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The Effect of Activin/TGFβ Signaling

in Mammary Epithelial and Breast Cancer Cells

by

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A thesis submitted to the Faculty of Graduate Studies and Research in partial fulfillment of the requirements for the degree of Doctor of Philosophy

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TABLE OF CONTENTS

ABSTRACT	6
RESUME	
PREFACE AND CONTRIBUTIONS OF AUTHORS	
ACKNOWLEDGEMENTS	
CLAIM TO ORIGINALITY	

CHAPTER I	16
GENERAL INTRODUCTION	16
1. Activin/TGFβ Signaling	17
1.1. Ligand	17
1.1.1. TGFβ	17
1.1.1.1. TGFβ isoforms, sites of synthesis and knockouts	17
1.1.1.2. TGFβ structure	18
1.1.2. Activin	19
1.1.2.1. Activin isoforms, sites of synthesis and knockouts	19
1.1.2.2. Activin structure	20
1.1.3. Other Ligands of the TGFβ Superfamily	20
1.2. Receptors	21
1.2.1. Type I and Type II Receptors	21
1.2.1.1. Structure of the Receptors	22
1.2.2. Type III Receptor	23
1.3. Core Pathway - The Smads	24
1.3.1. Smad cloning	28
1.3.2. Smad structure	28
1.3.3. Activation Requires Smad Accessory Proteins	29
1.3.4. Smad Regulation	30
1.3.4.1. Smad Phosphorylation	30
1.3.4.2. Smad Dephosphorylation	30
1.3.4.3. Smad Acetylation, Ubiquitination and Sumoylation	31
1.3.5. Smad Nuclear and Cytoplasmic Shuttling	32
1.3.6. Smad Nuclear Signaling	32
1.3.6.1. Smads and Transcription Factors	33
1.3.6.2. Smads interactions with Co-activators and Co-repressors	36
1.3.7. Inhibitory Smads	36
1.5.6. Sinau Knockouts	37
1.4. Crosstark with Other Signaling Pathways	38
2. Biological Functions of Activin/ IGFp	39
2.1. Centular Promeration	39
2.2. Differentiation	40
2.3. Apopulsis	41 10
2.7. Extractional Matrix Frontection and Autoston	42 /2
	43

2.6. Development	43
2.7. Hormonal Regulation	44
2.8. Angiogenesis	
3. Mammary Gland Development	45
3.1. Hormonal control of Ductal and Alveolar Development.	47
4. Activin/TGFβ signaling in Mammary Gland Development	48
4.1. Ligand and Signaling Components Expression in the Breast	48
4.1.1. TGFβs and TGFβ receptors	48
4.1.2. Activin and activin receptors	
4.1.3. The Smads	49
4.2. Knowledge Gained from Mouse Models	50
4.3. Summary	52
5. Activin/TGFβ and breast cancer	. 53
5.1. Ligand expression and regulation	53
5.2 Receptor expression and regulation	54
5.3. Smad signaling	54
5.3.1. Cytostatic Response	54
5.3.2. Apoptosis	56
5.4. Receptor and Smad mutations	57
5.5. Mouse models in breast cancer	58
5.6. Summary	59
6. TGFβ and breast cancer metastasis	60
6.1. Tumor Promoting Effects of TGFβ	61
6.1.1. Immune suppression/evasion	61
6.1.2. Angiogenesis	62
6.1.3. Tissue invasion/Cellular adhesion	63
6.1.4. Epithelial to Mesenchymal Transition	64
6.2. Summary	65
7. Hypothesis and objectives of this work	66

CHAPTER II.	68
Smad Signaling Antagonizes Stat5-Mediated Growth And Differentiation Of	
Mammary Epithelial Cells	68
PREFACE	69
1. The Role of the Prolactin (PRL) Jak-Stat Pathway in Proliferation and	
Differentiation of the Mammary Gland	69
1.1. PRL and PRL Receptor	69
1.2. Jak-Stat signaling	70
1.3. Stat5 structure	73
1.4. Regulation of Stat5 activity	74
1.5. Stat5 gene regulation	75
2. PRL Jak-Stat pathway in breast cancer	76
3. PRL Jak-Stat pathway in breast cancer metastasis	77
4. Purpose of this study	77
ABSTRACT	78

INTRODUCTION	
MATERIAL AND METHODS	
RESULTS	88
DISCUSSION	100
FIGURES	

CHAPTER III.	
The p38 MAP Kinase Pathway Is Required For Cell Growth Inhibition Of	Human
Breast Cancer Cells In Response To Activin	122
PREFACE	123
1. MAPK signaling: A brief Overview	123
1.1. The p38 MAPK pathway	124
2. TGFβ signaling crosstalk with the MAPK pathways	
2.1. MAPK Activation by TGFβ	
3. Purpose of Study	
ABSTRACT	
INTRODUCTION	
MATERIALS & METHODS	
RESULTS	135
DISCUSSION	
FIGURES	

CHAPTER IV.	
The Death Adaptor Molecule RAIDD is as a Novel Activin Target Nec	cessary for
Activin-Induced Cell Growth Inhibition	
PREFACE	
1. TGFβ and Death Receptor Signaling	164
2. The Death Adaptor RAIDD	
3. Purpose of study	
ABSTRACT	
INTRODUCTION	
MATERIALS and METHODS	
RESULTS	
DISCUSSION	
FIGURES	

•

CHAPTER V.	
GENERAL DISCUSSION	
1. Defining the Effect of Activin/TGF β signaling on Mammary Gland D	evelopment
2. Mode of Inhibition of Activin in Breast Cancer Cells	
3. Impact of Thesis Discoveries on Breast Cancer	
_	

REFERENCES	
APPENDIX	
ABBREVIATIONS	
Refereed Paper in Its Published Format	

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ABSTRACT

Activin and TGF β , members of the TGF β superfamily, are pluripotent cytokines that are expressed in virtually every cell of the body. These factors play diverse roles in the body such as regulating early development of the embryo, differentiation, extracellular matrix formation, hematopoiesis, angiogenesis and immune functions. TGF β superfamily signaling is transduced by heteromeric serine/threonine kinase receptors at the cell surface and the intracellular mediator, the Smad complex. Following activation of the receptors, there is recruitment and phosphorylation the Smads. As a result the Smad proteins accumulate in the nucleus, bind co-activators or repressors and elicit or suppress transcription of target genes.

To date, the molecular signaling mechanisms for activin/TGF β in mammary gland growth and differentiation have not been fully elucidated. Our data identify a novel regulatory crosstalk mechanism by which activin/TGF β induced Smad signaling acts to antagonize Stat5 transactivation in mammary epithelial cells. We demonstrate an inhibitory effect of activin/TGF β on milk protein expression, specifically β casein. We further show that activin/TGF β inhibitory effect upon β casein expression is not due to changes in either Stat5 phosphorylation, translocation to the nucleus or binding on the Stat5 response element. We finally demonstrate that the Smads are required to block Stat5 transactivation by activin/TGF β and show that they are important mediators in activin/TGF β inhibitory response upon Stat5 target gene expression, in particular β casein and cyclin D1. Finally, we unveil the mechanism by which these two signaling

cascades antagonize their effects and find that activated Smads inhibit Stat5 association with its co-activator CBP, thus blocking Stat5 transactivation of its target genes. Thus, we define a novel crosstalk mechanism between two divergent signaling pathways that are involved in regulating mammary gland growth and differentiation

Whereas the role of TGF β signaling in breast cancer has been well characterized, we sought out to study the role and mechanism of action of activin in the human breast cancer T47D cells. We found that activin treatment of T47D cells leads to a potent inhibition of cell growth. We further show that activin induces the Smad, the p38-mitogen activated kinase pathways and the p38 downstream target ATF2. Finally, using specific inhibitors to block p38 MAPK, activin-mediated cell growth inhibition is completely abolished. Together, these results define a novel signaling mechanism induced by activin in breast cancer cells.

Finally in an attempt to identify genes regulated by activin in breast cancer cells, we discover the death adaptor molecule RAIDD as a novel target of activin signaling. We show that RAIDD mRNA and protein levels are potently upregulated by activin. Using antisense-oligos directed against RAIDD, we show that RAIDD expression is necessary in mediating activin inhibition in breast cancer cells. Hence, we define the involvement of a new player in activin mediated cell growth inhibition.

Collectively, these studies reveal novel mechanisms of the activin/TGF β signaling cascade in normal mammary epithelial cells and breast cancer cells.

RESUME

Activine et TGF β , membres de la superfamille TGF β , sont des cytokines pluripotentes. Ces facteurs jouent des rôles variés dans le corps tels que la régulation des étapes précoces du développement de l'embryon, la différenciation, la formation de la matrice extracellulaire, l'hématopoïèse, l'angiogénèse et les fonctions immunitaires. La voie de signalisation médiée par activine/TGF β est initiée suite à la fixation d'un ligand à un complexe de deux récepteurs de la famille des sérine/thréonine kinases. Après transactivation des récepteurs, les médiateurs intracellulaires Smads sont recrutés et phosphorylés. Il en résulte une accumulation des protéines Smads dans le noyau où elles vont se fixer à des coactivateurs ou des répresseurs pour activer ou réprimer la transcription de gènes cibles.

A ce jour, les mécanismes moléculaires de la voie de signalisation impliquant activine/TGF β dans la croissance de la glande mammaire et sa différenciation n'ont pas été complètement élucidés. Nos résultats identifient un nouveau mécanisme de régulation par «cross talk » au cours duquel activine/TGF β induisent la voie de signalisation des protéines Smads en antagonisant la transactivation de Stat5 dans les cellules épithéliales mammaires. Nous démontrons que activine/TGF β a un effet inhibiteur sur l'expression des protéines de lait, spécifiquement sur l'expression de la β caséine. De plus, nous montrons que l'effet inhibiteur de activine/TGF β en réponse a l'expression de la β caséine n'est pas du à des changements de phosphorylation de Stat5, de sa translocation dans le noyau ou de sa fixation sur ses éléments de réponses. Finalement, nous démontrons que Smad2, Smad3 et Smad4 sont requis afin de bloquer la transactivation de Stat5 en réponse à activine/TGF β ; par ailleurs nous montrons qu'ils

sont des médiateurs importants de la réponse inhibitrice de activine/TGF β en réponse à l'expression des gènes cibles de Stat5, en particulier β caséine et cycline D1. Ainsi, nous définissons un nouveau mécanisme de «cross talk » entre deux voies de signalisation divergentes qui sont impliquées dans la régulation de la croissance et de la différenciation de la glande mammaire par lequel la voie de signalisation des protéines Smad inhibe l'activation transcriptionnelle médiée par Stat5 dans les cellules épithéliales mammaires en inhibant l'association de Stat5 avec le cofacteur CBP.

Bien que le rôle de la voie de signalisation TGFβ dans le cancer du sein a été bien caractérisé, nous avons voulu étudier le rôle et le mécanisme d'action d'activine dans la lignée de cellules T47D du cancer du sein. Nous avons trouvé qu'un traitement des cellules T47D par activine conduit à une forte inhibition de la croissance cellulaire. De plus, nous montrons qu'activine induit Smad, les voies des kinases activées par les mitogènes (p38^{MAPK}) ainsi que ATF2, la cible en aval de p38^{MAPK}. Finalement, l'inhibition de p38^{MAPK} par des inhibiteurs spécifiques abolit totalement l'inhibition de la croissance cellulaire médiée par activine. Ces résultats définissent un nouveau mécanisme de signalisation induit par activine dans les cellules du cancer du sein.

Afin d'identifier les gènes impliquées dans l'inhibition par l'activine dans le cancer du sein, nous avons mis en evidence la protéine RAIDD comme une nouvelle cible de l'activine. En effet, l'activine augmente l'ARNm ainsi que le niveaux protéique de RAIDD. De plus, en utulisant des oligos antisenses pour RAIDD, nous avons montré que son expression est nécessaire à l'inibition par l'activine dans les cellules T47D. Avec ces resultats, nous mettons en evidence l'implication d'un nouvel acteur, la proteine RAIDD, dans l'inhibition cellulaire par l'activine.

L'ensemble de nos résultats mettent à jour de nouveaux mécanismes dans la cascade de signalisation activine/TGF β dans les cellules épithéliales mammaires normales ainsi que dans les cellules du cancer du sein.

"As an alternative to the traditional thesis format, the thesis can consist of a collection of papers of which the student is an author or co-author." (Quoted from McGill University guidelines for submitting a doctoral thesis at: http://www.mcgill.ca/gps/programs/thesis/guidelines/preparation/) In accordance with the above guidelines for thesis preparation and submission, I have included the following papers as the core of my thesis (CHAPTER II, III and IV).

- Cocolakis E., Drolet L., Ho W.Y.J., Haines E., Ali S. and Lebrun J.J. Smad Signaling Antagonizes Stat5-Mediated Growth And Differentiation Of Mammary Epithelial Cells. (manuscript to be submitted)
- Cocolakis E., Lemay S., Ali S. and Lebrun J.J. (2001) The p38 MAP Kinase Pathway Is Required For Cell Growth Inhibition Of Human Breast Cancer Cells In Response To Activin. J. Biol. Chem. 276: 18430-6.
- Cocolakis E. and Lebrun J.J. The Death Adaptor Molecule RAIDD is as a Novel Activin Target Necessary for Activin-Induced Cell Growth Inhibition. (manuscript in preparation)

I have included as the first chapter, an extensive literature review as an introduction to the thesis. CHAPTER II, Smad Signaling Antagonizes Stat5-Mediated Growth and Differentiation of Mammary Epithelial Cells, is a first authored manuscript in which I performed all the experiments and wrote the manuscript in collaboration with my supervisor Dr. Lebrun. This paper will soon be submitted for publication. CHAPTER III, The p38 MAP Kinase Pathway is required for Cell Growth Inhibition of Human Breast Cancer Cells in Response to Activin, is a first authored manuscript that I wrote and performed all the experiments under the supervision of Dr. Lebrun. This paper is reproduced from The Journal of Biological Chemistry by copyright permission from The American Society for Biochemistry and Molecular Biology Inc. publisher. A reprint copy is included in the appendix. CHAPTER IV, The Death Adaptor Molecule RAIDD is as a Novel Activin Target Necessary for Activin-Induced Cell Growth Inhibition is a manuscript in preparation that I wrote and performed all the experiments for under the supervision of Dr. Lebrun. Finally, CHAPTER V, includes a detailed discussion of the findings presented in the thesis. In order to maintain the focus of this thesis on the effect of activin/TGF β signaling in mammary epithelial and breast cancer cells, I have not included two publications to which I have made a substantial contribution.

- Valderrama-Carvajal H, Cocolakis E, Lacerte A, Lee EH, Krystal G, Ali S, Lebrun JJ. Activin/TGFβ induce apoptosis through Smad-dependent expression of the lipid phosphatase SHIP. Nat Cell Biol. 2002 Dec;4(12):963-9.
- Ho J, Cocolakis E, Dumas VM, Posner BI, Laporte SA, Lebrun JJ. The G protein-coupled receptor kinase-2 is a TGFβ-inducible antagonist of TGFβ signal transduction. EMBO J. 2005 Sep 21;24(18):3247-58.

For the first paper, I performed all the biological assays such as the Flow Cytometry experiments, the MTT assays and Annexin V staining. For the EMBOJ paper, I performed the Flow Cytometry assays and the RT-PCR experiments. I will discuss the implication of these papers to my thesis work in the final chapter.

The following is how the co-authors contributed to the papers in this thesis:

Loren Drolet helped reproduce some of the luciferase assays perfomed, CHAPTER II Figure 10, for statistical analysis and helped me with the cyclin D1 western blots. Joanne Wing Yee Ho performed some co-immunoprecipitation experiments that were presented in CHAPTER II discussion as "figure not shown" and contributed to useful discussions about the manuscript. Dr. Suhad Ali provided multiple reagents and invaluable insight for both manuscripts. Dr. Serge Lemay performed the RNAse protection assay Figure 2 CHAPTER III.

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This was an incredible journey and the lessons learned were invaluable. Firstly, I'd like to thank my mentor Dr. Jean-Jacques Lebrun for his patience, guidance and for allowing me the opportunity to develop my research skills. Alongside my supervisor, I extend my gratitude to the members of the Lebrun lab past and present for their help, support and friendship, especially Joanne Ho. I would also like to express my appreciation to Dr. Suhad Ali for her continuous counsel and advice. Furthermore, I wish to recognize all the students and staff at the Royal Victoria Hospital and more specifically the Hormones and Cancer Research Unit. In addition, my studies and work would not have been made possible without the continuing support of the Division of Experimental Medicine and the Experimental Medicine Graduate Student Society.

I am especially grateful to my wonderful parents and sister, without their love and continuous encouragement, none of this would have been possible. Finally, I would like to thank the love of my life, Billy Andriopoulos; you have been my pillar of strength throughout the final chapter of my PhD.

CLAIM TO ORIGINALITY

The present thesis, consisting of five chapters, was written by myself, Eftihia Cocolakis, under the supervision of my thesis director, Dr. Jean-Jacques Lebrun. The manuscript presented in CHAPTER II, will be submitted for publication and consists of original and unpublished data. CHAPTER III contains a refereed published paper consisting at the time of original and unpublished findings. CHAPTER IV is a manuscript in preparation composed of novel unpublished data.

The major novel findings of the presented thesis are as follows:

- 1. Activin/TGFβ induced Smad signaling inhibits Stat5 transactivation and gene upregulation in mammary epithelial cells.
- 2. Activin signaling via the Smad and the p38 MAPK pathways inhibits the growth of human breast cancer cells, T47D.
- 3. The death adaptor molecule RAIDD is a novel target of activin and is necessary in the inhibition of cell growth by activin in T47D cells.

CHAPTER I.

GENERAL INTRODUCTION

1. Activin/TGFβ Signaling

Activins and transforming growth factor β s (TGF β s) belong to a group of pluripotent polypeptide growth factors, called the TGF β superfamily. These proteins exert diverse roles on different target tissues throughout the body and control a plethora of biological functions including cell growth, differentiation, apoptosis, migration, adhesion, and embryogenesis.

1.1. Ligand

1.1.1. TGFβ

TGF β 1 is the prototype founding family member of the superfamily. TGF β 1 was initially discovered in combination with TGF- α (EGF) as a factor called sarcoma growth factor (SGF). This factor was shown to transform rat fibroblasts and induce their growth in soft agar^{1,2}

1.1.1.1. TGFβ isoforms, sites of synthesis and knockouts

To date the three TGF β isoforms identified in mammals are TGF β 1, TGF β 2, and TGF β 3. They are highly homologous and arise from distinct genes on different chromosomes. TGF β is primarily produced by T cells³, however, platelets, neutrophils, macrophages, bone, placenta, kidneys and the endometrium are also rich sources of TGF β s. Although the three TGF β isoforms have similar biological functions *in vitro*, their *in vivo* patterns of expression differ. Indeed, this is consistent with the dissimilar

phenotypes in TGF β knockout mice models. Greater than 50% of TGF β 1 null mice die *in utero* due to vasculogenesis and hematopoiesis defects. The surviving TGF β 1 knockouts develop inflammatory disease and pass away within a month after birth^{4-7 8}. In contrast, mice lacking TGF β 2 die perinatally due to malformations of tissues and organs during development⁹. Finally, TGF β 3 knockouts die from abnormal lung development and cleft palate after they are born^{10, 11}.

1.1.1.2. TGFβ structure

Mature TGF β s are 25 kilodalton (kDa) homodimers composed of two 12.5 kDa polypeptides. TGF β s are initially synthesized as large precursor proteins, the 55kDa pre-proTGF β s. Shortly after synthesis, the preproTGF β s dimerize. The pre-proprotein contains a hydrophobic signal peptide, an N-terminal pro-domain and a biologically active peptide at the C-terminus^{12, 13}. The biologically active peptide contains 7-9 cysteines that form intramolecular disulfide bonds which form the cysteine knot that is characteristic to almost all the TGF β family members. Upon removal of the signal peptide, the biologically active peptide is cleaved by a furin-like endoproteinase¹⁴. This pro-peptide also known as the latency associated peptide (LAP), remains non-covalently attached to the active peptide and prevents binding of mature TGF β to its receptors^{13, 15}. This way TGF β s can be maintained in large inactive extracellular reserves. LAP can associate with other latent TGF β associated proteins (LTBPs) such as fibroblast growth factor receptor¹⁶⁻²⁰. LTBPs function to enhance secretion by targeting the complex to the extracellular matrix or to the cell surface where activation takes place. Futhermore,

LTBPs stabilize the TGF β -LAP complex and ensure that TGF β is folded properly^{21, 22}. TGF β s are rendered active once LAP dissociates. The precise mechanism by which active TGF β s are released is not completely understood.

1.1.2. Activin

Activin was first purified from porcine follicular fluid based on its ability to stimulate FSH secretion from the pituitary^{23, 24}. Since then, multiple functions have been assigned to activin in a wide range of tissue. Activin's roles throughout the body are diverse and include the regulation of; embryo development, stem cell biology, reproductive biology, erythroid differentiation, systemic inflammation, cell death, wound healing and fibrosis.

1.1.2.1. Activin isoforms, sites of synthesis and knockouts

Located on different chromosomes, five isoforms of the activin monomeric subunits (βA , βB , βC , βD , and βE) have been identified; however the precise biological function for the latter three is not clear^{25, 26}. The β subunit was initially attributed to activin's antagonist, inhibin. Inhibin is composed of both β and α subunits, giving rise to inhibin A ($\alpha \beta A$) and inhibin B ($\alpha \beta B$). The β subunits of activins form homo or heterodimers giving rise to activin A ($\beta A\beta A$), activin AB ($\beta A\beta B$), activin B ($\beta B\beta B$), etc. Amongst all activins, activin A has been most extensively studied.

The βA and βB subunits are expressed in most tissues and cell types, whereas the βC and βE are mostly found in the liver^{27, 28} ²⁹. Knockout studies of the differenct activin

subunits have highlighted their importance *in vivo*. Whereas mice lacking the activin βC and βE subunits have no obvious abnormalities³⁰, the βA knockouts die perinatally of craniofacial defects^{31,32}. On the other hand, βB knockout mice are viable and display defective eyelids, reproductive anomalies, incomplete mammary gland development and an absence of lactation^{33, 34}.

1.1.2.2. Activin structure

Similarly to TGF β , activin β subunits are produced as pre-proprotein containing an Nterminal signal peptide, a prodomain and the C-terminal biologically active peptide. The biologically active peptide contains 8 cysteine residues forming the cysteine knot. After cleavage at a furin recognition site, the biologically active 25kDa activin is made up of two monomer subunits held together by a disulfide bond³⁵. Dimerization and processing of activins occurs within the cell before their secretion³⁶. Unlike TGF β , which is secreted in its latent form, activins are secreted in their dimeric form as biologically active peptides³⁷.

1.1.3. Other Ligands of the TGFβ Superfamily

The superfamily consists of more than 42 human encoded-members, 7 in *Drosophila melanogaster* and 4 in the nematode *Caenorhabditis elegans*. In addition to both TGF β s and activins, the superfamily consists of inhibins, nodal, leftys, myostatin, bone-morphogenic proteins (BMPs), growth/differentiation factors (GDFs) and Mullerian inhibiting substance with pleitropic roles throughout the body. For example, myostatin

is an important regulator of muscle growth (reviewed in 38). As the name suggests, the BMPs play a critical role in bone development, mesoderm formation, heart and cartilage development (reviewed in 39). Mullerian inhibiting substance causes the regression of the Mullerian ducts which otherwise gives rise to the fallopian tubes, uterus, and upper vagina (reviewed in 40).

1.2. Receptors

Activin and TGF β signal through transmembrane serine threonine kinase receptors⁴¹. Based on homology of the TGF β superfamily of receptors, they are subdivided into two classes; the type I receptors and the type II receptors. These receptors exist as homodimers at the cell surface in the absence of ligand. Each are glycoproteins of approximately 55 and 70kDa respectively. Type III receptors are accessory receptors that lack any intrinsic kinase activity. Whereas in humans there are approximately 42 TGF β superfamily ligands, there are only 7 type I receptors (activin receptor-like kinases, ALKs 1-7) and 5 type II receptors (T β RII, ActRIIA, ActRIIB, BMPRII, MISRII). Multiple ligands interact with the few receptor complexes that exist, allowing for binding promiscuity. Depending on which receptor the ligands bind to, determines the intracellular signaling that is induced.

1.2.1. Type I and Type II Receptors

Different names have been attributed to the type I receptors depending on the groups that cloned them simultaneously. The activin type I receptor is known as ALK4 (activin-receptor like kinase 4)⁴² or ActRIB (activin receptor type IB)⁴³. Activin A mainly binds

ALK4. Recently, evidence suggests that activins B and AB, preferentially bind ALK7⁴⁴. Receptors for the β C or β E subunits are largely unknown. The TGF β type I receptor is known as ALK5⁴⁵ and T β RI⁴⁶. TGF β can also signal through another type I receptor, ALK1^{42, 46, 47}. Whereas ALK4 and ALK5 are expressed in different cells, ALK1 is mainly expressed at sites of angiogenesis, with highest expression in endothelial cells⁴⁷. One TGF β type II receptor exists, T β RII⁴⁸, and there are two activin type II receptors, ActRIIA and ActRIIB^{49, 50}. Activin A binds ActRIIA with a three to four fold lower affinity in comparison to ActRIIB.

1.2.1.1. Structure of the Receptors

Both receptor types consist of three domains: the extracellular, transmembrane and intracellular domains. The major distinction between the two types of receptors is the conserved amino acid sequence within the glycine and serine rich (GS) juxtamembrane domain and the kinase domain within the intracellular domain of the type I receptors.

The extracellular domains of the type I and II receptors are approximately 150 amino acids and are glycosylated. The fold of the receptors is controlled by 10 or more cysteines where three cysteines form a distinct cluster near the transmembrane domain^{51, 52}.

Within the intracellular region of the type I receptor exist two very important domains, the GS and the kinase domain. The GS domain contains a repeated glycine and serine sequence directly preceding the kinase domain. Upon binding to ligand, the type II receptor can interact with the type I receptor. Heterocomplex formation will allow for the constitutively active type II receptor to transphosphorylate the type I receptor. More specifically transphosphorylation occurs within the GS domain, on the serine and threonine residues,⁵³ which subsequently activates signaling. The kinase domain contains a L45 loop sequence that is critical for signal specificity and recruitment of the intracellular mediators, the Smad proteins⁵⁴⁻⁵⁶.

1.2.2. Type III Receptor

In addition to type I and II receptors, ligand crosslinking methods revealed the existence of additional TGF β binding proteins. In comparison to the type I and II, the type III receptors are higher in molecular weight. Betaglycan and endoglin (or CD105) are two examples of type III receptors. They are both single transmembrane proteins that exist as homodimers. Betaglycan, a proteoglycan containing membrane glycoprotein, binds TGF β and facilitates its interaction with the type II receptor^{57, 58}. Specifically, betaglycan has higher affinity to TGF β 2 than TGF β 1 and TGF β 3^{57, 59}. Betaglycan has also been shown to interact with inhibin which promotes interaction with the activin type II receptor. Signaling is henceforth blocked because it competes with activin for receptor binding⁶⁰. Endoglin is abundant in endothelial cells and contains a transmembrane region and a cytoplasmic tail homologous to betaglycan⁶¹. Endoglin may interact with several members of the TGF β superfamily including TGF β 1, TGF β 3 and activin^{62, 63}.

1.3. Core Pathway - The Smads

In the TGF β superfamily, the Smad proteins are the key propagators of the intracellular signal, Figure 1. They act directly downstream of the receptors at the plasma membrane and then translocate to the nucleus and interact with various co-factors to modulate the transcription of target genes. In total, 8 mammalian Smads, 4 *Drosophila* Smads, and 3 Smads in *C.elegans* are known to exist. Smads may be subdivided into three classes: the receptor Smads (R-Smads), the common-partner Smads (Co-Smads) and the inhibitory Smads (I-Smads), Figure 2. There are 5 mammalian R-Smads in which Smad1, Smad5 and Smad8 act downstream of the BMP and anti-Mullerian receptors, and Smad2 and Smad3 propagate the signal for the TGF β , activin and Nodal receptors. There is 1 Co-Smad, Smad4 that binds the R-Smads, and 2 I-Smads, Smad6 and Smad7, that are involved in signal downregulation.



Figure 2. Smad proteins and their structural elements



Adapted from: Massague J. et al. Genes Dev. 2005; 19: 2783-2810

1.3.1. Smad cloning

The first member of the Smad family to be discovered through genetic screens was the *Drosophila* Mothers against Decapentaplegic (DPP) gene (Mad), which is required for the DPP/TGF β response⁶⁴. Along with the discovery of Mad, a separate group discovered additional components of the TGF β family called the Sma genes in *C.elegans*⁶⁵. Henceforth arose the Smad, a contraction of "Sma" and "Mad" to describe the TGF β superfamily signal mediators⁶⁶. Subsequently, the Smads were either cloned by screening cDNA libraries or by searching EST based databases⁶⁷. Smad4 was initially identified by screening pancreatic cancer for gene mutations and was termed deleted in pancreatic carcinoma locus 4 (DPC4)⁶⁸.

1.3.2. Smad structure

Smads have an approximate length of 500 amino acids, consisting of two major domains joined together by a linker region. The N-terminus contains a Mad-homology 1 domain (MH1) whereas in the C-terminus there exists a Mad-homology 2 domain (MH2), Figure 2. The MH1 domain is highly conserved amongst all Smads with the exception of Smad6 and Smad7. On the other hand, the linker domain varies across to all Smads, whereas the MH2 domain is conserved. The MH1 domain is involved in nuclear importing, interaction with nuclear proteins and binding to DNA. Interestingly, a 30 base pairs insert encoded by exon 3 in the MH1 domain of Smad2 inhibits DNA binding⁶⁹. The MH2 domain mediates type I receptor recognition, Smad oligomerization and interaction with cytoplasmic retention proteins, nuclear pore complex proteins and DNA-binding cofactors. The L3 loop in the R-Smad MH2 domain

and the L45 loop of the type I receptor governs the specificity of interaction between R-Smad and type I receptor. The L45 loop of the TGF β and activin type I receptors are identical which permits activation of the same Smads, Smad2 and Smad3^{55, 56}. The interaction between R-Smad and type I receptor is stabilized by the phosphorylated GS motif of the type I receptor binding to the Smad sequence downstream of the L3 loop⁷⁰. At the extreme C-terminal region of the MH2 domain, the R-Smads contain a Serine-X-Serine motif that is phosphorylated by the type I receptor. Once phosphorylated, the R-Smads (Smad2 and Smad3 for activin/TGF β signaling) whose MH1 and MH2 domains are initially associated, unfold and subsequently interact with Co-Smad (Smad4), forming heterocomplexes⁷¹.

1.3.3. Activation Requires Smad Accessory Proteins

Efficient activation and receptor interaction upon activin and TGF β stimulation requires the Smad anchor for receptor activation (SARA)^{72, 73}. SARA is a FYVE domain protein that is anchored to the plasma membrane through interactions with phosphatidylinositol-3-phosphate. Initiation of the TGF β signal occurs through binding of Smad2/3 to SARA and the receptors in early endosomes^{74, 75 76}.

The TGF β receptor Smad complex is also stabilized through its interaction with Disabled-2 (Dab2)⁷⁷. Furthermore, the ras GTPase activating protein (GAP)-binding protein Dok-1 has been shown to interact with the activin receptor. Upon activin stimulation, Dok-1 associates with Smad3 and is required for signaling⁷⁸.

1.3.4. Smad Regulation

Smad proteins can be regulated through various forms of post-translational modifications such as phosphorylation, acetylation, sumoylation and ubiquitination.

