

MINIREVIEW

Activin Signaling and Its Role in Regulation of Cell Proliferation, Apoptosis, and Carcinogenesis

YE-GUANG CHEN,* QIANG WANG,* SHI-LUNG LIN,† C. DONALD CHANG,† JODY CHUNG,‡ AND SHAO-YAO YING†¹

**State Key Laboratory of Biomembrane and Membrane Biotechnology, Department of Biological Sciences and Biotechnology, Tsinghua University, Beijing 100084, People's Republic of China; †Department of Cell and Neurobiology, Keck School of Medicine, University of Southern California, 1333 San Pablo Street, Los Angeles, California 90033; and ‡Department of Molecular Biology and Biochemistry, Keck School of Medicine, University of Southern California, 1441 Eastlake Avenue, Los Angeles, California 90089*

Activins, cytokine members of the transforming growth factor- β superfamily, have various effects on many physiological processes, including cell proliferation, cell death, metabolism, homeostasis, differentiation, immune responses endocrine function, etc. Activins interact with two structurally related serine/threonine kinase receptors, type I and type II, and initiate downstream signaling via Smads to regulate gene expression. Understanding how activin signaling is controlled extracellularly and intracellularly would not only lead to more complete understanding of cell growth and apoptosis, but would also provide the basis for therapeutic strategies to treat cancer and other related diseases. This review focuses on the recent progress on activin-receptor interactions, regulations of activin signaling by ligand-binding proteins, receptor-binding proteins, and nucleocytoplasmic shuttling of Smad proteins. *Exp Biol Med* 231:534–544, 2006

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¹ To whom requests for reprints should be addressed at Department of Cell and Neurobiology, Keck School of Medicine, University of Southern California, 1333 San Pablo Street (BMT-403), Los Angeles, CA 90033. E-mail: sying@hsc.usc.edu

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Introduction

Ever since activins were isolated and characterized based on the secretion of follicle stimulating hormone (FSH) by the anterior pituitary gland (1, 2), many other functions have been found to be exerted by activin, including their roles in cell proliferation, differentiation, apoptosis, metabolism, homeostasis, immune response, wound repair, and endocrine function (3, 4). This review is an update of our previous minireview entitled "Regulation of cell proliferation, apoptosis, and carcinogenesis by activin" (*EBM* 227:75–87, 2002) and focuses on the recent development in the roles activins play in cell growth and carcinogenesis.

Activins are members of the transforming growth factor- β (TGF- β) superfamily, which includes activins, inhibins, TGF- β s, bone morphogenetic proteins (BMPs), growth and differentiation factor (GDF), Nodal, myostatin, Müllerian-inhibiting substance, lymphocyte inhibitory factor (LIF), and others. Members of the TGF- β family exert a wide range of biological effects on various cell types. Activins, similar to other members of the TGF- β superfamily, interact with two types of cell surface transmembrane receptors (types I and II) which have intrinsic serine/threonine kinase activities in their cytoplasmic domains (5). Activin binds to type II activin receptor (ActRII/IIB), leading to the recruitment, phosphorylation, and activation of type I activin receptor (ALK4, also known as ActRIB). The activated ALK4 transiently interacts with and then phosphorylates Smad 2 and Smad 3, two of the cytoplasmic Smad proteins. The phosphorylated Smad2 and

Smad3 form a heterocomplex with Co-Smad (Smad4), and the resulting Smad complex accumulates in the nucleus, binds to the promoter region of the target genes, and regulates their expression (6, 7). Increasing biochemical and developmental evidence also suggests non-Smad pathways in activin signal transduction. Examples include the RhoA-ROCK-MEKK1-JNK and MEKK1-p38 pathways, which lead to the control of actin cytoskeleton reorganization and epithelial cell migration and contribute to the physiologic and pathological effects of activins on epithelial morphogenesis (8).

