Hynes, 2002) (Figure 1). For example, the  $\beta 1$  subunit can pair with twelve different  $\alpha$  subunits, and forming twelve distinct integrins with different ligand binding properties. Other integrin subunits, like  $\beta 5$ , can only pair with one  $\alpha$ -subunit ( $\alpha v$ ). Although most integrins mediate cell-ECM adhesions, certain integrins, including those with a  $\beta 2$ -subunit, mediate cell-cell adhesion (Hynes, 2002).

### 2.2.1 Integrin structure

Integrin  $\alpha$  and  $\beta$  subunits contain large extracellular (700-1100 residues), small transmembrane and short cytoplasmic domains (30-50 residues) (Figure 2).

#### *The integrin extracellular domains*

Integrin  $\alpha$  subunits contain four or five domains. They are  $\beta$ -propeller, the 'inserted' (I), Thigh, Calf-1 and Calf-2 domains. At the N-terminal region, seven repeats of about 60 amino acids fold into a single domain, called the  $\beta$ -propeller. In half of integrin  $\alpha$  subunits, including  $\alpha 1$  and  $\alpha 2$ , a module of about 200-residues is inserted between repeat 2 and 3 of the  $\beta$ -propeller domain, this insert is called I domain, and also referred to as von Willebrand factor-type A domain (Heino, 2000; Humphries, 2000). I-domain contains a divalent cation-binding motif, called metal ion-dependent adhesion site or MIDAS motif, which is proposed to play a key role for a metal-dependent integrin-ligand interaction and ligand binding specificity in the I-domain containing integrins (Springer and Wang, 2004). Beneath the integrin  $\alpha$  subunit  $\beta$ -propeller domain, there is a large portion of the  $\alpha$  subunit extracellular domain of about 500 amino acids. The crystal structure shows presence of three  $\beta$ -sandwich domains in this region, called the thigh, calf-1 and calf-2 domains (Takagi and Springer, 2002).

The integrin  $\beta$  subunit contains four domains. One of them is the I-like domain that has detectable sequence homology to the I domain present in certain  $\alpha$  subunits (Takagi and Springer, 2002). The I-like domain contains two adjacent metal coordination sites, the ADMIDAS (adjacent to MIDAS) and LIMBS (ligand-associated metal binding site) (Xiong et al., 2001; Xiong et al., 2003).

The extracellular I- and I-like domains are major ligand-binding sites, allowing integrins to specifically bind to their ligands in both a conformation- and a divalent cation-dependent manner (Springer et al., 2004). In I-domain containing integrins (e.g.  $\alpha 1$  and  $\alpha 2$  integrins), ligand binding is mediated by the I-domains. In other integrins (e.g.  $\alpha v$  integrins), ligand binding is mediated by a  $\beta$ -propeller domain from the  $\alpha$  subunit in combination with the I-like domain in the  $\beta$  subunit (Arnaout, 2002).



### 2.2.2 Integrin-mediated cell-matrix adhesions

Using integrins, cells sense and respond to their surrounding ECM environment (Miranti and Brugge, 2002). Distinct integrins can bind to either a specific ECM or several ECM proteins (Hynes, 2002). For example, at least eight integrins, including integrin  $\alpha 5\beta 1$ , can bind to FN, and at least five integrins, including integrin  $\alpha 6\beta 4$ , bind to laminin. The  $\beta 1$ -integrins  $\alpha 1\beta 1$ ,  $\alpha 2\beta 1$ ,  $\alpha 10\beta 1$  and  $\alpha 11\beta 1$  are the common receptors for native collagens (Heino, 2000) while denatured or degraded collagen can also be recognized by integrin  $\alpha v\beta 3$  (Davis, 1992). Part of this thesis is focused on the function of integrin  $\alpha v\beta 3$ , which can bind a number of ECM proteins, including fibronectin, fibrinogen, vitronectin, osteopontin and proteolysed collagen type I.

When cells anchor to ECM, integrin engagement leads to formation of membrane-associated protein complexes at sites called cell-matrix adhesions (Zamir and Geiger, 2001). Cell-matrix adhesions are able to provide dynamic bi-directional linkages between the ECM and the intracellular cytoskeleton. These membrane-spanning links play critical roles in regulation of ECM assembly, rearrangements of the cytoskeleton, transduction of signaling as well as in the control of cell morphogenesis, migration, proliferation, differentiation and survival (Hynes, 2004).

#### *Cell-matrix adhesive structures*

Different types of adhesive structures in which integrins intracellularly link to actin filaments, are known to include focal complexes, focal adhesions and fibrillar adhesions with different molecular compositions (Zamir and Geiger, 2001). Hemidesmosomes are a separated class of cell-matrix adhesive structures where integrins are connecting basement membrane on the outside of the cell to the intracellular keratin intermediate filaments (Garrod, 1993).

Focal complexes are formed when cells start to spread and form lamellae. They are small (approx.  $1\mu\text{m}$ ), dot-like adhesions present at the edges of the lamellipodia. The formation of focal complexes is induced by the small GTPase Rac1. Focal complexes serve as the precursors of focal adhesions (Geiger et al., 2001).

Focal adhesions are relatively well-characterized adhesion structures (Geiger et al., 2001). They are flat, elongated structures and are several square microns in area. Focal adhesions locate near the periphery of cells, anchor actin-filament bundles and mediate strong adhesion to the substrate. So far, focal adhesions are known to contain more than 50 distinct components and the small GTPase RhoA is promoting the formation of focal adhesions. Cytoskeleton proteins including vinculin, talin, paxillin and tyrosine phosphorylated proteins such as FAK are present in these protein complexes. Integrin  $\alpha 5\beta 1$  and  $\alpha v\beta 3$  are adhesion receptors mostly found in focal adhesions.

Fibrillar adhesions are elongated or dot-like structures along actin stress fibers that mostly associate with soft fibronectin fibrils and are located in the centre of the cells (Geiger et al., 2001). Fibrillar adhesions are formed when integrin drives movement on lamellae towards the cell body. The formation of fibrillar adhesions leads to the stretch of cell surface fibronectin and formation of long fibronectin fibrils.

In fact, *in vivo* adhesion events also occur in three-dimensions (3D), where cell adheres to 3D mesh-like fibers rather than two-dimensional (2D) rigid substrates. A new type of cell-matrix adhesions—3D-adhesions is defined when cells adhere to a pliable 3D-environment (Cukierman et al., 2001), which may be similar to cell-matrix adhesions present *in vivo*. It should be noted that the cell-ECM adhesions found in 3D environments clearly differs from those typically observed in 2D. For

example, the 3D adhesions generally appear to be smaller (Cukierman et al., 2002). The characterization of 3D-adhesions will be discussed in section 2.7.1.

Hemidesmosomes are found in the epidermis and provide stable adhesion of epithelial cells to the underlying basement membrane (Garrod, 1993). It is known that the extracellular domain of integrin  $\alpha6\beta4$  mediates cell adhesion to laminin, and that the intracellular domain indirectly binds to keratin intermediate filaments. Hemidesmosomes are proposed the sites for integrin  $\alpha6\beta4$ -triggered singling events (Borradori and Sonnenberg, 1999).

## 2.3 INTEGRIN SIGNALING

Integrins lack intrinsic enzyme activity. However, cytoplasmic tails of integrins associate with numerous adaptor proteins that link integrins to cytoplasmic kinases and transmembrane growth factor receptors that all possess kinase activity. Thereby, integrin engagement is able to trigger diverse intracellular signaling events, including the activation of focal adhesion kinase (FAK), Src-family kinases, integrin-linked kinase (ILK), phosphatidylinositol 3-OH kinase (PI-3K), protein kinase C,  $Ca^{2+}$ , different types of mitogen-activated protein kinases (MAPKs) ((extracellular signal-regulated kinases (ERKs), c-Jun NH2-terminal kinase (JNK) and p38 MAPK)), and the Rho family of small GTPases Cdc42, Rac1 and RhoA (Giancotti and Ruoslahti, 1999). Below, I will focus on describing three signaling pathways FAK, MEK/ERK1/2 and the small GTPases, which are closely correlated with my present study.

### 2.3.1 FAK signaling

FAK is one of abundant protein-tyrosine kinases at focal adhesions (Guan et al., 1991; Hanks et al., 1992; Schaller et al., 1992). Upon integrin clustering, FAK is recruited to focal adhesions and co-localized with integrins. A recent study showed that FAK could associate with integrins through the integrin-associated proteins talin and paxillin (Schlaepfer et al., 2004). FAK functions as a signaling mediator that recruits and interacts with SH2-domain- and SH3-domain-containing proteins, leading to transduction of numerous signaling pathways. FAK signaling is critically involved in the control of various cellular functions, including cell adhesion, spreading, migration, proliferation and survival (Parsons, 2003). Here, I will selectively describe a couple of FAK-pathways identified upon integrin activation.

Integrin engagement causes autophosphorylation of FAK at Tyr397 (Schaller et al., 1994), which creates a binding site for SH2-domain-containing proteins, mainly Src-family kinases (Calalb et al., 1995). When a FAK/Src signaling complex is formed, the scaffold protein paxillin is bound to FAK and phosphorylated by Src at Tyr31 and Tyr118. Then paxillin together with the docking protein p130CAS that binds to FAK after Src activation leads to recruitment and activation of the scaffold proteins Crk and Nck (Richardson and Parsons, 1996; Schlaepfer and Hunter, 1998). The signaling involved in this pathway branches and activates downstream signaling pathways, regulating different cellular functions. For example, the FAK→Src→paxillin pathway critically controls the turn over of focal adhesions (Wozniak et al., 2004).

The FAK→Src→p130CAS→Crk pathway results in recruitment of DOCK180 (human counterpart of the *C.elegans* gene *mbc* and *ced-5*, an exchange factor for Rac)/ELMO complex that was shown to stimulate GTP-loading of Rac1 (Brugnera et al., 2002). This pathway may provide a mechanism for activation of the small GTPase Rac1 at focal adhesion (Parsons, 2003).

The activated Src kinase also phosphorylates FAK at Tyr925, allowing docking of Grb2 leading to activation of a key signaling pathway from FAK to Grb2→ Ras→ mSOS (guanine 5'-triphosphate exchange factor, GEF) → Raf (MAPK kinase kinase) → MEK (MAPK kinase) → ERK1/2 (Cobb and Goldsmith, 1995; Hill and Treisman, 1995; Marshall, 1995; Schlaepfer and Hunter, 1998). This pathway may be involved in the control of cell proliferation and survival.

### 2.3.2 The Rho family of small GTPases

The p21-Rho family belongs to the p21-Ras superfamily of small GTPases. At least 20 Rho-proteins have been identified and are roughly divided into five groups, Rho-like, Rac-like, Cdc42-like, Rnd-like and RhoBTB subfamilies (BurrIDGE and Wennerberg, 2004). The Cdc42, Rac1 and RhoA are the best known, 'classical' Rho GTPases.