1.3.4.1. Smad Phosphorylation

Phosphorylation of R-Smads by the type I receptor permits Smad2 and Smad3 to bind their common partner Smad4 and accumulate in the nucleus. Recently, multiple kinases have been shown to attenuate the Smad. Indeed, the MAP kinase extracellular signal-regulated (ERK), protein kinase C (PKC), calmodulin kinase II (CamKII), G1 cyclin dependent kinases Cdk2/3 and G-coupled receptor kinase 2 (GRK2) may phosphorylate either Smad2 and/or Smad3 in their linker domains or their MH1 domains and consequently block signal transduction⁷⁹⁻⁸³. Furthermore, no effect or enhancement of the Smad transcriptional effect occurs when the Smad2/3 linker domain is phosphorylated by c-Jun terminal kinase (JNK), Rho/ROCK and p38 mitogen activating protein kinase (MAPK)⁸⁴⁻⁸⁶.

1.3.4.2. Smad Dephosphorylation

Whereas phosphorylation is critical in activation of the Smad pathway and in the mediation of the TGF β biological effect, downregulation of the signal is also vital in maintaining a normal cellular response. R-Smad dephosphorylation induces dissociation of the R-Smad-Smad4 complex and export out of the nucleus into the cytoplasm. Recently, the intensely sought after Smad phosphatase, protein phosphatase 1-alpha

(PPM1A/PP2C α) was identified⁸⁷. PPM1A dephosphorylation of Smad2/3 induces nuclear export and is imperative in the attenuation of the TGF β signal⁸⁷.

1.3.4.3. Smad Acetylation, Ubiquitination and Sumoylation

Acetylation is yet another post-translational modification of proteins in which there are various functional consequences. The functional effects of protein acetylation include modulation of protein-DNA and protein-protein interactions and inhibition of nuclear export. p300, an acetyltransferase, has been shown to acetylate the MH2 domain of Smad3 which subsequently upregulates transcriptional activity⁸⁸. Furthermore, p300 may also acetylate Smad7 at sites where ubiquitin moieties attach and thus prevent receptor induced ubiquitination⁸⁹.

Ubiquitination may target proteins for degradation or it may act as a signal similar to phosphorylation. Smad2, Smad3, Smad4, and Smad7 are polyubiquitinated and targeted to the 26S proteosome for degradation⁹⁰⁻⁹². The Homologous to the E6-accessory protein C-terminus (HECT)-domain E3 ligases Smad ubiquitin regulatory factors (Smurf1 and Smurf2), the ubiquitin ligases Tiul1, SCF/Roc1, NEDD4/2, HxN3, SCF b-TrCP1, Ectodermin, and Arkadia⁹²⁻⁹⁶ target the Smads for degradation. In addition, the ubiquitin ligase Itch may add only limited ubiquitin moieties to improve its interaction with the TGF β type I receptor⁹⁷.

Multiple reports claim that Smad4 sumoylation may influence its activity depending on the factor bound to it⁹⁸⁻¹⁰².

1.3.5. Smad Nuclear and Cytoplasmic Shuttling

The distribution of Smads within a cell consists of shuttling between the cytoplasm and Smad2 and Smad3 can be imported into the nucleus through a transport nucleus. receptor independent mechanism. A hydrophobic corridor in their MH2 domains interact with the nucleoporins Nup153 and Nup214^{103, 104}. However Smad3 has additionally been reported to interact with the transport receptor importin. Smad3 has a nuclear localization sequence (NLS) within its MH1 domain which interacts with importins^{105, 106}. In contrast to Smad3, Smad2 is unable to interact with importins due to the extra insert in its MH1 domain. In addition, nuclear export of Smad2 and Smad3 is also thought to be due to their interaction with Nup153 and Nup214¹⁰³. Interestingly they possess a nuclear export sequence (NES) but do not interact with the nuclear exporter CRM1¹⁰⁷. On the other hand, a NES within Smad4's linker region interacts with CRM1 and exports Smad4 to the cytoplasm¹⁰⁸. Upon Smad4 interaction with the phosphorylated Smad2/3, the NES is masked causing the complex to remain nuclear. Once the R-Smads are dephosphorylated, Smad4 NES is uncovered and Smad4 is subsequently exported from the nucleus by CRM1^{109, 110}.

1.3.6. Smad Nuclear Signaling

All Smads possess the ability to induce transcription. Whereas Smad2 cannot bind DNA due to its extra exon, Smad3 and Smad4 may interact weakly with DNA. The β -hairpin loop within the MH1 domain allows for Smad3 and Smad4 to bind the Smad Binding Element (SBE), 5'-CAGAC-3'⁶⁹. At natural promoters, Smad interaction with transcription factors that bind DNA adjacent to the SBE, allows for higher affinity binding for both factors. GC-rich motifs in certain gene promoters may also bind Smad3

and Smad4¹¹¹. Smads interactions with various co-activators, co-repressors or transcription factors allow for widespread flexibility and bestow specificity of the TGF β /activin signal within the cell. Therefore, the intracellular DNA binding partners that interact with the Smads will determine what genes will be transcribed and henceforth the final biological outcome.

1.3.6.1. Smads and Transcription Factors

Smads interact with a wide range of DNA transcription factors through either their MH1 or MH2 domains, Table 1. The interaction between Smads and transcription factors is cell context specific and grants the versatility of the activin/TGF β signal. Smad2, Smad3 and Smad4 interact with various transcription factors including the bHLH, bZIP, Forkhead, Homeodomain, nuclear receptor, Runx and zinc finger protein families, amongst others (reviewed in ¹¹²). Through these interactions they either positively or negatively regulate a multitude of genes.

Table 1. Smad-Binding Transcription Factors

	Interacting		
Smad-binding	Smad and		
partners	domains	Features/mechanisms of action	Defenences
bHLH family			Kelefences
E2F4/5	Smad3 (MH2)	Recruitment of n107 to Smad2 to made	1 107
		myc gene	
Max	Smad3 (MH1)	Max inhibits transmisting of the local state	108
		wax minors transcription activation by Smad3	100
MyoD	Smad3 (MH1-	Interference of MyoD/E protein/DNA complex	109
	linker)	formation	
TFE3	Smad3/4	Synergistic cooperation on TGF-B target genes	110-112
		such as PAI-1, Smad7	
bZIP family			1
ATF2	Smod2/4 (MIII)		
1.7772	Siliau3/4 (MHI)	Stimulation of ATF2 transactivation	113
ATF3	Smad3 (MH2)	Repression of the Id1 promoter	114
c-Fos	Smad3 (MH2)	Cooperation on AP-1-dependent TGE-8 target	115
		genes	
c-Jun, JunB, JunD	Smad3 Smad4	Positively and negatively regulate Smod	115,116
		activity	
CEBΡα, β, δ	Smad3 (MH1)	Smad3 inhibits CEBP's transactivation	117,118
Forkhead family			I
FoxH1/FAST	Smad2/3	Formation of activin-responsive factors on the	105,119,120
		activin-responsive promoters	
FoxO	Smad2/3	Regulation of p21Cip1	121
Homeodomain	<u> </u>		
nrotein			
Dlx1	Smod4		- 100
	Sinau4	Inhibits Smad4 signaling	122
Milk/Mixer	Smad2 (MH2)	Recruitment of Smad2/Smad4 activators to the	120,123
		activin-responsive complex	
Nuclear receptor			
family			
Androgen recentor	Smad3 (MH2)	Province of the life of the party of the	124.126
(AR)	Sinado (WI12)	activity and of AD activity	124-120
(activity and of AR activity	
Estrogen receptor	Smad3/4(MH2)	Repression of Smad target genes	126,127
Glucocorticoid	Smad3 (MH2)	Inhibition of Smad3 transactivation activity	128
receptor			
LINIE4	0		
ПINC4	Smad3/4	Cooperative activation	129
RXR	Smad3 (MH2)		130
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Vitamin D3 receptor	Smad3 (MH1)	Coactivation of ligand-induced transactivation of vitamin D receptor	131
Runx family			
CBFA1/Runx2/AML	Smad2/3 (MH2)	Regulation of immune responses	132-134
Zinc finger protein family			
GATA3	Smad3	Recruits Smad3 to GATA sites to cooperatively activate transcription	135
Gli∆C-ter	Smad2/3/4	Unknown	136
OAZ	Smad4 (MH2)	Formation of BMP-responsive activator complex	137
Sp1	Smad2 (MH1)Smad4 (MH2)	Cooperative activation of TGF-β target genes, e.g., p15Ink4B, p21Cip1, Smad7, PAI-1, and collagen	133,138
YY1	Smad4 (MH1)	Complex with Smads and GATA	139,140
ZNF198	Smad3 (MH2)	Unknown	141
Others			
β-catenin	Smad4	Wnt-dependent activation of LEF1 target genes	142-144
HIF-1α	Smad3 (MH1, MH2)	Cooperation of TGF- β with hypoxia pathway and angiogenesis	145
IRF-7 (IRFs)	Smad3 (MH2)	Smad3 activation of IRF-7 transactivation function	146
Lef1/TCF	Smad2/3/4 (MH1, MH2)	Smad coactivation of LEF1 signaling	142,147,148
MEF2 (MADS box)	Smad3	Smad3 represses the transcription activity of MEF2	149
Menin	Smad2/3 (MH2)	Facilitate Smad DNA binding	150
NFкB p52	Smad3	Coactivation of KB site	151
NICD	Smad3 (MH2)	Coactivation of NICD-RBP-Jk complex to regulate the Notch targets	135,152
p53	Smad2/4	Synergism and antagonism	153-155
Pax8	Smad3	Smad3 reduces Pax8 DNA binding	156
SRF	Smad3	Mediate TGF-β-induced SM22α transcription	157

Adapted from ¹⁰⁶.

1.3.6.2. Smads interactions with Co-activators and Co-repressors

In addition to cooperating with transcription factors, Smads may also recruit coactivators or co-repressors to their transcriptional complexes to further control activin/TGF β signaling. Co-activators, such as the CREB binding protein (CBP) and p300, enhance transcription by bridging the RNA polymerase II complex with the transcription factor/Smad complex. In contrast, co-repressors such as TG3-interacting factor (TGIF), Sloan-Kettering Institute proto-oncogene (Ski) and Ski-related novel gene (SnoN) repress activin/TGF β mediated gene activation by binding Smads. More specifically, suppression of gene activation occurs by Smads/co-repressor complex either on their own or through their binding to chromatin-condensing histone deacetylases, (reviewed in ¹¹²).

1.3.7. Inhibitory Smads

Smad6 and Smad7 are the two inhibitory Smads in vertebrates. Whereas Smad6 inhibits the BMP pathway, Smad7 inhibits both the activin/TGF β and BMP signaling^{164,165, 166}. The MH2 domain in I-Smads is highly homologous to that of R-Smad and Smad4. Their MH1 domain is disparate and is dissimilar to other Smads. However, the I-Smad MH2 domain does not possess the SXS motif of phosphorylation that the R-Smad contains. Smad7 inhibits the activin/TGF β signal through three mechanisms. First, Smad7 competes for binding with Smad2/3 to the activated type I receptor therefore blocking signal mediation by the R-Smads^{165, 166}. Second, Smad7 is involved in targeting receptor degradation by the recruitment of the ubiquitin ligase Smurf^{167, 168}.

Another recent role for Smad7 is induction of receptor dephosphorylation and degradation by recruiting the protein phosphatase PP1/GADD34 to the activated receptor complex¹⁶⁹. A negative feedback loop is involved in the downregulation of the activin/TGF β signal via upregulation of Smad7 gene transcription. More specifically, the upregulation occurs upon activation of R-Smad/Smad4 by activin/TGF β induction. Furthermore, TGF β signaling induces translocation of Smad7 from the nucleus to the cytoplasm where upon receptor binding signaling is attenuated¹⁷⁰. Finally, evidence for Smad7's role in transcriptional regulation is based on its transactivation potential, interaction, and acetylation by p300⁸⁹. In addition to activin/TGF β induction of Smad7, its expression is also increased by interferon- γ STAT signaling, TNF- α induced NF- κ B, epidermal growth factor receptor (EGFR) and other tyrosine kinases^{171, 172}.

1.3.8. Smad knockouts

The Smad2 and Smad4 knockout mice are embryonic lethal¹⁷³⁻¹⁷⁶. While the Smad2 deficient mice die *in utero* due to a lack of anteriorposterior axis formation and no mesoderm formation, the Smad4 knockout's lethality is due to defective visceral endoderm leading to gastrulation defects. The Smad3 knockout phenotype is less severe. Although the mice are viable, they display reduced body size, metastatic colorectal tumor development, accelerated wound healing, impaired mucosal immunity and massive inflammation¹⁷⁷⁻¹⁸⁰. Although it appears that Smad2 and Smad3 are functionally similar, besides their differences in DNA binding, the phenotype of their respective knockout mice are dissimilar. This suggests that Smad2 may play a more pertinent role in embryo development. Recently, the functional role of Smad7 *in vivo*

was elucidated through the generation of mice lacking exon I of Smad7. The Smad7 exon I knockout mice are viable displaying a reduction in body size, and an impaired immune system¹⁸¹.

1.4. Crosstalk with Other Signaling Pathways

It has become increasingly apparent that $TGF\beta$ responses are not only regulated by the Smads but also other signaling pathways. The TGF_β receptors activate Smadindependent pathways that can directly crosstalk with the Smad pathway but can also allow for Smad-independent biological responses by TGFB. Besides the mitogenactivated protein kinases (MAPKs) which will be covered in detail in CHAPTER III, TGFB can signal through the phosphatidyl inositol-3-kinase (PI3K)/Akt pathway and Rho family members. The PI3K pathway plays an important role in regulating antiapoptotic/survival signals, epithelial to mesenchymal transition (EMT) and protein synthesis. For example, activation of the PI3K/Akt inhibits TGF\beta-induced apoptosis in primary mammary epithelial cells and in the HC11 mouse mammary epithelial cell line¹⁸². Interestingly, inhibition of the PI3K pathway reduces phosphorylated Smad2 by $TGF\beta$ which consequently prevents EMT, a process that is important in mediating tumor cell invasion to surrounding tissue in which TGF β plays a prominent role¹⁸³. TGF β activation of the small GTPases, RhoA, Rac and Cdc42 may also lead to EMT by affecting membrane ruffling, stress fiber formation and lamellipodia formation¹⁸⁴. In summary, TGF β crosstalk mechanisms lead to the regulation of the final biological outcome.

2. Biological Functions of Activin/TGF^β

Activin and TGFβ regulate a plethora of biological activities including cellular proliferation, differentiation, adhesion, apoptosis, extracellular matrix production, immune regulation, embryogenesis, hormonal control, tumor suppression, angiogenesis and tumor promotion. The physiological effects of these factors are manifested in a cellular specific manner. Although activin and TGFβ share identical signaling machinery, targeted *in vivo* disruption of the ligands and their receptors result in mice with varying phenotypes. However, a study has revealed a similar transcriptome regulated by both signaling pathways¹⁸⁵. Using cell lines overexpressing the activated form of both the activin type I (ALK4) and TGFβ type I (ALK5) receptors, the transcriptomes induced by each signaling pathway were investigated. Interestingly, no differences between the two pathways induced by these genes *in vitro* were observed¹⁸⁵. These findings allude to a functional redundancy between both pathways in the regulation of the biological effect.

2.1. Cellular Proliferation

One of the most important biological functions of activin and TGF β is their ability to induce cell cycle arrest in certain cells. Indeed, in the last few years a tremendous amount of knowledge on the cytostatic effect of these factors has been gathered. Activin and TGF β play a vital role in growth inhibition of epithelial, hematopoietic, neuronal and endothelial cells. TGF β mediates cell growth inhibition by directly affecting cell cycle components, particularly those involved in the G1 phase of the cell cycle, and

through repression of mitogenic transcription factors¹⁸⁶⁻¹⁹¹. Activin and TGF β signaling upregulate expression of the cyclin dependent kinase inhibitors, p15^{INK4B} and p21CIP1^{/WAF1}, which through a tightly controlled mechanism leads to the inactivation of G1 phase cyclin dependent kinases^{127, 144, 187, 188, 192, 193}. Additionally, TGF β rapidly represses expression of the mitogen c-myc which is involved in inhibition of p15^{INK4B} and p21CIP1^{/WAF1} ¹¹³. Besides c-myc, both activin and TGF β signaling downregulate the differentiation transcription factors Id1, Id2, and Id3 ¹²⁰. Id proteins (Id1–Id4) are negative regulators of basic helix–loop–helix (bHLH) transcription factors. They promote cell growth, inhibit differentiation, and play critical roles in development and cancer¹⁹⁴. Although today, it is widely accepted that TGF β inhibits growth of multiple cell types, TGF β was initially discovered as a factor that induced anchorage-independent growth of fibroblasts^{195, 196}. Thus, TGF β mitotic ability is still observed in certain transformed cells and immortalized fibroblasts¹⁹⁷.

2.2. Differentiation

Both activin and TGF β can regulate the differentiation of a wide spectrum of cells including immune, erythroid, neuronal, mesenchymal, keratinocytes, bronchial epithelial and colon carcinoma cells. For instance, during early pregnancy activin regulates the differentiation of human cytotrophoblasts¹⁹⁸. Furthermore, activin is involved in the regulation of branching morphogenesis in the lung, kidney and prostate (reviewed in ¹⁹⁹). Differentiation by TGF β and activin is controlled either directly by modulating differentiation-specific genes, or by influencing cell adhesion or proliferation (reviewed in ²⁰⁰). For example, activin can cause differentiation of erythroleukemic cells, induction of hemoglobin synthesis and inhibition of cellular division²⁰¹⁻²⁰³.

2.3. Apoptosis

The apoptotic function of activin and TGF β has been investigated in many cell types and in most cases their signaling pathways are pro-apoptotic. Indeed, they have been shown to induce apoptosis in epithelial cells, endothelial cells, hematopoietic stem cells, lymphocytes, hepatocytes, and neurons, as well as in breast cancer, gastric cancer, hepatic cancer, lymphoma, ovarian cancer, and prostate cancer cells (reviewed in ²⁰⁴). TGF_β and activin induced apoptosis is frequently a Smad-mediated process. Through Smad signaling, they may induce the expression of pro-apoptotic genes such as the TGF β -inducible early-response gene (TIEG1), death associated protein kinase (DAPK) and SH2-domain containing inositol-5-phosphate (SHIP)²⁰⁵⁻²⁰⁷. Furthermore, TGFβ may upregulate proapoptotic factors (ie, Bax), and/or downregulate antiapoptotic factors (ie, Bcl-2 and Bcl-xL) and activate caspases that partake in the apoptotic effector system²⁰⁴. On the other hand, other factors may cooperate with TGF β to induce death in different types of cells. For instance, TGF β and tumor necrosis factor α (TNF- α) may synergize to induce apoptosis in transformed fibroblasts by reducing levels of Bcl-2 and Bcl-xL²⁰⁸. TGF_β may also antagonize pro-survival signals and by doing so induces apoptosis. For example, Smad3 binds to the pro-survival kinase Akt allowing for TGFB to induce its apoptotic effect^{209, 210}. Moreover their role in inducing apoptosis *in vivo* is critical for proper organ development. For example, after lactation, mammary glands display elevated TGFB3 levels which subsequently induces programmed cell death

during involution²¹¹. Depending on the cellular system, activin and TGF β are deathinducing agents, however, the precise mechanisms involved in their pro-apoptotic function are still poorly defined and they are cell and context specific.

2.4. Extracellular Matrix Production and Adhesion

Tissue homeostasis and function depends on the regulation of extracellular matrix production and turnover. Activin/TGF\beta signaling tightly controls the production of major constituents of the extracellular matrix and matrix regulatory enzymes such as collagens, fibronectin and protease inhibitors such as plasminogen activator inhibitor I (PAI-1), and tissue inhibitor of metalloproteinases (TIMPs)²¹². For instance, Smads in cooperation with other transcription factors regulate the expression of PAI-1^{116, 212-215}. In addition, JNK activation by TGF β regulates fibronectin expression²¹⁶. During tumorigenesis, TGF β may cause the degradation of basement membrane components which subsequently leads to a loss of cellular-matrix adhesion. TGF β mediates this effect through direct activation of proteolytic enzymes such as matrix metalloproteases 2 and 9 (MMP2 and MMP9). This leads to degradation of type IV collagen in the basement membrane^{217, 218}. TGF_β and activin induced loss of cell-to-cell adhesion properties is characterized by its ability to decrease E-cadherin and regulate the expression of other cytoskeletal proteins²¹⁹. Loss of adhesion caused by TGF_β induces epithelial to mesenchymal transition (EMT) allowing cells to become more motile and This morphogenic response is imperative in TGFB's role in regulating invasive. embryogenesis and the pathology of cancer.

2.5. Immune Regulation

Activin and TGF β signaling play a critical role in regulating the immune system. Indeed, TGF β has been characterized as the most powerful immunosuppressor in mammals²²⁰. TGF β 's essential role in maintaining proper immune regulation is evident from the TGF β 1 knockout mice. These mice die from immune deregulation complications^{5, 221}. Furthermore at the cellular level, TGF β inhibits the proliferation and functional differentiation of immune cells including, natural killer cells, T lymphocytes, neutrophils, macrophages, and B cells. Additionally, TGF β 's immunosuppressive capabilities have a direct effect on tumor progression. More specifically, TGF β derived from tumors suppress T-cell activation allowing tumors to escape immune surveillance (reviewed in ²²²).

2.6. Development

TGF β , activin and their signaling components play a crucial role in embryo development. The imperative role of these signaling components is obvious from lethal phenotypes of the knockout models. TGF β 1, ALK4, T β RII, ActRIIA-ActRIIB double knockout, Smad2 and Smad4 knockout mice die during embryo development^{4, 175, 223-226}. Among the multiple defects in development TGF β 2 and TGF β 3 null mice have pronounced lung development impairment leading to perinatal death^{9, 10}. Activin β A knockout mice die postnatally from craniofacial defects³¹. In *xenopus* embryos, truncated activin receptor inhibits mesoderm induction²²⁷. In all, TGF β superfamily signaling members play a regulatory role in early post implantation mouse embryonic

and extraembryonic angiogenesis, vasculogenesis and development of the eyes, heart, left-right asymmetry, craniofacial, nervous and gonads (reviewed in ²²⁸).

2.7. Hormonal Regulation

Activin's role as an important regulator of hormones was evident upon its original identification as a stimulator of FSH production in the pituitary^{23, 24, 229}. Recently, activin has not only been shown to regulate FSH but also LH production via Smad signaling²³⁰⁻²³². Furthermore, *in vitro* data suggest that activin strongly inhibits growth hormone and corticotrophin (ACTH) secretion from the pituitary²³⁻²³⁵. On the other hand, activin may stimulate progesterone, GnRH and hCG production in placental cells²³⁶.

2.8. Angiogenesis

Activin/TGF β has an imperative biological effect on angiogenesis, a process by which blood vessels deliver nutrients and oxygen to cells. TGF β signaling component's vital role in angiogenesis is evident in the TGF β 1 and T β RII knockout mice that die *in utero* due to defective angiogenesis and vasculogenesis²²⁴. Moreover, mice with null mutations in genes encoding ALK1, ALK5 and endoglin have defective angiogenic phenotypes²³⁷⁻²⁴⁰. TGF β 1 may stimulate fibroblasts and epithelial cells to produce a vital angiogenic growth factor called vascular endothelial growth factor (VEGF). VEGF acts directly on endothelial cells to induce proliferation and migration²⁴¹. Interestingly, two TGF β signaling pathways are stimulated in endothelial cells. Not only is the Smad2/3 pathway induced through ALK5, but due to high expression of ALK1 in

endothelial cells⁴⁷, the Smad1/5 pathway is also activated. While TGF β binding to ALK5 seems to play a role in vascular maturation, ALK1 binding stimulates endothelial cell proliferation²⁴². TGF β 's ability to balance signaling between ALK1 and ALK5 allows for the regulation of vascular homeostasis. A major role for activin and TGF β is to induce angiogenesis of tumor cells which is crucial for tumor growth and invasion leading to metastasis.

3. Mammary Gland Development

Mammary gland development is an ongoing process throughout the lifetime of a reproductive female. This continuing process is under the control of multiple growth factors such as estrogen, progesterone, prolactin (PRL), TGF β and activin. Development of the mammary gland begins in the embryo where the rudimentary mammary epithelium is formed, Figure 3. At puberty, a network of ductal branches invades the fat pad forming terminal end buds (TEBs) under the control of ovarian hormones. During pregnancy, reproductive hormones induce massive epithelial proliferation which allows for lateral branching of the ducts forming lobuloalveolar structures. Alveoli are lined with milk secreting epithelial cells surrounded by myoepithelial cells that envelop a circular lumen. Upon lactation, terminally differentiated lobular alveoli secrete milk. Once suckling ceases, two stages of involution occur. The first is induced because of milk stasis where there is extensive remodeling of the alveolar structures due to apoptosis. It is a stage that is characterized by regulation of apoptotic and anti-apoptotic genes and downregulation of milk protein gene expression²⁴³⁻²⁴⁵. One of the main signaling molecules that is upregulated and

responsible for inducing apoptosis during the initial phase of involution is TGF β 3. The second stage of involution is defined by the destruction of the lobuoloaveolar structures due to a loss of circulating hormones and induction of protease genes^{244, 245}.

Figure 3. Mammary Gland Development



Mammary Gland Development Images taken from ²⁴⁶

3.1. Hormonal control of Ductal and Alveolar Development

Mammary growth from birth to the onset of puberty is minimal and proportional to that of the growth of the body. Genetic and tissue transplant experiments have implicated the requirement of certain genes during the initial fetal development of the mammary gland including Lef-1, Msx1, Msx2 and PTHrP^{247 248}. The sex steroid hormones estrogen and progesterone are critical for mammary ductal and alveolar development. Evidence from the estrogen receptor and progesterone receptor knockouts confirm their necessity for ductal development and for lobuloalveolar development respectively. During early puberty, estrogen, growth hormone and local production of insulin like growth factor-1, IGF-1, induces the growth of mammary ductal epithelial cells²⁴⁹. Initial alveolar proliferation is due to the synergistic action of prolactin and progesterone²⁵⁰. Other factors such as several cytokines including RANK-L, and members of the epidermal growth factor, EGF, family are also important for lobuloalveolar development^{251, 252}. During pregnancy and lactation, prolactin, placental lactogens, progesterone and local growth factors influence extensive proliferation of the lobuloalveolar epithelium. Prior to lactation, both progesterone and placental lactogen levels fall. During lactation, the lobuloalveolar epithelium becomes secretory, allowing for the synthesis of milk proteins and lactogenic enzymes.

4. Activin/TGFβ signaling in Mammary Gland Development

The mammary gland is a major endocrine target tissue for activin and TGF β . They appear to play a role in the regulation of mammary epithelium growth and differentiation at all stages of the gland's development including involution. The role of TGF β in this gland has been studied more extensively in comparison to activin, due to the generation of multiple transgenic mice. The importance of activin in mammary gland development stems from the expression of activin subunits and more specifically the phenotype of activin β B subunit knockout mice.

4.1. Ligand and Signaling Components Expression in the Breast

4.1.1. TGFBs and TGFB receptors

TGF β isoforms are expressed in the mammary gland at almost all physiological stages except lactation. During lactation, although there is extensive downregulation of all isoforms, there are trace levels of TGF β 2 mRNA^{211, 253, 254}. In virgin mice, TGF β 1 surrounds the ducts and accumulates in the periductal extracellular matrix where it maintains the spaces between the ducts²⁵³. Functional *in vivo* studies reveal that pellets slowly releasing TGF β 1/2/3 that are implanted in the mammary end buds of mice, inhibit ductal growth^{253, 255}. Similar studies performed with TGF β implants did not effect lobuloalveolar development²⁵⁶. During pregnancy, low levels of TGF β 1 and even lower levels of TGF β 2 are found in alveoli and in the ducts whereas TGF β 3 is highly expressed in these structures²⁵³. At involution, an initial increase of TGF β 3 is due to milk stasis and a subsequent increase in TGF β 1 and TGF β 2. At this stage of mammary

gland development, TGF β induces massive apoptosis resulting in restructuring and restoration of the gland back to its virgin state.

The type I and type II TGF β receptors are expressed in both the ductal epithelial and stromal cells in the virgin, pregnant, and involuting breast suggesting that these aforementioned cells are responsive to TGF β^{257} .

4.1.2. Activin and activin receptors

Both activin and its receptors are expressed in mammary tissue²⁵⁸⁻²⁶⁰. Functionally, activin inhibits the growth of both primary and transformed mammary epithelial cells. In addition activin suppresses tubule formation observed in human mammary organoids in response to hepatocyte growth factor/scatter factor (HGF/SF), suggesting a role for activin in regulating mammary cell growth and morphogenesis²⁵⁸. Furthermore, the presence of activin in its dimeric form in the cystic fluid of fibrocystic disease implies a local production and secretion of this protein in the human breast.

The expression of activin components is elevated during mid to late lactation and depressed during both involution in the mammary epithelium and stroma²⁶¹. Elevated levels of phosphorylated Smad3 during lactation in mammary epithelial cells are indicative of activin signaling²⁶¹. It has beens suggested that the downregulation of TGF β during lactation is to avoid apoptosis and that activin signaling permits proper lactation while restricting hyperproliferation of the tissue²⁶¹.

4.1.3. The Smads

A study in which the role for Smad3 in mammary gland development is investigated, found that all Smads are expressed throughout all stages of development¹⁷⁸. Although

still present, expression of all Smads decreases during lactation in the gland. For Smad2 and Smad4, the decrease is sustained at early stages of involution and is restored at day 6 of involution¹⁷⁸. Furthermore, when Smad3 null glands and Smad3 expressing glands are transplanted into the fat pads of nude mouse hosts, apoptosis occurs during involution more in the Smad3 expressing glands. This suggests that Smad3 contributes to the induction of apoptosis during involution¹⁷⁸.

4.2. Knowledge Gained from Mouse Models

The expression pattern of TGF β and activin in the mouse suggests that they may have roles in regulating branching morphogenesis, lactation, and involution. An animal model system developed to elucidate the *in vivo* role of activin has highlighted its importance in mammary gland development. In particular, deletion of the activin β B subunit, ablating three of the dimeric β molecules (activin B, activin AB and inhibin B), causes incomplete mammary development and an absence of lactation²⁶². Interestingly, when the mammary glands of β B knockout mice are transplanted into wild-type mice, they can develop normally²⁶². However, in order for the gland to undergo proper development, it requires that the site of transplantation of the mammary epithelium be an active stromal tissue such as the fat pad. This suggests that stromal β B production can compensate for the epithelial deficiency²⁶².

Invaluable insight in understanding the function of TGF β in the mammary gland has been achieved via gain of function and loss of function transgenic animals. The first TGF β transgenic mouse to be developed was a constitutively active TGF β 1 from the mouse mammary tumor virus (MMTV) promoter. This mouse resulted in the inhibition

of ductal development without affecting alveolar growth²⁶³. On the other hand, when TGF β 1 was expressed using a milk protein specific promoter, whey acidic protein (WAP)-TGF β 1 alveolar development was significantly inhibited which resulted in the suppression of lactogenesis²⁶⁴. Interestingly, transplantation of the transgenic mouse's mammary epithelium into the fat pad of wildtype mice barred normal mammary development. This observation implies that the TGF β 1 effect on lobuloalveolar development is due to an autocrine rather than a paracrine effect²⁶⁵. This means that TGF β 1 is not affecting the production of a factor in the stroma that may be inducing the (WAP)-TGF β 1 phenotype. In summary, these transgenic mouse models, using developmentally restricted promoters, illustrate that TGF β inhibits proliferation within the mammary epithelium in response to either the hormones of puberty or pregnancy however the molecular mechanisms in inducing this effect are unknown.