Activin and Activin-Binding Proteins

Activin. The TGF- β family comprises at least 42 members in humans, which are all characterized by a distinct cysteine knot scaffold structure (9, 10). Activins and inhibins are structurally related, sharing common β subunits, with a nine-cysteine distribution pattern similar to TGF- β s (7, 11, 12). Activins are dimeric proteins composed of two β subunits (activin-A [$\beta\alpha\beta\alpha$], activin-AB [$\beta\alpha\beta\beta$], or activin-B [$\beta\beta\beta\beta$]), which are linked by a single covalent disulfide bond, while inhibins are heterodimers of a β subunit and the structurally related α subunit (inhibin-A [$\alpha\beta\alpha$] and inhibin-B [$\alpha\beta\beta$]) (5, 13). In humans, genes encoding for four different activin/inhibin β subunits have been identified ($\beta\alpha$, $\beta\beta$, $\beta\gamma$, $\beta\delta$). The expression of activin C ($\beta\gamma\beta\gamma$), E ($\beta\delta\beta\delta$), AC ($\beta\alpha\beta\gamma$), AE ($\beta\alpha\beta\delta$), CE ($\beta\gamma\beta\delta$), and BC ($\beta\beta\beta\gamma$) has been demonstrated, but little is known about their function and stability (14, 15). A recent study showed that activin C stimulated DNA synthesis and proliferation of AML12 cells in serum-free medium (16). Activin C also exerts its action independently of the activin receptor signaling and has activities opposite to those of activin A. The $\beta\gamma$ subunit appears to attenuate activin activities by forming a heterodimer with a $\beta\alpha$ subunit and subsequently preventing the formation of biologically active activins (16). Accordingly, overexpression of activin C or activin E in the mouse liver inhibits regenerative DNA synthesis of hepatic cells and induces apoptosis in human and rat hepatoma cells (17, 18). However, targeted deletion of the genes encoding $\beta\gamma$ and $\beta\delta$ does not lead to abnormality in the liver (19).

Activin-Binding Proteins. Several activin-binding proteins, which play important roles in regulating the activin signaling, have been identified.

Follistatins. Follistatins are soluble extracellular proteins and function as mediators of cell growth, development, and differentiation in many tissues and organs. Follistatins bind activins with high affinity, block the interaction between activins and their cell-surface receptors, and consequently inhibit the signaling activity of activins (20). Follistatin consists of a 63-residue amino (N)-terminal segment, followed by three successive follistatin domains termed FSD1, FSD2, and FSD3, each of which contains ten cysteine residues. Alternative splicing generates three follistatin isoforms: FS288, FS303, and FS315. FS315 does

not interact with cell-surface proteoglycans and is the predominant circulating form of the protein (20). In addition to its interaction with the cell surface through a basic heparin-binding sequence (HBS; residues 75–86), the FSD1 is also essential for suppressing activin biological activity (21). Follistatin has ten times higher binding affinity for activin A than for activin B, suggesting that the determinants for follistatin binding differ between the two isoforms of activin (22).

Domain mapping has identified the region containing amino acid residues 85–109 in activin A to be involved in follistatin binding (23). Binding of follistatin to this region would mask the residues that are important in the interaction of activin with both ActRII (Ser90, Leu92, and Lys102) and ALK4 (Met91, Ile105, and Met108) (24–26). In fact, activin interacts with follistatin through a much bigger region, as shown by recent crystal structures of the activin A-follistatin (FS288) complex, revealing that two follistatin molecules embrace one activin dimer and bury one-third of its residues and its receptor binding sites (27).

FLRG. FLRG (follistatin-related gene), also known as follistatin-like 3, is a recently characterized follistatin domain containing secreted glycoprotein. Similar to follistatin, FLRG also binds to activins, myostatins, and BMPs (28–31). It is possible that the residues, which are important for activin binding, are located in the conserved regions between the two proteins. FLRG differs from follistatin in lacking the third follistatin domain and a consensus heparin-binding sequence. Although both follistatin and FLRG have similar functions in binding members of the TGF- β superfamily and neutralizing their activities, different expression patterns and distinct regulations are observed. FLRG is highly expressed in the placenta, testes, skin, and cardiovascular tissues, whereas the expression of follistatin is high in the pituitary and ovaries (20). Interestingly, the expression of FLRG is induced by TGF- β in a Smad-dependent manner (32), suggesting cross-talking between the TGF- β family members.

