

# MINIREVIEW

## The Regulation of Expression of Integrin Receptors (44078)

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**Abstract.** The integrins are a family of cell surface receptors that mediate cell-extracellular matrix and cell-cell interactions. The quantities and activities of these receptors are modulated during a wide variety of biological processes. A variety of agents have been found to affect expression of integrins and their function. These include cytokines, hormones, and pharmacologic agents. Mechanisms regulating integrin expression and function include regulation of protein levels by transcriptional or posttranscriptional mechanisms, alteration of protein structure by alternative splicing of mRNA, mobilization to the cell surface of preexisting intracellular stores of integrins, and modulation of receptor activity (inside-out signaling). We review studies that assess the effects of external agents on integrin levels using the cytokine TGF $\beta$  as an example. We also review studies that analyze integrin regulation with an emphasis on the control of integrin gene transcription. This review shows that the strategies for integrin modulation are quite complex. This regulatory sophistication is likely necessary, given the critical role that integrins play in the myriad social interactions of cells.

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Integrins are a family of cell surface receptors which mediate cell-extracellular matrix and cell-cell adhesion. They are heterodimers made up of one larger  $\alpha$  and one smaller  $\beta$  subunit (for a review see Ref. 1). They are generally grouped into families based on the  $\beta$  subunit. One  $\beta$  subunit can generally bind one of several different  $\alpha$  subunits to yield a unique receptor. However the  $\alpha_v$  subunit is unique. It is able to bind one of several different  $\beta$  subunits, so it is often considered as defining its own family. Since the initial characterization of the integrin family in the late 1980s, there have been numerous reports of integrin modulation during such processes as development, wound healing, inflammation, thrombosis, tumorigenesis, and metastasis. The mechanisms of regulation have also been investi-

gated, yielding insights into their complexity. This review is intended to summarize and synthesize the results of these studies. We will first discuss, using transforming growth factor- $\beta$  (TGF $\beta$ ) as an example, mediators that can signal a cell to up- or downregulate integrin receptors. We will then discuss the mechanisms by which a cell can control the presence of an active integrin molecule on its surface. These mechanisms can be broadly characterized as (i) regulation of protein levels by transcriptional or posttranscriptional mechanisms, (ii) alternative splicing of mRNA, (iii) mobilization of preexisting intracellular stores, and (iv) conformational control (inside-out signaling).

### Mediators That Regulate Integrin Levels

Many studies have examined the effects of signaling molecules, drugs, or other agents on integrin levels. Changes at the protein level are most commonly shown by FACS analysis, immunoprecipitation, or immunostaining. Parallel changes are also commonly shown at the mRNA level. In this section, we will review in detail the effects of

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TGF $\beta$  on integrins. We will then briefly cover other agents that can mediate changes in integrins.