Rho GTPases act as molecular switches and functionally switch intracellular signaling pathways by cycling between an inactive GDP- and an active GTP-bound conformation (Raftopoulou and Hall, 2004) (Figure 3). The guanine nucleotide exchange factors (GEFs) stimulate the formation of active GTP-bound GTPases, while the GTPase-activating proteins (GAPs) promote GTPase inactivation by stimulating GTP-hydrolysis activity. The guanine nucleotide dissociation inhibitors (GDIs) are proposed to function as inhibitors of GTPase activation by inhibiting the dissociation of GDP from the inactive GTPase. Below, I will expand the discussion of the GEF family.

The GEFs is a large family. The largest group of GEFs is the Db1 family where around 60 members are found that serve as GEFs for the Rho family of the GTPases RhoA, Rac1 and cdc42 (Schmidt and Hall, 2002). The Db1 members typically contain the Db1-homology (DH) and pleckstrin homology (PH) domains tandem repeat (Hart et al., 1991). The PIX family (PAK-interactive exchange factors) is a newly identified member of the Db1 family of GEFs. PIX/PAK complexes enrich in Cdc42- and Rac-1-induced focal complexes and can mediate Cdc42 to Rac1 signaling (Manser et al., 1998). Because all the members of Db1 family contain PH domain, many of them may bind to phospholipids. Moreover, an additional family of Rho GEFs, the DOCK180/ELMO lacking DH-PH tandem domains, is identified as Rac GEFs involved in the p130CAS→Crk pathway (Kiyokawa et al., 1998a) described in section 2.3.1.

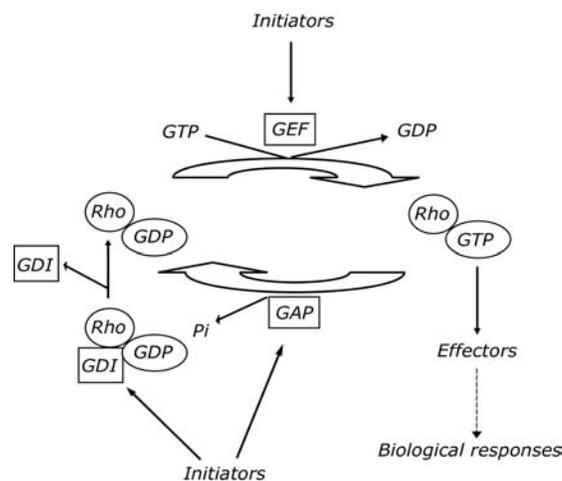


Figure 3 A biochemical model of regulation of activity of the Rho family of small GTPases. The cycle between the active, GTP-bound, and the inactive, GDP-bound, Rho GTPases is regulated by three classes of regulators: guanine nucleotide exchange factors (GEFs); GTP-activating proteins (GAPs); and guanine nucleotide dissociation inhibitors (GDIs). The extracellular signals (initiators) modulate these three regulators and affect the Rho GTPase activity, and active Rho GTPases can interact with distinct effectors, resulting in various biological responses.

Integrin engagement is critically involved in activation of these small GTPases. Integrin ligation can rapidly activate Cdc42 and Rac1 (Price et al., 1998). Integrin-mediated cell adhesion can also activate Rho in an actin cytoskeleton-independent manner (Ren et al., 1999). Anchorage-dependent phosphorylation of p130CAS on tyrosine results in its association of an SH2/SH3-containing adaptor protein Crk and the recruitment of DOCK180, leading to Rac activation (Kiyokawa et al., 1998b).

The p21-activated protein kinases (PAKs) are a family of serine threonine kinase, which can function downstream effectors of Cdc42 and Rac1 (Bar-Sagi and Hall, 2000). PAK1 plays a role in controlling cytoskeleton organization and cell migration (Sells et al., 1997; Zhang et al., 2002). Anchorage-mediated activation of PAK1 is associated with the Rac1 and the SH2/SH3-dapter protein Nck (Bagrodia and Cerione, 1999; del Pozo et al., 2000; Li and She, 2000). However, PAK activation can also occur in the absence of Cdc42 or Rac activation by PIX (Obermeier et al., 1998).

Rho signaling pathways often crosstalk with distinct oncogenic signaling cascades, including those downstream of Ras (Malliri and Collard, 2003). Integrin signaling mediated by Ras superfamily-proteins include an activation of signaling through ERK (Grb2 → Ras → mSOS → Raf → MEK → ERK pathway, as mentioned in section 2.3.1).

Rho GTPases controls various cellular functions, including cytoskeleton reorganization, cell adhesion, spreading, morphology, migration, proliferation and malignant transformation (Jaffe and Hall, 2002; Malliri and Collard, 2003). Rho A induces the formation of focal adhesions and assembly of stress fibers (Ridley and Hall, 1992). Cdc42 promotes filopodia formation (Kozma et al., 1995) and controls polarity signals directing cell migration (Allen et al., 1998; Nobes and Hall, 1999). Rac1 is required for the formation of actin-rich lamellipodia protrusion that is proposed to be a main driving force for cell movement (Ridley and Hall, 1992).

The role of Rho family of the small GTPases in the control of the G1-cell cycle progression will be discussed in section 2.4.2.

### 2.3.3 MEK/ERK1/2 signaling

The extracellular signaling-regulated kinase 1/2 (ERK1/2) is a type of mitogen-activated protein kinases (MAPKs), and is activated commonly by oncogenic stress. Importantly, integrin engagement also activates ERK1/2 signaling cascades which control a variety of cellular functions, including gene expression, cell proliferation, differentiation and survival (Howe et al., 2002; Nishida and Gotoh, 1993).

Integrin-mediated activation of ERK1/2 requires other signaling, including Raf/MEK1, PAK1 and/or FAK (Howe et al., 2002).

Cell attachment-dependent ERK1/2 activation requires Raf1/MEK1 signaling. Integrin-mediated cell adhesion is required for phosphorylation of Raf1 and activation of MEK1, and MEK1 mediated activation of ERK1/2 (Chen et al., 1996; Renshaw et al., 1997). Cell attachment may also be required to couple Ras activation to MEK1 and ERK1/2 activation (Lin et al., 1997b; Renshaw et al., 1997). The integrin activated Ras → Raf → MEK1 → ERK1/2 signalling cascade triggers a wide cellular response.

Cell attachment-dependent ERK1/2 activation also requires another important mediator, PAK1. The ability of PAK1 to regulate ERK1/2 may be due to a direct phosphorylation of Raf1, leading to MEK1 to ERK1/2 activation (Frost et al., 1997; King et al., 1998). The activity of PAK1 is suggested

to be involved in the formation of MEK1/ERK1/2 complexes and ERK1/2 activation in newly adhering cells (Eblen et al., 2002). In addition, upon cell adhesion, PAK1 can mediate MEK1 phosphorylation and subsequent activation of ERK1/2 (Slack-Davis et al., 2003).

The involvement of FAK in cell attachment-mediated ERK1/2 activation is controversial. Integrin-mediated transient activation of ERK1/2 was shown to be dependent on FAK (Chen et al., 1994). Upon cell attachment, autophosphorylation of FAK results in formation of the p130CAS/Shc/Grb2/SOS complex (Polte and Hanks, 1997; Schlaepfer et al., 1994; Schlaepfer and Hunter, 1997; Vuori et al., 1996), which may link the Ras→Raf→MEK1→ERK1/2 cascade because SOS signaling is a guanine nucleotide exchange factor for Ras activation (Egan and Weinberg, 1993; Khosravi-Far et al., 1995). However, others reported that FAK is not involved in activation of ERK1/2 because overexpression of constitutively active FAK failed to activate ERK1/2 (Frisch et al., 1996a). In addition, overexpression of dominant negative FAK in fibroblast prevented FAK activation, but failed to inhibit ERK1/2 activation by cell attachment to fibronectin (Lin et al., 1997a). Therefore, both FAK-dependent and -independent pathways may activate ERK1/2.

Integrin-mediated cell adhesion regulates ERK1/2 nuclear translocation and phosphorylation of its downstream transcriptional targets, including Elk-1, leading to immediate-early gene induction (Aplin et al., 2001).

The role of ERK1/2 signaling in the control of cell proliferation and survival will be discussed in section 2.4.2 and 2.4.4, respectively.

## **2.4 INTEGRIN CONTROL OF CELL PROLIFERATION AND SURVIVAL**

Anchorage to the ECM is required for proliferation and survival of all normal tissue cells. As the major cell adhesion receptors for the ECM, integrins play key roles in these processes (Ruoslahti and Reed, 1994).

### **2.4.1 Anchorage-dependent G1-cell cycle progression**

In order to control cell proliferation, anchorage regulates key cell cycle components during cell cycle progression (O'Neill et al., 1986). Here, I will focus on the effects of anchorage on the G1-phase of the cell cycle.

Progression through the G1-phase is controlled by the sequential activation of cyclin-dependent kinases (Cdks), in association with their regulatory subunits, cyclins. D-type cyclins, including cyclin D1 and D2, form active complexes with Cdk4 and Cdk6, and cyclin E1 and E2 form complexes with Cdk2. Cyclin D-Cdk4/6 and cyclin E-Cdk2 complexes are the main driving factors for the cell cycle progression through the G1-phase (Sherr and Roberts, 1999).

The activities of cyclin-Cdk complexes are regulated through the binding of two classes of cyclin-dependent kinase-inhibitors (Cdk-inhibitors or CDKI). The INK4CDKI family members, including p15<sup>INK4b</sup>, p16<sup>INK4a</sup>, p18<sup>INK4c</sup> and p19<sup>INK4d</sup>, specifically inhibit cyclin D-Cdk4/6 activity by direct interaction with and sequestration of Cdk4/6 (Sherr and Roberts, 1995). The CIP/KIP family members, including p21<sup>CIP1</sup> and p27<sup>KIP1</sup>, bind to cyclin D-Cdk 4/6 and cyclin E-Cdk2 complexes. At higher levels, p21<sup>CIP1</sup> and p27<sup>KIP1</sup> function as cyclin E-Cdk2 inhibitors, leading to cell cycle arrest. However, at lower levels, p21<sup>CIP1</sup> and p27<sup>KIP1</sup> actually promote the assembly, stability and nuclear retention of cyclin D-Cdk4 and cyclin D-Cdk6 complexes (LaBaer et al., 1997). Therefore, the relative

levels of cyclin, Cdk and CDKI proteins dictate whether a cell will progress through the G1 phase (Coleman et al., 2004).

