

Proteinase-activated Receptor 4 and Cell Apoptosis

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In memory of my beloved Dad

Chin Pau Kong

1958 – 2000

*For everyone in my family...
especially my mum and Yong*

Declaration

This dissertation is the result of my own work and includes nothing that is the outcome of work done in collaboration except where specifically indicated in the text.

This dissertation is also not substantially the same as any that I have submitted for a degree or diploma or other qualification at any other University.

Ai-Yen Chin
September 2013

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Ai-Yen Chin

In response to injury, the collagen-producing cells fibroblasts and myofibroblasts play an important role in promoting extracellular matrix deposition and release of inflammatory mediators in order to repair the damaged tissue. However, persistence and over-activity of these cells is associated with excessive collagen deposition and hence development of fibrosis, a pathological scarring process that leads to destruction of organ architecture and impairment of organ function. Removal of fibroblasts and myofibroblasts during fibrogenesis by apoptosis is therefore required for the normal resolution of tissue repair responses.

Proteinase-activated protein 4 (PAR₄) belongs to a subfamily of multifunctional G protein-coupled receptors which are activated by the proteolytic unmasking of a tethered peptide ligand that resides within their N-terminus. In addition to its well-studied role in platelet function, PAR₄, like the other PAR family members, is thought to be involved in pro-inflammatory responses and fibroproliferative processes. However, the role of PAR₄ in these processes remains largely unknown.

The hypothesis of this thesis is that during injury, PAR₄ expression is upregulated and this somehow contributes to apoptosis. To test this, the expression of PAR₄ was examined in two types of fibroblasts, cultured from human lung and renal explants. Results indicate that PAR₄ is not expressed in these cultured fibroblasts. Surprisingly, contradictory to a previous observation, exposure of lung fibroblasts to lipopolysaccharide did not consistently induce PAR₄ expression. As an alternative to the use of PAR₄-expressing fibroblasts, a stable PAR₄-expressing human cell line (HEK-PAR₄) was generated. Using these cells in an *in vitro* signalling assay, PAR₄ was found to confer responsiveness to PAR₄ activating peptide but not to a serine protease cathepsin G, which was previously shown to activate PAR₄ in platelets. Interestingly, the observation that cathepsin G-treated cells elicit a reduced signalling response to the stimulatory action of PAR₄ activating peptide suggests that cathepsin G might cleave PAR₄ at the ECL2 domain and cause PAR₄ to be unresponsive to the PAR₄ AP.

Next, serine proteases cathepsin G and trypsin were demonstrated as apoptosis inducers for human lung and renal fibroblasts. They induced pronounced morphologic changes in the fibroblasts (which do not express PAR₄). In HEK-PAR₄ cells, cathepsin G induced similar apoptotic level in comparison to empty vector control. Together, these findings suggest that cathepsin G can trigger apoptosis independently of PAR₄. On the other hand, PAR₄ activating peptide triggered higher percentage of apoptosis in HEK-PAR₄ cells compared to empty vector control, suggesting that apoptosis is mediated by PAR₄ signalling in this case.

Epithelium has a role in modulating a variety of inflammatory processes through the production and release of inflammatory cytokines. Apoptosis of damaged epithelium during inflammation has been reported to promote fibroblast growth and collagen deposition. In the last part of this thesis, media derived from confluent epithelial cell cultures were demonstrated to induce proliferation of lung and renal fibroblasts in a concentration dependent manner. This observation preliminarily supports the idea that epithelial cell injury may promote the proliferation of fibroblasts via the secretion of multiple cytokines.

In conclusion, this thesis demonstrates that apoptosis can be induced, first, by cathepsin G and trypsin in human primary bronchial fibroblasts and human primary renal fibroblasts independently of PAR₄, and second, by activation of PAR₄ in a non-fibroblastic PAR₄-expressing cell line.

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Chapter 1

Introduction

1.1 Fibrogenesis

Repair of damaged tissues is an essential biological process that allows the ordered replacement of dead or damaged cells after injury, allowing tissue architecture to restore and regain normal organ function. Fibrogenesis is a mechanism of wound healing and repair. Generally, it can be classified into three phases: (1) induction, (2) inflammation and matrix synthesis, and, (3) resolution (KUNCIO *et al.*, 1991).

1.1.1 Induction

The induction of conditions necessary for the establishment of active fibrogenesis and matrix remodelling represents the first phase of fibrogenesis. Injury caused by autoimmune or allergic reactions, environmental particulates, infection or mechanical damage often results in the disruption of normal tissue architecture, initiating a healing response. Acute damage to endothelial cells leads to the release of inflammatory mediators and initiation of a clotting cascade. Stimulation of the clotting cascade results in the cleavage of fibrinogen by thrombin to form a fibrin plug, which together with fibronectin, hold damaged tissues together and

provide a provisional matrix for the recruitment of inflammatory cells, fibroblasts and other resident cells (MUTSAERS *et al.*, 1997; CHAMBERS *et al.*, 2003). During induction phase, platelets aggregate and produce large amounts of platelet-derived growth factor (PDGF), which is a potent chemoattractant for fibroblasts, and transforming growth factor- β (TGF- β), a strong stimulant to fibroblast proliferation (SEPPÄ *et al.*, 1982; POSTLETHWAITE *et al.*, 1987; KUNCIO *et al.*, 1991). Furthermore, activated fibroblasts themselves secrete TGF- β and collagenases, hence enhancing their growth and motility (KUNCIO *et al.*, 1991).

1.1.2 Inflammation and Matrix Synthesis

Inflammatory cells propagate at the injury sites through the secretion of chemokines, cytokines and growth factors. Neutrophils are the first cells recruited, followed by the macrophages that infiltrate damaged tissue and secrete fibrogenic cytokines. Among many cytokines, interleukin (IL)-4, IL-13 and TGF- β are highly significant and exhibit pro-fibrotic activities by recruitment, activation and proliferation of macrophages, fibroblasts and myofibroblasts (CLARK, 1989; KUNCIO *et al.*, 1991). Macrophages are vital for normal healing. The healing process is impaired if their infiltration is prevented. They are a source of chemoattractants and growth factors, including PDGF, TGF- β and tumour necrosis factor- α (TNF- α). They act in concert with neutrophils to phagocytose debris and invading pathogenic microorganisms. TGF- β 1 secreted by macrophages then causes the fibroblasts to differentiate into myofibroblasts and initiate the production of matrix proteins, predominantly types I and III collagen, which increase the tensile strength of the wound (MUTSAERS *et al.*, 1997). Type III collagen is often deposited initially in higher ratios, but as fibrogenesis proceeds, type III collagen decreases relative to type I (JIMENEZ *et al.*, 1984; DEAN *et al.*, 1988; KUNCIO *et al.*, 1991). An imbalance in the production of stimulatory chemokines and growth factors can result in excess secretion of pro-fibrotic

cytokines and over-activation of myofibroblasts, leading to fibrosis (see **Section 1.2**) (ERJEFÄLT *et al.*, 1996; ELOVIC *et al.*, 1998; GAULDIE, 2002; PIGUET, 2003).

1.1.3 Resolution

The third phase, the resolution phase of wound healing, consists of an orchestrated cellular reorganisation guided by a fibrin-rich scaffold formation, wound contraction, closure and re-epithelialisation (WILSON and WYNN, 2009). Myofibroblasts migrate along the extracellular matrix (ECM) network and repair the wound. They also form stress fibres and α -smooth muscle actin (α -SMA) which confer high contractile activity within myofibroblasts. TGF- β also induces a contractile response, regulating the orientation of collagen fibres. (MIRASTSCHISKI *et al.*, 2004; HINZ, 2006; FARAHANI and KLOTH, 2008). The attachment of myofibroblasts to the ECM at specialised sites called the fibronexus pulls the wound together, reducing the size of the lesion during the contraction phase. The degree of ECM laid down and the quantity of activated myofibroblasts determine the amount of collagen deposition (SINGER, 1982; THANNICKAL and HOROWITZ, 2006). The rapid synthesis and degradation of connective tissue proteins is known as remodelling. The degradation of wound collagen and other matrix proteins are controlled by a variety of collagenases and the other metalloproteinases from granulocytes, macrophages, epidermal cells and fibroblasts. Imbalance of collagen synthesis and degradation will cause scar formation (MUTSAERS *et al.*, 1997). The resolution of inflammation through the removal of inflammatory cells and activated myofibroblasts by apoptosis and phagocytic pathways often leaves minimal damage and restores normal tissue architecture. However, delayed removal of myofibroblasts and the resistance of cells to apoptosis signals potentially cause fibrotic diseases (see **Section 1.2**) (THANNICKAL and HOROWITZ, 2006; FATTMAN, 2008). A tightly

regulated repair response following tissue injury is therefore critical.

1.2 Fibrosis

Fibrosis is the deregulation of fibrogenesis and continued exposure to chronic injury. Fibrosis is a pathological feature of most chronic inflammatory diseases. It is characterised by interstitial hypercellularity, matrix accumulation and atrophy of epithelial structures that lead to loss of normal function and organ failure. In spite of having distinct aetiological and clinical manifestations, most chronic fibrotic disorders have in common a persistent irritant that sustains the production of growth factors, proteolytic enzymes, angiogenic factors and fibrogenic cytokines, which stimulate the deposition of connective tissue elements that progressively remodel and destroy normal tissue architecture (WYNN, 2008).

Epithelium damage has an important role at the onset of fibrosis. During injury, damaged epithelial cells become activated and cytokines, growth factors and chemoattractants are secreted to activate and recruit macrophages to the injury sites (KISSELEVA and BRENNER, 2008). Macrophages then secrete TGF- β 1 which promotes fibroblasts activation and proliferation (KISSELEVA and BRENNER, 2006). Activated fibroblasts and myofibroblasts will produce high amounts of TGF- β 1 and extracellular reactive oxygen species (ROS) (**Section 1.2.1.2**) which facilitate apoptosis of damaged epithelial cells (WAGHRAY *et al.*, 2005). Similar responses to injury have been described for pulmonary epithelium and kidney epithelium (ZEISBERG *et al.*, 2001; THANNICKAL and HOROWITZ, 2006). See **Chapter 6** for further details.

1.2.1 Aetiological Factors in Fibrosis

1.2.1.1 TGF- β 1

TGF- β 1 is not expressed constitutively and is strongly upregulated during injury and inflammation. Macrophages are the major source of TGF- β 1 in fibrosing organs (BATALLER and BRENNER, 2005). Overexpression of TGF- β 1 in transgenic mice caused fibrosis in multiple organs, indicating that TGF- β 1 is a major pro-fibrogenic cytokine (BATALLER and BRENNER, 2005). Another fibrogenic factor, connective tissue growth factor (CTGF), is a downstream mediator of TGF- β 1 responses and it acts as a chaperone that augments TGF- β 1 signalling. CTGF binds to TGF- β 1 and increases its affinity to the TGF- β 1 receptor, causing a sustained, enhanced response (LEASK and ABRAHAM, 2004). It regulates cellular apoptosis, fibroblast proliferation, angiogenesis and deposition of ECM. These mechanisms of CTGF signalling have been documented in fibrogenesis in lungs, liver, kidneys and skin (PERBAL, 2004).

TGF- β is normally secreted as an inactive complex that is bound to a latency-associated peptide (LAP), a protein that prevents the binding of TGF- β 1 with its receptors (BUDINGER *et al.*, 2006). Once activated, TGF- β binds to its cell membrane type I and type II serine/threonine kinase receptors (**Figure 1.1**). This triggers the phosphorylation and activation of both Smad2 and Smad3. Phosphorylated Smad2/3 bind to Smad4 and translocate into the nucleus where they control the transcription of TGF- β -responsive genes (MENG *et al.*, 2013). ZHAO *et al.* (2002) has demonstrated that fibroblasts from Smad3 knockout mice did not synthesize collagen in response to TGF- β 1 and the mice were resistant to bleomycin-induced pulmonary fibrosis. In fibrosis, a multitude of mechanisms lead to a hyperactive TGF- β /Smad signalling and thus enhance post-translational activation of TGF- β protein (MENG *et al.*, 2013).

TGF- β is involved in many fundamental biological processes such as cell proliferation, cell migration, cell differentiation, ECM deposition and immune responses. TGF- β disrupts the balance between ECM synthesis and degradation, including an increase in the synthesis of matrix components and a parallel decrease in the matrix proteolytic activity (BRENMOEHL *et al.*, 2009). An increase in the expression of TGF- β 1 has been demonstrated in fibrotic tissues and regions of increased ECM deposition.

TGF- β is present in normal human bronchoalveolar lavage fluid. High levels of TGF- β 1 were found in the lungs in animal models of pulmonary fibrosis. Transient overexpression of TGF- β 1 in rat lung using adenovirus resulted in prolonged and severe pulmonary fibrosis (SIME *et al.*, 1997). Bleomycin-induced lung fibrosis was blocked in mice lacking the TGF- β 1-dependent Smad3 signalling pathway (BONNIAUD *et al.*, 2004; BUDINGER *et al.*, 2006). TGF- β is also present at the sites of ECM deposition in patients with cryptogenic fibrosing alveolitis. Furthermore, alveolar macrophages and epithelial cells from patients with pulmonary fibrosis highly express TGF- β 1 (XU *et al.*, 2003). In renal fibrosis, TGF- β can stimulate interstitial fibroblasts, mesangial cells and tubular epithelial cells to undergo myofibroblastic activation or transition, leading to the formation of matrix producing fibrogenic cells. In contrast, the inhibition of TGF- β suppresses renal fibrotic lesions and prevents progressive loss of kidney functions (LIU *et al.*, 2006).

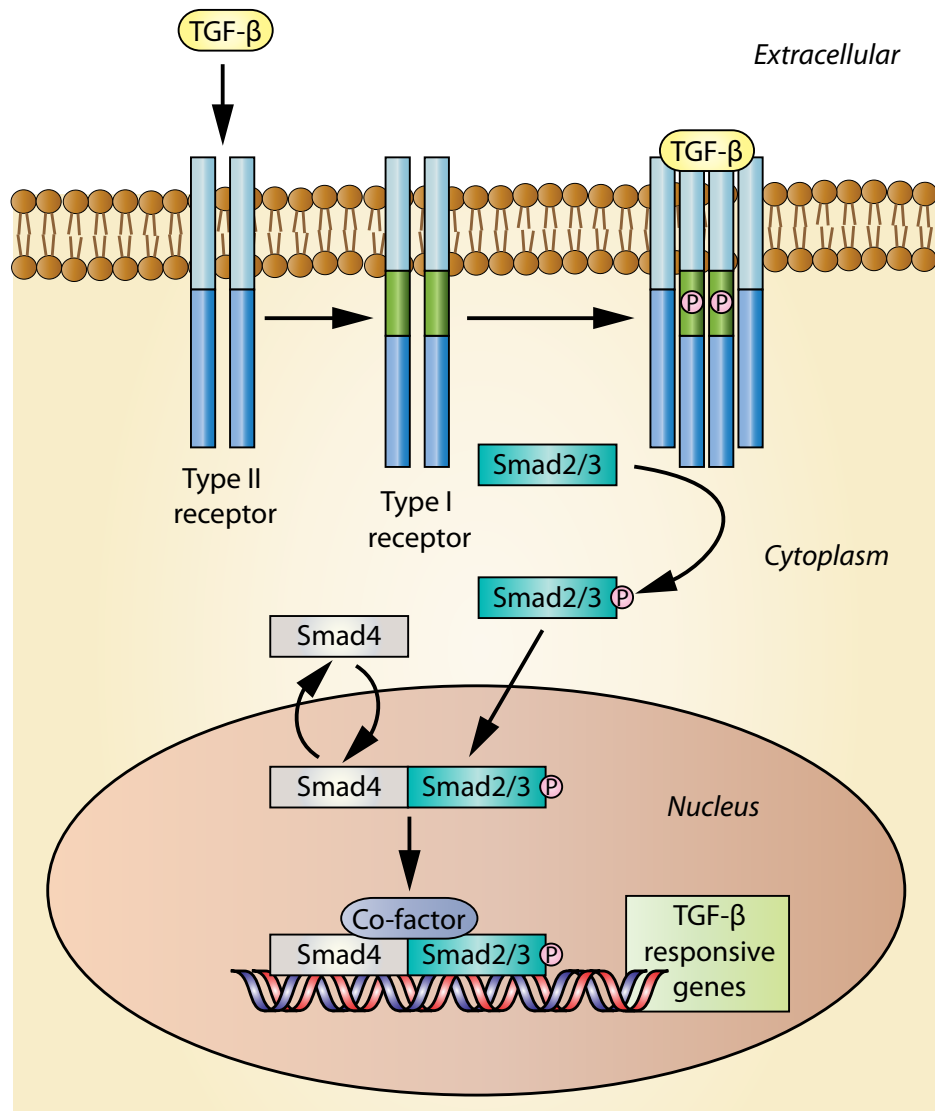


Figure 1.1: TGF- β /Smad signalling Pathway. Binding of TGF- β to the type II receptor results in phosphorylation and activation of the type I receptor. The activated type I receptor then phosphorylates Smad2/3 that promote dimer or trimer formation with Smad4, followed by nuclear translocation. Smad complexes together with their co-factor modulate transcription of TGF- β target genes. Adapted from MENG *et al.*, 2013.

1.2.1.2 ROS

Oxidative stress caused by an increase in ROS is closely related with fibrosis. Neutrophils, eosinophils, alveolar macrophages and alveolar epithelial cells contribute to ROS production in the lung (PIOTROWSKI and MARCZAK, 2000). Anti-oxidant compounds such as N-acetylcysteine has been demonstrated to protect against the tissue damage and pulmonary fibrosis induced by bleomycin (an oxygen-sensitive anti-cancer drug known to cause pulmonary fibrosis as a side effect) (SERRANO-MOLLAR *et al.*, 2003). In addition, Manoury and colleagues showed that NADPH oxidase-deficient p47phox-null mice were resistant against the development of bleomycin-induced lung fibrosis, indicating that NADPH oxidase-derived ROS production contributes to the development of pulmonary fibrosis (MANOURY *et al.*, 2005). In the kidney, ROS is a key factor in glomerulosclerosis and tubulointerstitial fibrosis. Renal ROS can be produced by fibroblasts, endothelial cells, vascular smooth muscle cells, mesangial cells, tubular cells and podocytes (GILL and WILCOX, 2006). Anti-oxidants are effective in inhibiting several models of fibrosis, however, none of these has been effective in clinical trials (KISSELEVA and BRENNER, 2008).

1.2.1.3 Resident Fibroblasts

Resident fibroblasts and myofibroblasts are the major collagen-producing cells in organs including the lungs, kidneys, liver and skin. Depending on the ECM deposition, fibroblasts remain quiescence or differentiate into myofibroblasts. Fibroblasts proliferate and differentiate into myofibroblasts in response to the changes in the mechanical stress of the ECM (HINZ, 2007). In fibrotic lung, the majority of myofibroblasts arise from the resident fibroblasts such as peribronchiolar and perivascular adventitial fibroblasts. These resident fibroblasts upregulate α -SMA, vimentin and collagen in response to fibrogenic stimuli (PHAN, 2002; HINZ, 2007). In

fibrotic kidney, myofibroblasts arise from cortical fibroblasts. Cortical fibroblasts are quiescent cells with a low turnover rate under normal condition. However, they proliferate and produce excess matrix proteins in response to injury (ZEISBERG *et al.*, 2000; QI *et al.*, 2006).

In addition, there are several other resident cell types which also contribute to fibrosis. Fibrocytes, pericytes and vascular smooth muscle cells are the additional sources of myofibroblasts in lung and kidney fibrosis (ZHANG *et al.*, 1994; DESMOULIÈRE *et al.*, 2003). Furthermore, epithelial cells have been identified as crucial precursors of fibroblasts, via epithelial-mesenchymal transition (EMT). EMT normally occurs physiologically during embryonic development. However, there is evidence which support EMT during fibrosis in lungs and kidneys (OKADA *et al.*, 1997; ABE *et al.*, 2001) (See **Section 1.3.1.1 & 1.3.2.3**).

1.2.1.4 Fibrocytes

Fibrocytes are circulating connective tissue progenitor cells which are implicated in fibrosis in the skin, kidneys, lungs and liver. Fibrocytes originate from bone marrow. They account for 20% of cells in the lungs of animal models with lung injury (EPPERLY *et al.*, 2003). They have dual characteristics of lymphoid cells and fibroblasts. Fibrocytes express CD34, CD45 and collagen I but negative for α -SMA. In response to injury, fibrocytes migrate in the blood to the injured organ. The number of infiltrating fibrocytes correlates with the intensity of fibrosis (BUCALA *et al.*, 1994). They are not only involved in the collagen deposition, they also secrete growth factors and cytokines that promote ECM deposition in the area of fibrosis. They can also differentiate into myofibroblasts (QUAN *et al.*, 2006).

1.3 Clinical Models of Fibrosis

1.3.1 Pulmonary Fibrosis

Pulmonary fibrosis is the abnormal formation of fibre-like scar tissue in the alveoli and interstitium of the lungs, resulting in the thickening of the tissues and an irreversible loss of the tissues' ability to transfer oxygen into the bloodstream (CHAPMAN, 1999). There are a number of conditions and risk factors associated with the disease, including smoking, occupational hazards, and viral and bacterial infections (JAKAB, 1990; MELICONI *et al.*, 1996; BAUMGARTNER *et al.*, 1997, 2000). In some patients, chronic pulmonary fibrosis develops without an identifiable cause, a condition called idiopathic pulmonary fibrosis (IPF) (PARDO *et al.*, 2005). It is characterised by alveolar epithelial cell (AEC) injury, fibroblast proliferation and excessive ECM deposition in the lung parenchyma. The accumulation of fibroblasts and myofibroblasts specifically between the vascular endothelium and alveolar epithelium disrupts the architecture of the lung (QUNN *et al.*, 2002). The main feature of IPF is the presence of fibroblastic/myofibroblastic foci (areas of active fibrogenesis, which are widely dispersed throughout the lung parenchyma) (RAMOS *et al.*, 2001; PARDO *et al.*, 2005). If the disease progresses, the lung tissues eventually thicken and become stiff, leading to breathlessness. Misdiagnosis is common as the origin and development of the disease are not completely understood (SELMAN *et al.*, 2001; PARDO *et al.*, 2005).

IPF accounts for $\sim 55\%$ of lung diseases classified as idiopathic interstitial pneumonia. IPF is uncommon in people aged under 50 years (MELTZER and NOBLE, 2008). Disease prevalence of IPF in the UK is approximately 15,000 and it has been estimated that approximately 5,000 new cases are diagnosed every year (NAVARATNAM *et al.*, 2011). The prognosis for individuals with IPF is poor, with a 5-year survival rate which is worse than several types of cancer (DU BOIS, 2012).

1.3.1.1 Cellular Mechanism of Pulmonary Fibrosis

It has been suggested that IPF involves abnormal wound healing in response to aberrant alveolar epithelial injury. Epithelial cell death is a prominent feature of fibrotic lung diseases. Continuous mechanical stretch of alveolar epithelium by forced ventilation results in pulmonary injury and fibrosis. AECs are in the alveolus to respond to injurious events by both proliferating to replace alveolar type I cell loss and by transdifferentiating into fibroblast/myofibroblast to promote repair (KIM *et al.*, 2006). The excessive formation of active fibroblasts/myofibroblasts leads to the exaggerated accumulation of ECM which causes irreversible destruction of lung parenchyma (SELMAN *et al.*, 2001; THANNICKAL *et al.*, 2004). The severity of fibrosis is inversely related to the efficiency of alveolar epithelial repair. A dysfunctional epithelial repair with a delay in appropriate re-epithelialisation could lead to fibrosis. Increased damage of the pulmonary epithelial cells leads to an increase in cytokine release, causing fibroblast activation and differentiation which is implicated in the pathogenesis of IPF (PLATAKI *et al.*, 2005). By preventing apoptosis of epithelial cells using an anti-Fas ligand (FasL) antibody, Kuwano and colleagues (1999a) were able to prevent the development of fibrosis in animal models of bleomycin-induced lung fibrosis.

EMT has been implicated in the pathogenesis of pulmonary fibrosis, AECs are the source of EMT in injured lungs. Biopsies from fibrotic human lungs showed epithelial cells with mesenchymal features, suggesting the possibility of EMT during fibrogenesis (TANJORE *et al.*, 2009). Alveolar epithelium consists of two types of epithelial cells, elongated alveolar type I cells which are responsible for gas exchange, and, cuboidal alveolar type II cells which synthesise and secrete surfactant (YANO *et al.*, 1997). Alveolar type II cells are the pulmonary multipotent progenitors which are capable

of self proliferating and differentiating into alveolar type I cells and fibroblasts during injury. During fibrosis, both alveolar cell types change morphology and gene expression patterns, downregulate of pulmonary epithelium markers and upregulate fibroblast specific markers (WILLIS *et al.*, 2006).

Furthermore, TGF- β 1 derived from epithelial cells is implicated in both AEC apoptosis and EMT. KIM *et al.* (2006) demonstrated that the treatment of AEC on matrigel with exogenous TGF- β 1 leads to AEC apoptosis whereas AECs on fibronectin undergo EMT through activation of endogenous TGF- β 1. These results indicate that an initiating stimulus leads to AEC apoptosis and enhanced alveolar permeability, then later AECs within a fibrin-rich provisional matrix undergo EMT and contribute to fibrosis (KIM *et al.*, 2006).

The origin of lung fibroblasts during pulmonary fibrosis is believed to be derived from proliferation of resident lung interstitial fibroblasts, differentiation of fibrocytes or EMT. Resident fibroblasts within the lung likely make a major contribution to the population of myofibroblasts which are recruited and mobilised during fibrosis. Prior animal studies have demonstrated that *in situ* proliferation contributes to the lung fibroblast population (ZHANG *et al.*, 1994). A few studies have suggested that lung fibroblast development during injury responses may also be derived from bone marrow progenitor cells (fibrocytes) that contribute to the fibrogenic process (HASHIMOTO *et al.*, 2004; PHILLIPS *et al.*, 2004; KIM *et al.*, 2006). Furthermore, KIM *et al.* (2006) demonstrated AECs (particularly type II AECs) as the progenitors for fibroblasts *in vivo* and the provisional ECM as a key regulator of epithelial transdifferentiation during fibrogenesis. TANJORE *et al.* (2009) showed that 30% of the fibroblasts in fibrotic lung were derived from lung epithelium via EMT in the bleomycin-induced lung fibrosis model.

Lung myofibroblasts may derived from resident fibroblasts, fibrocytes and the lung epithelium (HINZ, 2007). Based on the studies that myofibroblasts arise *de novo* and on the kinetics of the induction of α -SMA expression, the perivascular and peribronchiolar adventitial fibroblasts are suggested as precursors (ZHANG *et al.*, 1994). Circulating fibrocytes have been reported to migrate to tissue injury sites and differentiate into myofibroblast (ABE *et al.*, 2001). Furthermore, both EMT and EndoMT have been suggested as intrapulmonary precursors. The persistence of the myofibroblasts is thought to be of significant in the propagation of fibrosis with evolution to terminal end stage fibrotic lung disease.

1.3.1.2 Treatment

The pharmacological treatment that is currently available for IPF is clearly inadequate and drugs to treat lung scarring are still in the experimental phase (SELMAN *et al.*, 2001; MORRISEY, 2003). Corticosteroids have been used as a mainstay of the other forms of pulmonary fibrosis. However, no studies have demonstrated a consistent benefit of corticosteroid monotherapy in the treatment of IPF (MUNSON *et al.*, 2010). IPF patients receiving medication for gastroesophageal reflux have longer survival compared to those not on treatment (LEE *et al.*, 2011). Pirfenidone, an anti-fibrotic agent with anti-inflammatory and anti-oxidant properties through TNF- α and TNF- β pathways, has been assessed in patients with IPF in four Phase III trials (AZUMA *et al.*, 2005; TANIGUCHI *et al.*, 2010; NOBLE *et al.*, 2011). The meta-analysis of change in lung function shows a great consistency of treatment effect of pirfenidone in all four studies. Fewer overall deaths and significantly fewer on-treatment deaths related to IPF occurred in the pirfenidone group than in the placebo group. In all of the studies, pirfenidone was tolerated well. Commonly reported adverse events included gastrointestinal symptoms, photosensitivity, and dizziness.

1.3.2 Renal Fibrosis

The loss of renal function during kidney disease may occur rapidly and reversibly, as in the case of acute kidney injury (AKI); whereas in chronic kidney disease (CKD), the renal function declines slowly with no prominent symptoms in early stages of disease. It has been reported that patients who survived from AKI had significant risk for the development of progressive CKD and end-stage renal disease. Both AKI and CKD may progress to end-stage renal disease in which renal replacement therapy is required (LIM *et al.*, 2012). The annual incidence of end-stage renal disease generated from AKI survivors may account for quarter of the increase in end-stage renal disease incidence (PRUNOTTO *et al.*, 2012).

Renal fibrosis is the final manifestation of chronic kidney disease which is characterised by tubulointerstitial fibrosis and glomerulosclerosis with excessive deposition and accumulation of ECM components in the renal interstitial and tubulointerstitial cells, including collagen types I, III and IV, fibronectin, laminin and proteoglycans (EDDY, 2000; SCHIEPPATI and REMUZZI, 2005). In the early response to kidney injury, there is an expanding population of interstitial cells and deposition of collagen (LIN *et al.*, 2008; HUMPHREYS *et al.*, 2010). These cells are embedded in the basement membrane of peritubular capillaries (HUMPHREYS *et al.*, 2010; CHANG *et al.*, 2012). Interstitial fibroblasts, tubular epithelial cells and mesangial cells are the key fibrogenic cells in the injured kidney (EDDY, 2000). Tubulointerstitial inflammation is believed to play a central role in the development and progression of renal fibrosis. Interstitial inflammation is associated with ROS and increased angiotensin II activity, with their combined effects leading to disruption in glomerulotubular continuity, development of hypoxia, and impairment of protective auto-regulation of glomerular blood flow resulting in glomerulosclerosis. Close correlations of

the extent of fibrosis and the decrease of organ function have been shown in the kidney (RUIZ-ORTEGA *et al.*, 2006).

1.3.2.1 Glomerulosclerosis

Glomerulosclerosis is the progressive sclerosis and fibrosis of the glomeruli, leading to loss of the filtration surface area and hence renal dysfunction. This process occurs in the glomeruli which are affected by immune, hypertensive or metabolic injuries (BRADY, 1994; SAVAGE, 1994). Glomerular endothelial cells are the key effector cells in the inflammatory processes within the glomerulus. Endothelial injury causes the loss of anti-coagulant properties, resulting in the adhesion of platelets and their aggregation within the glomerular capillaries (JOHNSON, 1991). The surface expression of cell adhesion molecules (CAMs) changes in injured endothelial cells and this facilitates the infiltration of monocytes and macrophages in the glomeruli (BRADY, 1994; SAVAGE, 1994). Indeed, the release of chemokines by injured or activated endothelial cells may further attract inflammatory cells to the glomeruli and lead to their activation (STAHL, 1995; WENZEL and ABBOUD, 1995). The interactions between glomerular endothelial cells with circulating leukocytes and platelets may initiate glomerulosclerosis. Changes in the glomerular endothelium may also activate the underlying mesangial cells. Mesangial cells are able to synthesis and release pro-inflammatory cytokines and chemokines as well as fibrogenic growth factors such as PDGF (ABBOUD, 1993). Furthermore, mesangial cells acquire an α -SMA positive myofibroblast phenotype in response to TGF- β released during injury. They have also been demonstrated to be capable of synthesizing collagens type I and III and degrade ECM by the release of matrix metalloproteinases (EL NAHAS *et al.*, 1997). An imbalance between excessive synthesis and decreased breakdown of the glomerular ECM will lead to glomerulosclerosis.

1.3.2.2 Renal Tubulointerstitial Fibrosis

Renal tubulointerstitial fibrosis is a common pathway in progressive renal impairment and the proximal tubular epithelial cells play a vital role in this process. The tubulointerstitial space is composed of tubules and surrounding interstitium. Renal tubulointerstitial fibrosis is characterised by increased proliferation of fibroblasts and accumulation of matrix proteins in the renal interstitium (EDDY, 1996; NANGAKU, 2004). Chronic inflammation generally precedes the development of fibrosis and inflammatory cytokines are important mediators of fibrogenesis. The severity of tubulointerstitial inflammation and fibrosis has been considered as a vital determinant of progressive renal injury and long-term prognoses for both human and experimental glomerulonephritis (KONDO *et al.*, 2001). The area of active interstitial fibrosis predominantly exhibits a peritubular (rather than a perivascular) distribution (KOESTERS *et al.*, 2010). Moreover, in proteinuric nephropathies with progressive injury of the glomerular filtering barrier, abnormal uptake of ultrafiltered proteins by proximal tubular cells induces release of TGF- β 1, hence promoting interstitial fibrogenesis (ABBATE *et al.*, 2002). Patients with tubulointerstitial fibrosis have a poor prognosis and the condition often progresses to end-stage renal failure. End-stage renal failure is characterised by inflammation, scarring of glomeruli (glomerulosclerosis), scarring of the tubules and the interstitial cells (tubulointerstitial fibrosis), and tubular atrophy, which together result in loss of nephrons (STRUTZ, 1995).

1.3.2.3 Cellular Mechanism of Renal Fibrosis

Fibroblasts are not particularly abundant in normal kidneys when compared with lungs, lymphoid nodes, and spleens (MARKOVIĆ-LIPKOVSKI, 2002). During renal fibrogenesis, about 36% of new fibroblasts come from local EMT, about 14–15% from the bone marrow-derived circulating mesenchymal cells (fibrocytes), and the rest

from other resident cell types proliferation (IWANO *et al.*, 2002). Hence, EMT is a major contributor to the pathogenesis of renal fibrosis. Tubular epithelial cells can acquire a mesenchymal phenotype leading to a substantial increase in the number of myofibroblast during fibrosis (ZEISBERG and KALLURI, 2004). EMT during kidney fibrosis correlates with the expression of fibroblast specific protein-1 (FSP-1). FSP-1 identifies tubular epithelial cells undergoing transition in damaged nephrons and the number of fibroblasts. These FSP-1-positive epithelial cells traverse through damaged tubular basement membrane and accumulate in the interstitium of the kidney where they lose their epithelial markers and gain a fibroblast phenotype (OKADA *et al.*, 1996; IWANO *et al.*, 2002).

Fibroblasts are the resident interstitial cells of the kidneys which mainly cause renal tubulointerstitial fibrosis. In tubulointerstitial fibrosis, fibroblasts proliferate, migrate and synthesis growth factors and matrix proteins, contributing to the development of renal tubulointerstitial fibrosis. The tubules and peritubular capillaries ultimately disappear, the fibroblasts transform into myofibroblasts and increase in number and the mononuclear cells infiltrate into the interstitium, resulting in the formation of the interstitial scar (MARKOVIĆ-LIPKOVSKI, 2002).

It appears that the loss of the normal, homeostatic microenvironmental is the main cause of myofibroblast differentiation in fibrosis. The cross talk between epithelial cells and fibroblasts is crucial for the maintenance of the local homeostatic microenvironment (HINZ *et al.*, 2012). Several progenitors have been proposed in addition to local fibroblasts, including circulating fibrocytes, local pericytes and resident epithelial cells, through EMT (ZEISBERG and KALLURI, 2004; LIN *et al.*, 2008). The number of infiltrated fibrocytes correlates with the intensity of interstitial fibrosis in patients with glomerulonephritis (OKON *et al.*, 2003).

Pericytes are the major source of precursors of scar-producing myofibroblasts during kidney fibrosis. They are mesenchyme-derived perivascular cells aligned with the peritubular capillaries of the interstitium (ALLT and LAWRENSON, 2001). Unlike fibroblasts, they have important functions in regulating microvascular stability, angiogenesis, capillary permeability, capillary flow and capillary basement membrane synthesis (ALLT and LAWRENSON, 2001). Pericytes are found within the glomerular and tubulointerstitial compartments (SMITH *et al.*, 2012). Pericytes detach from the interstitial capillary within hours of the induction of renal injury (LIN *et al.*, 2008). Using a mouse model that expresses enhanced green fluorescent protein (EGFP) under the regulation of collagen 1 α 1 promoter, LIN *et al.* (2008) demonstrated that activation of pericytes and peritubular fibroblasts contributed significantly to interstitial myofibroblast population in experimental renal fibrosis.

Although endothelial cells produce PDGF and TGF- β in fibrosing kidneys, injured epithelial cells are the major source of these cytokines, and the TGF- β activator integrin α v β 6 is restricted to kidney epithelium (MA *et al.*, 2003; CHEN *et al.*, 2011b). In normal and diseased kidneys, the TGF- β receptor is widely expressed in the kidney epithelium and pericytes, whereas the synthesis of ligand TGF- β is most upregulated in injured tubular epithelium (WU *et al.*, 2013). TGF- β has been identified as an important cytokine during loss of epithelial cells known as tubular atrophy (MIYAJIMA *et al.*, 2000; MA *et al.*, 2003; SATO *et al.*, 2003). Increased TGF- β expression by epithelium is accompanied by the activation of intracellular signalling pathways and downstream effectors in the epithelium itself (SATO *et al.*, 2003). Blocking TGF- β and its downstream effectors can attenuate kidney injury and fibrosis (SATO *et al.*, 2003). KOESTERS *et al.* (2010) have shown that overexpression of TGF- β 1 in renal tubules in a transgenic mouse model induced peritubular fibrosis of local degeneration of nephrons. They demonstrated that the initial response of

tubular cell-derived TGF- β 1 consisted of robust peritubular cell proliferation and collagen deposition. Then, nephrons became degenerated with tubular dedifferentiation and proceeded to a total decomposition of tubular cells by autophagy. The fibrosis seen in between intact tubules and in areas of tubular decomposition were resulted from myofibroblasts that were derived from local fibroblasts. Ultimately, the remnants of tubular basement membrane collapsed and embedded into a dense collagenous fibrous tissue (KOESTERS *et al.*, 2010).

Macrophage infiltration is often associated with the degree of renal fibrosis. Macrophages infiltrating the kidneys produce various pro-inflammatory cytokines including TNF- α , IL-1 β and metalloproteinases (DOWDY *et al.*, 2005). Depletion of macrophages during fibrogenesis reduces fibrosis, suggesting that macrophages also contribute in some way to fibrosis (RICARDO *et al.*, 2008). On the other hand, macrophages that take up apoptotic cells exhibit anti-inflammatory properties and may contribute to the resolution of inflammation (KLUTH, 2007). Thus, macrophages likely play multiple, and often opposing, roles in kidney disease and repair.

1.3.2.4 Treatment

The treatments for chronic kidney disease has greatly improved following the introduction of drugs targeting the renin-angiotensin system, allowing proteinuria reduction and better control of blood pressure (ONUIGBO, 2011). Angiotensin-converting enzyme inhibitors and angiotensin II receptor type I blockers are the first line drugs in combating renal fibrosis (BOOR *et al.*, 2007). High dosage (ADAMCZAK *et al.*, 2003) or combination (WOLF and RITZ, 2005) of these both drugs show potential in experimental studies to halt progression of renal fibrosis in the early stages. In addition, renin inhibitors are potential drugs for the treatment of renal fibrosis in

rats, however, its clinical effects on human remain to be determined (PILZ *et al.*, 2005).

Kidney injury is always associated with the release of growth factors such as TGF- β by inflammatory cells which can provoke EMT. Recombinant human bone morphogenic protein (BMP)-7 is the endogenous antagonist of TGF- β -induced EMT in the kidney and elsewhere (ZEISBERG *et al.*, 2003). Mice with renal fibrosis that have been systemically treated using the cytokine BMP-7 showing reversal of EMT and repair of damaged tubular structures with repopulation of healthy tubular epithelial cells. A significant decrease in the number of EMT-derived and bone marrow-derived fibroblasts was observed (MORRISSEY *et al.*, 2002; ZEISBERG *et al.*, 2003). Interestingly, in non-uraemic type I diabetic patients who received pancreas transplantation, a reduction in interstitial collagen deposition and atrophic tubules was observed after 10 years of transplantation, indicating remodelling of renal lesions (FIORETTO *et al.*, 2006).

Due to the complexity and variability of organ fibrosis, it is difficult to establish an anti-fibrotic therapy for clinical application. Thus, effective therapies to prevent or to reverse existing fibrotic lesions are not yet available for any organ. However, some strategies have been proposed, such as modulation of inflammation, pharmacological prevention of ECM deposition and inhibition of pro-fibrotic growth factors (WYNN and RAMALINGAM, 2012).

1.4 Proteinase-activated Receptors

Proteinase-activated receptors (PARs) have been implicated in a number of diseases including cancer and inflammation of the cardiovascular, respiratory, gastrointestinal, musculoskeletal and nervous systems. PAR activation induces the upregulation of pro-inflammatory mediators and adhesion molecules, vasodilation and enhanced vascular permeability, suggesting the involvement of PARs in inflammation and tissue repair (COCKS and MOFFATT, 2000; VERGNOLLE *et al.*, 2001). Studies of PAR-deficient mice have provided unique insights into the strategies for drug development. Thus, PARs have become attractive targets for the development of therapeutic drugs.

PARs are a group of G protein-coupled receptors (GPCRs) that possess a unique mechanism of activation. Unlike the other GPCRs that have agonist-receptor systems, PAR activation is dependent on the specific cleavage of the extracellular N-terminus by proteinases such as thrombin, trypsin and cathepsin G (CG). Proteolytic unmasking of the N-terminal tail of the PARs reveals a tethered ligand sequence which interacts with the extracellular loop 2 (ECL2) of the PARs to trigger a sequence of events (VU *et al.*, 1991a; HOLLENBERG and COMPTON, 2002) (**Figure 1.2**). Synthetic peptides that mimic the final five to seven amino acids of the tethered ligand sequence can also specifically activate PARs, providing useful pharmacological tools to understand the physiology of these receptors. To date, four members of the PARs family have been identified: PAR₁, PAR₂, PAR₃ and PAR₄. They have been shown to be differentially expressed in humans and mice and between tissues (ORTIZ-STERN *et al.*, 2012). Several endogenous proteinases are able to activate the members of the PARs family. For instance, thrombin activates PAR₁, PAR₃ and PAR₄; trypsin activates PAR₂, PAR₄ and to a lesser extent PAR₁; CG activates PAR₄; mast cell tryptase can activate PAR₂ (VERGNOLLE *et al.*, 2001)(**Table 1.1**).

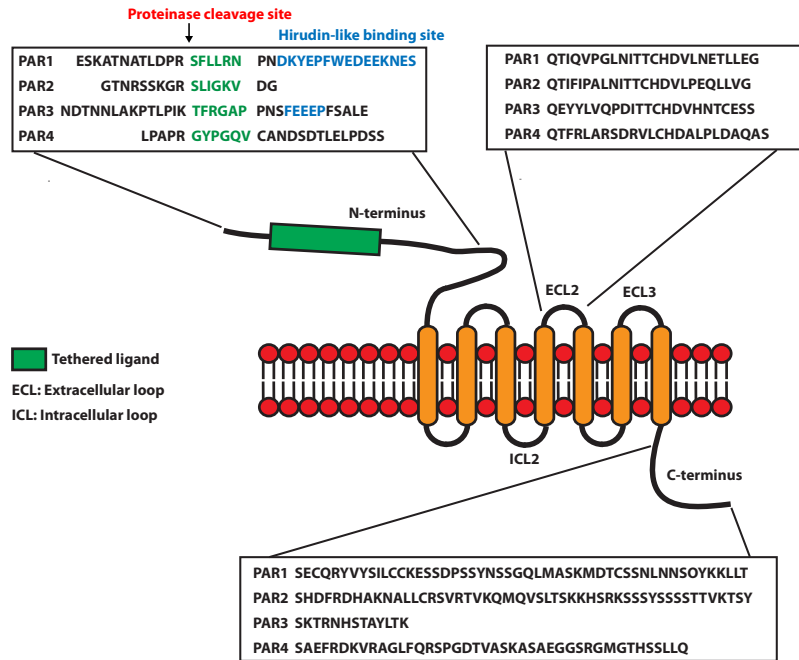


Figure 1.2: Structure of PAR and Their Activation. The proteinase cleaves PARs at a specific cleavage site and unmasks a tethered ligand which then interacts with the ECL2 to initiate signalling. The amino acid sequences of the tethered ligand, the ECL2 and the intracellular C-terminus of human PARs are presented in the boxes. Hirudin-like binding domain sequences for PAR₁ and PAR₃ are printed in blue (Adapted from STEINHOFF *et al.*, 2005).

Table 1.1: A Summary of PARs and Their Activating Proteases.

	PAR ₁	PAR ₂	PAR ₃	PAR ₄
Amino acid composition	425 aa	395 aa	374 aa	385 aa
Cleavage site	LDPR ⁴¹ ↓S ⁴² FLLRN	SKGR ³⁴ ↓S ³⁵ LIGKV	LPIK ³⁸ ↓T ³⁹ FRGAP	PAPR ⁴⁷ ↓G ⁴⁸ YPGQV
Tethered ligand sequence	SFLLRN	SLIGKV	TFRGAP	GFPGQV
Selective agonist peptide	TFLLRN-NH ₂	SLIGKV-NH ₂	None known	GYPGQV-NH ₂ AYPGQV-NH ₂
Activatory protease	Thrombin	Trypsin	Thrombin	CG
	Trypsin	Tryptase		Thrombin Trypsin
Inhibitory protease	CG	Elastase	CG	None known
	Proteinase 3	Chymase	Elastase	
	Elastase	CG		
Phenotype of knockout	Chymase			
	Partial embryonic lethality, Normal haemostasis	No embryonic lethality Impaired leukocyte migration	No embryonic lethality Impaired platelet activation	No embryonic lethality Loss of platelet activation

1.4.1 Discovery and Gene Structure

1.4.1.1 PAR₁

PAR₁ was the first member of the PAR family to be cloned and the first receptor for which this unique mechanism of activation was described (VU *et al.*, 1991a). The interest in PAR₁ was initially driven by research on the receptor responsible for thrombin-induced activation of platelets (VERGNOLLE *et al.*, 2004). The observation that thrombin can mediate responses in cells which were distinct from its role in the blood clotting cascade led to the discovery of PAR₁ (WEKSLER *et al.*, 1978; BAR-SHAVIT *et al.*, 1983a,b; BABICH *et al.*, 1990). PAR₁ was cloned in the same year by two laboratories using the strategy of expressing RNA from thrombin-responsive cells of humans and hamsters in oocytes of *Xenopus* (RASMUSSEN *et al.*, 1991; VU *et al.*, 1991a). Sequencing of the cDNA revealed that it encodes a protein of 425 amino acid residues with a poly-adenines (poly-A) tail (VU *et al.*, 1991a). The receptor contains eight hydrophobic domains, an N-terminal signal sequence and the seven transmembrane spanning characteristic of GPCRs (VU *et al.*, 1991a). A potential cleavage site for thrombin (LDPR⁴¹↓S⁴²FLLRN, where ↓ is the cleavage site) has been identified within the N-terminal region of PAR₁ (OSSOVSKAYA and BUNNETT, 2004).