**TGF $\beta$ .** A number of peptide growth factors have been shown to regulate integrin levels. The best studied of these regulatory molecules are members of the transforming growth factor- $\beta$  family, referred to here collectively as TGF $\beta$ . Even as the first studies demonstrating the structure of integrins were being completed, the effects of TGF $\beta$  on integrins were being investigated (2). TGF $\beta$  increases  $\beta_1$  integrin expression on several cell types at both the protein and mRNA level (2–7). In some cases, however, increases of  $\beta_1$  integrin dimers occur not due to increased synthesis of  $\beta_1$  but due to increases of its  $\alpha$  subunit partner (3, 8) or to faster maturation of the  $\beta_1$  subunit (2). In these cases, it has been suggested that the  $\beta$  subunits are normally expressed in excess and that stimulation by TGF $\beta$  increases assembly with the limiting  $\alpha$  partner. Indeed, Jaspers *et al.* showed that overexpressing  $\alpha_4$  by transfection with  $\alpha_4$  cDNA increased the rate of maturation of the  $\beta_1$  integrin precursor as well as the quantity of  $\beta_1$  integrins on the cell surface (9). Other examples of integrins that are increased by TGF $\beta$  stimulation include  $\alpha_1$  (10),  $\alpha_2$  (6–8, 11),  $\alpha_3$  (7, 8),  $\alpha_5$  (5, 6, 8, 12),  $\alpha_v$  (12),  $\beta_3$  (13),  $\beta_5$  (6, 12), and  $\beta_6$  (6). In many cases TGF $\beta$  is found only to increase the expression of integrins that are already present on cells. In other cases, TGF $\beta$  is found to initiate synthesis of a particular integrin. For example Janat *et al.* (13) reported *de novo* synthesis of  $\beta_3$  upon stimulation with TGF $\beta$ 1 in rabbit vascular smooth muscle cells. Likewise, Zambruno *et al.* (6) reported *de novo* expression of  $\beta_6$  mRNA in keratinocytes upon stimulation with TGF $\beta$ 1. Many of the effects of TGF $\beta$  are cell-type specific. For example,  $\alpha_3$  is increased on guinea pig airway epithelial cells after stimulation with TGF $\beta$ 1 (8) but is decreased on keratinocytes (6). Additionally  $\alpha_5$  is increased on several cells by TGF $\beta$ 1 but decreased on *ras*-transformed hepatocytes (10). TGF $\beta$  can also inhibit the activity of other cytokines which may increase a particular integrin. Rinaldi *et al.* showed that, in synovial cells, the increase in  $\alpha_3$  induced by  $\gamma$ -interferon (IFN- $\gamma$ ) can be inhibited by TGF $\beta$  (14). Although most of these studies used exogenously added TGF $\beta$ , at least one example has been offered of autocrine TGF $\beta$  inducing integrin expression (5).

It is apparent from these studies that the control of integrin expression by TGF $\beta$  is complex. Given that TGF $\beta$  has been shown to induce extracellular matrix molecules themselves, a recurring theme appears to be that TGF $\beta$  induces an increase in extracellular matrix and enhances the ability of the cells to respond to this increase. However, the above examples of cell-type specificity and varying mechanisms of regulation, such as increases in mRNA, changes in assembly of dimers, and cooperative effects with other cytokines, indicates a complex system which may be influenced by numerous factors.

**Other Growth Factors and Cytokines.** A number of other growth factors can regulate integrin levels. Most of these have not yet been sufficiently studied to compare ef-

fects on different cell types or on many different integrin subunits. These growth factors include PDGF-AB (15); PDGF-BB (16); EGF (17); NGF (18); acidic FGF (18); basic FGF (7); IL-4 (19); IL-1 $\beta$  (14, 20–22); IL-6 (23);  $\beta$  family chemokines (MCP-1, MIP-1 $\alpha$ , RANTES) (24); tumor necrosis factor- $\alpha$  (TNF- $\alpha$ ) (14, 25, 26); TNF- $\beta$  (27); IFN- $\gamma$  (14, 26); M-CSF (28, 29); and GM-CSF (29). Several signaling molecules and hormones such as retinoic acid (30, 31), 1,25-dihydroxyvitamin D $_3$  (32), and corticosterone (33, 34) have also been shown to have effects.

**Pharmacologic Agents.** Several pharmacologic agents have the ability to regulate integrin levels. This is often in the context of interruption of a known signaling pathway, or in the pharmacologic induction of differentiation. Examples include phorbol esters (25, 35–39), the tyrosine kinase inhibitor genistein (40), forskolin (which increases cAMP levels) (41), gossypol (a biphenolic compound from the *Portia* tree which has been used as an anti-inflammatory and anti-tumor agent) (42), thalidomide (43), and dexamethasone (18).

**Mechanical Factors.** Mechanical stress can also alter integrin levels. Carvalho *et al.* showed that mechanical strain on human osteosarcoma cells can increase  $\beta_1$  integrin mRNA and cause changes in protein distribution (44). Somewhat paradoxically, stress deprivation of rabbit anterior cruciate ligaments increased staining for  $\beta_1$  integrin (45).

**Infectious Agents.** Infectious agents which have so far been found to have an effect on integrin levels include *Pneumocystis carinii* (46), HIV (47, 48), and cytomegalovirus (49).

Table I summarizes mediators found to regulate integrin levels.