Cell anchorage to ECM is required during the G-1 phase firstly for induction of cyclin D and activation of Cdk4 and Cdk6, and secondly for promotion of cyclin E-Cdk2 activity (Fang et al., 1996; Gad et al., 2004). Cell attachment to the ECM results in reduction of the Cdk2-inhibitors p21<sup>CIP1</sup> and p27<sup>KIP1</sup>, whereas cells in suspension display higher levels of p21<sup>CIP1</sup> and p27<sup>KIP1</sup> (Gad et al., 2004; Strömblad et al., 1996; Zhu et al., 1996). In suspension, Cdk2 associates with p21<sup>CIP1</sup>, leading to an impaired cyclin E-Cdk2 activity concomitant with a block of the cell cycle in G1-phase (Fang et al., 1996; Strömblad et al., 1996; Zhu et al., 1996). It appears that anchorage-dependent regulation of p21<sup>CIP1</sup> is important for proper control of cyclin E-Cdk2 activity.

#### 2.4.2 Control of G1-cell cycle components by integrin signaling

Anchorage-activated integrin signaling, including FAK, MAPKs (ERK and JNK), PI-3K, ILK and Rac1, play key roles in the control of cell cycle progression of the G1-phase (Giancotti and Ruoslahti, 1999). These signaling components converge to regulate the activities of Cdks and the expression of cyclin D1. For example, integrin-mediated sustained ERK1/2 activation was shown to promote cyclin D1 expression in growth factor-treated fibroblasts (Roovers et al., 1999). In addition, upon integrin ligation, active Rac1 promotes cyclin D1 synthesis and thereby controls cell cycle progression through the G1-phase (Mettouchi et al., 2001), while Rho appears to maintain the correct timing of cyclin D1 expression in the G1-phase (Yamamoto et al., 1993).

The small GTPases Ras and Rho are also important regulators of p21<sup>CIP1</sup> and p27<sup>KIP1</sup>. Overexpression of an active Ras mutant induced p21<sup>CIP1</sup> while Rho signaling suppressed the induction of p21<sup>CIP1</sup> and thereby promoted DNA synthesis (Olson et al., 1998). RhoA has been implicated to control the mid-late G1-phase and to downregulate p27<sup>KIP1</sup> (Hirai et al., 1997).

#### 2.4.3 Proteasomal proteolysis in cell cycle

The proteasome pathway is a major intracellular proteolytic mechanism that controls various cellular processes, including the cell cycle. Ubiquitination targets proteins for proteasomal proteolysis and involves the coordinated actions of an E1 ubiquitin-activating enzyme, an E2 ubiquitin-conjugating enzyme, and an E3 ubiquitin-protein ligase. The last one delivers multiple ubiquitin molecules to the target protein and forms the ultimate polyubiquitin chain that serves as the signal for recognition and proteolysis by the 26S proteasome unit (Hochstrasser, 1996). The 26S proteasome is composed of a barrel-shaped 20S catalytic chamber, capped at each end by 19S complexes (Hershko and Ciechanover, 1998). A number of cell cycle components are targeted by proteasomes, including cyclins (A, B, D, E), E2F, Rb, p53, p21<sup>CIP1</sup> and p27<sup>KIP1</sup> (Blagosklonny et al., 1996; Boyer et al., 1996; Hofmann et al., 1996; King et al., 1996; Koepp et al., 1999; Pagano et al., 1995; Scheffner et al., 1993). The proteasome-mediated proteolysis of these components critically determines the periodicity of the cell cycle.

The transcriptional regulation of p21<sup>CIP1</sup> has been extensively studied (Gartel and Tyner, 1999). However, the regulation of p21<sup>CIP1</sup> levels by post-transcriptional mechanisms is still elusive. The p21<sup>CIP1</sup> protein has a short half-life, and is commonly degraded by the proteasome (Blagosklonny et al., 1996; Cayrol and Ducommun, 1998; Sheaff et al., 2000; Toutilou et al., 2001).

In most cases, proteasomal degradation is preceded by ubiquitination. For example, the polyubiquitination of p27<sup>KIP1</sup> mediated by a SCF (Skp/Cull/F-box protein)-ubiquitin-ligase complex leads to degradation of p27<sup>KIP1</sup> by the proteasome (Pagano et al., 1995). However, although p21<sup>CIP1</sup>

can be ubiquitinated, proteasomal degradation of p21<sup>CIP1</sup> does not require ubiquitination (Sheaff et al., 2000). It has also been shown that the C8  $\alpha$ -subunit of the 20S proteasome can directly interact with the C-terminus of p21<sup>CIP1</sup>, leading to rapid degradation of p21<sup>CIP1</sup> (Touitou et al., 2001). Consistently, a recent report indicated that disruption of essential components of the ubiquitination mechanism did not influence endogenous p21<sup>CIP1</sup> degradation (Chen et al., 2004). However, it has been unclear if integrin-mediated anchorage to the ECM might regulate proteasome-dependent proteolysis.

#### 2.4.4 Control of cell survival by integrin signaling

##### *Apoptosis*

Apoptosis is a form of programmed cell death and is an intrinsic cellular self-destructive suicide process essential for the control of tissue development and homeostasis. Defects in apoptotic pathways promote expansion of neoplastic cells, and enhance the escape of tumor cells from surveillance by the immune system, leading to tumorigenesis. Defects of apoptosis also cause cancer cell resistance to chemotherapy and irradiation.

Apoptosis is a highly regulated, stepwise process, starting with disruption of cellular membranes, following by a break of the cytoplasmic and nuclear skeletons, extrusion of the cytosol, degradation of the chromosomes and fragmentation of the nucleus. Eventually, the shrunk cell corpse is engulfed by neighboring cells or macrophages in the tissue and disappears typically within 24 h (Wyllie et al., 1980).

At least two apoptosis-inducing pathways have been well characterized. The intrinsic pathway is mediated by mitochondria upon intracellular stress and/or deprivation of survival factors. The extrinsic pathway is initiated by membrane death receptors activated by extracellular factors (Ashkenazi and Dixit, 1998). Both pathways involve the activation of cysteine aspartyl-specific proteases known as caspases that cleave their cellular substrates important for the cell and genome integrity, leading to the characteristic morphological and biochemical changes of apoptosis (Green, 2000).

Upon cellular stress, mitochondria release a number of apoptotic factors, such as cytochrome c, Smac/DIABLO (Second Mitochondrial Activator of Caspase) and HtrA2 (Jiang and Wang, 2004; Wang, 2001) promoting the intrinsic apoptotic pathway. Cytochrome c promotes apoptosis activating factor 1 (Apaf1) and initiator caspase 9, resulting in the formation of a complex known as the apoptosome, which triggers downstream caspase cascades including cleavage and activation of the executor caspase-3, and -7. Smac/DIABLO bind to and antagonize inhibitors of apoptotic proteins and thereby promote apoptosis (Suzuki et al., 2001; Wang, 2001). In fact, the change of mitochondrial membrane permeability is a central event, tightly controlled by the Bcl-2 family members, including proapoptotic proteins Bad, Bax, Bak, Bid, Bim, Noxa, and PUMA (p53-upregulated modulator of apoptosis) and the antiapoptotic proteins Bcl-2, Bcl-XL, and Bcl-W. These proteins either reside in or can translocate to mitochondria.

The extrinsic apoptotic pathway is typically activated by ligation of transmembrane death receptors including tumor suppressor factor receptor (TNFR), CD95 (FAS) and death receptor 5 (DR5) with their respective corresponding ligand TNF, FASL and TRAIL-R (TNF-related apoptosis inducing ligand-receptors 1). Upon ligand binding, these receptors promote the formation of death-inducing signaling complexes that lead to the activation of membrane-proximal initiator caspases including caspase-8 and -10, and these in turn cleave and activate executor caspase 3 and -7. In fact, there is extensive cross-talk between the intrinsic and extrinsic apoptotic pathways, which is proposed to lead to amplification of the apoptotic signals (Fulda et al., 2001).

In addition to caspase-dependent apoptosis mechanism mentioned above, apoptosis can also occur in the absence of caspase activity (Chipuk and Green, 2005).

The tumor suppressor p53 is a critical regulator of both intrinsic and extrinsic apoptotic pathways. The p53-mediated apoptosis mechanism will be discussed in section 2.6.1.

#### *Control of apoptosis by integrin signaling*

Anchorage to ECM is required for survival of many types of normal cells, including epithelial cells, and loss of anchorage leads to cell death by apoptosis (Frisch and Francis, 1994; Meredith et al., 1993). Importantly, not only loss of anchorage but also lack of specific integrin-mediated contact to the ECM can lead to apoptosis, although the cells are still firmly attached by other cell to ECM contacts (Montgomery et al., 1994; Petitclerc et al., 1999). To this end, integrin-activated signaling pathways, including FAK, PI-3K/Akt and MEK1/ERK1/2, can control both cell survival and apoptosis (Howe et al., 1998).

Overexpression of constitutively active FAK could prevent epithelial cell apoptosis (Frisch et al., 1996b). Inhibition of FAK triggered apoptosis in several types of cells (Hungerford et al., 1996; Xu et al., 1996). The mechanisms for FAK control of cell survival and apoptosis may be associated with PI-3K (Chen and Guan, 1994) whose downstream target Akt is critical for adhesion-dependent survival pathway by suppressing apoptosis (Khwaja et al., 1997). Integrin-activated FAK may also promote cell survival by repressing p53-dependent apoptosis (Ilic et al., 1998).

In addition, integrin-activated ERKs may regulate adhesion-dependent survival of epithelial cells (Frisch and Screaton, 2001). Upon integrin ligation, active ERK1/2 translocates to the nucleus where it activates a number of transcriptional genes that can promote cell survival (Schulze et al., 2001). In addition, integrin  $\alpha v \beta 3$  mediates a sustained activation of MEK1/ERK1/2 in endothelial cells, which may promote cell survival during angiogenesis (Eliceiri et al., 1998). Moreover, integrin-mediated activation of ERK1/2 may promote anchorage-dependent melanocyte cell survival (Conner et al., 2003).

As mentioned above, specific integrins are required for suppression of apoptosis in certain cell types and situations. Mechanistically, integrins  $\alpha 5 \beta 1$  and  $\alpha v \beta 3$  binding to fibronectin, are efficient in upregulating Bcl-2 (Matter and Ruoslahti, 2001; Zhang et al., 1995b), an antiapoptotic protein that can protect cells against apoptosis. Recently, integrin  $\alpha 5 \beta 1$ -mediated cell attachment was shown to promote cell survival through the inhibition of a Bit1/AEX complex -mediated mitochondrial apoptosis independent of caspase activity (Jan et al., 2004). However, other integrins, including the fibronectin receptor integrin  $\alpha v \beta 1$ , do not provide this survival effect. Moreover, integrin  $\alpha v \beta 3$  mediates endothelial cell survival associated with inhibition of p53 activity (Strömblad et al., 1996) as well as activation of the transcription factor nuclear factor kappa B (Scatena et al., 1998). Moreover, integrin  $\alpha v \beta 3$  elevated the Bcl-2 to Bax ratio and promoted glioma, melanoma and endothelial cell survival (Petitclerc et al., 1999; Strömblad et al., 1996; Uhm et al., 1999). Overexpressed unligated integrin  $\alpha v \beta 3$  may associate with activate caspase 8 in epithelial cells, leading to a death-receptor-initiated apoptosis (Stupack et al., 2001).