1.4.1.2 PAR₂

PAR₂ was found by screening a mouse genomic library with an oligonucleotide probe based on the bovine substance K receptor. A clone encoding a protein of 395 amino acid residues with a poly-A tail was identified (NYSTEDT *et al.*, 1994, 1995). The proteinase cleavage sites for the murine and human PAR₂ are identical (SKGR³⁴↓S³⁵LIGKV) but the proteolytically revealed tethered ligand is not conserved (SLIGKV in humans and SLIGRL in mice) (NYSTEDT *et al.*, 1994; OSSOVSKAYA and

BUNNETT, 2004). Sequence comparison of murine and human PAR₁ with murine PAR₂ showed ~30% homology. PAR₂ exhibits the hallmark of PAR₁ in terms of the tethered-ligand mechanism for its activation by trypsin (NYSTEDT *et al.*, 1994; OSSOVSKAYA and BUNNETT, 2004).

1.4.1.3 PAR₃

The discovery of PAR₂ and the absence of PAR₁ in murine platelets prompted a continued search for more thrombin receptors, resulting in the discovery of PAR₃ (CONNOLLY *et al.*, 1996). Connolly and colleagues (1996) provided evidence for the presence of the second thrombin receptor from their observations that platelets derived from PAR₁ deficient mice still responded to thrombin. Subsequently, ISHIHARA *et al.* (1997) used degenerate primers to conserved domains of PAR₁ and PAR₂ to screen RNA from rat platelets and then employed the sequence obtained to identify human PAR₃. Human PAR₃ gene encodes a protein of 374 residues and shows ~28% sequence homology to human PAR₁ and PAR₂. Like PAR₁ and PAR₂, PAR₃ is a typical GPCR with a thrombin cleavage site within the extracellular N-terminal region at LPIK³⁸↓T³⁹FRGAP.

1.4.1.4 PAR₄

The identification of PAR-like sequences by searching expressed sequence tag databases using the coding region of PAR₂ lead to the discovery of murine PAR₄ (ISHII *et al.*, 1994; KAHN *et al.*, 1998). Human PAR₄ was then discovered by searching the DNA sequence databases with amino acid sequences derived from PAR₁, PAR₂ and PAR₃ (XU *et al.*, 1998). The cDNA sequence of human PAR₄ encodes a protein of 385 residues, with a potential cleavage site for thrombin and trypsin within the extracellular N-terminal region at PAPR⁴⁷↓G⁴⁸YPGQV (KAHN *et al.*, 1998; XU *et al.*, 1998). PAR₄ alignment to the other PAR family members showed ~30%

sequence homology, with some differences in the N- and C-terminal domains (XU *et al.*, 1998).

1.4.2 Mechanisms of PAR Activation

Unlike the typical GPCRs in which the cellular activation events are initiated by the small hydrophilic molecules that bind reversibly to the receptors' extracellular and transmembrane domains to elicit cellular responses, PARs have a unique mechanism of activation (WETTSCHURECK and OFFERMANN, 2005). Initially established for PAR₁, this activation mechanism appears as a general paradigm for the PAR family members (VU *et al.*, 1991a). PARs are activated by an unusual irreversible proteolytic mechanism in which the protease binds to and cleave a specific site within the receptors' N-terminal domain. This reveals a tethered ligand that binds intramolecularly to the body of the receptor to initiate transmembrane signalling (STEINHOFF *et al.*, 2005). This tethered ligand mechanism has become the hallmark characteristic of the PAR family. Synthetic peptide which mimics the tethered ligand can also activate the receptor (NYSTEDT *et al.*, 1994).

1.4.2.1 PAR₁ Activation

The structural and functional determinants for proteolytically activated receptor have been investigated in detail in the case of the thrombin receptor and its activating peptides (VU *et al.*, 1991a). The extracellular N-terminal domain of human PAR₁ contains a sequence of charged, hirudin-like residues (D⁵¹KYEPF⁵⁶) that is distal to the thrombin cleavage site. The anion binding site on thrombin will bind to this hirudin-like domain, which serves to temporarily concentrate thrombin at the surface of the receptor (OSSOVSKAYA and BUNNETT, 2004). The importance of the hirudin-like domain is determined by the finding that its deletion markedly

diminishes the ability of thrombin to activate PAR₁ while its presence allows the full recovery of the activity (VU *et al.*, 1991a; BOUTON *et al.*, 1995). Thrombin cleaves PAR₁ at LDPR⁴¹↓S⁴²FLLRN to expose the tethered ligand SFLLRN, which binds and activates the cleaved receptor, resulting in signal transduction (VU *et al.*, 1991a; OSSOVSKAYA and BUNNETT, 2004). VU *et al.* (1991b) demonstrated the importance of the cleavage recognition sequences by replacing LDPR with DDDK, the recognition site for the protease enterokinase, resulting in abolished thrombin responses and making the receptor susceptible to enterokinase activation.

In addition, blocking the cleavage site by antibodies or mutation of the cleavage site prevents the thrombin cleavage and signalling. The interaction between the ECL2 and the tethered ligand is crucial for signalling and proper receptor function. Hence, the ECL2 is a critical determinant of the specificity of the PARs, making important contributions to the receptor structure and function, and is not simply a passive link between the transmembrane domains (GERSZTEN *et al.*, 1994; LERNER *et al.*, 1996).

A synthetic peptide that mimics the tethered ligand domain (S⁴²FLLRNPNDKYEPF) can directly activate intact PAR₁ without the specific cleavage of the extracellular N-terminal domain by thrombin. Peptides as short as six residues, (S⁴²FLLRN) are also fully active (VU *et al.*, 1991a) (**Figure 1.3**).

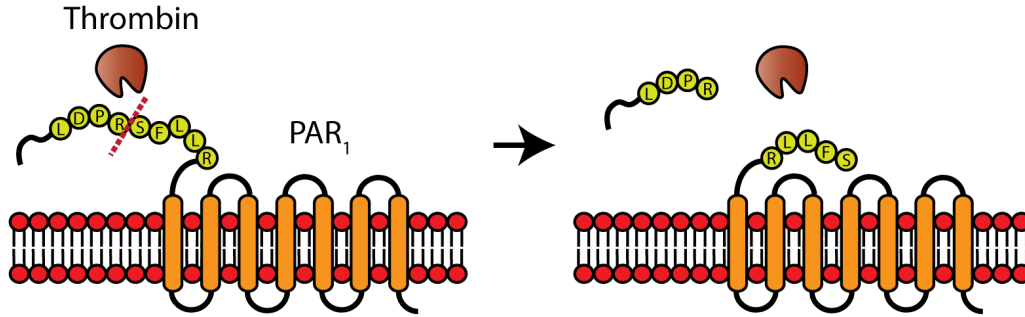


Figure 1.3: PAR₁ Activation. Thrombin cleaves human PAR₁ at its N-terminus, exposing the tethered ligand SFLLRN.

1.4.2.2 PAR₂ Activation

Trypsin cleaves PAR₂ at SKGR³⁴↓S³⁵LIGKV to reveal the N-terminal tethered ligand SLIGKV in humans (NYSTEDT *et al.*, 1994). Mutation or substitution of the domain in the trypsin cleavage site prevents the activation of PAR₂. Analysis of proteinase cleavage of peptide sequences corresponding to the human PAR₂ N-terminus revealed the Arg³⁴↓Ser³⁵ bond as the site for trypsin cleavage and tryptase (MOLINO *et al.*, 1997). Similar to PAR₁, synthetic peptide corresponding to the tethered ligand domain (SLIGKV) can activate PAR₂ without the requirement of receptor cleavage (NYSTEDT *et al.*, 1995; BÖHM *et al.*, 1996)(**Figure 1.4**).

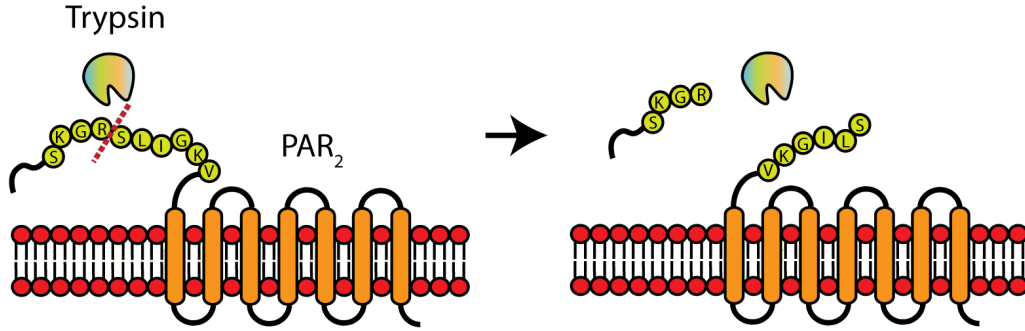


Figure 1.4: PAR₂ Activation. Trypsin cleaves human PAR₂, exposing the ligand sequence SLIGKV.

1.4.2.3 PAR₃ Activation

Similar observations indicate that thrombin cleaves PAR₃ at LPIK³⁸↓T³⁹FRGAP to reveal a new N-terminus (TFRGAP) that may interact with the receptor as a tethered ligand and mutation of the cleavage site would prevent the activation (ISHIHARA *et al.*, 1997). Synthetic peptides corresponding to this putative tethered ligand can activate PAR₁ and PAR₂ (HANSEN *et al.*, 2004; KAUFMANN *et al.*, 2005) but not PAR₃ (ISHIHARA *et al.*, 1997). The reason for this discrepancy is unknown. Another unexpected and unexplained observation is that murine PAR₃ does not appear to signal itself via its thrombin-revealed sequence. Rather, it appears to function as a co-receptor for PAR₄, perhaps allowing thrombin localisation through binding to its hirudin-like sequence and facilitating signalling at low thrombin concentration (NAKANISHI-MATSUI *et al.*, 2000) (**Figure 1.5**). PAR₃ contains a hirudin-like site (FEEFP) that is distal to the thrombin cleavage site, which interacts with thrombin (ISHIHARA *et al.*, 1997).

1.4.2.4 PAR₄ Activation

Thrombin, CG and trypsin can cleave PAR₄ at PAPR⁴⁷↓G⁴⁸YPGQV to reveal the tethered ligand and a peptide corresponding to the proteolytically revealed tethered ligand domain, GYPGQV, can directly activate PAR₄. Mutation of the cleavage site prevents activation by thrombin, CG and trypsin, but not by the synthetic peptide. This observation showed the importance of proteolytic cleavage for receptor activation (KAHN *et al.*, 1998; XU *et al.*, 1998). In contrast to the other thrombin receptors, PAR₄ lacks a hirudin-like binding site for thrombin. Thus, PAR₄ is a low affinity receptor for thrombin while PAR₁ and PAR₃ are high affinity thrombin receptors (KAHN *et al.*, 1998; XU *et al.*, 1998) (**Figure 1.5**).

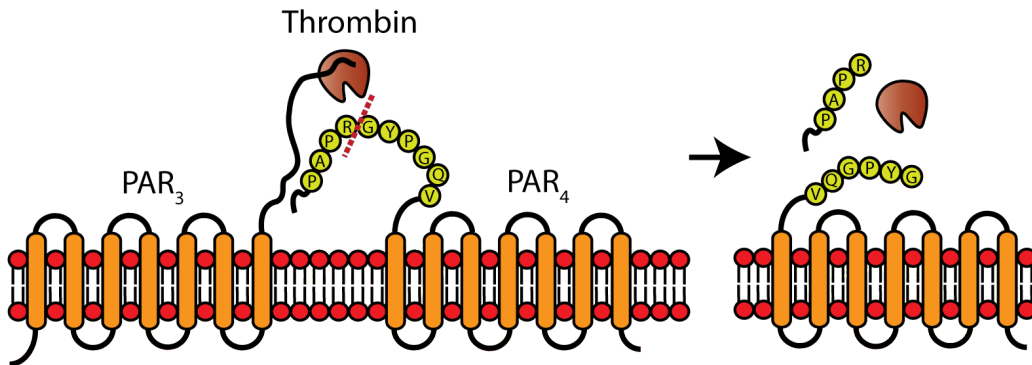


Figure 1.5: PAR₄ Activation. PAR₃ acts as a cofactor for PAR₄ cleavage by thrombin, exposing the tethered ligand GYPGQV in the human PAR₄ N-terminus.

1.4.3 Activation of Multiple signalling Cascades by PARs

Mammalian G-proteins are trimeric proteins made up of α , β and γ subunits. To date, there are four classes of G α subunits: G $_s$, G $_i$, G $_{q/11}$ and G $_{12/13}$. The functional consequences of their activation are believed to be mediated by their α subunit (WETTSCHURECK and OFFERMANN, 2005). G $_s$ α subunits activate adenylyl cyclase whereas G $_i$ α subunits inhibit adenylyl cyclase, all α -subunits of the G $_{q/11}$ class activate phospholipase C- β (PLC β) and G $_{12/13}$ α subunits regulate cell processes via the guanine triphosphate (GTP)ase-activating proteins and guanine nucleotide exchange factors (CABRERA-VERA *et al.*, 2003).

1.4.3.1 PAR $_1$ signalling

PAR $_1$ interacts with several G α subunits, in particular G $_i$, G $_{q/11}$ and G $_{12/13}$, which accounts for the pleiotropic action of its ligands (MACFARLANE *et al.*, 2001). The major pathway of coupling is through G $_{q/11}$ subunits. G $_{q/11}$ subunits play a major role in coupling since thrombin signalling in fibroblasts and platelets that express PAR $_1$ is attenuated by the microinjection of G $_{q/11}$ α subunits antibodies (BAFFY *et al.*, 1994). G $_{q/11}$ subunits activate PLC β , leading to the generation of inositol 1,4,5-triphosphate (InsP3) which mobilises intracellular Ca $^{2+}$ and diacylglycerol (DAG) and then activates protein kinase C (PKC). FEE *et al.* (1994) showed that thrombin-stimulated InsP3 generation and Ca $^{2+}$ mobilisation were blunted in mutant fibroblasts that expressed low levels of PLC β but normal levels of other phospholipases.

PAR $_1$ coupling with G $_{12/13}$ subunits was revealed through studies on thrombin stimulated platelets and astrocytoma cells (OFFERMANN *et al.*, 1994; ARAGAY *et al.*, 1995) where thrombin stimulates the incorporation of

a GTP analog into $G_{12/13}$ subunits in platelets, and thrombin-stimulated DNA synthesis is blocked by microinjection of antibodies to $G_{12/13}$ subunits in the astrocytoma cells. PAR_1 also couples to G_i subunits, which inhibit adenylyl cyclase and suppress the formation of cyclic adenosine monophosphate (cAMP) (HUNG *et al.*, 1992). Furthermore, PAR_1 activates multiple signalling pathways downstream of coupling to G-proteins, including the activation of phosphatidylinositol 3 (PI3) (MALARKEY *et al.*, 1995), extracellular signal-regulated kinase/mitogen-activated protein kinase (ERK/MAPK) pathway (VOURET-CRAVIARI *et al.*, 1993), and the Src family tyrosine kinases (SABRI *et al.*, 2000).

1.4.3.2 PAR_2 signalling

Less is known about the signalling mechanism for PAR_2 . Activators of PAR_2 stimulate generation of InsP3 and mobilisation of Ca^{2+} in PAR_2 transfected cell lines, indicating, but not confirming that PAR_2 coupling and signalling via $G_{q/11}$ subunits and possibly G_i subunits (MACFARLANE *et al.*, 2001).

In enterocytes and transfected epithelial cells, the activation of PAR_2 stimulates release of arachidonic acid and rapid generation of prostaglandins E_2 (PGE_2) and $F_{1\alpha}$, indicating activation of phospholipase A2 and cyclooxygenase-1 (KONG *et al.*, 1997; OSSOVSKAYA and BUNNETT, 2004). PAR_2 activation on smooth muscle and neuronal cells has been shown to activate PLC (BERGER *et al.*, 2001b) and PKC (OKAMOTO *et al.*, 2001a), respectively.

The agonists of PAR_2 strongly activate the MAPK cascade in rat aortic smooth muscle cells (BELHAM *et al.*, 1996) and jun amino-terminal kinase (JNK1/2) and p38 MAPK in human keratinocytes (KANKE *et al.*, 2001). MACFARLANE *et al.* (2005) reported that intracellular calcium mobilisation

in keratinocytes is a vital determinant of PAR₂ nuclear factor-kappaB (NFkB) signalling. Also, PAR₂ activation of ERK1/2 has been studied in a variety of cells including cardiomyocytes (SABRI *et al.*, 2000) and smooth muscle cells (BELHAM *et al.*, 1996).

PAR₂ was also shown to mediate Factor Xa that activates ERK1/2 in coronary artery smooth muscle cells (KOO *et al.*, 2002). VOURET-CRAVIARI *et al.* (2003) showed that endothelial PAR₂ activation induced activation of small molecule G-protein, Rho-A, Rac and p21 activated kinase (PAK).

1.4.3.3 PAR₄ signalling

PAR₃-mediated signalling events are pretty much unclear and it has not been shown to signal through G-proteins (HANSEN *et al.*, 2004; ARORA *et al.*, 2007). PAR₄ was shown to couple to G_q and G_{12/13} but not G_i in mice lung fibroblast (FARUQI *et al.*, 2000). PAR₄ signalling has been reported to activate MAPK signalling in vascular smooth muscle cells (BRETSCHNEIDER *et al.*, 2001), mice cardiomyocytes (SABRI *et al.*, 2003b), and human lung endothelial cells (FUJIWARA *et al.*, 2005).

1.4.4 Termination of PAR signalling

Due to the unique irreversible mechanism of PAR activation, tethered ligand remains bound to the receptor while PARs are activated, the activation state of the PARs therefore would be expected to elicit continuous signalling. However, PAR-mediated responses appear to be transient in nature with rapid desensitisation and receptor internalisation that tightly regulate PAR signalling (MACFARLANE *et al.*, 2001; HOLLENBERG and COMPTON, 2002). Studies have shown that sequences within intracellular receptor domains and C-terminal tail regulate the

receptor desensitisation and internalisation. The mechanism of desensitisation varies between different PARs, probably due to structural differences, especially in the intracellular loop 3 and C terminus (MACFARLANE *et al.*, 2001; HOLLENBERG and COMPTON, 2002; OSSOVSKAYA and BUNNETT, 2004). Receptor desensitisation and internalisation mechanisms have been well studied for PAR₁ and PAR₂ but little is known for PAR₃ and PAR₄ (OSSOVSKAYA and BUNNETT, 2004).

1.4.4.1 Disarming and Amputation of Tethered Ligand by Proteases

Many proteases can disable PAR activation by removing/ destroying the tethered ligand or by cleaving the binding domain in ECL2, resulting in the generation of receptors which are unresponsive to activating proteases (OSSOVSKAYA and BUNNETT, 2004).

Neutrophil, CG, elastase and proteinase 3 can abolish thrombin signalling by cleaving the activation site of PAR₁, whereas chymase (an abundant mast cell proteinase) has been shown to render keratinocytes unresponsive to thrombin, indicating that it can inactivate PAR₁ (MOLINO *et al.*, 1995; RENESTO *et al.*, 1997; SCHECHTER *et al.*, 1998). CG and elastase inactivate trypsin signalling by removing the N-terminal epitopes of PAR₂ but PAR₂ is still able to respond to the PAR₂ agonist peptide (DULON *et al.*, 2003).

Surprisingly, some proteinases can cleave PARs both at their activation and disabling sites and the net result depends on the efficiency of cleavage at different sites (OSSOVSKAYA and BUNNETT, 2004). For example, CG can activate PAR₁ at the activation site Arg⁴¹-Ser⁴², but the major cleavage site is at Phe⁵⁵-Trp⁵⁶, which removes the tethered ligand and thus disables the receptor (MOLINO *et al.*, 1995; OSSOVSKAYA and BUNNETT, 2004). In

the case of tryptase, it can cleave PAR₂ at Lys⁴¹-Val⁴² site which inactivates the receptor, but the activating cleavage is more important since tryptase activates PAR₂ (MOLINO *et al.*, 1997; OSSOVSKAYA and BUNNETT, 2004).

In human platelets, CG disables PAR₁ but activates PAR₄, whereas in murine platelets, CG disables PAR₃ and abolishes its co-receptor function for PAR₄, thus preventing platelet responses to thrombin (CUMASHI *et al.*, 2001).

1.4.4.2 Desensitisation and Internalisation

Ligand occupation of the GPCR induces the translocation of the members of G protein receptor kinase (GRK) family from the cytosol to the activated receptor at the cell surface. GRKs are serine-threonine kinases that phosphorylate activated GPCRs, usually within the C-terminal domain or intracellular loop 3. Phosphorylation then triggers the membrane translocation of arrestins, which interact with GRK-phosphorylated GPCRs to disrupt the interaction between GPCRs and G proteins, thus terminate the signal (OSSOVSKAYA and BUNNETT, 2004).

The expression levels of receptors at the cell surface are determined by the balance between removal by internalisation and replenishment by recycling or mobilisation of intracellular pools (OSSOVSKAYA and BUNNETT, 2004). PAR₁ and PAR₂ are rapidly internalised after activation and directed to lysosomes for degradation (HOXIE *et al.*, 1993). However, approximately 25% of the receptors are recycled back to the cell surface in order to maintain the amount of receptors at the cell surface and in the intracellular pool (HOXIE *et al.*, 1993).

PAR₁ activation leads to rapid phosphorylation at its C-terminal by several GRKs including GRK3 and GRK5. It was thought that PAR₁

signalling is desensitised by its interaction with β -arrestin 1. However, this interaction with β -arrestin 1 was found to have an important role in the receptor phosphorylation state but not essential for internalisation and downregulation of the receptor (WOLFE *et al.*, 2007). Instead, the internalisation and targeting of phosphorylated PAR₁ to degradation pathway involves deubiquitylation of the receptor, which leads to the clathrin and dynamin-dependent processes (PAING *et al.*, 2006; CHEN *et al.*, 2011a).

Activated PAR₂ is rapidly phosphorylated on a stretch of serine and threonine residues at the C-terminal domain, a process which is important for the recruitment of β -arrestins to the receptor. In contrast to PAR₁, the interaction between PAR₂ and β -arrestin is crucial for the desensitisation of signalling, receptor internalisation and targeting to lysosomes (DEFEA *et al.*, 2000; SEATTER *et al.*, 2004). The PAR₂- β -arrestin complex is targeted to early endosomes, and then to lysosomes in a process that involves deubiquitylation of the receptor (DÉRY *et al.*, 1999; DEFEA *et al.*, 2000; HASDEMIR *et al.*, 2009). The mechanism of lysosomal degradation of PARs is still unclear.

The mechanisms regulating the trafficking of PAR₃ and PAR₄ remain largely unknown. PAR₄ desensitisation has been shown to be slower than PAR₁ as PAR₄ is not rapidly phosphorylated in the C-terminal domain, possibly due to a lack of sites for GRK phosphorylation in the C-terminal domain (SHAPIRO *et al.*, 2000) (**Figure 1.6**).

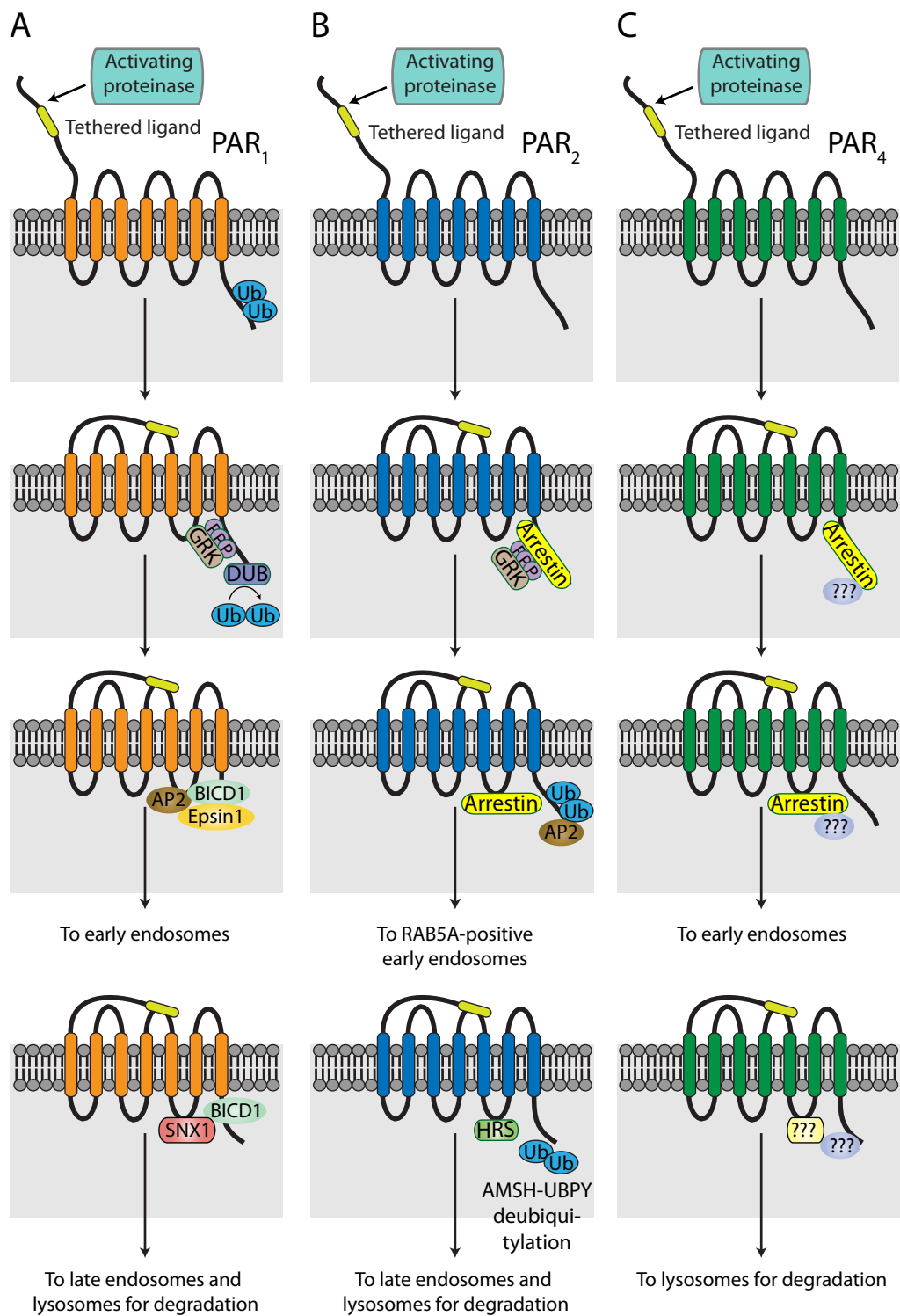


Figure 1.6: Intracellular Trafficking of Activated PARs. PAR activation is irreversible and activated receptors are targeted to the lysosomes for degradation. (A) Following activation, PAR₁ is rapidly phosphorylated at its C-terminal by several GRKs including GRK3 and GRK5. The internalisation and degradation of activated PAR₁ involves deubiquitylation of the receptor which leads to its interaction with the clathrin adaptor protein AP2 and epsin 1. C-terminal of PAR₁ is important for specifying lysosomal targeting. Sorting nexin 1 (SNX1) (a membrane-associated lysosomal sorting protein) and bicaudal D homolog 1 (BICD1) are vital for the translocation of PAR₁ from plasma membrane to lysosomes for degradation. (B) In contrast to PAR₁, the interaction between PAR₂ and β -arrestin is crucial for the desensitisation of signalling, receptor internalisation and targeting to lysosomes. The PAR₂-arrestin complex is targeted to RAB5A-positive early endosomes then to lysosomes that involve the deubiquitylation of PAR₂. (C) The mechanism regulating PAR₃ and PAR₄ remain largely unknown. Due to the low level of PAR₄ C-terminal phosphorylation, PAR₄ desensitisation is slower than PAR₁. Adapted from RAMACHANDRAN *et al.*, 2012.

The internalisation of both PAR₁ and PAR₂ is mediated by a clathrin-mediated mechanism. Their internalisation requires GTPase dynamics that mediates the detachment of clathrin-coated pits (BÖHM *et al.*, 1996; DÉRY *et al.*, 1999; TREJO *et al.*, 2000). β -arrestins play an important role in endocytosis of many GPCRs by serving as adaptor proteins that link GRK-phosphorylated receptors to clathrin (OSSOVSKAYA and BUNNETT, 2004) (**Figure 1.7**).

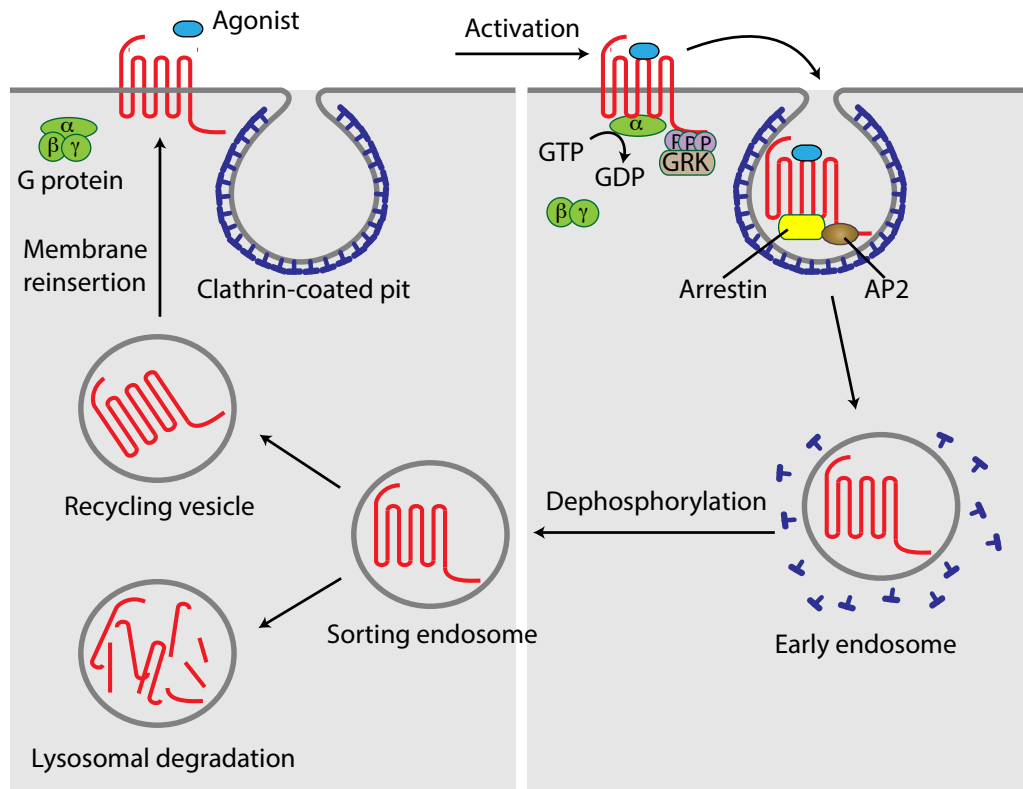


Figure 1.7: Mechanisms that Regulate PAR Desensitisation and Internalisation. Once activated, PARs are rapidly phosphorylated and form a complex with β -arrestin. The PAR-arrestin complex is then endocytosed via clathrin-coated pits and targeted to early endosome. The GTPase dynamics mediates detachment of clathrin-coated pits. Then, PARs are dephosphorylated by protein phosphatases. Finally, PARs are either reinserted into the membrane or targeted to lysosomes for degradation. Adapted from RAMACHANDRAN *et al.*, 2012.

1.4.5 PARs in Physiology and Pathophysiology

PARs are expressed in various tissues and cells throughout mammalian body. The specificities of their involvement in various processes remain to be verified. The PAR-mediated events are complicated as the signalling depends on the availability of the activating or disabling proteases, protease inhibitors and co-factors or anchoring proteins (OSSOVSKAYA and BUNNETT, 2004; STEINHOFF *et al.*, 2005). In addition, the lack of specific PAR antagonists and the difficulties in extrapolating data obtained from animal models to human diseases make it difficult to determine the precise roles of PARs in human body (OSSOVSKAYA and BUNNETT, 2004).

Genetically modified animals have been used to study the role of PARs *in vivo*. Approximately 50% of PAR₁-knockout mice die before birth (CONNOLLY *et al.*, 1996). Embryonic lethality was not associated with the deletion of PAR₂, PAR₃ or PAR₄, suggesting a specific role for PAR₁ in development (MAJOR *et al.*, 2003). PAR₁-knockout mice were hemostatically normal, indicating that deletion of PAR₁ has no effect on thrombin-induced platelet activation (DARROW *et al.*, 1996). Decrease in the leukocytes rolling and delayed onset of inflammation were observed in PAR₂-deficient mice, suggesting the involvement of PAR₂ in inflammation LINDNER *et al.* (2000). PAR₃-deficient mice demonstrated a marked reduction in response to thrombin, demonstrating that PAR₃ is a thrombin receptor on murine platelets and contributes to thrombin-induced platelet activation in mice. However, persistent thrombin responses suggest the presence of another thrombin receptor in mice (KAHN *et al.*, 1998; ISHIHARA *et al.*, 1998). PAR₄-deficient mice are completely insensitive to thrombin, indicating the importance of PAR₄ in mouse platelet (SAMBRANO *et al.*, 2001).

1.4.5.1 Respiratory System

The human respiratory tract expresses all four PAR members that distribute differently in the airway structures (**Table 1.2**).

Table 1.2: PAR Expression on Different Cell Types in Lung.

PAR	Cell Types	References
PAR ₁	Fibroblasts,	TREJO <i>et al.</i> (1996); CHAMBERS <i>et al.</i> (1998)
	epithelial cells,	ASOKANANTHAN <i>et al.</i> (2002)
	endothelial cells,	D'ANDREA <i>et al.</i> (1998); KATAOKA <i>et al.</i> (2003)
	smooth muscle cells	LAN <i>et al.</i> (2000); WALKER <i>et al.</i> (2005)
PAR ₂	Fibroblasts,	AKERS <i>et al.</i> (2000); MATSUSHIMA <i>et al.</i> (2006)
	epithelial cells,	KNIGHT <i>et al.</i> (2001); ASOKANANTHAN <i>et al.</i> (2002)
	smooth muscle cells	D'ANDREA <i>et al.</i> (1998); SCHMIDLIN <i>et al.</i> (2001)
PAR ₃	Fibroblasts,	RAMACHANDRAN <i>et al.</i> (2006)
	epithelial cells,	SHIMIZU <i>et al.</i> (2000); ASOKANANTHAN <i>et al.</i> (2002)
	endothelial cells	KATAOKA <i>et al.</i> (2003)
PAR ₄	Fibroblasts,	RAMACHANDRAN <i>et al.</i> (2007)
	epithelial cells,	SHIMIZU <i>et al.</i> (2000); ASOKANANTHAN <i>et al.</i> (2002)
	endothelial cells,	KATAOKA <i>et al.</i> (2003)
	smooth muscle cells	LAN <i>et al.</i> (2000)

PAR₁ and PAR₂ are important in the inflammatory and fibroproliferative processes. PAR₁-knockout mice are partially protected from bleomycin-induced lung fibrosis (HOWELL *et al.*, 2005). Similarly, PAR₂-null mice develop considerably less inflammation in the airway than the mice which overexpress PAR₂ (SCHMIDLIN *et al.*, 2002). An *in vitro* study showed that PAR₁ and PAR₂ can induce proliferation of lung fibroblasts (HOWELL *et al.*, 2005). Their expression are upregulated during the development of pulmonary diseases. Increased protein levels of PAR₁ was detected by immunohistochemistry in lung tissues of patients with pulmonary fibrosis (HOWELL *et al.*, 2005; BLANC-BRUDE *et al.*, 2005) and in early stage of pulmonary fibrosis associated with scleroderma (BOGATKEVICH *et al.*, 2005).

PAR₁ expression decreases in fibroblasts following prostaglandin E₂ (PGE₂) exposure (SOKOLOVA *et al.*, 2005). An increased expression of PAR₂ was detected in the bronchial epithelium of asthmatic patients (KNIGHT *et al.*, 2001). PAR₂ expression is also elevated following exposure to a variety of inflammatory stimuli, including smoke, respiratory viruses, bacterial products and allergens (OSTROWSKA *et al.*, 2007). PAR₄ expression on bronchial fibroblasts was reported to be induced following exposure to inflammatory stimuli, such as lipopolysaccharide (LPS) and TNF- α (RAMACHANDRAN *et al.*, 2007).

PAR activation may also promote the inflammatory processes in the respiratory tract, inducing the release of pro-inflammatory cytokines and mediators in cell cultures relevant to airway diseases. PAR₁ and PAR₂ activations enhance the expressions of matrix metalloproteinase-9 and granulocyte-macrophage colony-stimulating factor (GM-CSF), which are the important mediators of inflammation. PAR₁ is also involved in the inflammatory cell recruitment in response to bleomycin injury, collagen accumulation and expressions of pro-fibrotic factors such as CTGF and TGF- β 1 (HOWELL *et al.*, 2005). PAR₂ activation induces the release of IL-6, IL-8 and PGE₂ in primary human bronchial epithelial cells (ASOKANANTHAN *et al.*, 2002; KAWABATA *et al.*, 2004; KAWABATA and KAWAO, 2005). PAR₄-mediated signalling has been suggested to contribute to a pro-inflammatory reaction, in which it plays a critical pro-inflammatory role in neutrophil rolling and adherence. Neutrophilic responses were diminished as a result of PAR₄ inhibition (VERGNOLLE *et al.*, 2002; SLOFSTRA *et al.*, 2007).

PAR agonists can induce the rapid and sustained formation and release of prostanoids from a wide variety of cell and tissue types. For example, PAR₁ AP causes PGE₂ release from human bronchial epithelial cells

(ASOKANANTHAN *et al.*, 2002) and human lung fibroblasts (SOKOLOVA *et al.*, 2005). Human cultured bronchial airway epithelial cells release PGE₂ following exposure to PAR₂ AP (ASOKANANTHAN *et al.*, 2002). PGE₂ promotes inflammatory processes in most organ systems, but produces predominantly anti-inflammatory effects in the lung. It appears to have a role in limiting the inflammatory response and tissue repair processes (VANCHERI *et al.*, 2004). Trypsin induces PGE₂ release from airway smooth muscle cells independently of PAR₂, suggesting that PAR₄ which is also a trypsin receptor may induce PGE₂ release from airway smooth muscle (CHAMBERS *et al.*, 2003). PAR₄ AP can also induce PGE₂ release from the cultured bronchial epithelial cells (ASOKANANTHAN *et al.*, 2002). These findings indicate that PAR-mediated PGE₂ production within the airway may inhibit fibrosis through a number of mechanisms.

Infiltration of immune cells has been shown to be inhibited in PAR₂ deficient mice, where allergic inflammation of the airway and neuroinflammation occurred (NOORBAKHSI *et al.*, 2006). In pancreatitis, PAR₂ is activated by leaked trypsin, which mediates both pro-inflammatory and anti-inflammatory responses (KOMATSU *et al.*, 2012). Involvement of PAR₂ in regulating airway tone has a dual role: protective bronchodilatory response and detrimental bronchoconstriction. The activation of PAR₂ causes relaxation in the main bronchi and trachea but produces contractile responses from the isolated smaller intrapulmonary bronchi. These findings suggest that PAR₂ might be protective in the larger airways but detrimental in the smaller bronchioles as it increases airway resistance by contraction (RICCIARDOLO *et al.*, 2000; KAWABATA and KAWAO, 2005).

PAR₄ may also play a pro-fibrotic role. The concentrations of thrombin and/or CG in bronchio-alveolar lavage fluid in patients with IPF or pulmonary fibrosis are much higher than those in healthy controls. Thus, thrombin and/or CG receptors such as PAR₁ and/or PAR₄ are responsible

for the pathogenesis of lung fibrosis (HERNÁNDEZ-RODRÍGUEZ *et al.*, 1995; KIMURA *et al.*, 2005). Stimulation of PAR₄ in alveolar epithelial cells induced an increase in α -SMA expression and a decrease in epithelial cell marker E-cadherin, suggesting that PAR₄ stimulation induces EMT in these cells (ANDO *et al.*, 2007b).

In contrast, PAR₄ may suppress pulmonary fibrosis by countering PAR₁-stimulated proliferation of fibroblasts (RAMACHANDRAN *et al.*, 2007). Exposure of human primary bronchial fibroblasts to pro-inflammatory stimuli induced expression of functional PAR₄ on the fibroblasts. In these TNF- α stimulated fibroblasts, thrombin no longer induced proliferation, and a PAR₄ AP caused a reduction in fibroblast cell number (RAMACHANDRAN *et al.*, 2007). Furthermore, induction of PAR₄ expression enables signalling of CG, which usually silences PAR₁ and PAR₂, to evoke a calcium signalling responses (RAMACHANDRAN *et al.*, 2007).

PAR₄ agonists can stimulate the release of IL-6, IL-8 and PGE₂ with an increase in cytoplasmic Ca²⁺ concentration in human respiratory epithelial cell lines (ASOKANANTHAN *et al.*, 2002). PAR₄ stimulation causes mobilisation of Ca²⁺ from intracellular stores in the initial peak response (phospholipase C β -dependent mobilisation of Ca²⁺) and enhances Ca²⁺ entry through the store depletion-operated Ca²⁺ pathway in the delayed phase in mouse lung AECs (ANDO *et al.*, 2007a).

PAR₄ can be activated by CG at sites of vascular injury. PAR₄ is the CG receptor on human platelets and the activation of PAR₄ by CG is crucial for neutrophil-dependent platelet activation (SAMBRANO *et al.*, 2000). PAR₄ is also involved in the late phase of platelet aggregation in which it sustains the aggregation in response to thrombin when PAR₁ becomes rapidly inactivated (KAHN *et al.*, 1998; MACFARLANE *et al.*, 2001).

1.4.5.2 Renal System

The kidney expresses PAR₁, PAR₂ and PAR₄, particularly PAR₂ (RASMUSSEN *et al.*, 1991; NYSTEDT *et al.*, 1995; HOLLENBERG, 2003). PAR₄ mRNA has been identified from both renal cortex and medulla and expression has been reported in podocytes and from human tubular epithelial cells at low levels. The role of PAR₄ in kidney has not been studied in detail (GUI *et al.*, 2003; HARRIS *et al.*, 2009)(**Table 1.3**).

Table 1.3: PAR Expression on Different Cell Types in Kidney.

PAR	Cell Types	References
PAR ₁	human glomerular epithelial cells, human glomerular mesangial cells, podocytes, glomerular endothelial cells, ubterstitial peritubular cells	RONDEAU <i>et al.</i> (2001), SAKAI <i>et al.</i> (2009)
PAR ₂	epithelial cells, mesangial cells, blood vessel walls, infiltrating renal inflammatory cells, collecting duct cells	D'ANDREA <i>et al.</i> (2001), TANAKA <i>et al.</i> (2005), XIONG <i>et al.</i> (2005), BERTOG <i>et al.</i> (1999) GRANDALIANO <i>et al.</i> (2003)
PAR ₄	tubular epithelial cells, podocytes	GUI <i>et al.</i> (2003) HARRIS <i>et al.</i> (2009)

Both PAR₁ and PAR₂ have functional roles in renal pathophysiology. PAR₁ is involved in renal inflammation. The treatment of PAR₁-knockout mice with PAR₁-AP protects them from renal injury, while PAR₁-AP caused glomerulonephritis in the wild-type control (CUNNINGHAM *et al.*, 2000). The contribution of PAR₂ to renal inflammation has been studied using knockout mice that highlight the importance of PAR₂ in the development of inflammation. Both SU *et al.* (2005) and CHIGNARD and PIDARD (2006) have demonstrated that PAR₂-knockout mice had substantially less inflammation compared to the wild type mice. Elevated expression levels of PAR₂ mRNA and protein have been shown in the proximal tubular cells, infiltrating interstitial mononuclear cells and glomerular epithelial cells in patients with IgA nephropathy. The PAR₂ mRNA levels correlate directly with the extent of fibrosis (GRANDALIANO *et al.*, 2003).

PAR₁ activation causes vasoconstriction of the afferent arteriole whereas PAR₂ activation causes vasodilation mainly via the release of nitric oxide in the kidney (MURAMATSU *et al.*, 1992; SAIFEDDINE *et al.*, 2001). Thrombin or PAR₁ agonist peptide TFLLR-amide caused a marked reduction in renal perfusion flow (GUI *et al.*, 2003), whereas activation of PAR₂ causing vasodilation of the afferent arteriole, resulted in an increase in perfusion flow in the kidney (HOLLENBERG *et al.*, 2003). These findings suggest that there is an increase in the glomerular filtration rate with PAR₂ activation and a decrease in the glomerular filtration rate with PAR₁ activation (GUI *et al.*, 2003). These effects may be of particular importance in the setting of renal diseases where the tissues may be exposed to serine proteinases (HOLLENBERG *et al.*, 2003).

As proximal tubular cells appear to be the predominant site of PAR₂ expression in the kidney, PAR₂ agonists have been proposed to regulate fluid and electrolyte secretion in the kidneys. BERTOGLIO *et al.* (1999) has

shown that PAR₂ can regulate chloride secretion in murine tubular cells. Tryptase and factor Xa were shown to stimulate proliferation of renal fibroblasts and mesangial cells, respectively (KONDO *et al.*, 2001; TANAKA *et al.*, 2005), suggesting a role for PAR₂ in renal fibrosis. PAR₂ induced cell proliferation is suggested to be mediated via EGF-receptor and downstream MAPK signalling (CHIGNARD and PIDARD, 2006).