Cripto. Human Cripto, Mr 36,000 molecule, is the prototypical member of the epidermal growth factor–Cripto–FRL–Criptic (EGF-CFC) protein family. Members of the EGF-CFC family share the six cysteine residues in the central region (amino acids 77–113 of Cripto); however, Cripto shows little resemblance to EGF and does not bind to EGF receptors (33, 34). Cripto does not bind directly to activin, and activin type II receptors seem to be required for the formation of a Cripto-activin complex (35). Cripto exists in two forms, a membrane-bound form and a soluble secreted form. The membrane-bound Cripto anchors to the lipid bilayer of cell surfaces by using a glycosylphosphatidylinositol molecule as a co-receptor for Nodel, an activin-like TGF- β family member (36). The soluble secreted Cripto acts as a growth factor–like signaling molecule (37, 38). A Cripto receptor has not been defined yet, but Cripto was found to interact with Glypican-1 (39) and indirectly with ErbB-4 (40) as well as fibroblast growth

factor receptor (41). Cripto plays an important role in embryonic development in zebrafish and *Xenopus* (42, 43).

It has been shown that Cripto binds Nodal *via* its EGF-like domain and interacts with ALK4 *via* its CFC domain to promote Nodal signaling (44). In contrast, Cripto inhibits activin signaling in many cell lines (35, 45) by inhibiting the recruitment of the signaling type I receptor, ALK4. The actions of Cripto to block activin signaling are dependent on the EGF-like domain of Cripto (35). The molecular mechanisms of the functions of Cripto remain to be elucidated.

Activin Receptors and the Regulation of Receptors Activity. *Activin Receptors.* Activins and other members of the TGF- β superfamily exert their biological effects by interacting with two types of transmembrane receptors that have intrinsic serine/threonine kinase activities. Type I receptors, referred to as ALKs (for activin receptor-like kinases), include ALK 1–7 (46). Functional studies have established that ALK4 is the *bona fide* type I receptor for activin. A recent study also suggests that ALK7 functions as a type I receptor for activin AB and activin B (47). The combination of ActRIIA and ALK7, preferred by activin AB and activin B but not by activin A, is responsible for the activin-mediated secretion of insulin from pancreatic β cell line, MIN6 (47).

Ligand-Receptor Binding. Recent structural analysis studies shed light on ligand-receptor interactions. Activin, similar to other members in the TGF- β superfamily, forms a butterfly-shaped dimer linked by an interchain disulfide bond, and each monomer of the dimer comprises one α -helix and nine β -sheets to form a curled “hand” structure that contains a wrist region, a fingertip region, and a knuckle region (25, 48, 49). Crystal structures of activin A bound to its type II receptor revealed that the ligand residues in the knuckle region are involved in type II receptor binding (24, 25). In the activin A-ActRIIB complex, activin adopts some very flexible conformations that may account for its binding affinity to the receptors, and the ligand-receptor binding may also be influenced by the membrane-restricted setting of the receptors (49, 50). The ActRIIB-activin A interface involves hydrophobic, charged, and polar residues in both ActRIIB and activin A. The residue Lys102 in the knuckle region of activin A appears to be highly critical, since when it is changed to Glu, the mutant completely loses its ability to bind ActRII (51). Based on the structure of BMP7 complexed with its type I receptor ALK3 (also called BMPRIA), it was proposed that activin associates with type I and type II receptors *via* different regions, contacting ALK4 through the residues in the wrist region (25, 50). Indeed, the replacement of the residue Met108 with Ala or Glu in this region of activin A led to significantly lower signaling activity, even though the mutant still retained wild-type-like binding affinity for ActRII (26). The defect of the M108A mutant in forming a cross-linked complex with ALK4 in the presence of ActRII indicates that the ability of M108A to bind ALK4 was disrupted. Mutagenesis studies

have identified five hydrophobic amino acid residues in the ALK4 extracellular domain (Leu40, Ile70, Val73, Leu75, and Pro77) that likely constitute the binding surface for activin (52).

Specificity of Receptor-Smad Interaction. The receptor-regulated Smad proteins (R-Smad) can be divided into two groups. Group 1 contains Smad2 and Smad3, which bind to and are phosphorylated by the activated type I receptors of TGF- β and activin; Smad1, 5, and 8 make up the second group and are activated by BMP type I receptors. The specific receptor-Smad interaction is mainly determined by the discrete structural motifs in type I receptors and R-Smads: the L45 loop in the kinase domain of type I receptors and the L3 loop in the MH2 domain of R-Smads (53–55). The amino acid sequence of the L45 loop is conserved among the type I receptors that have similar substrate specificity; that is, ALK4 and ALK5 (also known as T β RI) have a similar L45 loop sequence, which is different from that of BMP type I receptors. Similarly, Smad2 and Smad3, substrates for ALK4 and ALK5, respectively, share the same L3 loop sequence, which is distinct from that of Smad 1, 5, and 8 (56).