## Control of Gene Expression

A long-term modulation of integrin functions can occur with changes in integrin protein levels. This can be controlled by modulation of gene transcription, or by posttranscriptional mechanisms. Studies of regulatory regions of integrin genes have begun to unravel the complex control mechanisms that regulate integrin gene transcription. A number of integrin promoter regions have been characterized, including  $\alpha_2$  (50),  $\alpha_4$  (51–53),  $\alpha_5$  (54),  $\alpha_L$  (CD11a) (55),  $\alpha_M$  (CD11b) (56–59),  $\alpha_X$  (CD11c) (60),  $\alpha_v$  (61),  $\alpha_{IIB}$  (62),  $\beta_1$  (63),  $\beta_2$  (CD18) (64, 65),  $\beta_3$  (66), avian  $\beta_3$  (67), and mouse  $\beta_7$  (68) (Table II). All of these promoters lack both TATA and CAAT boxes except  $\alpha_{IIB}$ , which contains a CAAT box (69), and  $\alpha_4$  which contains both TATA and CAAT boxes.

**Sp1.** All of the characterized promoters except  $\alpha_4$  and mouse  $\beta_7$  have been shown to contain Sp1-binding sites. In most eukaryotic promoters the TATA box binds the complex TFIID, which plays a central role in the initiation of mRNA synthesis. Sp1 has been suggested to serve to anchor TFIID in the absence of TATA boxes (70). Chen *et al.* (59) showed that in the case of  $\alpha_M$  (CD11b), Sp1 binding at one

**Table I. Reported Integrin Regulatory Molecules**

Integrin	Mediator	Cell type	How shown	References	
$\alpha_1$	IL-1 $\beta$ , TNF- $\alpha$ , IFN- $\gamma$	Synovial cells	Staining, FACS	14	
	NGF, aFGF, dexamethasone (decreases)	PC 12 pheochromocytoma	Northern, I.P.	18	
$\alpha_2$	TGF $\beta$	<i>ras</i> -transformed hepatocytes	I.P., Northern	10	
	Retinoic acid, PMA, TNF- $\alpha$	Endothelial cells	I.P.	25	
	PDGF ab	Normal fibroblasts	I.P.	15	
	PDGF bb	Normal fibroblasts	Northern	16	
	EGF	Squamous cell carcinoma	I.P., ELISA	17	
	IL-1 $\beta$	MG-63 osteosarcoma	RT-PCR	22	
	TGF $\beta$	Endothelial cells, colon carcinoma	I.P., Northern	7, 11	
$\alpha_3$	bFGF	Endothelial cells	I.P., Northern	7	
	PMA	K562 leukemic cells	Northern, FACS, nuclear run-on	37, 114	
$\alpha_4$	PDGF ab	Normal fibroblasts	I.P.	15	
$\alpha_4$	M-CSF	Macrophages	I.P.	28	
	PMA (decreases)	Myeloid cell lines U937 and HL60	FACS, Northern, nuclear run-on (transcription constant)	35, 38	
$\alpha_5$	PDGF ab	Normal fibroblasts	I.P.	15	
	IL-1 $\beta$	Synovial cells, osteosarcoma lines	RT-PCR	14, 20–22	
	IL-6	Corneal epithelium	RT-PCR	23	
	TGF $\beta$	Colon carcinoma, keratinocytes, endothelial cells	RNAse protection, I.P., Northern	5–7	
	bFGF	Endothelial cells	I.P.	7	
	M-CSF	Macrophages	I.P.	28	
	PMA	Myeloid cell lines U937 and HL60	FACS, Northern	35, 38	
	$\alpha_v$	Retinoic acid	Melanoma	Northern	30
		1 $\alpha$ ,25-Dihydroxyvitamin D <sub>3</sub>	Osteoclasts	Northern, nuclear run-on	32
		IL-4	Bone marrow macrophages	Northern	19
TGF $\beta$		Keratinocytes	Northern	6	
$\alpha_L$	Polyunsaturated fatty acids	Neutrophils	FACS	115	
	PMA	Myeloid cell lines U937 and HL60	Northern, nuclear run-on	35	
$\alpha_M$	$\beta$ family chemokines (MCP-1, MIP-1 $\alpha$ , RANTES)	Monocytes	FACS	24	
	PMA	Myeloid cell lines U937 and HL60	Northern, nuclear run-on	35	
$\alpha_X$	$\beta$ family chemokines (MCP-1, MIP-1 $\alpha$ , RANTES)	Monocytes	FACS	24	
	PMA	Myeloid cell lines U937 and HL60	FACS, Northern, nuclear run-on	35, 36	
$\alpha_{IIb}$	PMA	K562 leukemic cells	Northern, FACS, nuclear run-on	37, 114	
$\beta_1$	PDGF ab	Normal fibroblasts	I.P.	15	
	IL-6	Corneal epithelium	RT-PCR	23	
	TGF $\beta$	Endothelial cells	I.P., Northern	7	
	Retinoic acid	Teratocarcinoma	I.P.	31	
	Corticosterone	Osteoblasts, bone	I.P., Northern, staining	33, 34	
$\beta_2$	Genistein	Myelomonocytic cells THP-1 and HL60	FACS	40	
	PMA	Myeloid cells HL60	Northern, nuclear run-on (no change in transcription)	35, 36	
	Gossypol	Neutrophils	FACS	42	
$\beta_3$	Thalidomide (decreases)	Neutrophils	FACS	43	
	bFGF	Endothelial cells	I.P.	7	
	GM-CSF	Macrophages	I.P., Northern	29	
	PMA	K562 leukemic cells	Northern, FACS, nuclear run-on	114	
	TNF- $\alpha$ , IFN- $\gamma$ (decreases)	Endothelial cells	FACS, Northern	26	
$\beta_4$	Forskolin	Schwann cells	Northern	41	
$\beta_5$	M-CSF	Macrophages	I.P., Northern	29	
$\beta_6$	TGF $\beta$	Keratinocytes	Northern	6	
$\beta_7$	PMA	Myeloid cell lines U937 and HL60	Northern, nuclear run-on	35	
	TNF $\beta$	Lymphocytes	FACS	27	