1.5 Apoptosis

Apoptosis is a fundamental physiological event in the normal development and homeostatic processes to maintain a balance between cell proliferation and cell death. It is form of programmed cell death that requires the activation of specific enzymes and signalling pathways, offering potential for pharmacological manipulation. It results in the dismantling of the entire cell within the context of membrane-enclosed vesicles that can be recognised and engulfed by phagocytes. Hence, it prevents the release of intracellular components from dying cells and the activation of innate immune responses. Apoptosis is critical for the maintenance of postnatal adult tissue homeostasis as it eliminates the damaged or infected resident cells, inflammatory cells and mesenchymal cells that are involved in wound healing. Orchestrated death and removal of these cells is necessary for the restoration of normal cellular homeostasis and the maintenance of the tissue architecture and organ function (SARASTE and PULKKI, 2000; LIU *et al.*, 2002; THANNICKAL and HOROWITZ, 2006).

Failure to clear unwanted cells by apoptosis will prolong inflammation due to the release of their toxic contents. Excessive apoptosis causes extensive cell loss, leading to the failure of clearing the apoptotic cell debris and eventually the amplification of inflammation and the possibility of forming scar tissue (HAGIMOTO *et al.*, 1997a; MATUTE-BELLO *et al.*,

2001). Enhanced apoptosis of epithelial cells, fibroblasts and myofibroblasts occurs in fibrosis (POLUNOVSKY *et al.*, 1993; KAPETANAKI *et al.*, 2013).

Apoptosis can be triggered by external stimuli, such as soluble cell death ligands, which are released during inflammatory responses or intrinsic stimuli due to an alteration of the cellular function and metabolism (TANG *et al.*, 2008). It is characterised by a selection of morphological features, such as loss of plasma membrane asymmetry and attachment, cell shrinkage, chromatin condensation and chromosomal DNA fragmentation (LIU *et al.*, 2002). These morphological changes are a consequence of characteristic molecular and biochemical events occurring in an apoptotic cell. During early apoptosis, the cell rounds up, loses contact with its neighbouring cells and shrinks. Then, the chromatin in the nucleus condenses and aggregates into dense compact masses, the plasma membrane blebs or buds, and finally the cell is fragmented into compact membrane-enclosed structures called the apoptotic bodies which contain cytosol, condensed chromatin and organelles. The apoptotic bodies are engulfed by macrophages and thus are removed from the tissue without causing an inflammatory response (SARASTE and PULKKI, 2000).

Apoptosis is different from the necrotic mode of cell death. Necrosis is an accidental, unplanned death occurring in response to sudden and severe cell injury due to hypoxia, toxins, extreme temperatures or attack by complement and lytic viruses (SAVILL, 1994). The plasma membrane is damaged and becomes abnormally permeable, resulting in a loss of membrane integrity, swelling and rupture of the cells. The cellular contents are released uncontrolled into the cellular environment, which causes damage to the surrounding cells and provokes tissue injury and inflammation (SAVILL, 1994).

Caspases are a family of cysteine proteases which play an important role in the execution of apoptosis (ALIKHANI *et al.*, 2004). Caspases are synthesized as inactive zymogens in the cell, which are known as pro-caspases and are activated by proteolytic cleavage into a heterodimer consisting of a large (20 kDa) and a small (10 kDa) subunits. A heterotetramer consisting of two small and two large subunits then forms an active caspase with two active sites (THORNBERRY *et al.*, 1997; BUDIHARDJO *et al.*, 1999; ALIKHANI *et al.*, 2004). The pro-apoptotic caspases can be divided into a group of initiator caspases including pro-caspase-2, -8, -9 and -10, and a group of executioner caspases including pro-caspase-3, -6, and -7. The initiator caspases are recruited to and activated at the death-inducing signalling complexes in response to either the ligation of the cell surface death receptors (extrinsic pathway) or the signals originating from inside the cell (intrinsic pathways) (EARNSHAW *et al.*, 1999; PLATAKI *et al.*, 2005).

The caspase cascade can be activated by an extrinsic or intrinsic pathway. Caspase-8 activation is part of the cytoplasmic (extrinsic) pathway of apoptosis while caspase-9 activation is usually associated with the mitochondrial (intrinsic) pathway of apoptosis (GREEN, 2000). The extrinsic or death receptor pathway involves the activation of death receptors present in the cell membrane such as Fas and TNF-receptor 1. These receptors contain cysteine-rich extracellular subdomains that allow them to recognize their ligands specifically and an intracellular death domain that is crucial for the transduction of the apoptotic signal. Binding of the death ligand to its receptor leads to the activation of an adaptor protein called the activated death domain and the subsequent activation of pro-caspase-8 or -10. Activated caspase-8 then directly activates the effector caspases, caspase-3 and caspase-7, which execute the apoptotic cell death programme (GOLTSEV *et al.*, 1997; IRMLER *et al.*, 1997).

The intrinsic pathway is initiated by the intracellular stress signals such as DNA damage and oxidative stress that will activate the BH3-only (pro apoptotic), member of the B cell lymphoma-2 (Bcl-2) family proteins, translocate from the cytosol to the mitochondrion. There they induce the release of cytochrome c from the mitochondrial intermembrane space to the cytosol. Cytochrome c then binds to the apoptotic protease-activating factor 1 (Apaf-1), which undergoes an adenosine 5'-triphosphate (ATP)-dependent conformational change and forms the multimeric complex known as the apoptosome. The apoptosome will activate the initiator caspase, caspase-9, which will subsequently activate caspase-3 and caspase-7 and execute apoptosis (ZOU *et al.*, 1997; SRINIVASULA *et al.*, 1998; THANNICKAL and HOROWITZ, 2006) (**Figure 1.8**).

Accumulating evidence supports the importance of apoptosis as a potential pathogenic mechanism in fibrosis. Components of the Fas-FasL ligand (Fas-FasL) immunological pathway have been detected in patients with IPF (KUWANO *et al.*, 1999b). The Fas-FasL pathway is an important apoptosis-signalling pathway. Fas antigen is a cell surface protein that mediates apoptosis. It is expressed in various cells and tissues including kidney, lung, liver and heart. FasL is a cell surface molecule that belongs to TNF (SUDA *et al.*, 1993). It is expressed predominantly in the activated T-lymphocytes and in the organs including small intestines, kidney, testis and lung (SUDA *et al.*, 1993). Removal of fibroblasts and myofibroblasts by programmed cell death is required for the normal resolution of tissue repair responses. Resistance of these cells to apoptosis may result in a chronic inflammation or fibrosis (KISSELEVA and BRENNER, 2008).

AEC apoptosis with subsequent fibrosis is well documented in the bleomycin-induced fibrosis model of IPF (HAGIMOTO *et al.*, 1997b,c). LEE *et al.* (2004) showed that activation of Fas pro-apoptosis pathway together with TGF- β overexpression causes apoptosis in AEC which is essential for

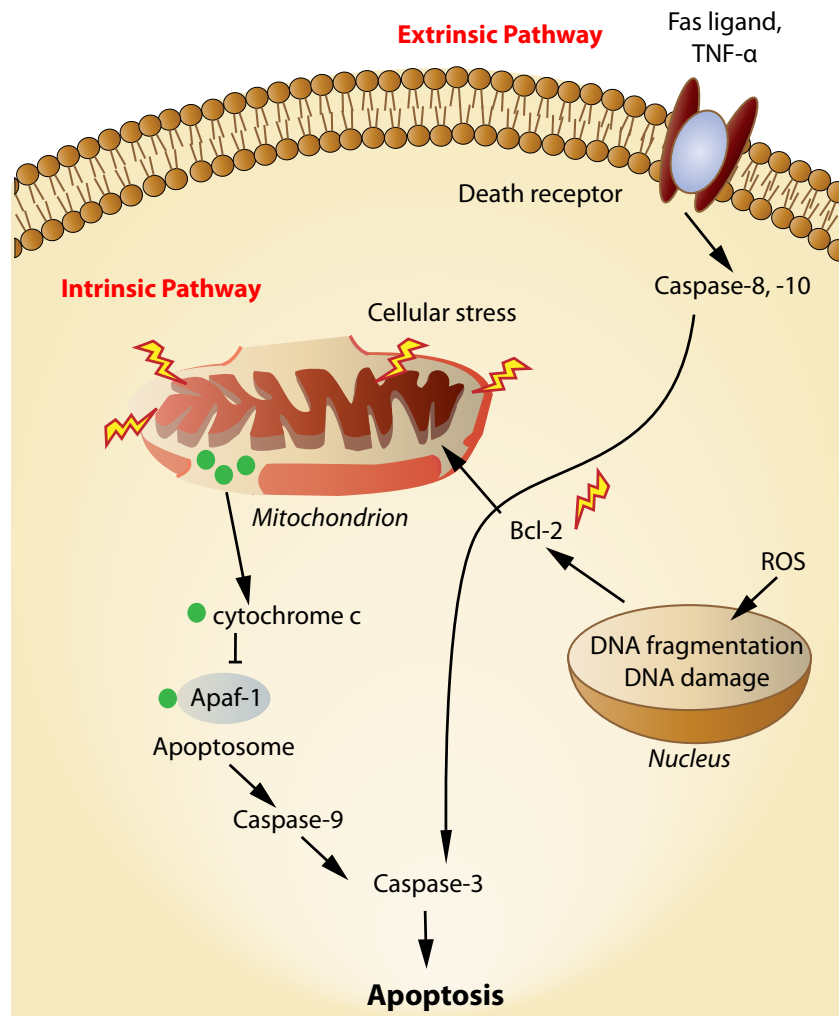


Figure 1.8: Representative of Major Intrinsic and Extrinsic Pathways of Apoptosis. In extrinsic pathway, binding of death ligand to the death receptor mediates the activation of initiator caspase-8. Activated caspase-8 initiates the effector caspase and leads to apoptosis. In intrinsic pathway, intracellular stress and DNA damage induce the release of cytochrome c from the mitochondrion and contribute to the formation of apoptosome. The apoptosome activates caspase-9 which is another initiator caspase and execute the apoptosis. Adapted from HAVASI and BORKAN, 2011.

the induction of pulmonary fibrosis in mice. Furthermore, ROS generated by mitochondria has been linked to increased cellular oxidative stress and apoptosis of AECs. It has been shown by the early induction of ROS-dependent AEC apoptosis in murine model of bleomycin-induced pulmonary fibrosis (WALLACH-DAYAN *et al.*, 2006). Exaggerated apoptosis of epithelial cells causes deranged tissue homeostasis and contributes to fibrosis (HUMPHREYS *et al.*, 2010; KOESTERS *et al.*, 2010).

CG and elastase are highly present in the active phase of inflammation. OWENS (1995) demonstrated that CG and elastase are expressed on the cell surface of polymorphonuclear leukocytes neutrophil (PMN). They can be upregulated by pro-inflammatory mediators. Apoptotic PMN accumulated in lung as a result of the interference of CG and elastase with phagocytosis of apoptotic cells by alveolar macrophages, leading to the retention of apoptotic cells in the lungs. Failure of PMN removal may contribute to chronic inflammatory diseases (VANDIVIER *et al.*, 2002; GUZIK *et al.*, 2007).

Apoptosis occurs in both human and animal kidneys during acute kidney injury. Apoptosis can be detected in the kidneys after ischaemia, toxin exposure, inflammation and sepsis. Recent studies have indicated that injured tubular epithelial cells either undergo apoptosis or remain in a state of G2/M arrest with characteristic phenotypic changes, including flattened morphology and loss of polarity. Moreover, exaggerated apoptosis of epithelial cells also causes deranged tissue homeostasis and contributes to fibrosis (HUMPHREYS *et al.*, 2010; KOESTERS *et al.*, 2010). Proximal tubule epithelial cells are highly susceptible to apoptosis. Apoptosis of parenchymal cells is one of the major factors which contributing to the loss of renal function during the progression of kidney disease. Counterbalancing the loss of epithelial cells is the activation of proliferative pathways in an attempt to recreate tubules within the kidney (HAVASI and BORKAN, 2011).

1.6 Thesis Hypothesis

The main hypothesis of this thesis is that PAR₄ is expressed in both lung and renal fibroblasts, and PAR₄ activating peptide and cathepsin G can induce apoptosis in fibroblasts via PAR₄-dependent and independent mechanisms.

1.7 Aims

1. To study the expression of PARs in lung and renal fibroblasts (Chapter 3).
2. To study whether TGF- β 1 can differentiate fibroblast into myofibroblast (Chapter 3).
3. To generate a stable PAR₄-expressing transgenic cell line using HEK293 cells (termed HEK-PAR₄ cells) (Chapter 4).
4. To determine if cathepsin G and PAR₄ activating peptide can trigger apoptosis in fibroblasts and HEK-PAR₄ cells (Chapter 5).
5. To examine the effect of media derived from confluent epithelial cell cultures on fibroblast proliferation and differentiation (Chapter 6).

Chapter 2

General Materials and Methods

2.1 Materials and Reagents

Dulbecco's Modified Eagles Medium (DMEM), sodium pyruvate, antibiotic/antimycotic (penicillin G sodium, streptomycin sulphate and amphotericin B), foetal bovine serum (FBS), trypsin EDTA, Roswell Park Memorial Institute (RMPI) medium, G418, Opti-MEM media and Lipofectamine were purchased from Gibco (Paisley, UK). dNTPs, random primers, Cy3 goat anti-mouse IgG, and CyQUANT cell proliferation assay kit were obtained from Invitrogen (Paisley, UK). Fibroblast growth medium and TGF- β 1 were purchased from Promocell (Heidelberg, Germany). Anti-prolyl 4-hydroxylase, rabbit polyclonal anti- α SMA and polyclonal anti-collagen I were purchased from Abcam (Cambridge, UK). NucleoSpin RNA II Kit was obtained from Macherey-Nagel (Duren, Germany). Primers were purchased from MWG Eurofins (Ebersberg, Germany). Taq DNA polymerase and restriction enzymes (XhoI and HindIII) were obtained from New England Biolabs (Hitchin, UK). Qiagen miniprep Kit was obtained from Qiagen (Crawley, UK). Fermentas RT kit was purchased from Fermentas (Opelstrasse, St. Leon-Rot, Germany). PAR antibodies, anti- α -tubulin and goat anti-mouse IgG HRP were purchased from Santa Cruz Biotechnology, Germany). Cathepsin G was purchased from EPC

(Missouri, USA). Fluo-3 acetoxymethyl ester (Fluo-3 AM) was purchased from Cambridge Biolabs and later Invitrogen (Cambridge, UK). Both human and rat PAR₄ APs were purchased from Peptides International (Kentucky, USA). The enhanced chemilumescence (ECL) western blotting detection reagents and donkey anti-rabbit HRP were obtained from GE Healthcare (Amersham, Buckinghamshire, UK). Glycerol/PBS solution AF1 was purchased from Citiflour (London, UK). XL1-Blue supercompetent cells was obtained from Stratagene Europe (Amsterdam, Netherlands). Coomassie Brilliant Blue was purchased from Bio-Rad Laboratories Ltd (Hertford, UK) FITC-conjugated Annexin V was purchased from IQ product (DL Groningen, Netherlands). Caspase-3 and cleaved caspase-3 antibodies were purchased from Cell Signalling Technology (Hertford, UK). All other chemicals and reagents were purchased from Sigma-Aldrich (Poole, Dorset, UK) unless otherwise stated.

2.2 Cell Culture

Human primary bronchial fibroblast (HPBF) and human primary renal fibroblast (HPRF) cultures were established from bronchial and renal tissue explants, respectively. Renal tissue explants were obtained under informed written consent from patient undergoing nephrectomy. Ethics approval was obtained from the Hull and East Riding Local Research Ethics Committee (12/SC/0474) for lung specimen, Hull and East Yorkshire Hospitals NHS Trust (Hull, UK), with approval of the local ethics committee (Elsy no CHH 341) for kidney specimen.

Cell cultures were established using methods based on previously published papers (AKERS *et al.*, 2000; RAMACHANDRAN *et al.*, 2007). Briefly, explants were dissected into pieces $\leq 1 \text{ mm}^3$, placed into individual wells of a 24-well culture plate with 500 μl of DMEM containing in v/v

10% FBS, 1% sodium pyruvate, and 1% antibiotic/antimycotic (penicillin G sodium, streptomycin sulphate and amphotericin B) and then incubated at 37°C in a humidified atmosphere of air containing 5% CO₂. The medium was changed at least twice a week. After 3 weeks, confluent fibroblasts were seen growing out from the explants. The cells were then harvested by trypsinization and transferred to 25 cm² flasks with 5 ml of fresh fibroblast growth medium. These cells were cultured for further a 1 or 2 weeks until confluent islands of cells were observed. Then, the cultures were passaged with a split ratio of 1:3 into 75 cm² flasks in 10 ml fresh fibroblast growth medium. The purity of the fibroblast culture was confirmed by staining with anti-vimentin and anti-prolyl 4-hydroxylase antibodies and by observing the typical spindle shape and characteristic swirls formation when confluent. See **Section 2.7**.

HEK293 cells were routinely maintained in DMEM complete growth medium containing in v/v 10% FBS, 1% sodium pyruvate, and 1% antibiotic/antimycotic (penicillin G sodium, streptomycin sulphate and amphotericin B). Cells were harvested by washing with 5 ml of phosphate buffered saline (PBS) and dissociating the cells from the flask using fresh 5 ml of PBS. The cultures were passaged with a split ratio 1:5 into 75 cm² flasks approximately every 2 days with 10 ml fresh growth medium.

2.3 Quiescing of HPBF and HPRF

Prior to certain experiments, cells were cultured in a serum free media consisting of fibroblast growth media supplemented with antibiotic/antimycotic only. This was to arrest cell division and to elucidate the specific effects of single agonist without interference from FBS components.

2.4 mRNA Extraction

Cells were cultured in 25 cm² flasks with 5 ml of complete growth medium. Total RNA was prepared using the NucleoSpin RNA II Kit as per manufacturer's instructions. Using the NucleoSpin RNA methods, cells are lysed by incubation in a solution containing large amounts of chaotropic ions which will immediately inactivate ribonuclease (RNase) and create appropriate binding conditions which favour absorption of RNA to the silica membrane. Contaminating DNA which is also bound to the silica membrane is then removed by a recombinant DNase (rDNase) solution. Simple washing steps with two different buffers remove salts, metabolites and macromolecular cellular components. Finally, pure RNA is eluted under low ionic strength condition with diethylpyrocarbonate (DEPC) water. The mRNA was quantified with a GeneQuant spectrophotometer (Amersham, UK).

2.5 Reverse Transcription (RT)

cDNA was synthesized using the Fermentas RT kit. The reagents used were summarised in (Table 2.1).

Table 2.1: Reagents Used in a RT Reaction.

Reagent	Volume (Final Volume = 20 μ l)	Final Concentration
5 \times RT Buffer	4 μ l	1 \times
dNTPs (10 mM)	1 μ l	0.5 mM
Random Primers (3 μ g/ μ l)	0.2 μ l	30 ng/ μ l
RNase Inhibitor (40 U/ μ l)	0.5 μ l	20 U
Reverse Transcriptase (200 U/ μ l)	1 μ l	200 U
mRNA	Variable	2 μ g
DEPC water	Added to 20 μ l	-

Briefly, the reaction was cycled at 25°C for 10 min for random primer annealing, 50°C for 30 min to allow reverse transcription, 85°C for 5 min to inactivate reverse transcriptase, followed by a final hold at 4°C. The reaction was carried out in TC-3000 Personal 25-well Thermal Cycler (Bibby Scientific, UK).

2.6 Polymerase Chain Reaction (PCR)

PCRs were performed for 35 cycles. Denaturation at 94°C for 30 sec, primer annealing at 59°C for 30 sec and elongation at 72°C for 30 sec. The reagents used are summarised in **Table 2.2**. All reactions included an initial denaturation at 94°C for 2 min and final extension at 72°C for 10 min. PCR was carried out in TC-3000 Personal 25-well Thermal Cycler (Bibby Scientific, UK).

Table 2.2: A Typical PCR Reaction to Amplify PARs.

Reagent	Volume (Final Volume = 50 μ l)	Final Concentration
10 \times PCR Buffer	5 μ l	1 \times
dNTPs (10 mM)	1 μ l	0.5 mM
Forward Primer (20 pM)	1 μ l	0.4 pM
Reverse Primer (20 pM)	1 μ l	0.4 pM
Taq Polymerase (250 U)	0.25 μ l	1.25 U
cDNA	Variable	2 μ g
DEPC Water	Added to 50 μ l	-

All experiments included a control where the cDNA was omitted from the reaction mixture as well as a mock reverse transcription containing all the RT-PCR reagents, except the reverse transcriptase (no RT control).

The PCR product was separated on a 1.3% agarose gel, stained with ethidium bromide (0.75 $\mu\text{g}/\text{ml}$) and visualised under ultraviolet light. Images were obtained using an Epichemi system (consisting of a Epichemi dark room, high resolution deeply cooled scientific grade digital CCD and 3UV transilluminator) coupled to a Labworks 4.0 image acquisition and analysis software (UVP Laboratory Products, Cambridge, UK).

2.7 Immunocytochemical Staining

HPBFs or HPRFs were seeded on cover slips and grown in 6-well plates with 2 ml of fibroblast complete growth medium. Once confluent, cells were washed with PBS, fixed with 4% paraformaldehyde for 20 min, and washed 3 times with PBS. The cells were then permeabilised using 0.1% Triton X-100 in PBS for 15 min at room temperature. After 3 further washes with PBS, the cells were incubated with blocking solution (1% BSA in PBS) for 20 min and washed 3 times with PBS. Then, the cells were incubated with primary antibody. The irrelevant isotype matched antibody was used as a negative control. After washing 3 times with PBS, the cells were incubated with biotinylated antibody at 1:100 at room temperature for 40 min. Again, the cells were washed 3 times with PBS and incubated with streptavidin conjugated peroxidase enzyme at 1:100 for another 40 min at room temperature. After 3 washes with PBS, the cells were incubated with 200 μl of 3,3'-diaminobenzinetetrahydrochloride (DAB) for 5 min. The cells were then washed 3 times with distilled water and mounted with glycerol based gelatine. Finally, slides were visualised under a light microscope (Nikon) and images were taken with a Nikon Coolpix 930 digital camera at 10 \times magnification.

2.8 Immunofluorescent Staining for α -SMA

After 24 h treatment with TGF- β 1 (10 ng/ml), fibroblasts were washed with PBS, fixed with 4% paraformaldehyde for 20 min, and then washed 3 times with PBS. The cells were then permeabilised using 0.1% Triton X-100 in PBS for 15 min at room temperature. After 3 washes with PBS, the cells were incubated with blocking solution (1% BSA in PBS) for 20 min and washed 3 times with PBS. Then, the cells were incubated with 50 μ l of monoclonal anti-actin, α -smooth muscle clone 1A4 (5 μ g/ml) for 40 min at room temperature. As a negative control, the irrelevant isotype matched antibody IgG2a (5 μ g/ml) was used in place of the primary antibody. After a further 3 washes with PBS, the cells were incubated with 50 μ l of Cy3 goat anti-mouse (1:200) for 40 min at room temperature in dark. The cells were then washed 3 times with PBS, followed by mounting on a slide using the glycerol/PBS solution, AF1, and sealing with nail polish. Slides were visualized under a fluorescent microscope (Nikon) with FITC or Cy3 filter.

2.9 Intracellular Calcium Mobilisation Assay

Calcium signalling assays were performed using the methods described by COMPTON *et al.* (2001). Cells at 70-85% confluence in 75 cm² flasks were washed and harvested with PBS (without calcium or magnesium). Cells were pelleted and resuspended in 500 μ l of normal culture medium containing 0.25 mM sulphinyprazole and 7 μ M of Fluo-3 acetoxymethyl ester (Fluo-3 AM) in DMSO. The cells were then incubated at room temperature for 25 min whilst gently shaking, allowing the fluorescent probe to be taken up by the cells. The cells were washed by adding 4.5 ml of PBS and centrifuged to remove the excess Fluo-3 AM, then resuspended in 300 μ l of calcium assay buffer (CAB) (150 mM sodium chloride, 250 μ M sulphinyprazole, 3 mM potassium chloride, 10 mM glucose, 20 mM HEPES and 280 nM calcium chloride, pH 7.4). 100 μ l of cell suspension was then

added to the calcium assay cuvette containing 1.9 ml of CAB and a magnetic flea to keep the cells suspended. Increases in intracellular calcium levels were measured at room temperature using a fluorospectrometer (Photo Technology International), set to measure the Fluo-3 AM with excitation at 480 nm and emission at 530 nm. The increase in fluorescence measured at 530nm were expressed as a percentage of the maximum fluorescence signal after the addition of 2 μ M calcium ionophore.

2.10 Generation of Whole Cell Lysate

Cells were passaged into 25 cm² culture flasks and allowed to reach over 85% confluence. Cells were then harvested, pelleted by centrifugation at 500 \times g for 5 min and lysed by adding 500 μ l Laemilli's sample buffer (containing 2% SDS, 10% glycerol, 50 mM Tris-HCl (pH 6.8), 5 mM EDTA, 0.008% bromophenol blue and 0.5% β -mercaptoethanol). The cell lysates were then transferred into a 1.5 ml eppendorf tube. Cell lysates were heated to 100°C on a heat block for 10 min and centrifuged at 13,200 \times g for 10 min at 4°C.

2.11 SDS Polyacrylamide Gel Electrophoresis (SDS-PAGE)

Gel forming apparatus was constructed as per the manufacturer's instructions. A 12.5% SDS-PAGE gel was made according to **Table 2.3** and adding N,N,N',N'-tetramethylethylenediamine (TEMED) last, quickly mixed before adding to gel former, 5ml per gel. Propan-2-ol was pipette onto the top of the gel to get rid of bubbles and ensure a flat surface. The gel was then left to set for 30-60 min at room temperature. Once the gel is set, propan-2-ol was poured off and the gel surface was washed with dH₂O

for two times and dried. Then, the stacking gel was made according to **Table 2.4** and adding TEMED last, quickly mixed and added to the gel former filling it to the top. A 12 sample comb was then inserted into the gel and the gel was left to set for another 30 min at room temperature.

Table 2.3: 12.5% SDS-PAGE Gel.

12.5% SDS-PAGE Gel (Final Volume = 8 ml)		
Reagents	Volume	Concentration
Acrylamide/Bis-acrylamide, 30% solution	3.33 ml	12.5%
1.5 M Tris pH 8.8	2 ml	375 mM
10% SDS	80 μ l	0.1%
10% Ammonia Persulphate (APS)	80 μ l	0.1%
Deionised Water	2.5 ml	-
TEMED	8 μ l	-

Table 2.4: 6% Stacking Gel.

6% Stacking Gel (Final Volume = 5 ml)		
Reagents	Volume	Concentration
Acrylamide/Bis-acrylamide, 30% solution	2.6 ml	6%
0.5 M Tris pH 6.8	1.25 ml	78 mM
10% SDS	50 μ l	0.1%
10% Ammonia Persulphate (APS)	50 μ l	0.1%
Deionised Water	2.6 ml	-
TEMED	5 μ l	-

Proteins were separated in 12.5% SDS-PAGE gel and the gel was run in a vertical gel electrophoresis unit in electrode buffer consisting of 25 mM Tris base, 190 mM glycine and 0.1% SDS, pH 8.3. The gel former was placed into the gel tank and enough electrode buffer was poured into the internal gel former reservoir until the buffer was levelled with the top of the gels and the remaining buffer was poured into gel tank up to the max fill mark, ensuring that the bottom of the gels were submerged in the buffer.

10 μ l of Precision Plus ProteinTM Dual colour standards (BIO-RAD) was used as size markers on the gels. 20 μ l of the samples were loaded into sample wells alongside 10 μ l of protein standard. Electrophoresis was carried out at 100 V for approximately 2 h or until the blue dye had run to the bottom of the gel.

2.12 Western Blotting

The proteins on the gel were electrotransferred to a nitrocellulose membrane using the Invitrogen i-blot dry blotting system as per the manufacturer's instructions. The membrane was then blocked with 5% w/v non-fat powdered milk in PBS containing 0.1% Tween 20 (PBS-Tween) at room temperature for 1 h to block the non-specific binding. The non-fat milk solution was then removed and the membrane washed 4×10 min with PBS-Tween. The membrane was then incubated with primary antibody (in PBS-tween containing 5% non-fat milk) at 4°C overnight on a rocker. Following 4 washes with PBS-Tween for 10 min, the membrane was then incubated with HRP conjugated secondary antibody (in PBS-Tween containing 5% non-fat milk) at room temperature for 1 h. The secondary antibody was then removed by 4 washes with PBS-Tween.

Protein bands on the membrane were visualised by enhanced chemiluminescence (ECL) according to manufacturer's instructions. Briefly, ECL reagent A and B were mixed together in equal volumes and applied to the protein binding surface and incubated at room temperature for 1 minute. Excess reagent was then removed and the membrane photographed using a UVP Laboratory Products Epichem II Darkroom setup to measure chemiluminescence. Bands were visualised using Lab Works Image Acquisition and Analysis software (UVP Laboratory Products, Cambridge, UK). Pictures were taken every 5 min for 20 min. Finally, bands were

quantified using ImageJ software.

2.13 Statistical Analysis

Statistical analyses were carried out using IBM SPSS 19. All data were expressed as mean \pm SEM. Paired t test was used to compare values between two groups. Differences between control and experimental groups were performed using a one-way ANOVA for repeated measures, followed by Dunnett's post hoc test for multiple comparisons. A value of $p < 0.05$ was considered as significant.

Chapter 3

Characterisation and Detection of PAR Expression in Primary Human Fibroblasts and Myofibroblast Differentiation

3.1 Introduction

Fibroblasts are ubiquitous mesenchymal cells that display a spindle-shaped elongated cellular phenotype with elliptical nuclei. They have a thin cytoplasm with abundant granular materials and electron microscopy reveals a well-developed rough endoplasmic reticulum and a golgi apparatus (LEMLEY and KRIZ, 1991; CAMELLITI *et al.*, 2005). They are widely distributed in the stroma of many tissues of most vertebrate organisms. Fibroblasts are involved in the maintenance of tissue structure and the assembly of ECM by producing factors including growth factors, cytokine and matrix metalloproteinases which are necessary to maintain a balance between the synthesis and the degradation of connective tissue components (CAMELLITI *et al.*, 2005).

Fibroblasts play central roles in tissue homeostasis and repair. Lung fibroblasts, renal mesangial cells and renal fibroblasts express little to no α -SMA in their resting state (ELGER *et al.*, 1993; BARNES and GORIN, 2011). During fibrogenesis, fibroblasts become activated, migrate into the damaged tissue and contribute to the inflammatory responses by secreting cytokines and chemokines that drive the recruitment of leukocytes (RAMACHANDRAN *et al.*, 2006). Fibroblasts then differentiate into contractile and highly synthetic myofibroblasts that are involved in promoting wound closure, ECM deposition and tissue remodeling (HINZ *et al.*, 2007). Fibroblasts are present in the adventitia of vascular structures and airways in the normal adult lung. In adult kidney, fibroblasts can be found in the renal cortex and medulla (CAMELLITI *et al.*, 2005; QI *et al.*, 2006; PHAN, 2008).

The activation and differentiation of fibroblasts into myofibroblasts were first described by GABBIANI *et al.* (1971). Myofibroblast differentiation and persistence are mainly dependent on the mechanical resistance of the ECM together with the action of pro-fibrotic TGF- β 1 (HINZ *et al.*, 2007). During wound healing or progressive fibrotic events after injury, activated fibroblasts highly express α -SMA along with the extracellular mesenchymal matrix proteins, collagen types I and III, and cellular fibronectin upon activation by TGF- β , PDGF, or TNF- α (JARNAGIN *et al.*, 1994; SCHNAPER and KOPP, 2003). The differentiation of the myofibroblasts from fibroblasts involves the formation of proto-myofibroblasts (DESMOULIÈRE *et al.*, 2005). The proto-myofibroblast phenotype is characterised by the increased expression of fibronectin (HINZ *et al.*, 2007; HINZ, 2007) and specifically the expression of the alternately spliced ectodysplasin-A (ED-A) isoform, which is not expressed by fibroblasts. Proto-myofibroblasts do not express α -SMA and thus are distinct from myofibroblasts, suggesting that proto-myofibroblast is an intermediate in the process of myofibroblastic differentiation (HINZ, 2007) (**Figure 3.1**).

Myofibroblasts display cytoplasmic stress fibres (actin microfilaments) and are connected to each other by adherens and gap junctions. They are also in contact with the ECM by focal contact (fibroneexus), a transmembrane complex made up of intracellular contractile microfilaments and the ECM protein fibronectin (POWELL *et al.*, 1999). They are present in many tissues in the body and play an important role in tissue remodelling after inflammation or injury. They are responsible for the synthesis and accumulation of the interstitial ECM components such as collagen types I and III as well as fibronectin during wound healing and at the sites of scarring and fibrosis (GABBIANI *et al.*, 1971). Myofibroblasts can produce cytokines and are capable of augmenting or down-regulating the inflammatory response. Myofibroblasts regress and disappear by apoptosis on wound epithelialisation. When myofibroblast activities become excessive and persists, beneficial tissue repair turns into the detrimental tissue deformities characteristic of organ fibrosis (HINZ, 2007).

Depending on the type of tissue to be remodelled, myofibroblast precursor cells are recruited from different sources, resident fibroblasts seem to be the most common among these (HINZ *et al.*, 2007). Other myofibroblast progenitors are fibrocytes, pericytes, EMT or endothelial-mesenchymal transition (EndoMT) (**Figure 3.2**). Hence, damaged organs seem to recruit myofibroblast precursors from several sources to satisfy the temporarily high demand of cells with tissue remodeling activity. (HAO *et al.*, 2006; HE LI *et al.*, 2009). In normal wound healing, the contractile activity of myofibroblasts is terminated when the tissue is repaired, α -SMA expression decreases and myofibroblasts disappear by apoptosis. In pathological wound healing, myofibroblast activity persists, leading to tissue deformation, which is particularly evident in hypertrophic scars developing after injury. Besides, WAGHRAY *et al.* (2005) has demonstrated that myofibroblast secretion of H_2O_2 plays a role in alveolar epithelial apoptosis and retardation of epithelial regeneration.

Thus, myofibroblasts are important in promoting ECM deposition, release of inflammatory mediators and epithelial injury, all of which are considered as key factors in the cycle of injury and fibrosis. Myofibroblasts have been demonstrated to be involved in fibrosis of the lung (HASHIMOTO *et al.*, 2004), kidney (DIREKZE *et al.*, 2003) and liver (FORBES *et al.*, 2004).

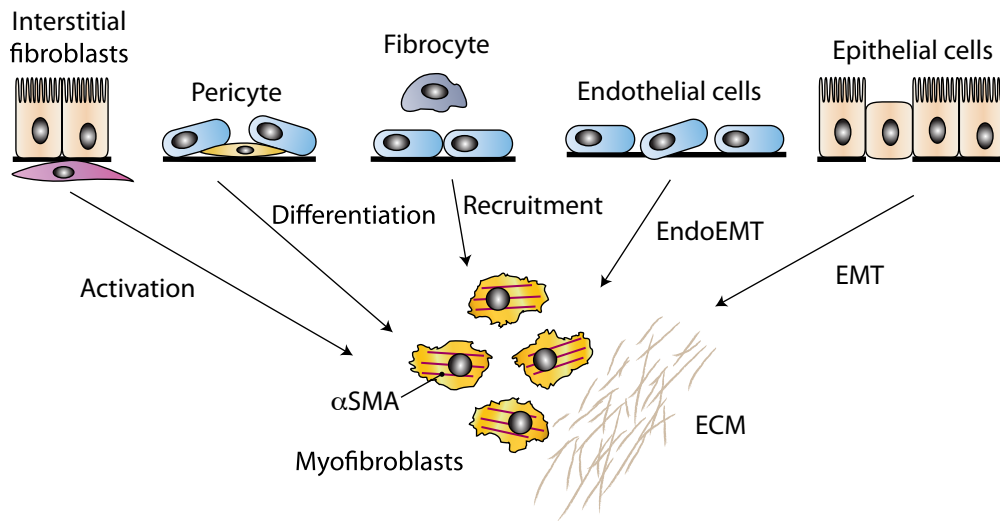


Figure 3.2: Multiple Origins of Myofibroblasts. Myofibroblasts can be derived from phenotypic activation from interstitial fibroblasts, differentiation from pericytes, recruitment from circulating fibrocytes, EndoEMT and EMT. Adapted from LIU, 2011.

TGF- β , PDGF and basic fibroblast growth factor-2 (bFGF-2) are the three main growth factors that have been shown to be associated with myofibroblast differentiation (FLOEGE *et al.*, 1992). Among these cytokines, TGF- β is well recognised as a pluripotent cytokine that drives organ fibrosis. It is a strong inducer of fibroblast differentiation to myofibroblasts by inducing expression of α -SMA. Increased expression of TGF- β and its downstream Smad signalling have been demonstrated in a variety of animal models and human diseases associated with fibrosis

(ABBATE *et al.*, 2002; GABBIANI, 2003; DESMOULIÈRE *et al.*, 2003). Recently, WU *et al.* (2013) has demonstrated that TGF- β 1 released from the injured kidney tubular epithelial cells stimulated pro-fibrotic cytokine production that promoted the proliferation and transition of pericytes to myofibroblasts. Pro-fibrotic cytokine production was reversed by TGF- β receptor 1 kinase inhibitor SB431542 in TGF- β 1-treated tubular epithelial cells, showing the importance role of TGF- β 1 and tubular epithelial cells in kidney fibrosis. Besides, TGF- β 1 upregulates expression of fibronectin and its integrin receptors was observed in lung fibroblasts which is linked to the induction of myofibroblast differentiation (THANNICKAL *et al.*, 2003). Conversely, α - and γ -interferon (IFN) decrease the expression of α -SMA in myofibroblasts by either transdifferentiating them back to the fibroblast state or by down-regulating the amount of α -SMA in the cell (POWELL, 2000).

3.1.1 Distribution of PARs

The widespread tissue distribution of PARs strongly implies their potential roles in a variety of biological processes (**Tables 3.1** and **Table 3.2**). However, the specificities of these remain to be fully elucidated. PARs are self-activated by a tethered ligand that becomes exposed after extracellular N-terminal cleavage by proteinase. PAR activation depends on the concentration of the active enzyme and agonist in the extracellular fluid and the existence of uncleaved PARs at the surface of the target cells where they can be activated by proteolysis and coupled to signalling pathways (DÉRY *et al.*, 1998).

Table 3.1: PAR Distribution.

PAR	Tissues	References
PAR ₁	Lung airway, platelets, kidney, nervous system, immune system, cardiomyocytes	CHAMBERS <i>et al.</i> (2000); VU <i>et al.</i> (1991a) CUNNINGHAM <i>et al.</i> (2000) CONANT <i>et al.</i> (2002) ROCHE <i>et al.</i> (2003); SABRI <i>et al.</i> (2002)
PAR ₂	Lung airway, kidney, cardiovascular system, platelets, nervous system	AKERS <i>et al.</i> (2000); BERTOG <i>et al.</i> (1999) KOO <i>et al.</i> (2002); STORCK <i>et al.</i> (1996) LOURBAKOS <i>et al.</i> (2001) OKAMOTO <i>et al.</i> (2001b)
PAR ₃	Lung airway, platelets, immune system	RAMACHANDRAN <i>et al.</i> (2006) ISHIHARA <i>et al.</i> (1997) BAR-SHAVIT <i>et al.</i> (2002)
PAR ₄	Lung airway, platelets, endothelium	ASOKANANTHAN <i>et al.</i> (2002) SAMBRANO <i>et al.</i> (2000) HAMILTON <i>et al.</i> (2001); SABRI <i>et al.</i> (2003a)

3.2 Aims

This chapter aims to:

1. Establish human primary bronchial and renal fibroblast cultures from bronchial sections and renal tissue explants, respectively.
2. Study the fibroblastic phenotype of the cultured cells through staining with fibroblast specific markers.
3. Examine the expressions of PARs in these cultured cells.
4. Differentiate fibroblasts into myofibroblasts by treatment with TGF- β 1.
5. Characterise the myofibroblasts through staining with α -SMA and Western blotting.

Table 3.2: PARs on Fibroblasts in Different Tissues.

PAR	Cell Types	References
PAR ₁	Human bronchial fibroblast, gingival fibroblast, cardiac fibroblast, synovial fibroblasts, human kidney glomerular mesangial cells, rat kidney glomerular epithelial, rat kidney mesangial cells.	RAMACHANDRAN <i>et al.</i> (2006) HOU <i>et al.</i> (1998) SABRI <i>et al.</i> (2002) HIRANO <i>et al.</i> (2002) CHOUDHURY <i>et al.</i> (1996) LAPING <i>et al.</i> (1997)
PAR ₂	Human bronchial fibroblast, mouse kidney cortical duct cells rat kidney afferent arteriole	RAMACHANDRAN <i>et al.</i> (2006) AKERS <i>et al.</i> (2000) BERTOG <i>et al.</i> (1999) TROTTER <i>et al.</i> (2002)
PAR ₃	Human bronchial fibroblast	RAMACHANDRAN <i>et al.</i> (2006)
PAR ₄	Human bronchial fibroblast	ASOKANANTHAN <i>et al.</i> (2002)

3.3 Methods

3.3.1 Cell Culture

HPBFs and HPRFs were cultured as described in **Section 2.2**. Fibroblasts between passages 2 and 5 at 80-95% confluence were used for all of the experiments described in this Chapter.

3.3.2 Immunocytochemical Staining

HPBFs and HPRFs were stained as described in **Section 2.7**.

To stain for fibroblastic markers, anti-prolyl 4-hydroxylase (5 μ g/ml) or monoclonal anti-vimentin (0.25 mg/ml) antibodies were used. The isotype matched IgG1 (for prolyl 4-hydroxylase staining) or mouse ascitic fluid IgM (for vimentin staining) was used as a negative control. The secondary antibody, biotinylated goat anti-mouse antibody was used at 1:100 dilution. The PAR antibodies were used according to **Table 3.3**.

Table 3.3: Immunocytochemical Staining for PARs Expression.

PAR	Primary Antibody	Isotype antibody	Secondary antibody
PAR ₁	PAR ₁ (10 µg/ml)	IgG1 (10 µg/ml)	biotinylated goat anti-mouse antibody (1:100)
PAR ₂	PAR ₂ (10 µg/ml)	IgG2a (10 µg/ml)	biotinylated goat anti-mouse antibody (1:100)
PAR ₃	PAR ₃ (10 µg/ml)	Rabbit IgG (10 µg/ml)	biotinylated goat anti-rabbit antibody (1:100)
PAR ₄	PAR ₄ (10 µg/ml)	Goat IgG (10 µg/ml)	biotinylated rabbit anti-goat antibody (1:100)

3.3.3 PAR₄ Induction Assay

Cells were placed into 25 cm² flasks and allowed to grow to 70-80% confluence. The cells were then quiesced in serum free media for 24 h (see **Section 2.3**) before treatment with LPS (100 ng/ml) for 24 h as described in RAMACHANDRAN *et al.* (2007).

3.3.4 RT-PCR Detection of PARs

Fibroblasts were cultured in 25 cm² flasks with 5 ml of fibroblast growth medium. Total RNA was extracted and reverse transcription of HPBF and HPRF mRNA were carried out as described in **Sections 2.4** and **2.5**. 2 µg of cDNA product was subsequently used in the PCR reaction in the final volume of 50 µl in TC-3000 Personal 25-well Thermal Cycler (Bibby Scientific, UK) as described in (see **Section 2.6**).

Primers were ordered according to the published sequences in RAMACHANDRAN *et al.* (2006), except that PAR₄ was designed using Primer-BLAST. All primers were synthesized by MWG Eurofins. The sequences of oligonucleotides used to amplify PARs and β -actin are summarised in **Table 3.4**. The PCR products were analysed as described in **Section 2.6**.

Table 3.4: PCR Primer Sequences for PAR and β -actin.

Target	Primer Sequence	Product Size
PAR ₁	5'-CACGGATCCTATTTTTCCGGCAGTGATTGG-3' 3'-CACGAATTCTCAAATGATAGACACATAACAGACCCT-5'	450 bp
PAR ₂	5'-TGAAGATTGCCTATCACATAC-3' 3'-GGCTCTTAATCAGAAAATAATGCA-5'	550 bp
PAR ₃	5'-TCCCCTTTTCTGCCTTGGAAG-3' 3'-AAACTGTTGCCCACACCAGTCCAC-5'	500 bp
PAR ₄	5'-TCACCTGCCTGGCGCTGTTG-3' 3'-CGTTGGAAGAGCCCTGCCCCG-5'	340 bp
β -actin	5'-CGTGGGCCGCCCTAGGCACCA-3' 3'-TTGGCCTTAGGGTTCAGGGGG-5'	242 bp

3.3.5 Intracellular Calcium Mobilisation Assay

Calcium signalling assay was performed as described in **Section 2.9**. Agonists used were: PAR₁ AP (TFLLRN), 100 μ M; PAR₂ AP (SLIGKV), 100 μ M; and PAR₄ AP (AYPGQV), 100 μ M. As the peptides were reconstituted in 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid (HEPES), this was used as a negative control.

3.3.6 TGF- β 1 Treatment for Immunofluorescent Staining of α -SMA

HPBFs and HPRFs were seeded on coverslips and grown in 6-well plates with 2 ml of fibroblast complete growth media. Once reaching the desired confluency (80%), cells were treated with TGF- β 1 (10 ng/ml) for 24 h before proceeding for staining as described in **Section 2.8**.

3.3.7 Preparation of Whole Cell Lysates

HPBFs or HPRFs were passaged into 25 cm² culture flasks and allowed to reach over 70% confluence. Once reaching the desired confluency, cells were treated with TGF- β 1 (10 ng/ml) for 24 h. Cells were then harvested by centrifugation at $500 \times g$ for 5 min and lysed by adding 500 μ l Laemilli's sample buffer as described in **Section 2.10**.

3.3.8 SDS-PAGE and Western Blotting

Protein samples were separated on a 12.5% SDS-PAGE gel before transferring to a nitrocellulose membrane using the i-blot system (Invitrogen, UK) as described in **Sections 2.11** and **2.12**. The membrane was then blocked with 5% milk solution, incubated with primary and secondary antibodies as described in **Section 2.12**. Finally, the blot was visualised using the ECL detection system as describe in **Section 2.12** .