Functional Difference in Smad2 and Smad3. Although Smad2 and Smad3 are structurally very similar, they have some functional differences in transducing signals for activin receptors. For example, Smad2 and Smad3 behave differently in regulating the transcription of a homeobox gene, *gooseoid*, through different interaction with Smad4 and a transcription factor FAST-2 (forkhead activin signal transducer-2) (57). The major structural difference between Smad2 and Smad3 is at the MH1 domain, and the second insertion at the MH1 domain of Smad2 may interfere with DNA binding (58). Therefore, the MH1 domain of Smad3 but not Smad2 is able to directly bind DNA (58–60). The absence of this insertion in the Smad2, as a product of alternative splicing with a deletion of exon 3 of the Smad2 gene, occurs naturally in mammalian cells, resulting in a gain of function in binding the activator protein-1 (AP-1) sites of the p3TP-lux promoter, which contains three repeats of AP-1 elements and the plasminogen activator inhibitor-1 (PAI-1) promoter (61).

In FAST-2-mediated transcriptional regulation using the activin-responsive element derived from *Xenopus* Mix.2 promoter as a reporter, Smad3 but not Smad2 alone was able to stimulate the transcription. In addition, Smad3 inhibits the transactivation of the promoter induced by co-expression of Smad2, Smad4, and an active activin type-I receptor. The Mad homology 1 (MH1) domain of Smad3 was found to be indispensable for the dual regulatory function of Smad3. However, this Smad3-specific function could not be manifested in Smad2 mutants that were devoid of the two amino acid insertions (at the MH1 domain) that comprise the major structural difference between Smad2 and Smad3. These findings indicate that other structural motifs are involved in determining the regulatory activity of Smad3 and the most N-terminal portion of Smad3 was

crucial for its function (62). The unique function of Smad3 in modulating the FAST-2-mediated transcription is contributed to by a subtle difference in the structural features at the MH1 domain. Indeed, studies using cells deficient in Smad2 for biochemical and cell biological assays and Smad3-deficient mice also demonstrate that there is a clear difference between Smad2 and Smad3 during development (63).

The Regulation of Receptor Activity. *Inhibin and Betaglycan.* Inhibins are heterodimers of $\alpha\beta$ subunits and share the inhibin/activin βA or βB subunit with activins. They are potent antagonists of activins in a subset of activin-responsive cells, including pituitary gonadotropes (13, 64, 65). Although it has long been thought that inhibin antagonizes activin by competing for the binding to the activin signaling receptors, the molecular basis of the selective actions of inhibins was only recently elucidated. Betaglycan, a proteoglycan known as a type III TGF- β receptor, binds inhibin, and the binding affinity increases about 30-fold in cells co-expressing ActRII and betaglycan (66). ALK4 is excluded from this ternary inhibin-betaglycan-ActRII complex. Betaglycan also forms a complex with ActRIIB and BMPRII, thereby sequestering them away from activin or BMP (66, 67).

BAMBI. BAMBI is a transmembrane protein that lacks an intracellular kinase domain but has sequence similarity with the extracellular domain of the type I receptors, and thereby functions as a general negative modulator for BMP, activin, and TGF- β (68). BAMBI is highly conserved and has been identified in zebrafish, mice, rats, and human beings. The human homolog, also known as nma (non-metastatic gene A), might play an important role by providing cancer cells with an escape mechanism from TGF- β -mediated inhibition of cell growth. Knockdown of BAMBI expression with antisense oligonucleotides restored the inhibitory effect of TGF- β in several human gastric carcinoma cell lines (69). Furthermore, overexpression of BAMBI inhibits the response of tumor cells to TGF- β signaling, and the expression of BAMBI is activated by the Wnt/ β -catenin signaling in colorectal tumor cells (70). The expression of BAMBI is also regulated in male germ cells, a finding correlating well with the previous observation that a decrease of activin activity is critical in gonadocyte differentiation (71).