Loss of function studies further reveal the role of TGF β signaling in the breast. Dominant negative T β RII receptor expression via a MMTV promoter, resulted in precocious alveolar hyperplasia and lactation in virgin mice²⁶⁶. Recently, a conditional knockout of T β RII in fibroblasts revealed reduced ductal elongation²⁶⁷. Furthermore, these mice lacked both mature ducts and terminal endbuds highlighting the importance of stromal TGF β on gland development²⁶⁷. Hence loss of TGF β signaling in the stroma, altered paracrine signaling to the mammary epithelium. Finally, overexpression of a constituvely active TGF β type I receptor (ALK5TD) mutant using the MMTV promoter in mice exhibited depressed lobuloaveolar development during pregnancy²⁶⁸. The importance of TGF β in the mammary gland is further illustrated by TGF β 1-null heterozygous mice. These animals display accelerated ductal outgrowth during puberty

and alveolar expansion during pregnancy due to an increase in mammary epithelial cell proliferation²⁶⁹. This suggests that TGF β normally acts as an inhibitor of ductal elongation and branching.

Whereas, as mentioned earlier, Smad2 and Smad4 knockouts are lethal, Smad3-null mutant mice survive postnatally. Analysis of the Smad3 knockout mice reveals that the mammary gland of virgins show delayed development¹⁷⁸. However, when given appropriate hormonal stimulation, the Smad3 null mammary epithelium develops normally and undergoes full functional differentiation¹⁷⁸. Future conditional knockouts will further address the relative contribution of each Smad in mammary gland development.

4.3. Summary

It is clear from a variety of studies looking at TGF β /activin signaling components expression, within various stages of mammary gland development, that they induce a myriad of effects. *In vivo* studies using exposure to exogenous sources or transgenic expression of constitutively active protein have shown what TGF β can do in the mammary gland. These have generally led to the conclusion that TGF β has a prominent role in regulating pattern formation by the epithelium, perhaps via interactions with the stroma, and is involved in fate decisions by individual cells. Although no transgenic mice models have been generated to investigate activin signaling within the mammary gland, the activin β B knockout mouse alludes to an important function activin in the regulation of mammary differentiation and lactation. However, the signaling pathways activated by activin and TGF β leading to these aforementioned effects are not yet fully characterized.

5. Activin/TGF β and breast cancer

TGF β signaling has been described as a double-edged sword in cancer²⁷⁰. This description was coined due to its dual and contrasting role in tumor biology. In early stages of tumorigenesis TGF β is a potent inhibitor of tumor cell growth where its signaling components have been characterized as tumor suppressive. In contrast, TGF β also has the potential to drive malignant progression, invasion, and metastasis. Although activin's increasingly vital role in breast cancer pathogenesis and metastasis emerges exponentially, most of the focus to date has been on TGF β .

5.1. Ligand expression and regulation

In primary human breast cancers, TGF β localization concentrates around epithelial tumor cells, while the flanking stromal cells are negative. Multiple studies have found a positive correlation between TGF β expression by primary breast cancer and advanced tumor progression²⁷¹⁻²⁷⁴. Furthermore, many breast cancers synthesize and secrete high levels of TGF β^{275} . These studies implicate TGF β as a promoter of breast cancer progression rather than an inhibitor of tumorigenesis.

Initial systemic localization studies of activin subunits display positive expression in breast tissue whereas malignant breast lesions are negative²⁵⁹. This suggests that the absence of activins in carcinoma tissue may facilitate abnormal cell proliferation. Furthermore, there is a downregulation of activin and its signaling components in high

grade breast cancers, suggesting a role for activin in breast tumor development²⁷⁶. However, subsequent reports have also correlated increased activin expression with increased bone metastasis. Fascinatingly, activin may thus be implicated in the progression of breast cancer metastasis²⁷⁷.

5.2 Receptor expression and regulation

Interestingly, two studies have reported diminished T β RII expression in early and late stages of human breast cancer²⁷⁸. This decreased expression of T β RII correlates with an increase risk of developing invasive breast cancer²⁷⁸. ALK5 expression was observed in epithelial cell cultures derived from malignant breast tissue²⁷⁹. *In vitro*, numerous breast carcinoma cell lines, express all TGF β and activin signaling components. Some exceptions include the MDA-MB-468 which lacks Smad4, and ZR-75-1 and T47D, where T β RII is not detected²⁸⁰.

5.3. Smad signaling

5.3.1. Cytostatic Response

Escape of cellular proliferation inhibition is a defining hallmark of cancer. TGF β mediated inhibition of cellular proliferation is associated with its ability to block tumorigenesis. TGF β /Smad signaling increases expression of p21CIP1^{/WAF1} in the human mammary epithelial cell line MCF-10A²⁸¹. In breast cancer cells, TGF β growth inhibititory response could be restored once the T β RII is reintroduced into the cells through the induction of cell cycle inhibitors p21CIP1^{/WAF1} and p27²⁸². Interestingly, it

has been reported that TGFβ receptors and Smad activity are still present when breast cancer cells lose their cytostatic response²⁸³. The inability for TGFβ to induce the cytostatic response is apparent in breast cancer metastasis^{284, 285}. Indeed, the loss of TGFβ cytostatic response in breast cancer cells has been associated with a defective repression of c-myc²⁸⁴ and induction of the cell cycle inhibitor p15 by the Smads²⁸⁵. Furthermore, the transcription factor C/EBPβ is central in regulating c-myc and p15^{INK4B} by TGFβ signaling²⁸⁵. In metastatic breast cancer, TGFβ's inability to regulate cell growth inhibition may be due to an increase in the inhibitory isoform LIP of C/EBPβ²⁸⁵.

A limited study on MCF7 cells showed that, as well as expressing the activin receptors, these cells produced activin subunit proteins²⁶⁰. Indeed, activin was found to cause G1 cell cycle arrest and hence inhibit MCF7 cell growth. Later studies have shown that activin inhibits cellular proliferation by increasing expression of $p15^{INK4B}$ which reduced expression of cyclin A and subsequently leading to retinoblastoma protein phosphorylation²⁸⁶.

The effects of activin on a panel of breast cancer cell lines that were ER positive or negative were investigated²⁸⁷. The ER-positive cell lines in the study were inhibited by activin, whereas the ER-negative cell lines were not. In two of the ER-negative cell lines, resistance to the growth-inhibitory effects of activin were explained by down-regulation of the activin receptors. In two other ER-negative cell lines, MDA-MB-231 and MDA-MB-468, activin insensitivity was not due to reduced activin receptor levels. Instead, the failure of the MDA-MB-468 cell line to respond to activin was explained by loss of Smad4 expression in these cells. Transfection of Smad4 into these cells rendered

them sensitive to inhibition by activin. The other activin resistance/ER-negative cell line, MDA-MB231, expressed both Smad4 and Smad2. In this case, additional studies revealed that these cells lacked a functional ActRI²⁸⁷. These studies demonstrate that there is a loss of activin signaling components in more aggressive estrogen receptor negative cell lines suggesting a role for this pathway in tumor progression.

5.3.2. Apoptosis

Cancer cells ability to evade apoptotic signals allows for their survival. Resistance to TGFβ-induced apoptosis may be an essential component of tumorigenesis, particularly for cancers arising from tissues in which $TGF\beta$ is a prominent regulator of apoptosis. Indeed, TGF β mediated apoptosis is important in restructuring the mammary epithelium during involution²¹¹. TGF β downregulates the mitochondrial anti-apoptotic factors Bcl-2 and Bcl-X_L in mouse mammary epithelial cells inducing apoptosis^{288, 289}. As mentioned previously, TGFB is a death-inducing factor in breast cancer cells. TGFB has been shown to induce cell death in MCF7 breast cancer cells through a substantial downregulation of Bcl-2 and Bcl- X_L mRNA²⁹⁰. In addition, TGF β may sensitize cells for other pro-apoptotic stimuli. For example, when dominant negative TBRII was introduced in the breast cancer cell line MCF7, these cells became resistant to TNF-ainduced cell death²⁹¹. Furthermore, breast cancer cells treated with Tamoxifen lead to an upregulation of TGF β and subsequent cell death²⁹². In addition, the ability of TGF β to induce apoptosis in lymphocytes may be a critical component for the immunosuppressive effect of TGFB during tumorigenesis which will be reviewed further

in subsequent sections. Although a well-documented phenomenon, the biochemical mechanism responsible for TGF β induced apoptosis in breast cancer remains elusive.

5.4. Receptor and Smad mutations

TGF β and activin signaling component mutations are often associated with human cancer. Indeed, the T β RII and the ActRII genes contain a poly-adenine tract in their kinase domains that is often mutated in human cancers such as gastric, pancreatic, lung, and brain (reviewed in ²⁹³). Cumulative point mutations in the kinase domain of T β RII are present only in advanced recurrent breast cancers and not in primary breast tumors²⁹⁴. While there are no reports of ALK4 mutations in breast cancer, conflicting data on the incidence of mutations in ALK5 exist. One particular study reveals that metastatic breast cancers possess a point mutation in the kinase domain of ALK5. The authors hence suggest that the loss of ALK5 signaling via TGF β is imperative in the progression of metastasis²⁹⁵. Yet another study has challenged these finding having reported after examining metastatic breast cancers that no such mutations in ALK5 were detected²⁸³.

Mutations of the gene encoding Smad2 occur in a limited number of colon, lung, liver and cervical carcinomas²⁹⁶⁻²⁹⁸. On the other hand, there is only one reported case where Smad3 is highly downregulated in gastric cancer²⁹⁹. Smad4 is the most frequently mutated Smad gene in cancer, especially of pancreatic origin³⁰⁰ and is the only known Smad mutation in breast cancer³⁰¹. Furthermore, Smad4 is mutated and deleted in hepatocellular, bladder, biliary tract, ovarian, intestinal, colorectal, lung, prostate and cervical cancers³⁰¹. In addition, Smad4 is absent in breast cancer cell lines and invasive ductal carcinomas^{302, 303}. These studies support a role for Smad4 in the development of breast cancer

Taken together, the low number of reported mutations in $TGF\beta$ /activin signaling components in breast cancer may be due to the dual role of these factors to not only inhibit tumorigenesis but also induce metastasis.

5.5. Mouse models in breast cancer

Evidence of TGF β having prominent tumor suppressive properties in the mammary gland is supported by transgenic mice studies. An increase in TGFB1 expression in the breast effectively decreases the number of tumors when MMTV-TGFB1 mice are crossed with a tumor forming MMTV-TGFa mouse²⁶³. Moreover, MMTV-TGF_{β1} inhibits mammary tumor development in mice challenged with the chemical carcinogen 7,12-dimethylbenz(α)anthracene (DMBA)²⁶³. In the same line of evidence, the incidence, number and size of developing tumors increases dramatically in the breast when dominant negative T β RII is overexpressed in mouse epithelium (MMTV-DNIIR) when challenged with DMBA³⁰⁴. The MMTV-neu mouse is a well characterized model that develops adenocarcinomas that metastasize to the lung³⁰⁵. Introduction of the activated form of the TGF β type I receptor (ALK5TD) fused to an MMTV promoter in neu expressing mice in the mammary epithelium (MMTV-neu) developed fewer tumors. On the other hand, MMTV-DNIIR administration into the neu mice lead to shortened tumor latency²⁶⁸. While having no effect on normal mammary gland development, the conditional knockout of Smad4, Smad4^{MMTVcreKO}, resulted in hyperproliferative

mammary epithelial cells. These cells subsequently differentiated to a squamous epithelial phenotype³⁰⁶.

The above mouse models clearly define TGF β signaling as functioning to inhibit tumor formation. In contrast, evidence exists characterizing TGF β as having a defining role in promoting cancer and metastasis. This is observed in the MMTV- ALK5T Δ D/MMTVneu mice, where there is an increase in tumor metastasis to the lung²⁶⁸. On the other hand, blocking TGF β signaling with MMTV-DNIIR in the neu mice resulted in fewer metastases²⁶⁸. TGF β 's ability to promote metastasis was further demonstrated when mice with inducible polyomavirus middle-T-tumors were crossed against mice with inducible expression of TGF β 1. More specifically, the progeny displayed an elevated lung metastasis phenotype³⁰⁷.

5.6. Summary

TGF β has an important role in normal mammary biology as a potent regulator of mammary epithelial proliferation, mammary ductal and alveolar development, and postlactation involution of the mammary gland. Hence, it is not surprising that TGF β signaling plays an important role in mammary carcinogenesis. Mulitple studies that have been described support TGF β 's ability to inhibit breast tumorigenesis. TGF β can potently inhibit breast cancer cell growth. There mutation in or loss of expression of members of the TGF β signaling pathway including T β RII and ALK5 in some human breast cancers, indicating that human breast cancers may develop resistance to TGF β 's antiproliferative effects. Furthermore, there is decreased breast cancer formation in human patients with elevated levels of TGF β . Through upregulation of TGF β , the

antiestrogen tamoxifen inhibits breast cancer cell growth. Furthermore, *in vitro* studies presented suggest that the mechanisms for resistance to the growth-inhibitory effects of TGF β are key cellular events during mammary carcinogenesis. Activin signaling components are expressed in breast tissue and a loss of their expression correlates with increasing breast cancer grade. Moreover, activin is known to induce cell cycle arrest n breast cancer cells however, the precise signaling mechanisms are not fully elucidated.

6. TGFβ and breast cancer metastasis

Recent evidence has attributed a novel role for TGF β , not only as a tumor suppressor in early stages of tumorigenicity but also as promoter of metastasis in advanced cancer. A cell model was developed to demonstate how TGFB can switch from a tumor suppressor to a prometastastic factor in the course of carcinogenic progression³⁰⁸. In this model, the TGF β induced switch occurred at the transition from histologically low to high grade breast cancer ³⁰⁸. Genetic or epigenetic changes that occur during this transition alter the cellular interpretation of the TGF β signal³⁰⁸. TGF β has also been shown to be a major effector of breast tumor metastasis in vivo. Indeed, when TGFB signaling was blocked in the metastatic breast cancer cell line MDA-MB-231 and injected into immunodeficient mice, less tumors metastasized to the bone³⁰⁹. Furthermore, parathyroid hormone-releasing peptide (PTHrP), which is associated with metastatic disease, was induced in tumor cells by TGF β^{309} . Groups of genes directly involved in mediating bone metastasis have been revealed in the MDA-MB-231 cell line³¹⁰. Two genes, IL11 and CTGF, are induced by TGF β through Smad signaling, contributing to osteolytic bone metastases³¹⁰.

6.1. Tumor Promoting Effects of TGFβ

The stroma and microenvironment directly influence the initiation, promotion, or progression of a cancer. Human breast cancers are characterized by desmoplasia, fibroblast proliferation and remodeling of the extracellular matrix³¹¹. TGF β 's protumorigenic role is defined by its ability to affect both the carcinoma cell directly and the surrounding stroma. The importance of TGF β signaling on stroma is displayed in an *in vivo* mouse model. T β RII knockout in mammary gland fibroblasts leads to a promotion of tumor growth and invasiveness. In conjunction, there is an increase in hepatocyte growth factor (HGF), macrophage stimulating protein (MSP) and TGF- α mediated signaling networks²⁶⁷. This study suggests that TGF β regulates various growth factors that promote breast cancer in the stroma²⁶⁷.

TGF β tumor promoting effects are due to its ability to induce immune suppression, angiogenesis, tissue invasion, extracellular matrix deposition and epithelial to mesenchymal transition.

6.1.1. Immune suppression/evasion

Tumor cells express tumor-specific antigens that are detected by the body's immune system which leads to their elimination. By acquiring the ability to evade immunosurveillance, cancer cells can develop and progress. TGF β secretion is a major mechanism by which the tumor can suppress the immune system. TGF β immunosuppressive role in cancer progression is supported by the fact that cancer cells

are able to produce and secrete $TGF\beta^{312}$. Experimental models and specimens from cancer patients contain elevated levels of $TGF\beta^{313}$. *In vivo* and *in vitro* evidence associate $TGF\beta$ as a potent immunosuppressor. $TGF\beta$ produced by T cells can blocks production of interleukin 2 (IL-2) to inhibit IL-2-dependent proliferation of T cells³. $TGF\beta$ also inhibits the differentiation of T cells, and prevents naïve T cells from acquiring cytotoxic or helper functions²²⁰. $TGF\beta$ has been implicated in *in vivo* tumorigenesis through its effect on natural killer (NK) cell activity³¹⁴. Neutralizing antibodies against $TGF\beta$ block MDA-MB-231 local tumor and metastasis formation in NK-competent mice but not in NK-deficient mice³¹⁴. This study suggests that $TGF\beta$ allows for the highly metastatic breast cancer cell line MDA-MB-231 to metastasize by inhibiting NK cells, further supporting the role for tumor secreted $TGF\beta$ as a suppressor of the host immune surveillance³¹⁴.

6.1.2. Angiogenesis

Angiogenesis is necessary for proper nutrient and oxygen supply to the tumor. The formation of new microvasculature by capillary sprouting is a prerequisite for tumor growth. This process allows for intravasation of the blood system which paves the way for metastasis. In human breast tumors, increased TGF β is associated with an augmentation of microvessel density, correlating with poor patient prognosis³¹⁵. A potent inducer of angiogenesis is vascular endothelial growth factor (VEGF) whose expression is regulated by TGF β in breast cancer cells³¹⁶. Through TGF β 's direct effect on the formation of a new vasculature to the tumor, it promotes tumorigenesis.

6.1.3. Tissue invasion/Cellular adhesion

Cancer cell invasiveness requires a motile cellular phenotype and the ability for tumor cells to degrade their extracellular milieu. TGF β induction of the homeobox transcription factor CUTL1, a poor prognosis factor for metastatic breast cancer, regulates the expression of multiple genes regulating cell motility, tumor cell invasiveness, and extracellular deposition³¹⁷. Additionally, both Smad dependent and independent mechanisms are involved with TGF β -induced tumor cell invasiveness. This includes a PI3K/Akt dependent and Smad independent mechanism by which TGF β induces motility in metastatic breast cancer cells³¹⁸.

In normal situations, TGF β increases production of the extracellular matrix proteins collagen and fibrinogen while decreasing matrix degradation enzymes such as collagenase. During breast tumorigenesis, TGF β augments these extracellular matrix degrading enzymes, increasing proteolytic activity of cancer cells. One of these factors is urokinase-type plasminogen activator (uPA), which plays a key role in tumor matrix degradation and promotes tumor progression³¹⁹. By increasing its expression, TGF β allows for the invasiveness of breast cancer cells. Furthermore, TGF β activation is enhanced by the production of proteases and plasmin by tumor cells³²⁰.

In summary, by increasing the proteolytic activity and decreasing the adhesiveness of cancer cells, TGF β acts to promote breast tumor invasion.

6.1.4. Epithelial to Mesenchymal Transition

Potential lethality arising from solid tumors stems from their ability to invade surrounding tissue and metastasize to target organs. In order for the tumors to invade they must undergo the aforementioned process of dedifferentiation EMT. This transitional process is characterized by a loss of cell-cell junction proteins such as E-Cadherin and gain of mesenchymal proteins such as vimentin. Furthermore, this process is typified by a loss of cell polarity, repression of epithelial markers, and cytoskeletal reorganization. Motility of these cells may only occur upon transition from their initial epithelial origin to fibroblastoid cells. The newly mobile cells are now invasive and capable of degrading the basement membrane and interstitial matrix. Therefore, alterations in stromal and growth will lead to eventual metastasis.

In both normal and transformed mammary epithelial cells, TGF β may induce morphological changes characteristic of EMT^{219, 321, 322}. These morphological changes include reorganization of the actin cytoskeleton, downregulation of adhesion and cytoskeletal molecules and expression of mesenchymal markers^{219, 321}. For example, TGF β may downregulate expression of the epithelial markers E-Cadherin, ZO-1, vinculin and keratin. In contrast, it may upregulate expression of the mensenchymal markers vimentin and N-Cadherin. These specific aforementioned changes induce alterations in cell morphology and motility^{184, 219, 323}.

Cooperation between the TGF β Smad pathway and other pathways such as activated Ras, ERK MAPK, p38 MAPK, NF κ B and PI3K are all involved in EMT (reviewed in ³²⁴). For example, in Ras transformed breast carcinomas, Smad signaling cooperates with NF κ B contributing to EMT *in vitro* and metastasis *in vivo*³²⁵. TGF β may also

induce EMT in a Smad independent mechanism. Through ALK5 interaction with the polarity protein Par6, TGF β stimulation results in dissolution of the actin cytoskeleton and tight junctions through degradation of RhoA³²⁶. Smad3 and Smad4 have been shown to act cooperatively with Rho and p38 to induce stress fibre formation thus inducing EMT. Transcriptional regulation of EMT by TGF β involves multiple targets such as Id genes, the SNAIL family of zinc finger proteins, two-handed zinc finger/homeodomain proteins, basic helix-loop-helix proteins, and high motility group box-containing proteins (reviewed in ³²⁴). Therefore, through multiple mechanisms TGF β induces EMT allowing for tumors to invade surrounding tissue leading to their metastasis.

6.2. Summary

TGF β inhibits primary tumor development and growth by inducing cell cycle arrest and apoptosis during the early phase of epithelial tumorigenesis. When tumor cells become resistant to growth inhibition by TGF β due to inactivation of the TGF β signaling pathway or aberrant regulation of the cell cycle in later stages of tumor progression, the role of TGF β becomes one of tumor promotion. This suggests a pro-oncogenic role for TGF β in addition to its tumor suppressor role. Through various alterations in the complex TGF β signaling and cell cycle pathways, human cancers resist TGF β -mediated inhibition of proliferation. As we have seen, TGF β can exert effects on tumor and stromal cells as well as alter the responsiveness of tumor cells to TGF β to stimulate invasion, angiogenesis, and metastasis, and to inhibit immune surveillance. Furthermore, when epithelial cells lose autocrine TGF β responsiveness they procure a growth advantage leading to malignant progression.

7. Hypothesis and objectives of this work

Activin and TGF β signaling are pluripotent cytokines with diverse roles within different organs throughout the body, with the mammary gland being one of the key target tissues. In fact their signaling components are regulated throughout mammary gland development. Animal model systems developed to elucidate the *in vivo* role of activin and TGF β have further highlighted their importance in mammary gland development. Collectively, these *in vitro* and *in vivo* findings emphasize a role of these TGF β family members in negatively regulating mammary growth and differentiation. However, the precise signaling mechanism of action of activin and TGF β in the breast remains to be dissected.

A plethora of studies evaluating the effects of TGF β in breast carcinogenesis have been performed, defining TGF β as a potent inhibitor of growth in early stages of tumorigenesis and a promoter of metastasis. Evidence of activin's anti-proliferative effects in breast cancer are highlighted by studies looking at expression of activin signaling subunits in high grade breast cancers. These studies reveal that a loss of activin signaling correlates with high grade breast cancer suggesting it may play a role in breast cancer development. The limited data obtained from few studies mentioned in CHAPTER I describing the localization of activin and its effects in breast cancer cells suggest that resistance to the growth-inhibitory effects of activin involve changes to the activin signaling pathway. Hence, the contribution of activin, and the activin signaling pathway to breast tumorigenesis have not been defined.

In order to better understand the role of activin/TGF β signaling pathway in normal mammary gland biology and the pathogenesis of breast cancer, the objectives of my

doctoral thesis work were as follows. The first objective was to elucidate the role of activin and TGF β signaling in the mediation of growth and differentiation of the mammary gland. This study was performed in mammary epithelial cells where I looked at the activin/TGF β signaling effect on the prolactin Jak/Stat pathway which is one of the central hormones regulating the development of the breast. The second objective of my project was to analyze the effect of activin in breast cancer and to dissect the molecular mechanism governing activin's role in breast carcinogenesis. Hence, I unveiled for the first time the activation of a Smad-independent pathway downstream of activin, the p38 MAPK. Furthermore, I showed that activin is a potent inhibitor of breast cancer cell growth and this effect is mediatiated through activin induced p38 MAPK activation. Finally, the third objective of my doctoral work was to identify the target genes involved in activin mediated cell growth inhibition of human breast cancer cells. As such, I have found a novel activin target gene, the death adaptor protein RAIDD, which is potently upregulated upon activin signaling. Moreover, I show that RAIDD expression is necessary in inducing activin mediated cell growth inhibition.

CHAPTER II.

Smad Signaling Antagonizes Stat5-Mediated Growth And Differentiation Of Mammary Epithelial Cells

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PREFACE

As described in CHAPTER I, multiple studies underlining the relevance of activin and TGF β signaling in the breast exist. However, the precise signaling mechanisms regulated have not been defined. Therefore, in this study, we sought out to elucidate the effect of activin and TGF β signaling on mammary gland growth and differentiation. In the following paper, we dissected the molecular mechanism regulated by activin/TGF β signaling in mammary epithelial cells. One of the key signaling pathways involved in mammary gland differentiation and proliferation is the prolactin Jak-Stat pathway. As such, I have included as a prelude to this paper, a detailed account of prolactin Jak/Stat signaling and its role in the biology of the mammary gland. Finally, I have described prolactin Jak/Stat's role in breast carcinogenesis in order to understand the implications of the work presented in this chapter.

1. The Role of the Prolactin (PRL) Jak-Stat Pathway in Proliferation and Differentiation of the Mammary Gland

1.1. PRL and PRL Receptor

PRL is a polypeptide hormone that is synthesized and secreted mainly by cells in the pituitary. PRL exerts a vast array of biological functions and is studied extensively for its effects on mammary gland development and lactation. PRL's imperitive role in this gland is well illustrated by a lack of lobuloaveolar development in the PRL knockout mouse³²⁷. Therefore PRL deficiency results in a mammary gland resembling that at early puberty.

The PRL receptor (PRLR) belongs to the class I cytokine receptor superfamily that includes among others the receptors for multiple interleukins, growth hormones and erythropoietin³²⁸. PRLR knockout mice at puberty lack ductal branching which further confirms the necessity of this cytokine in mammary gland development³²⁹. Furthermore, PRLR heterozygote animals (PRLR^{+/-}) are not able to lactate due to reduced ductal branching during puberty and depressed lobuloalveolar development during pregnancy. Moreover, during pregnancy there is a complete failure of lobuloalveolar development when PRLR^{-/-} mammary epithelium is transplanted into the fat pads of a normal mouse³²⁹.

1.2. Jak-Stat signaling

The Jak-Stat pathway has emerged as the main transducer of the PRL signal. PRL signaling commences with ligand binding to the PRLR, Figure 4. Because the receptor lacks any intrinsic kinase domain it utilizes the cytoplasmic tyrosine kinase, Janus kinase-2 (Jak2) to transduce its signal³³⁰. Jak2 is constitutively associated to the PRLR. PRL induction of PRLR oligomerization brings two Jak2 molecules in close proximity so they may transphosphorylate each other³³¹. Once activated, Jak2 tyrosine phosphorylates the receptor³³² allowing for recruitment of SH2-domain containing proteins such as the transcription factor: signal transducer and activator of transcription (Stat) family³³³. Jak2 subsequently phosphorylates Stat5 on a conserved tyrosine residue (Tyr694) which leads to receptor dissociation and dimerization of the Stat5 molecules³³⁴. Stat5 dimers then translocate into the nucleus and bind to a specific sequence known as the γ -interferon-activated sequence (GAS) motif. Sequences containing the GAS motif
include those expressed in milk protein genes. Stat5 exists in two isoforms, Stat5a and Stat5b. The two unique isoforms are encoded by separate genes and share approximately a 90% homology. Stat5a was originally identified as a mammary gland factor (MGF) in sheep mammary glands activated by PRL³³⁵.

A definite role for Stat5 in mammary gland development was demonstrated via gene targeting. The Stat5a knockouts have impaired lactation and lobuloalveolar development³³⁶. Furthermore, they display a reduction in alveoli number and a failure of alveoli functional differentiation³³⁶. The Stat5b knockout phenotype also exhibits diminished lobuloalveolar development but to a lesser extent than Stat5a. In contrast, a more dramatic phenotype occurs in the Stat5a/b double knockout in comparison to that of the single knockouts³³⁷. Therefore, knockout studies done thus far suggest that Stat5 plays a vital role in alveolar proliferation, differentiation and expansion in the mammary gland.

Figure 4. Prolactin Induced JAK-STAT Signaling



1.3. Stat5 structure

Stat5 belongs to the Stat family of latent cytoplasmic proteins that range from a molecular weight of 90 to 100 kDa. The Stat family contains 8 members; Stat1 (a and β), Stat2, Stat3, Stat4, Stat5a, Stat5b and Stat6. Stats contain six domains that are functionally and structurally conserved. More specifically, they include the aminoterminal, coiled-coil, DNA-binding, linker, SH2, and transactivation domains. The amino-terminal domain is the major site of protein-protein interaction. Furthermore, it is implicated in both Stat nuclear translocation³³⁸ and interaction with nuclear co-activators such as CBP/p300³³⁹. The coiled-coil domain is made up of four α -helices forming a hydrophilic surface allowing for protein interaction^{340, 341}. Moreover, the coiled-coil domain is involved in receptor binding, activation and nuclear export^{342, 343}. The linker domain separates the DNA-binding domain with the SH2 domain and is able to mediate transcription³⁴⁴. The SH2 domain represents the most highly conserved Stat motif³³³ and is essential for receptor recognition of the phosphotyrosine docking sites^{345, 346 347}. Furthermore the SH2 domain is required for Stat dimerization and determines the specificity of dimer formation^{346, 348}. The carboxyl-terminus transactivation domain is the least conserved and thus most variable domain amongst the Stats³⁴⁹. Truncated isoforms of Stats that lack the transactivation domain are not able to drive transcription³⁵⁰. This domain mediates the interaction of a variety of nuclear coactivators facilitating chromatin modification and transcriptional activity³⁵¹. Stat5 transactivation domain interacts directly with CBP/p300 and enhances PRL mediated transcriptional activity³⁵². Importantly, serine residues on the transactivation domain

have also been shown to regulate transcriptional activity^{353, 354}. For example, serine phosphorylation of Stat5 has been to shown to promote its stability³⁵⁵.

1.4. Regulation of Stat5 activity

Downregulation of Stat5 activity exists at multiple levels of the signaling cascade such as the receptor, Jak2 and Stat5 itself. Various phosphatases such as the SH2 domaincontaining tyrosine phosphatase (Shp-2)^{356, 357}, cytoplasmic protein-tyrosine phosphatase 1B (PTP1B)³⁵⁸, serine/threonine protein phosphatase 2A (PTP2A)³⁵⁹ and T-cell proteintyrosine phosphatase (TC-PTP)³⁶⁰ are capable of regulating Stat5 activity. For example, TC-PTP dephosphorylates and deactivates PRL induced Stat5 in the nucleus³⁶⁰. Stat5 activity is also regulated by the protein inhibitor of activated Stats (PIAS) family³⁶¹. PIAS function as small ubiquitin-related modifier 1-tethering protein ligases which may regulate localization, stability, and activity of a variety of proteins. For example, PIAS3 is capable of specifically inhibiting Stat5. Suppressors of cytokine signaling (SOCS) proteins also possess the capability to modulate Stat5 activity.

Eight members of this family exist including SOCS1-7 and cytokine-inducible SH2 protein (CIS). These proteins are characterized by a central SH2 domain and a unique carboxyl terminus motif called the SOCS box. This unique box is implicated specifically in the binding machinery of the ubiquitin-proteosomal system. Amongst other cytokines, PRL is able to induce expression of SOCS proteins³⁶². As such, SOCS-3 is able to inhibit PRL-induced Stat5 activation. Furthermore, SOCS-1 interacts directly with Jak2 and subsequently targets it for degradation³⁶³. Another level of Stat5

regulation is through the ubiquitin proteosomal degradation system. More specifically, Stat5 ubiquitination and targeted degradation downregulates Jak-Stat signaling³⁶⁴.

1.5. Stat5 gene regulation

The main effect of activated Stat5 lies in its ability to bind DNA and induce transcription of target genes. Stat5 dimers recognize and bind to a canonical gamma interferon (IFN- γ)-activated (GAS)-like site with a general palindromic sequence of 8 base pairs (TTCNNNGA). Stat5's capacity to activate transcription is determined by the nuclear co-activators it recruits and their ability for basic transcriptional machinery interaction and chromatin modification. Stat5 has been shown to interact with numerous transcription factors and co-regulators such as the glucocorticoid receptor³⁶⁵, centrosomal P4.1-associated protein (CPAP)³⁶⁶, N-myc interactor (Nmi)³⁶⁷, Stat5 and receptor corepressor (SMRT)³⁶⁸, p100³⁶⁹, ERK³⁷⁰ and CBP/p300³⁵², all of which act as either co-activators or co-repressors to Stat5 mediated gene modulation. For example, interaction of Stat5 with the glucocorticoid receptor protects Stat5 from inactivation by dephosphorylation, and enhances its activation ^{365, 371}. CBP/p300 bind the transactivation domain of Stat5 and is essential for its activation^{339, 372-374}.