For PAR blots, primary antibodies were: mouse anti-human PAR₁ (1:200), mouse anti-human PAR₂ (1:200), rabbit anti-human PAR₃ (1:200) and rabbit anti-human PAR₄ (1:200); secondary antibody was: donkey anti-mouse HRP (PAR₁ and PAR₂) and donkey anti-rabbit HRP (PAR₃ and PAR₄).

For collagen type I and α -SMA blots, primary antibodies were: rabbit polyclonal anti- α -SMA (1:100) and rabbit polyclonal anti-collagen type I (1:5000); secondary antibody was: donkey anti-rabbit HRP (1:5000).

For α -tubulin loading control, mouse monoclonal IgG1 anti- α -tubulin (1:1000) was used as the primary antibody and goat anti-mouse IgG HRP (1:2000) was used as secondary antibody.

3.4 Results

3.4.1 HPBFs and HPRFs stain positively for Fibroblast Specific Markers

To study the fibroblastic phenotypes of the cultured cells, immunocytochemical stainings using the fibroblast specific markers anti-prolyl 4-hydroxylase and anti-vimentin antibodies were performed. Both HPBFs and HPRFs cultures showed no detectable staining with the negative control antibodies (**Figure 3.3A & B**; and **Figure 3.4A & B**). HPBFs and HPRFs were positively stained by the anti-prolyl 4-hydroxylase and anti-vimentin antibodies (**Figure 3.3C & D**; and **Figure 3.4C & D**), showing the characteristic fibroblastic phenotypes.

3.4.2 PARs detected by RT-PCRs in HPBFs and HPRFs

RT-PCRs were performed to investigate PAR expression in fibroblasts. RT-PCR of cDNAs derived from confluent HPBFs indicated mRNA expressions for PAR₁, PAR₂ and PAR₃ but not PAR₄ (**Figure 3.5A**). The intensities of the bands for PAR₁ and PAR₃ were higher than that for PAR₂. Prior to certain experiments, fibroblasts were cultured in a serum free media consisting of fibroblast growth media supplemented with antibiotic/antimycotic only. Thus, RT-PCR on cDNAs isolated from HPBFs that had been placed in serum free media for 24 h was performed to investigate whether PAR expression was altered when quiesced compared to fibroblasts grown in full growth media. There was no detectable difference in the PAR mRNA expression profile for quiescent HPBFs (**Figure 3.5B**) compared to that for HPBFs in full growth media (**Figure 3.5A**). In PAR₄ induction experiments, HPBFs were treated with LPS (100 ng/ml) for 24 h before mRNA extraction. mRNA expression for PAR₄ was not consistent.

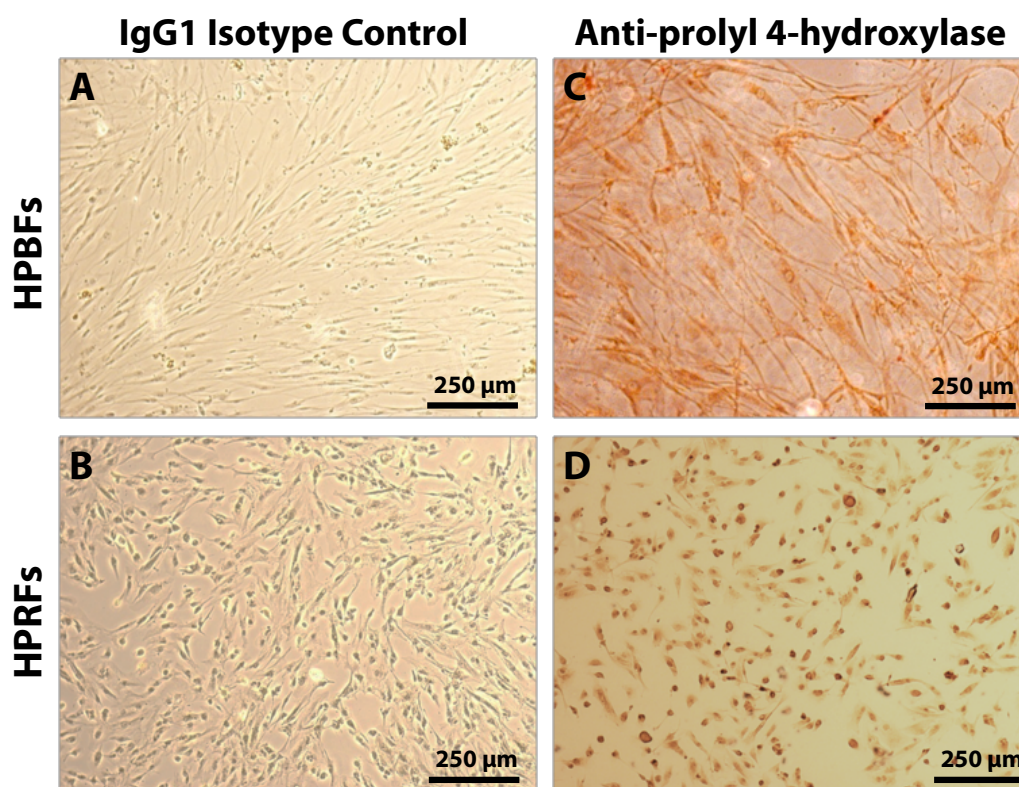


Figure 3.3: HPBFs and HPRFs were Positively Stained for Prolyl 4-hydroxylase. HPBFs and HPRFs were seeded on cover slips and grown in 6-well plates with 2 ml of fibroblast complete growth medium. Once confluent, cells were fixed with 4% paraformaldehyde, permeabilised with 0.1% Triton X-100 and blocked with 1% BSA/PBS. Cells were then incubated with the relevant isotype controls (A & B) or anti-prolyl 4-hydroxylase antibody (C & D). A secondary antibody conjugated to biotin was used to detect primary antibody. Streptavidin and DAB development were used to detect secondary antibody binding. Positive staining is indicated by the development of a brown colour. Results are representative of five independent experiments.

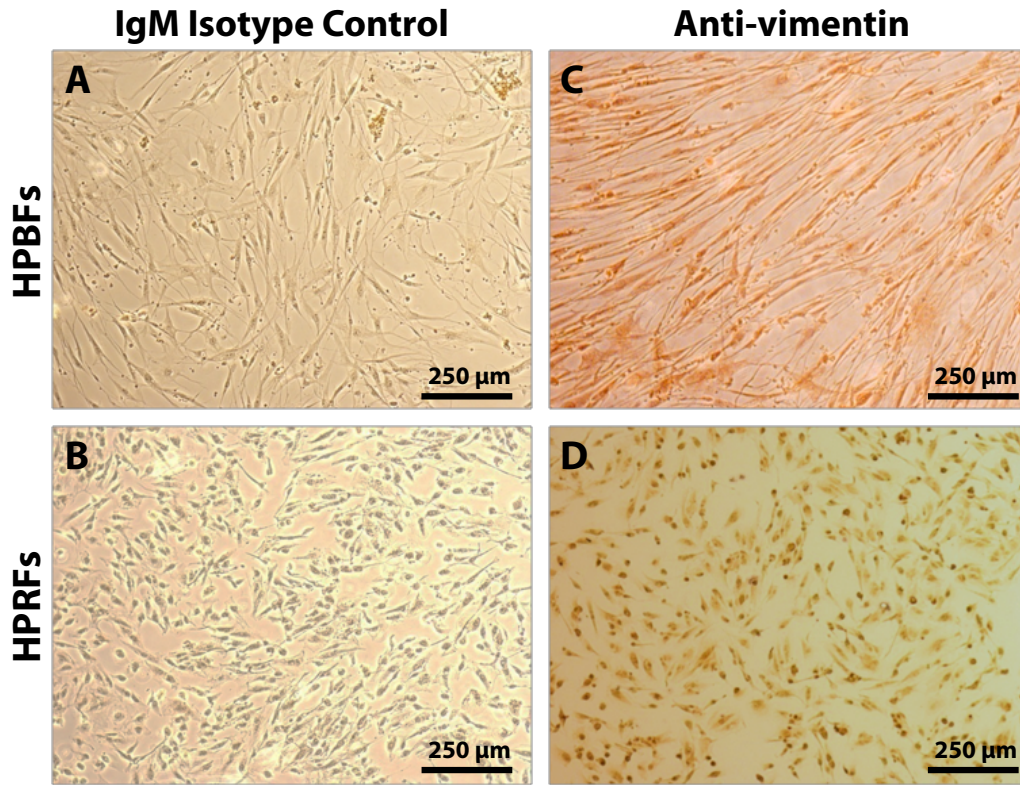


Figure 3.4: HPBFs and HPRFs were Positively Stained for Vimentin. HPBFs and HPRFs were seeded on cover slips and grown in 6-well plates with 2 ml of fibroblast complete growth medium. Once confluent, cells were fixed with 4% paraformaldehyde, permeabilised with 0.1% Triton X-100 and blocked with 1% BSA/PBS. Cells were then incubated with the relevant isotype controls (A & B) or anti-vimentin antibody (C & D). A secondary antibody conjugated to biotin was used to detect primary antibody. Streptavidin and DAB development were used to detect secondary antibody binding. Positive staining is indicated by the development of a brown colour. Results are representative of five independent experiments.

Over ten independent experiments, the PAR₄ band was observed only in three experiments (for example, **Figure 3.5C**), but not in the remaining seven experiments. No band was observed in the negative controls where reverse transcriptase (RT) enzyme or no template control reactions (NTC) where cDNA was omitted. See **Section 2.6** .

To ensure the PAR₄ primers were functional, LN CAP cells (androgen-sensitive human prostate adenocarcinoma cells derived from a left supraclavicular lymph node metastasis) were used as a positive control. LN CAP cells are known to express PAR₁, PAR₂ and PAR₄. RT-PCR of cDNAs derived from confluent LN CAP cells showed mRNA expressions for PAR₁, PAR₂ and PAR₄ but not PAR₃ (**Figure 3.6**), indicating that the PAR₄ primers were functional.

For HPRFs, RT-PCR of cDNAs derived from cell cultures showed mRNA expressions of PAR₁ and PAR₂ but not PAR₃ and PAR₄ (**Figure 3.7A**). In addition, RT-PCR of cDNAs isolated from HPRFs that had been placed in serum free media for 24 h was carried out. The mRNA expression profiles for quiescent HPRFs and HPRFs grown in full growth media were comparable (**Figures 3.7A & 3.7B**). In PAR₄ induction experiments, no mRNA expression for PAR₄ was detected (**Figure 3.7C**), indicating that renal fibroblasts do not express PAR₄ after LPS stimulation.

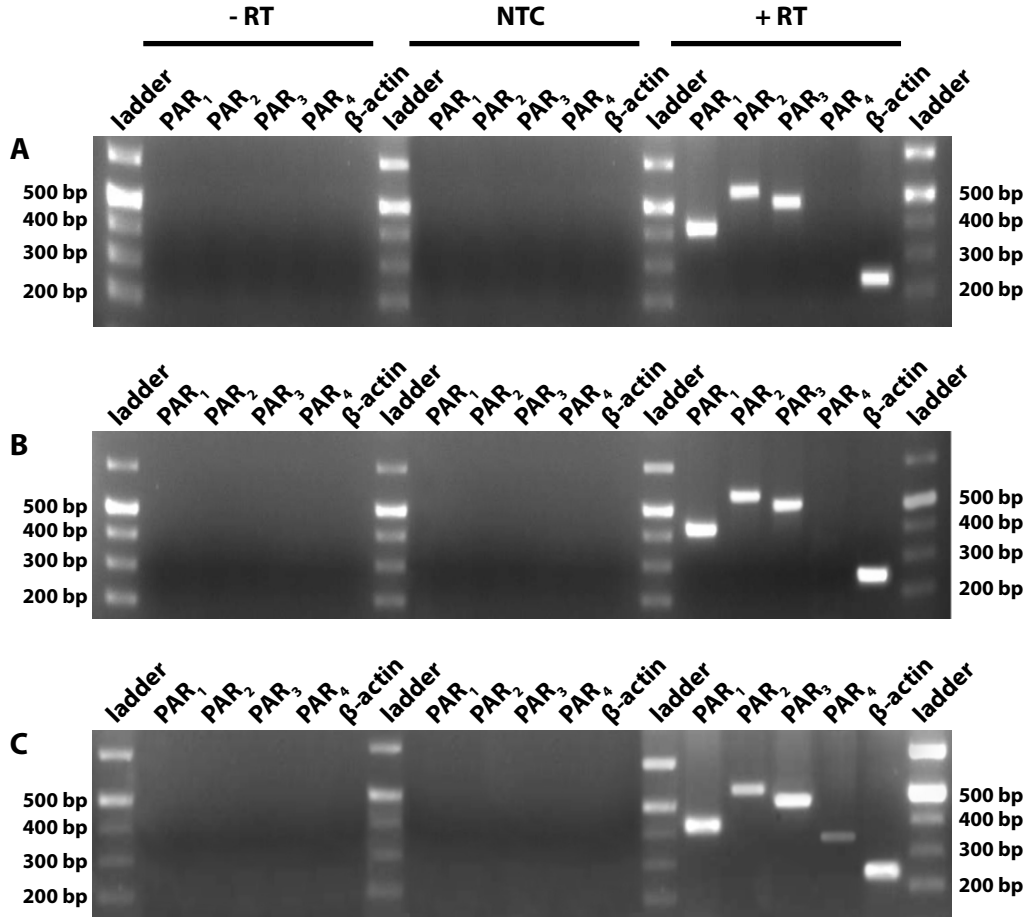


Figure 3.5: RT-PCR Detection of PAR mRNA in HPBFs. HPBFs were cultured in (A) Complete growth media; (B) Serum free media for 24 h; (C) LPS (100 ng/ml) under serum free condition. RNAs were extracted and reverse transcribed. PCR was carried out for 35 cycles using primers specific to PAR₁, PAR₂, PAR₃ or PAR₄. β -actin primers were included as a positive control. No template controls (NTC) and no reverse transcriptase (-RT) samples were included. Expected band sizes: PAR₁ (450 bp), PAR₂ (550 bp), PAR₃ (500 bp), PAR₄ (340 bp) and β -actin (242 bp). Results are representative of ten independent experiments performed with HPBFs cultured from ten different tissue samples.

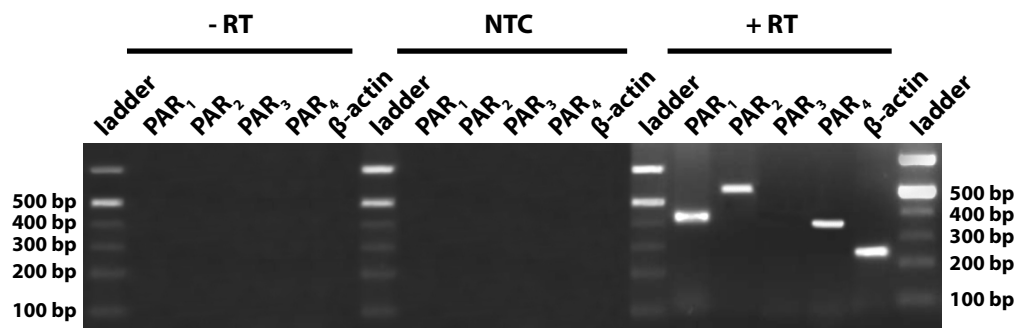


Figure 3.6: RT-PCR Detection of PAR₄ mRNA in LN-CAP cells. RNAs were extracted and reverse transcribed by RT-PCR (35 cycles) using primers specific to PAR₁, PAR₂, PAR₃ or PAR₄. β -actin primers were included as a positive control. No template controls (NTC) and no reverse transcriptase (-RT) samples were included as negative controls. Expected band sizes: PAR₁ (450 bp), PAR₂ (550 bp), PAR₃ (500 bp), PAR₄ (340 bp) and β -actin (242 bp). Results are representative of three independent experiments.

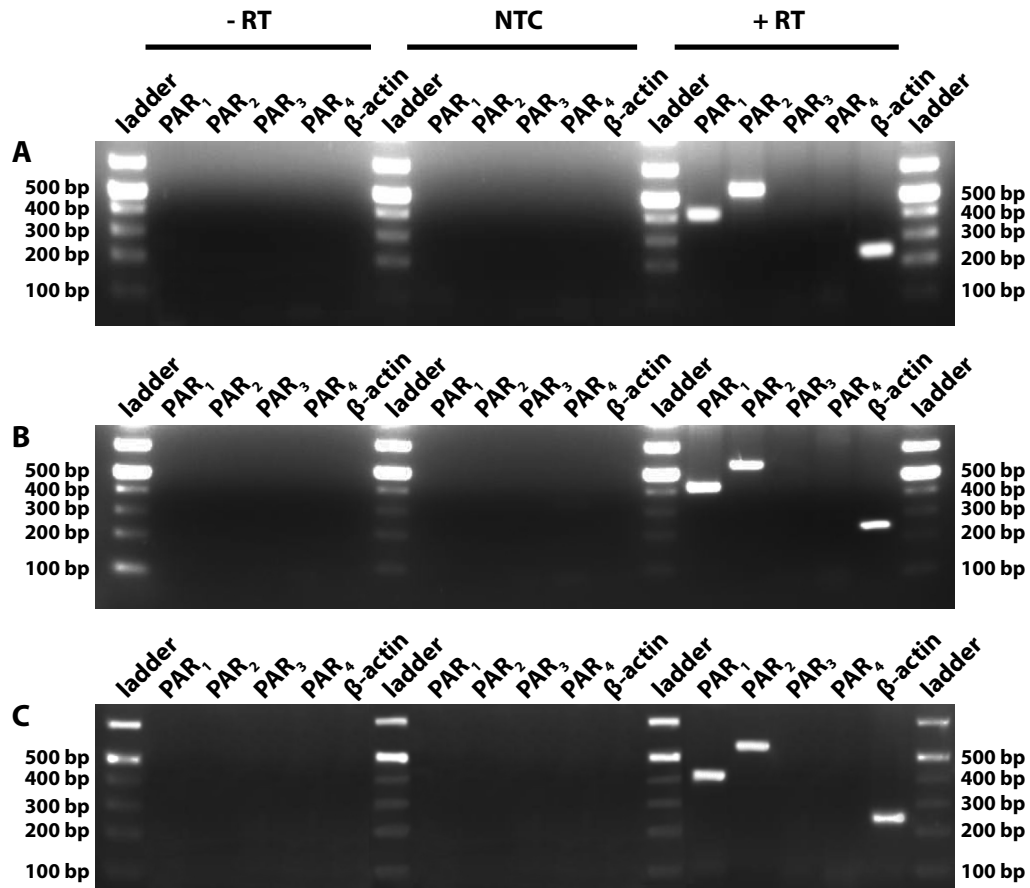


Figure 3.7: RT-PCR Detection of PAR mRNA in HPRFs. HPRFs were cultured in (A) Complete growth media; (B) Serum free media for 24 h; (C) LPS (100 ng/ml) under serum free condition. RNAs were extracted and reverse transcribed. PCR was carried out for 35 cycles using primers specific to PAR₁, PAR₂, PAR₃ and PAR₄. β -actin primers were included as a positive control. No template controls (NTC) and no reverse transcriptase (-RT) samples were included. Expected band sizes: PAR₁ (450 bp), PAR₂ (550 bp), PAR₃ (500 bp), PAR₄ (340 bp) and β -actin (242 bp). Results are representative of ten independent experiments performed with HPBFs cultured from ten different tissue samples.

3.4.3 Detection of PARs on HPBFs and HPRFs by Calcium Assay

Western blotting analysis failed to detect expression of PAR proteins despite including lysates of cells which have been previously shown to express PARs (**Figure 3.8**). Therefore, an intracellular calcium mobilisation assay was performed to confirm the presence of active PARs in HPBFs and HPRFs. However, PAR₃ expression could not be investigated using this assay because there is no available known PAR₃ AP. Both PAR₁ AP and PAR₂ AP caused elevations in intracellular calcium levels in both HPBFs (**Figure 3.9B & 3.9C**) and HPRFs (**Figure 3.9G & 3.9H**), indicating that PAR₁ and PAR₂ are expressed and functional in these cells. For PAR₄, only HPBFs treated with LPS for 24 h showed an increase in the calcium level (**Figure 3.9E & 3.9J**). HEPES was used as a negative control and no calcium increase was observed (**Figure 3.9A & 3.9F**). These results are consistent with the findings by RT-PCRs (**Figures 3.5 & 3.7**).

3.4.4 Immunocytochemical Staining of PARs in HPBFs and HPRFs

As PAR₃ could not be studied using a calcium mobilisation assay, immunocytochemical staining using DAB was performed. HPBFs were positively stained by PAR₁, PAR₂ and PAR₃ antibodies. LPS-treated HPBFs were also positively stained by the PAR₄ antibody (**Figures 3.10**). Consistent with the RT-PCR results, HPRFs were only positively stained by PAR₁ and PAR₂ antibodies (**Figures 3.11**).

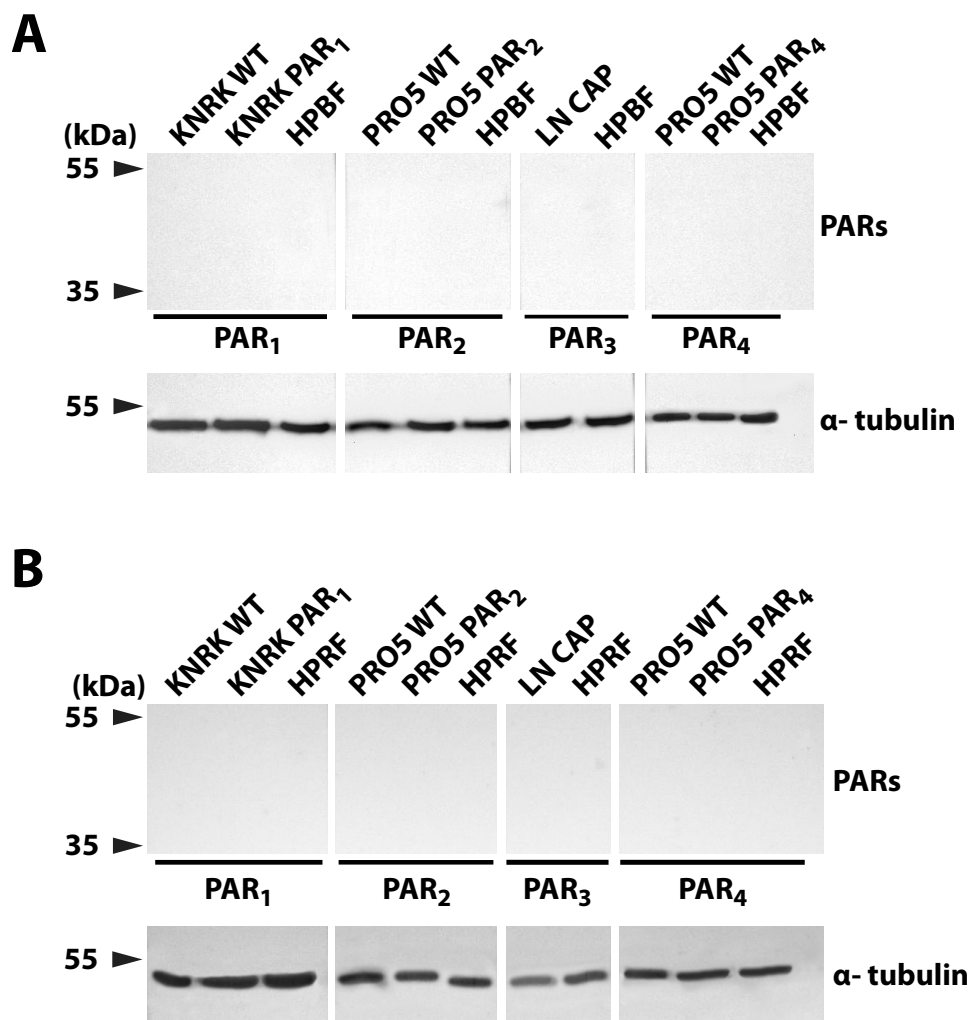


Figure 3.8: Western Blot Detection of PAR Expression. (A) HPBFs and (B) HPRFs were analysed for the expression of PARs. Various cell lines expressing different PARs (along with the corresponding WT cells which do not express PARs as negative controls) were included as controls. Cell lysates were obtained and then subjected to SDS-PAGE followed by immunoblotting with antibodies against PAR₁ (ATAP2), PAR₂ (SAM11), PAR₃ (H-103) and PAR₄ (C-20). α -tubulin was used as a loading control. 20 μ g of protein was loaded to each lane. Expected band sizes: PAR₁ ~47 kDa, PAR₂ ~44 kDa, PAR₃ ~43 kDa, PAR₄ ~38 kDa and α -tubulin ~52 kDa. Results are representatives of two independent experiments.

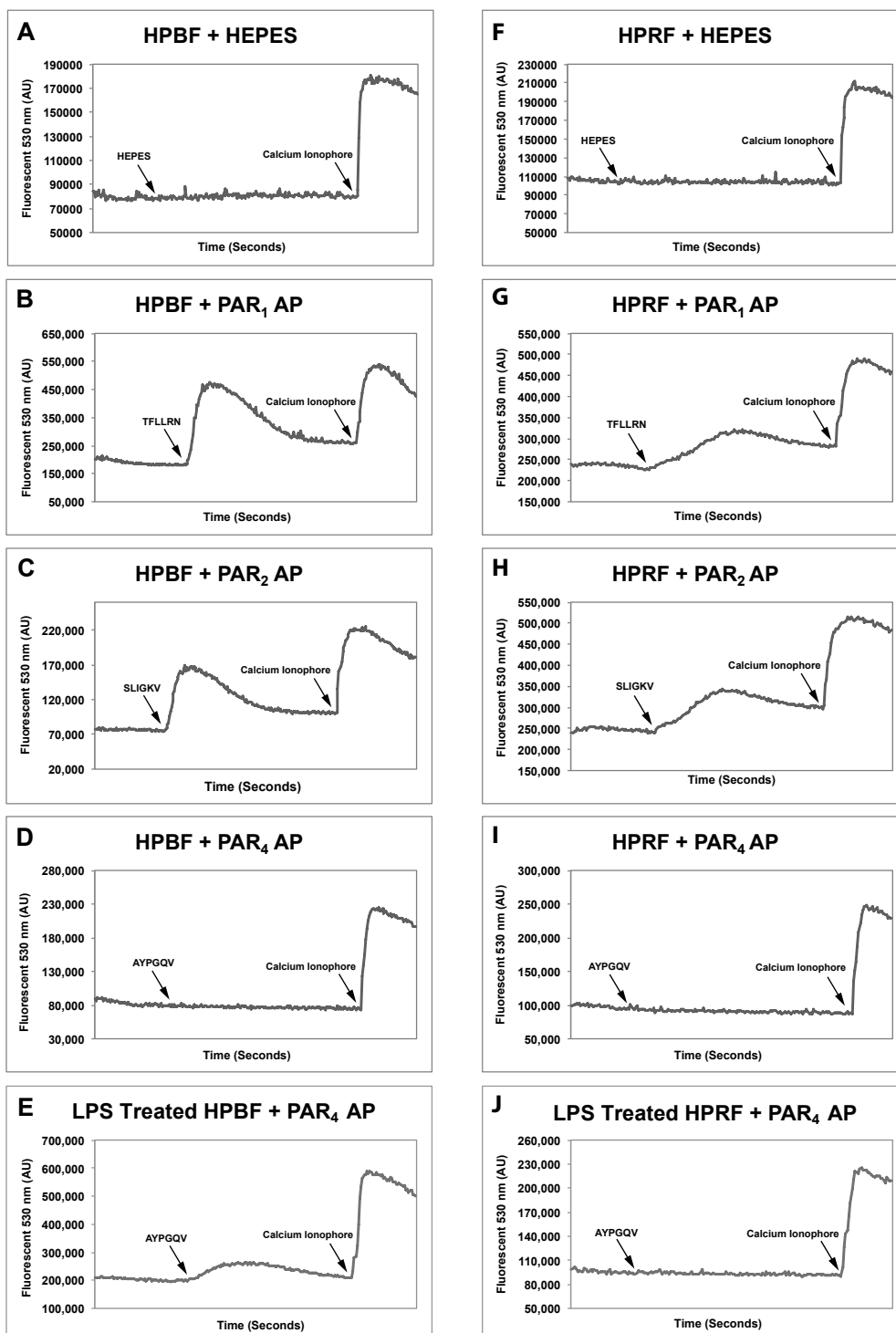


Figure 3.9: Calcium Responses to PAR Agonists in HPBFs and HPRFs.

Cells at 70-85% confluence in 75 cm² flasks were harvested and incubated with Fluo-3 AM at room temperature for 25 min. Cells were then washed and resuspended in calcium assay buffer. Functional PAR activities were assessed by treating (A–E) HPBFs or (F–J) HPRFs with (A & F) HEPES as negative control, (B & G) PAR₁ AP (TFLLRN, 100 μ M), (C & H) PAR₂ (SLIGKV, 100 μ M), (D & I) PAR₄ (AYPGQV, 100 μ M), and, (E & J) PAR₄ (AYPGQV, 100 μ M). In E and J, the cells were pre-treated with LPS before the calcium assay. An increase in fluorescence (E530) monitored by fluorescence spectrophotometer is indicative of calcium mobilisation. Arrows indicate the time when test agonists were added. These results represent data from three independent experiments.

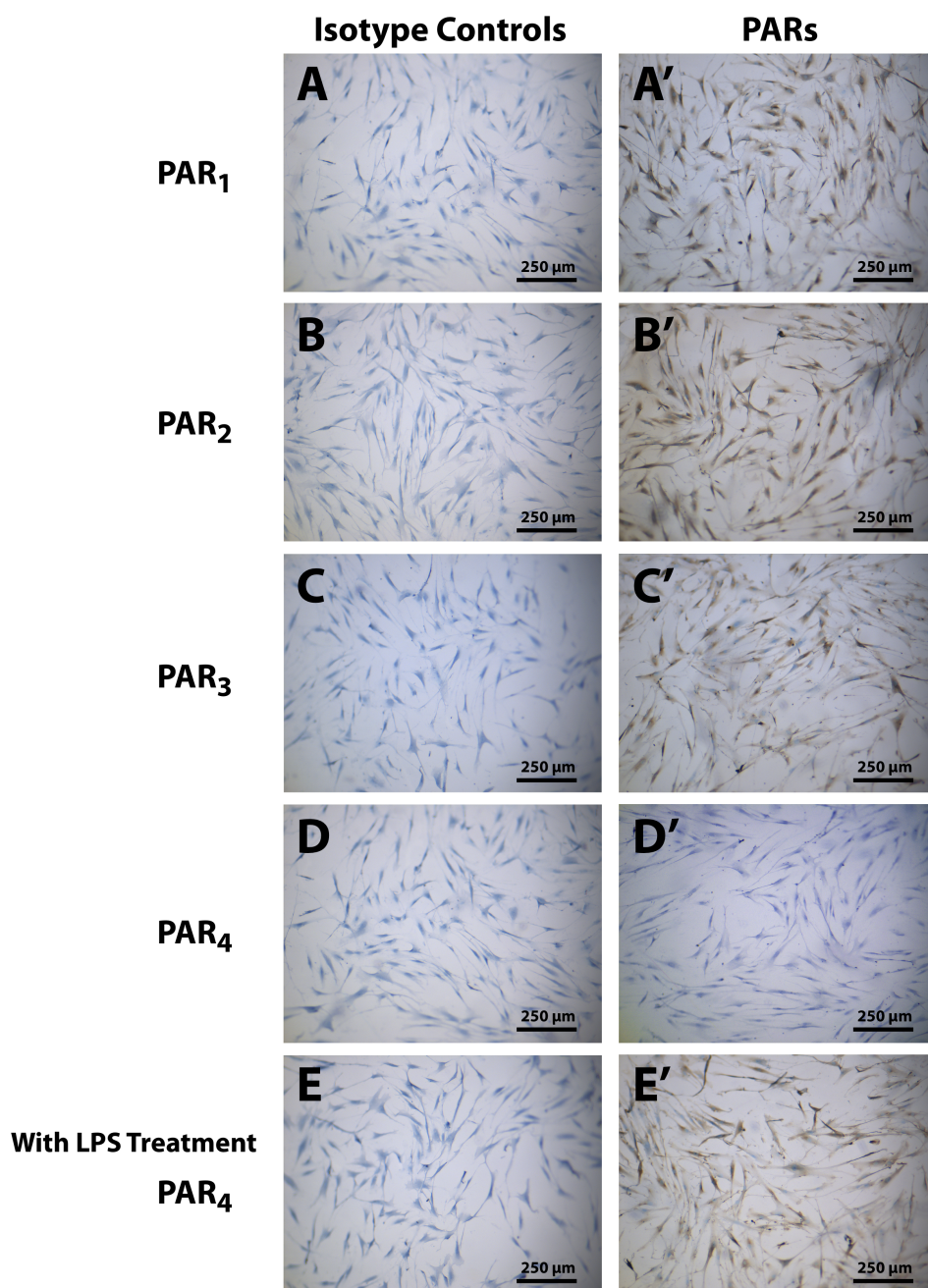


Figure 3.10: Immunocytochemical Staining of PARs in HPBFs. HPBFs were seeded on cover slips and grown in 6-well plates with 2 ml of fibroblast complete growth medium. For PAR₄ induction, quiescent HPBFs were treated with LPS (100 ng/ml) for 24 h. After blocking with 1% BSA/PBS, HPBFs were stained with primary antibodies: (A) Mouse IgG1, (A') PAR₁ (ATAP2), (B) Mouse IgG2a, (B') PAR₂ (SAM11), (C) Rabbit IgG, (C') PAR₃ (H-103), (D) Goat IgG, (D') PAR₄ (C-20), (E) Goat IgG, and, (E') PAR₄ (C-20). A secondary antibody conjugated to biotin was used to detect primary antibody. Streptavidin and DAB development were used to detect secondary antibody binding. Positive staining is indicated by the development of a brown colour. All samples were also counterstained with haematoxylin. Left panels (A–E) are the isotype controls for corresponding anti-PAR antibodies. E and E' represent HPBFs treated with LPS. These pictures represent results from three independent experiments.

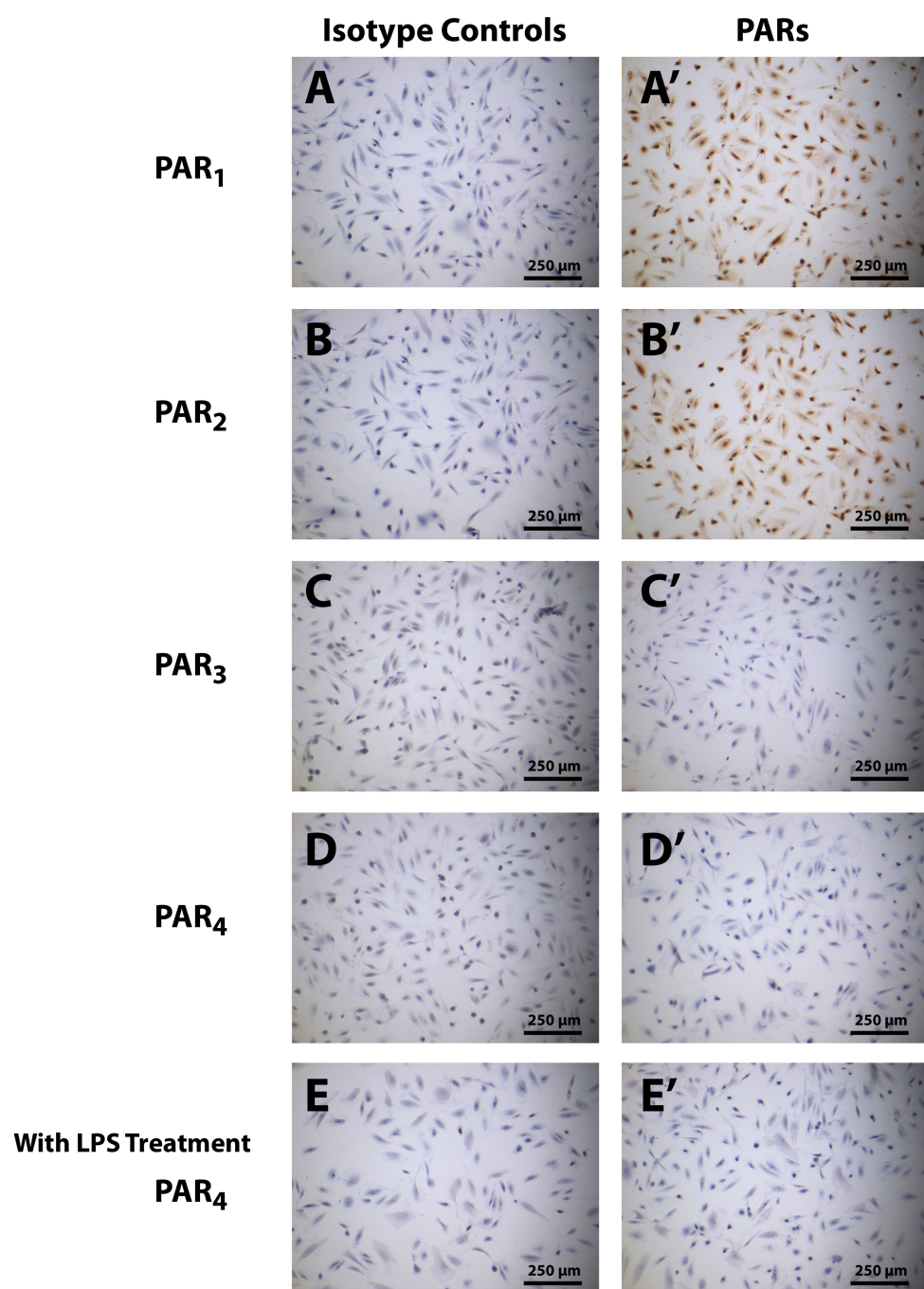


Figure 3.11: Immunocytochemical Staining of PARs in HPRFs. HPRFs were seeded on cover slips and grown in 6-well plates with 2 ml of fibroblast complete growth medium. For PAR₄ induction, quiescent HPBFs were treated with LPS (100 ng/ml) for 24 h. HPRFs were stained with primary antibodies: (A) Mouse IgG1, (A') PAR₁ (ATAP2), (B) Mouse IgG2a, (B') PAR₂ (SAM11), (C) Rabbit IgG, (C') PAR₃ (H-103), (D) Goat IgG, (D') PAR₄ (C-20), (E) Goat IgG, and, (E') PAR₄ (C-20). A secondary antibody conjugated to biotin was used to detect primary antibody. Streptavidin and DAB development were used to detect secondary antibody binding. Positive staining is indicated by the development of a brown colour. All samples were also counterstained with haematoxylin. Left panels (A–E) are the isotype controls for corresponding anti-PAR antibodies. E and E' represent HPBFs treated with LPS. These pictures represent results from three independent experiments.

3.4.5 Immunofluorescent Characterisation of Human Lung and Renal Myofibroblasts

TGF- β is the most potent inducer of α -SMA expression and fibroblast to myofibroblast differentiation, Therefore, TGF- β 1 was used to stimulate differential expression of α -SMA in HPBFs and HPRFs. Various concentrations of TGF- β 1 were used in order to determine the optimal concentration for the induction of α -SMA expression (See **Appendix**). The effect of TGF- β 1 (10 ng/ml) addition to the culture medium was examined on the phenotypic transformation of fibroblasts to myofibroblasts. Immunofluorescent staining with anti- α -SMA antibody showed increases in the levels of α -SMA in TGF- β 1-treated HPBFs and HPRFs in comparison to the untreated controls (**Figure 3.12**).

3.4.6 TGF- β 1 induces Collagen Type I and α -SMA expressions in lung and renal fibroblasts

In order to confirm the results above, Western blot analysis was performed using collagen type I and α -SMA antibodies. Untreated fibroblasts or fibroblasts treated with 10 ng/ml TGF- β 1 were used. TGF- β 1-treated fibroblasts exhibited higher levels of collagen type I and α -SMA expression than untreated fibroblasts (**Figure 3.13**). Thus, this data further supports the finding that both lung and renal fibroblasts upregulate α -SMA and collagen type I in response to the stimulation of exogenously added TGF- β 1.

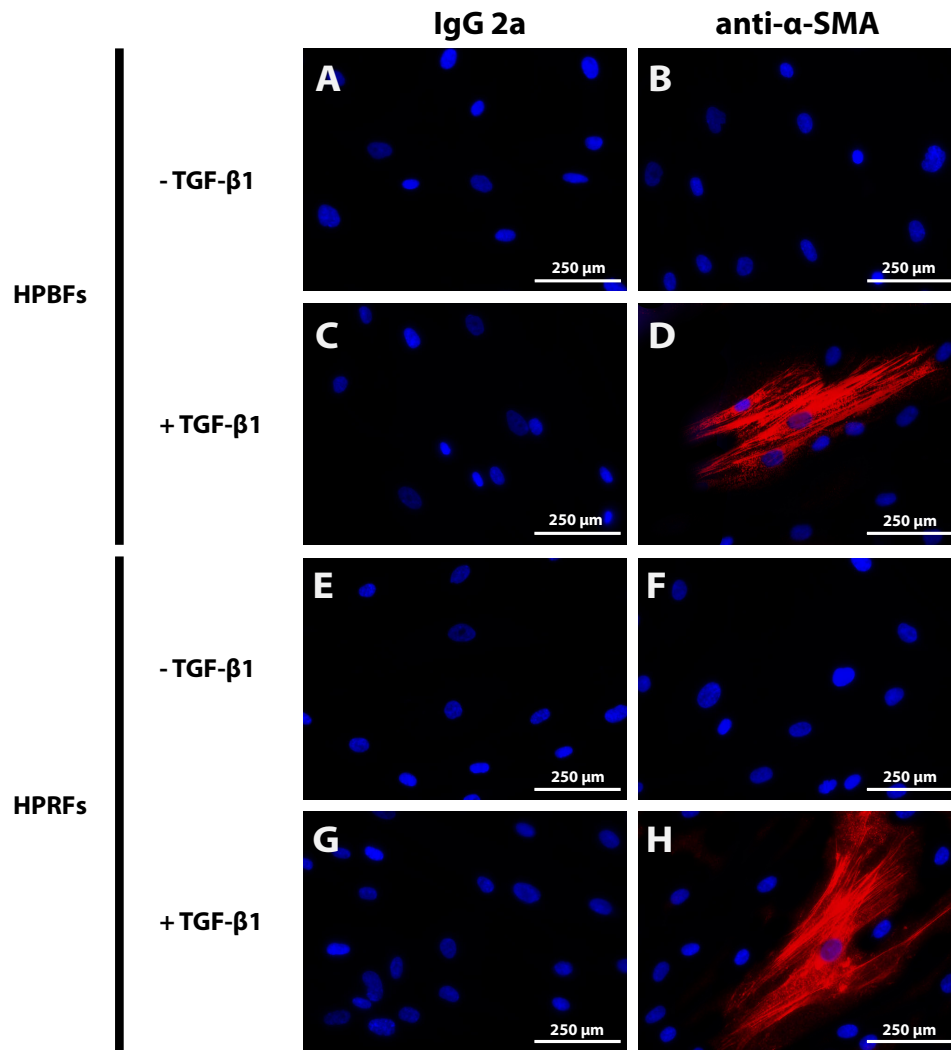


Figure 3.12: α -SMA expression increases in HPBFs and HPRFs after TGF- β 1 treatment. HPBFs and HPRFs were seeded on cover slips and grown in 6-well plates with 2 ml of fibroblast complete growth medium. For α -SMA expression induction, quiescent HPBFs and HPRFs were treated with TGF- β 1 (10 ng/ml) for 24 h. Cells were then fixed, permeabilised and blocked with 1% BSA/PBS. Untreated HPBFs (A & B) and HPRFs (E & F) were stained with (A & E) mouse IgG2a negative control antibody or (B & F) mouse anti- α -SMA antibody. Similarly, TGF- β 1-treated HPBFs (C & D) and HPRFs (G & H) were stained with (C & G) mouse IgG2a negative control antibody (D & H) or mouse anti- α -SMA antibody. All samples were also stained for nuclei (blue) using DAPI. Red depicts α -SMA. These images represent results from three independent experiments.

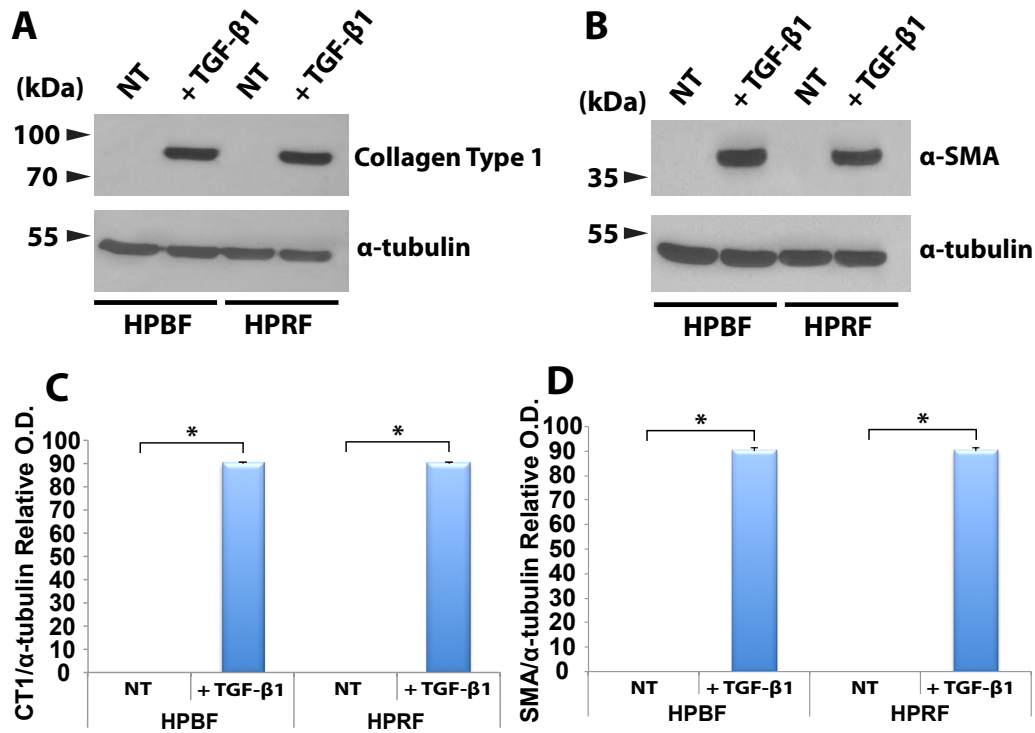


Figure 3.13: Collagen Type I and α -SMA are detected by Western blotting in TGF- β 1-treated HPBFs and HPRFs. Amounts of collagen type I (A & C) and α -SMA (B & D) in HPBFs and HPRFs, either untreated or treated with TGF- β 1, were analysed using Western blotting. Quiescent HPBFs and HPRFs were stimulated with TGF- β 1 (10 ng/ml) under serum free conditions for 24 h. Cell lysates were obtained and then subjected to SDS-PAGE followed by immunoblotting with antibodies against collagen type 1, α -SMA and α -tubulin. α -tubulin was used as a loading control. Expected band sizes: collagen type I (\sim 90 kDa), α -SMA (\sim 42 kDa) and α -tubulin (\sim 52 kDa). (C & D) Results were quantitated and summarised in a bar chart, where optical densities were normalised to α -tubulin loading controls. Results are expressed as mean \pm SEM of three independent experiments. * indicates $p < 0.05$ compared with untreated samples in paired t-test.