ARIPs. Recent studies indicate that the cell surface level of ActRIIs, the primary receptors for activins and related ligands, is regulated by a group of proteins called ARIPs (activin receptor-interacting proteins) (72–74). ARIP1 contains several protein-protein interaction domains, including two WW domains and five or six PDZ domains. In addition to interacting with ActRIIs, ARIP1 can also bind to Smads, glutamate receptors, adhesion proteins, PTEN, and β -catenin, implying that it plays an important role in signal cross-talking (72, 73, 75, 76). In contrast, ARIP2, a small protein that has only one PDZ domain (74), decreases the expression levels of ActRIIs in the plasma membrane

and reduces their response to ligands. Apparently, ARIP2 functions as an adaptor protein by recruiting RalBP1 (*via* the COOH-terminus) to ActRII (through the PDZ domain). Then, RalBP1 works with the small GTP-binding protein Ral to regulate the endocytosis of ActRIIs.

Dapper2. In the search for Dishevelled (Dvl)-binding proteins, Dapper was found to function as a general antagonist of Wnt signaling to inhibit both the canonical β -catenin pathway and the non-canonical c-Jun N-terminal kinase pathway (77, 78). Inhibition of maternal Dapper expression results in the loss of the notochord and head structures in *Xenopus* embryos, suggesting an important role of Dapper in modulating Wnt signaling for normal vertebrate development. Interestingly, Frodo, which has high similarity to Dapper and was also identified as a Dvl-interacting protein, has been shown to promote Wnt signaling (79). Recently, Frodo was proposed to mediate signaling directly from Dvl to TCF in a β -catenin-independent way (80). Dapper2, which is divergently related to Dapper, interferes with Nodal signals in mesoderm induction in zebrafish (81). Knockdown of Dapper2 expression by antisense oligonucleotides enhanced expression of mesoderm markers, whereas its overexpression resulted in eye fusion, a phenotype resembling that from mutation of Nodal coreceptor one-eye pinhead. Biochemical analysis studies demonstrated that Dapper2 specifically associates with ALK5 and Activin/Nodal type I receptor ALK4 and targets receptors for lysosomal degradation (81). Therefore, Dapper2 controls endocytosed receptor transport from late endosomes to lysosomes for degradation. By modulating the cell surface protein level of receptors, Dapper2 may function to fine-tune Nodal/activin signaling in the mesoderm formation. The function of Dapper proteins could be complex, as recent work suggests that both Dapper1 and Dapper2 are required for Wnt signaling in zebrafish embryogenesis (82). Further investigation is needed to establish the physiological role of Dappers in a spatial-temporal manner.

BMP-3. BMP-3, unlike other members of the TGF- β superfamily, inhibits biological activities of other BMPs and TGF- β s in a variety of mammalian systems (83). In *Xenopus* embryos, unlike BMP-2, BMP-4, and BMP-7, which are all potent ventralizing agents, BMP-3 induces dorsalization (83, 84). These effects of BMP-3 are similar to those of the BMP antagonists noggin, chordin, and follistatin. BMP-3 β , a molecule 83% homologous to BMP-3, can also antagonize BMP-like ligands and Nodal-like proteins (84). BMP-3 also interferes with activin signaling (78) and binds to ActRIIB, a common type II receptor for activin-related proteins that is unable to activate R-Smads (78).

Small-Molecule Receptor Inhibitors. Specific small-molecule inhibitors of the signaling machinery have great potential therapeutic uses to target human diseases. Thus, there is considerable interest in two recently developed competitive inhibitors for the ATP binding site in the kinase

domain of ALK5 (86, 87). These inhibitors, SB-431542 and SB-505124, also inhibit ALK4 and ALK7, which share similar substrate specificity with ALK5. However, these small-molecule receptor inhibitors have no effect on ALK1-, ALK2-, ALK3-, or ALK6-induced Smad signaling, or on the activities of other protein kinases, suggesting that the inhibition of the receptors is remarkably specific (86, 87). SB-431542 has been shown to inhibit the TGF- β -induced proliferation of human osteosarcoma cells (88) and TGF- β -promoted cell proliferation, angiogenesis, and motility in malignant glioma (89, 113). The effect of these molecules in activin-dependent physiopathological systems remains to be determined.