*Note.* Many of the reported effects are complex and may be related to the individual experimental conditions reported. The reader is cautioned to refer to individual references for details. All mediators increase the integrin except where noted. I.P., immunoprecipitation; RT-PCR, reverse transcriptase–polymerase chain reaction; ELISA, enzyme-linked immunosorbent assay.

**Table II.** Reported Integrin Promoter Regions and Putative Consensus Binding Sites

Subunit	Promoter characterized?	Consensus sequences in promoter
$\alpha_1$	No	
$\alpha_2$	Yes (50)	Sp1, Ap-1, AP-2, GATA, PU.1, possible estrogen receptor-binding site
$\alpha_3$	No	
$\alpha_4$	Yes (51–53)	TATA, CAAT, Sp1, AP-1, AP-2, PU, MyoD, ets
$\alpha_5$	Yes (54)	Sp1, AP-1, AP-2, ets
$\alpha_6$	No	
$\alpha_v$	Yes (61)	Sp1, ets, GATA
$\alpha_L$ (CD11a)	Yes (55)	Sp1, oct, PU
$\alpha_M$ (CD11b)	Yes (56–59)	Sp1, AP-2, PU, ets, RAR
$\alpha_X$ (CD11c)	Yes (60)	Sp1, AP-1, AP-2, PU, <i>c-myc</i> , NF $\kappa$ B, oct, hept, RA
$\alpha_{IIb}$	Yes (human and mouse) (62, 69, 71, 116–118)	CAAT, Sp1, CP-2, GATA, ets
$\beta_1$	Yes (63)	Two independent promoters. Sp1, NF-1, AP-1, oct
$\beta_2$ (CD18)	Yes (64, 65)	SP1, RAR, ets
$\beta_3$	Yes (66)	Sp1, PU, two putative megakaryocytic elements
$\beta_4$	No	
$\beta_5$	No	
$\beta_6$	No	
$\beta_7$	Yes (mouse) (68)	AP-2, myeloid motifs, PU, E (myoD), ets, NF-AT, GATA-3, HMG, RAR

of the Sp1-binding sites was necessary for promoter activity. Additionally this factor was found to bind only in U937 myeloid cells which express  $\alpha_M$ , but not in HeLa cells, which do not express this integrin subunit. These authors proposed that binding of the transcription factor PU.1, which is myeloid specific, allows binding of Sp1, which then results in transcription.