In response to PRL induced activation of Stat5, milk gene proteins such as β casein, whey acidic protein, and β lactoglobulin are upregulated³⁷⁵. Stat5 is also necessary in inducing expression of the cell cycle regulator cyclin D1 by PRL in mammary epithelial cells³⁷⁶.

2. PRL Jak-Stat pathway in breast cancer

Whereas the role of PRL in mammary gland development, growth, and differentiation is obvious, the involvement of PRL in the induction and progression of human breast cancer is subject of great debate. In humans, some studies claim that high PRL levels correlate with the risk of breast cancer in postmenopausal women, while others claim that there is no correlation³⁷⁷⁻³⁷⁹. In rodents however, evidence of an association between increased PRL secretion and tumorigenesis via chemical carcinogens exists³⁸⁰. Furthermore, mammary tumors develop in transgenic mice overexpressing PRL³⁸⁰. Both PRL and its receptor are present in breast cancer cell lines and mammary tumors, creating an autocrine-paracrine effect of PRL^{381, 382}. Interestingly, the use of various PRL blocking techniques interferes with the autocrine-paracrine loop in the human breast cancer cell line T47D and subsequently suppresses cellular proliferation^{381, 383, 384}. In contrast, PRL has also been implicated as an inhibitor of breast cancer due to its ability to upregulate the tumor suppressor Breast Cancer 1 (BRCA1) in breast cancer cells³⁸⁵.

The exact role for Stat5 in the growth and survival of mammary tumor cells remains to be elucidated. Importantly, in leukemias and lymphomas, Stat5a and Stat5b are constitutively phosphorylated^{386, 387}. Moreover, a high proportion of human breast cancers have reported Stat5 to be activated and localized in the nucleus³⁸⁸. At a molecular level, the aforementioned observations may be explained by Stat5's ability to regulate cell cycle progression and survival. More specifically, this occurs through regulation of the cell cycle regulatory proteins cyclin D1 and the anti-apoptotic factor Bcl-X_L ^{376, 389}. However, no reports link regulation of these proteins by Stat5 to breast

cancer development. Clinically, patients whose tumors displayed elevated levels of active Stat5 resulted in a favorable prognosis³⁹⁰.

3. PRL Jak-Stat pathway in breast cancer metastasis

The major cause of death in patients with breast cancer is due to metastasis. PRL has recently been defined as an invasion suppressor hormone in breast cancer cells³⁹¹. More specifically, PRL activation of Jak2 plays a critical role in the inhibition of breast cancer cell invasion capacity. This vital inhibition may stem from a negative regulation of both the MAPK (ERK1/2) and Smad pathways³⁹¹. This is further supported by Stat5's capability to suppress breast cancer cell invasion³⁹². Excitingly, Stat5's invasive suppression potential is the biological link where elevated Stat5 activation leads to improved breast cancer patient prognosis³⁹⁰.

4. Purpose of this study

In order to elucidate the effect of activin and TGF β signaling on mammary gland growth and differentiation, we looked at activin/TGF β induced Smad crosstalk with prolactin induced Jak/Stat pathway.

In this study, we define a novel crosstalk mechanism in which activin/TGF β induced Smad signaling antagonizes one of the key players involved in mammary gland growth and differentiaion, Stat5.

ABSTRACT

Two critical signaling cascades within the mammary epithelial tissue are the TGF_β/Smad and the Jak/Stat pathway. Interestingly, opposing physiological effects between these two signaling pathways are prominent in the regulation of mammary gland development and breast carcinogenesis. However, the exact nature of the biological network existing between the Smad and Stat signal transduction pathways has remained elusive. Our results identify a novel regulatory crosstalk mechanism by which activin/TGF\beta-induced Smad signaling acts to antagonize prolactin-mediated Jak/Stat signaling. While these two pathways appear to signal in a linear manner in the cytoplasm they converge to antagonize their effects on target gene expression within the nucleus. Our data show that ligand-induced activation of Smad2, 3 and 4 leads to a direct inhibition of Stat5 transactivation, leading to inhibition of Stat5-mediated target gene expression, such as β casein and cyclin D1, thereby blocking vital processes for mammary gland growth and differentiation. Finally, we unveiled the mechanism by which these two signaling cascades antagonize their effects and found that activated Smads inhibit Stat5 association with its co-activator CBP, thus blocking Stat5 transactivation of its target genes.

INTRODUCTION

Mammary gland growth and differentiation is a complex process regulated by steroids, polypeptide hormones, and growth factors. Among those, prolactin and TGF β family members, play a major role in the regulation mammary gland development. Prolactin is required for lobuloalveolar formation of the mammary ducts during pregnancy and lactation. On the other hand, TGF β has an opposite effect, inducing apoptosis during mammary gland involution and inhibiting milk protein expression ^{211, 393}. Transgenic mouse models developed to investigate the *in vivo* response to TGF β indicate that TGF β inhibits proliferation in response to the hormones that regulate mammary gland development^{264, 394, 395}. The effect of activin on the development of the mammary gland stems from the activin bB subunit knockout mouse. Deletion of the activin β b subunit, through ablation of three of the dimeric β molecules (activin B, activin AB and inhibin B), results in mice with the phenotype of incomplete mammary development and an absence of lactation²⁶².

Prolactin signal transduction is induced by formation of a homodimeric complex of two molecules of prolactin receptor (PRLR), which lack intrinsic kinase activity but are constitutively associated with the intracellular tyrosine kinase Jak2 ^{332, 396, 397}. Prolactin-induced receptor homodimerization brings their associated Jak2 molecules in close proximity allowing for their transactivation as well as phosphorylation of the PRLR ³³¹. These phospho-tyrosine residues on both Jak2 and the PRLR then create docking sites for the recruitment and activation of the transcription factor Stat5 via its SH2 domain ³⁹⁸. Once phosphorylated, Stat5 homodimerizes and translocates into the nucleus to bind

response elements on target gene promoters, such as those encoding milk gene proteins and cell growth regulators ^{399, 376}. The importance of Stat5a in the mammary gland development is further highlighted by the Stat5a knockout mouse which show no lobuloalveolar development during pregnancy and a complete absence of lactation ³³⁶. The physiological role and importance of Stat5 has been subsequently extended, as many cytokines including growth hormone, erythropoietin, thrombopoietin, granulocytemacrophage-colony-stimulating factor and most interleukins also signal through Stat5 400-405

TGF β family members transduce their signals by binding to serine/threeonine kinase receptors (type I and type II). Following ligand binding to the type II receptor, the type I receptor is recruited to the complex and transphosphorylated by the type II kinase domain. This in turn will lead to activation and phosphorylation of the Smad proteins, the main downstream effector molecules for these receptors. The activated type I receptor phosphorylates receptor-regulated Smads (R-Smads), Smad2 and 3, on their carboxyl-terminal serine residues (SxS motif). Phosphorylation allows for heterotrimerization of two phosphorylated R-Smad subunits with one common partner Smad4 subunit ⁴⁰⁶⁻⁴⁰⁸. Subsequently, the Smad heterotrimer translocates into the nucleus where it associates with various transcription factors, co-activators or co-repressors to regulate expression of target genes in a cell and tissue specific manner ⁴⁰⁹. Activin and TGF β inhibits milk protein synthesis and secretion in explants isolated from mid-pregnant mice ^{253, 410, 411}, no role for activin in the regulation of lactation has yet been

established. In this study, we show that both activin and TGF β , through the Smad pathway, potently regulate this process by antagonizing prolactin/Stat5 target gene expression.

The Stat5 and Smad pathways play a critical role in regulating mammary gland development. These two signaling pathways oppose their effects and the resulting balance between these two antagonistic pathways allows for proper regulation of mammary epithelial cell growth and differentiation. However, the mechanisms by which these two signaling cascades regulate each other remain unknown. This led us to investigate the molecular crosstalk mechanisms existing between the Smad and Stat signal transduction pathways. We identified a novel regulatory crosstalk mechanism by which activin/TGF β -induced Smad signaling led to direct inhibition of Stat5-mediated gene transcription regulating differentiation and growth. Furthermore, we showed that activin/TGF β signaling greatly reduced Stat5 interaction with its co-activator CBP, thereby inhibiting Stat5 transactivation capacity.

MATERIAL AND METHODS

Reagents: Ovine prolactin (Sigma-Aldrich), human TGFβ1 (PeproTech, Inc), Activin A (Dr. Y Eto and Ajinomoto Co.). Monoclonal antibodies to STAT5 (BD Transduction Laboratories), to phospho-Stat5Y-694 (Intermedico), to cyclin D1 (NeoMarkers, Fremont CA), to Stat5A (Intermedico), to phosphoSmad2 (Cell Signaling), to hemagglutin (HA) (Roche Diagnostics), to phosphoSmad3 (Chemicon), to Smad2/3 (Santa Cruz), to βtubulin (Sigma), to Jak2 (Upstate Biotechnologies); goat anti-mouse horseradish peroxidase (Santa Cruz), to ERK1/2 (Cell Signaling) goat anti-rabbit horseradish peroxidase (Sigma-Aldrich); Lumi-light plus kit (Roche Diagnostics).

Plasmid constructs: Expression plasmid encoding MGF-Stat5 (pXM-MGF/STAT5) and the rat βcasein promoter (-344/-1) were obtained from Dr. Bernd Groner (Institute for Biomedical Research, Frankfurt am Main, Germany). The promoter construct 3TPluc was obtained from Dr. Joan Massague (Howard Hughes Medical Institute, Memorial Sloan-Kettering). The promoter construct XPAL7 was obtained from Dr. Bernard Turcotte (Hormones and Cancer Research Unit, Montreal, Canada). Cytomegalovirus expression plasmid pR/CMV vector (Invitrogen) containing cDNA encoding for the PRLR long form was obtained from Dr. Paul Kelly (INSERM Endocrinologie Moleculaire, Faculté de Médecine Necker, Paris, France). GAL4-STAT5a was obtained form Dr. Bernard Callus. The cyclin D1 (D1-944) luciferase promoter construct was generously provided by Dr. Linda Schuler (Department of

Comparative Biosciences, University of Wisconsin-Madison, Madison, USA). Dominant negative Smad2 (DNSmad2) and dominant negative Smad3 (DNSmad3) were generated as previously described⁴¹². Activin type I receptor mutant (ALK4mL45) was generated as previously described⁴¹³. The 5XSTAT5-luc reporter was made by cloning a doublestranded oligonucleotide (5'-

CTAGCTGTGGAC<u>TTCTTGGAA</u>TTAAGGGACTTTTGTGTGGAC<u>TTCTTGGAA</u>TT AAGGGACTTTTGTGTGGGAC<u>TTCTTGGAA</u>TTAAGGGACTTTTGTGTGGAC<u>TTCT</u> <u>TGGAA</u>TTAAGGGACTTTTG TGTGGAC<u>TTCTTGGAA</u>TTAAGGGACTTTTGC -3'), containing 5X Stat5 binding sites from the bovine βcasein promoter, into pTA-luc

(Clontech Laboratories).

Cell Culture and transfections: HC11 cells (obtained from Dr. Nancy Hynes, Friedrich Miescher Institute, Basel, Switzerland and Dr. Bernd Groner, Institute for Biomedical Research, Frankfurt am Main, Germany) were cultured for 2 days in RPMI 1640 supplemented with 10% fetal bovine serum, 10ng/ml epidermal growth factor, 5µg/ml insulin, 50units/ml penicillin/streptomycin. At confluency HC11 cells were induced for 2 days RPMI 1640 supplemented with 10% fetal bovine serum, 1µM hydrocortisone, 5µg/ml insulin, 50units/ml penicillin/streptomycin. Cells were starved overnight in RPMI supplemented 0.5mg/ml fetuin and 10 µg/ml transferrin and stimulated with 5µg/ml ovine prolactin, 1µM hydrocortisone and 5µg/ml insulin (HIP) to produce β casein. Mouse embryonic fibroblasts (MEF, MEFSmad4(-/-)) were obtained from Dr. Christian Sirard, Brain Tumor Research Center, McGill University, Montreal,

Canada. CHO and MEF cells were maintained in 10% fetal bovine serum, 50units/ml penicillin/streptomycin in DMEM.

Cell lysis and Western blotting: Total cell extracts were collected as follows. Cells were lysed in 300 μ l of lysis buffer (10 mM Tris-HCl, pH 7.5, 5 mM EDTA, 150 mM NaCl, 30 mM sodium pyrophosphate, 50 mM sodium fluoride, 1 mM sodium orthovanadate, 10% (v/v) glycerol, 0.5% Triton X-100) containing protease inhibitors (1 mM phenylmethylsulfonyl fluoride, 2 mg/ml leupeptin, 5 mg/ml aprotinin) for 5 min at 4 °C. The lysates were then centrifuged at 14,000 rpm for 10 min at 4 °C.

Cytoplasmic and nuclear extracts were prepared as follows. The cells were lysed with a hypotonic buffer (10 mM HEPES-KOH, pH 7.9, 1.5 mM MgCl₂, 10 mM KCl, 0.5 mM dithiothreitol, 1 mM Na₃VO₄, 20 mM NaF, 1 mM phenylmethylsulfonyl fluoride, 5 μ g/ml aprotinin, and 2 μ g/ml leupeptin) and vortexed for 1 min. Cells were pelleted at 14,000 rpm for 15 min at 4 °C, and the supernatant was collected (cytoplasmic fraction). The pellet was then washed 3× with phosphate-buffered saline and lysed with a high salt buffer (20 mM HEPES-KOH, pH 7.9, 25% glycerol, 420 mM NaCl, 1.5 mM MgCl₂, 0.2 mM EDTA, 1 mM Na₃VO₄, 20 mM NaF, 5 μ g/ml aprotinin, and 2 μ g/ml leupeptin). Vortexed at 4 C for 30 min, centrifuged at 14,000 rpm for 15 min at 4 °C and the supernatant was collected (nuclear fraction).

Cell extracts were separated on polyacrylamide gels, transferred onto nitrocellulose and incubated with specific antibodies as indicated. Immunoreactivity was revealed by chemiluminescence (Lumi-Light Plus Western Blotting substrate, Roche) according to

the manufacturer's instructions and measured using an Alpha Innotech Fluorochem Imaging system (Packard Canberra).

Northern blot analysis: HC11 cells were cultured to differentiate and then treated or not with HIP, 0.5nM Activin A or both. Total RNA was extracted using Trizol (Invitrogen). Each sample (20 μ g) was then separated on agarose gels (1% agarose in 0.04M 3-(N-morpholino)propanesulfonic acid; 0.01M sodium acetate; 10mM EDTA, pH 8.0; and 2.5M formaldehyde) and transferred to nylon membranes. A probe for mouse β casein was labeled using the Random Priming Kit (Roche) and added to the hybridization solution (0.5 NaPO4, pH 7.2, 1mM EDTA, pH 8.0, 7% SDS, 1% BSA, and 200mg/ml salmon sperm DNA). Results were revealed using a phosphorimager Cyclone Storage Phosphorscreen (Packard Canberra).

RT PCR: Differentiatied HC11 cells were treated for 24 hours with HIP and subsequently with or without Actinomycin D, Actinomycin D and 0.5 nM activin or Actinomycin D and 100pM TGFb from 0 to 24 hours. Total RNA was extracted using Trizol reagents (Invitrogen). Reverse transcription of total cellular RNA using random primers was carried out using Superscript Reverse Transcriptase (Invitrogen) as per the manufacturer's instruction. Subsequently, amplification of cDNA to obtain products for β casein and GAPDH was performed. The PCR conditions were as follows: 30 cycles (94°C for 30 s, 60°C for 30 s, 72°C for 1 min 30 s).

EMSA: EMSA were performed as previously described⁴¹⁴. $6\mu g$ of nuclear extracts were incubated with the Stat5 binding site from the bovine β casein promoter (5'-

AGATTTCTAGGAATTCAATCC-3')³³⁵ (20,000 cpm) for 30 min on ice in 20 μ l of electrophoretic mobility shift assay (EMSA) buffer (10 mM HEPES (pH 7.6), 2 mM NaHPO₄, 0.25 mM EDTA, 1 mM DTT, 5 mM MgCl₂, 80 mM KCl, 2% glycerol, 100- μ g/ml poly(dI-dC)). Supershift experiments were performed by adding anti-Stat5a 30 min prior to the binding reaction at a dilution of 1:500. A 4% polyacrylamide gel that was prerun for 2 h at 200 V in 0.25× TBE buffer (22.5 mM Tris-borate (pH 8.0), 0.5 mM EDTA). The samples were run on gel for 1 h at 200 V in 0.25xTBE at room temperature. The gels were dried and revealed using a phosphorimager Cyclone Storage Phosphorscreen (Packard Canberra).

Luciferase assays: CHO and MEFs were transciently co-transfected with 2 μ g of different promoter constructs (3TP-luc, β caseinlux, 5XSTAT5-luc, pXPAL7) and with varying combinations and concentrations of cDNAs encoding PRLR, MGF-STAT5, Smad2, Smad3, Smad4, GAL4-STAT5a, DNSmad2, DNSmad3, ALK4, ALK4mL45, and the β galactosidase and 3TP-Luc gene reporter construct. CHO cells were transfected using lipofectamine 2000 reagent as per the manufacturers instructions (Invitrogen) and MEFs were transfected with lipofectamine Plus as per the manufacturers instructions (Invitrogen). Luciferase activity was measured (EG&G Berthold Luminometer) and normalized to the relative β galactosidase activity.

Statistical Analysis: Results are expressed as mean \pm SD of three or more separate independent experiments. Statistical analysis was assessed by one-way ANOVA or the unpaired *t* test, as indicated in figure legends, using GraphPad Prism 4 software (GraphPad Software, Inc.). Statistical analyses were meant to compare fold induction

(percentage of control) of TGF β /activin-treated samples among themselves within each experiment. Additional post-ANOVA tests were performed when necessary to compare all data with HIP-treated control Bonferroni's Multiple Comparison test GraphPad Prism. For all statistical analyses and tests, a p value < 0.05 was considered significant and is indicated on the top of the error bars by an asterisk.

RESULTS

Activin and TGF β inhibit lactogenic hormone-induced milk gene: The signals that regulate mammary gland development also coincide with those that are involved in milk protein production ⁴¹⁵. Originally derived from a mammary epithelial cell line isolated from mid-pregnant BALB/c mouse mammary gland tissue, HC11 cells can be differentiated with lactogenic hormone stimulation to synthesize the milk protein β casein ^{416, 417}. HC11 cells have often been used as a model system to study mammary gland differentiation ³⁹⁹.

To investigate the role of activin/TGF β on mammary gland differentiation we examined the effects of these two growth factors on the regulation of expression of the milk protein β casein. HC11 cells were differentiated and subsequently treated or not with either prolactin, activin, or a combination of both for different periods of time and β casein mRNA level was assessed using Northern blot analysis. As shown in Fig.1a, prolactin induced a strong up-regulation of β casein mRNA levels at all time points analyzed while activin alone had no effect. However, when cells were treated with both activin and prolactin, simultaneously, β casein mRNA levels were strongly suppressed (Fig. 1a). The same results were obtained in cells treated with TGF β (data not shown).

To then investigate whether the decrease in prolactin-induced β casein mRNA levels upon activin treatment was followed by a decrease in β casein protein levels, HC11 cells were treated or not with prolactin, activin or a combination of both factors and total cell lysates were analyzed by Western blot using an anti- β casein antiserum. As shown in

Fig.1b (upper panel), while prolactin significantly increased β casein protein levels, this effect was almost completely blocked in the presence of activin. Reprobing of the membrane with an anti-Erk1/2 antibody showed equal loading of proteins (Fig.1b, lower panel). Previous studies have shown that in vitro optimal Stat5-mediated ßcasein gene expression is achieved upon treatment of mammary epithelial cells with a combination of lactogenic hormones containing glucocorticoid (such as hydrocortisone), insulin and prolactin^{418, 419}. As such, we treated differentiated HC11 cells with hydrocortisone, insulin and prolactin (HIP) for 24 hours, in either the presence or absence of TGF β or activin and subsequently examined the effect upon β case in protein expression. Whereas HIP induced a robust increase in β casein protein levels, both activin and TGF β completely inhibited its expression (Fig.1c, upper panel). The membrane was stripped and reprobed with anti-Erk1/2 antibody to show equal loading of the proteins (Fig.1c, lower panel). Together these results indicate that activin and TGF β are strong inhibitors of prolactin or HIP-mediated ßcasein gene expression in mammary epithelial cells, suggesting the existence of a direct cross-talk mechanism between these two growth factor family signaling pathways.

Jak/Stat Expression Levels and β casein Protein Stability are not affected by Activin/TGF β ; To rule out that the inhibitory activin/TGF β effect observed on prolactin-induced β casein expression was merely due to a change in Jak or Stat expression level we examined the expression of Jak2 and Stat5 in HC11 cells upon activin/TGF β treatment from 4 to 24 hours. As shown in Fig.1d, we observed no change

in their expression, indicating that activin/TGF β regulation of β casein expression is not a result of changes in Jak2 or Stat5 expression levels.

Lactogenic hormone treatment can augment the rate of ßcasein mRNA transcription two to four fold. However, this is not sufficient to explain the drastic increase in ßcasein mRNA which can rise seventeen to twenty five fold above basal levels ⁴²⁰. This net increase is in fact due to a direct transcriptional activation of the ßcasein gene coupled to stabilization of β casein mRNA ⁴²¹. To then examine whether activin/TGF β could also affect ßcasein mRNA stability, HC11 cells were treated for 24 hours with lactogenic hormones (HIP) to increase ßcasein mRNA levels and subsequently treated with the transcriptional inhibitor actinomycin D. ßcasein mRNA levels were then examined by RT PCR analysis. As shown in Fig.2 (left panel), in control HC11 cells treated with actinomycin D alone, we observed a significant decrease in ßcasein mRNA levels after 16 hrs, while the levels remained constant at earlier time points. Activin (middle panel) or TGFB (right panel) treatment of the cells did not affect Bcasein mRNA stability as degradation rate was identical to that observed for the control cells (left panel). GAPDH mRNA levels were analyzed in parallel as a negative control (Fig.2). These results indicate that activin/TGFB do not affect Bcasein mRNA stability but rather act at the transcriptional level.

Activin/TGFβ Does Not Affect Lactogenic Hormone Induced Phosphorylation and Nuclear Translocation of Stat5: Following phosphorylation by the Jak2 kinase, Stat5 rapidly accumulates in the nucleus to regulate transcription of target genes. To determine

whether activin/TGF β signaling could affect Stat5 phosphorylation and nuclear translocation, HC11 cells were treated or not with HIP in the presence or absence of activin for 0 to 60 min. Cytoplasmic and nuclear fractions were purified and analyzed by Western blot analysis using a specific phospho-Stat5 antibody. As shown in Fig.3a (upper panel), HIP rapidly induced Stat5 phosphorylation and this effect was unaltered by activin treatment. Equal loading of the proteins was assessed by reprobing the membrane with an anti-Stat5 antibody (Fig.3a, bottom panel). Similarly, Stat5 nuclear translocation in response to HIP treatment was not antagonized by activin (Fig.3b). The nuclear fraction membranes were reprobed with an anti-TBP for equal loading (Fig.3b, lower panel). Proper activin signaling in these cells was verified by reprobing of the membrane with a phospho-Smad3 antibody. As shown in Fig.3c, activin rapidly induced Smad3 phosphorylation in a time dependent manner. These results indicate that activin does not affect HIP-induced phosphorylation and nuclear accumulation of Stat5 and suggests that the antagonistic effect observed for activin on HIP-induced β casein expression takes place at a step further downstream within the nucleus.

Activin/TGF β Treatment does not affect Stat5 binding to the β casein Promoter: β casein gene expression is mediated through direct binding of Stat5 to the β casein gene promoter. We then investigated whether activin/TGF β could interfere with Stat5 DNA binding, using electromobility shift assay (EMSA). HC11 cells were treated from 0 to 120 minutes with HIP, activin or both, nuclear fractions were isolated and EMSA was performed using the Stat5 binding site (TTCNNNGAA) from the β casein promoter as a probe. As illustrated in Fig.4a, HIP induced a very rapid and transient DNA/protein complex formation while activin alone had no effect.

Interestingly, co-treatment of the cells with HIP and activin did not affect HIP-induced Stat5 DNA binding. The same results were observed in response to TGF β (Fig.4b). The presence of Stat5 in the HIP-induced DNA-protein complex was ensured by supershift experiment using a polyclonal antibody against Stat5. As shown in Fig.4b, (lanes 5, 6), addition of anti-Stat5a resulted in a supershift of the complex in HIP-treated extracts. Together, these results indicate that the decrease of β casein mRNA and protein levels by activin/TGF β is not due to an inhibition of Stat5 binding to the β casein promoter.

Activin/TGF β Inhibit Activation of the β casein gene Promoter in response to lactogenic hormones: In trying to understand the mechanism by which activin/TGF β act to inhibit β casein synthesis, we next investigated their effects at the level of transcription of the β casein gene promoter. For this, HC11 cells stably expressing the β casein gene promoter fused to the luciferase gene were treated from 4 to 24 hours with either lactogenic hormones, activin, TGF β or a combination of both. As shown in Fig.5, whereas HIP increased β casein luciferase activity in a time dependent manner, this effect was strongly inhibited by activin and TGF β (Fig.5). Activin and TGF β treatments alone did not affect β casein luciferase activity (Fig.5). These results demonstrate that activin and TGF β robustly block lactogenic hormone induction of the β casein gene promoter activity.

Stat5 Mediated Transcription is Blocked by Activin/TGF β Treatment: The β casein gene promoter construct encompasses the proximal part of the promoter that includes Stat5 binding sites, but also contains regulatory regions for other transcription factors such as the CCAAT enhancer binding protein C/EBP β , Oct1 ⁴²²⁻⁴²⁴. To delineate if the changes in β casein expression are a result of activin/TGF β induced alterations in Stat5 specific activation of the β casein gene promoter, we made an artificial promoter containing five tandem repeats of the Stat5 response elements fused to the luciferase gene (5XStat5-luc) and generated HC11 stable cell lines expressing this 5XStat5-luc (HC11-5XStat5-luc). As shown in Fig.6a, the three positive clones that were selected all strongly responded to the HIP treatment, as measured by the luciferase activity. Interestingly, while TGF β alone had no effect on this reporter construct, it strongly inhibited HIP-induced 5XStat5 luciferase activity, demonstrating the TGF β antagonizes Stat5-mediated transcriptional activity (Fig.6a).

To further extend our results to human mammary epithelial cells, we transfected MCF10A cells with the 5XStat5-luc reporter construct and examined the TGF β response on HIP-induced Stat5 transactivation. As shown in Fig.6b, HIP treatment induced a strong increase of 5X-Stat5-luc promoter activity and this effect was also robustly antagonized by TGF β . Together these results indicate that TGF β signaling directly block HIP-induced Stat5 activation in both mouse and human mammary epithelial cells, thereby leading to inhibition of milk gene protein expression.

Smad signaling blocks Stat5-induced gene transcription: To then address the molecular mechanisms by which activin/TGF β antagonizes Stat5 signaling, we next investigated the role of the Smad pathway, the main regulatory pathway downstream of activin/TGF β . For this, CHO cells were co-transfected with the β casein luciferase reporter construct, cDNAs encoding Stat5 and PRLR in the presence or absence of varying combinations of cDNAs encoding Smad2, Smad3, and Smad4. Cells were then stimulated overnight with HIP or TGF β alone or in combination. As shown in Fig.7a, TGF β significantly repressed HIP-induced β casein (left panel) and 5XStat5 (right panel) luciferase activity. Interestingly, overexpression of Smad3 alone or in combination with Smad4 significantly potentiated the TGF β inhibitory effect on HIP-induced luciferase activity for both promoter constructs (Figs.7b, c). Furthermore, as shown in Fig.7c (middle and left panels), a similar result was obtained in response to activin and with overexpression of Smad2. Together, these data indicate that the Smad proteins play a critical role in mediating activin/TGF β inhibition of lactogenic hormone-induced β casein gene promoter activation.

Having demonstrated that overexpression of the Smads could potentiate activin/TGF β mediated inhibition of prolactin/Stat5 β casein gene promoter activation, we next examined the effect of blocking Smad signaling on the activin/TGF β response. For this we used dominant negative Smad2 and dominant negative Smad3, in which the carboxyl-terminus serine residues were mutated to alanine and hence cannot be phosphorylated by the receptor ⁴¹². Likewise, we also used a mutant form of the activin type I receptor ((ALK4mL45) in which the three critical residues for interaction site with

Smad2 and Smad3 (N265, D267 and N268 within the L45 loop of the receptor) were mutated to alanine. The resulting mutant receptor, fails to recruit the Smads and is unable to mediate activin signaling 412 .

The efficiency of the dominant negative Smads (DNSmads) and the mutant receptor (ALK4mL45) was first assessed using the activin/TGF β responsive promoter construct 3TPluc. As shown in Fig.7d, DN Smad2, DN Smad3 and the mutant receptor (ALK4mL45) all strongly inhibited activin-induced 3TPluc activity. We then assessed the effect of overexpressing DNSmad2, DNSmad3 or ALK4mL45 in CHO cells transfected with cDNAs encoding the PRLR, and Stat5, along with β casein or 5XStat5-luc reporter constructs. Whereas in the control transfected cells HIP/activin treatment led to inhibition of β casein-luc and 5XStat5-luc luciferase activity, overexpression of DNSmad2, DNSmad3 and ALK4mL45 completely reversed these effects clearly highlighting the important role played by the Smads in mediating the inhibitory effect of activin/TGF β on Stat5 driven promoters (Fig.7e).

Smad signaling in response to activin/TGF β is centrally controlled by the common partner Smad4. Hence to further demonstrate the involvement of Smad pathway in mediating activin/TGF β inhibition of β casein gene expression and Stat5 activation we used murine embryonic fibroblasts (MEFs) established from wild type or Smad4 knockout mice ⁴²⁵. Inactivation of Smad4 expression has been shown to prevent activin/TGF β signaling and target gene transcriptional activation ^{207, 425}. Wild-type and Smad4 null mutant MEFs were co-transfected with either β casein promoter or 5XStat5

promoter, Stat5 and PRLR. Subsequently cells were treated or not with HIP, TGF β or HIP/TGF β . Although in the wild type MEFs, HIP-induced β casein promoter and 5XStat5 luciferase activity was antagonized by TGF β , this effect was completely abolished in the Smad4 deficient MEFs (Fig.7f). Furthermore, restoring Smad4 expression in the Smad4 null mutant MEFs also restored the TGF β inhibitory effect on HIP-induced β casein gene expression and Stat5 activation, clearly indicating the importance of the Smad pathway in repressing Stat5 mediated gene activation (Fig.7f).

Collectively these results demonstrate that the Smad pathway strongly suppresses Stat5mediated gene activation. Furthermore we show that the Smad pathway is necessary in mediating activin/TGF β antagonistic effect on Stat5 transcriptional activation.

The Transactivation capacity of Stat5 is Repressed Potently by the Smads: The transactivation domain of Stats is essential to drive transcription.⁴²⁶. To evaluate the involvement of activin/TGF β signaling via the Smads on Stat5 transactivation ability we co-transfected CHO cells with a GAL4 responsive promoter fused to the luciferase gene (pXPAL7) with a chimeric construct containing the GAL4 DNA binding domain and the carboxyl-terminus Stat5 transactivation domain (GAL4-Stat5a) ⁴²⁷. The cells were also transfected with or without increasing concentrations of Smad3/4. As shown in Fig.8, whereas TGF β induced a 27% decrease in GAL4-Stat5a induced luciferase activity, increasing concentrations of Smad proteins led to a parallel increasing inhibition of the luciferase activity by TGF β to reach 55% repression at the highest Smad concentration.