3.5 Discussion

The purity of confluent cultures of fibroblasts grown from finely dissected pieces of tissue in fibroblast growth media were assessed by their morphological appearance and immunocytochemical staining for the fibroblast specific markers: prolyl 4-hydroxylase and vimentin. Prolyl 4-hydroxylase is a critical enzyme for collagen formation. It is a putative marker of collagen producing cells and also a cytoplasmic marker of human fibroblasts (SMITH *et al.*, 1998). Vimentin is a member of the intermediate filament family of proteins. It is responsible for maintaining cell integrity and exists as a dynamic structure in fibroblasts (CLARKE and ALLAN, 2002). Although anti-vimentin antibody can react with the abundant intermediate filaments of fibroblasts, this antibody also labels the other cells types such as the vascular endothelial cells and the neurons that contain intermediate filaments. Given the morphology differences between these cell types, anti-vimentin is a suitable tool for reliable identification of fibroblasts (CAMELLITI *et al.*, 2005). In this study, along with the morphological appearance, both HPBFs and HPRFs were positively stained for prolyl 4-hydroxylase and vimentin, confirming the fibroblastic nature of these cells.

RAMACHANDRAN *et al.* (2006) have demonstrated that HPBFs express mRNA for PAR₁, PAR₂ and PAR₃, but not PAR₄. The RT-PCR results presented above are consistent with this previously published data. This observation was reproducible in different tissue samples. In contrast, the PAR expression profile in HPRFs is different from the one in HPBFs. The findings described herein demonstrate that only PAR₁ and PAR₂ were expressed in HPRFs. To date, there is no evidence that PAR₃ and PAR₄ are expressed in human renal fibroblasts. Interestingly, RT-PCR data in this study inconsistently showed that LPS induced PAR₄ expression in HPBFs. This is somewhat inconsistent with the previous findings that LPS reproducibly induced expression of functional PAR₄ in HPBFs under the

same experimental conditions (RAMACHANDRAN *et al.*, 2007). This difference might be due to several factors such as age, gender and smoking habit of the donors or underlying disease process. Besides, LPS treatment failed to induce PAR₄ expression in HPRFs, suggesting that there is no PAR₄ expression in human renal fibroblasts.

Reliable Western blot results could not be obtained using the anti-PAR antibodies available for this thesis in three different independent experiments (**Figure 3.8**). In contrast, BAE and REZAIE (2008); STRANDE and PHILLIPS (2009); BANFI *et al.* (2011); ZHANG *et al.* (2012) demonstrated positive Western blot results using the same PAR antibodies. This might be because different cell types were used in this thesis. Besides, the failure of the Western blotting for detecting PARs here might be due to insufficient amount of the proteins loaded (20 μ g total protein was used in this study). Also, the antibody may only effectively recognise PAR₄ protein in its native form. All of these could potentially cause the negative Western blot results. Hence, calcium assay and immunocytochemical staining using DAB were used to further confirm the PAR expressions in HPBFs and HPRFs. Following initial experiments, it was decided to use haematoxylin to facilitate the visualisation of cells stained with isotype controls.

Fibroblasts and myofibroblasts are often quiescent in nature. However, these cells become activated after injury. IPF and renal fibrosis strongly correlate with a substantial increase in the presence of activated fibroblasts in lung and kidney, respectively (POWELL, 2000). During wound healing, epithelial cells and myofibroblasts initially form a new basement membrane replacing the damaged membrane. Then, the epithelial stem cells undergo mitosis, proliferate and migrate along the newly formed basement membrane in response to various growth factors secreted by myofibroblasts. In order to limit the surface area of the damaged tissue, myofibroblasts are

connected to each other in a syncytium as they contain α -SMA and smooth muscle myosin isoforms. The ability of the myofibroblasts to contract the tissue mainly depends on the changes in the cellular cytoskeleton (the formation of stress fibres), the formation of the Rho-regulated focal contacts (fibronexus), and the integrin expression that allows attachment of the myofibroblasts to the ECM (POWELL, 2000). A few studies also suggested that the α -SMA expression is involved in the regulation of signal transduction and gene expression, including the ECM components, where α -SMA is found in abundance in areas of high ECM expression (LEIVONEN *et al.*, 2002; CHAQOUR *et al.*, 2006; WANG *et al.*, 2006). The number of myofibroblasts gradually decreases as the healing process of active fibrosis progresses to completion or termination. Persistence of the activated cells is associated with excessive collagen deposition and fibrosis (RAMOS *et al.*, 2006). Thus, a better understanding of the processes inducing the transformation of fibroblasts to myofibroblasts and the alterations of the biology of fibroblasts associated with this transformation are of great interest for drug discoveries.

Myofibroblasts are distinguishable from fibroblasts based on the expression and organisation of α -SMA (ZHANG *et al.*, 1994). The most widely used molecular marker for myofibroblast in research and clinical diagnostics is the *de novo* expression of α -SMA. Both HPBFs and HPRFs express little to no collagen type I and α -SMA in their resting state. However, upon activation *in vitro* or during disease, they highly express α -SMA along with extracellular mesenchymal matrix proteins collagen types I and III, and cellular fibronectin, which are the main features of myofibroblasts (BARNES and GORIN, 2011). Immunofluorescent staining results described in this chapter demonstrated that TGF- β 1-treated fibroblasts were stained positively for α -SMA. α -SMA-positive stress fibers appeared parallel to the long axis of the cells. These observations indicate that the cells have differentiated into myofibroblasts and are consisted with

the study demonstrated by SERPERO *et al.* (2006). This is further supported by Western blotting, which showed significant levels of collagen type I and α -SMA in TGF- β 1-treated fibroblasts but not in the untreated samples. In this study, collagen type I antibody was not used for the immunofluorescent staining because there might be cross reactivity with other forms of collagen in fibroblasts.

In conclusion, PAR₁, PAR₂ and PAR₃ are present in the human lung fibroblasts and only PAR₁ and PAR₂ are present in the human renal fibroblasts without LPS stimulation. The differences of PAR family expression in fibroblasts may be due to the different origins of the fibroblasts used. LPS was shown to induce PAR₄ expression in HPBFs but this was inconsistent. LPS did not induce PAR₄ in HPRFs. TGF- β 1 potently stimulates the production of collagen type I and α -SMA in both HPBFs and HPRFs. The levels of collagen type I and α -SMA for TGF- β 1 treated fibroblasts were significantly higher than that for untreated fibroblasts, suggesting that they differentiated into myofibroblasts. These results confirmed the ability of TGF- β 1 to stimulate α -SMA expression, consistent with its ability to promote myofibroblast differentiation.

Chapter 4

Generation of PAR₄-expressing Cell Line

4.1 Introduction

PAR₄ has a number of physiological roles. KAHN *et al.* (1998) first demonstrated that PAR₄ is an important thrombin receptor for the aggregation of both human and mouse platelets. Subsequently, SAMBRANO *et al.* (2001) demonstrated that mice lacking the PAR₄ gene showed an increased bleeding time, indicating the importance of PAR₄ signalling in coagulation events *in vivo*. PAR₄ is also present in endothelial cells and leukocytes (VERGNOLLE *et al.*, 2002).

With the exception of PAR₃, PARs can be activated by PAR APs. PAR APs are synthetic peptides having sequences designed based on the revealed tethered ligands that can activate the receptor. They mimic the PAR-mediated action of proteinases in a variety of tissues. These observations facilitate the study of the physiological and pharmacological properties of the PARs by investigating the potential consequences of activating PARs in bioassay systems *in vitro* and in *in vivo*. The synthetic PAR₄ AP (AYPGQV-NH₂) was designed based on the human PAR₄ tethered ligand sequence (HOLLENBERG and COMPTON, 2002).

PAR₄ AP is able to induce *in vivo* leukocyte rolling and adhesion to the endothelium in rat mesenteric venules, as monitored by intravital microscopy (VERGNOLLE *et al.*, 2002). The mechanisms by which PAR₄ recruits leukocytes to the inflammatory site via the endothelium is unknown, but PAR₄ has been detected by immunohistochemistry at the surface of neutrophils, endothelial cells and smooth muscle cells of the aorta in rats (VERGNOLLE *et al.*, 2002). These findings suggest that the pro-inflammatory effects of the PAR₄ agonists are mediated through PAR₄ activation on endothelial cells and/or leukocytes (VERGNOLLE *et al.*, 2002; KATAOKA *et al.*, 2003). HOLLENBERG *et al.* (2004) and HOULE *et al.* (2005) further demonstrated that PAR₄ plays a critical role in inflammatory responses. Activation of PAR₄ generates two hallmarks of the inflammatory response: oedema and granulocyte infiltration. PAR₄ AP caused oedema in rats (HOLLENBERG *et al.*, 2004) and increased the recruitment of granulocytes to the site of inflammation in the mouse paws (HOULE *et al.*, 2005). All of these observations strongly support a possible involvement of PAR₄ in inflammation.

PAR₄ is not expressed endogenously in human renal fibroblasts. To study the signaling pathway of PAR₄, a stable PAR₄-expressing cell line is generated in this chapter using HEK293 cells. HEK293 cells are a transformed cell line derived from human embryonic kidney cells with sheared adenovirus DNA. The exact origin of HEK293 cell is unknown and embryonic kidney cells may differentiate into a variety of cell types present in the body. They are polygonal in shape and exhibit epithelial morphology. They are semi-adherent cell line, they do not adhere well to culture plate and can easily detach. Because they are experimentally transformed, they are easy to culture and transfect and are commonly used as a model for examining a transfected receptor (THOMAS and SMART, 2005). HEK293 cells endogenously expressed PAR₁ and PAR₂ (GRISHINA *et al.*, 2005).

4.2 Aim

The aim of this chapter is to establish a stable PAR₄-expressing cell line using HEK293 cells.

4.3 Methods

4.3.1 Propagation of PAR₄-containing Plasmid

The plasmid containing pro-opiomelanocortin-AU1-hPAR₄ (POMC-AU1-hPAR₄) with the C-terminus tagged with a hemagglutinin 11(HA.11) epitope in pcDNA3.1 vector (**Figure 4.1**) was provided by Dr S. J. Compton and Dr Y. P. Xiao. The expected structure of this PAR₄ construct is depicted in **Figure 4.2**.

The bacterial transformation was carried out as per standard transformation protocol provided by Stratagene, UK. For each transformation, a 5 ml falcon tube was pre-chilled on ice before adding 50 μ l of XL1-Blue supercompetent *E. coli*. The cells were incubated on ice for 10 min with 0.5% β -mercaptoethanol, swirling at regular intervals. 1 μ l of vector DNA was added to the β -mercaptoethanol treated *E. coli*, swirled and incubated on ice for 30 min. The cells were then heat shocked at 42°C for 45 sec before placing back onto ice for further 2 min. 500 μ l of LB broth (pre-heated to 42°C) was then added and the cells were incubated at 37°C with shaking at 200 rpm for 60 min. After that, 4.5 ml of LB broth containing 5 μ l of 1 mg/ml ampicillin (100 μ g/ml final concentration in 5 ml) was added to 500 μ l of transformation reaction mixture and incubated at 37°C overnight.

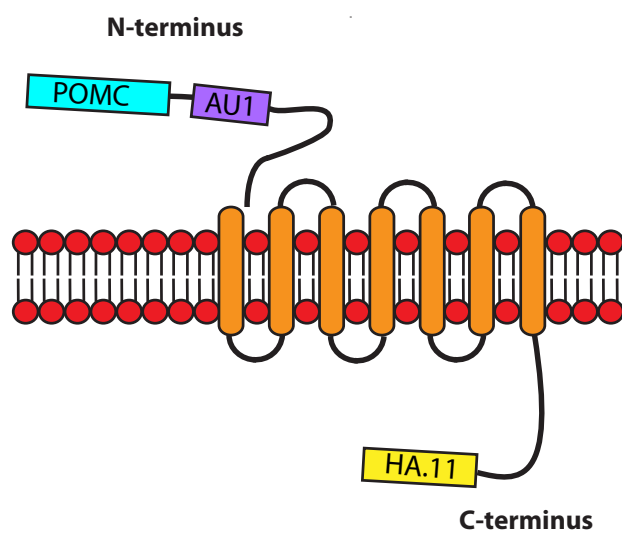


Figure 4.2: Schematic Structure of POMC-AU1-hPAR4-HA.11. The POMC signal peptide and AU1 are fused to the N-terminus and the HA.11 is fused to the C-terminus of hPAR4. The POMC signal peptide enables efficient expression of PAR4 whereas the AU1 and HA.11 epitope tags facilitate isolation and detection of the receptor.

Plasmid DNA was extracted from the overnight cultures using a Qiagen Miniprep Kit as per manufacturer’s instructions. To check if the purified plasmid contained the insert sequence, a restriction digest reaction was performed by incubating the reagents according to **Table 4.1** at 37°C for 1 h. Then, the sample was run on a 1.3% agarose gel alongside 1 kb Plus DNA Ladder. The DNA concentration was then determined using a Genequant spectrophotometer and an aliquot of the sample was sent to MWG Biotech for sequencing using T7 primers to further verify the insert.

Table 4.1: Reagent used in Restriction Digest Reaction.

Reagent	Volume	Final Concentration
10× NEB Buffer 2	2 μ l	1×
BSA	2 μ l	100 μ g/ml
Xho1	0.5 μ l	2000 U/ μ l
HindIII	0.5 μ l	2000 U/ μ l
Plasmid DNA	5 μ l	-
DEPC water	10 μ l	-

4.3.2 Preparation of PAR₄-expressing Cell Lines

4.3.2.1 Cell Culture

HEK293 cells were routinely maintained in DMEM complete growth medium containing in v/v 10% FBS, 1% sodium pyruvate, and 1% antibiotic/antimycotic (penicillin G sodium, streptomycin sulphate and amphotericin B).

The cells were harvested by washing with 5 ml of PBS and dissociating the cells from the flask using fresh 5 ml of PBS. The cultures were passaged with a split ratio 1:5 into 75 cm² flasks every 2 days with 10 ml fresh growth medium. A549 (human adenocarcinomic alveolar basal epithelial) cells were cultured in RPMI 1640 medium containing in v/v 10% FBS, 1%

sodium pyruvate, and 1% antibiotic/antimycotic (penicillin G sodium, streptomycin sulphate and amphotericin B). The cultures were passaged with a split ratio 1:5 into 75 cm² flasks approximately every 2 days with 10 ml fresh growth medium.

4.3.2.2 Cell Transfection

The transfection was carried out by using the Lipofectamine method (Invitrogen, UK), according to the manufacturer's protocol.

Briefly, HEK293 cells at 50-70% confluence in 65 mm petri dishes were used. 4 ml of Opti-MEM medium was applied to the cells after the normal growth medium was aspirated. Then, two 5 ml Falcon polystyrene round bottom tubes (labelled '1' and '2') containing 1 ml of Opti-MEM medium were prepared. 5 µg of vector DNA was added into tube 1 and 20 µl of lipofectamine was added into tube 2. Both tubes were then incubated at room temperature for 15 min. The content of tube 2 was poured directly into tube 1 after the incubation, vortexed for 4 sec and incubated at room temperature for a further 15 min. Finally, the mixture was applied to the cells after 4ml of Opti-MEM medium had been aspirated off. After 24 h incubation at 37°C 5% CO₂, the mixture medium was removed and 3 ml of fresh DMEM complete growth medium was added. The cells were then incubated for a further 24 h before being grown in DMEM complete growth medium containing G418 (1.4 g/l) for two weeks.

4.3.2.3 Single Cell Cloning

A single cell cloning procedure was carried out to obtain a cell line with optimum receptor expression. The transfected cells in 25 cm² flasks at 70-85% were counted using a haemocytometer and diluted using selective media to give a cell suspension with a final cell concentration of 5 cells per

ml. Cells were then pipetted into a 96-well plate with a volume of 200 μ l per well. After approximately two weeks, colonies of cells became visible in the wells and only the wells containing single visible colony were selected and transferred to 25 cm² flasks containing 5 ml of selective media. These cells were then left growing to reach \sim 70-80% confluence before intracellular calcium signalling measurements were performed to identify cells expressing functional receptor (See **Section 2.9**). PAR₄ AP was used as an agonist. Once a clone had been identified, this clone was taken through second and third rounds of single cell cloning to ensure that the final set of clones were derived from a single cell.

4.3.2.4 Storage of Frozen Cell Lines

The clone showing the highest increase in calcium following agonist activation as determined by calcium signalling experiments was selected as the expressing clone for all future analysis and passaged up into larger flasks before being frozen down in FBS with 10% dimethyl sulfoxide (DMSO) in liquid nitrogen for long-term storage.

4.3.3 RT-PCR Detection of PAR₄ in HEK-PAR₄ Cells

Cells were cultured in 25 cm² flasks with 5 ml of DMEM containing G418. Total RNA was prepared using the Nucleospin RNA II Kit and reverse transcription of empty vector control (with empty pcDNA3.1 vector) and HEK-PAR₄ mRNA were carried out as described in **Sections 2.4** and **2.5**. 2 μ g of cDNA products were amplified by PCR in 50 μ l final volume in TC-3000 Personal 25-well Thermal Cycler (Bibby Scientific, UK).

PCR detection of PAR₄ was carried out as described in **Section 2.6**. The sequences of oligonucleotides used in PCR to amplify PAR₄ and β -actin are summarised in **Table 3.4**. Reaction products were analysed as described in **Section 2.6**.

4.3.4 Preparation of Whole Cell Lysates

Cells were passaged into 25 cm² culture flasks and allowed to reach over 70% confluence. Cells were then harvested by centrifugation at $500 \times g$ for 5 min and lysed by adding 500 μ l Laemilli's sample buffer as described in **Section 2.10**.

4.3.5 SDS-PAGE and Western Blotting

Protein samples (20 μ g) were separated on a 12.5% SDS-PAGE gel before transferring to a nitrocellulose membrane using the i-blot (Invitrogen, UK) as described in **Sections 2.11** and **2.12**. The membrane was then blocked with 5% milk solution, incubated with primary and secondary antibodies as described in **Section 2.12**.

Primary antibodies were: mouse HA.11 antibody (1 μ g/ml); secondary antibody was: goat anti-mouse IgG HRP (1:2000). As a loading control, mouse monoclonal IgG1 anti- α -tubulin (1:1000) was used as the primary antibody and goat anti-mouse IgG HRP (1:2000) was used as secondary antibody. The blot was visualised using the ECL detection system as describe in **Section 2.12**.

4.3.6 Detection of PAR₄ Expression on HEK-PAR₄ Cells by Flow Cytometry

Empty vector control and HEK-PAR₄ cells were passaged into 6-well plate and allowed to reach over 85% confluence. Cells were then harvested by centrifugation at $400 \times g$ for 3 min. They were resuspended in 50 μ l of ice cold PBS and incubated with PAR₄ antibody (10 μ g/ml) for 30 min on ice and washed 2 times with ice cold PBS. The cells were then incubated with anti-goat IgG FITC (1:100) for 30 min on ice, in the dark and washed 2 times with PBS before analysing on a Becton Dickinson flow cytometry. A minimum of 10,000 events per sample were measured. Multiparameter data analysis was performed with CellQuest software (Becton-Dickinson).

4.4 Results

4.4.1 Verification of PAR₄ Plasmid

A restriction digest reaction was performed to check if the purified PAR₄ plasmid contained the insert sequence. Double digestion with HindIII and XhoI yielded two fragments on a 1.3% agarose gel, representing the pcDNA3.1 backbone (5428 bp) and the POMC-AU1-hPAR₄-HA.11 (1167 bp) insert (**Figure 4.3**). The presence and accuracy of POMC-AU1-hPAR₄-HA.11 insert was further confirmed by sequencing (data not shown).

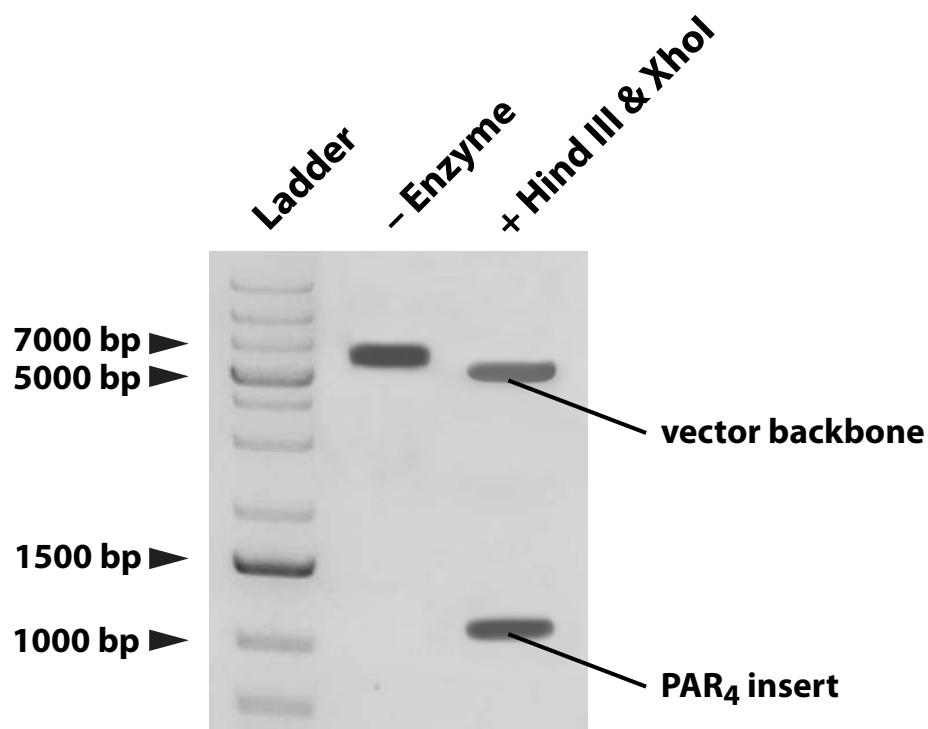


Figure 4.3: PAR₄ Plasmid Checked by Restriction Digest. pcDNA3.1-POMC-AU1-hPAR₄-HA.11 plasmid was incubated with or without HindIII and XhoI. In the presence of these enzymes, the plasmid was cut into two fragments, where the higher band corresponds to the pcDNA3.1 backbone (5428 bp) and the lower band corresponds to the POMC-AU1-hPAR₄-HA.11 insert (1167 bp).

4.4.2 Detection of PAR₄ Expression in HEK-PAR₄ Cells

To determine if the PAR₄ transgene was successfully introduced into HEK293 cells and was expressed in these cells, RT-PCR and flow cytometry were carried out.

4.4.2.1 PAR₄ mRNA Detected by RT-PCR

Empty vector control cells and four different transfected HEK-PAR₄ clones grown from four independent colonies were examined. No band was observed in the negative controls when no RT enzyme was added or no template control reactions (NTC) where cDNA was omitted (**Figure 4.4A**). While no band was detected in the empty vector control, a PCR product of an expected size of 340 bp was amplified from all four HEK-PAR₄ clones, demonstrating the presence of PAR₄ mRNA in these transfected cells (**Figure 4.4B**). As a positive control, a 242 bp band corresponding to β -actin was detected in all samples when β -actin primers were used (**Figure 4.4B**, lane 2-6).

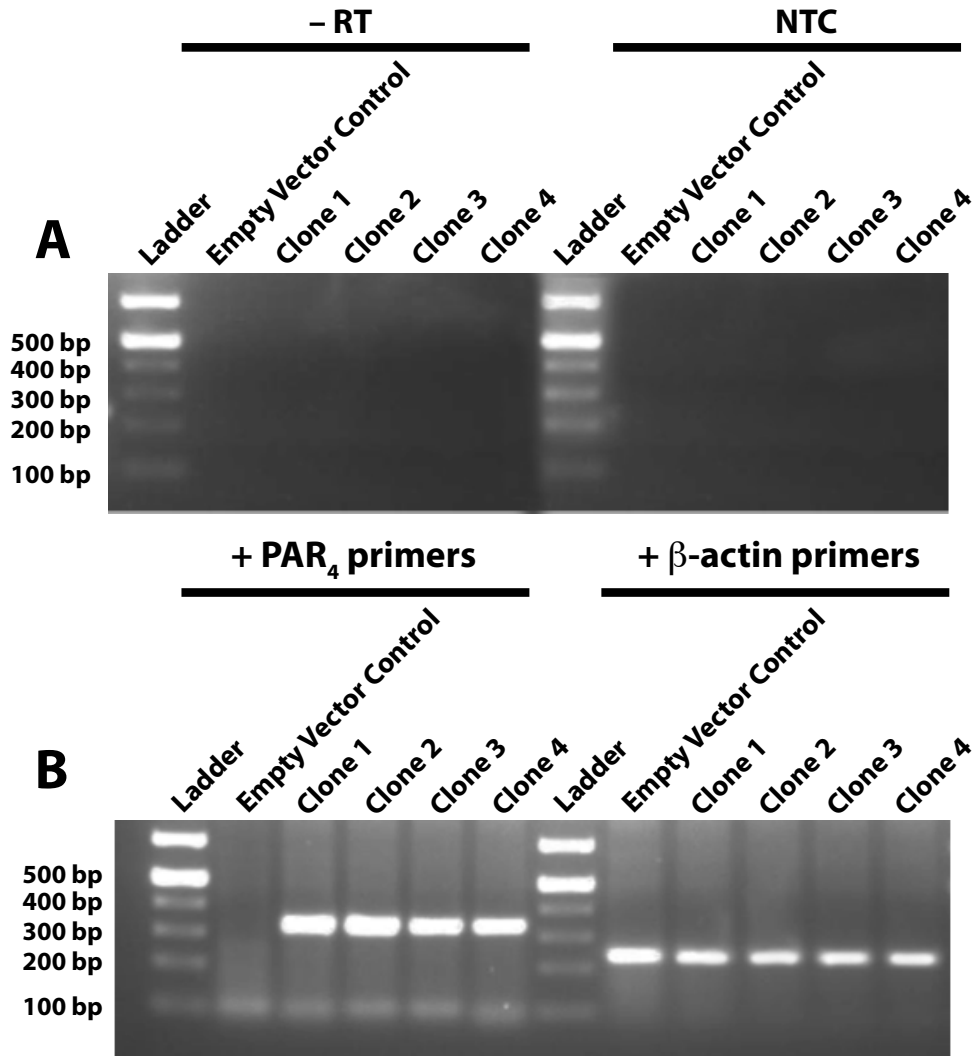


Figure 4.4: RT-PCR Detection of PAR₄ in HEK-PAR₄ Cells. Empty vector control or PAR₄-transfected (four clones) HEK cells were analysed by RT-PCRs. RNAs were extracted and reverse transcribed. PCRs were performed for 35 cycles using primers specific to PAR₄ or β -actin. β -actin primers were included as a positive control. No template controls (NTC) and no reverse transcriptase (-RT) samples were included with PAR₄ primers. These PCRs were done in parallel. Expected band sizes: PAR₄ (340 bp) and β -actin (242 bp). Results are representative of three independent experiments.

4.4.2.2 Detection of PAR₄ Protein by Western Blotting using HA.11 antibody

In chapter 3, it was shown that PAR₄ protein could not be determined by Western blotting using PAR₄ specific antibodies. As the PAR₄ transgene was tagged with HA.11, HA. 11 antibody was used to detect the presence of this transgene. **Figure 4.5** shows that PAR₄ protein was successfully expressed in the HEK- PAR₄ cells.

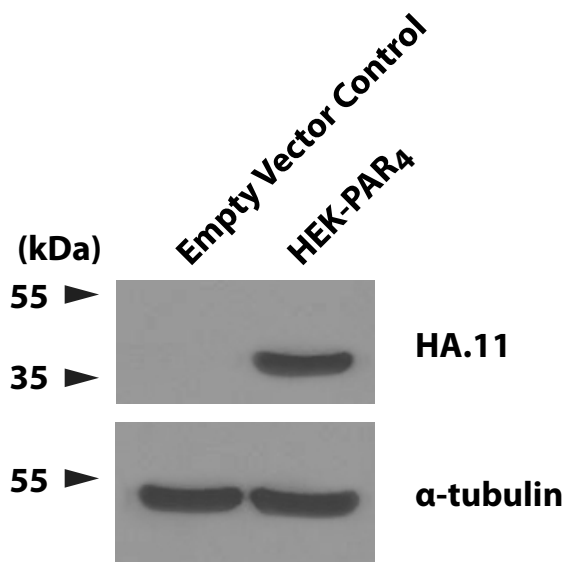


Figure 4.5: Detection of HA.11 tag of PAR₄ protein by Western blotting. Cells at 70-85% confluence in 25 cm² flasks were harvested and lysed. Cell lysates obtained were subjected to SDS-PAGE followed by immunoblotting with antibodies against HA.11 and α -tubulin. Expected band sizes: HA.11 (~38 kDa) and α -tubulin (~52 kDa). Results are representative of three independent experiments.

4.4.2.3 PAR₄ Protein Detected by Flow Cytometry

Flow cytometry analysis was also performed to determine the PAR₄ protein expression on HEK-PAR₄ cells. Flow cytometry data demonstrate that HEK-PAR₄ cells showed clear rightward shift in fluorescence when compared to empty vector control, indicating the surface expression of PAR₄ on HEK-PAR₄ cells (**Figure 4.6**).

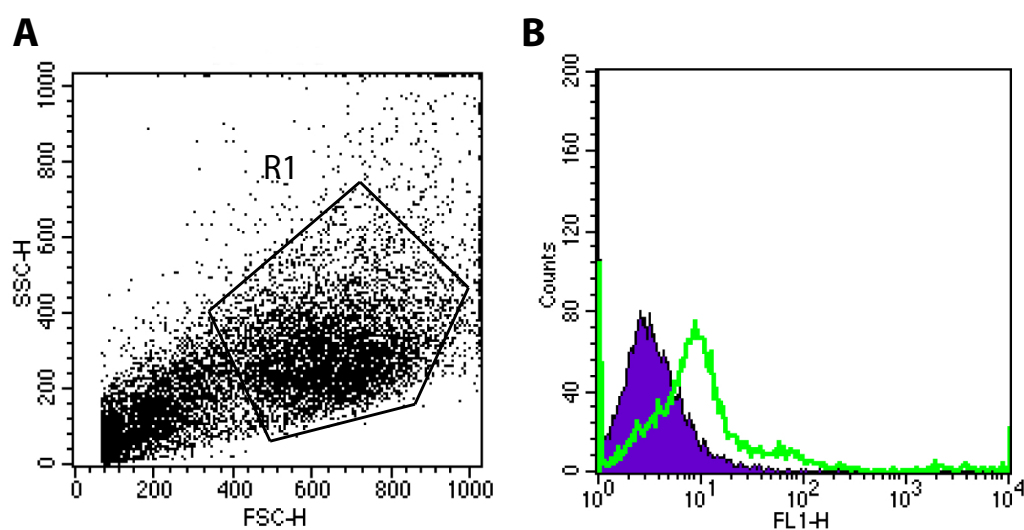


Figure 4.6: Detection of Cell Surface PAR₄ Expression on HEK-PAR₄ Cells by Flow Cytometry. Cells at 70-85% confluence in 6-well plate were harvested and incubated with anti-PAR₄ antibody. The cells were then incubated with anti-goat IgG FITC in the dark before analysing on a Becton Dickinson flow cytometry. (A) Cells were gated (R1) from the debris. (B) PAR₄ expression on gated HEK-PAR₄ cells (green line) was compared with the empty vector control cells (blue area). The histogram shows fluorescence intensity (x-axis) against number of events (y-axis). Data are representative of three independent experiments.

4.5 Discussion

PAR₄ activation is known to lead to pro-inflammatory effects. A greater understanding of PAR₄ activation and the its downstream signalling pathways could reveal novel targets for the treatment of inflammatory diseases as PAR₄ expression is upregulated during inflammation. In this chapter, stable cell line expressing functional PAR₄ (HEK-PAR₄ cells) was generated.

Results from RT-PCR (**Figure 4.4B**), Western blotting using HA.11 tag (**Figure 4.5**) and flow cytometry (**Figure 4.6**) all show that HEK293 cells have been successfully transfected with the PAR₄ transgene. Unfortunately, the anti-PAR₄ antibody (same PAR₄ antibody used in the flow cytometry experiment) was unable to produce reliable Western blotting results. One possible reason is that the antibody may only effectively recognise PAR₄ protein in its native form (e.g. in flow cytometry) but not in denatured condition (e.g. Western blotting).

In conclusion, a stable and functional PAR₄-expressing HEK293 cell line has been established, which is used in the functional studies of PAR₄ presented in the next chapters.

Chapter 5

PAR₄ Independent and Dependent Apoptosis Induction

5.1 Introduction

Apoptosis is thought to be involved in the development of fibrosis via three different mechanisms: (1) resistance to apoptosis of fibroblasts and myofibroblasts, (2) increased apoptosis of epithelial cells leading to inefficient re-epithelialisation, and (3) ineffective removal of apoptotic cells sustains a persistent inflammatory response (DRAKOPANAGIOTAKIS *et al.*, 2008). Fibroblasts and myofibroblasts are the primary matrix producing cells and excessive activation of these cells are considered to be the principal mediator of lung and renal fibrosis. The number of these cells closely correlates with the severity of fibrosis. Thus, fibroblast apoptosis is vital to the regression of scars and the restitution of healthy tissue during wound repair. Failure to eliminate excessive fibroblasts may contribute to severe fibrotic disease.

An increased amount of fibroblasts, myofibroblasts, resident glomerular cells and infiltrating leukocytes can be seen within the interstitium of scarred kidneys during the progression of clinical and experimental nephropathies. It has been proposed that efficient removal of these cells by

apoptosis is beneficial for the resolution of glomerulonephritis (SAVILL, 1994). Samples obtained from the alveolar surface of patients during lung repair contained peptides such as progesterone and glucocorticoids that can induce both fibroblast and endothelial cell death (SAVILL, 1994). Histological examination of lung tissue obtained from patients also revealed mesenchymal cell death within the airspace (POLUNOVSKY *et al.*, 1993). These studies indicate a role for apoptosis in eliminating the excessive fibrotic tissue and allowing the restoration of normal alveolar and kidney anatomy.

Serine proteases are a class of proteases where serine is the key enzymatic residue that initiates the proteolytic cleavage of the target proteins (KESSENBROCK *et al.*, 2011). Cathepsin G (CG), neutrophil elastase and proteinase 3 are the three main neutrophil serine proteases that are released during inflammation. These proteases are important for maintaining the balance between tissue protection and destruction during an inflammatory response (PHAM, 2008). During inflammation, neutrophils infiltrate and release granules containing proteinases, cytokines, chemokines and other enzymes at the site of injury. They also secrete collagenase and have the potential to recruit more neutrophils to the inflammatory site (GADEK *et al.*, 1984). Recruitment and activation of neutrophils are fundamental processes in the pathogenesis of fibrosis. Neutrophils can modify the inflammatory response by modulating the production of pro-inflammatory cytokines and anti-inflammatory mediators. They are important regulators of the inflammatory processes and hence serve as the potential targets for new therapeutic approaches against inflammatory diseases.

CG and trypsin are known to regulate cell signalling by cleaving and activating PARs (VESEY *et al.*, 2007). CG is stored in the azurophil granules in an active form and is secreted in limited amounts following

chemotactic and phagocytic stimuli. It is involved in clearance of internalised pathogens, proteolytic modification of chemokines and cytokines, activation and shedding of cell surface receptors, and apoptosis (PHAM, 2008). SHIMODA *et al.* (2007) reported that CG was a major mediator of tissue injury in ischaemic kidney during reperfusion. Prolonged neutrophil-mediated inflammation in the kidneys led to tubular apoptosis and development of tissue fibrosis. Compared to wild type mice, CG-deficient mice showed reduced mortality in response to ischaemic reperfusion induced damage. CG also acts as a monocyte chemoattractant in joint inflammation of rheumatoid arthritis. Monocyte chemotactic activity was detected in synovial fluid of rheumatoid arthritis patients which contained high concentrations of CG. The chemotactic activity was partially decreased by the treatment with CG inhibitors such as α 1-antichymotrypsin (ACT) and phenylmethylsulfonyl fluoride (PMSF) (MIYATA *et al.*, 2007).

The blockade of inflammation using steroids and other drugs has been the main focus for fibrosis treatment. However, the clinical benefits of such treatment are limited despite excellent anti-inflammatory efficacy of the agents used (MUNSON *et al.*, 2010). Thus, treatments that directly target fibroblasts would be desirable as fibroblasts are the key effector cells in fibrosis that produce excessive ECM. Therapies that promote fibroblast apoptosis during the repair phase after injury may facilitate recovery by eliminating excessive fibrotic tissue. Therefore, potential therapeutic targets in fibrosis may involve the administration of inducers of fibroblast apoptosis or the promotion of their mediators, provided that this can be achieved in a cell type specific manner. As CG and PAR₄ expression levels are upregulated during inflammation, CG may be important in PAR₄-mediated inflammation.

5.2 Aims

In **Chapter 3**, the purity of fibroblast cultures was assessed morphologically and immunocytochemically by staining for the fibroblast markers, vimentin and prolyl-4-hydroxylase. PAR expression in these fibroblasts was determined, and results indicate that PAR₄ is not present in these fibroblasts. PAR₄ is thought to be involved in pro-inflammatory responses and fibroproliferative processes (VERGNOLLE *et al.*, 2002; ANDO *et al.*, 2007b). Thus, as described in **Chapter 4**, a stable HEK-PAR₄ cell line was generated using HEK293 cells (human embryonic kidney cells) in order to study PAR₄. This chapter aims to investigate whether:

1. PAR₄ AP and CG can induce PAR₄ signalling in HEK-PAR₄ cells
2. CG and trypsin induce apoptosis
3. Activation of PAR₄ triggers apoptosis of HEK-PAR₄ cells.

5.3 Methods

5.3.1 Intracellular Calcium Mobilisation Assay

A calcium signalling assay was performed using the methods described in **Section 2.9**. Agonists used were: AYPGQV (100 μ M), CG (300 nM) and antagonist PMSF (1 mM).

5.3.2 Staining of Enzyme Activity After PAGE

For enzyme activity staining, the SDS-PAGE was prepared as described in **Section 2.11**. CG (300 nM) was added to casein (5 mg/ml) and the mixture was incubated at 37°C for 24 h. To inhibit CG enzymatic activity, PMSF was added to CG for 30 min before CG was added to casein. CG was inactivated in each sample before loading on the gel by heating at

100°C for 5 min.

After electrophoresis, gel was fixed in 50% ethanol containing 10% acetic acid for 30 min and washed with 50% methanol containing 10% acetic acid for another 30 min. Gel was then stained with 0.1% v/v Coomassie brilliant blue (CBB) in 20% methanol containing 10% acetic acid overnight. After that, gel was destained in 50% methanol containing 10% acetic acid. The solution was replenish several times until background of the gel was fully destained.

5.3.3 Acridine Orange Apoptosis Assay

HPBFs and HPRFs were cultured in 24-well plates with 500 μ l of fibroblast growth medium and allowed to grow to 70-80% confluence before quiescing in serum free media for 24 h. Quiescent cells were then treated with different apoptosis inducers for a further 24 h. As a negative control (no treatment), PBS was used to treat the quiescent cells. To inhibit the enzyme activity of CG and trypsin, 1 mM PMSF was added to the CG and trypsin for 30 min before being added to the cells for 24 h.

Acridine orange (2.5 μ g/ml) was added to the cells before visualising using a fluorescent microscope (Nikon) with a filter for green fluorescence (525 nm). Detection of apoptotic cells was performed on the basis of nuclear morphology and rounding up of cells that were losing adhesion. Cells with condensed chromatin, rounded morphology and fragmented DNA were classified as apoptotic. Five microscopic fields at 60 \times magnification with approximately 800 cells were randomly selected, and the number of apoptotic cells was counted.

5.3.4 Annexin V Binding to Phosphatidylserine (PS) Flow Cytometry Assay

HEK-PAR₄ cells were passaged into 6-well plates and allowed to reach over 70-80% confluence before treating with different apoptosis inducers for a further 24 h. In the enzyme inhibition assay, 1 mM PMSF was added to CG and trypsin for 30 min before being added to the cells for 24 h.

Next, the cells were resuspended in 100 μ l of calcium buffer (10.9 mM HEPES, 140 mM sodium chloride and 2.5 mM calcium chloride) and incubated with 10 μ l of FITC-conjugated Annexin V for 20 min on ice, in the dark. 1 μ l of propidium iodide (PI) (stock concentration: 1 mg/ml) was added before analysing on a Becton Dickinson flow cytometer. A minimum of 10,000 events per sample were measured. Multiparameter data analysis was performed with CellQuest software (Becton-Dickinson). Cells were analysed using a fluorescence intensity histogram.

5.3.5 Preparation of Whole Cell Lysates

HPBFs or HPRFs were passaged into 25 cm² culture flasks and allowed to reach over 70% confluence. Once reaching the desired confluency, cells were treated with different apoptosis inducers for 24 h. Cells were then harvested by centrifugation at $500 \times g$ for 5 min and lysed by adding 500 μ l Laemilli's sample buffer as described in **Section 2.10**.

5.3.6 SDS-PAGE and Western Blotting

Protein samples were separated on a 12.5% SDS-PAGE gel before transferring to a nitrocellulose membrane using i-blot (Invitrogen, UK) as described in **Sections 2.11** and **2.12**.

The membrane was blocked with 5% milk solution, and then incubated with primary and secondary antibodies as described in **Section 2.12**. Primary antibodies were: rabbit caspase-3 (1:500) and rabbit cleaved caspase-3 (1:500); secondary antibody: donkey anti-rabbit HRP (1:5000). As a loading control, mouse monoclonal IgG1 anti- α -tubulin (1:1000) was used as primary antibody and goat anti-mouse IgG HRP (1:2000) was used as secondary antibody. The blot was visualised using the ECL detection system.

5.4 Results

5.4.1 Functional Characterisation of HEK-PAR₄ Cells by CG

5.4.1.1 CG does not activate PAR₄

To determine whether the PAR₄ developed in these HEK-PAR₄ cells is functional, a calcium mobilisation assay was performed. Exposure of empty vector control to the PAR₄ AP (100 μ M) showed no calcium response (**Figure 5.1A**). A robust increase in intracellular calcium ($60 \pm 4.5\%$ of calcium ionophore) was detected in the HEK-PAR₄ cells in the presence of PAR₄ AP (100 μ M) (**Figure 5.1B**). A549 cells that possess functional PAR₄ were used as a positive control and a calcium response ($35 \pm 2.4\%$ of calcium ionophore) was detected when PAR₄ AP was added (**Figure 5.1C**).

To test whether CG activates PAR₄, a calcium mobilisation assay was performed. 300 nM CG failed to induce a calcium response as the intracellular calcium did not change during acute incubation with CG (**Figures 5.1E & 5.1F**). **Figure 5.2** shows the summary of the calcium mobilisation in empty vector control, HEK-PAR₄ and A549 cells in response to PAR₄ and CG.

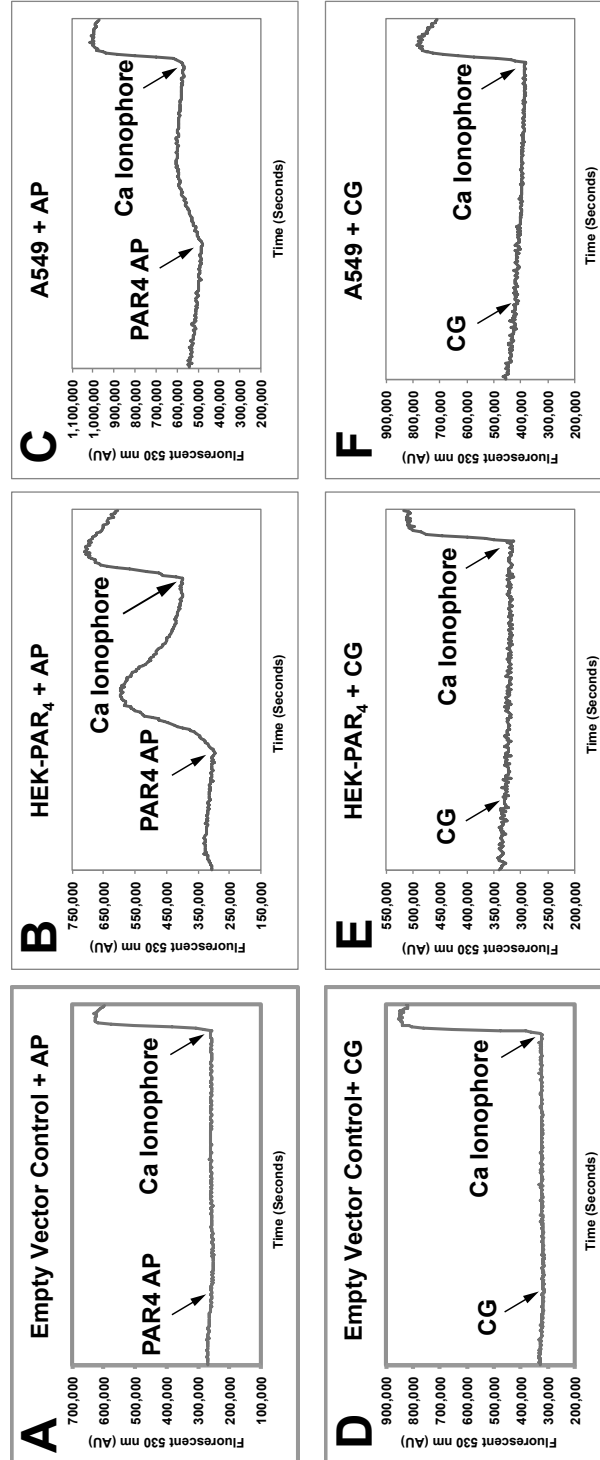


Figure 5.1: Calcium Signalling Assay for PAR₄ Cells in Response to PAR₄ AP or CG. Cells at 70-85% confluence in 75 cm² flasks were harvested and incubated with Fluo-3 AM at room temperature for 25 min. Cells were then washed and resuspended in calcium assay buffer. Empty vector control (A & D) or PAR₄-expressing HEK cells (B & E) and A549 cells (C & F) were assayed for calcium mobilisation in the presence of 100 μ M PAR₄ AP (AYPGQV) (A–C) or 300 nM CG (D–E). An increase in fluorescence (E530) monitored by fluorescence spectrophotometry is indicative of calcium mobilisation. Arrows indicate the time when test agonists were added. Data shown are representative of five independent experiments.