**Ets.** Another putative transcription factor-binding site which is common to multiple integrin promoters is that of the ets family of transcription factors. Ets consensus binding sites have been described in the promoters of  $\alpha_{IIb}$  (71),  $\alpha_v$  (61),  $\alpha_4$  (52),  $\alpha_5$  (54),  $\alpha_M$  (56), and  $\beta_2$  (65). These sequences have been shown to be important in control of transcription of integrins. Rosen *et al.* carried out a detailed analysis of the  $\alpha_4$  promoter (52). There is a short sequence –42 to –76 bp from the transcription start site that is necessary for transcription in Jurkat cells which express  $\alpha_4$ . This sequence showed no activity in HeLa cells which do not express  $\alpha_4$ . This sequence contains three ets-binding sequences. Gel retardation assays showed two complexes: one, which showed slower electrophoretic mobility, was found only in Jurkat cells, while a faster migrating complex was found in both Jurkat and HeLa cells. The faster moving

complex contained the ets family proteins GABP $\alpha$  and GABP $\beta$ . Using a panel of antibodies, the authors found evidence to suggest that the additional protein in the slower band was an ets-related protein but was not Ets-1, Ets-2, PU.1, or GABP $\alpha$ . The two downstream sites were sufficient to bind ets proteins, while the upstream site alone was not. However, the presence of the upstream site was required for the full, slower-moving complex to form. Deletion of this 5' site also caused formation of another complex which was shown to contain Ets-1. In summary, the ets site farthest downstream is sufficient to bind GABP $\alpha$ /GABP $\beta$  and does have some promoter activity. Including the adjacent upstream site causes binding of Ets-1, which causes more efficient transcription. If the third ets site, farther upstream is included, Ets-1 does not bind, an unidentified ets protein does bind, and transcription is further stimulated.

Ets recognition sequences have also been implicated in the activity of the  $\beta_2$  (CD18) promoter. Böttinger *et al.* used deletion analysis to find a short sequence from –81 to –35 that showed promoter activity (65). DNA footprint analysis showed that this region had two protected segments, suggesting binding of at least two transcription factors. Both segments contained ets-binding sequences, with the upstream sequence being inverted. This short promoter sequence was sufficient for tissue-specific expression and phorbol ester inducibility. The authors noted two strong bands on gel-shift assays. One complex is likely GABP $\alpha$ /GABP $\beta$  based on immunologic data and binds both ets regions. The other complex forms only in myeloid cells and also binds to both regions. This second transcription factor is ets related but otherwise yet unknown. The upstream segment binds GABP $\alpha$ /GABP $\beta$  more strongly, while the downstream segment binds the myeloid-specific factors more strongly.

Tissue-specific gene transcription was also attributed to presence of an ets-binding sequence in the promoter of the megakaryocyte/platelet integrin  $\alpha_{IIb}$  gene (71). These authors showed that megakaryocyte-specific  $\alpha_{IIb}$  expression was due to a cooperative interaction between GATA-1 (an erythroid and megakaryocyte specific transcription factor) and Ets-1. Transfection of a –75-bp promoter fragment into megakaryocytic cells resulted in reporter activity. The same construct had no activity in HeLa cells. However, if HeLa cells were co-transfected with plasmids expressing Ets-1 or GATA-1, activity of the promoter was restored. This effect was additive when both Ets-1 and GATA-1 were included.

In summary, putative Ets binding sites have been found in a number of integrin promoters. In the cases of  $\alpha_4$ ,  $\alpha_{IIb}$ , and  $\beta_2$ , these sites have further been shown to be functional in transcriptional regulation. For  $\alpha_{IIb}$ , the ets site was found to be important in controlling tissue-specific expression of the gene product.