This finding demonstrates that Smad signaling efficiently blocks Stat5 transactivation ability leading to inhibition of milk gene protein production.

Stat5 Target Gene Cyclin D1 is Inhibited by Activin/TGFB: In the mammary gland Stat5 regulates milk gene protein production and cell differentiation but also controls expression of genes involved in cell cycle progression and survival. Interestingly, prolactin/Stat5 and activin/TGFB/Smad signaling have opposed effects on mammary epithelial cell growth and survival. Having shown that activin/TGF\beta-induced Smad signaling inhibited Stat5 transactivation and ßcasein production we next investigated whether Smad could also antagonize Stat5-mediated gene expression of other target genes, in particular those involved in Stat5-induced cell growth, such as cyclin D1. Indeed, prolactin signaling via Stat5 has been shown to induce cyclin D1 proximal promoter and increase in cyclin D1 protein expression in the mammary epithelial cells PRE-1 ^{376, 428}. To investigate whether the lactogenic stimulation (HIP) could also induce an increase in cyclin D1 protein expression in HC11 cells, we treated differentiated HC11 cells from 0 to 8 hours with HIP. As seen in Fig.9a, HIP induced a very rapid and transient increase in cyclin D1 protein levels peaking at 4 hours and returning back to basal levels at 8 hours. The membrane was then probed with anti-βtubulin as a loading control. We then sought to evaluate the effect of activin/TGF β on HIP induced cyclin D1 protein levels. Differentiated HC11 cells were treated for 2 hours with or without HIP, TGF^β or both. Whereas HIP induced an increase in cyclin D1 protein, TGF^β was able to completely reverse HIP induction of cyclin D1 back to basal levels (Fig.9b). To then evaluate whether the TGF β antagonistic effect was mediated at the transcriptional level,

we used the proximal cyclin D1 promoter fused to luciferase (cyclinD1-944), which has previously been shown to be activated by prolactin in a Stat5 dependent manner ³⁷⁶. CHO cells were transfected with the cyclinD1-944 reporter construct, Stat5, PRLR and β galactosidase cDNAs and stimulated overnight with HIP, TGF β or both. As shown in Fig.9c, HIP treatment induced cyclin D1 gene promoter activity and this effect was significantly reversed in the presence of TGF β .

Finally to evaluated the role of the Smad pathway in antagonizing Stat5-mediated cyclin D1 gene promoter activation. CHO cells were transiently co-transfected with cyclinD1-944, Stat5, PRLR, β gal with or without a combination of Smad2, Smad3 and Smad4. As shown in Fig.9d, in the absence of overexpressed Smad proteins TGF β induced a 20% reversal effect of HIP-induced cyclin D1 gene promoter activity. Interestingly, overexpression of the Smad proteins resulted in a clear potentiation of the TGF β antagonistic effect to approximately 50% reversal of HIP-induced cyclin D1 gene promoter activity (Fig.9d). These results demonstrate that activin/TGF β -inhibition of Stat5-induced cyclin D1 protein expression requires the Smad pathway. In all, these findings reveal that another Stat5 target gene, cyclin D1, activation is repressed by activin/TGF β mediated Smad signaling.

Activin/TGF β signaling reduces Stat5 interaction with CBP: We next wanted to elucidate the mechanism by which activin/TGF β -mediated Smad signaling blocked Stat5 transactivation of its target genes. It was previously shown that the co-activator CBP/p300 physically interacts with Stat5 to regulate Stat5-mediated gene expression ³⁵².

In fact, CBP/p300 binds the transactivation domain of various Stat family members and is essential for their activation ^{339, 372-374}. Henceforth, to determine whether activin/TGF β would reduce Stat5 interaction with CBP, CHO cells were transfected with PRLR, Stat5 and HA-tagged CBP. Cells were subsequently treated for 25 minutes with or without HIP, TGF β or both, before being lysed and immunoprecipitated with an anti-HA antibody, affinity conjugated to matrix beads and revealed by western blot analysis with the anti-Stat5 antibody. As shown in Fig.10, HIP treatment of the cells induced increased association between HA-CBP and Stat5. However, when the cells were treated with TGF β this interaction was significantly diminished. Equal level of protein levels were ensured by reprobing membranes with anti-HA and ant-Stat5 antibodies (Fig.10). Furthermore, total cell lysates were probed with anti-phosphoStat5 and antiphosphoSmad3, to ensure proper ligand stimulation (Fig.10). These results indicate that activin/TGF β inhibit Stat5 interaction with the co-activator CBP.

DISCUSSION

Mammary gland growth and differentiation is regulated by an assembly of signaling networks in response to various hormones and growth factors and alterations within these signaling cascades represent underlying causes of a variety of human diseases. such as breast cancer. Interestingly, the final outcome of mammary epithelial cell behavior and biological responses are in fact controlled by the way these pathways interact with each other to form signaling networks, a mechanism referred as crosstalk. Two critical signaling cascades within the mammary epithelial tissue are the activin/TGFB/Smad signaling and the Jak/Stat pathway. These two pathways oppose their physiological effects and are eminent in the regulation of mammary gland development and breast carcinogenesis. However, the exact nature of the biological network existing between the Smad and Stat signal transduction pathways has remained elusive. Our results underlined a novel crosstalk mechanism in which the intracellular mediators of activin/TGF β signaling, the Smad proteins, inhibit Stat5 regulated gene expression. These antagonistic effects take place in the nucleus and we showed that while activin/TGFβ-mediated Smad signaling does not prevent Stat5 phosphorylation, translocation and DNA binding, it blocks Stat5 association with the co-activator CBP, thereby inhibiting Stat5 transactivation.

Crosstalk mechanisms between distinct signaling pathways are key in providing an integrated response and regulating homeostasis. A previous study indicated that interferon- γ signaling through the Jak/Stat pathway could downregulate TGF β signaling ¹⁷¹. In fact, the existence of a direct effect of the Jak/Stat pathway towards TGF β

signaling is also supported by the fact that prolactin inhibits TGF_β-induced apoptosis in primary mammary epithelial cells. Inhibition of TGFB-induced apoptosis is carried out by induction of the kinase Akt in a PI3K-dependent manner¹⁸². However, the reciprocal effect of the TGFB/Smad signaling on Stat signaling has to date remained inconclusive. For instance, in mouse lymphocytes, TGF^β immunosuppressive effects are partly mediated through negative inhibition of IL-2 and IL-12 induced phosphorylation of Jak/Stat proteins $^{429, 430}$. However, in human T cells and natural killer cells, TGF β had no effect on IL-2 and IL-12 induced Jak/Stat phosphorylation ⁴³¹. Pregnant mice overexpressing the whey-acidic protein (WAP) promoter-driven transforming growth factorß cDNA displayed increased apoptosis in pregnant and lactating mammary glands associated with decreased lactation ^{264, 265, 432}. Added to the fact that all three isoforms of TGF_β are upregulated during involution ^{211, 254, 433}, it has been suggested that reduced milk protein expression may be due to a decrease in lobuloaveoli. However, our findings demonstrate that the TGFB/Smad signaling pathway tightly regulate Jak/Stat signaling in mammary gland through a direct crosstalk mechanism leading to inhibition of Stat5 transactivation of its target genes by Smad signaling.

In this study, we show that both β casein and cyclin D1 induced expression are regulated by activin/TGF β signaling. Cyclin D1 is an important cell cycle regulator that controls lobuloalveolar proliferation. Furthermore, cyclin D1 knockout mice fail to undergo proper lobuloalveolar proliferation during pregnancy, a phenotype shared by PRL and PRLR knockout mice ^{399, 434, 435}, consistent with the fact PRL regulates cyclin D1 gene promoter through Stat5 signaling ⁴²⁸. TGF β 's antagonistic effect on lactogenic hormone

induction of cyclin D1, implicates TGF β in a regulatory role of *in vivo* mammary gland development. This regulatory role allows for the differentiation phase of late pregnancy to occur by regulating proliferation of the lobuloaveoli. Moreover, activin/TGF β Smad signaling inhibition on cyclin D1 suggests that the effect of activin/TGF β Smad signaling is broad, potentially encompassing all Stat5 target genes and biological systems.

We observed that activin/TGF β signaling significantly reduces Stat5 association with the co-activator CBP. Interestingly, CBP/p300 can bind Smad2, Smad3 and Smad4, and contribute to their full activation ⁴³⁶⁻⁴³⁸. Thus, our data suggest that the Smads may compete with Stat5 for CBP/p300 binding, thereby inhibiting Stat5 transactivation ability. Such mechanism is reminiscent of Stat1 α competition with Smad3 for CBP/p300 binding. Stat1 α binding to CBP/p300 allows interferon- γ to block TGF β induced transcription of type I collagen by inhibiting Smad activities⁴³⁹. The competition model by which the Smads are sequestering CBP/p300 away from Stat5 can potentially be applied to other Stat molecules where CBP/p300 binding is essential for their activation.

Our findings unveiled strong antagonistic crosstalk mechanism between the Smad and Stat signaling pathway in regulating mammary gland. The potent tumor suppressor and growth inhibitory effects of activin/TGFβ pathway are well established in mammary epithelial and breast cancer cells ^{440, 441}. This is consistent with an antagonistic role played by the Smad towards prolactin signaling which is known to induce proliferation and survival in breast cancer cells ^{376, 383, 442}. TGFβ also displays a dual role in cancer

where as the tumor progresses TGF β acts to promote tumor metastasis ¹⁷¹. Interestingly, prolactin also exhibit a dual role, as in later stages of tumor development prolactin acts as an invasion suppressor hormone ³⁹¹. Thus, once again our data are consistent with these observations and suggest that the antagonistic crosstalk mechanism existing between the two pathways is critical to mammary cell growth and differentiation, and also regulates breast cancer formation and tumor metastasis.

The importance of molecular crosstalk mechanisms and their final biological outcomes are emphasized in this paper. Understanding how two prominent pathways, the activin/TGF β /Smad and prolactin Jak/Stat pathways act to antagonize their effects has provided insight into their relative contributions to mammary gland differentiation. Future studies may thus address whether they are applicable to other biological systems.

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FOOTNOTES

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FIGURES

Figure 1. Activin/TGF β inhibits lactogenic hormone induced β casein expression in mouse mammary epithelial cells. (A) HC11 cells were differentiated and subsequently treated for 8, 16 and 24 hours with prolactin, activin or prolactin/activin, and total RNA was analyzed by Northern blot using a specific probe for β casein (upper panel). Equal loading was assessed by ethidium bromide staining (lower panel). (B) Differentiated HC11 cells were treated with prolactin, activin, prolactin/activin for 24 hours and total cell lysates were analyzed by Western blot assay using a specific antibody against β casein (upper panel) or ERK1/2 (lower panel) as a loading control. (C) Differentiated HC11 cells were treated with or without HIP, activin, HIP/activin, TGF β , HIP/TGF β for 24 hours and total cell lysates were analyzed by Western blot assay using a specific antibody against β casein (upper panel) or ERK1/2 (lower panel) as a loading control. (C) Differentiated HC11 cells were treated with or without HIP, activin, HIP/activin, TGF β , HIP/TGF β for 24 hours and total cell lysates were analyzed by Western blot assay using a specific antibody against β casein (upper panel) or ERK1/2 (lower panel) as a loading control. (D) HC11 cells were treated with activin from 0, 4, 8, 16 and 24 hours and total cells lysates were analyzed by Western blot using specific antibodies against Jak2 (upper panel), Stat5 (middle panel) and β tubulin (lower panel).

Α











Fig. 1Activin/TGF β inhibits lactogenic hormone induced β casein expression in mouse mammary epithelial cells
Figure 2. Activin/TGFB do not affect milk protein mRNA stability.

Following treatment for 24 with HIP, differentiated HC11 cells were treated with either actinomycin D, actinomycin D/activin or actinomycin D/TGF β . Cells were then collected from 0 to 24 hours and total RNA was isolated. Reverse transcription reactions were performed using random primers and cDNAs were amplified for 30 cycles using specific oligonucleotides to β casein and GAPDH as a control.

Figure 3. Stat5 phosphorylation and translocation to the nucleus is unaffected by activin/TGF β signaling.

(A and B) HC11 cells were treated with HIP or HIP/activin from 0 to 60 minutes and cytoplasmic and nuclear fractions were isolated. Western blots were performed using specific antibodies against phosphoStat5, Stat5, and TBP. (C) HC11 cells were treated for the indicated time periods with activin or HIP/activin. Nuclear fractions were analyzed by Western blot using specific antibodies against phosphoSmad3 and TBP.



Fig. 2 Activin/TGF β do not effect milk protein mRNA stability

С





HIP: _ - - + + + + Activin: 0 15 30 60 0 15 30 60 Nucleus Wb: phosphoSmad3 Wb: TBP

Fig. 3 Stat5 phosphorylation and translocation to the nucleus is unaffected by activin/TGF\beta signaling

Figure 4. Activin/TGF β signaling do not inhibit Stat5 binding to the Stat5 binding element on the β casein promoter.

(A) Nuclear extracts from HC11 cells were isolated after treatment with HIP, HIP/activin or activin from 0 to 120 minutes. Electromobility shift assays were performed, using a 21 base pairs double stranded oligonucleotide encompassing the Stat5-binding site of the bovine β casein promoter as a probe. (B) EMSA on nuclear extracts treated or not with HIP, HIP/TGF β or TGF β for 20 minutes were performed. Supershifts were performed with a polyclonal antibody against Stat5a (lanes 5-6).





A







Figure 5. Bcasein promoter activation is potently inhibited by activin/TGFB.

HC11 cells which are stably transfected with the rat β casein promoter (-344/-1) were treated with or without HIP, activin or HIP/activin (left panel) or HIP, TGF β or HIP/TGF β (right panel) for 4, 8, 16 and 24 hours. Luciferase were subsequently performed. For statistical analysis, Two-way ANOVA was performed with a post-ANOVA Bonferroni's Multiple Comparison test. **p<0.01 as compared with HIP alone treatment. *** p<0.001 as compared with HIP alone.

Figure 6. Activin/TGFβ block Stat5-mediated transcription.

(A) HC11 clonal cells expressing a luciferase reporter driven by five Stat5 binding sites (5XStat5-luc) clone #2, clone #10, and clone #15 were treated or not with HIP, TGF β , HIP/TGF β for 16 hours and the response was measured by luciferase assay. (B) Human mammary epithelial cells, MCF10A cells, were co-transfected with 5XSta5-luc, long PRLR, MGF/Stat5a and β galactosidase and luciferase assays were performed after 16 hour treatment with or without HIP, TGF β or the combination of the two. For statistical analysis, an One-way ANOVA with a post-ANOVA Bonferroni's Multiple Comparison test (A and B), ***p<0.001 versus HIP treatment alone.



Fig. 5 β casein promoter activation is potently inhibited by activin/TGF β .



Fig. 6 Activin/TGFβ block STAT5-mediated transcription

Figure 7. Smads regulate activin/TGFβ inhibition of Stat5-mediated transcription.

(A, B, C, E) CHO cells were transciently transfected with either a 344 base pairs of the proximal βcasein promoter fused to the luciferase gene (βcasein-lux) or 5XStat5-luc and long PRLR, MGF/Stat5, ßgalactosidase. (A) Transfected CHO cells were treated with or not HIP, activin or HIP/activin (left panels) or HIP, TGFB, HIP/TGFB (right panels) for 16 hours and luciferase assays were performed (**B** and **C**) In addition CHO cells were also co-transfected with or without various combinations of full length Smad2, Smad3 and Smad4 as indicated. Subsequently, cells were treated with either HIP or HIP/activin (left panels) and HIP/TGFB (right panels). Luciferase activity is represented as % induction of the indicated promoter β casein-lux (B panel) and 5XStat5-luc (C panel) as compared to HIP only treated samples. (D) CHO cells were transfected with 3TPluc, β galactosidase and either dominant negative Smad2 (DNSmad2), dominant negative Smad3 (DNSmad3) or the activin type I receptor mutant (ALK4mL45) cDNAs. After treatment with activin for 16 hours luciferase activity was measured. (E) CHO cells were co-transfected with β casein-lux (left panel) or 5XStat5-luc (right panel) and DNSmad2 or DNSmad3 or ALK4mL45. After 16 hours treatment with HIP alone or HIP/activin, luciferase assays were performed. Luciferase activity is assessed by % induction of the indicated promoter as compared to HIP only treated samples. (F) Smad4(+/+) MEFs (left panel) and Smad4(-/-) MEFs (middle and right panel) were transfected with ßgalactosidase, long PRLR, MGF-Stat5, ßgalactosidase and ßcasein-luc (upper panel) or 5XStat5-luc (lower panel) with or without Smad4. The HIP, TGF β and HIP/TGFB response was measured after 16 hours by luciferase assay. For statistical analysis, One-way ANOVA with a post-ANOVA Bonferroni's Multiple Comparison test was performed, *p<0.05, **p<0.01, ***p<0.001 as compared to HIP only treatments.







Fig. 7 Smads regulate activin/TGF β inhibition of STAT5-mediated transcription



Figure 8. Stat5 transactivation is blocked by the Smads.

CHO cells were transfected with β galactosidase, XPal7, GAL4-STAT5TAD and with or without Smad3, Smad4 or Smad2, Smad3, Smad4 from 1µg to 4µg. Cells were treated with HIP or HIP/TGF β overnight and luciferase assays were performed. Values are represented as % repression as compared to non-TGF β treated samples. For statistical analysis, One-way ANOVA followed by post-test for linear trend were performed, p<0.001 for increasing Smad concentrations.

Figure 9. Stat5 target gene cyclin D1 induction is blocked by Activin/TGFβ Smad signaling.

(A). Differentiated HC11 cells were treated from 0 to 8 hours with HIP and western blot analysis was performed using cyclin D1 antibody (upper panel) and β tubulin (lower panel). (B) Differentiated HC11 cells were treated with or without HIP, TGF β , HIP/TGF β for 2 hours and total cell lysates were analyzed by Western blot assay using a specific antibody against cyclin D1 (upper panel) or β tubulin (lower panel) as a loading control. (C) CHO cells were transfected with the 944 base pairs proximal cyclin D1 promoter (cyclinD1-944) along with long PRLR, MGF/Stat5, β galactosidase. Cells were treated overnight with or without HIP, TGF β , HIP/TGF β . Luciferase activity was assessed. (D) CHO cells were transfected with cyclinD1-944, long PRLR, MGF/Stat5 and bgalactosidase with or without Smad2, Smad3, and Smad4 cDNAs. Cells were treated for 16 hours with or without HIP or HIP/TGF β . Luciferase activity was assessed. Values are represented as % repression as compared to HIP alone treatment. For statistical analysis, One-way ANOVA with a post-ANOVA Bonferroni's Multiple Comparison test was performed (C), ***p<0.001 versus HIP treatment alone. An unpaired t test was performed (D), **p<0.01 versus mock transfected cells.



Fig. 8. STAT5 transactivation is blocked by the Smads



Fig.9. Stat5-induced cyclin D1 expression is blocked by activin/TGF β Smad signaling

Figure 10. Activin/TGFβ Smad signaling inhibits Stat5 interaction with CBP.

CHO cells were transfected with PRLR, MGF/Stat5, and HA-CBP. Cells were subsequently treated and total cell lysates were extracted. Cell lysates from CHO cells stimulated with or without HIP, TGF β , HIP/TGF β for 25 minutes were immunoprecipitated with an anti-HA affinity matrix and analyzed by Western blot with an anti-Stat5 antibody (top panel) and an anti-HA antibody (second panel). Total cell lysates representing 10% of the immunoprecipitating input were analyzed by Western blot using antibodies to phosphoStat5, phosphoSmad3, Stat5A and HA as controls.





CHAPTER III.

The p38 MAP Kinase Pathway is required for Cell Growth Inhibition of Human Breast Cancer Cells in Response to Activin

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PREFACE

As we defined in CHAPTER II a novel mechanism by which TGF β and activin regulate mammary gland development, we wanted to investigage the effect of these family members in the diseased state of this organ. Whereas many studies have been conducted evaluating TGF β signaling mechanisms in breast cancer, as seen in CHAPTER I, activin induced signaling pathways in mammary carcinogenesis remained elucive. Furthermore, while Smads are key players in TGF β signaling, accumulating evidence indicate that other pathways are also induced downstream of their receptors. As such, some key signaling pathways that are activated downstream of TGF β family members are the mitogen activating protein kinases (MAPKs). Hence, I have included an introduction on MAPK signaling and crosstalk with TGF β pathways in order to better understand the paper presented in this chapter.

1. MAPK signaling: A brief Overview

MAPK signal transduction is induced in response to a wide array of extracellular stimuli. Classically, the MAPK signaling cascade involves three activation steps. The MAPK kinase kinase (MAPKK) will activate the MAPK kinase (MAPKK) which will in turn activate the MAPK. MAPK phosphorylate proteins on serine and threonine residues. Hence, MAPK rapidly target a multitude of substrates including protein kinases and transcription factors. The members of this family are subdivided into three groups: the extracellular-signal regulated kinases (ERKs), the stress activated kinases JNK and p38.

1.1. The p38 MAPK pathway

The p38 MAPK pathway is activated in response to physiological stress, osmotic stress, inflammatory stimuli, and ultraviolet exposure⁴⁴³. To date, five p38 isoforms have been identified (p38 α , β , β 2, γ and δ)⁴⁴⁴⁻⁴⁴⁸. Shortly after the discovery of the first p38 isoform, a target for an anti-inflammatory drug (SB203580) which binds pyridinyl imidazole derivatives was termed cytokine suppressive anti-inflammatory drugs binding protein (CSBP) which was identical to p38⁴⁴⁹. The p38 inhibitor, SB203580, binds to the ATP pocket of p38 and thus inhibits its enzymatic activity⁴⁵⁰. p38 α and β are ubiquitously expressed whereas p38y is found mostly in skeletal muscle. p388 is predominantly expressed in lung, kidneys, testis, pancreas and small intestine. The MAPKKK that are known to be involved in the cascade are MEKK1-4, MLK2/3, DLK, ASK1, Tpl2, and TAK1. The MAPKK are MKK3 and MKK6 (reviewed in ⁴⁵¹). Some substrates for p38 include the serine threonine specific kinases, the MAP-kinase activated protein kinases MAPKAPK2 and MAPKAPK3, which in turn phosphorylate the small heat shock protein HSP27, ATF1, MNK. Furthermore, the transcription factor ATF2, CREB, MEF2C, CHOP, Elk-1 and SAP-1 are also substrates of p38 (reviewed in ⁴⁵²). ATF2 and CREB once activated bind to cAMP response (CRE) elements on the promoters of target genes⁴⁵³. The p38 MAPK pathway is involved in the regulation of inflammation, apoptosis, proliferation, development, cellular differentiation, and tumor suppression.

2. TGFβ signaling crosstalk with the MAPK pathways

The integration of complex signaling cascades contributes to the final TGF β biological effect. Increasing evidence has highlighted the importance of other signal pathways either being activated by TGF β or having a direct effect on Smad signaling. In addition, TGF β s not only signal through the canonical Smad pathway but induction may occur through pathways such as the ERK mitogen activating protein kinase (MAPK) pathway, the JNK pathway and the p38 MAPK pathway. MAPK pathway activation by TGF β is cell specific.

2.1. MAPK Activation by TGFβ

Multiple examples in the literature exist where TGFβ activates the ERK, JNK and p38 MAPK pathways. Depending on the kinetics of TGFβ induced MAPK activation determines the involvement of the Smad pathway. For instance, TGFβ activation of the MAPK pathways with slow kinetics suggests, in some instances, a Smad-dependent transcriptional response. For example, TGFβ activation of Smads leads to upregulation of GADD45b which activates MKK4 and subsequently p38⁴⁵⁴. On the other hand, TGFβ activation of MAPKs with quick kinetics implies that they are a direct non-transcriptional target of this signaling pathway⁴⁵⁵. This observation is supported by studies performed using Smad4-deficient cells, dominant-negative Smads or studies performed using mutated TGFβ type I receptors, defective in Smad activation⁴⁵⁵. Using Smad4-deficient cells, TGFβ stimulation can still activate JNK⁴⁵⁶. Also, TGFβ may still induce p38 phosphorylation when using a mutant TGFβ type I receptor that cannot phosphorylate Smad2/3⁴⁵⁷. Finally, there is also evidence demonstrating convergence of

the MAPKs and the Smads. For instance, the downstream target of p38 MAPK, activating-transcription factor 2 (ATF2), interacts with Smad3 and Smad4, leading to a synergistic effect of both pathways¹¹⁹. Furthermore, both the Smad and JNK pathway synergize their effects via their interaction between c-Jun and Smad3^{121, 458, 459}.

Activation of the p38 MAPK and JNK pathways, by TGF β , occurs via various MAPKKK, amongst others. The biochemical link between the TGF^β receptors and the MAPK cascade has not been sufficiently defined. It has been suggested that XIAP (Xlinked inhibitor of apoptosis) may be the link between the receptor and TGF β induced activation of TAK1, but direct interaction has yet to be determined⁴⁶⁰. TGF β induced activation of MAPKKK TGF^β activated kinase 1 (TAK1)⁴⁶¹ which is enhanced by the scaffold protein TAK1 activator (TAB1)⁴⁶², positively regulates JNK and p38 MAPK⁴⁶¹. TAB1 may also interact with Smad7 leading to p38 activation by TAK1⁴⁶³. Evidence also indicates that TGF β activates JNK by a hematopoietic progenitor kinase (HPK-1) that phosphorylates TAK1 activating JNK⁴⁶⁴. TGFB can further activate JNK and subsequently c-Jun through MKK 4^{458} . Through TGF β type II receptor interaction with the death adaptor protein Daxx, TGFB activates the MAPKKK ASK-1 then JNK and induces apoptosis⁴⁶⁵. Finally, depending on the cell line, TGF_β can regulate the Rholike GTPases, Rac and Cdc42, inducing activation of JNK and p38 pathways. As illustrated by these multiple examples, TGF β may activate the MAPKs through a variety The biological consequences of TGFB induced MAPK activation remain of kinases. poorly characterized.

3. Purpose of Study

The aim of this study was to determine the effect of activin in breast cancer cells and to delineate the signaling pathways triggered downstream of activin. We demonstrate for the first time that activin induced an inhibition of cell growth in human breast cancer cells through activation of the p38 MAPK pathway. Moreover, at the time when this study was undertaken there were no published cases by which activin could convey its signal through a Smad-independent process. Hence, this was one of the first reports published demonstrating that activin can signal through the p38 MAPK pathway. We further showed that the p38 MAPK pathway is necessary for activin mediated cell growth repression.

ABSTRACT

Activin, a member of the TGF β family inhibits cell growth in various target tissues. Activin interacts with a complex of two receptors that upon activation phosphorylate specific intracellular mediators, the Smad proteins. The activated Smads interact with diverse DNA binding proteins and co-activators of transcription in a cell specific manner, thus leading to various activin biological effects. In this study, we investigated the role and mechanism of action of activin in the human breast cancer T47D cells. We found that activin treatment of T47D cells leads to a dramatic decrease in cell growth. Thus activin appears as a potent cell growth inhibitor of these breast cancer cells. We show that activin induces the Smad pathway in these cells but also activates the p38mitogen activated kinase pathway, further leading to phosphorylation of the transcription factor ATF2. Finally, specific inhibitors of the p38 kinase (SB202190, SB203580, and PD169316) but not an inactive analogue (SB202474) or the MEK-1 inhibitor PD98059 completely abolish the activin-mediated cell growth inhibition of T47D cells. Together, these results define a new role for activin in human breast cancer T47D cells and highlight a new pathway utilized by this growth factor in the mediation of its biological effects in cell growth arrest.

INTRODUCTION

Activin, a member of the TGF β family, regulates cell growth of various cell types. Activin interacts with a complex of two receptors (type I & type II), both containing an extra-cellular domain, a single transmembrane region and a large intracellular domain that contain a serine/threonine kinase domain. The type II receptor which is constitutively phosphorylated ⁴⁶⁶ transphosphorylates the type I receptor (ALK4) upon ligand stimulation, on serine and threonine residues ^{53, 467, 468}. The activated receptor complex then recruits the two receptor-regulated Smad2 and Smad3 ⁴⁶⁹⁻⁴⁷². Following binding and phosphorylation by the activin type I receptor, Smad2 and Smad3 are released to the cytoplasm where they associate with the common-partner Smad4 before being translocated to the nucleus ⁴⁷²⁻⁴⁷⁵.

Both Smad3 and Smad4 but not Smad2 can directly bind DNA elements (Smad binding element, SBE) and activate the transcription of the target genes ⁴⁷⁶. However, the DNA binding affinity of the Smads is low ⁶⁹ and they usually require the presence of other DNA binding proteins to efficiently interact with the promoters of their responsive target genes. As a result, the SBE elements are often found close to the DNA binding element of other transcription factors. Among those are the FAST family members, FAST1 ¹²⁵ and FAST2 ¹¹¹, TFE3 ²¹³, fos and Jun ¹²¹, Sp1 ⁴⁷⁷, CBP/p300 ⁴⁷⁸, Evi-1 ⁴⁷⁹, ATF2 ¹¹⁹.

The Smad proteins are central elements in the activin receptor signaling pathway but are not the sole pathway activated by this receptor complex. Other members of the TGF β super family have been shown to activate different signaling pathways, in addition to the Smads. TGF β itself can activate a member of the MAPKKK family of kinases, TAK1 (TGF activated kinase) ⁴⁶¹. TAK1 then activates the stress-activated kinase p38 and the transcription factor ATF2, a member of the b-ZIP family of DNA binding proteins ¹¹⁹. *In vitro* studies also suggested that the transcription factor ATF2 could interact with the MH1 domains of two activin responsive Smads, Smad3 and Smad4 ^{119, 480}. Both TGF β and the Müllerian inhibiting substance (MIS) were also shown to mediate some of their biological effects through an NFkB-mediated pathway ^{440, 481}. It is therefore conceivable that activin also utilizes other signaling pathways to transduce its signals.

Activin, its receptors and the Smads are expressed in myoepithelial cells as well as in a certain number of human breast cancer cell lines ^{258, 260}, suggesting a role for this growth factor and its downstream effectors, the Smads, in mammary cell growth and differentiation. Several reports have recently implicated TGFβ family members or their downstream signaling pathways in the regulation of breast cancer cell growth. Indeed, Smad4 can restore cell growth arrest in MDA-MB-468 cells, a breast cancer cell line in which the Smad4 gene is deleted ⁴⁸². Genetic mutations or loss of expression of the activin and TGFβ receptors is also found in human breast cancers ^{259, 295}. Finally, TGFβ and MIS mediates cell growth arrest in breast cancer by reducing NFkB DNA binding activity ^{440, 481} and activin itself can modulate cell growth of the breast cancer cells MCF7 ²⁵⁸.

In the present study, we investigated the role and mechanism of action of activin in breast cancer cells. We show here for the first time that activin strongly inhibits cell

growth of the human breast cancer cell line T47D. In addition, our results indicate that activin induce the Smad pathway in these cells but also activate the p38 MAP kinase pathway. Activation of this pathway further leads to phosphorylation of the transcription factor ATF2. Furthermore, we show that specific inhibitors of the p38 MAP kinase pathway fully antagonize the activin-mediated cell growth arrest in T47D cells. Thus, this highlights for the first time the involvement of this p38 kinase pathway downstream of the activin receptor signal transduction pathways leading to cell growth arrest.