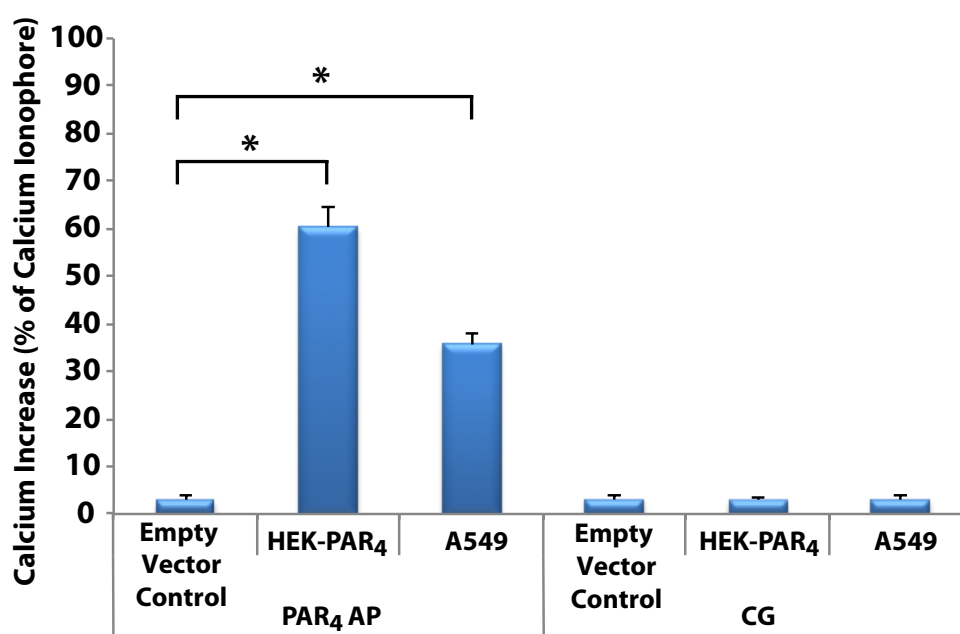


Figure 5.2: Summary of the Calcium Mobilisation for PAR₄ Cells in Response to PAR₄ AP or CG. The data in Figure 5.1 were quantitated and summarised in a bar chart, where the calcium response was expressed as a percentage of the calcium ionophore mean response (maximum obtainable response). Results are expressed as mean \pm SEM of five independent experiments. * indicates $p < 0.05$ compared with empty vector control in one way-ANOVA with Dunnett's post hoc test.

5.4.1.2 Examination of CG Enzyme Activity

As no calcium response was observed in the experiments above in the presence of CG, a possible reason might be that the CG used was inactive. To eliminate this possibility, the ability of CG to cleave casein (a known CG substrate, CONSIDINE *et al.* (2002)) was tested. As shown in **Figure 5.3**, casein can clearly be seen at ~ 35 kDa. Following CG treatment, casein is degraded by CG and a cluster of bands at smaller molecular weights were detected. Importantly, this degradation of casein was prevented when CG was pre-incubated with its inhibitor PMSF. These results indicate that the CG used in this study was active, and thus the negative results described in **Section 5.4.1** are not due an inactive CG.

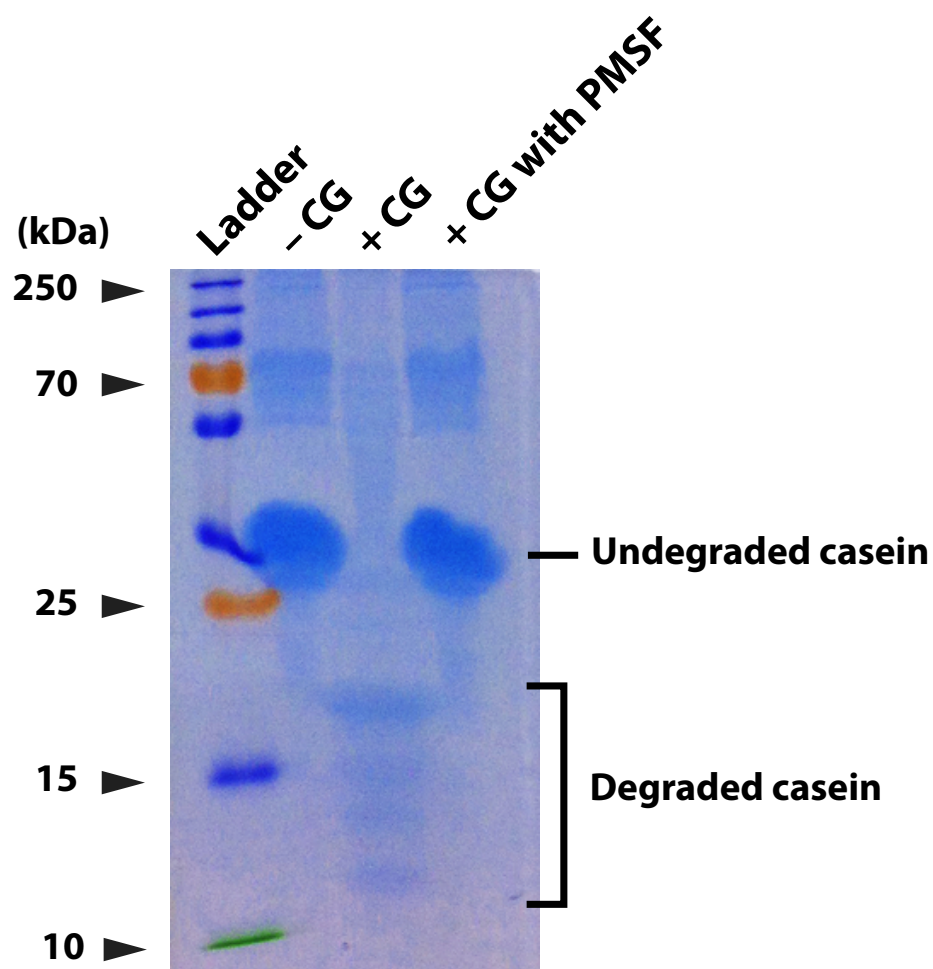


Figure 5.3: Confirmation that Cathepsin G is enzymatically active. Casein was incubated at 37°C for 24 h without CG (A), with 300 nM CG (B), or, with 300nM CG pre-treated with PMSF (C). Samples were then subjected to SDS-PAGE. Gel was fixed and stained with 0.1% v/v CBB overnight to visualise the protein bands.

5.4.1.3 CG inhibits PAR₄

As CG did not activate PAR₄, the possibility that CG could inhibit PAR₄ was investigated. CG (300 nM) was added before PAR₄ AP. Compared to the reactions with PAR₄ AP alone without CG (**Figure 5.4B & 5.4C**), the amplitude of the response to PAR₄ AP was reduced after incubation with CG in HEK-PAR₄ ($17 \pm 3.3\%$ of calcium ionophore) and A549 cells ($15 \pm 1.6\%$ of calcium ionophore) (**Figures 5.4E, 5.4F & 5.4J**), indicating that CG could somehow inhibit PAR₄. In addition, PMSF (1 mM) was used to inhibit CG enzyme activity to test if the calcium could be increased. As expected, the magnitude of the calcium responses increased back to the levels observed when PAR₄ AP alone was added, HEK-PAR₄ ($51 \pm 5.2\%$ of calcium ionophore) and A549 ($38 \pm 2.9\%$ of calcium ionophore) (**Figures 5.4H & 5.4I**, compared to **Figure 5.4B & 5.4C**).

To investigate whether the reduced calcium response was due to the cleavage of PAR₄ AP by CG, PAR₄ AP and CG were mixed together and incubated for 30 min before performing the calcium assay. The results obtained (**Figure 5.7**) were similar to the observations when PAR₄ AP and CG were added sequentially (**Figures 5.5**), indicating that CG did not cleave PAR₄ AP.

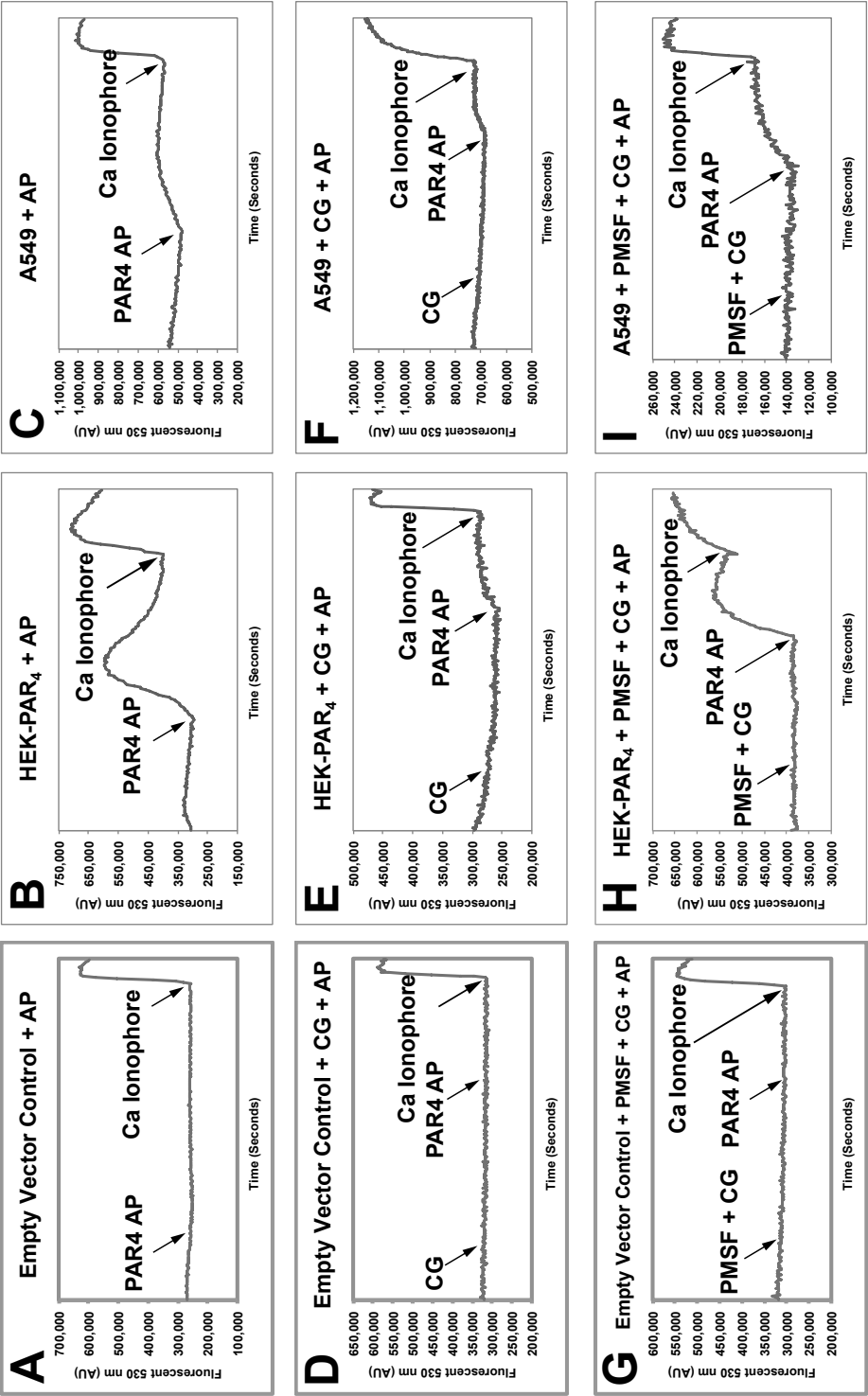


Figure 5.4: Calcium Signalling Assay for PAR₄ Cells in Response to Sequential Addition of PAR₄ AP and CG. Cells at 70-85% confluence in 75 cm² flasks were harvested and incubated with Fluo-3 AM at room temperature for 25 min. Cells were then washed and resuspended in calcium assay buffer. (A–F) Empty vector control or PAR₄-expressing HEK cells and A549 cells were assayed for calcium mobilisation after the addition of PAR₄ AP alone (A–C), 300 nM CG followed by 100 μ M PAR₄ AP (AYPGQV) (D–F), or, 300 nM CG which had been pre-incubated with 1 mM PMSF, followed by 100 μ M PAR₄ AP (AYPGQV) (G–I). An increase in fluorescence (E530) monitored by fluorescence spectrophotometry is indicative of calcium mobilisation. Arrows indicate the time when test agonists were added. Data shown are representative of five independent experiments.

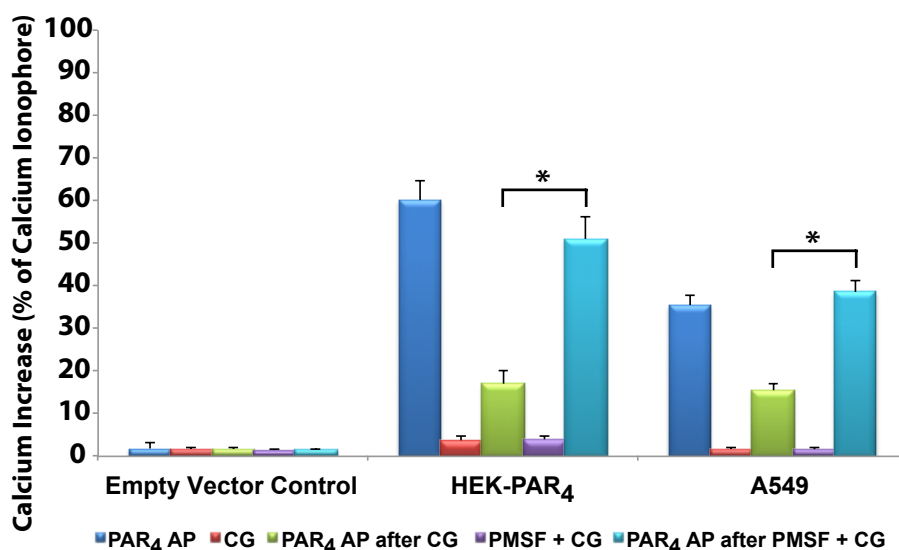


Figure 5.5: Summary of the Calcium Mobilisation for PAR₄ Cells in Response to Sequential Addition of PAR₄ AP and CG. The data in Figure 5.4 were quantitated and summarised in a bar chart, where the calcium response was expressed as a percentage of the calcium ionophore mean response (maximum obtainable response). Results are expressed as mean \pm SEM of five independent experiments. * indicates $p < 0.05$ comparison of calcium response by paired t-test.

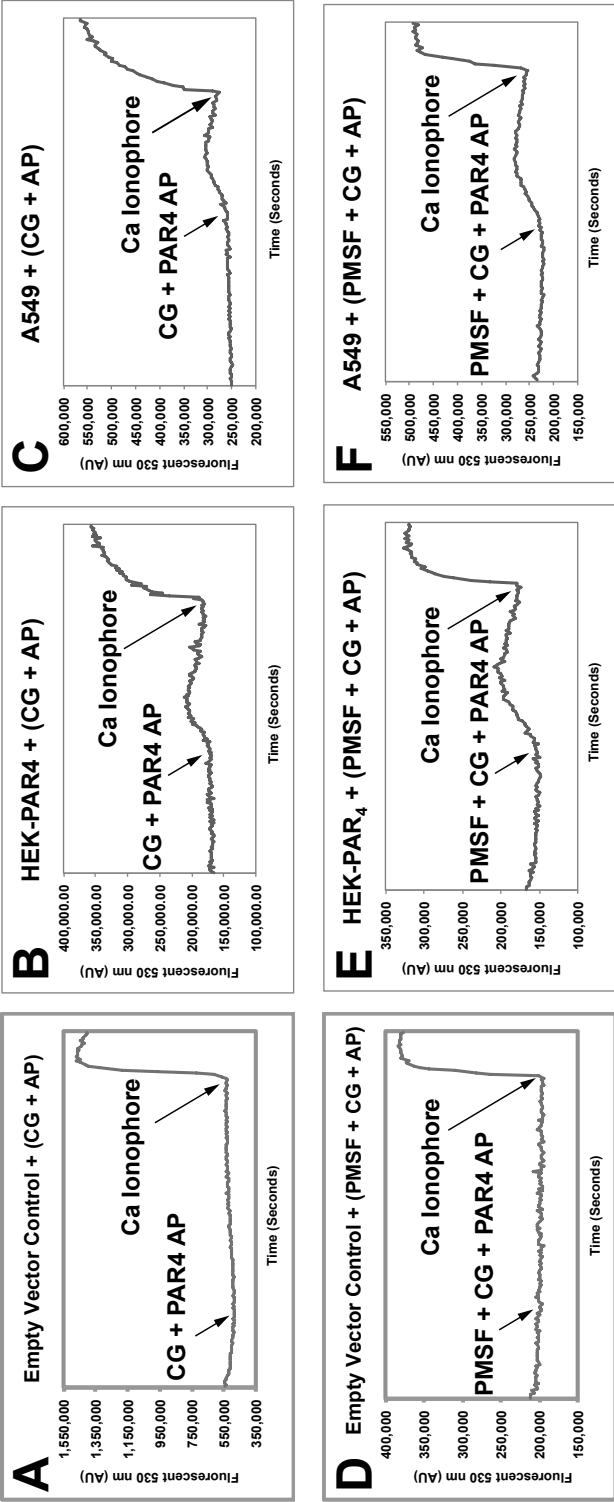


Figure 5.6: Calcium Signalling Assay for PAR₄ Cells in Response to Pre-mixed PAR₄ AP and CG. Cells at 70-85% confluence in 75 cm² flasks were harvested and incubated with Fluo-3 AM at room temperature for 25 min. Cells were then washed and resuspended in calcium assay buffer. Empty vector control (A & D) or PAR₄-expressing HEK cells (B & E) and A549 cells (C & F) were assayed for calcium mobilisation after the addition of a mixture of 300 nM CG and 100 μ M PAR₄ AP (AYPGQV) (A–C), or, a mixture of 1 mM PMSF, 300 nM CG and 100 μ M PAR₄ AP (AYPGQV) (D–F) . An increase in fluorescence (E530) monitored by fluorescence spectrophotometry is indicative of calcium mobilisation. Arrows indicate the time when test agonists were added. Data shown are representative of five independent experiments.

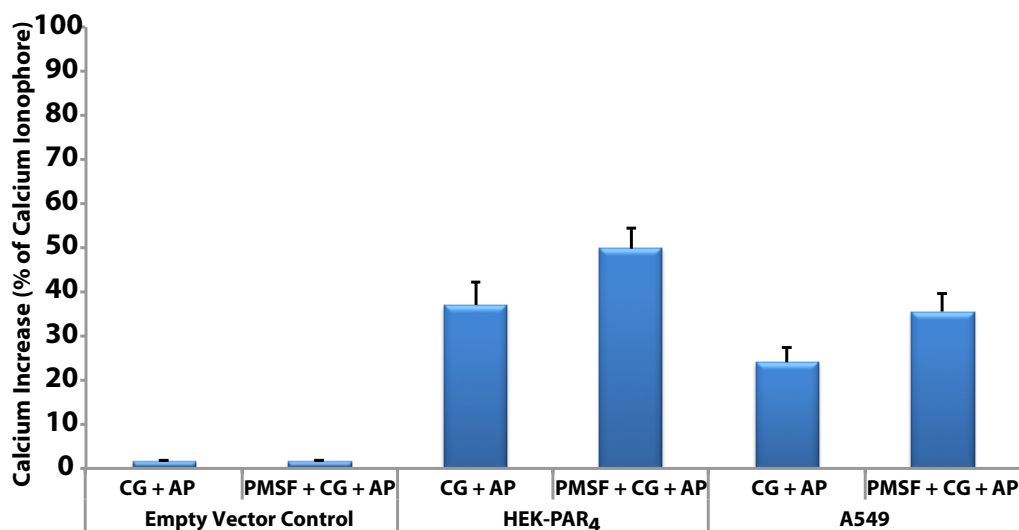


Figure 5.7: Summary of the Calcium Mobilisation for PAR₄ Cells in Response Pre-mixed PAR₄ AP and CG. The data in Figure 5.6 were quantitated and summarised in a bar chart, where the calcium response was expressed as a percentage of the calcium ionophore mean response (maximum obtainable response). Results are expressed as mean \pm SEM of five independent experiments. * indicates $p < 0.05$ compared with empty vector control in one way-ANOVA with Dunnett's post hoc test.

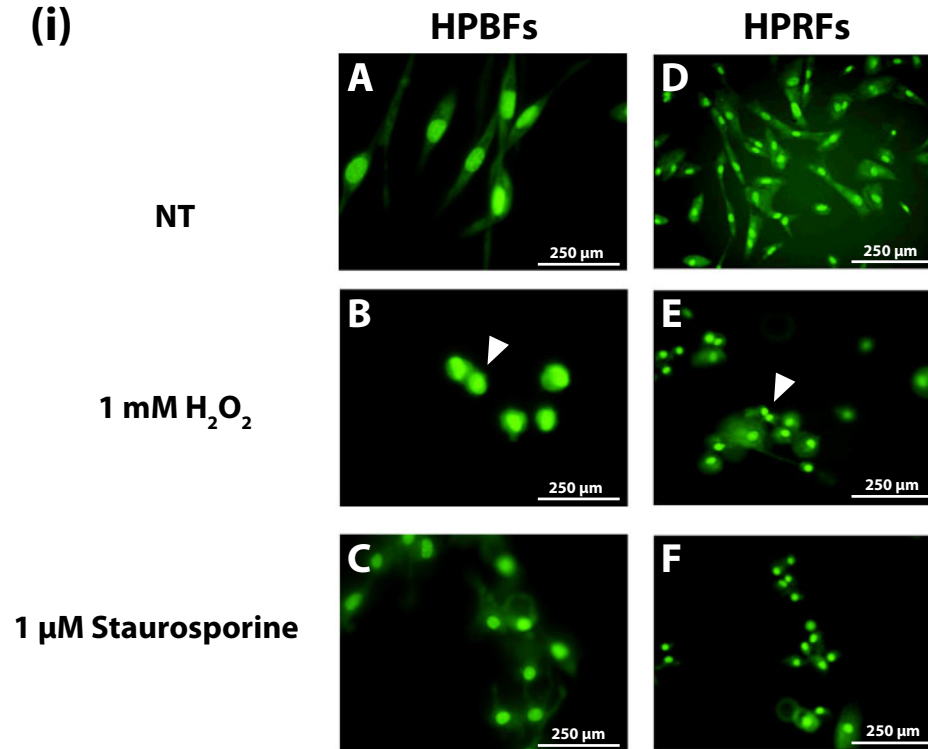
5.4.2 Apoptosis Induction in HPBFs and HPRFs

To test response to apoptosis inducing agents, HPBFs and HPRFs were treated with hydrogen peroxide (H_2O_2) (1 mM) and staurosporine (1 μM) and then stained with acridine orange that will binds to DNA. Without treatment with these agents, HPBFs and HPRFs showed a flattened and spread appearance with bright green chromatin (**Figure 5.8A**). However, pronounced chromatin condensation were observed in > 90% of cells treated with H_2O_2 or staurosporine (**Figures 5.8A & 5.8B**).

Next, to determine whether CG and trypsin induced apoptosis in fibroblasts, HPBFs and HPRFs were treated with CG or trypsin for 24 h under serum free conditions. In the presence of CG, fibroblasts appeared as stellate shape and the cells lost cell-cell contacts (**Figure 5.9A**). CG induced apoptosis in both HPBFs and HPRFs in a concentration dependent fashion (**Figures 5.9B & 5.9C**). While 300 nM GC caused $22 \pm 1.2\%$ of HPBFs to become apoptotic and $42 \pm 8.4\%$ of HPRFs to become apoptotic, 600 nM CG induced $86 \pm 1.5\%$ and $85 \pm 4.8\%$ apoptosis in HPBFs and HPRFs, respectively (**Figures 5.9B & 5.9C**, blue bars). Pre-incubation of CG with 1 mM PMSF, a serine protease inhibitor, caused only minimal amounts of apoptotic cells (**Figures 5.9B & 5.9C**, red bars).

Treatment of HPBFs and HPRFs with trypsin also induced apoptosis in a dose-dependent manner (**Figure 5.10**). At 250 nM, trypsin induced a significant $73 \pm 10\%$ apoptosis in HPBFs and a significant $36 \pm 7.4\%$ apoptosis in HPRFs. When the concentration of trypsin was increased to 500 nM, $95 \pm 2.7\%$ and $66 \pm 4.8\%$ apoptotic cells were observed in HPBFs and HPRFs, respectively (**Figures 5.10B & 5.10C**, blue bars). This apoptosis-inducing activity of trypsin was significantly suppressed when it was pre-incubated with 1 mM PMSF before being added to the cells (**Figures 5.10B & 5.10C**, red bars).

(i)



(ii)

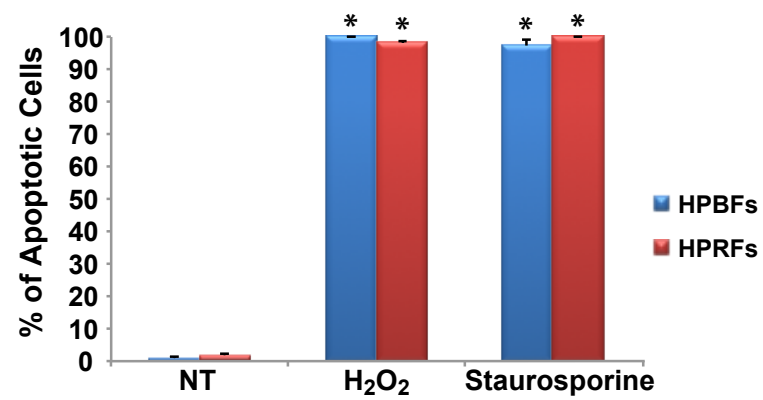


Figure 5.8: H₂O₂ and Staurosporine Induce Apoptosis in HPBFs and HPRFs. Cells at 70-85% confluence in 24-well plates were quiesced. Quiescent cells were then treated with different apoptosis inducers for 24 h. Then, acridine orange was added to the cells before visualising with fluorescent microscope. (i) HPBFs: (A) No treatment (NT); (B) H₂O₂ and (C) Staurosporine. HPRFs: (D) NT; (E) H₂O₂ and (F) Staurosporine. White arrowheads indicate apoptosis fibroblasts. Data shown are representative of six independent experiments. (ii) Apoptotic cells were quantified. Error bars represent mean \pm SEM of six independent experiments. * indicates $p < 0.05$ compared to NT in one way ANOVA with Dunnett's post hoc test.

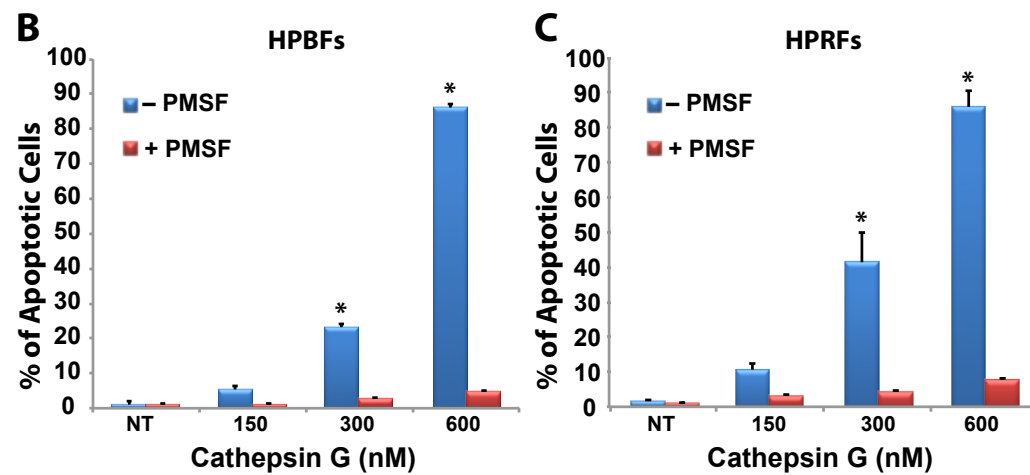
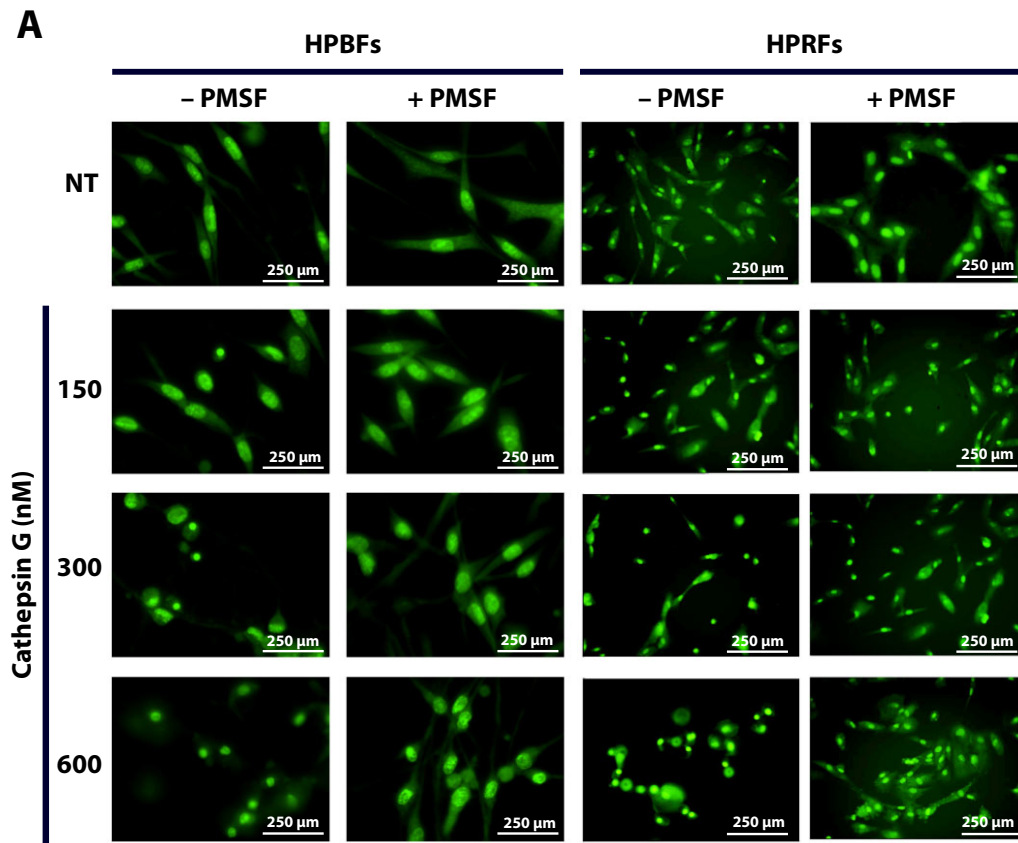


Figure 5.9: CG Induced Apoptosis in HPBFs and HPRFs in a Concentration Dependent Fashion. Cells at 70-85% confluence in 24-well plates were quiesced. Quiescent cells were then treated with different apoptosis inducers for 24 h. Then, acridine orange was added to the cells before visualising with fluorescent microscope. (A) HPBFs and HPRFs were treated with CG at various concentrations as indicated, either with or without pre-incubation with 1 mM PMSF. No CG was added in the untreated sample (NT). Pictures shown are representatives of six independent experiments. (B & C) Apoptotic cells were quantified. Error bars represent mean \pm SEM of six independent experiments. * indicates $p < 0.05$ compared to NT in one way ANOVA with Dunnett's post hoc test.

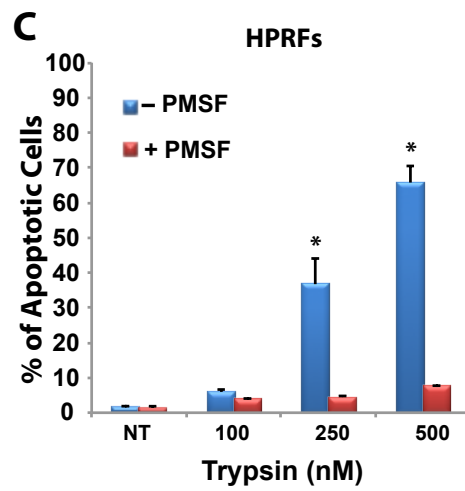
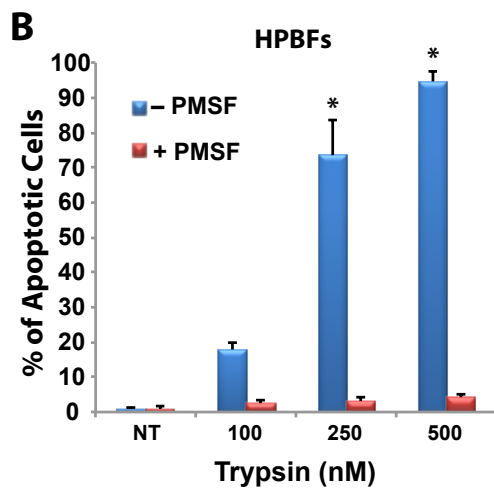
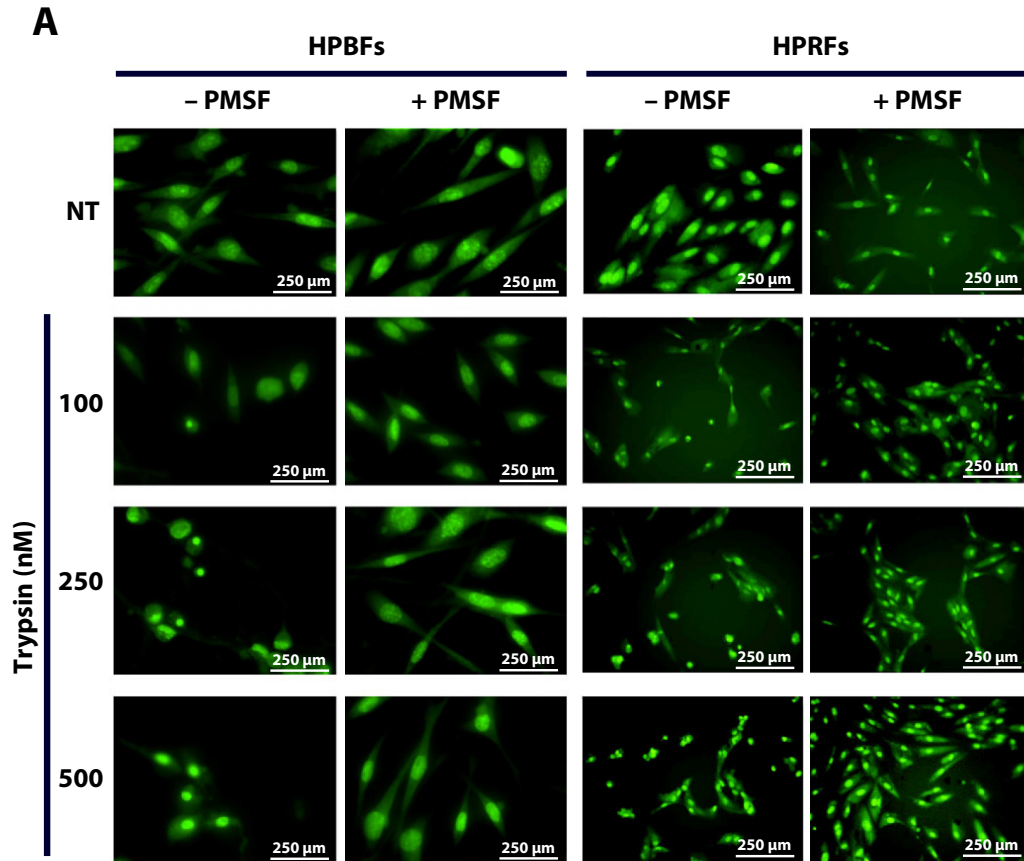


Figure 5.10: Trypsin Induced Apoptosis in HPBFs and HPRFs in a Concentration Dependent Fashion. Cells at 70-85% confluence in 24-well plates were quiesced. Quiescent cells were then treated with different apoptosis inducers for 24 h. Then, acridine orange was added to the cells before visualising with fluorescent microscope. (A) HPBFs and HPRFs were treated with trypsin at various concentrations as indicated, either with or without pre-incubation with 1 mM PMSF. No trypsin was added in the untreated sample (NT). Pictures shown are representatives of six independent experiments. (B & C) Apoptotic cells were quantified. Error bars represent mean \pm SEM of six independent experiments. * indicates $p < 0.05$ compared to NT in one way ANOVA with Dunnett's post hoc test.

In order to confirm the induction of apoptosis, Western blot analysis was performed using antibodies specific to caspase-3 or cleaved caspase-3. During apoptosis, caspase-3 is cleaved into two active forms of caspase-3, the p17 and p19 forms (~ 17 or ~ 19 kDa, respectively). The presence of these caspase-3 fragments in both HPBFs and HPRFs treated with H_2O_2 , staurosporine, CG (**Figures 5.11 & 5.12**) or trypsin (**Figures 5.13, 5.14 & 5.15, 5.16**) indicates that apoptosis occurred in these samples. The intensities of cleaved caspase-3 bands increased when the concentrations of CG and trypsin increased. These cleaved caspase-3 fragments were not observed in the untreated sample and in the samples where CG and trypsin were pre-treated with PMSF (**Figures 5.11, 5.12, 5.13, 5.14 & 5.15, 5.16**).

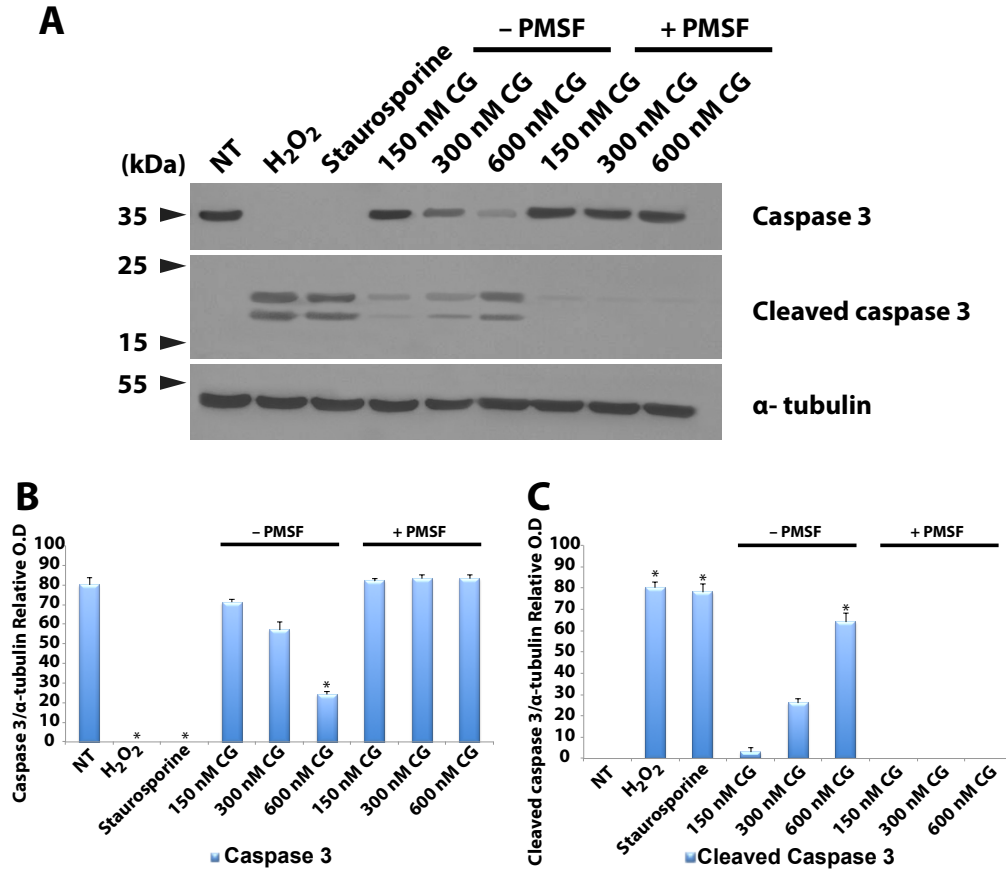


Figure 5.11: Cleaved Caspase-3 Fragments were Detected in Bronchial Fibroblasts Treated with CG. Quiescent cells were treated with different apoptosis inducers for 24 h. Cell lysates were obtained and then subjected to SDS-PAGE followed by immunoblotting with antibodies against caspase-3 and cleaved caspase-3. (A) HPBFs were treated with 1 mM H₂O₂, 1 μ M staurosporine or various indicated concentrations of CG (with or without 1 mM PMSF pre-treatment). None of these agents were added in the untreated sample (NT). α -tubulin was used as a loading control. Expected band sizes: caspase-3 ~35 kDa, cleaved caspase-3 ~17 kDa and ~19 kDa, and α -tubulin ~52 kDa. (B) Results were quantitated and summarised in a bar chart, where optical densities were normalised to α -tubulin loading controls. Results are expressed as mean \pm SEM of three independent experiments. * indicates $p < 0.05$ compared with NT in one way ANOVA with Dunnett's post hoc test.

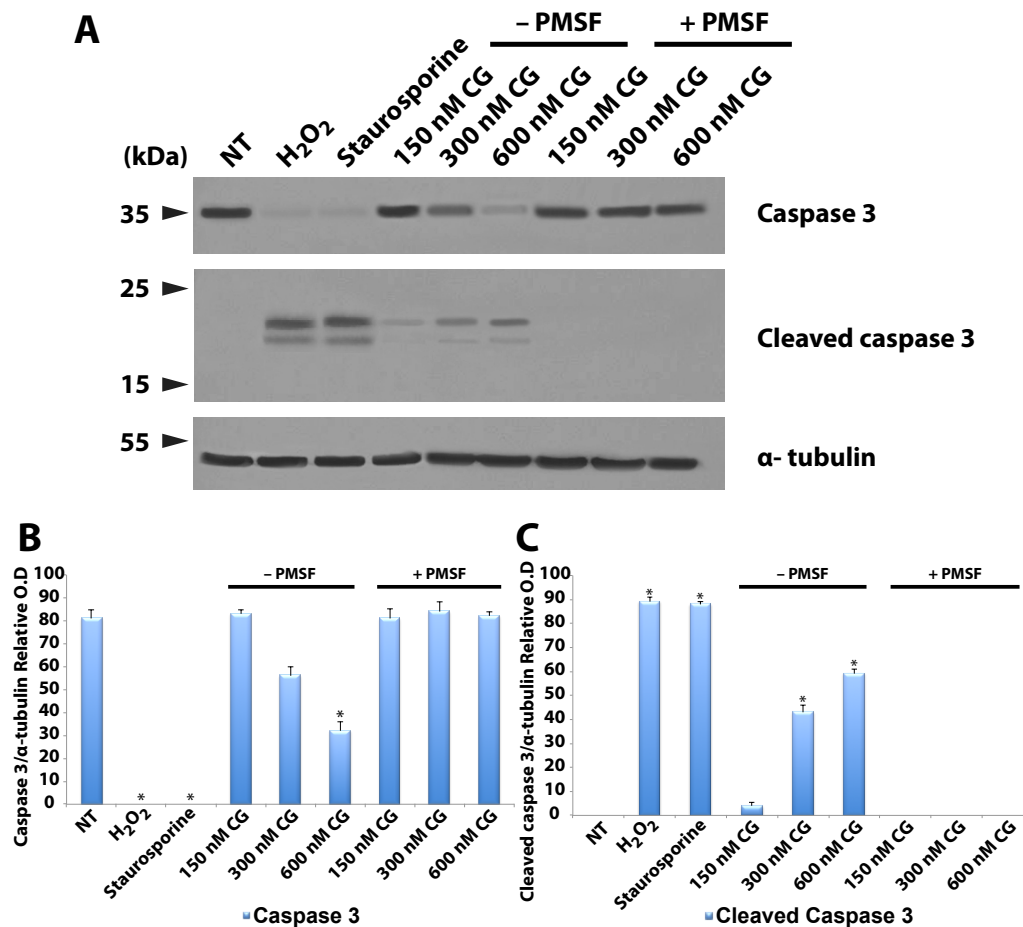


Figure 5.12: Cleaved Caspase-3 Fragments were Detected in Renal Fibroblasts Treated with CG. Quiescent cells were treated with different apoptosis inducers for 24 h. Cell lysates were obtained and then subjected to SDS-PAGE followed by immunoblotting with antibodies against caspase-3 and cleaved caspase-3. (A) HPRFs were treated with 1 mM H₂O₂, 1 μ M staurosporine or various indicated concentrations of CG (with or without 1 mM PMSF pre-treatment). None of these agents were added in the untreated sample (NT). α -tubulin was used as a loading control. Expected band sizes: caspase-3 ~35 kDa, cleaved caspase-3 ~17 kDa and ~19 kDa, and α -tubulin ~52 kDa. (B) Results were quantitated and summarised in a bar chart, where optical densities were normalised to α -tubulin loading controls. Results are expressed as mean \pm SEM of three independent experiments. * indicates $p < 0.05$ compared with NT in one-way ANOVA with Dunnett's post hoc test.