The Downstream Smad Effectors and the Regulation of Their Activities. R-Smad and Co-Smad proteins consist of the sequence-conserved amino-terminal Mad homology 1 (MH1) domain, the carboxyl-terminal MH2 domain, and the sequence-divergent middle linker region. The MH1 domain is mainly involved in DNA binding and the interaction with other transcription factors. The MH2 domain contributes to transcriptional activation, Smad-Smad interaction, Smad-receptor interaction, and association with other binding proteins and transcription factors (5, 90, 91). The linker region provides a binding site for Smurfs, ubiquitin E3 ligases, and thus is involved in Smad ubiquitination and proteasome-mediated degradation (92–95). Inhibitory Smads (I-Smads: Smad6 and Smad7) form a distinct subclass of Smads that act in the opposite manner to R-Smads and antagonize signaling. Observations of recently identified Smad binding proteins, their roles in regulation of Smad activities, and our current understanding of the nucleocytoplasmic shuttling of Smad proteins are briefly summarized below.

Regulation of Smad Activity. The activity of Smad is regulated positively or negatively by a variety of signal inputs (6, 7, 56, 78, 96). The linker region of the Smad also contains the phosphorylation sites for ERK, CDK, and Ca²⁺-calmodulin-dependent kinase II; phosphorylation of this region by these kinases negatively regulates Smad activity (97–99).

First, Smad proteins function in the nucleus as transcription factors. This transcriptional activity is dependent on the recruitment of other coactivators, such as CBP and p300 (100), or corepressors, such as c-Ski and SnoN (101, 102). The *DLX* genes constitute a subfamily of vertebrate homeobox genes that are structurally similar to the *Drosophila* *distal-less* gene, and they play a central role in appendage development, neurogenesis, and hematopoiesis (103, 104). Recent evidence shows that DLX1 is expressed in hematopoietic cells in a lineage-dependent manner. DLX1 interacts with Smad4 and blocks the differentiation of a hematopoietic cell lineage induced by activin A (105).

Second, at steady state, R-Smads are predominantly cytoplasmic, and Smad4 is distributed throughout the cytoplasm and nucleus; however, upon ligand stimulation

both R-Smads and Smad4 accumulate in the nucleus (106). The Smads shuttle between the cytoplasm and the nucleus in both basal and activated states (107, 108). However, the R-Smads are continuously being dephosphorylated in the nucleus at a low rate by a yet unidentified phosphatase. This dephosphorylation allows R-Smads to dissociate from Smad4 and move to the cytoplasm (107, 108). If the receptors are still active, R-Smads are rephosphorylated, form complexes with Smad4, and relocate to the nucleus. If the receptors are no longer active, then the Smad proteins accumulate in the cytoplasm over time (108).

Lastly, Smad4 contains a nuclear export signal (NES) and a nuclear localization signal (NLS) in the linker region. The nuclear exporter CRM1 binds to the NES of Smad4, and the nuclear importer importin- α binds to the NLS to facilitate Smad4 nucleocytoplasmic shuttling (106, 109, 110). Smad3 also contains a basic NLS in its MH1 domain that is thought to bind directly to importin- β ; mutation of this NLS prevents Smad3 from accumulating in the nucleus, even when the cells are treated with TGF- β (111, 112). The Smad2 MH1 domain does not bind to importin- β (113, 155) due to the presence of a unique insert sequence in the exon 3 of Smad2 (112). Instead, there is an alternative pathway for Smad2 shuttling that does not involve classical signals (107, 113, 114). The Smad2 nucleocytoplasmic shuttling is independent of transport receptors. It is mediated by direct interactions of the MH2 domain with nucleoporins, particularly Nup214 and Nup153, which are present on the cytoplasmic and the nuclear side of the nuclear pore complex, respectively. The MH2 domain of Smad3, which is closely related to that of Smad2, also binds to components of the nuclear pore complex (114). The fact that Smad3 has a greater tendency to be in the nucleus as compared to Smad2 and that it can readily activate TGF- β transcriptional responses in the absence of signaling when overexpressed may be due to its ability to interact with both the nucleoporin complex and importin- β . CRM1 is not involved in the ATP-dependent export of Smad2 and Smad3 from the nucleus, suggesting that an alternative exporter is involved in their active exporting out of the nucleus (108).