MATERIALS & METHODS

Cell culture and Proliferation Assay: T47D cells were cultured in Dulbeco Modified Eagles Medium (DMEM) in the presence of 10% fetal calf serum. For proliferation assay, cells were plated in triplicates in 96-well dishes, at 5,000 cells/100ul in 2% FCS serum. Cells were treated with stimulated or no with activin (0.5 nM) and grown over a 5 day period. Cell proliferation was assessed using direct cell counting and the non-radioactive MTT cell proliferation assay for eukaryotic cells (Cell Titer 96, Promega G 4000). Absorbance was measured at 570 nm with a reference wavelength at 450 nm, using a Bio-tek Microplate reader.

Transfection and Reporter Assay: T47D cells (10^7 cells) were transfected by electroporation (Biorad Gene Pulser II) in 500 µl of PBS (240 Volts and 975 µF) with 10 µg of each of the indicated cDNAs. Following transfection, cells were plated in 6 well dishes in DMEM (10% FCS) for 24 hours recovery. The following day, cells were starved overnight in DMEM without serum and stimulated or no with activin (0.5nM) for 16 hours. Then, cells were washed once with PBS and lysed in 250 µl of lysis buffer (1% Triton X-100; 15 mM MgSO4; 4 mM EGTA; 1 mM DTT; 25 mM glycylglycine) on ice. The luciferase activity of each sample was measured using 45 ul of cell lysate (EG&G Berthold Luminometer) and normalized to the relative β -galactosidase activity.

RNAse Protection Assay: RNAse protection assay was performed using the hcc-2 template set and RiboQuant kit from Pharmingen (San Diego, CA) according to the manufacturer's instructions, with minor modifications. Radiolabeled antisense RNA

probes were prepared by in vitro transcription of the hcc-2 templates with T7 RNA polymerase in the presence of α -³²P UTP (NEN, Boston, MA). After DNAse I digestion, phenol-chloroform extraction, and ethanol precipitation, the probes were quantified. RNA samples (5 µg) were dried in a vacuum centrifuge and resuspended in 20 µl hybridization buffer containing 8x105 cpm of radiolabeled probes. Hybridization (overnight at 56 C), RNAse A/T1 digestion (1 hour at 30 C), proteinase K digestion, phenol-chloroform extraction, ethanol precipitation and gel resolution (5% polyacrylamide, 8 M urea sequencing gel) were carried out according to the instructions contained in the RiboQuant RNAse protection assay kit. A yeast tRNA-only reaction was included as a negative control to ensure complete RNAse digestion. Undigested RNA probes were also resolved on each gel to ensure their integrity and to serve as size markers. The cell cycle genes represented in the assays and the size of corresponding protected probe/mRNA duplexes were as follows: p130, 400 bp; Rb, 352 bp; p107, 317 bp; p53, 283 bp; p57, 252 bp; p27, 227 bp; p21, 202 bp; p19, 182 bp; p16, 163 bp; p14/p15, 133 bp; L32 riboprotein (L32, used as a housekeeping control), 113 bp; and GAPDH, 96 bp. The dried gel was exposed to X-Ray film. The positions of the protected probes were confirmed by plotting on a semi-log graph.

Western blot analysis: T47D cells were plated at 10^6 cells/ml in 6 well dishes in DMEM (10% FCS). The following day, cells were starved for an overnight period and stimulated or no with activin for different period of time as indicated. Total cell extracts were prepared from these cells were then separated on a polyacrylamide gel, transferred onto nitrocellulose and incubated with the indicated specific antibody overnight at 4°C (p38 (NEB, cat#9212), phosphop38 (NEB, cat#9210), ATF2 (NEB, cat# 9222),

phosphoATF2 (Santa Cruz, cat#8398), Smad2/3 (Santa Cruz, cat# 8332), phosphoSmad2 (UBI, cat# 6829), Smad4 (Santa Cruz, cat# 7966), ERK1/2 (NEB, cat#9102), phosphoERK1/2 (NEB, cat#9101). Following incubation, the membranes were washed twice for 10 min in washing buffer (50 mM Tris-HCl pH 7.6; 200 mM NaCl; 0.05% Tween 20) and incubated with a secondary antibody coupled to peroxidase (Santa Cruz at a 1/10,000 dilution) for 1 hour at room temperature. Then, the membranes were washed four times for 15 min in the washing buffer and immunoreactivity was normalized by chemiluminescence (Lumi-Light Plus Western Blotting substrate, Boehringer) according to the manufacturer's instructions and revealed using an Alpha Innotech Fluorochem (Packard Canberra).

RESULTS

Activin Inhibits T47D Human Breast Cancer Cell Growth: Although activin and its receptors are expressed in a number of breast cancer cell lines, the role of activin in the regulation of breast cancer cell growth has not been fully investigated yet. To analyze the role of activin in regulating growth of human breast cancer cells, we utilized the human breast cancer cell line T47D that endogenously expresses the activin-responsive Smad2, Smad3 and Smad4 ²⁸⁰. Using a cell growth and viability assay (MTT assay), we show that activin treatment of T47D cells leads to a significant inhibition in their growth, apparent as early as day 2 and reaching 40% inhibition at day 3 (Fig.1A). To verify that activin affects cell growth and not the metabolic rate of the cell, direct cell counting was also performed. As shown in Fig.1B, activin stimulation of T47D cells for three days also results in clear cell growth inhibition. Therefore, activin appears as a potent cell growth inhibitor for T47D breast cancer cells.

Activin Modulates Cell Cycle Regulators in Breast Cancer Cells: TGF β family members regulate cell growth through different mechanisms. They often mediate cell cycle arrest through up regulation of the three cyclin dependent kinase inhibitors p15^{INK4B}, p21CIP1^{/WAF1} and p27^{186, 188, 483}. Since activin exerts a strong effect on cell growth in T47D (Fig.1), we analyzed its effects in modulating gene expression levels of different cyclin dependent kinase inhibitors as well as of other cell cycle regulatory genes. For this, we examined the level of mRNA species of different cell cycle regulators, using a highly sensitive and specific ribonuclease protection assay (RPA). As shown in Fig.2, T47D cells were stimulated for different periods of time with activin (0.5

nM). Total RNA from un-stimulated or stimulated cells were extracted and hybridized with multiple antisense probes for human cell cycle regulators (p15, p16, p18, p19, p21, p27, as well as for p53, p57, p107 p130, the Retinoblastoma protein (Rb) and the two house keeping genes L32 and GAPDH). As shown in Fig.2, a modest but reproducible ligand-dependent increase in the mRNA level of p21^{CIP1/WAF1} was observed. This is consistent with a micro-array analysis of T47D cells treated for 8 hours with activin, that shows a 1.7 fold increase in p21^{CIP1/WAF1} mRNA level (JJL, unpublished data). mRNA levels for p15^{INK4B} were also consistently increased upon activin treatment, though at a lower level than p21^{CIP1/WAF1}. This experiment was repeated three times and showed consistent results. None of the other cell cycle regulators (p130, Rb, p107, p53, p57, p27, p19, p18, p16) or house keeping genes (L32, GAPDH) mRNA levels showed any significant or reproducible difference in response to activin (Fig.2). Our attempts to detect p15^{INK4B} and p21^{CIP1/WAF1} protein levels in these cells were unsuccessful, probably due to low level of expression of theses two proteins. This suggests that, at least part of the activin effect on cell growth arrest in T47D cells is mediated through up-regulation of p15^{INK4B} and p21^{CIP1/WAF1}.

Activin Induces Smad2 Phosphorylation in T47D Cells: To then analyze the role of the Smad pathway in T47D cells, we first examined the activation state of Smad2, following activin stimulation. Cells were starved for an overnight period and treated with 0.5 nM activin for different period of time, as indicated in Fig.3. Total cell lysates were separated by SDS-PAGE electrophoresis and resolved proteins were transferred to a nitrocellulose membrane for western blotting analysis. The membrane was probed with a specific antibody to phospho-Smad2 that recognizes the two phosphorylated serine residues in the C-terminal end of the MH2 domain of Smad2 (SSXS). As shown in Fig.3, upper panel, activin treatment of T47D cells leads to a clear phosphorylation of Smad2, as early as 15 min. following ligand stimulation of the cells. The membrane was stripped and reprobed with a polyclonal antibody that recognizes both Smad2 and Smad3 (Fig.3, middle panel) and subsequently with a monoclonal antibody to Smad4 (Fig.3, lower panel) and shows equal levels of all Smads in all samples. This data indicates that the Smad pathway is functional in T47D cells and is activated in response to activin stimulation.

Activin Induces 3tplux and ARE-Lux Promoters in T47D Cells: To further examine the activation of the activin receptor/Smad pathway in T47D cells, we analyzed the ability of activin to induce two activin receptor/Smad responsive promoter constructs (3TPLux and ARE-Lux). T47D cells were transiently co-transfected as shown in material and methods with the promoter construct 3TPLux or ARE-Lux and an expression vector encoding the co-activator Fast1. As shown in Fig.4A, activin treatment of T47D cells led to a 2.6 and 2.7 fold induction for 3TPLux and ARE-Lux/Fast1, and an expression vector encoding a constitutively active form of the activin type I receptor (ALK4 T Δ D). This point mutation replaces threonine 206 by an aspartic acid and renders the receptor constitutively active even in the absence of ligand or type II receptor ⁵³. As shown in Fig.4B, ALK4 T Δ D mimics activin effects on the activation of the two promoter constructs, leading to a 3.2 and 2.7 fold induction for 3TPlux and ARE-Lux/Fast1 respectively. Finally, to confirm the involvement of the Smad pathway, a

dominant negative form of Smad3, which lacks the MH2 domain (Smad3 Δ C) was transfected in T47D cells together with 3TPLux. Deletion of the C-terminal domain of Smad3 results in the loss of homo and heterodimerization with the wild type Smad4 as well as in its ability to induce a reporter construct ⁴⁸⁴. Cells were stimulated or not with activin and as seen in Fig.4C, over expression of Smad3 Δ C completely blocks activin-induced 3TPLux activity. Together, these results confirm that the activin receptor/Smad pathway is functional in breast cancer cells.

Activin Activates The p38 Kinase Pathway in T47D Cells: Recently, the p38 mitogen-activated protein kinase (MAPK) pathway was shown to regulate gene expression in response to TGF β ⁴⁸⁰. To assess the role of this pathway in activinmediated cell growth inhibition of breast cancer cells, T47D cells were starved overnight and stimulated with 0.5 nM of activin for different periods of time as indicated in Fig.5A. Total cell lysates were analyzed by immunoblot using specific antibodies directed against the phosphorylated form of the p38 kinase (pp38) and the normal form of p38 (p38). As shown in Fig.5A, upper panel, activin treatment of the T47D cells results in a clear increase in p38 phosphorylation in a time dependent manner. Activin effect is maximal at 20 to 40 min. and then decreases to return to basal level. The membrane was stripped and reprobed with an antibody directed against p38 and shows equal amount of the p38 kinase in all lanes (Fig.5A, lower panel).

We then analyzed the activin effects on the phosphorylation of the transcription factor ATF2, a downstream target of the p38 kinase. Total cell lysates were analyzed by immunoblot using specific antibodies directed the phosphorylated ATF2 (pATF2) or

ATF2 (ATF2). As shown in Fig.5B (upper panel), there is a time-dependent phosphorylation of the transcription factor ATF2 following activin treatment of the cells. The phosphorylation of ATF2 correlates with the activation of the p38 MAP kinase and shows a maximum phosphorylation at 40 min. The membrane was stripped and reprobed with an anti-ATF2 antibody and shows equal amount of the transcription factor in all lanes (Fig 5B. lower panel). Together, these data demonstrate that the p38 MAP kinase/ATF2 pathway is activated in T47D cells in response to activin.

The p38 Kinase Inhibitor PD169316 Blocks Activin-Induced p38 and ATF2 **Phosphorylation:** To further confirm the involvement of the p38 MAP kinase pathway downstream of the activin receptor, T47D cells were treated with a specific p38 kinase inhibitor (PD169316) or DMSO as a control. Cells were then stimulated or not with activin for 30 min. and total cell lysates were analyzed by Western blotting using different antibodies directed against phosphop38 or p38, phospho-ATF2 or ATF2. As shown in Fig. 6A (upper panel), in the presence of DMSO, activin induces phosphorylation of the kinase p38, confirming that previously seen (Fig.5). However, in the presence of the specific p38 kinase inhibitor (PD169316), this activin effect on p38 phosphorylation is abolished (Fig. 6A, upper panel). The membrane was stripped and reprobed with an antibody directed against p38 and shows equal amount of proteins in all lanes (Fig. 6A, lower panel). Similarly, as shown in Fig.6B, upper panel, activin induces phosphorylation of the transcription factor ATF2 in the presence of DMSO but this activin-induced effect is abolished in the presence of the p38 kinase inhibitor (PD169316). Equal amount of protein in all lanes was ensured by stripping and reprobing of the membrane with an anti-ATF2 antibody (Fig.6B, lower panel).

The p38 Kinase Inhibitors Antagonize Activin-Induced Cell Growth Arrest in **Breast Cancer Cells:** In order to evaluate the contribution of the p38 kinase pathway in activin-mediated cell growth inhibition in T47D cells, we used different p38 kinase specific inhibitors (SB202190, SB203580, PD169316), or an inactive analog (SB202474) and the MEK1/ERK1/2 inhibitor (PD98059) as controls, in both MTT (Fig.7A) and direct cell counting assays (Fig.7B). T47D cells were cultured in DMEM, 2% serum for three days and stimulated or not with 0.5 nM of activin in the presence or the absence of the different inhibitors. As shown in Fig.7A and 7B, after three days, cell growth is reduced by 40% in activin-treated cells as compared to untreated cells, similar to that previously observed in Fig.1A and 1B. However, in the presence of each the three specific p38 kinase inhibitors (SB202190, SB203580, PD169316), the inhibitory effect of activin on cell growth is abolished. On the other hand, the activin effect on cell growth inhibition is maintained in samples treated with the inactive form of the p38 kinase inhibitor (SB202474), or with the MEK1/ERK1/2 inhibitor (PD98059). Our results indicate that p38 kinase specific inhibitors nearly completely reverse the activin effect. As p38 kinase inhibitors could affect TGFB receptor activity ⁴⁸⁵ we examined their effect on activin-induced Smad2 phosphorylation. As shown in Fig.7C, while activin-induced p38 phosphorylation is inhibited by pretreatment of the cells with all three active forms of p38 kinase inhibitors, we observed no significant inhibitory effect on Smad2 phosphorylation under the same conditions. Thus it is likely that the antagonistic effect exerted by the p38 inhibitors on activin-induced cell growth arrest is mediated through inhibition of the p38 kinase pathway downstream of the activin receptor.

As activin is potent cell growth inhibitor in many different cell lines, the effect of the p38 kinase inhibitors were also analyzed in several activin-responsive cell line such as K562, CHO and MCF7. Interestingly, the activin inhibitors could reverse the activin effects on cell growth arrest in all cell line tested (data not shown). This indicates that the contribution of the p38 MAP kinase pathway to activin-mediated cell growth arrest is critical.

Activin Effect on Cell Growth Arrest is Not Mediated Through the MEK1/ERK1/2 MAP Kinase Pathway: The absence of effect of the MEK1/ERK1/2 inhibitor (PD98059) on activin-mediated cell growth arrest (Fig.7) suggests that activin does not modulate the MAP kinase MEK1/ERK1/2 pathway to arrest cell growth. The MEK1/ERK1/2 pathway is known to be involved in cell proliferation in response to various growth factors. To confirm that activin does not modulate or inhibits activation of this pathway in response to growth factors, T47D cells were starved overnight and stimulated with EGF (20 ng/ml) for different periods of time in the absence or presence of 1 nM of activin (Fig.8). Total cell lysates were then analyzed by Western blotting using an antibody directed against phospho-ERK1/2 (α -PERK). As shown in Fig.8 (upper panel), EGF very rapidly and transiently induces the phosphorylation of ERK1/2 (p42/p44). However, activin co-stimulation of the cells does not affect EGF-induced ERK1/2 phosphorylation. The membrane was stripped and reprobed with an anti-ERK antibody and shows equal amount of MAP kinase in all samples. Together this indicates that the activin effect on cell growth arrest in T47D cells is not mediated through the MEK1/ERK1/2 MAP kinase pathway.

DISCUSSION

Members of the TGF β family of growth factors are important factors in regulating cell growth inhibition hence it is critical to characterize their intracellular signaling mechanisms. While it is known that activin signals through activation of Smad proteins, the activation of other intracellular signaling pathways and their contribution to activinmediated cell growth inhibition remain to be characterized. In this paper we have examined the role of activin in mediating cell growth inhibition of breast cancer cells. Our results indicate that activin induce the Smad pathway in T47D cells and emphasize the involvement of the p38 MAP kinase pathway in activin-induced cell growth inhibition of these breast cancer cells.

Abnormalities in the signaling pathways of activin/TGF β have been clearly linked to various cancers, including breast cancer ⁴⁸⁶. We analyzed activin effects on the regulation of cell growth of human breast cancer cells. Using the human breast cancer cell line T47D, we found that activin has a profound and significant effect on the growth of these cells. We further investigated how activin triggers its effects in this cell line. Activin treatment of T47D cells leads to rapid phosphorylation of the receptor-regulated Smad2. Furthermore, both activin or the constitutively active form of the activin type I receptor (ALK4T Δ D) induce the two promoter constructs 3TPLux and ARE-Lux and this effect is completely abolished in the presence of an over expressed dominant negative form of Smad3 (Smad3 Δ C). All together, these results suggest that the activin receptor/Smad pathway is activated and can regulate the activin response in breast
cancer cells, confirming the central role played by the Smad proteins in the mediation of the activin response.

The p38 MAP kinase is involved in regulating cellular responses to stress and cytokines ^{444, 449, 487, 488}. p38 kinase is activated and phosphorylated at the Thr (180)-Tyr (182) site by the two closely related dual specificity protein kinases MKK3 and MKK6^{489,490}. The activated p38 kinase has been shown to phosphorylate several transcription factors such as ATF2 ⁴⁴³ and Max ⁴⁹¹, Elk-1 ⁴⁹² and indirectly CREB via activation of Nrf2 ⁴⁹³, Stat1 ⁴⁹⁴, MEF-2 ⁴⁹⁵. The p38 pathway is activated in response to TGF^β in C2C12, Mv1LU and 293 cells $^{119, 480}$. TGF β can induce phosphorylation of both p38 and the transcription factor ATF2 in these cell lines. In addition, p38 and ATF2 can contribute to the activation of the synthetic reporter construct 3TPLux in these cells but the physiological significance of this pathway in the mediation of the TGF β effects remains unclear. We show here that activin induces the p38 kinase pathway in T47D cells leading to phosphorylation of both the p38 kinase and the transcription factor ATF2. Furthermore, we show that the p38/ATF2 pathway is required to transduce the activin effects on cell growth inhibition. Indeed, different specific p38 kinase inhibitors, but not their inactive analog or the MEK inhibitor can totally reverse the activin effect on cell growth inhibition. This highlights a new role for the p38 kinase pathway in the control of cell growth and proliferation downstream of the activin/TGFB super family of growth factors. TGFB family members often require the presence of parallel or synergistic pathways to the Smads to carry on their full biological effects of these growth factors and diversity of the Smad-interacting partners may contribute to signal specificity ⁴⁹⁶. In

143

future studies, it will be interesting to examine the level of interaction between the Smad and the p38 kinase pathways in response to activin in T47D cells, as *in vitro* studies have suggested that the Smads could physically interact with the transcription factor ATF2^{119,} ⁴⁸⁰

Signaling by the MAPK family is organized hierarchically in three different steps. MAPK, such as p38, are phosphorylated by MAPK-kinases (MAPKKS), such as MKK3 and MKK6 in the case of p38. The MAPKKs are themselves activated and phosphorylated by the MAPKK-kinases (MAPKKS), such as MLK, TAK and ASK1 kinases act as MAPKKKs. Finally, the MAPKKKs are regulated by cell surface receptors or other external stimuli ^{497, 498}. It will be interesting to identify the upstream kinases and other partner proteins involved in the activin-mediated p38 activation that are acting between the activin receptor complex and the p38 kinase in the signaling cascade. Recent reports indicated TAK-1 a member of the MAPKKK family is activated by several cytokines including TGF β ⁴⁶¹ and the bone morphogenetic protein ⁴⁶⁰. TAK1 is a potent activator of the p38 kinase ⁴⁹⁹. It will, therefore, be interesting to determine whether or not TAK1 also lies downstream of the activin receptor complex signaling cascade.

It was also recently shown that the Müllerian Inhibitory substance (MIS) represses the growth of breast cancer cells by regulating the NFkB pathway⁴⁸¹. TGF β effect on cell growth inhibition of breast cancer has also been shown to be associated with a reduced

144

NFkB activity ⁴⁴⁰. This suggests that different member of the TGF β super family may regulate cell growth by utilizing different signaling pathways in the same target tissues. Interestingly, TAK1 was also shown to lead to NFkB activation ⁴⁸⁰, suggesting a potential role for this factor downstream of the activin receptor.

Our results indicate that activin strongly represses the cell growth of the breast cancer cells T47D. Further characterization of the downstream target genes that are modulated in T47D cells in response to activin will greatly enhance our understanding of its mechanism of action on cell growth regulation. Our data suggest that at least some of these targets could be the cyclin dependent kinase inhibitors. However, it will remain to determine if other cell cycle regulators as well as apoptosis regulators are also regulated by activin in these cells. Indeed, identification of the target genes, involved in the regulation of cell cycle and/or apoptosis will be of importance to shed light on the activin receptor mechanism of action in breast cancer cells.

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FOOTNOTES

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Abbreviations: TGF β , transforming growth factor β ; bp, base pair; ALK, activin receptor like kinase; CDK, cyclin dependent kinase; CDKI, cyclin dependent kinase inhibitor; Fast1, forkhead activin signal transducer-1.

FIGURES

Fig. 1: Activin induces cell growth arrest of the breast cancer cell line T47D. T47D cells were grown in 2% FCS DMEM over a 5 day period in the presence or the absence of 0.5 nM activin. Cell proliferation was assessed by (A) MTT colorimetric assay in triplicates and (B) direct cell counting. Values are expressed in arbitrary units.



Figure 1. Activin induces cell growth arrest of the breast cancer cell line T47D

Fig. 2: Expression of cell cycle genes in T47D cells in response to activin. Total RNA $(5 \ \mu g)$ obtained from T47D cells treated for 0, 4, 8, 16 or 24 hours with activin (0.5 nM). RNase protection assay was performed with radiolabeled probes for the indicated human cell cycle genes and 2 housekeeping control genes (L32 and GAPDH), as described in Materials and Methods. The positions of the protected probes are shown to the left of the autoradiography. Yeast tRNA (lane 6) is shown as a negative control. Undigested probes (lane 7) were used as size standards.



Figure 2. Expression of cell cycle genes in T47D cells in response to activin

Fig. 3: Activin induces Smad2 phosphorylation in T47D cells: T47D cells were treated with 0.5 nM activin for 0, 15, 30 and 60 min. Cell lysates were analyzed by Western blot using a specific antibody to phospho-Smad2 (Upper panel). The membrane was stripped and reprobed with an anti-Smad2/3 antibody (middle panel) and an anti-Smad4 antibody (lower panel).



Figure 3. Activin induces Smad2 phosphorylation in T47D cells

Fig. 4: Activin induces 3TPLux and ARE-Lux promoters in T47D cells: (A) T47D cells transfected with the activin receptor/Smad responsive promoter constructs 3TP-Lux or ARE-Lux/Fast1 reporter constructs were stimulated with activin 16 hours. The luciferase activity was normalized to the relative β -galactosidase values. Results represent means and standard deviations of three independent experiments. (B) T47D cells transfected with the promoter constructs 3TP-Lux or ARE-Lux/Fast1 reporter constructs in the presence or the absence of the constitutively active form of the activin type I receptor (ALK4 T Δ D). The luciferase activity was normalized to the relative β -galactosidase values. Results represent means and standard deviations of three independent experiments. (C) T47D cells were transfected with the promoter construct 3TP-Lux in the presence or the absence of the truncated form of Smad3 (Smad3 Δ C) and stimulated with activin 16 hours. The luciferase activity was normalized to the relative β -galactosidase values. Results represent means and standard deviations of three independent experiments. (C) T47D cells were transfected with the promoter construct 3TP-Lux in the presence or the absence of the truncated form of Smad3 (Smad3 Δ C) and stimulated with activin 16 hours. The luciferase activity was normalized to the relative β -galactosidase values. Results represent means and standard deviations of three independent experiments.



Figure 4. Activin induces 3Tplux and ARE-Lux promoters in T47D cells

Fig. 5: Activin induces the p38 kinase pathway in T47D cells: T47D cells were starved overnight and stimulated with 0.5 nM of activin for 0, 5, 15, 30, 60 and 90 min. (A) Total cell lysates were analyzed by immunoblot using specific antibodies directed against the phosphorylated form of the p38 kinase (pp38) (upper panel). The membrane was stripped and reprobed with an anti-p38 (p38) antibody (lower panel). (B) Similarly, total cell lysates were analyzed by immunoblot using a specific antibody directed against the phosphorylated ATF2 (pATF2) (upper panel). The membrane was stripped and reprobed with an anti-p38 (p38) antibody directed against the phosphorylated ATF2 (pATF2) (upper panel). The membrane was stripped and reprobed with an anti-ATF2 (ATF2) antibody (lower panel).



Figure 5. Activin induces the p38 kinase pathway in T47D cells

Fig. 6: The p38 kinase inhibitor PD169316 blocks activin-induced p38 and ATF2 phosphorylation: T47D cells were pretreated with DMSO or with a specific p38 inhibitor (PD169316) at 10 μ M for 1 hour before being stimulated with activin for 30 min. (A) Total cell lysates were analyzed by immunoblot using a specific antibody directed against the phosphorylated form of the p38 kinase (pp38) (upper panel). The membrane was stripped and reprobed with an anti-p38 (p38) antibody (lower panel). (B) Similarly, total cell lysates were analyzed by immunoblot using a specific antibody directed against the phosphorylated ATF2 (pATF2) (upper panel). The membrane was stripped and reprobed with an anti-p38 (p38) antibody (lower panel). (B) Similarly, total cell lysates were analyzed by immunoblot using a specific antibody directed against the phosphorylated ATF2 (pATF2) (upper panel). The membrane was stripped and reprobed with an anti-ATF2 (ATF2) antibody (lower panel).



Figure 6. The p38 kinase inhibitor PD169316 blocks activin-induced p38 and ATF2 phosphorylation

A

Fig. 7: p38 kinase inhibitors antagonize activin-induced cell growth arrest in breast cancer cells: T47D cells were cultured in DMEM, 2% serum for three days and stimulated or no with 0.5 nM of activin in the presence or the absence of 10 uM of the different p38 kinase specific inhibitors (SB202190, SB203580, PD169316), or an inactive analog (SB202474) and the MEK1/ERK1/2 inhibitor (PD98059) as controls. Cell growth was assessed by (A) MTT colorimetric assay in triplicates and (B) direct cell counting. Values represent means and standard deviations of five separate experiments and are expressed as percentage of inhibition compared to the control. (C) T47D cells were pretreated with DMSO or with the p38 inhibitors (SB202190, PD169316 or SB203580) at 10 μ M for 45 min. before being stimulated with activin for 15 min. Total cell lysates were analyzed by immunoblot using specific antibodies directed against the phosphorylated form of Smad2 (pSmad2, upper panel), the phosphorylated form of p38 kinase (p38, lower panel).



Figure 7. p38 kinase inhibitors antagonize activin-induced cell growth arrest in breast cancer cells

Fig. 8: Activin effect on cell growth arrest is not mediated through the MAP Kinase pathway: T47D cells were starved overnight and stimulated with EGF (20 ng/ml) for different period of times in the absence or presence of 1 nM of activin. Total cell lysates were then analyzed by Western blotting using an antibody directed against phospho-ERK1/2 (upper panel). The membrane was stripped and reprobed with an anti-ERK1/2 antibody (lower panel).





CHAPTER IV.

The Death Adaptor Molecule RAIDD is as a Novel Activin Target Necessary for Activin-Induced Cell Growth Inhibition

Effihia Cocolakis and Jean-Jacques Lebrun

PREFACE

As a direct continuation of CHAPTER III, we decided to characterize the intracellular target genes that relay activin effects on cell growth inhibition in human breast cancer cells by gene profiling using affymetrix DNA microarrays. As such, we identified the death adaptor molecule RAIDD as a novel target of activin signaling. I have included a brief introduction on RAIDD in order to better comprehend the study that follows.

1. TGFβ and Death Receptor Signaling

The prototypic death receptor pathway involves TNF- α and FasL signaling through their respective receptors TNF-RI (tumor necrosis factor receptor I) and Fas, leading to intracellular signaling with an end biological outcome of apoptosis. An important pathway activated by FasL is through the death adaptor molecule Daxx that directly interacts with Fas. Indeed, Daxx interaction with Fas leads to ASK-1 (apoptosis signal-regulating kinase 1) activation and subsequent activation of JNK, leading to apoptosis⁵⁰⁰, ⁵⁰¹. Interestingly, a yeast-two hybrid screening has identified Daxx as a binding partner of the TGF β type II receptor. Daxx interacts with the cytoplasmic tail of the receptor, and its carboxyl-terminus was also shown to act as a dominant-negative inhibitor of TGF β -induced apoptosis and to regulate TGF β -induced apoptosis⁴⁶⁵. Furthermore, antisense oligonucleotides to Daxx inhibit TGF β -induced apoptosis⁴⁶⁵. This study was the first to link a death adaptor protein to a member of the TGF β superfamily and define a novel pathway in the induction of apoptosis. To date, no death adaptor molecules have been shown to be involved within the activin signaling pathway.

2. The Death Adaptor RAIDD

The death adaptor molecule RAIDD (for RIP-associated ICH-1/CED-3-homologous protein with a death domain) was initially identified in the NCBI GenBank expressed-sequence tag (EST) data base based on its homology with the prodomain of the human ICE-like protease ICH-1 or procaspase-2⁵⁰². Subsequent to the initial discovery, another group idenfied RAIDD as the molecule CRADD (for caspase and RIP adaptor with death domain) through a similar database screening⁵⁰³. RAIDD is constitutively expressed, with highest expression in the adult heart, testis, liver, skeletal muscle, fetal liver and kidney. Located on chromosome 22, the RAIDD gene encodes for a 200 amino acid protein with a relative molecular weight of approximately 22 kDa.

RAIDD is composed of a N-terminal CARD (caspase activation and recruitment domain) which shares high homology with caspase-2. The C-terminus is composed of a DD (death domain) whose sequence is similar to that of other DD-containing proteins involved in death receptor signaling. Through homotypic interactions, the DD of RAIDD interacts with the DD of RIP (receptor interacting protein). RIP is a serine threonine kinase involved in the death receptor pathway. Similarly, through homotypic interactions via its CARD domain, RAIDD recruits and activates caspase-2 zymogens⁵⁰². RAIDD was found to promote apoptosis by recruiting caspase-2 to TNF-RI in the presence of RIP and the death adaptor molecule TRADD. Dominant negative forms of RAIDD, however, did not abrogate TNF- α -mediated cell death, suggesting that TNF- α signaling does not require RAIDD to induce apoptosis⁵⁰².

165

3. Purpose of study

Based on our previous study in which we showed that activin induces cell growth arrest in human breast cancer cells through the p38 MAPK pathway, we sought out to investigate the target genes donwnstream of activin signaling. We show that activin induces a strong upregulation of RAIDD mRNA and protein levels in T47D breast cancer cells. Furthermore, RAIDD is required for activin mediated cell growth inhibition of these cells.

ABSTRACT

Activin, a prominent member of the transforming growth factor- β (TGF β) superfamily of pluripotent cytokines plays a crucial role in growth control of multiple several cell types. Here we identify a novel activin target gene encoding RAIDD (RIP-associated ICH-1/CED-3-homologous protein with a death domain), a death adaptor protein involved in TNF-RI (tumor necrosis factor receptor 1) induced signaling that mediates programmed cell death by TNF- α . We reveal that activin upregulates RAIDD protein levels in human breast cancer cells. We further show that RAIDD increase in protein levels is not limited to breast cancer cells but also to human hepatocarcinoma cells. Finally, using antisense oligonucleotides to RAIDD, we demonstrate that RAIDD expression is necessary for activin mediated cell growth arrest.