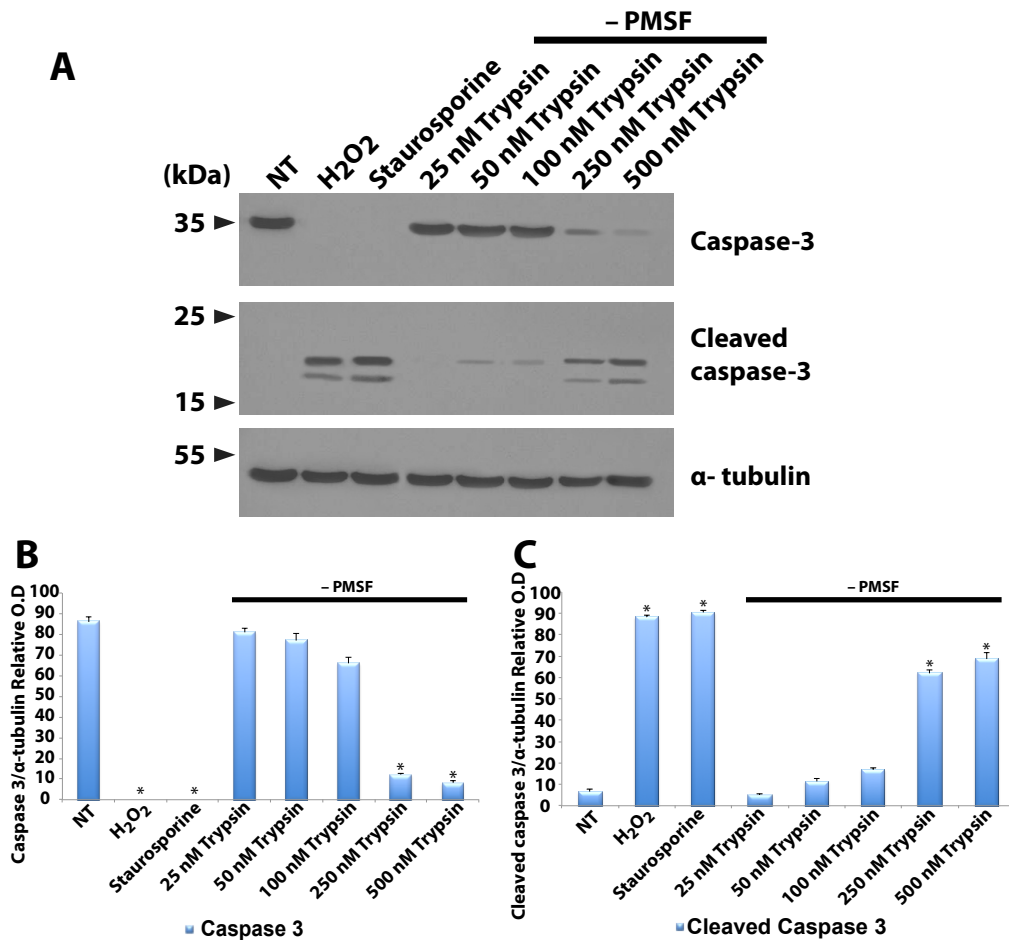


Figure 5.13: Cleaved Caspase-3 Fragments were Detected in Bronchial Fibroblasts Treated with Trypsin. Quiescent cells were treated with different apoptosis inducers for 24 h. Cell lysates were obtained and then subjected to SDS-PAGE followed by immunoblotting with antibodies against caspase-3 and cleaved caspase-3. (A) HPBFs were treated with 1 mM H₂O₂, 1 μ M staurosporine or various indicated concentrations of trypsin. None of these agents were added in the untreated sample (NT). α -tubulin was used as a loading control. Expected band sizes: caspase-3 ~35 kDa, cleaved caspase-3 ~17 kDa and ~19 kDa, and α -tubulin ~52 kDa. (B & C) Results were quantitated and summarised in a bar chart, where optical densities were normalised to α -tubulin loading controls. Results are expressed as mean \pm SEM of three independent experiments. * indicates $p < 0.05$ compared with NT in one-way ANOVA with Dunnett's post hoc test.

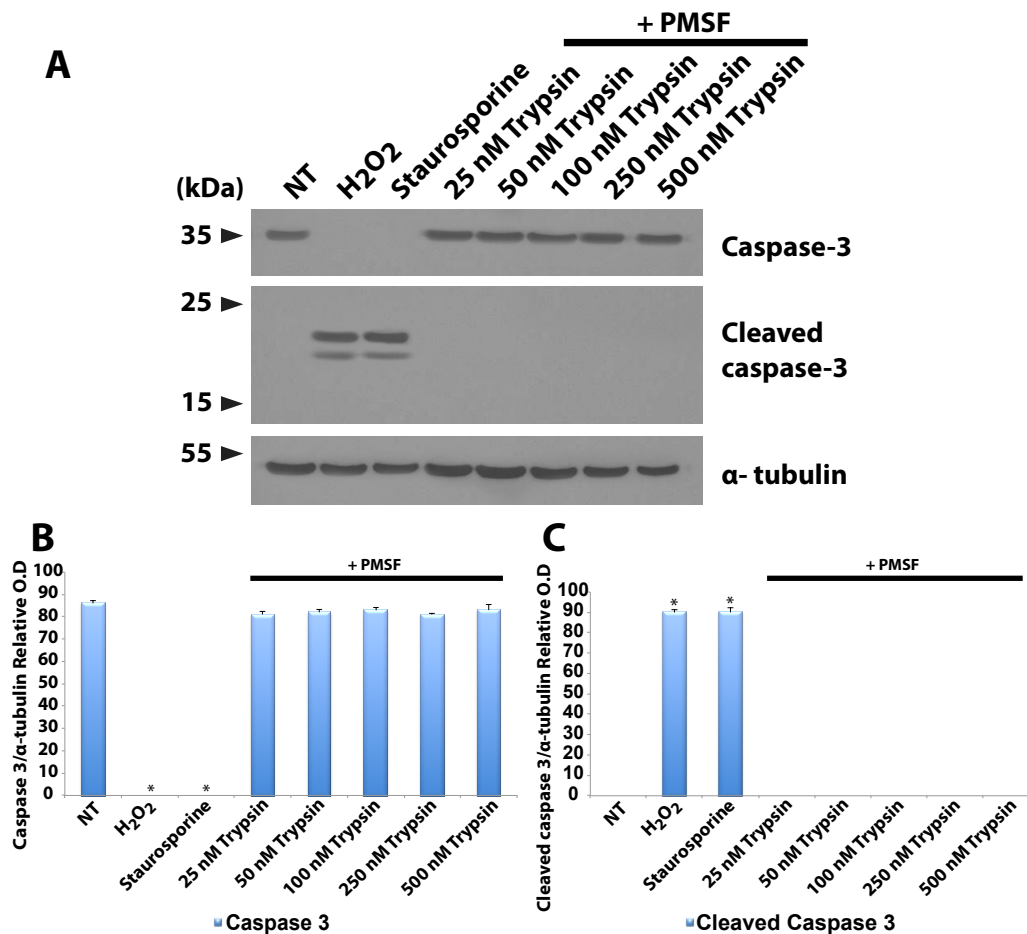


Figure 5.14: No Cleaved Caspase-3 Fragments were Detected in Bronchial Fibroblasts Treated with Trypsin Pretreated with PMSF. Quiescent cells were treated with different apoptosis inducers for 24 h. Cell lysates were obtained and then subjected to SDS-PAGE followed by immunoblotting with antibodies against caspase-3 and cleaved caspase-3. (A) HPBFs were treated with 1 mM H₂O₂, 1 μ M staurosporine or various indicated concentrations of trypsin where trypsin was pre-treated with 1 mM PMSF. None of these agents were added in the untreated sample (NT). α -tubulin was used as a loading control. Expected band sizes: caspase-3 ~35 kDa, cleaved caspase-3 ~17 kDa and ~19 kDa, and α -tubulin ~52 kDa. (B & C) Results were quantitated and summarised in a bar chart, where optical densities were normalised to α -tubulin loading controls. Results are expressed as mean \pm SEM of three independent experiments. * indicates $p < 0.05$ compared with NT in one-way ANOVA with Dunnett's post hoc test.

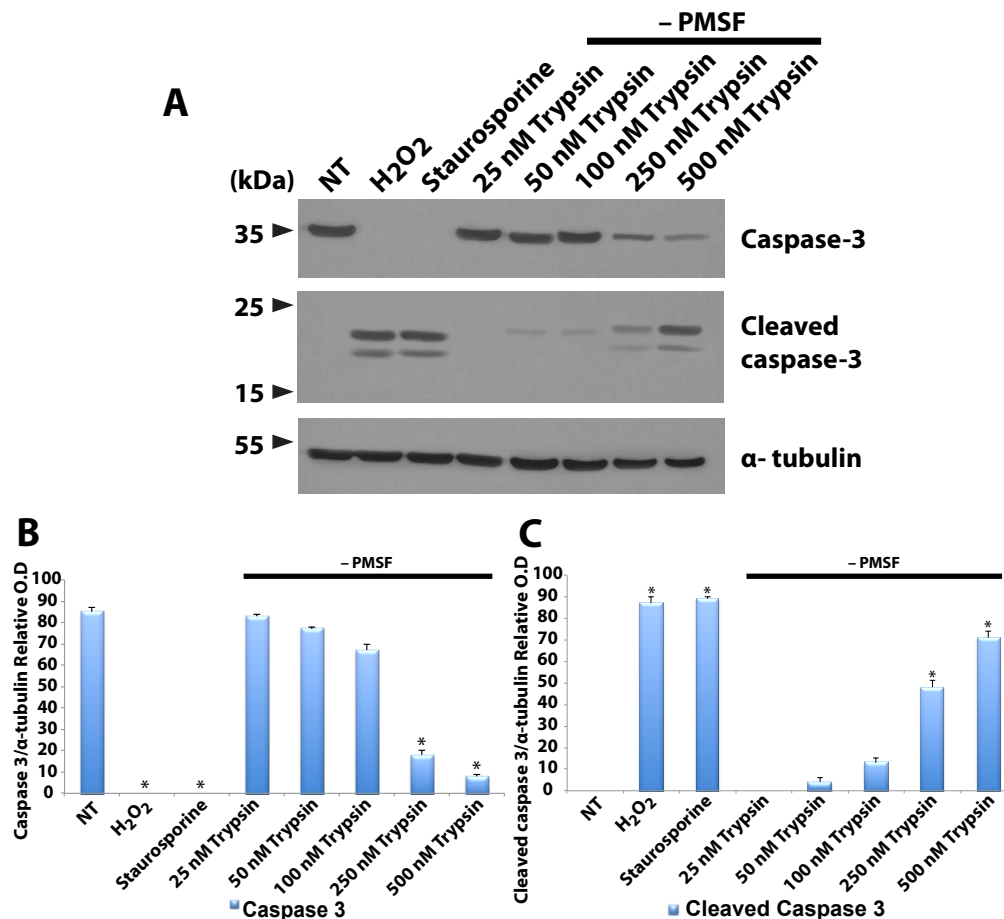


Figure 5.15: Cleaved Caspase-3 Fragments were Detected in Renal Fibroblasts Treated with Trypsin. Quiescent cells were treated with different apoptosis inducers for 24 h. Cell lysates were obtained and then subjected to SDS-PAGE followed by immunoblotting with antibodies against caspase-3 and cleaved caspase-3. (A) HPRFs were treated with 1 mM H₂O₂, 1 μ M staurosporine or various indicated concentrations of trypsin. None of these agents were added in the untreated sample (NT). α -tubulin was used as a loading control. Expected band sizes: caspase-3 ~35 kDa, cleaved caspase-3 ~17 kDa and ~19 kDa, and α -tubulin ~52 kDa. (B & C) Results were quantitated and summarised in a bar chart, where optical densities were normalised to α -tubulin loading controls. Results are expressed as mean \pm SEM of three independent experiments. * indicates $p < 0.05$ compared with NT in one-way ANOVA with Dunnett's post hoc test.

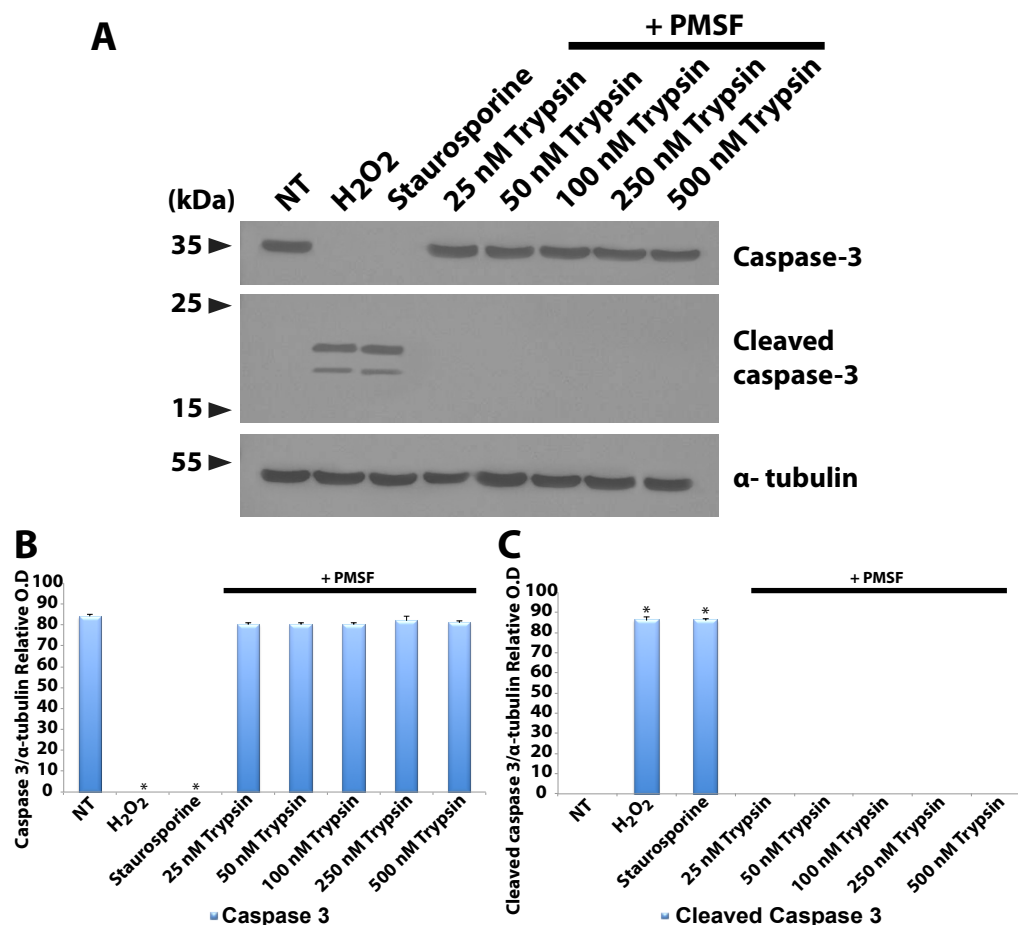


Figure 5.16: No Cleaved Caspase-3 Fragments were Detected in Renal Fibroblasts Treated with Trypsin Pretreated with PMSF. Quiescent cells were treated with different apoptosis inducers for 24 h. Cell lysates were obtained and then subjected to SDS-PAGE followed by immunoblotting with antibodies against caspase-3 and cleaved caspase-3. (A) HPRFs were treated with 1 mM H₂O₂, 1 μ M staurosporine or various indicated concentrations of trypsin where trypsin was pre-incubated with 1 mM PMSF. None of these agents were added in the untreated sample (NT). α -tubulin was used as a loading control. Expected band sizes: caspase-3 \sim 35 kDa, cleaved caspase-3 \sim 17 kDa and \sim 19 kDa, and α -tubulin \sim 52 kDa. (B & C) Results were quantitated and summarised in a bar chart, where optical densities were normalised to α -tubulin loading controls. Results are expressed as mean \pm SEM of three independent experiments. * indicates $p < 0.05$ compared with NT in one-way ANOVA with Dunnett's post hoc test.

5.4.3 Apoptosis Induction in HEK-PAR₄ Cells

Acridine orange staining is suboptimal for use with empty vector control and HEK-PAR₄ cells to detect apoptotic cells as some cells did not contain a recognisable nucleus and only the cytoplasm was stained by acridine orange (**Figure 5.17**). Therefore, FITC-Annexin-V staining using flow cytometry was used to detect apoptosis in empty vector control and HEK-PAR₄ cells. **Figure 5.18** shows representative flow cytometry dot-plots of FITC-Annexin V (FL1)/ propidium iodide (PI) (FL2) dual colour flow cytometry.

HEK-PAR₄ cells were used to investigate whether PAR₄ activation triggered apoptosis in the presence of PAR₄ AP and CG. First, as positive controls for determination of apoptotic index using this FITC-Annexin V flow cytometry assay, empty vector control and HEK-PAR₄ cells were treated with H₂O₂ and staurosporine. Results showed that >70% of apoptotic cells were detected in these samples (**Figure 5.19A**, $p < 0.05$). After 24 h treatment with PAR₄ AP, the amounts of apoptotic cells in empty vector control and HEK-PAR₄ samples were $6 \pm 0.35\%$ and $41 \pm 2\%$, respectively (**Figure 5.19B**). 20 nM CG induced 16% apoptotic cells in both empty vector control and HEK-PAR₄ cells. When treated with 300 nM CG, the numbers of apoptotic cells doubled to $30 \pm 9.25\%$ and $29 \pm 4.7\%$ in empty vector control and HEK-PAR₄ cells, respectively. It is statistically significant compared to the untreated sample. Blocking the CG activity with PMSF reduced apoptosis to less than 10% in both empty vector control and HEK-PAR₄ cells.

To further confirm these results, Western blot analysis was performed using caspase-3 and cleaved caspase-3 antibodies. The presence of the bands corresponding to cleaved caspase-3 fragments indicates that the cells underwent apoptosis (**Figures 5.20 & 5.21**).

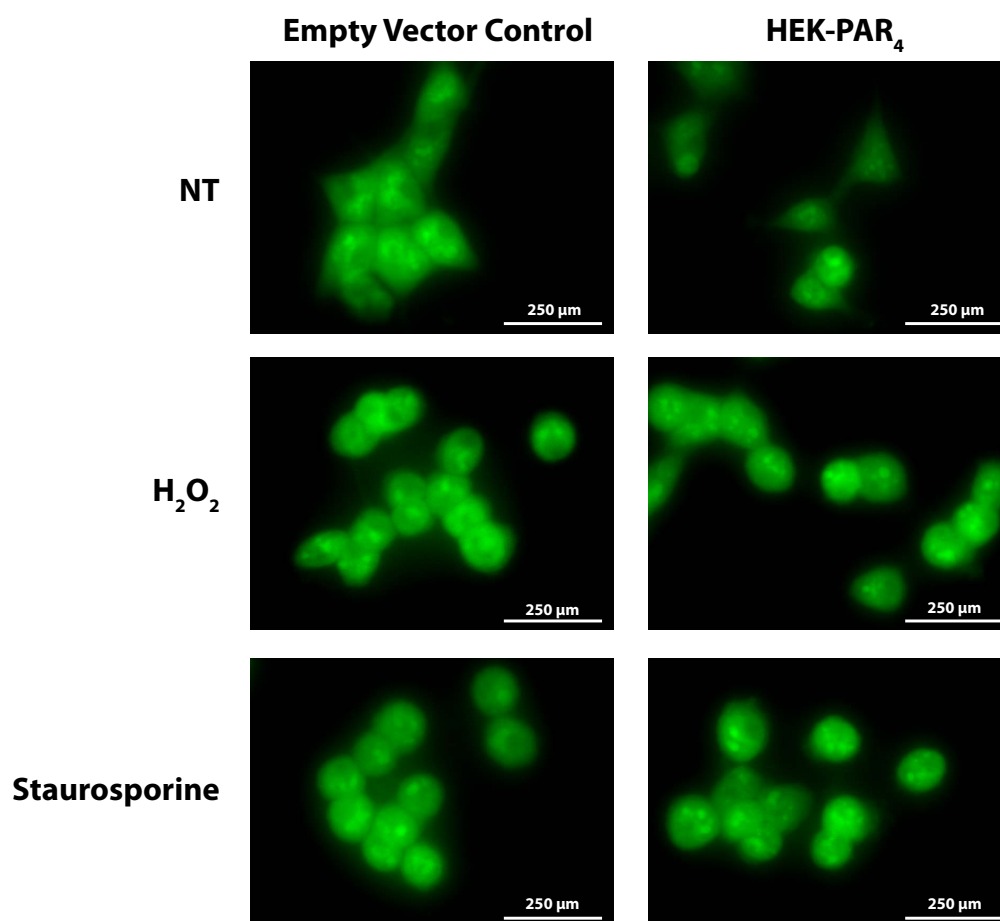


Figure 5.17: HEK-PAR₄ Cells Treated with H₂O₂ and Staurosporine in Acridine Orange Apoptosis Assay. Cells at 70-85% confluence in 24-well plates were quiesced. Quiescent cells were then treated with different apoptosis inducers for 24 h. Then, acridine orange was added to the cells before visualising with fluorescent microscope. Empty vector control or HEK-PAR₄ cells were treated with 1 mM H₂O₂ or 1 μM Staurosporine. No H₂O₂ or staurosporine was added in the untreated samples (NT). Results are representative of three independent experiments.

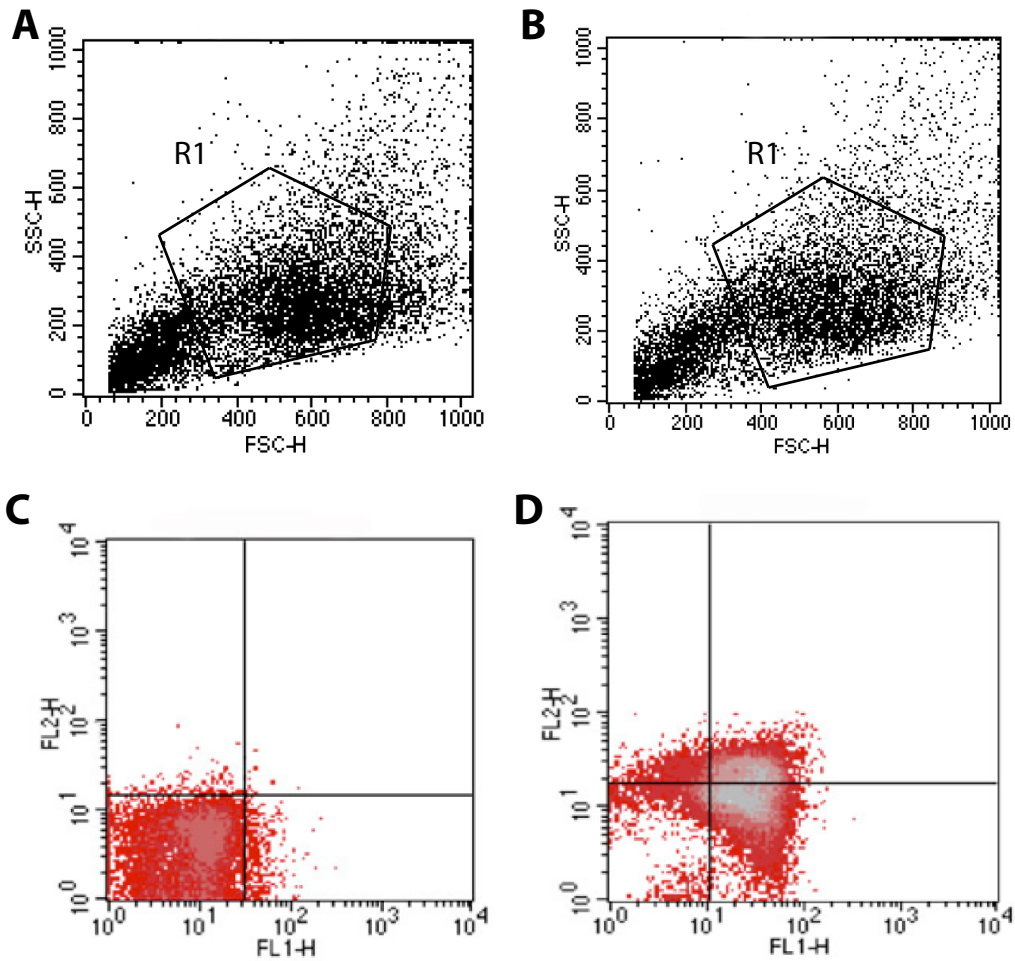


Figure 5.18: Representative Flow Cytometry Dot-plots of FITC-Annexin V (FL1)/ PI (FL2) Dual Colour Flow Cytometry. Cells at 70-85% confluence in 6-well plate were quiesced and treated with different apoptosis inducers for 24 h. The cells were then incubated with FITC-conjugated Annexin V and propidium iodide in the dark. Binding of Annexin V/PI to empty vector control and HEK-PAR₄ cells that were exposed to different apoptosis inducers were evaluated by flow cytometry. (A) Untreated empty vector control. (B) Empty vector control was treated with 1 mM H₂O₂ for 24 h. (C & D) Cells depicted in lower quadrants showed intact cytoplasmic membrane integrity (PI-negative), where the bottom left quadrant (Annexin V-negative) represents viable cells and the bottom right quadrant (Annexin V-positive) represents apoptotic cells. Cells depicted in the top left (Annexin V-negative/PI positive) and top right (Annexin V-positive/PI-positive) quadrants represent necrotic and late apoptotic cells, respectively.

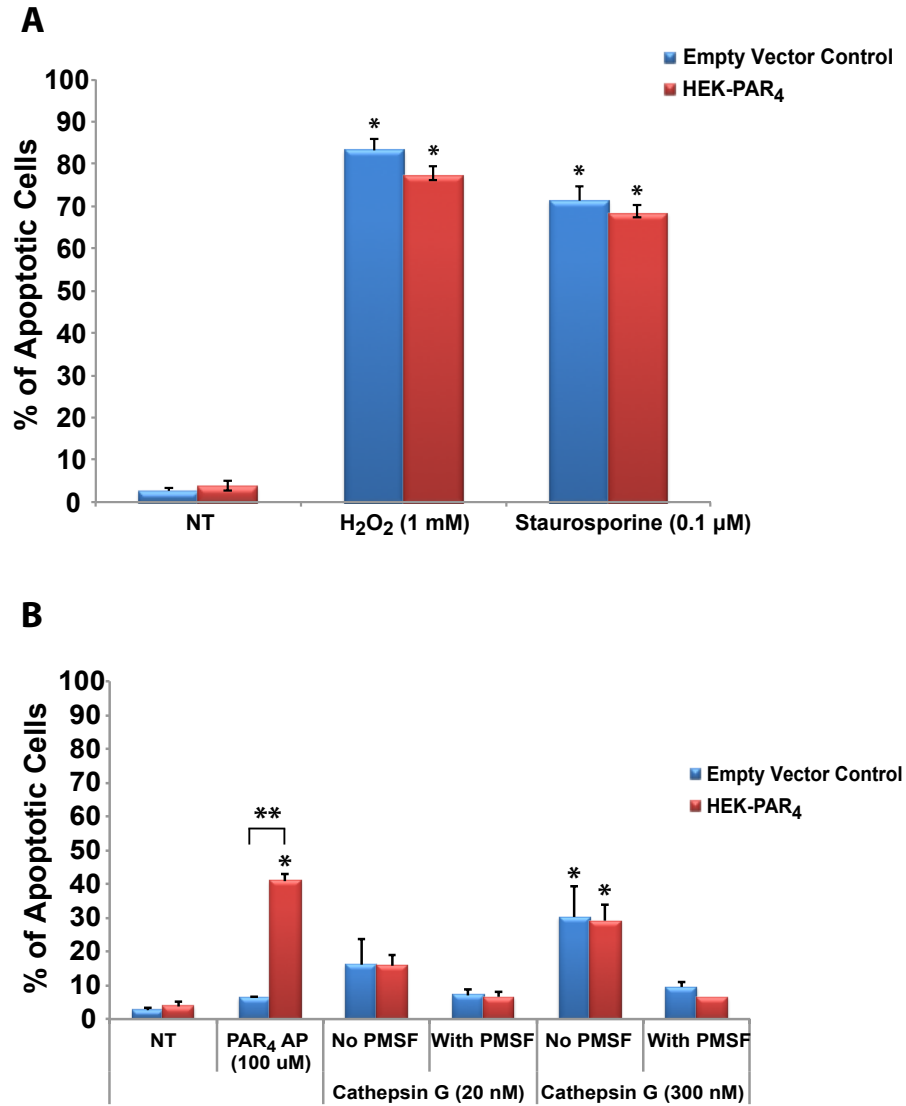


Figure 5.19: Summary of Annexin V Apoptosis Assay. (A) Empty vector control and (B) HEK-PAR₄ cells were treated with H₂O₂, Staurosporine, PAR₄-AP or CG. Results are expressed as percentage of apoptotic cells, presented as the mean \pm SEM of five independent experiments. * indicates $p < 0.05$ compared with NT in one way ANOVA with Dunnett's post hoc test. ** indicates $p < 0.05$ between empty vector control and HEK-PAR₄ cells in one way ANOVA with Bonferroni post hoc test.

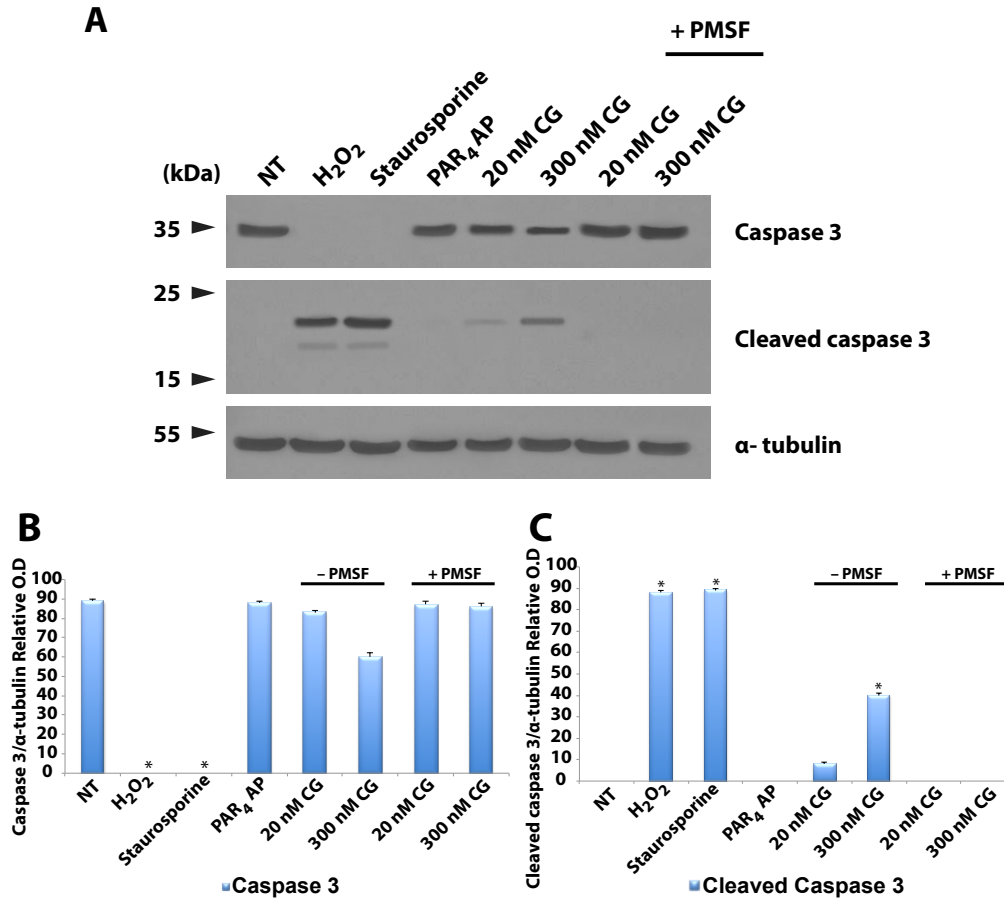


Figure 5.20: Cleaved Caspase-3 Fragments were Detected by Western Blotting in CG treated Empty Vector Control. Quiescent cells were treated with different apoptosis inducers for 24 h. Cell lysates were obtained and then subjected to SDS-PAGE followed by immunoblotting with antibodies against caspase-3 and cleaved caspase-3. Empty vector controls were treated with 1 mM H₂O₂, 1 μ M staurosporine, 100 μ M PAR₄ AP or 20 nM and 300 nM CG (with or without 1 mM PMSF pre-treatment). None of these agents were added in the untreated samples (NT). α -tubulin was used as a loading control. Expected band sizes: caspase-3 (\sim 35 kDa), cleaved caspase-3 (\sim 17 kDa and 19 kDa) and α -tubulin (\sim 52 kDa). (B) Results were quantitated and summarised in a bar chart, where optical densities were normalised to α -tubulin loading controls. Results are expressed as mean \pm SEM of two independent experiments. * indicates $p < 0.05$ compared with NT in one-way ANOVA with Dunnett's post hoc test.

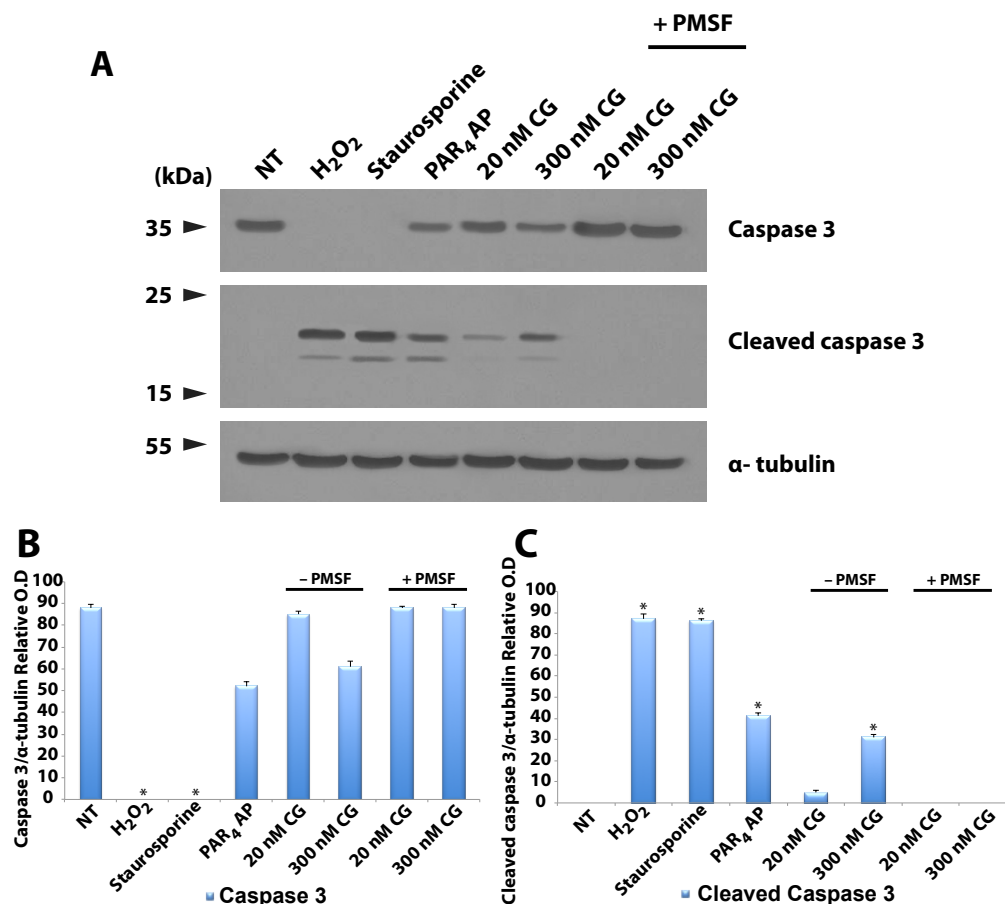


Figure 5.21: Cleaved Caspase-3 Fragments were Detected by Western Blotting in PAR₄ AP and CG treated HEK-PAR₄ Cells. Quiescent cells were treated with different apoptosis inducers for 24 h. Cell lysates were obtained and then subjected to SDS-PAGE followed by immunoblotting with antibodies against caspase-3 and cleaved caspase-3. (A) HEK-PAR₄ cells were treated with 1 mM H₂O₂, 1 μ M staurosporine, 100 μ M PAR₄ AP or 20 nM and 300 nM CG (with or without 1 mM PMSF pre-treatment). None of these agents were added in the untreated samples (NT). α -tubulin was used as a loading control. Expected band sizes: caspase-3 (\sim 35 kDa), cleaved caspase-3 (\sim 17 kDa and 19 kDa) and α -tubulin (\sim 52 kDa). (B) Results were quantitated and summarised in a bar chart, where optical densities were normalised to α -tubulin loading controls. Results are expressed as mean \pm SEM of two independent experiments. * indicates $p < 0.05$ compared with NT in one-way ANOVA with Dunnett's post hoc test.

5.5 Discussion

Apoptosis is a precisely regulated physiological form of cell death that leads to the elimination of intact cells by phagocytes without causing tissue injury (SAVILL, 1994). The pathogenesis of fibrosis might involve apoptotic defects. Wound healing and resolution of tissue injury are associated with apoptosis of activated fibroblasts and myofibroblasts, while tissue scarring and fibrosis are associated with an inappropriate decrease in apoptosis of these cells (DESMOULIÈRE *et al.*, 1995).

Serine proteases degrade proteins through their ability to catalyse the hydrolysis of covalent peptide bonds. The discovery of the PARs revealed a new intracellular signalling role for serine proteases that is in addition to their degradation function, provided new insight into the study of PARs (RUSSELL *et al.*, 2010). Several experimental animal models demonstrated the importance of neutrophils in initiation and maintenance of the inflammatory response. Depletion of neutrophils abrogates inflammation in experimental arthritis (WIPKE and ALLEN, 2001; TANAKA *et al.*, 2006), chronic inflammatory lung diseases (PARK *et al.*, 2006; CHUA *et al.*, 2007), and tissue damage following ischemia/reperfusion injury (SISLEY *et al.*, 1994; SHIMODA *et al.*, 2007). In patients with cystic fibrosis, the levels of CG and elastase are greatly increased (SOMMERHOFF *et al.*, 1990). These findings suggest a potential role for CG and trypsin in generating the pathologic manifestations of fibrosis. Trypsin is known to activate PAR₂ (NYSTEDT *et al.*, 1995) and PAR₄ (XU *et al.*, 1998). Both HPBFs and HPRFs expressed PAR₂ while PAR₄ expression could be upregulated when HPBFs were stimulated with pro-inflammatory cytokines (see **Section 3.4.2**, RAMACHANDRAN *et al.*, 2007). PAR₄ is thought to be involved in pro-inflammatory responses (VERGNOLLE *et al.*, 2002; ANDO *et al.*, 2007b). A greater understanding of PAR₄ activation and the ultimate downstream signalling pathways could reveal targets for the treatment of inflammatory diseases.

In PAR₄ functional studies using calcium mobilisation assay, PAR₄ activation by PAR₄ AP results in brisk rise in intracellular calcium, whereas CG stimulation does not affect intracellular calcium. In addition, CG does not activate PAR₄ in A549 cells which endogenously express PAR₄. These differences in the effect of PAR₄ AP versus CG suggest that CG might not contribute to the proteolytic cleavage of PAR₄. As the concentration, temperature and incubation time potentially affect the action of CG, various concentrations, temperatures and incubation times were tested. All results showed no calcium response (See **Appendix**). The experimental evidence implicating PAR₄ cleavage as the mechanism mediating CG actions is more tenuous and direct evidence that CG cleaves PAR₄ has never been reported. Furthermore, CUMASHI *et al.* (2001) demonstrated that CG did not trigger aggregation in murine platelets and SABRI *et al.* (2003b) also demonstrated that human PAR₄ conferred responsiveness to thrombin and PAR₄ AP but not to CG. These studies and experimental data reported herein demonstrate that CG acts independently of PAR₄. Together this suggests that CG does not proteolytically activate PAR₄.

Interestingly, the results presented here indicate that CG might inhibit, rather than activate, PAR₄. When the cells pretreated with CG before the addition of PAR₄ AP, the amplitude of the calcium response to PAR₄ AP was reduced. Also, when CG was pretreated with 1 mM PMSF (as shown in **Figure 5.3**, CG (300 mM) action was completely blocked using 1 mM PMSF), the magnitude of the calcium responses were similar to those observed when PAR₄ AP alone was added. Furthermore, in order to investigate whether the reduced calcium response was due to the cleavage of PAR₄ AP by CG, PAR₄ AP and CG were mixed together before performing the calcium assay. Results obtained were similar to the observation when PAR₄ AP and CG were added sequentially, indicating that CG did not cleave PAR₄ AP. Hence, the inhibiting action of CG on HEK-PAR₄ and

A549 cells suggests that CG might cleave at a secondary site within the ECL2 domain of PAR₄, causing PAR₄ to be unresponsive to the PAR₄ AP.

In contrast, SAMBRANO *et al.* (2000) demonstrated that CG could activate PAR₄ in human platelets and lead to platelet aggregation. The differences in CG responses between the findings presented in this chapter and SAMBRANO *et al.* (2000) might be due to the cell specific differences in post-translational processing of PAR₄, such as phosphorylation and glycosylation. Although it is currently unclear if glycosylation happens to and affects PAR₄. It is known that the N-linked glycosylation of a receptor may regulate conformation, folding or stability, as well as protect the receptor from proteolytic degradation (XIAO *et al.*, 2011). N-linked glycosylation in ECL2 is important for optimal receptor cell surface expression, receptor stability and function (XIAO *et al.*, 2011). The extent of glycosylation of a receptor could influence the receptor activation. NAKAYAMA *et al.* (2003) demonstrated that trypsin was able to cleave PAR₁ but did not activate PAR₁ in the endothelial cells, whereas XIAO *et al.* (2011) demonstrated that trypsin could activate PAR₁ in epithelial cells. This difference could be explained by the different extent of glycosylation of PAR₁ in different cell types. PAR₁ expressed in platelets and endothelial cells is not heavily glycosylated (BRASS *et al.*, 1992), whereas PAR₁ expressed in epithelial cells is highly glycosylated (XIAO *et al.*, 2011).

Data obtained here suggest that CG does not activate PAR₄ in this HEK-PAR₄ cell line. Instead, the observation that CG-treated cells elicit a reduced signalling response to the stimulatory action of PAR₄ AP suggests that CG might inhibit PAR₄, at least in these HEK-PAR₄ cells. Thus, further studies are required to investigate if CG cleaves PAR₄ at another site to cause the inhibition. This could be done by first identify the other possible CG cleavage sites and then test the effects of mutations to these

sites. As discussed above, PAR activation can also be regulated by glycosylation, thus it would be interesting to study the effect of glycosylation in PAR₄ function.

This chapter also attempts to examine whether CG and trypsin could induce fibroblast cell death. After 24 h treatment with CG and trypsin, fibroblasts showed a reduction in size, progressive loss of cell-cell contacts and detachment from the plates. The addition of progressively higher concentrations of CG and trypsin to fibroblasts produced an increase in the percentage of apoptotic cells, suggesting that both CG and trypsin can induce apoptosis in HPBFs and HPRFs. The serine protease inhibitor PMSF partly interferes with the interaction of CG and trypsin with the receptor by specifically binds to their serine residues (YAMAZAKI and AOKI, 1997). When CG and trypsin were pre-treated with PMSF, the number of apoptotic cells dramatically reduced. The inhibitory effect of PMSF on fibroblast apoptosis in the presence of CG and trypsin suggests that the active catalytic site of the proteases is required for triggering apoptosis. These results were further supported by the observation of caspase-3 cleavage (an indication of apoptotic event) using Western blotting. This study is comparable to the study demonstrated by SABRI *et al.* (2003b). They demonstrated that CG can trigger detachment-induced apoptosis (anoikis) and activate caspase-3 in cardiomyocytes. In addition, RAMACHANDRAN *et al.* (2007) demonstrated CG reduced cell number in TNF- α -treated HPBF where PAR₄ was induced.

Some proteases from the circulation, exocrine glands and inflammatory cells can cleave PARs and thereby regulate inflammation, healing, pain and homeostasis (COTTRELL *et al.*, 2004). During inflammation, both CG and PAR₄ can be up-regulated by pro-inflammatory mediators (SOMMERHOFF *et al.*, 1990; OWEN *et al.*, 1995; RAMACHANDRAN *et al.*, 2007). Hence, the second aim of this chapter was to examine if CG and PAR₄ AP could

induce apoptosis in HEK-PAR₄ cells when PAR₄ is activated. The acridine orange assay did not reliably identify apoptosis in empty vector control and HEK-PAR₄ cells (see **Figure 5.17**). Therefore, FITC-Annexin V flow cytometry was performed. The apoptotic cells were assessed by the binding of Annexin V to the phosphatidylserine (PS) exposed on the cell membrane. Annexin V is a calcium ion dependent phospholipid binding protein that has a high affinity for PS and binds to cells with exposed PS. It is conjugated to FITC and thus serves as a sensitive probe for flow cytometric analysis of cells that are undergoing apoptosis. The loss of cell membrane phospholipid asymmetry during early phases of apoptosis is accompanied by exposure of PS to the outer membrane. The movement of PS to the extracellular membrane surface is a characteristic event of cells undergoing apoptosis. As the externalisation of PS occurs in the earlier stages of apoptosis, FITC-Annexin V staining can identify apoptosis at an earlier stage than the other assays based on the nuclear changes such as DNA fragmentation (RIEGER *et al.*, 2011). FITC-Annexin V staining is typically used in conjunction with PI to allow identification of early apoptotic cells (Annexin V positive, PI negative). Cells negative for both PI and Annexin V staining are viable cells; PI-negative and Annexin V-positive cells are early apoptotic cells; PI-positive and Annexin V-negative cells are necrotic cells; whereas PI-positive and Annexin V-positive cells are primarily cells in late stages of apoptosis (RIEGER *et al.*, 2011).