Interestingly, Smad-binding proteins in the cytoplasm and the coactivators or corepressors in the nucleus may be involved in modulating the Smad nucleocytoplasmic shuttling through their interactions with Smads. For example, the purified Smad-binding domain (SBD) of the cytoplasmic Smad anchor for receptor activation protein (SARA) inhibits nuclear accumulation of the Smad2 MH2 domain (113), whereas FoxH1 overexpression leads to Smad2 nuclear accumulation in the absence of ligands (107, 115). Furthermore, the presence of Smad4 binding partners in the nucleus, such as the corepressor proteins SnoN and Ski, may also contribute to the nuclear retention of Smad4 in unstimulated cells (101, 102).

Smad-Independent Signal Pathways of Activin. Although the Smad pathway is the well-established central mediator for the TGF- β superfamily members from the

receptors to the nucleus, activation of Smad alone cannot account for all of the downstream signaling events of TGF- β /activin activation. Increasing biochemical and developmental evidence supports an alternative: non-Smad pathways in TGF- β signaling. TGF- β receptors can directly interact with or phosphorylate non-Smad proteins, initiating parallel signaling that cooperates with the Smad pathway in eliciting physiological responses (116). The results obtained from *in vitro* cell models imply that the small GTPase Ras and the mitogen-activated protein kinases (MAPKs) ERKs, p38, and c-Jun N-terminal kinases (JNKs) are involved in the TGF- β signaling (117).

Activins play a critical role in epidermis remodeling that involves epithelial cell movement. The MEKK1-JNK cascade is required for eyelid closure in mammals. It was demonstrated that the MEKK1-JNK cascade transmits TGF- β and activin signals to control epithelial cell movement in a Smad4-independent way (118). It was also revealed that activin A induced p38 phosphorylation and inhibited ERK1/2 phosphorylation in K562 cells (119). In keratinocytes, activins can activate MEKK1-dependent phosphorylation of JNK and c-Jun in a RhoA-dependent but Rac- and CDC42-independent way (8). Furthermore, activins stimulate p38 activity by a RhoA-independent mechanism in MEKK1-deficient keratinocytes. Interestingly, neither pathway is dependent on Smad activation, although the mechanism by which activins activate RhoA or MEKK 1 remains unclear. Dok-1, a Ras GAP-binding protein and a target of protein tyrosine kinases-like Src and Abl (121), has been suggested to mediate activin signaling to Smad proteins by binding to ActRIIA and ALK4 (120). Although Dok-1 cannot be tyrosine phosphorylated in response to activin signaling (120), it remains interesting to determine whether or not it functions as an adaptor mediating the signaling from receptor to GTPase in a non-Smad pathway. Indeed, TAK1, originally identified as a TGF- β activated kinase, has been suggested to mediate activin A signaling by the MKK3-p38 MAPK pathway to activate the expression of neurogenin3, a transcription factor essential for the differentiation of pancreatic endocrine cells (122).

Regulation of Cell Proliferation, Apoptosis, and Carcinogenesis by Activin

Activins regulate the growth and differentiation in numerous types of cells. The actions of activins on cell growth and differentiation are mainly through the Smad-dependent pathways. For instance, activin A induces growth inhibition of Hep3B cells by downregulating Bcl-xL (anti-apoptotic) expression *via* Smad2 or Smad3 (123). HepG2 cells treated with activin showed increased gene expression of the cyclin-dependent kinase inhibitor p15INK4B and induced cell cycle arrest (124). Activin is strongly expressed in wounded skin, and overexpression of activin in the epidermis of transgenic mice improves wound healing and enhances scar formation (127). Conversely, inhibition of

activin activities in the skin delays wound healing but improves the quality of the healed wound. In addition to effecting cell growth, activin regulates the morphogenesis of branching organs such as the prostate, lung, and kidney (125), and it regulates the differentiation of human trophoblast tissues during early pregnancy (126).

TGF- β and BMP have been shown to be essential for the maintenance of stem cell renewal. Similarly, activin/Nodal signaling through Smad2/3 is also necessary to maintain the pluripotent status of human embryo stem cells (hESCs), and in order that WNT and TGF β /activin/nodal signaling collaborate in maintaining pluripotency (128, 129). Inhibition of activin/Nodal signaling by follistatin, overexpression of Lefty or Cerberus-Short, or the activin receptor inhibitor SB431542 induces hESC differentiation (128). Furthermore, activin A is secreted by mouse embryonic feeder layers, and culture medium enriched with activin A is capable of maintaining hESCs in the undifferentiated state for over 20 passages in feeder-free cultures (130).