**PU.1.** Another member of the ets family which has tissue-specific activity is the lymphoid and myeloid-specific transcription factor PU.1. It is found primarily in macrophages and B cells (72). Its binding sequence has been noted

in the promoters of  $\alpha_L$  (55),  $\alpha_M$  (56),  $\alpha_X$  (60),  $\alpha_2$  (50),  $\alpha_4$  (51),  $\beta_3$  (66), and mouse  $\beta_7$  (68) genes. Pahl *et al.* studied the role of PU.1 in transcriptional control of  $\alpha_M$  (CD11b) in myeloid versus non-myeloid cells (58). They showed that a PU.1 site at -20 bp relative to the transcriptional start site is functional and necessary for promoter activity. Another consensus PU.1 site at -130 does not bind PU.1. The active PU.1 site appears to be responsible for much of the tissue-specific activity. However, it cannot be solely responsible, since PU.1 is also expressed in B cells though  $\alpha_M$  is not.

**Other Consensus Sites.** A number of other consensus sequences for DNA-binding proteins have been identified in integrin promoters. Many of these putative sites have not yet been tested directly for activity in controlling integrin expression. However, there are intriguing possibilities. AP-1 sites are known to mediate transcriptional stimulation by phorbol esters (73) and by TGF $\beta$  (74). The promoter regions of  $\alpha_2$  (50),  $\alpha_4$  (51),  $\alpha_5$  (54),  $\alpha_X$  (60), and  $\beta_1$  (63) have consensus AP-1 sites. Expression of most of these genes have been shown to be responsive to one or both of these molecules. The responses however, are complex. For example, although  $\alpha_4$  and  $\alpha_5$  both contain AP-1 sites, phorbol ester-induced differentiation of U937 promonocytic cells causes an increase in  $\alpha_5\beta_1$  and a decrease in  $\alpha_4\beta_1$  (35, 38), though the decrease in  $\alpha_4$  may be due to posttranscriptional mechanisms (35). T cells (75) or MG-63 osteosarcoma cells (39) also showed no change or a decrease in  $\alpha_4$  in response to phorbol ester treatment. Although the  $\beta_1$  promoter has several elements which could be responsive to TGF $\beta$  stimulation, when Cervella *et al.* transfected reporter constructs into MG-63 osteosarcoma cells the constructs showed no responsiveness to TGF $\beta$  (63).

Several integrin promoters have retinoic acid response elements.  $\alpha_M$  (CD11b) (56),  $\alpha_X$  (CD11c) (60),  $\beta_2$  (CD18) (64), and mouse  $\beta_7$  (68) have all been noted to contain these sites.  $\alpha_M$  (CD11b) has been shown to be responsive to retinoic acid in the HL-60 myeloid cell line. However, the  $\alpha_M$  promoter also contains an AP-2-binding site. AP-2 can itself be stimulated by retinoic acid (76). In addition,  $\alpha_V$  and  $\beta_1$ , which have not been noted to have retinoic acid response elements in their promoters, are in fact increased by retinoic acid (30, 31, 77). Neither  $\alpha_V$  nor  $\beta_1$  have AP-2 consensus sites. Clearly, the effects are complex, and responsiveness to retinoic acid cannot be predicted simply on the presence or absence of a putative binding site.

### Alternative Splicing

Another mechanism by which cells can regulate integrin function is by alternative splicing. Alternative splicing has been found in several integrins including  $\alpha_3$  (78),  $\alpha_6$  (78-81), mouse  $\alpha_6$  (82),  $\alpha_7$  (83, 84),  $\alpha_{1B}$  (85), drosophila PS2 $\alpha$  (86),  $\beta_1$  (87-92),  $\beta_3$  (93, 94), human  $\beta_4$  (95, 96), and mouse  $\beta_4$  (97). Changes in splicing have been noted during development (82, 83) and tumorigenesis (98). Alternative splicing has also been noted to be tissue specific (78, 87, 88, 99, 100). Functional differences in alternatively spliced