INTRODUCTION

The transforming growth factor β (TGF β) superfamily of pluripotent growth factors consists of over 42 members including activins, TGF β s and bone morphogenic proteins (BMPs) among others, regulating a vast array of physiological and pathophysiological processes throughout the body. These polypeptides affect cell growth, differentiation and apoptosis in almost all cell types, including those of epithelial, endothelial and hematopoietic origin⁵⁰⁴.

Activin, their receptors and the Smads are widely expressed in all tissues and the regulatory role played by these growth factors is of central importance to human diseases. Indeed, mutations or deletions within these genes are often the underlying basis for human cancers. Interestingly, the involvement of these growth factors in human cancer is multifaceted. While they initially contribute tumor suppression by efficiently inhibiting cell proliferation, the TGF β growth inhibitory responses in cancer cells are often replaced by invasive and pro-metastatic responses as tumors progress, highlighting the dual role of TGF β as both a tumor suppressor and tumor promoting agent.

Activin signal transduction begins with ligand binding to a single-transmembranespanning, constitutively auto-phosphorylated serine/threonine kinase, type II receptor. Upon ligand binding, the type II receptor recruits and transphosphorylates the type I receptor within a juxtamembrane glycine and serine-rich region, rendering type I's kinase active. The activated type I receptor then phosphorylates the intracellular mediators known as the receptor-regulated Smads (R-Smads) Smad2 and Smad3, on serine residues with their carboxyl-terminus. Activation of the R-Smads allows for heterodimerization with common partner Smad4. Subsequently, the Smad heterocomplex translocates to the nucleus where it can associate with either co-activators or co-repressors to elicit or repress transcription of target genes⁵⁰⁴.

In the present study we describe a novel target gene of activin signaling, the death adaptor molecule RAIDD (RIP-associated ICH-1/CED-3-homologous protein with a death domain). We show that RAIDD mRNA and protein levels are upregulated in response to activin in human breast cancer (T47D) cells and human heptocarcinoma (HUH7) cells. Finally we demonstrate that RAIDD expression is necessary in mediating activin cell growth inhibition. Our data, implicate for the first time RAIDD as target in the mediation of activin's anti-proliferative effect.

MATERIALS and METHODS

Cell culture and Proliferation Assay: T47D and HUH7 cells were cultured in Dulbeco Modified Eagles Medium (DMEM) in the presence of 10% fetal calf serum. For proliferation assay, cells were plated in triplicates in 96-well dishes, at 5,000 cells/100ul in 2% FCS serum. Cells were treated with stimulated or no with activin (0.5 nM) and grown over a 3 day period. Cell proliferation was assessed the non-radioactive MTT cell proliferation assay for eukaryotic cells (Cell Titer 96, Promega G 4000). Absorbance was measured at 570 nm with a reference wavelength at 450 nm, using a Bio-tek Microplate reader.

Reverse-transcription PCR: T47D cells were treated with or without 0.5 nM activin from 2 to 8 hours, and total RNA was extracted using Trizol reagents (Invitrogen). Reverse transcription of total cellular RNA using oligo-dT primers was carried out using Stratacript Reverse Transcriptase (Stratagene) as per the manufacturer's instruction. Subsequently, amplification of cDNA to obtain products for RAIDD and GAPDH was performed. The PCR conditions were as follows: 30 cycles (94°C for 30 s, 58°C for 30 s, 72°C for 1 min).

Western analysis: Cells were cultured in DMEM, 2% fetal calf serum and stimulated or not with 0.5 nM activin for different periods of time as indicated in the figures. Total cell extracts were separated on a 12% polyacrylamide gel, transferred onto nitrocellulose and incubated with the indicated specific antibodies (anti-RAIDD, Santa-Cruz; anti-tubulin, Sigma). Immunoreactivity was revealed by chemiluminescence (Lumi-Light Plus Western Blotting substrate, Roche) according to the manufacturer's instructions and measured using an Alpha Innotech Fluorochem Imaging system (Packard Canberra).

Antisense Oligonucleotide (AS-Oligo) Treatment: Phosphorothioate-derivatized antisense RAIDD and control oligonucleotides (C-oligos) (20 bp) were synthesized. The AS-oligo was 5'-GGGCGGCCTTCAGCCCCATG-3', and the C-oligo was 5'-TCAGACTGGCTCTCTCCATG-3'. Cells were plated in the presence or absence of 50 μ M RAIDD AS-oligo or control C-oligo for 12 h and then stimulated with 0.5 nM activin. MTT assays were performed 72 h of ligand stimulation.

Statistical Analysis: Results are expressed as mean \pm SD of three or more separate independent experiments. Statistical analysis was assessed by one-way ANOVA as indicated in the figure legend, using GraphPad Prism 4 software (GraphPad Software, Inc.). Statistical analyses were meant to compare fold induction of activin-treated samples among themselves within each experiment. For all statistical analyses and tests, a p value < 0.05 was considered significant and is indicated on the top of the error bars by an asterisk.

RESULTS

RAIDD is novel target gene of Activin signaling in human breast cancer cells T47D: We have previously shown that activin induces cell-growth inhibition in human breast cancer (T47D) cells⁴⁴¹. To identify novel activin target genes which may be responsible for mediating the growth-inhibitory effect, we performed Affymetrix human Gene Chip U95A microarray experiments using activin-treated T47D cells. From our microarray experiments, we found the mRNA level of the death adaptor protein RAIDD to be significantly increased T47D cells treated for 2 and 8 hours with activin (5.8 and 5.3, respectively), Fig.1a. The activin-induced increase in RAIDD mRNA levels was verified by RT–PCR using primers specific for RAIDD. As shown in Fig.1b, activin induces an increase in RAIDD mRNA levels at 2 hours and is maintained at 8 hours. Hence, the micro-array data was confirmed demonstrating an increase in the RAIDD transcript by activin treatment.

Activin increases RAIDD protein levels: To then investigate whether the activin induced increase in RAIDD mRNA levels was followed by an increase in RAIDD protein levels, T47D cells were treated or not with activin for 2 to 24 hours and total cell lysates were analyzed by Western blot using an anti-RAIDD antibody. As shown in Fig.2a (upper panel), activin induced an increase in RAIDD protein levels starting at 8 hours and maintained until 24 hours. Reprobing of the membrane with an anti-βtubulin antibody showed equal loading of proteins (Fig.2a, lower panel). We also wanted to investigate whether the effects of activin on RAIDD protein levels could be extended to other cell types. Therefore, we treated the human hepatocarcinoma cell line HUH7 with activin from 0 to 24 hours and evaluated RAIDD expression by Western blot analysis.

Activin was able to induced RAIDD protein levels in HUH7 cells as seen in Fig.2b (upper panel). The blot was reprobed with a β tubulin antibody as a control for equal loading Fig.2b (lower panel). Thus our findings demonstrate that activin is a key regulator of RAIDD expression in both breast and liver cancer cells.

RAIDD is necessary for activin induced cell growth inhibition: In order to evaluate the contribution of the RAIDD in activin-mediated cell growth inhibition in T47D cells, we used anti-sense phosphorothioated oligos targeted towards RAIDD mRNA or a scrambled oligo as a negative contro in MTT assays, Fig.3. T47D cells were cultured in DMEM, 2% serum for three days and stimulated or not with 0.5 nM of activin in the presence or the absence of the antisense oligos. As shown in Fig. 3, after three days, cell growth is reduced by 40% in activin-treated cells as compared to untreated cells. However, in the presence of the RAIDD antisense oligo (AS-RAIDD), the inhibitory effect of activin on cell growth is abolished. On the other hand, the activin effect on cell growth inhibition is maintained in samples treated with the control scrambled oligo (AS-CTL). Our results indicate that antisense RAIDD completely reverse the activin effect. These data demonstrate that activin acts as a potent cell growth inhibitor and that this effect requires the death adaptor protein, RAIDD.

DISCUSSION

In this study, we demonstrate that RAIDD is a novel activin target gene and that its expression is necessary for mediating activin's growth inhibitory effect in breast cancer cells. The essential role of activin in inducing cell growth inhibition in a variety of cells and physiological conditions is well documented; however, the molecular mechanisms enabling this process are far from being clear. The identification of RAIDD as a target gene of activin signaling and its involvement in the inhibition of cell growth now provides a novel explanation for activin-induced cell growth inhibition.

The widespread expression of the activin-receptors, and RAIDD suggest that this mechanism may be a common method by which activin inhibits cell growth throughout the body. Indeed, we show that activin also upregulates RAIDD expression in human hepatocarcinoma cells. Activin has also been shown to induce apoptosis in various liver cells. It would be interesting to investigate whether RAIDD is involved in this biological process in other activin target tissues such as the liver.

Many types of tumour cells develop a resistance to activin-induced growth inhibition and concomitantly acquire the ability to release activin⁵⁰⁵. Once released, activin- may induce apoptosis in nearby lymphocytes, enabling the tumour cells to evade destruction by the cellular components of the immune system. Furthermore, there is a downregulation of activin and its signaling components in high grade breast cancers, suggesting a role for activin in breast tumor development²⁷⁶. As such, a loss of response to activin-induced cell growth inhibition may be crucial in the development of breast cancer. Observations such as these highlight the importance of activin-induced cell growth inhibition in many different pathological processes.

174

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FIGURES

Figure 1. Transcriptional Regulation of RAIDD Gene by Activin. Total RNA from T47D cells stimulated with activin for the indicated periods. (A) Results from Affymetrix human Gene Chip U95A microarray for RAIDD mRNA levels. (B) RT-PCR reactions were performed using oligo-dT and cDNAs were amplified using oligonucleotides specific to RAIDD and GAPDH.



Figure 1. Activin increases RAIDD mRNA levels in T47D human breast cancer cells.

Α.

Figure 2. Activin induces RAIDD protein expression. (A) T47D and (B) HUH7 cells were stimulated with activin for various times. Total cell lysates were analysed by immunoblotting using a specific polyclonal antibody against RAIDD (top). Equal loading was confirmed with an anti- β tubulin antibody (bottom).


Figure 2. Activin increases RAIDD protein levels.

Figure 3. Inhibition of RAIDD expression prevents activin induced cell growth inhibition. T47D cells were treated for 12 hours with or without 50 μ M AS-RAIDD or AS-CTL, prior to activin stimulation. Cell viability was assessed 72 hours after 0.5nM activin treatment via MTT assays. For statistical analysis, One-way ANOVA was performed with ** p<0.05.



Figure 3. Antisense-RAIDD antagonizes activin induced cell growth inhibition in breast cancer cells .

CHAPTER V.

GENERAL DISCUSSION

1. Defining the Effect of Activin/TGF^β signaling on Mammary Gland Development

Activin and TGF β signaling components are present throughout the development of the mammary gland, playing a crucial role in maintaining cellular homeostasis. Control of cellular homeostasis within the mammary gland by activin/TGFB is thought to be due to its anti-proliferative and apoptotic effects. A critical regulator in breast development is the lactogenic hormone prolactin. Prolactin has a positive role in mammary gland biology. Through its main signaling effecter, Stat5, prolactin induces ductal and lobuloalveolar proliferation and differentiation. The final effect of prolactin signaling induced mammary differentiation is its ability to stimulate milk protein production through a direct transcriptional mechanism. It is therefore not surprising that activin/TGF β and prolactin signaling pathways crosstalk with each other, resulting in antagonistic physiological effects. We have defined a novel crosstalk mechanism by which activin/TGF^β induced Smad activation results in the inhibition of lactogenic hormone induced Stat5 transactivation by decreasing Stat5 interaction with the coactivator CBP. The discovery of this novel crosstalk mechanism in mammary epithelial cells between the Smad and Stat pathway has allowed us to better understand the role of activin/TGFβ signaling in mammary gland development.

1.1. Other Potential Mechanism by which Smads Inhibit Stat5 Transactivation

Although, activin/TGF β signaling appears to inhibit Stat5 interaction with CBP, TGF β treatment does not completely prevent Stat5 and CBP interaction, CHAPTER II Figure 10. Therefore, additional mechanisms by which Smad2/3/4 may inhibit the transactivation of Stat5 are possible. Upon activin/TGF β stimulation, the Smads may recruit a Stat5 co-repressor to the promoter and subsequently induce its inhibition. Otherwise, upon activin/TGF β signaling, Smad2/3/4 may compete for other co-activators of Stat5 transactivation, similar to what we have shown for CBP.

Smad recruitment of a co-repressor to the Stat5 complex may be visualized by EMSA. More specifically, an additional shift in the EMSA is achieved using the Stat5 binding site of β casein promoter, Chapter II Figure 4, in the lanes that were treated with HIP/activin or HIP/TGF β . However, we do not see such a shift. On the other hand, we cannot exclude the possibility that the Smads are recruiting a co-repressor to both the β casein and cyclin D1 promoters at a location other than the Stat5 binding site. However, a strong repression by Smad signaling on the artificial promoter construct containing five tandem repeats of the Stat5 binding site may be observed. The inhibitory effect of TGF β is abolished when using the Smad4 knockout MEFs and the dominant negative Smads, Chapter II Figure 7. The effect of Smad signaling appears to be specific for Stat5 transactivation and may be due to Smads recruitment of a Stat5 repressor such as a histone deacetylase. Indeed, Smad3 interaction with HDAC4 and 5, leads to repression of gene expression⁵⁰⁶. The other possibility is that Smad2/3/4 may recruit away a co-activator from the Stat5 complex which may subsequently affect its transactivation.

Stat5 has been shown to interact with numerous transcription factors and co-regulators such as the glucocorticoid receptor³⁶⁵, cetrosomal P4.1-associated protein (CPAP)³⁶⁶, Nmyc interactor (Nmi)³⁶⁷, STAT5 and receptor corepressor (SMRT)³⁶⁸, p100³⁶⁹, ERK³⁷⁰, CBP/p300³⁵², STAP-2/BKS⁵⁰⁷, NCoA-1/SRC-1⁵⁰⁸, Oct-1⁵⁰⁹, and ER α^{510} . All of the aforementioned act as either co-activators or co-repressors to Stat5 mediated gene modulation. To date, we are unable to observe any interactions between Stat5 and Smad2, Smad3 or Smad4 in our mammary epithelial cell system. Aside from CBP/p300, the Smads share other Stat5 binding partners such as the glucocorticoid receptor and NCoA-1/SRC-1. Perhaps, competition for binding with some of the essential binding partners is another mechanism by which the Smads are inhibiting Stat5 transactivation. For example, interaction of Stat5 with the glucocorticoid receptor protects Stat5 from inactivation by dephosphorylation and enhances its activation ^{365, 371}. Interestingly, the carboxyl-terminus domain of Smad3 may interact with the glucocorticoid receptor and inhibit Smad3 transactivation¹³⁴. However, if Smad3 was recruiting away the glucocorticoid receptor from Stat5, a decrease in nuclear Stat5 phosphorylation would be observed. Since this is not the case, a mechanism by which glucocorticoid receptor is regulated by the Smads in order to inhibit Stat5-mediated gene activation is unlikely.

Another potential candidate that may be regulated by activin/TGF β /Smad signaling is the nuclear receptor co-activator1 (NCoA-1) or steroid receptor co-activator 1 (SRC-1). Initially discovered as a factor that interacts with nuclear receptors by enhancing their transcription capabilities⁵¹¹, NCoA-1/SRC-1 may interact with the transactivation domain of Stat5, augmenting PRL-induced β casein activation⁵⁰⁸. Furthermore, NCoA- 1/SRC-1 may bind Smad3, enhancing the functional link between Smad3 and CBP/p300⁵¹². This interaction potentiates TGF β -induced Smad3-mediated transcription⁵¹². Henceforth, NCoA-1/SRC-1 may also be competed away from Stat5 by Smad signaling, allowing for the inhibition of HIP induced Stat5 target gene activation.

1.2. Tight Regulation of Stat5 Necessary for Maintaining Proper Mammary Gland Development

Opposing physiological effects between activin/TGFB signaling and the prolactin Jak-Stat pathway are prominent in the regulation of mammary gland development. We demonstrate a novel mechanism in which the intracellular mediators of activin/TGF β signaling, the Smad proteins, inhibit Stat5 regulated gene induction by the inhibition of Stat5 transactivation. Our results highlight a novel crosstalk mechanism between two important signal transducing pathways. Interestingly, constitutively active Stat5 expression in the mammary gland leads to an increase in cellular proliferation during pregnancy in mice accompanied by shrunken alveoli during late pregnancy and early lactation⁵¹³. The phenotype of the forced activation of Stat5 mouse highlights the importance of tight regulation of Stat5 activity in the mammary gland in order to prevent an abnormal phenotype. Our study, CHAPTER II, emphasizes the significance of activin and TGFB signaling within the breast to maintain proper Stat5 gene activation. It is possible that activin and TGFB induced inhibition of Stat5 transactivation is the mechanism by which Stat5 levels are monitored to avoid over-proliferation of the mammary epithelium and premature lactation.

2. Mode of Inhibition of Activin in Breast Cancer Cells

Although it appears that activin and TGF β activate similar intracellular signaling cascades, the ligands and their distinct receptors differ greatly in their pattern of expression. Many *in vivo* and *in vitro* studies define possible roles for TGF β in mammary gland development, breast cancer and breast cancer metastasis, activin induced signal transduction in this tissue remains elusive.

2.1. Activin induction of the p38 MAPK pathway

In our second study, we evaluate the effect of activin signaling in breast cancer cells. We have found that along with the canonical Smad pathway, the p38 MAPK pathway is induced by activin. Furthermore, we show that the p38 MAPK pathway is required for activin mediated cell growth inhibition. Using three specific p38 MAPK inhibitors we completely reverse activin inhibition in the breast cancer cell line T47D. A subsequent study performed to investigate activin's antiproliferative effects in breast cancer cells demonstrated that activin induced G1 arrest in T47D cells through enhanced expression of p15, reduced cyclin A expression, and reduced phosphorylation of the retinoblastoma (Rb) protein²⁸⁶. These authors were not able to see p38 MAPK activation by activin treatment. It is possible that their experimental conditions were dissimilar to ours and that although we both used T47D cells, inconsistencies among the same cell lines often Hence, one must always be cautious with results obtained when limiting exist. themselves to only one cell line. In fact, we were able to see p38 MAPK activation in other cell lines and another breast cancer cell line MCF7 (data not shown). Furthermore, we were able to see reversal of activin induced cell growth inhibition in MCF7 cells using the p38 MAPK pathway inhibitors.

We were the first to unveil that activin signals through Smad-independent pathway, the p38 MAPK pathway. Interestingly, studies performed subsequent to ours also observe activin induced activation of p38 MAPK pathway. For example, in the erythroleukemia cell line K562, activin induces p38 phosphorylation, mediating growth inhibition and hemoglobin synthesis⁵¹⁴. Furthermore, activation of p38 MAPK pathway by activin in lactotrophs inhibits the pituitary transcription factor Pit-1⁴¹². Suggesting that activin induced activation of p38 MAPK is not limited to breast cancer cells.

2.2. Contribution of the Smad and p38 MAPK Pathways in Activin Mediated Cell Growth Inhibition in Breast Cancer Cells

Activin induces p38 MAPK activation and is involved in inducing cell growth inhibition in T47D breast cancer cells. This complete reversal by the p38 MAPK inhibitors suggests that the p38 MAPK pathway is central in mediating cell growth inhibition by activin in T47D cells. However, we still observe phosphorylation of Smad2 and activation of activin receptor/Smad responsive promoter constructs 3TP-Lux and ARE-Lux/Fast1 constructs, Chapter III Figure 3 and 4. A subsequent study has revealed that the Smad pathway is involved in mediating cell cycle arrest by activin in T47D cells²⁸⁶. Thus it would be interesting to investigate the relative contribution of the Smad and p38 MAPK pathways in provoking cell growth arrest in breast cancer cells. Interestingly, *in vitro* studies reveal that interaction between the p38 downstream target ATF2 and Smad3/4, mediate transcriptional activation by TGF $\beta^{119, 480}$. Therefore in T47D cells, a similar mechanism may exist which entails a point of convergence of the p38 and Smad pathway through ATF2.

Activin stimulation increases the mRNA of the cell cycle dependant inhibitors, $p15^{INK4B}$ and $p21CIP1^{/WAF1}$, Chapter III Figure 2. This suggests that the activin inhibition of cell growth might be due in part to upregulation of $p15^{INK4B}$ and $p21CIP1^{/WAF1}$. Indeed, the activin/TGF β cytostatic response in multiple cell lines is mediated through a Smad dependent upregulation of $p15^{INK4B}$ and $p21CIP1^{/WAF1}$ 127, 144, 186, 187, 192, 515, 516. Furthermore, TGF β activation of p38 MAPK has also been shown to stabilize $p21CIP1^{/WAF1}$ levels⁵¹⁷. This implies that both the Smad and p38 MAPK pathways may be involved in regulating $p15^{INK4B}$ and $p21CIP1^{/WAF1}$ expression. As a consequence, this may mediate activin induced cell growth arrest in T47D breast cancer cells.

2.3. Contribution of Novel Target Genes Regulated by Activin Signaling to the Activin and TGFβ Signaling Pathways

In the fourth chapter of my thesis, we discovered a novel activin target gene that is necessary in the anti-proliferative effect of activin in T47D cells. RAIDD, a death adaptor molecule, is upregulated by activin treatment, and its expression is imperative in blocking cell growth of breast cancer cells by activin. Another death adaptor molecule, Daxx, as described earlier, is involved in mediating TGF β to induce apoptosis through direct interaction with the T β RII and activation of the JNK pathway⁴⁶⁵. Thus, we investigated RAIDD interaction with the activin receptors but we were unable to detect binding. What remains to be determined is the mechanism by which it mediates its anti-proliferative effects in breast cancer cells.

Interestingly, we have also characterized two other novel target genes, the inositol phosphatase Src homology 2 (SH2) domain-containing 5' inositol phosphatase (SHIP) and the protein G-coupled receptor kinase 2 (GRK2) that are strongly upregulated by

both activin and TGF β . SHIP is an inositol lipid phosphatase that hydrolyses the D-5' phosphate position of both phosphatidylinosytol-3,4,5-triphosphate and inositol-1,3,4,5-tetrakisphosphate, which is critical in the regulation of cell growth⁵¹⁸. Activin and TGF β induced Smad signaling results in a robust increase in SHIP levels in immune cells. Furthermore, this increase in SHIP expression is necessary in mediating apoptosis in these cells through the regulation of lipid metabolism. Based on these results we wanted to examine the role of SHIP in the regulation of cell growth arrest by activin in breast cancer cells. However, SHIP expression is restricted to the hematopoietic system thus we investigated activin's effects on the far more ubiquitously expressed homologue SHIP2⁵¹⁹⁻⁵²¹. Unfortunately, we were not able to see any regulation of SHIP2 by activin in breast cancer cells (data not shown). Perhaps, TGF β /activin-induced up-regulation of SHIP may be limited to hematopoietic cells and not to breast cancer cells. Most likely, in epithelial derived cancers, such as that of the breast, target genes like RAIDD, as we have demonstrated in CHAPTER IV, play an imperative role in controling activin's anti-proliferative effects.

We've also identified GRK2, a kinase involved in the desensitization of G proteincoupled receptors (GPCR), as a downstream target and regulator of the TGF β -signaling cascade. We show that GRK2 expression levels are upregulated in response to activin/TGF β signaling. Furthermore, GRK2 physically interacts with the MH1 and MH2 domains of the receptor-regulated Smads and phosphorylates their linker region on a specific single serine/threonine residue. GRK2-induced Smad phosphorylation blocks activin/TGF β -induced Smad activation, nuclear translocation and target gene expression. The net effect of GRK2 on activin/TGF β responses leads to an inhibition of their antiproliferative and proapoptotic functions. Interestingly, activin was also able to induce GRK2 protein expression levels in MCF7 breast cancer cells. This study is particularly exciting due to the potential development of antagonists for anticancer therapies to activin/TGF β Smad signaling. Recently, many studies have highlighted the therapeutic potential of various TGF β antagonists as antimetastatic drugs^{522, 523}. As such, a useful method in treating breast cancer metastasis may be through the modulation of GRK2 function.

3. Impact of Thesis Discoveries on Breast Cancer

Breast cancer is the most common cancer in women. One in every nine Canadian women will develop breast cancer in a lifetime and one in twenty-seven will die. In 2006, an estimated 22,200 Canadian women will be diagnosed with breast cancer and 5,300 will die of it. Furthermore, approximately 160 men will be diagnosed with breast cancer and 45 will die of it⁵²⁴. Deciphering the crosstalk mechanisms and key signaling pathways in breast tumorigenesis and metastasis is critical for the development of new therapies to treat human breast cancer.

It would not be surprising that Smad antagonism on Stat5 mediated gene activation is a common mode of action for activin/TGF β to block prolactin biological effects. Henceforth, a tight regulation of activin/TGF β signaling components in mammary gland development and carcinogenesis is necessary to sustain normal homeostasis. A high proportion of human breast cancers have reported Stat5 to be activated and localized in the nucleus³⁸⁸. Overexpressing Smads in these specific types of breast cancers would

block Stat5 activation, as we have shown *in vitro* in CHAPTER II, which could lead to a potential treatment of this disease. On the other hand, in more advanced stages of the disease, TGF β signaling promotes cancer progression. We have shown in a collaborative study that blocking prolactin signaling triggers the TGF β pathway, causing breast cancer cells to become more invasive³⁹¹. Hence, activin/TGF β mediated inhibition of Stat5 transactivation may be another means by which activin/TGF β may induce breast cancer metastasis by blocking prolactin anti-invasive signaling.

Besides the antagonistic crosstalk-mechanism between Smads and Stat5, we have identified two major players in activin induced breast cancer cell growth inhibition, the p38 MAPK pathways and the death adaptor RAIDD. The process by which mammary tissues become cancerous must involve a multistep component where genes and pathways are misregulated resulting in malignancy. An extensive analysis of the precise signaling mechanisms, crosstalk pathways and genes that are regulated by activin and TGF β signaling pathways will allow us to decipher their relative contributions to the development, differentiation, transformation and tumor progression of the mammary gland. Targeting specific pathways such as the p38 MAPK or particular genes like RAIDD would pave the way for a mechanism-based design of anti-cancer drugs that would be beneficial in the treatment of patients with breast cancer.

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APPENDIX

ABBREVIATIONS

ACTH, adrenocorticotropin hormone

ActRIB, activin receptor type IB

ActRII, activin type II receptor

ALK, activin-receptor like kinase

ASK, apoptosis-regulating-signal kinase

ATF-2, activating-transcription factor-2

ATP, adenosine tri-phosphate

bHLH, basic helix-loop-helix

BMP, bone-morphogenic protein

BRCA1, breast cancer 1

b-TrCP1, [beta]-transducin repeat-containing protein

bZIP, basic leucine zipper domain protein

CamKII, calmodulin kinase II

CBP, CREB binding protein

Cdk, cyclin dependent kinase

CIS, cytokine-inducible SH2 protein

Co-Smad, common-partner Smad

CPAP, cetrosomal P4.1-associated protein

CREB, cyclic AMP response element binding protein

CRM1, chromosomal region maintenance 1

CSBP, cytokine suppressive anti-inflammatory drugs binding protein

CTGF, connective tissue growth factor

Dab2, Disabled-2

DAPK, death associated protein kinase

DLK, dual leucine zipper-bearing kinase

DMBA, 7,12-dimethylbenz[α]anthracene

EGF, epidermal growth factor

EGFR, epidermal growth factor receptor

EMT, epithelial to mesenchymal transition

ERK, extracellular signal-regulated

FSH, follicular stimulating hormone

GAS, y-interferon-activated sequence

GDF, growth/differentiation factor

GnRH, Gonadotropin-Releasing Hormone

GRK2, G-coupled receptor kinase 2

GS, glycine serine

hCG, Human Chorionic Gonadotropin

HIP, hydrocortisone insulin prolactin

HECT, homologous to the E6-accessory protein C-terminus

HGF/SF, hepatocyte growth factor/scatter factor

HPK, hematopoietic progenitor kinase

ICH-1, Ice/ced-3

ICE, interleukin-1beta converting enzyme

IGF-1, insulin like growth factor-1

IL11, interleukin-11

I-Smad, inhibitory Smad

Jak, Janus kinase

JNK, c-Jun terminal kinase

LAP, latency associated peptide

Lef-1, Lymphoid enhancer factor-1

LH, luteinizing hormone

LTBP, latent TGF β associated protein

Mad, Mothers against DPP gene

MAPK, mitogen activating protein kinase

MAPKAPK, MAP-kinase activate protein kinase

MAPKK, MAPK kinase

MAPKKK, MAPKK kinase

MEF2C, myocyte enhancer factor 2C

MEK, mitogen activated and extracellular signal-regulated kinase

MEKK, mitogen activated and extracellular signal-regulated kinase kinase

MGF, mammary gland factor

MH1, Mad-homology 1 domain

MH2, Mad-homology 2 domain

MLK, mixed-lineage kinase

MMP, matrix metalloprotease

MMTV, mouse mammary tumor virus

MSP, macrophage stimulating protein

Msx, muscle segment homeobox

NICD, Notch intracellular domain

NEDD4/2, neural precursor cell expressed, developmentally down-regulated 4-2

NES, nuclear export sequence

NFκB, nuclear factor-kappaB

NK, natural killer

NLS, Nuclear localization sequence

Nmi, N-myc interactor

Nup, nucleoporin

PAI, plasminogen activator inhibitor

PI3K, phosphatidyl inositol-3-kinase

PIAS, protein inhibitor of activated Stats

PKA, protein kinase A

PP2A, protein phosphatase 2A

PP2C, protein phosphatase 2C

PPM1A, protein phosphatase 1alpha

PRL, prolactin

PRLR, PRL receptor

PTHrP, parathyroid hormone-releasing peptide

PTP, protein-tyrosine phosphatase

RAIDD, RIP-associated ICH-1/CED-3-homologous protein with a death domain

RIP, receptor interacting protein

ROCK, Rho-associated kinase

R-Smad, receptor Smad

SAP-1, sphingolipid activator protein

SAPK, stress activated protein kinase

SARA, Smad anchor for receptor activation

SCF, Skp1/Cullin1/F-box protein

Roc1, regulator of Cullins 1

SGF, sarcoma growth factor

SHIP, SH2-domain containing inositol-5-phosphate

Shp-2, SH2 domain-containing tyrosin phosphatase

Ski, Sloan-Kettering Institute proto-oncogene

SMRT, Stat5 and receptor corepressor

Smurf, Smad ubiquitin regulatory factor

SnoN, Ski-related novel gene

SOCS, Suppressors of cytokine signaling

STAT, signal transducer and activator of transcription

TAB, TAK1 activator

TAK1, TGF β activated kinase 1

TCF, T cell-specific factor

TC-PTP, T-cell protein-tyrosine phosphatase

TEB, terminal end bud

TGF- α , transforming growth factor

TGF β , transforming growth factor β

TGIF, TG3-interacting factor

TIEG1, TGF β -inducible early-response gene

TIMP, Tissue Inhibitor of Metalloproteinase

Tiul1, for TGIF interacting ubiquitin ligase 1

TNF- α , tumor necrosis factor- α

T β RI, TGF β type I receptor

T β RII, TGF β type II receptor

uPA, urokinase plasminogen activator

VEGF, vascular endothelial growth factor

WAP, whey acidic protein

The p38 MAPK Pathway Is Required for Cell Growth Inhibition of Human Breast Cancer Cells in Response to Activin*

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Activin, a member of the TGF β family inhibits cell growth in various target tissues. Activin interacts with a complex of two receptors that upon activation phosphorylate specific intracellular mediators, the Smad proteins. The activated Smads interact with diverse DNA binding proteins and co-activators of transcription in a cell-specific manner, thus leading to various activin biological effects. In this study, we investigated the role and mechanism of action of activin in the human breast cancer T47D cells. We found that activin treatment of T47D cells leads to a dramatic decrease in cell growth. Thus activin appears as a potent cell growth inhibitor of these breast cancer cells. We show that activin induces the Smad pathway in these cells but also activates the p38-mitogen-activated protein kinase pathway, further leading to phosphorylation of the transcription factor ATF2. Finally, specific inhibitors of the p38 kinase (SB202190, SB203580, and PD169316) but not an inactive analogue (SB202474) or the MEK-1 inhibitor PD98059 completely abolish the activin-mediated cell growth inhibition of T47D cells. Together, these results define a new role for activin in human breast cancer T47D cells and highlight a new pathway utilized by this growth factor in the mediation of its biological effects in cell growth arrest.