However, the functions of activin in embryonic stem cells are still dubious. In contrast to the effect of activin in maintaining pluripotency, activin A in combination with other factors has been used to induce embryonic stem cells to differentiate into pancreatic β cells (131). Activin A induces mesoderm and endoderm in mouse embryoid bodies (132). Furthermore, Activin A has also been used to induce human embryonic stem cells to differentiate into definitive endoderm in culture (133). Mouse embryonic stem cells can also be directed to differentiate into Rx⁺/Pax6⁺ neural retinal precursors in the SFEB culture combined with Dkk1, LeftyA, FCS, and activin (134). Activin A has also been demonstrated to have an inhibitory effect on murine hematopoietic stem cells (135).

Activin also induces apoptosis in multiple cells and tissues. In hematopoietic cells, TGF- β family members regulate apoptosis *via* the inositol phosphatase SHIP (SH2 domain-containing 5' inositol phosphatase), a central regulator of phospholipid metabolism. Activin/TGF- β -induced expression of SHIP results in the intracellular changes in the pool of phospholipids, as well as in the inhibition of both Akt/PKB phosphorylation and cell survival (136). Activin inhibits adrenal tumor growth by inducing x-zone apoptosis (137). In addition, activin/inhibin signaling can increase apoptosis in human adrenocortical cells and hematopoietic cells (136, 138). Activin C and E have also been shown to induce apoptosis in both human and rat hepatoma cells (139).

In addition to inducing apoptosis, activin may have an anti-tumorigenic effect. Activin inhibits proliferation of human tumor cells derived from gall bladder (140), prostate (141), and pituitary gland (142). The mRNAs encoding all three activin/inhibin subunits are expressed in breast carcinoma, fibroadenoma, and normal mammary tissue (143). Activin inhibits cellular proliferation of T47D breast cancer cells by enhancing the expression of p15 cyclin-

dependent kinase inhibitors, reducing cyclin A expression, and phosphorylating the retinoblastoma protein (144). In this regard, activin resembles the TGF- β effect on epithelial cells.

Activin A also exerts its tumor suppressor function as an inhibitor of angiogenesis. Neuroblastoma cells with restored activin A expression exhibit a diminished proliferation rate and form smaller xenograft tumors with reduced vascularity (145). Cells treated with activin A showed increased expression of cyclin-dependent kinase inhibitors p15^{INK1b}, p21^{CIP1}, and p27^{KIP1}, and decreased expression of vascular endothelial growth factor receptor-2, the receptor of a key angiogenic factor in cancer. Overexpression of the constitutively active ALK4 has the same effects, and these actions are mediated *via* the Smad2/Smad3 pathways. Consistent with the finding that decreased vascularity of the xenograft tumors, activin A inhibited several crucial angiogenic responses in cultured endothelial cells, such as the proteolytic activity, migration, and proliferation.

As with the many complicated functions of activin in cell proliferation and differentiation, the relationship between activin and carcinogenesis is not simple. Increased levels of activin A in human endometrial adenocarcinoma tissues have been proposed to be involved in carcinogenesis by reducing TGF- β -mediated signals that have inhibitory effects on these tissues (146). Activin A has been shown to mediate high N-cadherin expression on the carcinoma cell surface, and this is associated with tumor aggressiveness and a poor prognosis (147). Activin signaling has also been suggested to be active at the leading edge of ErbB2/Neu-induced tumors, even though the Smad-dependent TGF- β signaling is absent in these tumors. (148) Activin A can increase the proliferation of ovarian cancer cell lines SKOV3, OCC1, OVCAR3, and A2780-s, and this could be because activin A augmented invasion through Matrigel (149). This shows that activins can be tumorigenic or anti-tumorigenic, depending on the setting. It is far from clear whether their roles are causal or consequential; the molecular mechanisms for the actions of activin remain to be determined.

Conclusion

Activin A is pleiotropic and affects proliferation, differentiation, and apoptosis in a variety of cell types. Insight on the molecular basis for activin signal transduction has been gained; however, the actions of activin and the regulation and dysregulation of this molecule in the physiological and pathological conditions, respectively, remain to be elucidated.

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