## **2.5 MECHANISMS OF CANCER**

Today, more than a hundred distinct types of cancers are found in the human being, implicating the diversity and complexity of cancer. While cancer is a genetic disease associating with mutagenic alterations of oncogenes and tumor suppressive genes especially at the initial tumorigenic stage,

transformation of normal cells into cancerous derivatives must include multistep alterations. Recently, a number of essential alterations in cells were characterized as a self-sufficiency in growth signals, insensitivity to growth-inhibitory signals, evasion of apoptosis, limitless replicative potential, sustained angiogenesis, and tissue invasion and metastasis. These six steps that constitute the uncontrolled tumor growth are suggested as the hallmarks of cancer, were carefully reviewed by Hanahan and Weinberg (Hanahan and Weinberg, 2000).

### 2.5.1 The hallmarks of cancer

Cancer cells acquire a capacity for self-sufficiency. This was the first of the six capabilities to be defined, in large part because of the prevalence of dominant oncogenes (Ras) that were found to modulate mitogenic growth signals. Thereby, cancer cells became independent on exogenous growth factors and less relying on their surrounding microenvironment, because they can manipulate various own factors for growth stimulation through different molecular strategies. For example, cancer cells switch the types of integrin receptors that they express, benefiting ones that transmit pro-growth signals that can activate the SOS→Ras→Raf→MAPK mitogenic cascade (Aplin et al., 1998; Giancotti and Ruoslahti, 1999; Lukashev and Werb, 1998). In contrast, normal cells are extremely dependent on extracellular growth signals to proliferate.

Cancer cells also acquire a capacity of insensitivity to anti-growth signals (e.g. TGF- $\beta$ ) and thereby can grow out of control, leading to a disruption of the tissue homeostasis. For example, in many different types of cancers the pRb pathway, as governed by TGF- $\beta$ , is disrupted, which leads to release of E2Fs and promotion of cell proliferation (Fynan and Reiss, 1993). In contrast, normal cells sense the external stimuli and are able to correctly decide to proliferate, to be quiescent or to enter into a postmitotic, differentiated state.

In addition, cancer cells acquire the capacity of evading apoptosis, whereas normal cells will undergo apoptosis upon a variety of stimuli, including DNA damage, oncogenic stimuli and hypoxia or upon lack of extracellular stimuli from growth factors or ECM. Mutations in the *TPp53* gene and defects in the p53 pathway are the most common causes for cancerous cells to become resistant to apoptosis (Vogelstein et al., 2000).

Moreover, cancer cells acquire a capacity of limitless replicative potential, and when propagated in culture the cells appear to be capable of multiplying without limit — immortalization. In contrast, normal cells in culture have the capacity of approximately 60-70 doublings, a limited replication state, before becoming senescent.

Cancer cells also acquire the capacity of sustained angiogenesis in which new blood vessels are formed from pre-existed vessels. Angiogenesis is tightly regulated by a balance between positive and negative signals, including from soluble growth factors such as vascular endothelial growth factor (VEGF), cell adhesion receptors such as integrins, or negative signals, such as thrombospondin-1. Integrin  $\alpha v \beta 3$  is known to be critical for the control of angiogenic endothelial cell survival (Brooks et al., 1994; Strömblad and Cheresh, 1996).

Finally, cancer cells acquire the capacity of invasion and metastasis. Most types of tumor cells are able to move out of their original sites, invade to adjacent tissues and travel to distant sites where they may settle down. This process is called metastasis and is the cause of nearly all human cancer deaths (Sporn, 1996). Many adhesion molecules that mediate cell-cell adhesion and cell-ECM interactions are changed in cells achieving invasive or metastatic capacities. Despite their relative anchorage independence, cancerous cells still need integrins to promote growth, survival, migration and/or

metastasis (Bissell and Radisky, 2001; Wiseman and Werb, 2002). For example, integrin  $\alpha\beta3$  is critical for melanoma growth, invasion and metastasis (Hsu et al., 1998; Seftor, 1998). Moreover, the matrix-degrading proteases are aberrantly overexpressed and protease inhibitors are deregulated, which is associated with the capacity of tumor invasion and metastasis.

### 2.5.2 Malignant melanoma

Melanoma develops from malignant transformation of the pigment-secreting cells melanocytes. During embryonic development, melanocytes differentiate from neural crest progenitor cells and eventually reside in the basal epidermal layer mainly in the skin.

The proclivity for metastasis is a hallmark of melanoma, which leads melanoma to be the most common fatal cancer. For example, once cutaneous melanoma has progressed from the radial growth phase (RGP) to the vertical growth phase (VGP), the cure and survival rates of melanoma patients dramatically decline. Pathologically, most melanoma subtypes display a slow RGP, followed by a more rapid VGP (Clark et al., 1984) (See Figure 4). RGP melanoma cells extend upward in the epidermis but remain *in situ* and lack capacity to invade the dermis and metastasize, while VGP melanoma can invade the dermis and even deeper structures and metastasize to distant organs (Meier et al., 1998; Rusciano, 2000).

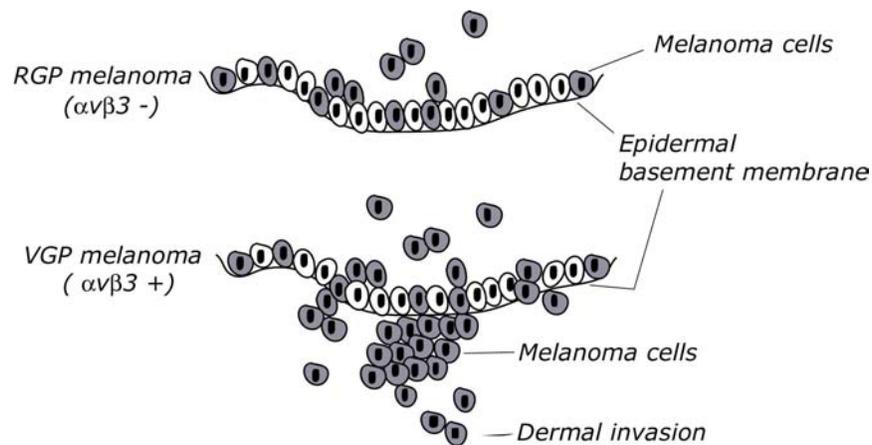


Figure 4 Schematic representation of melanoma growth at two stages: in situ melanoma, radial growth phase (RGP) melanoma that does not express integrin  $\alpha\beta3$ ; malignant melanoma, vertical growth phase (VGP) melanoma that expresses integrin  $\alpha\beta3$ .

As in many cancers, environmental factors are proposed to highly influence the development of melanoma. Exposure of ultraviolet (UV) light appears to be a causal factor for melanoma genesis (Chin, 2003).

The genetic changes play key role for the development of melanoma. Through analyzing mutations or deletions in the melanoma genome, multiple genetic defects are found, including the inactivation of tumor suppressor genes. The tumor suppressor *cyclin-dependent kinase inhibitor 2A* (*CDKN2A*) on chromosome 9p21 appears to be associated with melanoma susceptibility in people with familial melanoma (Hussussian et al., 1994). The *CDKN2A* locus (INK4 locus) encodes two tumor suppressors,

p16<sup>INK4a</sup> (inhibitor of cyclin D/Cdk4 or Cdk6) and p14<sup>ARF</sup> (p19<sup>ARF</sup> in mice, stabilizing p53 by abolishing HDM2-induced p53 degradation), leads to suppression of both the INK4A/cyclin D/Cdk4/pRb pathway and the ARF/p53 pathway. These two pathways are known to be critical for tumor suppression through regulation of cell proliferation and apoptosis, respectively.

However, several melanoma pathological surveys indicated that an absence or very low incidence (< 5 %) of point mutation or allelic loss of *TP53* in surgical specimens of primary and metastatic melanomas (Satyamoorthy et al., 2001; Yang et al., 2001). This suggests the existence of additional mechanisms that render p53 nonfunctional in melanoma.

Activation of oncogenes can be accomplished by activated mutations, including *Ras* and *RAF* family members. Activating mutations of *Ras* in melanoma have been observed at an incidence of 10-15 % (Chin, 2003). *NRAS* and *HRAS* are the two common types of mutations, which are proposed to play important roles in the RAS-signaling pathway in melanoma genesis. *BRAF* activation is one of the most frequent melanoma-associated genetic events, since approximately 60 % of melanomas was found to carry the *BRAFV599E* mutation (Davies, 2002). The *BRAF* mutations were found in both benign and malignant melanocytic lesions, which suggest a key role of *BRAF* in transformation and melanoma development (Chin, 2003).

Therapeutic resistance is another hallmark of malignant melanoma, since melanoma tumors are strongly refractory to both chemo- and radio-therapy. One strategy that is currently being tried to treat melanoma patients is gene transfer delivery to certain melanoma of an adenoviral vector expressing wt p53 (Sotomayor et al., 2002). However, it is unclear if this or other current efforts to find a cure for melanoma will be successful.

### 2.5.3 Integrin $\alpha\beta3$ in melanoma progression

Expression of integrin  $\alpha\beta3$  has been linked to malignant melanoma progression. For example, the vertical growth phase of malignant melanoma displays high expression levels of integrin  $\alpha\beta3$  as compared to horizontally growing melanoma in the epidermis (Albelda et al., 1990; Seftor et al., 1999; Van Belle et al., 1999). Overexpression of integrin  $\beta3$  through *in vivo* gene delivery of integrin  $\beta3$  gene promoted invasive melanoma growth from the epidermis into the dermis in three-dimensional (3D) skin reconstructs (Hsu et al., 1998). Integrin  $\alpha\upsilon$  was also shown to promote melanoma metastatic potential (Felding-Habermann et al., 1992). Moreover, integrin  $\alpha\beta3$  promoted melanoma cell survival as shown in a 3D-collagen gel model *in vitro*, and in full thickness human skin *in vivo* (Montgomery et al., 1994; Petitclerc et al., 1999). In addition, block of integrin  $\alpha\beta3$  by an antagonistic anti-integrin  $\alpha\beta3$  mab induced melanoma cell apoptosis and thereby prevented melanoma tumor growth in mice. Furthermore, re-constitution of the integrin  $\alpha\upsilon$  subunit into  $\alpha\upsilon$ -negative melanoma cells rescued cell survival in 3D-collagen as well as in human skin and restored melanoma tumor growth *in vivo* (Montgomery et al., 1994; Petitclerc et al., 1999). Recently, integrin  $\alpha\beta3$  was also found to bind to the endothelial cell adhesion molecular L1, and this adhesive interaction might promote migration of melanoma cells across the endothelium (Voura et al., 2001).