forms have been investigated. Niessen *et al.* found no change in ligand specificity with different isoforms of  $\alpha_6$  (101). Delwel *et al.* showed that PMA stimulation of  $\alpha_{6A}$  or  $\alpha_{6B}$  transfected cells resulted in better adhesion in  $\alpha_{6B}$  transfectants than in  $\alpha_{6A}$  transfectants, though PMA-induced phosphorylation of the  $\alpha$  subunit was much stronger in  $\alpha_{6A}$  variants (102). Hogervorst *et al.* showed that PMA-induced phosphorylation of  $\alpha_{6A}$  resulted in decreased adhesion to laminin (103). Balzac *et al.* investigated the function of the  $\beta_{1B}$  isoform. Using an antibody against the unique peptide region, they were able to demonstrate tissue specific expression. They found no difference in the ability of  $\beta_{1A}$  and  $\beta_{1B}$  isoforms to bind ligand, but they did show that, while  $\beta_{1A}$  was localized to focal adhesion,  $\beta_{1B}$  was not (104). In follow-up studies, Balzac *et al.* transfected the  $\beta_{1B}$  isoform into CHO cells. They found that this subunit was not capable of inducing tyrosine phosphorylation as was the endogenous or transfected human  $\beta_{1A}$ . Transfection of the  $\beta_{1B}$  subunit resulted in reduced adhesion and migration suggesting a dominant-negative effect (89). Fornaro *et al.* showed that cells expressing the  $\beta_{1C}$  variant showed less ability to proliferate in response to serum stimulation (105). Meredith *et al.* showed that when this  $\beta_{1C}$  subunit was transfected into mouse fibroblasts, it inhibited cell cycle progression in late G1 near the G1/S transition (106).

Most of the alternative splicing events that have been reported affect the cytoplasmic domain of the protein. One exception is the alternatively spliced Drosophila PS2  $\alpha$  protein. Zavortink reported that the splice event occurs in the extracellular domain and may be important in determining ligand specificity (107). Ziober also reported alternative splicing in the ligand-binding domain of human  $\alpha_7$  (84).

In summary, changes in integrin structure due to alternative splicing appear to affect the protein's function. Alternative splicing of the cytoplasmic domain results in altered responsiveness to posttranslational events, such as phosphorylation, as well as altered intracellular signaling by that integrin subunit. Splicing of the extracellular domain may affect ligand binding.

### Mobilization of Intracellular Stores

Neutrophils and monocytes express integrins of the  $\beta_2$  (CD 18) family. Miller *et al.* reported that when monocytes were stimulated with FMLP or other mediators the cell surface expression of  $\alpha_M\beta_2$  (Mac-1 or CD11b/CD18) and  $\alpha_X\beta_2$  (p150, 95, or CD11c/CD18) increased rapidly with a half-maximal time of 2 min. Using detergent permeabilization studies and electron microscopy it was shown that those molecules were held in intracellular vesicles and then mobilized to the cell surface after stimulation (108). Likewise in neutrophils  $\alpha_M\beta_2$  and  $\alpha_X\beta_2$  are found in intracellular granules (109, 110). When neutrophils are stimulated by chemoattractant molecules such as C5a, IL-8, or FMLP, or by ligation of the Fc $\gamma$  receptor, the cell surface expression of  $\alpha_M\beta_2$  is increased due to exocytosis (111). This mecha-

nism provides a means of rapid modulation of integrin function, occurring within minutes.

### Intracellular Control of Ligand Binding

This type of regulation, termed inside-out signaling, has been recently reviewed (1, 112, 113) and will not be discussed further here. Inside-out signaling is characterized by the presence of integrin molecules on the cell-surface that either do not bind ligand or bind with lower affinity. An intracellular change can then activate these molecules to produce an active receptor. This mechanism is also capable of yielding a very rapid increase in adhesion after appropriate stimulation.

### Summary

The regulation of integrins has been studied in many different cell types. Regulation of these molecules has turned out to be far more complex than a simple stimulus-response function. A given cell type can respond to multiple exogenous signals, and the same signal has different effects on different cells. Even at a single point of regulation, such as control of transcription, the mechanisms are complicated. In sum, it is clear that the regulation of integrins is complex and affords the cell many possible levels of control. This regulatory sophistication is likely necessary, given the critical role that integrins play in the myriad social interactions of cells.

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