Activin, a member of the $TGF\beta^1$ family, regulates cell growth of various cell types. Activin interacts with a complex of two receptors (types I and II), both containing an extracellular domain, a single transmembrane region, and a large intracellular domain that contain a serine/threonine kinase domain. The type II receptor, which is constitutively phosphorylated (1) transphosphorylates the type I receptor (ALK4) upon ligand stimulation, on serine and threonine residues (2-4). The activated receptor complex then recruits the two receptor-regulated Smad2 and Smad3 (5-8). Following binding and phosphorylation by the activin type I receptor, Smad2 and Smad3 are released to the cytoplasm where they associate with the common-partner Smad4 before being translocated to the nucleus (8-11).

Both Smad3 and Smad4 but not Smad2 can directly bind DNA elements (Smad binding element) and activate the transcription of the target genes (12). However, the DNA binding affinity of the Smads is low (13), and they usually require the presence of other DNA binding proteins to efficiently interact with the promoters of their responsive target genes. As a result, the Smad binding elements are often found close to the DNA binding element of other transcription factors. Among those are the FAST family members, FAST1 (14) and FAST2 (15), TFE3 (16), Fos and Jun (17), Sp1 (18), CBP/p300 (19), Evi-1 (20), and ATF2 (21).

The Smad proteins are central elements in the activin receptor signaling pathway but are not the sole pathway activated by this receptor complex. Other members of the TGF β superfamily have been shown to activate different signaling pathways, in addition to the Smads. TGF β itself can activate a member of the MAPKKK family of kinases, TAK1 (TGF-activated kinase) (22). TAK1 then activates the stress-activated kinase p38 and the transcription factor ATF2, a member of the b-ZIP family of DNA binding proteins (21). In vitro studies also suggested that the transcription factor ATF2 could interact with the MH1 domains of two activin responsive Smads. Smad3 and Smad4 (21, 23). Both TGF β and the Müllerian inhibiting substance (MIS) were also shown to mediate some of their biological effects through an NFkB-mediated pathway (24, 25). It is therefore conceivable that activin also utilizes other signaling pathways to transduce its signals.

Activin, its receptors, and the Smads are expressed in myoepithelial cells as well as in a certain number of human breast cancer cell lines (26, 27), suggesting a role for this growth factor and its downstream effectors, the Smads, in mammary cell growth and differentiation. Several reports have recently implicated TGF β family members or their downstream signaling pathways in the regulation of breast cancer cell growth. Indeed, Smad4 can restore cell growth arrest in MDA-MB-468 cells, a breast cancer cell line in which the Smad4 gene is deleted (28). Genetic mutations or loss of expression of the activin and TGF β receptors is also found in human breast cancers (29, 30). Finally, TGF β and MIS mediates cell growth arrest in breast cancer by reducing NF κ B DNA binding activity (24, 25), and activin itself can modulate cell growth of the breast cancer cells MCF7 (26).

In the present study, we investigated the role and mechanism of action of activin in breast cancer cells. We show here for the first time that activin strongly inhibits cell growth of the

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¹ The abbreviations used are: TGFβ, transforming growth factor β ; MAPK, mitogen-activated protein kinase; MAPKK, MAPK kinase; MAPKKK, MAPK kinase kinase; TAK1, TGF-activated kinase 1; ERK, extracellular signal-regulated kinase; MEK, MAPK/ERK kinase; MIS, Müllerian inhibiting substance; DMEM, Dulbecco's modified Eagle's medium; FCS, fetal calf serum; MTT, 3-[4,5-dimethylthiazol-2-yl]-2,5diphenyltetrazolium bromide; L32, L32 riboprotein; pp38, phosphoryl ated form of p38 kinase; EGF, epidermal growth factor; bp, base pair(s); ALK, activin receptor-like kinase; Fast1, forkhead activin signal transducer-1; STAT, signal transducers and activators of transcription.

human breast cancer cell line T47D. In addition, our results indicate that activin induces the Smad pathway in these cells but also activates the p38 MAPK pathway. Activation of this pathway further leads to phosphorylation of the transcription factor ATF2. Furthermore, we show that specific inhibitors of the p38 MAPK pathway antagonize the activin-mediated cell growth arrest in T47D cells. Thus, this highlights for the first time the involvement of this p38 kinase pathway downstream of the activin receptor signal transduction pathways leading to cell growth arrest.

MATERIALS AND METHODS

Cell Culture and Proliferation Assay—T47D cells were cultured in Dulbecco's Modified Eagle's Medium (DMEM) in the presence of 10% fetal calf serum. For proliferation assay, cells were plated in triplicates in 96-well dishes, at 5000 cells/100 μ l in 2% FCS. Cells were stimulated or not with activin (0.5 nM) and grown over a 5-day period. Cell proliferation was assessed using direct cell counting, and the non-radioactive MTT cell proliferation assay for eukaryotic cells (Cell Titer 96, Promega G 4000). Absorbance was measured at 570 nm with a reference wavelength at 450 nm, using a Bio-tek Microplate reader.

Transfection and Reporter Assay—T47D cells (10⁷ cells) were transfected by electroporation (Bio-Rad Gene Pulser II) in 500 μ l of phosphate-buffered saline (240 V and 975 microfarads) with 10 μ g of each of the indicated cDNAs. Following transfection, cells were plated in 6-well dishes in DMEM (10% FCS) for 24-b recovery. The following day, cells were starved overnight in DMEM without serum and stimulated or not with activin (0.5 nM) for 16 h. Then, cells were washed once with phosphate-buffered saline and lysed in 250 μ l of lysis buffer (1% Triton X-100, 15 mM MgSO₄, 4 mM EGTA, 1 mM dithiothreitol, 25 mM glycyl-glycine) on ice. The luciferase activity of each sample was measured using 45 μ l of cell lysate (EG&G Berthold luminometer) and normalized to the relative β -galactosidase activity.

RNase Protection Assay-RNase protection assay was performed using the hcc-2 template set and RiboQuant kit from PharMingen (San Diego, CA) according to the manufacturer's instructions, with minor modifications. Radiolabeled antisense RNA probes were prepared by in vitro transcription of the hcc-2 templates with T7 RNA polymerase in the presence of $[\alpha^{-32}P]UTP$ (PerkinElmer Life Sciences, Boston, MA). After DNase I digestion, phenol-chloroform extraction, and ethanol precipitation, the probes were quantified. RNA samples (5 µg) were dried in a vacuum centrifuge and resuspended in 20 µl of hybridization buffer containing 8×10^5 cpm of radiolabeled probes. Hybridization (overnight at 56 °C), RNase A/T1 digestion (1 h at 30 °C), proteinase K digestion, phenol-chloroform extraction, ethanol precipitation, and gel resolution (5% polyacrylamide, 8 M urea sequencing gel) were carried out according to the instructions contained in the RiboQuant RNase protection assay kit. A yeast tRNA-only reaction was included as a negative control to ensure complete RNase digestion. Undigested RNA probes were also resolved on each gel to ensure their integrity and to serve as size markers. The cell cycle genes represented in the assays and the size of corresponding protected probe/mRNA duplexes were as follows: p130, 400 bp; Rb, 352 bp; p107, 317 bp; p53, 283 bp; p57, 252 bp; p27, 227 bp; p21, 202 bp; p19, 182 bp; p16, 163 bp; p14/p15, 133 bp; L32 riboprotein (L32, used as a housekeeping control), 113 bp; and glyceraldehyde-3-phosphate dehydrogenase, 96 bp. An exposure was made of the dried gel onto x-ray film. The positions of the protected probes were confirmed by plotting on a semi-log graph.

Western Blot Analysis-T47D cells were plated at 10⁶ cells/ml in 6-well dishes in DMEM (10% FCS). The following day, cells were starved for an overnight period and stimulated or not with activin for different periods of time as indicated. Total cell extracts prepared from these cells were then separated on a polyacrylamide gel, transferred onto nitrocellulose, and incubated with the indicated specific antibody overnight at 4 °C (p38 (New England BioLabs, catalogue no. 9212), phosphop38 (New England BioLabs, catalogue no. 9210), ATF2 (New England BioLabs, catalogue no. 9222), phosphoATF2 (Santa Cruz Biotechnologies, catalogue no. 8398), Smad2/3 (Santa Cruz, catalogue no. 8332), phosphoSmad2 (Upstate Biotechnology Inc., catalogue no. 6829), Smad4 (Santa Cruz, catalogue no. 7966), ERK1/2 (New England Bio-Labs, catalogue no. 9102), and phosphoERK1/2 (New England BioLabs, catalogue no. 9101)). Following incubation, the membranes were washed twice for 10 min in washing buffer (50 mm Tris-HCl, pH 7.6; 200 mM NaCl; 0.05% Tween 20) and incubated with a secondary antibody coupled to peroxidase (from Santa Cruz; at a 1/10,000 dilution) for 1 h at room temperature. Then, the membranes were washed four times for



FIG. 1. Activin induces cell growth arrest of the breast cancer cell line T47D. T47D cells were grown in 2% FCS DMEM over a 5-day period in the presence or absence of 0.5 nM activin. Cell proliferation was assessed by (A) MTT colorimetric assay in triplicates and (B) direct cell counting. Values are expressed in arbitrary units.

15 min in the washing buffer, and immunoreactivity was normalized by chemiluminescence (Lumi-Light Plus Western blotting substrate, Roche Molecular Biochemicals) according to the manufacturer's instructions and revealed using an Alpha Innotech Fluorochem imaging system (Packard Canberra).

RESULTS

Activin Inhibits T47D Human Breast Cancer Cell Growth-Although activin and its receptors are expressed in a number of breast cancer cell lines, the role of activin in the regulation of breast cancer cell growth has not yet been fully investigated. To analyze the role of activin in regulating growth of human breast cancer cells, we utilized the human breast cancer cell line T47D, which endogenously expresses activin-responsive Smad2, Smad3, and Smad4 (31). Using a cell growth and viability assay (MTT assay), we show that activin treatment of T47D cells leads to a significant inhibition in their growth. apparent as early as day 2 and reaching 40% inhibition at day 3 (Fig. 1A). To verify that activin affects cell growth and not the metabolic rate of the cell, direct cell counting was also performed. As shown in Fig. 1B, activin stimulation of T47D cells for 3 days also results in clear cell growth inhibition. Therefore, activin appears as a potent cell growth inhibitor for T47D breast cancer cells.

Activin Modulates Cell Cycle Regulators in Breast Cancer Cells—TGF β family members regulate cell growth through different mechanisms. They often mediate cell cycle arrest through up-regulation of the three cyclin-dependent kinase inhibitors p15^{INK4B}, p21CIP1^{WAF1}, and p27 (32–34). Because activin exerts a strong effect on cell growth in T47D (Fig. 1), we analyzed its effects in modulating gene expression levels of different cyclin-dependent kinase inhibitors as well as of other cell cycle regulatory genes. For this, we examined the level of mRNA species of different cell cycle regulators, using a highly sensitive and specific ribonuclease protection assay. As shown in Fig. 2, T47D cells were stimulated for different periods of



FIG. 2. Expression of cell cycle genes in T47D cells in response to activin. Total RNA (5 μ g) obtained from T47D cells treated for 0, 4, 8, 16, or 24 h with activin (0.5 nm). An RNase protection assay was performed with radiolabeled probes for the indicated human cell cycle genes and two housekeeping control genes (L32 and glyceraldehyde-3phosphate dehydrogenase), as described under "Materials and Methods." The positions of the protected probes are shown to the *left* of the autoradiography. Yeast tRNA (*lane 6*) is shown as a negative control. Undigested probes (*lane 7*) were used as size standards.

time with activin (0.5 nm). Total RNA from unstimulated or stimulated cells were extracted and hybridized with multiple antisense probes for human cell cycle regulators (p15, p16, p18, p19, p21, p27, as well as for p53, p57, p107 p130, the retinoblastoma protein (Rb), and the two housekeeping genes L32 and glyceraldehyde-3-phosphate dehydrogenase). As shown in Fig. 2, a modest but reproducible ligand-dependent increase in the mRNA level of p21^{CIP1/WAF1} was observed. This is consistent with a microarray analysis of T47D cells treated for 8 h with activin, which shows a 1.7-fold increase in p21^{CIP1/WAF1} mRNA level.² mRNA levels for p15^{INK4B} were also consistently increased upon activin treatment, although at a lower level than p21^{CIP1/WAF1}. This experiment was repeated three times and showed consistent results. None of the other cell cycle regulators (p130, Rb, p107, p53, p57, p27, p19, p18, or p16) or housekeeping genes (L32 or glyceraldehyde-3-phosphate dehydrogenase) mRNA levels showed any significant or reproducible difference in response to activin (Fig. 2). Our attempts to detect p15^{INK4B} and p21^{CIP1/WAF1} protein levels in these cells were unsuccessful, probably due to the low level of expression of theses two proteins. This suggests that at least part of the activin effect on cell growth arrest in T47D cells is mediated through up-regulation of p15^{INK4B} and p21^{CIP1/WAF1}

Activin Induces Smad2 Phosphorylation in T47D Cells—To then analyze the role of the Smad pathway in T47D cells, we first examined the activation state of Smad2, following activin stimulation. Cells were starved for an overnight period and treated with 0.5 nm activin for a different period of time, as indicated in Fig. 3. Total cell lysates were separated by SDS-



FIG. 3. Activin induces Smad2 phosphorylation in T47D cells. T47D cells were treated with 0.5 nm activin for 0, 15, 30, and 60 min. Cell lysates were analyzed by Western blot using a specific antibody to phospho-Smad2 (*upper panel*). The membrane was stripped and reprobed with an anti-Smad2/3 antibody (*middle panel*) and an anti-Smad4 antibody (*lower panel*).

polyacrylamide gel electrophoresis, and resolved proteins were transferred to a nitrocellulose membrane for Western blotting analysis. The membrane was probed with a specific antibody to phospho-Smad2 that recognizes the two phosphorylated serine residues in the C-terminal end of the MH2 domain of Smad2 (SSXS). As shown in Fig. 3, *upper panel*, activin treatment of T47D cells leads to a clear phosphorylation of Smad2, as early as 15 min following ligand stimulation of the cells. The membrane was stripped and reprobed with a polyclonal antibody that recognizes both Smad2 and Smad3 (Fig. 3, *middle panel*) and subsequently with a monoclonal antibody to Smad4 (Fig. 3, *lower panel*) and shows equal levels of all Smads in all samples. These data indicate that the Smad pathway is functional in T47D cells and is activated in response to activin stimulation.

Activin Induces 3TPLux and ARE-Lux Promoters in T47D Cells-To further examine the activation of the activin receptor/Smad pathway in T47D cells, we analyzed the ability of activin to induce two activin receptor/Smad-responsive promoter constructs (3TPLux and ARE-Lux). T47D cells were transiently co-transfected as shown under "Materials and Methods" with the promoter construct 3TPLux or ARE-Lux and an expression vector encoding the co-activator Fast1. As shown in Fig. 4A, activin treatment of T47D cells led to a 2.6and 2.7-fold induction of 3TPLux and ARE-Lux, respectively, Furthermore, T47D cells were also co-transfected with 3TPLux or ARE-Lux/Fast1 and an expression vector encoding a constitutively active form of the activin type I receptor (ALK4 $T\Delta D$). This point mutation replaces threonine 206 by an aspartic acid and renders the receptor constitutively active even in the absence of ligand or type II receptor (4). As shown in Fig. 4B, ALK4 TDD mimics activin effects on the activation of the two promoter constructs, leading to a 3.2- and 2.7-fold induction of 3TPlux and ARE-Lux/Fast1, respectively. Finally, to confirm the involvement of the Smad pathway, a dominant negative form of Smad3, which lacks the MH2 domain (Smad3 Δ C), was transfected in T47D cells together with 3TPLux. Deletion of the C-terminal domain of Smad3 results in the loss of homo- and heterodimerization with the wild type Smad4 as well as in its ability to induce a reporter construct (35). Cells were stimulated or not with activin and, as seen in Fig. 4C, overexpression of Smad3 Δ C completely blocks activin-induced 3TPLux activity. Together, these results confirm that the activin receptor/

² J.-J. Lebrun, unpublished data.



FIG. 4. Activin induces 3TPLux and ARE-Lux promoters in T47D cells. A, T47D cells transfected with the activin receptor/Smad responsive promoter constructs 3TP-Lux or ARE-Lux/Fast1 reporter constructs were stimulated with activin 16 h. The luciferase activity was normalized to the relative β -galactosidase values. Results represent means and standard deviations of three independent experiments. B, T47D cells transfected with the promoter constructs 3TP-Lux or ARE-Lux/Fast1 reporter constructs in the presence or the absence of the constitutively active form of the activin type I receptor (ALK4 $T\Delta D$). The luciferase activity was normalized to the relative β -galactosidase values. Results represent means and standard deviations of three independent experiments. C, T47D cells were transfected with the promoter construct 3TP-Lux in the presence or absence of the truncated form of Smad3 (Smad3 ΔC) and stimulated with activin 16 h. The luciferase activity was normalized to the relative β -galactosidase values. Results represent means and standard deviations of three independent experiments.

Smad pathway is functional in breast cancer cells.

Activin Activates the p38 Kinase Pathway in T47D Cells-Recently, the p38 mitogen-activated protein kinase (MAPK) pathway was shown to regulate gene expression in response to TGF β (23). To assess the role of this pathway in activin-mediated cell growth inhibition of breast cancer cells, T47D cells were starved overnight and stimulated with 0.5 nm activin for different periods of time as indicated in Fig. 5A. Total cell lysates were analyzed by immunoblot using specific antibodies directed against the phosphorylated form of the p38 kinase (pp38) and the normal form of p38 (p38). As shown in Fig. 5A, upper panel, activin treatment of the T47D cells results in a clear increase in p38 phosphorylation in a time-dependent manner. Activin effect is maximal at 20-40 min and then decreases to return to basal level. The membrane was stripped and reprobed with an antibody directed against p38 and shows an equal amount of the p38 kinase in all lanes (Fig. 5A, lower panel).



FIG. 5. Activin induces the p38 kinase pathway in T47D cells. T47D cells were starved overnight and stimulated with 0.5 nM of activin for 0, 5, 15, 30, 60, and 90 min. A, total cell lysates were analyzed by immunoblot using specific antibodies directed against the phosphorylated form of the p38 kinase (pp38) (upper panel). The membrane was stripped and reprobed with an anti-p38 (p38) antibody (lower panel). B, similarly, total cell lysates were analyzed by immunoblot using a specific antibody directed against the phosphorylated ATF2 (pATF2) (upper panel). The membrane was stripped and reprobed with an anti-ATF2 (ATF2) antibody (lower panel).

We then analyzed the activin effects on the phosphorylation of the transcription factor ATF2, a downstream target of the p38 kinase. Total cell lysates were analyzed by immunoblot using specific antibodies directed against the phosphorylated ATF2 (pATF2) or ATF2 (ATF2). As shown in Fig. 5B (upper panel), there is a time-dependent phosphorylation of the transcription factor ATF2 following activin treatment of the cells. The phosphorylation of ATF2 correlates with the activation of the p38 MAPK and shows a maximum phosphorylation at 40 min. The membrane was stripped and reprobed with an anti-ATF2 antibody and shows an equal amount of the transcription factor in all lanes (Fig. 5B, lower panel). Together, these data demonstrate that the p38 MAPK/ATF2 pathway is activated in T47D cells in response to activin.

The p38 Kinase Inhibitor PD169316 Blocks Activin-induced p38 and ATF2 Phosphorylation-To further confirm the involvement of the p38 MAPK pathway downstream of the activin receptor, T47D cells were treated with a specific p38 kinase inhibitor (PD169316) or Me₂SO as a control. Cells were then stimulated or not with activin for 30 min, and total cell lysates were analyzed by Western blotting using different antibodies directed against phosphop38 or p38, phospho-ATF2 or ATF2. As shown in Fig. 6A (upper panel), in the presence of Me₂SO, activin induces phosphorylation of the kinase p38, confirming the previously seen results (Fig. 5). However, in the presence of the specific p38 kinase inhibitor PD169316, this activin effect on p38 phosphorylation is abolished (Fig. 6A, upper panel). The membrane was stripped and reprobed with an antibody directed against p38 and shows an equal amount of proteins in all lanes (Fig. 6A, lower panel). Similarly, as shown in Fig. 6B, upper panel, activin induces phosphorylation of the transcription factor ATF2 in the presence of Me₂SO, but this activin-induced effect is abolished in the presence of the p38



FIG. 6. The p38 kinase inhibitor PD169316 blocks activin-induced p38 and ATF2 phosphorylation. T47D cells were pretreated with Me₂SO or with the specific p38 inhibitor PD169316 at 10 μ M for 1 h before being stimulated with activin for 30 min. A, total cell lysates were analyzed by immunoblot using a specific antibody directed against the phosphorylated form of the p38 kinase (pp38) (upper panel). The membrane was stripped and reprobed with an anti-p38 (p38) antibody (lower panel). B, similarly, total cell lysates were analyzed by immunoblot using a specific antibody directed against the phosphorylated ATF2 (pATF2) (upper panel). The membrane was stripped and reprobed with an anti-ATF2 (ATF2) antibody (lower panel).

kinase inhibitor PD169316. An equal amount of protein in all lanes was ensured by stripping and reprobing of the membrane with an anti-ATF2 antibody (Fig. 6B, *lower panel*).

The p38 Kinase Inhibitors Antagonize Activin-induced Cell Growth Arrest in Breast Cancer Cells-To evaluate the contribution of the p38 kinase pathway in activin-mediated cell growth inhibition in T47D cells, we used different p38 kinasespecific inhibitors (SB202190, SB203580, PD169316) or an inactive analogue (SB202474) and an MEK1/ERK1/2 inhibitor (PD98059) as controls, in both MTT (Fig. 7A) and direct cell counting assays (Fig. 7B). T47D cells were cultured in DMEM. 2% serum for 3 days and stimulated or not with 0.5 nm activin in the presence or absence of the different inhibitors. As shown in Fig. 7, A and B, after 3 days cell growth is reduced by 40% in activin-treated cells as compared with untreated cells, similar to that previously observed in Fig. 1, A and B. However, in the presence of each the three specific p38 kinase inhibitors (SB202190, SB203580, PD169316), the inhibitory effect of activin on cell growth is abolished. On the other hand, the activin effect on cell growth inhibition is maintained in samples treated with the inactive form of the p38 kinase inhibitor SB202474 or with the MEK1/ERK1/2 inhibitor PD98059. Our results indicate that p38 kinase-specific inhibitors nearly completely reverse the activin effect. Because p38 kinase inhibitors could affect TGF β receptor activity (36), we examined their effect on activin-induced Smad2 phosphorylation. As shown in Fig. 7C, although activin-induced p38 phosphorylation is inhibited by pretreatment of the cells with all three active forms of



FIG. 7. p38 kinase inhibitors antagonize activin-induced cell growth arrest in breast cancer cells. T47D cells were cultured in DMEM, 2% serum for 3 days and stimulated or not with 0.5 nm activin in the presence or absence of 10 μ M of the different p38 kinase-specific inhibitors, SB202190, SB203580, and PD169316, or the inactive analogue SB202474 and the MEK1/ERK1/2 inhibitor PD98059 as controls. Cell growth was assessed by (A) MTT colorimetric assay in triplicates and (B) direct cell counting. Values represent means and standard deviations of five separate experiments and are expressed as percentage of inhibition compared with the control. C, T47D cells were pretreated with Me₂SO or with the p38 inhibitors (SB202190, PD169316, or SB203580) at 10 $\mu{\rm M}$ for 45 min before being stimulated with activin for 15 min. Total cell lysates were analyzed by immunoblot using specific antibodies directed against the phosphorylated form of Smad2 (pSmad2, upper panel), the phosphorylated form of p38 kinase (pp38, middle panel), or p38 kinase (p38, lower panel).

p38 kinase inhibitors, we observed no significant inhibitory effect on Smad2 phosphorylation under the same conditions. Thus it is likely that the antagonistic effect exerted by the p38 inhibitors on activin-induced cell growth arrest is mediated through inhibition of the p38 kinase pathway downstream of the activin receptor.

As activin is potent cell growth inhibitor in many different cell lines, the effect of the p38 kinase inhibitors were also analyzed in several activin-responsive cell lines such as K562, Chinese hamster ovary, and MCF7. Interestingly, the activin



FIG. 8. Activin effect on cell growth arrest is not mediated through the MAPK pathway. T47D cells were starved overnight and stimulated with EGF (20 ng/ml) for different period of times in the absence or presence of 1 nm activin. Total cell lysates were then analyzed by Western blotting using an antibody directed against phospho-ERK1/2 (upper panel). The membrane was stripped and reprobed with an anti-ERK1/2 antibody (lower panel).

inhibitors could reverse the activin effects on cell growth arrest in all cell lines tested (data not shown). This indicates that the contribution of the p38 MAPK pathway to activin-mediated cell growth arrest is critical.

Activin Effect on Cell Growth Arrest Is Not Mediated through the MEK1/ERK1/2 MAPK Pathway-The absence of effect of the MEK1/ERK1/2 inhibitor PD98059 on activin-mediated cell growth arrest (Fig. 7) suggests that activin does not modulate the MAPK MEK1/ERK1/2 pathway to arrest cell growth. The MEK1/ERK1/2 pathway is known to be involved in cell proliferation in response to various growth factors. To confirm that activin does not modulate or inhibit activation of this pathway in response to growth factors, T47D cells were starved overnight and stimulated with EGF (20 ng/ml) for different periods of time in the absence or presence of 1 nm activin (Fig. 8). Total cell lysates were then analyzed by Western blotting using an antibody directed against phospho-ERK1/2 (α -PERK). As shown in Fig. 8 (upper panel), EGF very rapidly and transiently induces the phosphorylation of ERK1/2 (p42/p44). However, activin co-stimulation of the cells does not affect EGF-induced ERK1/2 phosphorylation. The membrane was stripped and reprobed with an anti-ERK antibody and shows an equal amount of MAPK in all samples. Together this indicates that the activin effect on cell growth arrest in T47D cells is not mediated through the MEK1/ERK1/2 MAPK pathway.

DISCUSSION

Members of the TGF β family of growth factors are important factors in regulating cell growth inhibition; hence, it is critical to characterize their intracellular signaling mechanisms. Although it is known that activin signals through activation of Smad proteins, the activation of other intracellular signaling pathways and their contribution to activin-mediated cell growth inhibition remain to be characterized. In this paper we have examined the role of activin in mediating cell growth inhibition of breast cancer cells. Our results indicate that activin induces the Smad pathway in T47D cells and emphasize the involvement of the p38 MAPK pathway in activin-induced cell growth inhibition of these breast cancer cells.

Abnormalities in the signaling pathways of activin/TGF β have been clearly linked to various cancers, including breast cancer (37). We analyzed activin effects on the regulation of cell growth of human breast cancer cells. Using the human breast cancer cell line T47D, we found that activin has a profound and significant effect on the growth of these cells. We further investigated how activin triggers its effects in this cell line. Activin treatment of T47D cells leads to rapid phosphorylation of the receptor-regulated Smad2. Furthermore, both activin or the constitutively active form of the activin type I receptor (ALK4T Δ D) induce the two promoter constructs 3TPLux and ARE-Lux, and this effect is completely abolished in the presence of an overexpressed dominant negative form of Smad3 (Smad3 Δ C). All together, these results suggest that the activin receptor/Smad pathway is activated and can regulate the activin response in breast cancer cells, confirming the central role played by the Smad proteins in the mediation of the activin response.

The p38 MAPK is involved in regulating cellular responses to stress and cytokines (38-41). p38 kinase is activated and phosphorylated at the Thr¹⁸⁰-Tyr¹⁸² site by the two closely related dual specificity protein kinases MKK3 and MKK6 (42, 43). The activated p38 kinase has been shown to phosphorylate several transcription factors such as ATF2 (44), Max (45), and Elk-1 (46) and indirectly cAMP-response element-binding protein via activation of Nrf2 (47), STAT1 (48), and MEF-2 (49). The p38 pathway is activated in response to TGF β in C2C12, Mv1LU, and 293 cells (21, 23). TGF β can induce phosphorylation of both p38 and the transcription factor ATF2 in these cell lines. In addition, p38 and ATF2 can contribute to the activation of the synthetic reporter construct 3TPLux in these cells, but the physiological significance of this pathway in the mediation of the TGF β effects remains unclear. We show here that activin induces the p38 kinase pathway in T47D cells leading to phosphorylation of both the p38 kinase and the transcription factor ATF2. Furthermore, we show that the p38/ATF2 pathway is required to transduce the activin effects on cell growth inhibition. Indeed, different specific p38 kinase inhibitors, but not their inactive analogue or the MEK inhibitor can totally reverse the activin effect on cell growth inhibition. This highlights a new role for the p38 kinase pathway in the control of cell growth and proliferation downstream of the activin/TGF β superfamily of growth factors. TGF β family members often require the presence of parallel or synergistic pathways to the Smads to carry out their full biological effects and diversity of the Smad-interacting partners may contribute to signal specificity (50). In future studies, it will be interesting to examine the level of interaction between the Smad and the p38 kinase pathways in response to activin in T47D cells, because in vitro studies have suggested that the Smads could physically interact with the transcription factor ATF2 (21, 23).

Signaling by the MAPK family is organized hierarchically in three different steps. MAPK, such as p38, are phosphorylated by MAPK kinases (MAPKKS), such as MKK3 and MKK6, in the case of p38. The MAPKKs are themselves activated and phosphorylated by the MAPKK kinases (MAPKKKs), such as MLK, TAK, and ASK1 kinases, which act as MAPKKKs. Finally, the MAPKKKs are regulated by cell surface receptors or other external stimuli (51, 52). It will be interesting to identify the upstream kinases and other partner proteins involved in the activin-mediated p38 activation that are acting between the activin receptor complex and the p38 kinase in the signaling cascade. Recent reports indicated that TAK1, a member of the MAPKKK family, is activated by several cytokines, including TGF β (22) and bone morphogenetic protein (53). TAK1 is a potent activator of p38 kinase (54). It will be interesting, therefore, to determine whether or not TAK1 also lies downstream of the activin receptor complex signaling cascade.

It was also recently shown that the Müllerian Inhibitory substance (MIS) represses the growth of breast cancer cells by regulating the NF κ B pathway (25). The TGF β effect on cell growth inhibition of breast cancer has also been shown to be associated with a reduced NF κ B activity (24). This suggests that different members of the TGF β superfamily may regulate cell growth by utilizing different signaling pathways in the same target tissues. Interestingly, TAK1 was also shown to lead to NF κ B activation (55), suggesting a potential role for this factor downstream of the activin receptor.

Our results indicate that activin strongly represses the cell growth of T47D breast cancer cells. Further characterization of the downstream target genes that are modulated in T47D cells in response to activin will greatly enhance our understanding of its mechanism of action on cell growth regulation. Our data suggest that at least some of these targets could be the cyclindependent kinase inhibitors. However, it will remain to be determined whether other cell cycle regulators as well as apoptosis regulators are also regulated by activin in these cells. Indeed, identification of the target genes, involved in the regulation of cell cycle and/or apoptosis, will be important in shedding light on the activin receptor mechanism of action in breast cancer cells.

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