The main part of my thesis was to investigate integrin  $\alpha\upsilon$ -mediated melanoma cell survival mechanism.

## 2.6 THE TUMOR SUPPRESSOR p53

The p53 protein is a *bona fide* tumor suppressor. Upon various types of stress, including oncogenic stimuli and DNA damage, p53 is activated and triggers diverse cellular processes, including cell growth arrest and apoptosis. The importance of p53 for tumor suppression is underscored by the fact

that defects of p53 function occur in almost all human cancers. In approximately half of human cancers, p53 is inactivated directly as a result of mutations within the *TPp53* gene (Hollstein et al., 1999). Some cancers, although harbouring wild-type (wt) p53, are defective in the pathway of p53-activated cell cycle arrest or apoptosis due to viral infection, mouse double minute-1 (MDM2) overexpression, ARF or ATM deficiency (Wang et al., 2003). In melanoma, p53 is rarely mutated, but its function is somehow impaired (Satyamoorthy et al., 2001). p53 is also known as the ‘guardian of the genome’, since inactivation of p53 and p53 pathways accelerate genomic instability (Vogelstein et al., 2000). Loss of p53 functions promotes tumor progression, resistance to treatment and constitutes poor prognosis (Kirsch and Kastan, 1998).

Below, I will discuss certain aspects of p53 function and its regulatory mechanisms that are closely correlated with my present study.

### 2.6.1 Apoptotic activities of p53

Activation of apoptosis is an important function of the tumor suppressor p53. Numerous studies suggest that p53 triggers apoptosis through transcription-dependent and –independent mechanisms (Vousden and Lu, 2002), which contributes to the activation of the intrinsic mitochondrial as well as the extrinsic death receptor apoptotic pathways (discussed in section 2.4.4).

#### *Transcriptional-dependent apoptosis*

p53 serves as a tetrameric transcription factor through binding to specific DNA sequences (Ko and Prives, 1996) and transcriptionally controls apoptosis (Fridman and Lowe, 2003). p53 transcriptionally activates many proapoptotic Bcl-2 family members, including Bax, Bid, Noxa and PUMA (Miyashita et al., 1994; Nakano and Vousden, 2001; Oda et al., 2000a; Sax et al., 2002). These proteins are involved in induction of the intrinsic mitochondrial apoptotic pathway. p53 transactivates other apoptotic effectors, including Apaf1 (Soengas et al., 1999), which acts as a co-activator of caspase 9 and mediates activation of downstream caspase cascades leading to apoptosis. In addition, p53 also transrepresses many antiapoptotic genes, including Bcl-2, Bcl-XL and Survivin (Johnstone et al., 2002).

The death receptors FAS and PIDD (p53-induced protein with a death domain) are identified as the direct transcriptional targets of p53, these receptors are known to mediate an extrinsic apoptotic pathway (Lin et al., 2000; Maecker et al., 2000; Owen-Schaub et al., 1995). p53 may also activate apoptosis through engaging caspase 8 (Ding et al., 2000).

Moreover, p53 can also counteract survival signaling by its ability to transactivate PTEN, a negative regulator of PI-3K survival pathway (Fridman and Lowe, 2003).

#### *Transcriptional-independent apoptosis*

In the absence of transcription, p53 can elicit Bax-dependent apoptosis through translocation of Bax to mitochondria, leading to an increase in mitochondrial membrane permeability and subsequent release of cytochrome c (Chipuk et al., 2004; Chipuk et al., 2003). In addition, p53 can also directly translocate to mitochondria and mediate mitochondrial apoptosis (Mihara 2003). More recently, p53 was found to interact with the mitochondrial membrane protein Bak and form a p53-Bak complex. This complex can disrupt the interaction with Bak of the anti-apoptotic Bcl-2 member Mcl1, leading to a release of cytochrome c from mitochondria and subsequent activation of apoptosis (Leu et al., 2004).

Figure 5 summarizes p53-mediated apoptotic pathways.

### 2.6.2 p53 post-translational modifications

The tumor suppressor p53 is a tightly regulated protein. Several post-translational modifications are involved in the regulation of its stabilization, accumulation in the nucleus and transcriptional activation. These modifications include ubiquitination, sumoylation, neddylation, phosphorylation and acetylation (Bode and Dong, 2004; Harper, 2004). I will focus on discussing p53 ubiquitination, phosphorylation and acetylation.

Ubiquitin-mediated proteasome degradation is involved in regulation of p53. In unstressed cells, p53 is maintained at low levels through p53 interacting with MDM2, an ubiquitin ligase (Barak et al., 1993; Haupt et al., 1997). Because MDM2 is a transcriptional target of p53, MDM2-mediated proteasomal degradation of p53 constitutes a negative feedback mechanism (Oren, 1999; Wu et al., 1993). In addition, MDM2-independent mechanisms, such as JNK stimulation, can also promote degradation of p53 through the ubiquitin-proteasome system (Fuchs et al., 1998).

Phosphorylation and acetylation are two common post-translational modifications in the regulation of p53 (Brooks and Gu, 2003). So far, 17 p53 phosphorylation sites have been described in human cells upon DNA damage induced by ionizing radiation or ultraviolet-light irradiation (Bode and Dong, 2004). Among these, Ser 46 phosphorylation appears to be importantly involved in p53 apoptotic function upon UV stimuli (Oda et al., 2000b). Acetylations of p53 by the cofactor p300/CBP, a histone acetyl transferase, occur at multiple lysine residues in the carboxy-terminal regulatory domain. Of these, acetylation of Lys382 has been found to be involved in p53-mediated apoptosis. For example, a recent study showed that p300-mediated acetylation of Lys382 controls p53-dependent apoptosis upon DNA damage through regulation of PUMA/p21 expression (Iyer et al., 2004).

### 2.6.3 Regulation of p53 conformation

p53 has a flexible protein conformation. To this end, two distinct conformations have been identified in cells by use of conformation-specific monoclonal antibodies (Bell et al., 2002). The monoclonal antibodies PAb1620 and PAb246 are specific for a folded, active conformation of p53 (Cook and Milner, 1990). Several other antibodies, including PAb240, recognize an unfolded, inactive conformation of p53 and can bind to unfolded p53 proteins (Gannon et al., 1990; Legros et al., 1994; Vojtesek et al., 1995).

The p53 activity strictly depends on its active, folded conformation (Bullock and Fersht, 2001). Point mutations (structural mutations) often cause a shift of the folded, active p53 conformation to an unfolded, inactive form, leading to p53 inactivation. For example, p53R175H, one of the most common structural mutations within *TP53* gene, preferentially displays an unfolded, inactive PAb240 conformation. The structure mutation V143A displays a temperature-induced mutant conformation; at 32°C, it is recognized by PAb1620 and at 37°C by PAb240. Therefore, mutation-induced unfolding may explain p53 inactivation in more than half of human cancers. However, it is unclear whether the p53 conformation may affect the activity of wt p53 in tumor cells.

Several attempts are initiated to restore mutant p53 function as a new strategy for the development of tumor therapy. The restoration of an active conformation of mutant p53 originally derives from application of antibodies and peptides that could specifically bind to the p53 carboxy-terminus and promote p53 DNA-binding affinity (Abarzua et al., 1995; Selivanova et al., 1997). Rational designs then led to the identification of a short peptide, CDB3, with similar p53-activating properties (Friedler et al., 2002). Recently, a pharmacological rescue of mutant p53 conformation and function by a small compound CP31398 was achieved through stabilizing the active conformation of the p53-DNA binding domain (Foster et al., 1999). Furthermore, using a cell-based random screen of a chemical

library, PRIMA-1 (**p53 Reactivation and Induction of Massive Apoptosis**) was identified as capable of converting an unfolded conformation of mutant p53 to an active folded form, inducing apoptosis in a mutant p53-dependent manner (Bykov et al., 2002). PRIMA-1<sup>MET</sup>, an analogue of PRIMA-1 with increase activity (Bykov et al., 2005), was applied in part of my present study to investigate whether also the conformation of wt p53 could be manipulated pharmacologically. Another recent approach to activate p53 was achieved through stabilizing wt p53 by blocking its interaction with MDM2. This led to identification of Nutlin (Vassilev et al., 2004), and the small organic compound RITA (Issaeva et al., 2004). For example, RITA was found to induce a conformational change that blocks interaction of p53 with its negative regulators, including human homology of MDM2 (HDM-2), which targets p53 for proteasomal degradation. These strategies of p53-targeting may provide novel promising approaches that could contribute to the development of tumor therapy.

In section 2.5.2, I mentioned that p53 is rarely mutated in melanoma (Castresana et al., 1993; Lubbe et al., 1994; Montano et al., 1994). However, melanoma tumors are not sensitive to ionizing radiation or chemotherapy (Jenrette, 1996; Satyamoorthy et al., 2000), implicating that the p53-controlled functions may be disrupted. An impaired function of p53 is often found to be associated with defects in the signaling pathways that are upstream or downstream of p53 (Satyamoorthy et al., 2000; Soengas et al., 2001; Vousden and Lu, 2002), but an impaired p53 function may be caused by the p53 protein itself. In fact, a modulation of the p53 conformation was suggested to associate with the regulation of embryonic stem cell differentiation (Sabapathy et al., 1997). The inactivation of p53 by a conformational change could allow the differentiating cells to escape from apoptosis. The present study addressed the effects of p53 conformation on p53 activation and function in malignant melanoma.

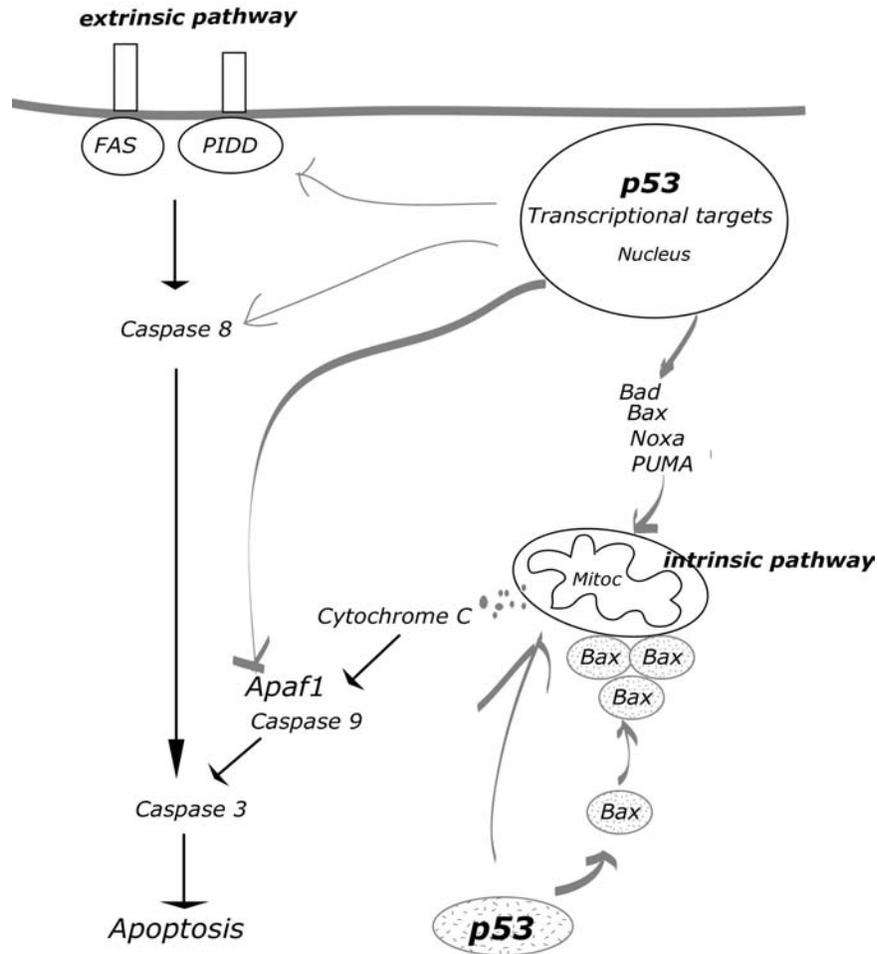


Figure 5 Schematic drawing of suggested p53-mediated apoptotic pathways related to the present investigation. p53 transcriptionally transactivates numerous downstream targets including Apaf1, Bad, Bax, Noxa and PUMA known to mediate an intrinsic mitochondrial apoptosis. p53 also directly translocates to mitochondria or targets to mitochondria through interactions with apoptotic proteins involving Bax in a transcription-independent manner. In addition, p53 regulates an extrinsic apoptotic pathway through transcriptional regulation of its downstream targets death receptors FAS and PIDD, and caspase 8.

## 2.7 THREE-DIMENSIONAL CELL CULTURE MODELS

### 2.7.1 Characteristics of 3D cell culture environment

In living organisms, tissue cells are growing in a 3D-microenvironment where they are communicating with one and another and interacting with their surrounding ECM. Therefore, in order to more closely reflect the situation *in vivo*, a 3D-culture environment may represent a useful model for researchers in cell biology. In contrast to conventional, regular 2D-cultures where artificial substrates such as plastic are probably distorting the cells by enforcing them to adjust to flat and rigid surface (Elsdale and Bard, 1972), the 3D-culture provides a more authentic environment. In fact, molecular composition of the 3D-ECM environment may facilitate to most cell proliferate and survival as they live inside the organisms (Cukierman et al., 2002).

Many studies have demonstrated that cells cultured in 3D generate different signaling and display different behavior as compared to those observed in 2D. For example, through its interaction with integrins, 3D-matrix can induce special 3D-matrix adhesion structures, called 3D-adhesions (Cukierman et al., 2002). They were elongated and spindle shape, and clearly morphologically different from the focal and fibrillar adhesions characterized on 2D-substrates (Zamir et al., 1999) (discussed in section 2.2.2). 3D-fibronectin-mediated adhesions are characterized with low levels of phosphorylated FAK, although the FAK protein is abundant. This differs from the highly phosphorylated FAK found in focal adhesions, implicating that 3D-ECM may transduce their specific signaling pathways (Cukierman et al., 2002). EGF-receptor signaling were also found to be different in response to cell adhesion within 3D-matrices as compared to attachment onto 2D-tissue culture plates (Cukierman et al., 2001; Wang et al., 1998). The differences in cell polarity and interaction with the surrounding ECM within 3D-culture might also dictate the susceptibility of normal and cancer cells to the cancer chemotherapy in terms of induction of apoptosis (Weaver et al., 2002). In a 3D-collagen model, the expression of matrix metalloproteinase 13 (MMP13) was upregulated through integrin  $\alpha 1\beta 1$  and  $\alpha 2\beta 1$ -mediated activation of ERK, JNK and p38 MAPK (Ravanti et al., 1999). Importantly, in a 3D-collagen model, integrin  $\alpha v$  was found to control melanoma cell survival (Montgomery et al., 1994), consistent with later findings *in vivo* (Petitclerk., 1999). The latter 3D-collagen model was applied in parts of my present study.

### 2.7.2 Examples of 3D cell culture models

#### *3D reconstituted basement membrane culture*

This model was developed in Mina Bissell's lab to mimic a microenvironment for mammary cells. This model has been used to study mammary breast carcinoma morphology, polarity, growth, survival and signaling, as well as application for the study of invasive, tumorigenicity in nude mice (Weaver et al., 1995).

#### *3D cell-derived fibronectin matrix*

3D-matrix derived from culture cells that contains fibronectin has been extensively used for growing cells under quasi-physiological conditions, yet its capacity to support specific molecular types of adhesions has not been determined (Vlodavsky, 1999; Vlodavsky et al., 1982).

#### *3D-collagen gel*

This model was first described by Elsdale and Bard (Elsdale and Bard, 1972) in 1972, containing dermal collagen type I that polymerize to form a 3D-fibrous network mimicking a dermal *in vivo*

environment for cell growth, where approximately 90 % of the protein is collagen type I. In the 3D-collagen, the morphological changes of fibroblasts were partially similar to those *in vivo*. The 3D-collagen gels have also been used to study cell motility (Friedl and Brocker, 2000), melanoma cell survival (Montgomery et al., 1994) and primary melanoma explants (Hegerfeldt et al., 2002).

*Peptide Hydrogel (BD<sup>TM</sup>PuraMatrix<sup>TM</sup>)*

The Peptide Hydrogel is a newly established model based on a scaffold formed by self-assembling peptides that comprise standard amino acid (1 % w/v) and 99 % water. Under physiological conditions, the peptide component self-assembles into a 3D hydrogel that exists in a nanometer scale fibrous structure with just the right porosity to slowly distribute nutrients and other necessary biological molecules to embedded cells, resulting in a realistic 3D-microenvironment. This model has been used to study cell differentiation, attachment, proliferation, invasion, and *in vivo* analyses of tissue regeneration (Semino et al., 2004; Semino et al., 2003; Zhang et al., 1995a).

### 3 AIMS OF THE PRESENT INVESTIGATION

Integrins function as transmembrane adhesion receptors that mediate cell interactions with their surrounding ECM. Upon ligation, integrins transduce numerous signaling pathways, leading to control of various cellular functions, including cell proliferation and survival. The overall aim of the present study was to investigate the role of integrin signaling in the control of cell proliferation and survival. The specific goals for each study in this thesis were:

- I. To develop a method that specifically analyzes integrin signaling without contribution of cell spreading
- II. To elucidate mechanisms of integrin signaling in control of Cdk2-inhibitors p21<sup>CIP1</sup> and p27<sup>KIP1</sup>
- III. To clarify mechanisms of integrin  $\alpha v$ -mediated melanoma cell survival
- IV. To assess mechanisms of integrin  $\alpha v$ -mediated inactivation of tumor suppressor p53

## 4 RESULTS AND DISCUSSION

### 4.1 An immobilized anti-integrin monoclonal antibody developed to examine specific integrin signaling independent of cell spreading (paper I)

Integrin signaling-mediated responses are commonly studied by allowing cell attachment to ECM proteins coated onto a solid surface. Upon ligation, integrin signaling is transduced into the cell, but parts of the signaling responses also stem from cell spreading (Chen et al., 1997). To analyze specific integrin-mediated responses independent of cell spreading, we developed a method engaging integrin signaling by use of an immobilized mab (JBS5) directed against the fibronectin receptor integrin  $\alpha 5\beta 1$ . In this case, this antibody acts as an agonistic integrin-ligating protein and promotes integrin signaling. Using this method, we found that cells plated onto immobilized mab JBS5 did not spread, but displayed a strong reduction of the Cdk2-inhibitors  $p21^{CIP1}$  and  $p27^{KIP1}$ . Therefore, this method can be used to analyze specific integrin signaling independent of cell spreading.

### 4.2 Integrin ligation activates proteasomal degradation of the Cdk2-inhibitor $p21^{CIP1}$ (papers I and II)

The Cdk2-inhibitors  $p21^{CIP1}$  and  $p27^{KIP1}$  are negatively regulated by anchorage during cell proliferation (Fang et al., 1996; Strömblad et al., 1996; Zhu et al., 1996). To address the role of integrin signaling in the regulation of  $p21^{CIP1}$  and  $p27^{KIP1}$ , three distinct cell lines were allowed to attach to different ECM proteins, including fibronectin and vitronectin. To analyze specific responses mediated by integrin signaling independent of cell spreading, an immobilized anti-integrin mab was used as described in paper I. To exclusively analyze the effect of integrin signaling, cells were exposed in the absence of serum to avoid any contribution from growth factor signaling. Our results showed that integrin-mediated cell attachment to ECM induced rapid downregulation of  $p21^{CIP1}$  and  $p27^{KIP1}$  but not integrin-independent attachment to poly-L-lysine. Surprisingly, we found that integrin ligation could activate proteasomal proteolysis, leading to degradation of  $p21^{CIP1}$  and  $p27^{KIP1}$ . Our results revealed the first example of integrin signaling capable of controlling protein stability. Moreover, we showed that ubiquitination was not required for integrin-mediated proteasomal degradation of  $p21^{CIP1}$ . This was an unexpected finding, but several other reports have also described mechanisms of an ubiquitin-independent degradation of  $p21^{CIP1}$ . For example, direct ubiquitination of  $p21^{CIP1}$  was not necessary for its turnover by the proteasome (Sheaff et al., 2000). A recent report also supported our finding that disruption of essential components for the ubiquitination mechanism did not influence endogenous  $p21^{CIP1}$  degradation (Chen et al., 2004). Moreover,  $p21^{CIP1}$  was suggested to directly bind to the C8  $\alpha$ -subunit of the 20S proteasome complex leading to degradation of  $p21^{CIP1}$  (Touitou et al., 2001). Therefore, integrin-induced proteolysis of  $p21^{CIP1}$  may represent a physiological proteasomal pathway that is independent of ubiquitination.

### 4.3 Integrin-activated Cdc42/Rac1 signaling pathway controls proteasomal degradation of $p21^{CIP1}$ (paper II)

Integrin-activated signaling pathways, including through FAK, PI-3K and ERK1/2, are critically involved in the control of cell proliferation (Giancotti and Ruoslahti, 1999). The small GTPases Cdc42, Rac1, and Rho have been indicated to be involved in the control of cell cycle progression through the G-1 phase, including control of cyclin D1 expression (Coleman et al., 2004). However, it was unclear if Cdc42 or Rac signaling induced by integrins may affect Cdk2 inhibitors. Using a GST-PAK1 pull down assay, we showed that integrin ligation could activate a Cdc42 to Rac1 signaling pathway. Importantly, we found that integrin-activated Cdc42 to Rac signaling could activate

proteasomal degradation of p21<sup>CIP1</sup>. However, block of signaling through FAK, MEK1/ERK1/2 or PI-3K did not revert the integrin-induced down-regulation of p21<sup>CIP1</sup> (Bao and Strömblad, unpublished results). Instead, we link the integrin-mediated down-regulation of p21<sup>CIP1</sup> to signaling by the small GTPases Cdc42 and Rac. Ras signaling has been shown to stimulate p27<sup>KIP1</sup> degradation and to regulate p21<sup>CIP1</sup> expression in response to growth factors (Hirai et al., 1997; Olson et al., 1998; Takuwa et al., 1999). Our finding that integrin activation of endogenous Cdc42/Rac1 signaling induces proteasomal degradation of the Cdk2-inhibitor p21<sup>CIP1</sup> might contribute to clarify the complex function of small GTPases in cell cycle progression.

Upon integrin ligation, the mechanism involved in cdc42-mediated subsequent activation of Rac1 is unclear. PIX, a Cdc42/Rac GEF has been suggested to link Cdc42 to Rac1 activation by coupling of the cdc42 effector PAK1 (Manser et al., 1998). However, it remains to be elucidated whether these exchange factors might be involved in integrin-mediated Cdc42 to Rac1 activation.

Integrin-activated Cdc42 and Rac1 are involved in the regulation cell spreading (Clark et al., 1998; Price et al., 1998). One may suspect that Cdc42/Rac1 promotes p21<sup>CIP1</sup> degradation through affecting cell spreading, since p27<sup>KIP1</sup> degradation was shown to be regulated by cell spreading (Huang et al., 1998). However, our results showed that suppression of Cdc42 or Rac1 did not block activation of FAK or ERK1/2 signaling induced by cell attachment, indicating the existence of integrin specific signaling. In addition, our results also showed that down-regulation of p21<sup>CIP1</sup> and p27<sup>KIP1</sup> could occur in the absence of cell spreading, when cells were attached onto immobilized mab JBS5 (paper I). Thereby we concluded that an integrin-induced signaling pathway through Cdc42/Rac1 specifically causes proteasomal proteolysis of p21<sup>CIP1</sup>.

#### **4.4 Integrin $\alpha v$ promotes melanoma cell survival by inactivating p53 (paper III)**

Integrin  $\alpha v$  has been found to be critical for melanoma cell survival *in vitro* and *in vivo* models (Montgomery et al., 1994; Petitclerc, et al 1999). In this study, we examined the mechanism of integrin  $\alpha v$ -mediated melanoma cell survival by using a 3D-collagen model mimicking the pathophysiological environment of malignant melanoma growth in dermis *in vivo*. We cultured integrin  $\alpha v$ -positive M21 and M0- $\alpha v$  cells, and corresponding  $\alpha v$ -negative M21L and M0 cells in 3D-collagen. We firstly confirmed previous findings that integrin  $\alpha v$  is required for melanoma cell survival in 3D-collagen (Montgomery et al., 1994). Importantly, we found that integrin  $\alpha v$  suppressed p53 DNA-binding activity in 3D-collagen. Furthermore, we showed that suppression of p53 by dominant negative p53 or p53-siRNA obviated the need for integrin  $\alpha v$  for melanoma cell survival in 3D-collagen and for melanoma tumor growth *in vivo*. This suggests that integrin-mediated inactivation of p53 functionally controls melanoma cell survival.

In addition, we investigated whether post-translational modifications by phosphorylation and acetylation may affect p53 activity. Our results showed that p53-K382-acetylation was downregulated in integrin  $\alpha v$ -positive M21 and M0- $\alpha v$  cells, associated with decreased p53 activity upon integrin  $\alpha v$  ligation, correlating with a downregulation of p300, a cofactor for p53 acetylation. Integrin  $\alpha v$  control of p300 may therefore play a role for p53-acetylation at K382.

We also examined the p53 transcriptional downstream targets Apaf1, Bax, Bcl-2 and PUMA, all are known to be involved in apoptosis regulation. We found that PUMA levels were markedly increased in integrin  $\alpha v$ -negative M21L and M0 cells as compared to M21 and M0- $\alpha v$  cells. Our results also indicated that PUMA might be a downstream target of p53 (Jeffers et al., 2003).

It has been suggested that unligated integrin  $\alpha\beta3$  may induce epithelial cell apoptosis in 3D-collagen by recruitment and activation of caspase-8 (Stupack et al., 2001). However, we found that loss of integrin  $\alpha\upsilon$  activated caspase 9 but not caspase 8, suggesting that loss of integrin  $\alpha\upsilon$  may activate a mitochondrial apoptosis pathway since caspase 9 is essential for p53-induced apoptosis (Soengas et al., 1999).

#### **4.5 Integrin $\alpha\upsilon$ -mediated p53 inactivation controls a MEK1-dependent melanoma cell survival pathway (paper III)**

Integrin-activated Raf/MEK/ERK1/2 signaling has been implicated in the control of cell survival (Howe et al., 2002), and anchorage is required for activating melanocyte ERK1/2 signaling (Conner et al., 2003). Although most melanoma cells in regular 2D-culture display an active ERK1/2 because of activated BRAF V599E mutation (Satyamoorthy et al., 2003), our results showed that activation of MEK1/ERK1/2 signaling depended on integrin  $\alpha\upsilon$  within 3D-collagen. Importantly, this integrin-activated signaling pathway was necessary for melanoma cell survival in 3D-collagen because block of MEK1 activity by specific inhibitor induced apoptosis. These results are consistent with an *in vivo* need for integrin  $\alpha\beta3$  for sustained vascular cell ERK1/2 activation during angiogenesis (Eliceiri et al., 1998). Furthermore, integrin  $\alpha\beta3$  was shown to trigger FAK as well as PAK1-mediated c-Raf-S338 phosphorylation in angiogenic endothelial cells leading to activation of MEK1 and ERK1/2 (Hood et al., 2003). However, we found neither FAK-Y397 or c-Raf-S338 phosphorylation, nor PAK1 kinase activity to be regulated by integrin  $\alpha\upsilon$  in melanoma cells in 3D-collagen (Bao et al, unpublished observations). However, surprisingly, we found that p53 acted upstream of MEK1 signaling and functionally controlled MEK1-mediated melanoma cell survival, since stable transfection with dnp53-His175 or p53-siRNA rescued integrin  $\alpha\upsilon$ -negative M21L cell MEK1 and ERK1/2 activities in 3D-collagen.

#### **4.6 Integrin $\alpha\upsilon$ induces an unfolded, inactive wt p53 conformation in melanoma cells (paper IV)**

p53 mutations cause unfolded conformation leading to inactivation of p53 (Cook and Milner, 1990; Gannon et al., 1990). However, no published study has addressed if wt p53 may adopt an unfolded conformation that could cause p53 inactivation in melanoma cells. To investigate how integrin  $\alpha\upsilon$  mediates p53 inactivation, we therefore analyzed wt p53 conformation in three distinct melanoma cell lines cultured in 3D-collagen by ELISA using the conformation-specific monoclonal antibodies (mab) PAb1620 and PAb240 to detect folded (active) and unfolded (inactive) conformations, respectively (Bykov et al., 2002). Firstly, we found that 3D-collagen could confer an inactive, unfolded wt p53 conformation (240 epitope) in all three melanoma cell lines. To examine the potential role of integrin  $\alpha\upsilon$  in the modulation of wt p53 conformation, we compared p53 conformation in  $\alpha\upsilon$ -positive M21 cells and a M21 subpopulation, M21L cells, that lacks integrin  $\alpha\upsilon$ . Surprisingly, we found that integrin  $\alpha\upsilon$  could enforce wt p53 into an inactive conformation within 3D-collagen. Importantly, the p53 conformation state was consistent with p53 activation and function, since integrin  $\alpha\upsilon$ -positive M21 cells that displayed an inactive conformation and also had low p53 activity and survived within 3D-collagen, whereas  $\alpha\upsilon$ -negative M21L cells that displayed an active conformation also displayed high p53 activity and p53-dependent apoptosis described in paper III. Therefore, our results suggest that the regulation of wt p53 conformation is critical for the integrin  $\alpha\upsilon$  control of melanoma cell survival in a 3D-environment. These results for the first time demonstrate a controlled wt p53 conformational regulation *in lieu* of p53 mutations in tumor cells, which may contribute to explain the lack of need for p53 mutations in malignant melanoma.

#### **4.7 PRIMA-1<sup>MET</sup> reactivates wt p53 conformation and its apoptotic function in melanoma cells** (paper IV)

PRIMA-1<sup>MET</sup>, an analogue of PRIMA-1 with increased activity, can revert an inactive, unfolded conformation of mutant p53 protein to an active, folded form (Bykov et al., 2002; Bykov et al., 2005). Our results suggested that PRIMA-1<sup>MET</sup> could also switch an unfolded, inactive wt p53 conformation to a folded, active form in three distinct melanoma cell lines within 3D-collagen. To examine if PRIMA-1<sup>MET</sup> could also activate melanoma cell apoptosis in a p53-dependent manner, the p53 protein was knocked-down by stably transfecting p53-siRNA (Brummelkamp et al., 2002) in M21 cells. We showed that PRIMA-1 activated melanoma cell apoptosis in a wt p53-dependent manner, which supports a role for regulation of wt p53 conformation in the control of melanoma cell survival.

We also investigated PRIMA-1<sup>MET</sup>-triggered apoptosis mechanisms by examining apoptotic proteins Apaf1 and PUMA levels in M21 and p53 knocked-down M21-p53siRNA cells. We indicated that PRIMA-1<sup>MET</sup> could induce a p53-dependent induction of transcriptional target PUMA, and that PUMA could be acting downstream of p53 in activation of apoptosis. Given that p53 can induce apoptosis by a direct localization to mitochondria (Mihara et al., 2003), that PRIMA-1 activated mutant p53 and elicited bax-dependent apoptosis in a transcriptional-independent manner (Chipuk et al., 2003), and that PRIMA-1 promoted mutant p53 translocation to the cytoplasm (Bykov et al., 2002), PRIMA-1<sup>MET</sup> may induce transcriptional-independent apoptosis in melanoma cells.

In addition, we found caspase 9 to be functionally involved in PRIMA-1<sup>MET</sup>-induced apoptosis. This indicates that PRIMA-1<sup>MET</sup> may activate a p53-dependent, mitochondrial apoptotic pathway.

#### **4.8 PRIMA-1<sup>MET</sup> suppresses melanoma xenograft tumor growth in mice in a wt p53-dependent manner** (paper IV)

Based on the fact that PRIMA-1<sup>MET</sup> could trigger melanoma cell apoptosis in 3D-collagen, we tested the effects of PRIMA-1<sup>MET</sup> on melanoma tumor growth *in vivo*. We found that PRIMA-1<sup>MET</sup> treatment suppressed M21 tumor growth carrying wt p53, but did not inhibit tumor growth of C8161 cells carrying a defective p53-truncation. This may suggest that PRIMA-1<sup>MET</sup> suppresses melanoma tumor growth depending on a functional p53. In addition, PRIMA-1<sup>MET</sup> also rendered no effect on tumor growth of M21-p53siRNA cells, strongly indicating that PRIMA-1<sup>MET</sup> suppression of melanoma tumor growth is dependent of wt p53.

We also found that an intermittent regimen treatment of PRIMA-1<sup>MET</sup> markedly inhibited FM88 melanoma tumor growth, indicating that PRIMA-1<sup>MET</sup> efficiently inhibits melanoma tumor growth of two distinct origins. However, surprisingly, continuous treatment (everyday) with PRIMA-1<sup>MET</sup>, was less efficient, for both FM88 and M21 cells (data not shown). This indicates that optimization of PRIMA-1<sup>MET</sup> dosing and regimen is an important issue. Nevertheless, our results clearly demonstrate proof of principle for efficacy of a wt p53-targeting compound inhibiting melanoma tumor growth.

#### **4.9 The 3D-collagen gel model for studying integrin signaling-mediated melanoma cell survival** (papers III and IV)

Using a three-dimensional collagen model mimicking a pathophysiological environment of melanoma growth in the dermis *in vivo*, we investigated regulatory mechanisms for integrin  $\alpha$ v-mediated melanoma cell survival. We found that wt p53 conformation, activity and apoptotic function were regulated by integrin  $\alpha$ v only within 3D-collagen. Moreover, integrin-activated MEK1/ERK1/2

signaling was only observed in 3D as well as the control of MEK1 signaling by integrin  $\alpha_v$ -mediated p53 regulation. Furthermore, regulation of wt p53 conformation and function by PRIMA-1<sup>MET</sup> was observed only in the 3D-collagen environment. Importantly, our results from the 3D-collagen environment were similar to our results on melanoma tumor growth *in vivo*: (1) Suppression of p53 activity rescued tumor growth of  $\alpha_v$ -integrin negative melanoma cells that otherwise did not grow. (2) PRIMA-1<sup>MET</sup> induced melanoma cell apoptotic death in 3D-collagen and also markedly suppressed melanoma xenograft tumor growth in mice. In fact, several studies have demonstrated that integrin-mediated cell-matrix interactions trigger different signaling and cellular behavior in 3D-environment as compared with regular 2D-culture conditions (Cukierman et al., 2002; Jacks and Weinberg, 2002). Our results reveal another example how important a 3D-environment can be for studying integrin-mediated cellular responses since we would not have been able to find any of the presented mechanisms if the studies had been performed under 2D-conditions. Notably, the application of 3D-culture models to study integrin function may more closely reflect the situations in living organisms.

## 5 CONCLUDING REMARKS

The present investigation reveals several new effects of integrin signaling in the control of cell proliferation and survival.

In response to interaction with the ECM, we found that integrins control the key cell cycle regulators p21<sup>CIP1</sup> and p27<sup>KIP1</sup> by activating a proteasomal proteolysis mechanism. This for the first time reveals that integrins are capable of controlling protein stability. An integrin-activated signaling pathway involving cdc42 and Rac1 is critically involved in the control of this proteasomal degradation of p21<sup>CIP1</sup>. A hypothetical model for integrin regulation of proteasomal proteolysis of p21<sup>CIP1</sup> is presented in Figure 6. Integrin-mediated proteasomal proteolysis might contribute to anchorage-dependent cell cycle control.

For the roles of integrins in control of melanoma cell survival, integrin  $\alpha v$  displays a similar mechanism as it acts in angiogenesis, where integrin  $\alpha v$  is capable of suppressing tumor suppressor p53 activity (Brooks et al., 1994; Eliceiri et al., 1998; Strömblad et al., 1996; Strömblad et al., 2002). Furthermore, integrin  $\alpha v$  inactivated p53 by inducing an unfolded wt p53 conformation and promoted MEK1 signaling, demonstrating the first example of a cell adhesion receptor that can control a conformational regulation of a tumor suppressor p53 in tumor cells *in lieu* of mutations. Through reactivating wt p53 conformation, the small organic compound PRIMA-1<sup>MET</sup> induced a marked p53 apoptotic function and suppressed melanoma xenograft tumor growth. This may provide a novel approach to the urgently needed development of melanoma therapy. Figure 7 illustrates a hypothetical model for the mechanism involved in integrin- $\alpha v$ -mediated melanoma cell survival.

Future studies would be necessary to pinpoint the remaining underlying molecular mechanisms that were not elucidated in the present study. For example, it would be interesting to address the signaling upstream of the small GTPases Cdc42 and Rac1 upon integrin ligation, and to address how small GTPases leads to proteasome degradation of p21<sup>CIP1</sup> through identifying more of the pathways involved. It would also be of exceptional interest to clarify how integrin  $\alpha v$  regulates wt p53 conformation in terms of investigating molecules or cofactors involved in this conformational regulation of wt p53, which act downstream of integrins  $\alpha v$ . Another future development that has already been initiated is to further develop new strategy for treatment of malignant melanoma, which could be useful in clinical trials in the future.

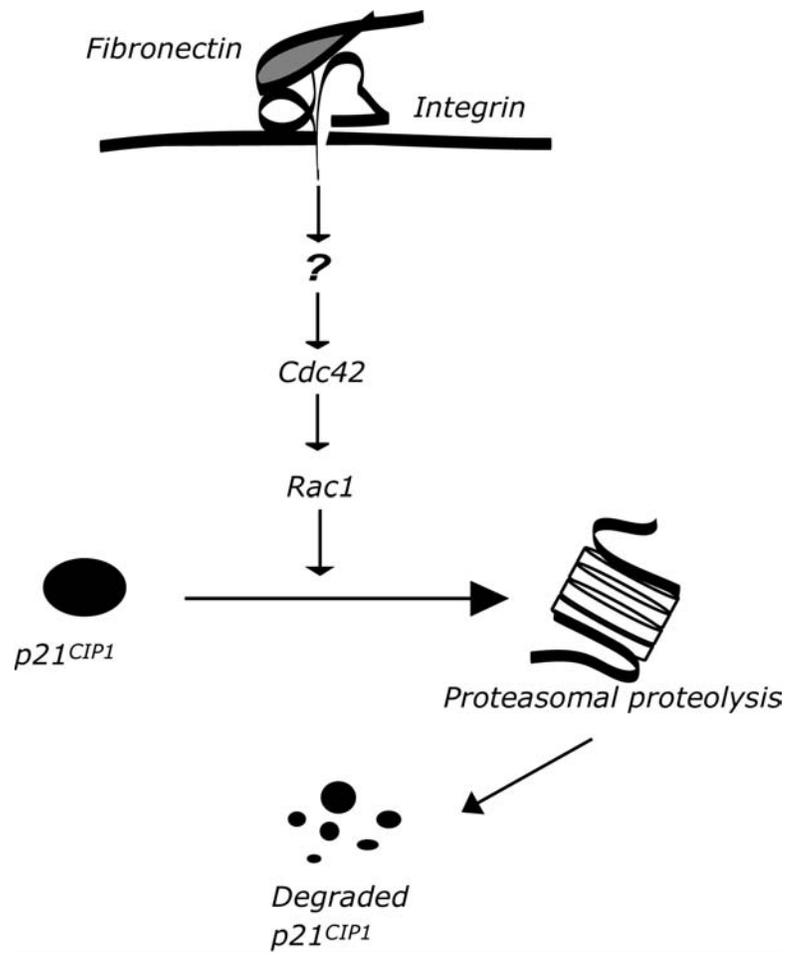


Figure 6 A hypothetical model for integrin regulation of proteasomal degradation of Cdk2-inhibitor p21<sup>CIP1</sup> through activating a Cdc42 to Rac1 signaling pathway. Integrin ligation to fibronectin leads to activation of a Cdc42 to Rac1 signaling pathway that promotes proteasomal proteolysis of p21<sup>CIP1</sup>.

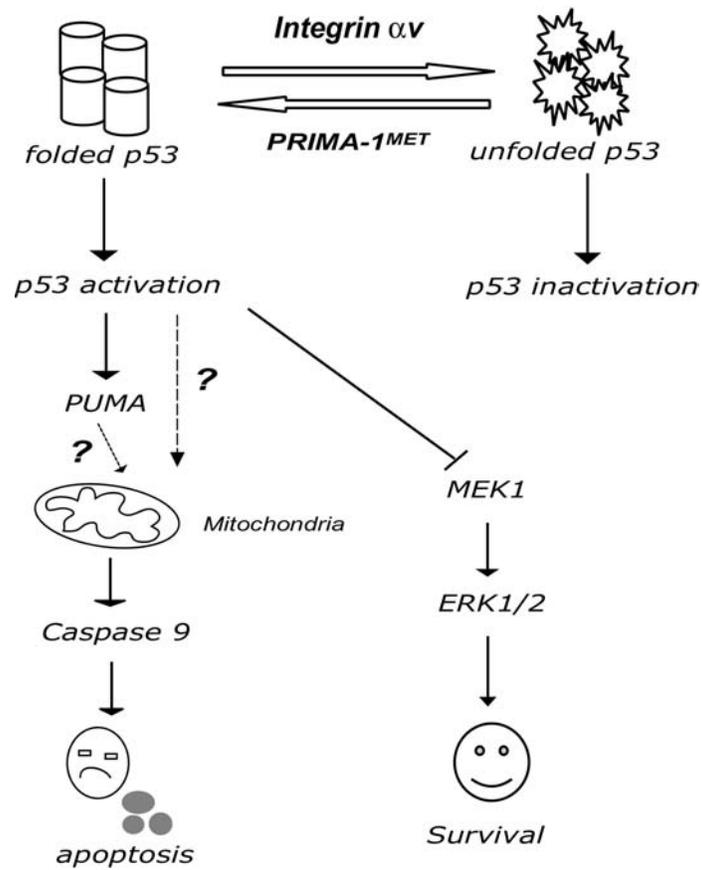


Figure 7 A hypothetical model for how integrin  $\alpha v$  may control melanoma cell survival. Expression of integrin  $\alpha v$  promotes p53 inactivation in 3D environment by inducing an unfolded p53 conformation. Lack of integrin  $\alpha v$  leads to upregulation of apoptotic protein PUMA, and enhancement of cleaved caspase 9, suggesting a mitochondrial apoptotic pathway. Lack of integrin  $\alpha v$  also leads to p53-dependent inhibition of a MEK1-ERK1/2-mediated melanoma cell survival pathway. PRIMA-1<sup>MET</sup> switches an unfolded p53 conformation to a folded form, leading to activation of p53 and melanoma cell apoptosis.

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