An apoptosis assay was performed to test if CG triggers apoptosis via PAR₄ signalling. The percentage of apoptotic cells induced by CG is concentration dependent (see **Appendix, Figure A.6**), where the numbers of apoptotic cells increased as the concentrations of CG were increased from 20 nM to 600 nM. However, there is no significant difference in the numbers of apoptotic cells between empty vector control and HEK-PAR₄ cells following treatment with 20 or 300 nM CG (**Figure 5.19**). This effect of CG is dependant on CG activity, as pre-treatment of

CG with PMSF reduced the numbers of apoptotic cells. However, activation of PAR₄ with PAR₄ AP induced higher level of apoptosis in HEK-PAR₄ cells (41%), whereas only 6% apoptotic cells were observed in the PAR₄ AP-treated empty vector control cells. Together, these results suggest that CG induces apoptosis independently of PAR₄.

It was hypothesised that in fibrosis, enhancement of fibroblast apoptosis is beneficial to the host. The results presented above suggest that CG, trypsin and PAR₄ AP have the potential to induce cell death. Importantly, this study provides the first evidence that CG can act as a potent apoptosis inducer in human cultured lung and renal fibroblasts. Results obtained here also suggest that CG induces apoptosis independently of PAR₄. As HPBFs, HPRFs, and HEK-PAR₄ cells all express PAR₁ and PAR₂, CG might act on the other PARs or via another mechanism to induce fibroblast apoptosis. Thus, this suggests that CG and trypsin might help in tissue repair by triggering fibroblast cell death during inflammation without PAR₄ expression. In contrast, PAR₄ AP induced a pronounced apoptosis in HEK-PAR₄ cells compared to the empty vector control, indicating a PAR₄-dependent apoptosis signalling pathway exists.

In conclusion, the results presented here suggest that CG and trypsin can induce fibroblasts apoptosis independently of PAR₄ and PAR₄ AP can trigger apoptosis in HEK-PAR₄ cells via PAR₄ signalling pathway. The local release of CG and trypsin in areas of inflammation may help tissue remodelling by triggering fibroblast cell death without PAR₄ expression. Although LPS failed to consistently induce PAR₄ expression in bronchial fibroblasts as demonstrated in chapter 3, it is still possible that bronchial fibroblasts express PAR₄ when expose to the pro-inflammatory mediators. In this case, fibroblast cell death can be triggered by PAR₄ activation. These PAR₄-dependent and independent mechanisms of cell death could reveal potential therapeutic targets for the treatment of fibrosis. A

potential problem for therapeutic manipulation is cell type specificity. Ideally, CG and trypsin should specifically induce apoptosis in fibroblasts while not affect the other cell types. Hence, further careful investigations to elucidate the regulation mechanisms of apoptosis in fibroblasts would contribute to the development of more specific therapies for IPF and renal fibrosis.

Chapter 6

Epithelial Cell-Derived Medium and PAR₄ Can Regulate Fibroblast Proliferation

6.1 Introduction

Epithelial cells attach to the basement membranes to provide context and architectural stability for the cell-cell contact. When the basement membrane is damaged by protease or disrupted by alteration in assembly, epithelial cells become activated, detach from damaged basement membranes and start secreting cytokines (ZEISBERG and KALLURI, 2004). Fibroblasts are the major ECM producer in the wound healing and excessive fibroblast proliferation is associated with excessive collagen deposition and fibrosis (RAMOS *et al.*, 2006). Damage of epithelial cells and disruption of a normal epithelial-fibroblast interaction are sufficient to promote fibroblast growth and excessive collagen deposition (ADAMSON *et al.*, 1988). Conversely, normal levels of fibroblast growth and collagen are seen in the cultured explants where little or no disruption of epithelial-fibroblast interaction takes place (ADAMSON *et al.*, 1988).

Several studies have implicated excessive apoptosis in epithelial cells as a potential mechanism of acute tissue injury and fibrosis (HAGIMOTO *et al.*, 1997c; NOMOTO *et al.*, 1997; KUWANO *et al.*, 1999b). Apoptosis of damaged epithelium can be caused by death receptor-mediated pathway (Fas-FasL), loss of contact to the basement membrane or intrinsic organelle-dependent pathway which involves lysosomal permeabilisation or mitochondria damage (KUWANO *et al.*, 2004). In a mouse model of bleomycin-induced pulmonary fibrosis, FasL mRNA was upregulated in infiltrating lymphocytes, and Fas was upregulated in bronchiolar and AECs in which excessive apoptosis was detected. Fas is a type I membrane receptor protein that belongs to the TNF receptor family which can induce apoptosis after binding to FasL (KUWANO *et al.*, 1999a). Blockade of either the Fas-FasL pathway or caspase inactivation by caspase inhibitors has been shown to prevent epithelial cell apoptosis and fibrosis. Hence, loss of epithelial cells through the Fas-mediated pathway has a critical role in tissue injury and organ dysfunction (KUWANO *et al.*, 1999a). In addition, HAGIMOTO *et al.* (2002) demonstrated that upregulation of Fas and FasL expression was observed in bronchiolar and AECs in lung tissue from IPF patients. Thus, apoptosis of lung epithelial cells by Fas ligation may be involved in the pathogenesis of pulmonary fibrosis.

Damaged epithelial cells synthesis and release pro- and anti-inflammatory molecules that can recruit and activate inflammatory cells and thus modulate a variety of inflammatory responses (KNIGHT *et al.*, 1994). Cytokines that are released by the epithelial cells include PGE₂, IL-1 α , PDGF, bFGF and TGF- β , which are involved in the regulation of fibroblast proliferation (HOLGATE *et al.*, 2000; KNIGHT and HOLGATE, 2003; SACCO *et al.*, 2004).

PGE₂ is a lipid mediator derived from cell membrane phospholipid and is a potent inhibitor of fibroblast functions, including migration (KOHYAMA *et al.*, 2001), proliferation (BITTERMAN *et al.*, 1986) and collagen synthesis (GOLDSTEIN and POLGAR, 1982). It is the key mediator of the suppressive effects of epithelial cells on fibroblasts (LAMA *et al.*, 2002; MOORE *et al.*, 2003). IL-1 α is an important inducer of PGE₂ and it suppresses fibroblast proliferation (PORTNOY *et al.*, 2006). Hence, loss of epithelial cells may cause a deficit of anti-proliferative factors, promoting the fibroblast proliferation and the development of fibrosis. Fibrosis may also result from either an inadequate generation of these suppressive factors by the epithelial cells or from an inadequate response of fibroblasts to these factors (HOSTETTLER *et al.*, 2008). PDGF is one of the most potent mitogens and chemoattractants for mesenchymal cells and it induces the proliferation of fibroblasts and synthesis of ECM (ROM *et al.*, 1988). bFGF is a potent stimulator of both fibroblast and endothelial cell proliferation and is associated with the fibroproliferative response (KUWANO *et al.*, 2004).

TGF- β is a potent cytokine associated with tissue fibrosis and structural remodelling (ANSCHER *et al.*, 1993; WESTERGREN-THORSSON *et al.*, 1993; SIME *et al.*, 1997; SAGARA *et al.*, 2002; BALZAR *et al.*, 2005). TGF- β expression is upregulated in AECs and macrophages in fibroproliferative lesions (MADTES *et al.*, 1994). The production of active TGF- β by epithelial cells at the sites of injury may be a critical event in healing processes. It is involved in the regulation of fundamental cell functions, including proliferation, differentiation, apoptosis and migration. Conversely, it also inhibits the proliferation of many cell types, emphasising the complexity of this cytokine (MCANULTY *et al.*, 1997). It has been shown to function as a potent mitogen on fibroblasts (MOSES *et al.*, 1994), inhibiting the growth of epithelial cells and vascular endothelial cells (TUCKER *et al.*, 1984; TAKEHARA *et al.*, 1987).

There are studies which demonstrated that PAR activation mediates the release of inflammatory cytokines during inflammation. Human respiratory epithelial cells produce IL-6, IL-8 and PGE₂ in response to PAR₄ agonist peptides (ASOKANANTHAN *et al.*, 2002). It has also been demonstrated that PAR₄ is involved in the induction of actin fibre formation in lung vascular endothelial cells (FUJIWARA *et al.*, 2005). Furthermore, PAR₄ stimulation induces EMT in primary cultured alveolar epithelial cells (ANDO *et al.*, 2007c). These findings suggest that PAR₄ appear to play a role in mediating cytokines release from different cell types during injury and inflammation.

6.2 Aims

Severe injury with dysfunctional epithelial repair processes results in prolonged disruption of the normal intercellular relationships, particularly between the epithelial cells and the fibroblasts (ADAMSON *et al.*, 1988). Hence, the hypothesis of this chapter is that accumulation of fibroblasts during fibrosis is regulated by a number of mediators that can direct their recruitment and proliferation, which are possibly released by the injured epithelial cells or the activation of PAR₄.

The aims of this chapter are to examine:

1. The effect of media collected from confluent epithelial cell cultures, which are thought to contain a number of cytokines released by the epithelial cells, on the proliferation of HPBFs and HPRFs.
2. The effect of PAR₄ activation on fibroblast proliferation.

6.3 Methods

6.3.1 Preparation of Conditioned Media

A549, normal rat kidney epithelial cells (NRK52E) and HEK-PAR₄ cells were used in this chapter.

To obtain conditioned medium, cells were passaged into 75 cm² flasks and allowed to reach 100% confluence. In experiments designed to study PAR₄-induced mediator secretion, human PAR₄-AP (100 μ M) was added to the flasks cultured with A549 or HEK-PAR₄ cells whereas rat PAR₄ AP (100 μ M) was added to the flasks cultured with NRK52E cells for 24 h. The cultured medium was collected, centrifuged at $400 \times g$ for 5 min to remove any cell debris, split into aliquots and stored at -80°C.

6.3.2 Proliferation Assay

HPBFs or HPRFs were cultured in 96-well plates with 200 μ l fibroblast growth medium and allowed to grow to 40-50% confluence. The cells were then quiesced in serum free media for 24 h (see **Section 2.3**). Next, the conditioned medium collected in **Section 6.3.1** was added to each well at different volumes and incubated for 24 h. Wells with fibroblast complete growth medium only were used as a negative control. After 24 h, the microplate was gently inverted and blotted onto paper towels to remove the medium from the wells. The microplate with cells was then frozen at -80°C for 24 h. Subsequently, the microplate was thawed at room temperature and the proliferation assay was performed using CyQUANT cell proliferation assay kit according to the manufacturer's instructions. This kit uses a proprietary green fluorescent dye (CyQUANT GR dye) which exhibits strong fluorescent enhancement when bound to cellular nucleic acids. The fluorescence of the samples in the microplate was measured

using a fluorescence microplate reader (Infinite 200) with excitation at 480 nm and emission at 520 nm.

6.3.3 Immunofluorescent Staining of α -SMA

HPBFs or HPRFs were seeded on the cover slips and grown in 6-well plates. Once the desired confluence (80%) was obtained, the cells were treated with fibroblast medium and conditioned medium at 1:1 ratio or solely the conditioned medium for 24 h before proceeding for staining as described in **Section 2.8**.

6.3.4 Generation of Whole Cell Lysates

HPBFs or HPRFs were passaged into 25 cm² culture flasks and allowed to reach over 80% confluence before treating with different conditioned media at different ratios for 24 h. The fibroblasts were then harvested by centrifugation at 500 \times g for 5 min and lysed by adding 500 μ l Laemilli's sample buffer as described in **Section 2.10**.

6.3.5 SDS-PAGE and Western Blotting

Protein samples were separated on a 12.5% SDS-PAGE gel before transferring to a nitrocellulose membrane using i-blot (Invitrogen, UK) as described in **Sections 2.11** and **2.12**.

The membrane was then blocked with 5% milk solution, incubated with primary and secondary antibodies as described in **Section 2.12**. Primary antibodies: rabbit polyclonal anti- α -SMA (1:100) and rabbit polyclonal anti-collagen type I (1:5000); secondary antibody: donkey anti-rabbit HRP. For loading control, mouse monoclonal IgG1 anti- α -tubulin (1:1000) was

used as primary antibody and goat anti-mouse IgG HRP (1:2000) was used as secondary antibody. The blot was visualised using the ECL detection system.

6.4 Results

6.4.1 Proliferation Assay

It is believed that during wound healing, the loss of epithelial cells will release mediators such as PDGF, TNF- α and FGF that can induce the proliferation of fibroblasts (Hostettler et al. 2008). Hence, the effect of epithelial cell-conditioned media (see **Section 6.3.1**) on fibroblast proliferation was evaluated using the CyQUANT cell proliferation assay kit. As TGF- β 1 has important roles in the pathogenesis of fibrosis and the potential in regulation of cell proliferation. Thus, the effect of TGF- β 1 on proliferation of HPBFs and HPRFs was tested. When grown in the presence of 1 ng/ml or 5 ng/ml TGF- β 1, the numbers of HPBFs and HPRFs were higher compared to the controls without TGF- β 1, particularly when they were treated with TGF- β 1 (5 ng/ml) (**Figure 6.1**). This indicates that TGF- β 1 induces proliferation of these fibroblasts. Hence, for the following proliferation experiments, TGF- β 1 was used as a positive control. However, the number of cells is slightly increased when treated with 10 ng/ml of TGF- β 1 (**Figure 6.1**).

To determine whether epithelial cell-conditioned media promotes fibroblast proliferation, HPBFs and HPRFs were cultured with A549 and NRK52E cell-derived conditioned media, respectively, for 24 h (see **6.3.1**). This led to a significant increase in the number of fibroblasts in a concentration dependent manner (**Figures 6.2 & 6.3**). The greatest proliferative activity was observed when 140 μ l conditioned medium was added to HPBFs ($p= 0.004$) and HPRFs ($p= 0.001$) (**Figures 6.2 & 6.3**,

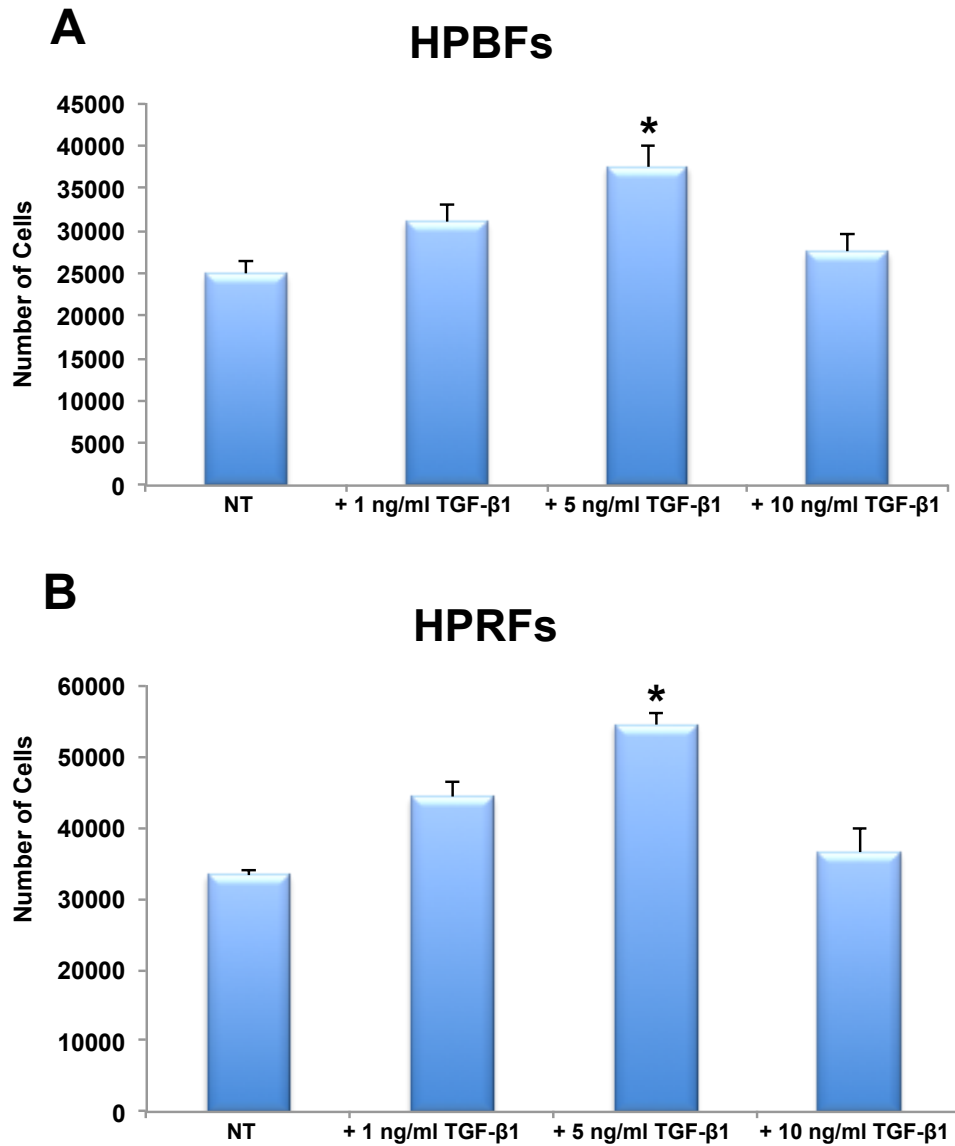


Figure 6.1: TGF- β 1 Induced Proliferation of HPBFs and HPRFs. (A) HPBFs and (B) HPRFs at 40-50% confluence in 96-well plate were quiesced and treated with different concentrations of TGF- β 1 as indicated. No TGF- β 1 was added to the untreated sample (NT). Numbers of cells were scored using CyQUANT cell proliferation assay kit. Results were presented as mean \pm SEM of six independent experiments. * indicates $p < 0.05$ *vs.* NT in one-way ANOVA with Dunnett's post hoc test.

blue bars). Proliferative activity decreased slowly after the peak but was still higher than the untreated samples (solely fibroblast growth medium, without any epithelial cell-derived conditioned media).

To examine the effect of epithelial cell-conditioned media on the fibroblast proliferation when PAR₄ is activated, A549 and NRK52E cells were stimulated with 100 μ M PAR₄ AP for 24 h before collecting the medium. The epithelial cell-conditioned media with activated PAR₄ induced the proliferation of both HPBFs and HPRFs in a dose dependent manner (**Figures 6.2 & 6.3**, red bars). In the presence of PAR₄ AP, the peak of proliferative activity was observed when 180 μ l of conditioned medium was added ($p= 0.041$) and 160 μ l in HPRFs ($p= 0.015$), respectively.

The effect of culture medium from HEK-PAR₄ cells on fibroblasts was then investigated to test if activation of PAR₄ leads to secretion of cytokines that induce fibroblast proliferation during inflammation (**Figure 6.4**). When lower amounts of HEK-PAR₄-derived conditioned medium (up to 10 μ l; with/without PAR₄ activation by PAR₄ AP) were used to treat the fibroblasts, the cell numbers for both HPBFs and HPRFs increased, indicating proliferation of the fibroblasts. When greater than 10 l of HEK-PAR₄-derived conditioned medium was added, the proliferative activity decreased. However, these proliferation activities are not statistically significant when compared to the controls where no HEK-PAR₄-derived conditioned medium was used. In addition, again, no statistical significance was observed when comparing the proliferation activities of cells treated in medium derived from PAR₄-activated culture to those treated in medium derived from culture without PAR₄ activation.

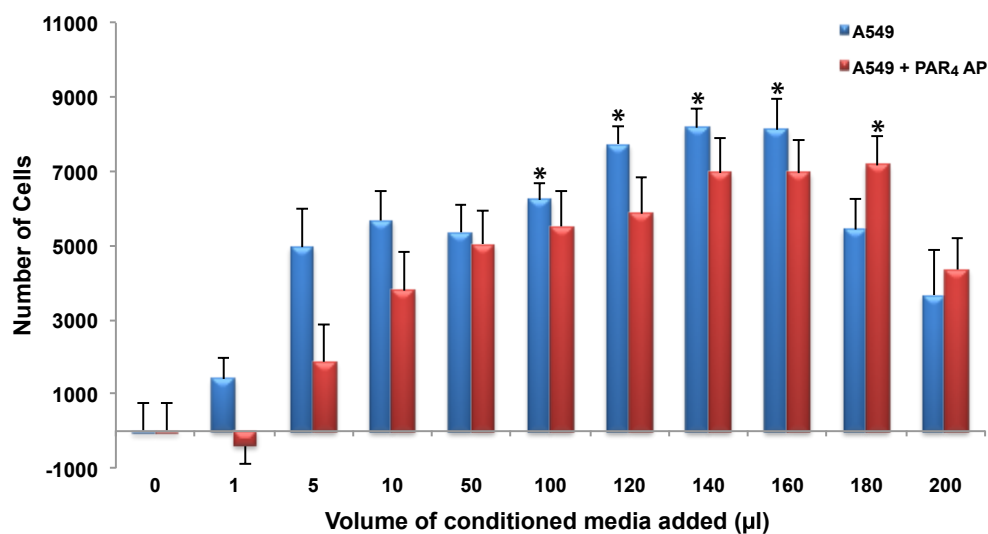


Figure 6.2: A549 Cell-derived Conditioned Medium Promotes Bronchial Fibroblasts Proliferation. A549 cells were cultured in the absence (blue) or presence (red) of 100 μ M PAR₄ AP for 24 h. The culture medium was collected and added to the fibroblast culture medium of HPBFs at the indicated volumes, such that each sample was grown in a total volume of 200 μ l, for a further 24 h period. Numbers of cells was scored using CyQUANT cell proliferation assay kit. Results are expressed as mean \pm SEM of six independent experiments. * indicates $p < 0.05$ vs. 0 μ l conditioned medium in one-way ANOVA with Dunnett's post hoc test.

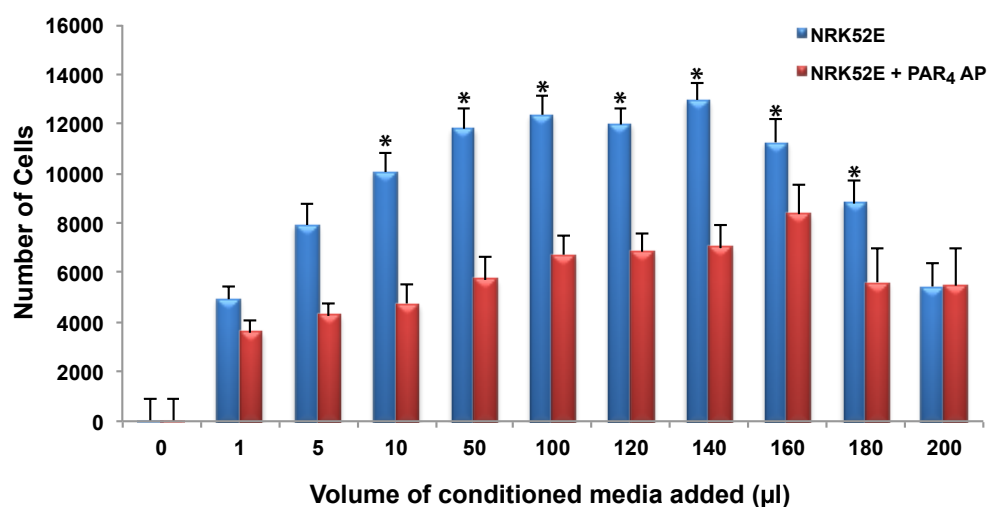


Figure 6.3: NRK52E Cell-derived Conditioned Medium Promotes Renal Fibroblasts Proliferation. NRK52E cells were cultured in the absence (blue) or presence (red) of 100 μ M PAR₄ AP for 24 h. The culture medium was collected and added to the fibroblast culture medium of HPRFs at the indicated volumes, such that each sample was grown in a total volume of 200 μ l, for a further 24 h period. Numbers of cells was scored using CyQUANT cell proliferation assay kit. Results are expressed as mean \pm SEM of six independent experiments. * indicates $p < 0.05$ vs. 0 μ l conditioned medium in one-way ANOVA with Dunnett's post hoc test.

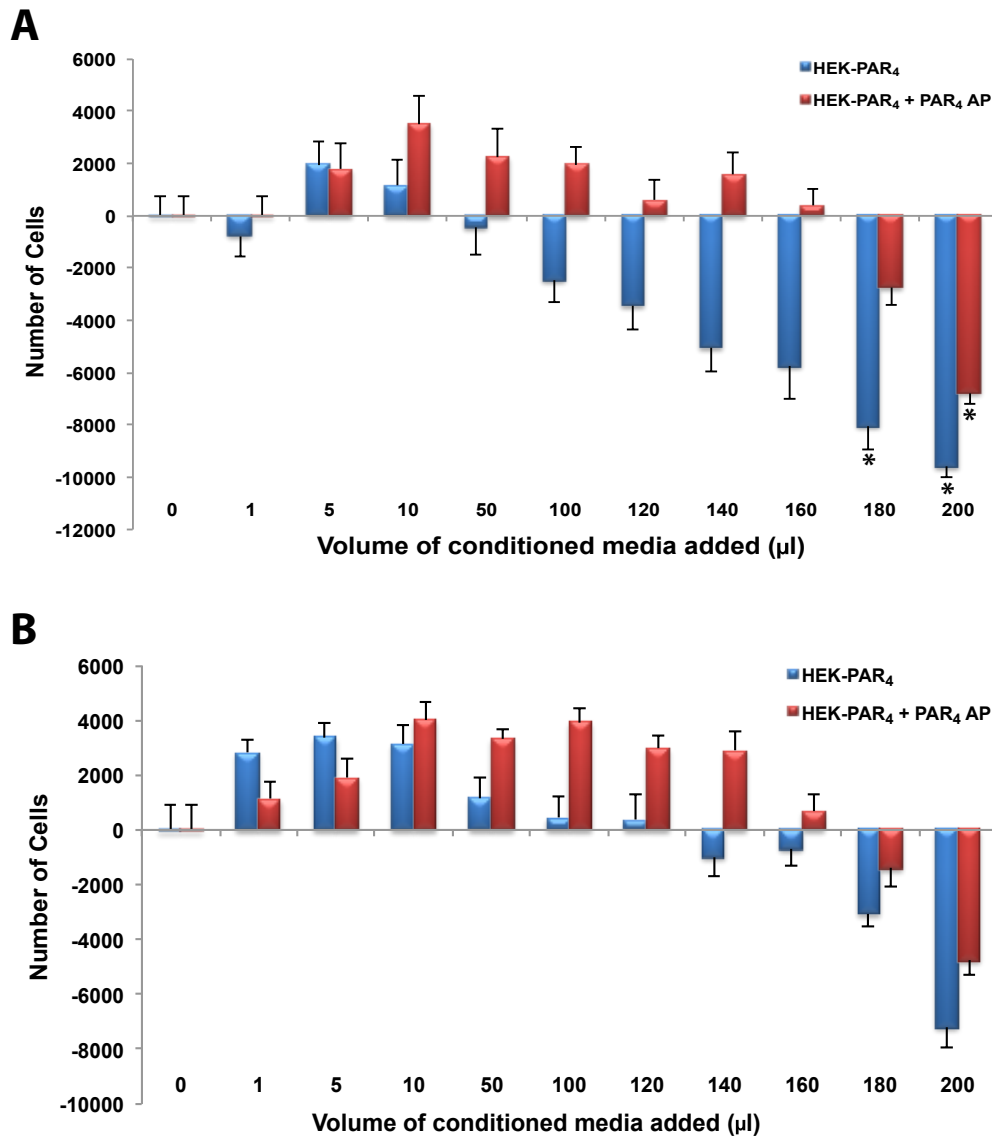


Figure 6.4: HEK-PAR₄ Cell-derived Conditioned Medium does not Promote Proliferation in Bronchial and Renal Fibroblasts. HEK-PAR₄ cells were cultured in the absence (blue) or presence (red) of 100 μ M PAR₄ AP for 24 h. The culture medium was collected and added to the culture medium of (A) HPBFs or (B) HPRFs at the indicated volumes, such that each sample was grown in a total volume of 200 μ l, for a further 24 h period. Numbers of cells were scored using CyQUANT cell proliferation assay kit. Results are expressed as mean \pm SEM of six independent experiments. * indicates $p < 0.05$ vs. 0 μ l conditioned medium in one-way ANOVA with Dunnett's post hoc test.

6.4.2 Immunofluorescent Staining for α -SMA

Immunofluorescent staining of α -SMA was used to investigate whether fibroblasts can differentiate into myofibroblasts in response to the epithelial cell-derived conditioned media. Both HPBFs and HPRFs did not differentiate into myofibroblasts in the absence of TGF- β 1 as no actin stress fibres were observed (**Figures 6.5A & 6.5E**, respectively). When treated with 1 ng/ml or 5 ng/ml of TGF- β 1, actin stress fibres appeared in neither HPBFs (**Figures 6.5B & 6.5C**) nor HPRFs (**Figures 6.5F & 6.5G**). However, at 10 ng/ml, TGF- β 1 could induce the differentiation of HPBFs and HPRFs into myofibroblasts, as shown by the appearance of actin stress fibres in the cells (**Figures 6.5D & 6.5H**).

To investigate whether conditioned media derived from epithelial cells could differentiate fibroblasts into myofibroblasts, immunofluorescent staining of α -SMA was performed. Only fibroblasts cultured with solely epithelial cell-conditioned medium or equal ratio of fibroblast growth medium and epithelial cell-conditioned medium were used for staining. As shown in **Figure 6.6 & 6.7**, none of the conditioned media could differentiate fibroblasts into myofibroblasts as no actin stress fibres were observed.

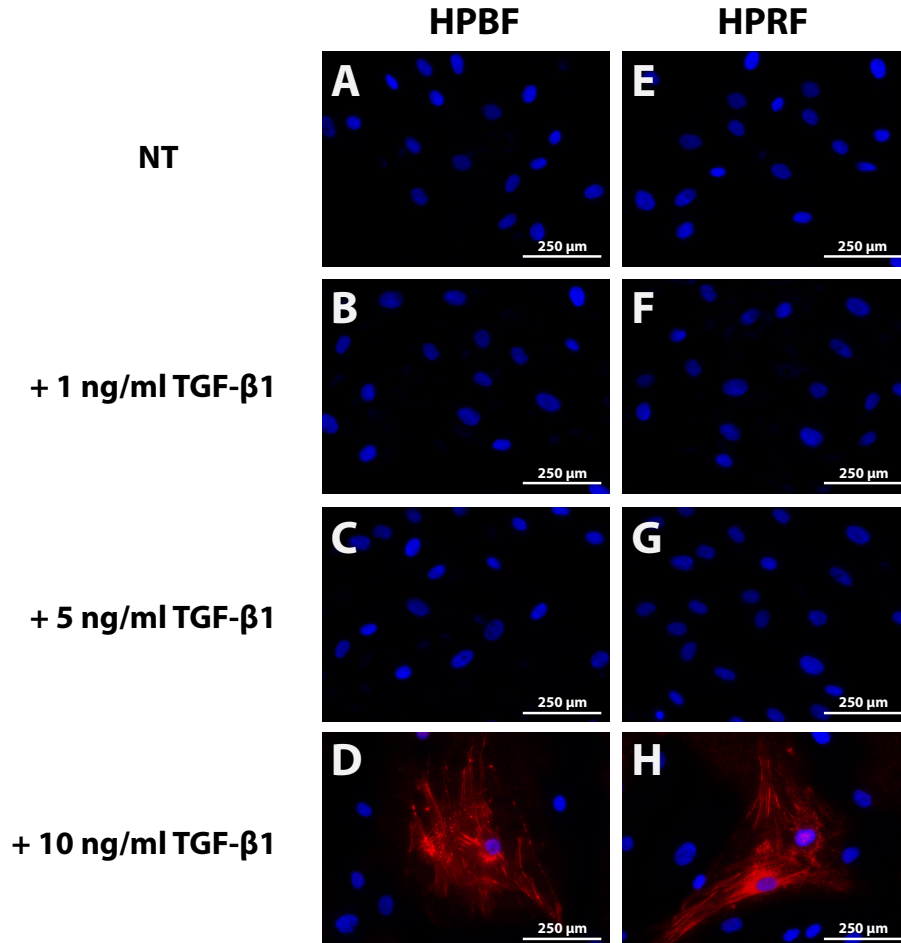


Figure 6.5: α -SMA Expression Observed in Bronchial and Renal Fibroblasts when Treated with 10 ng/ml TGF- β 1. Cells were seeded on cover slips and grown in 6-well plates. Cells at 70-85% confluence were quiesced and treated with different concentrations of TGF- β 1 as indicated. Cells were then fixed, permeabilised and blocked with 1% BSA/PBS. Finally, cells were stained with anti- α -SMA. All samples were also stained for nuclei (blue) using DAPI. These images represent results from three independent experiments.

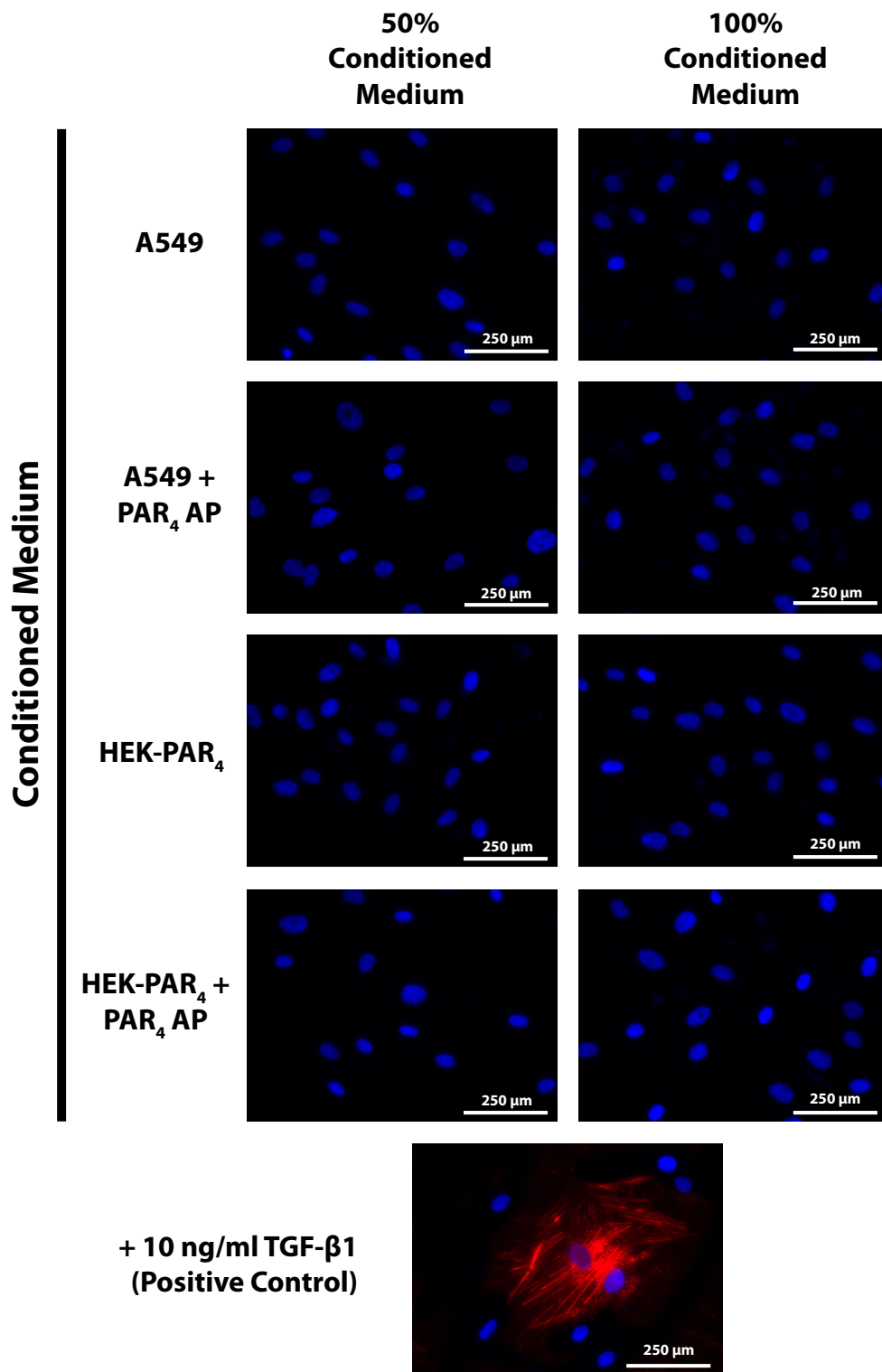


Figure 6.6: No α -SMA Expression Observed in Bronchial Fibroblasts after Cultured with Different Conditioned Media. The conditioned media used were collected from A549 culture, A549 culture with PAR₄ AP, HEK-PAR₄ culture, and HEK-PAR₄ culture with PAR₄ AP. HPBFs were seeded on cover slips and grown in 6-well plates. HPBFs at 70-85% confluence were quiesced. Quiescent HPBFs were cultured with fibroblast growth medium and epithelial cell-derived conditioned media at 50% or 100% epithelial cell-derived conditioned media. HPBFs treated with 10 ng/ml TGF- β 1 were used as a positive control. HPBFs were then fixed, permeabilised and blocked with 1% BSA/PBS. Finally, HPBFs were stained with anti- α -SMA. All samples were also stained for nuclei (blue) using DAPI. These pictures are representatives from three independent experiments.

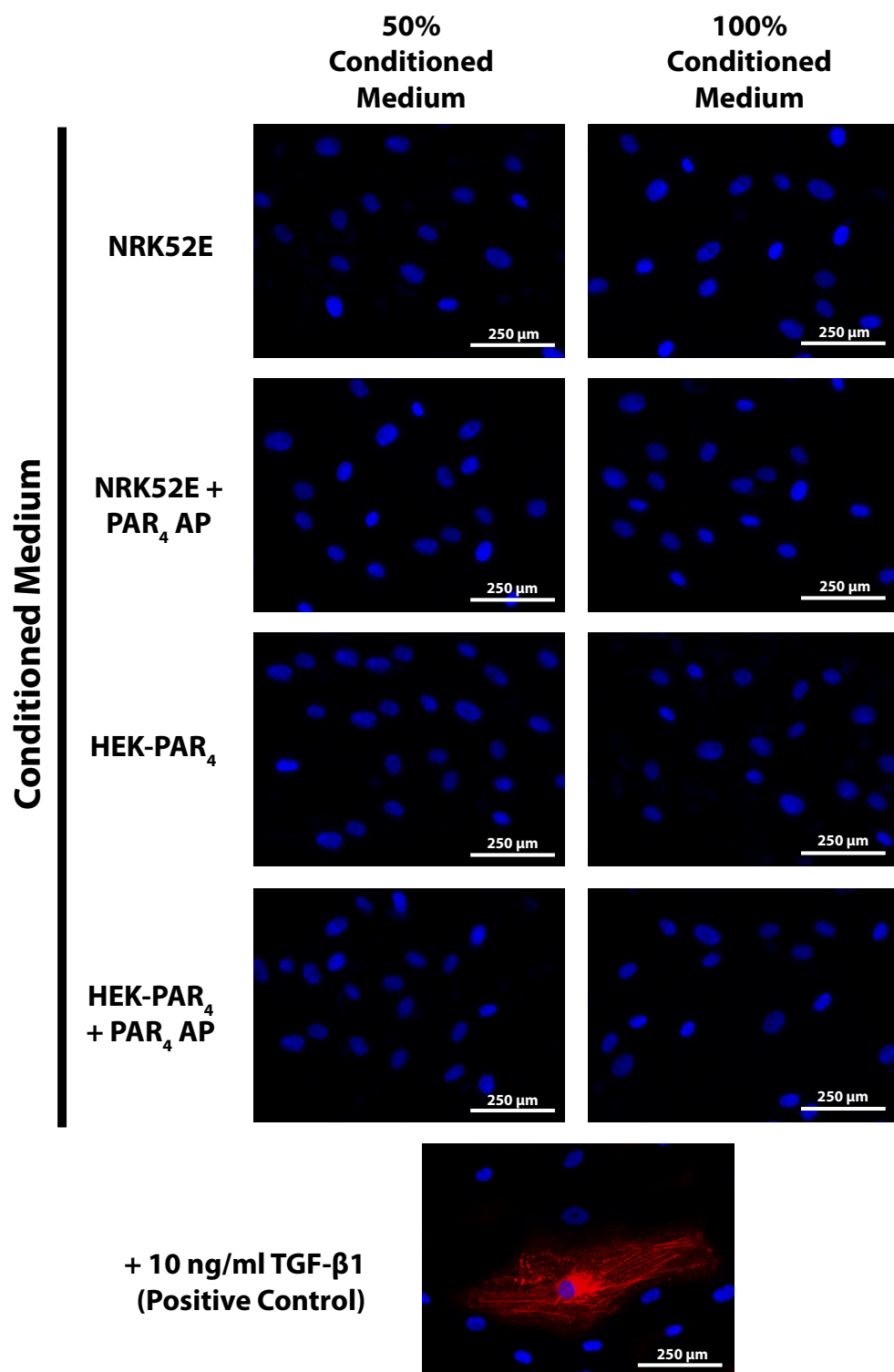


Figure 6.7: No α -SMA Expression Observed in Renal Fibroblasts after Cultured with Different Conditioned Media. The conditioned media used were collected from A549 culture, A549 culture with PAR₄ AP, HEK-PAR₄ culture, and HEK-PAR₄ culture with PAR₄ AP. HPRFs were seeded on cover slips and grown in 6-well plates. HPRFs at 70-85% confluence were quiesced. Quiescent HPRFs were cultured with fibroblast growth medium and epithelial cell-derived conditioned media at 50% or 100% epithelial cell-derived conditioned media. HPRFs treated with 10 ng/ml TGF- β 1 were used as a positive control. HPRFs were then fixed, permeabilised and blocked with 1% BSA/PBS. Finally, HPRFs were stained with anti- α -SMA. All samples were also stained for nuclei (blue) using DAPI. These pictures are representatives from three independent experiments.

6.4.3 Western Blotting

To further validate the results from immunofluorescent staining described in **Section 6.4.2**, Western blotting was performed. α -SMA and collagen type I were not detected in either HPBFs or HPRFs when cultured with epithelial cell-conditioned media (**Figures 6.8 & 6.9**), further indicating that they did not differentiate into myofibroblasts in these experiments.

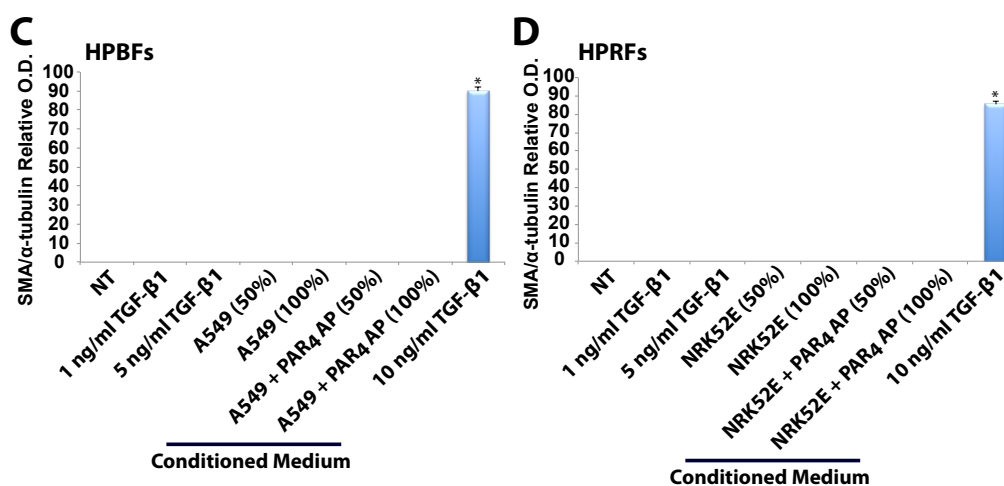
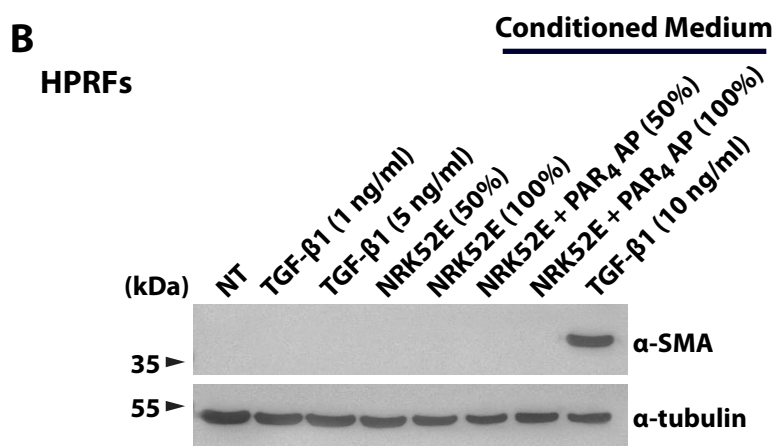
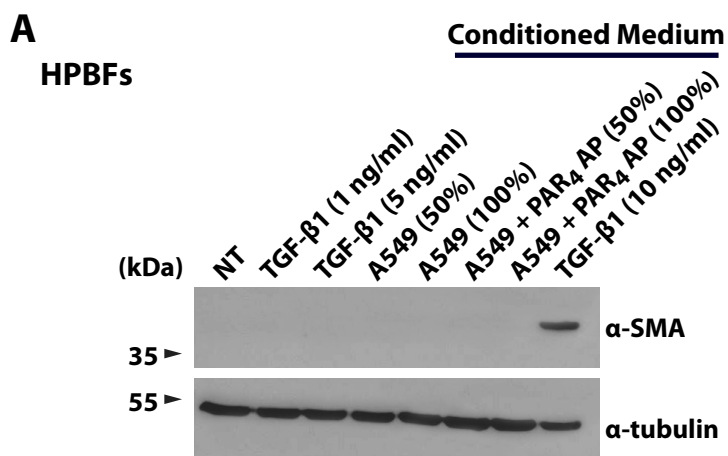


Figure 6.8: No α -SMA are detected by Western Blotting after Cultured with Different Conditioned Media. Quiescent (A) HPBFs or (B) HPRFs were cultured in the media as indicated for 24 h. Cell lysates were obtained and then subjected to SDS-PAGE followed by immunoblotting with antibodies against α -SMA and α -tubulin. α -tubulin was used as a loading control. Expected band sizes: collagen type I (~ 90 kDa), α -SMA (~ 42 kDa) and α -tubulin (~ 52 kDa). (C & D) Results were quantitated and summarised in a bar chart, where optical densities were normalised to α -tubulin loading controls. Results are expressed as mean \pm SEM of three independent experiments. * indicates $p < 0.05$ compared with untreated samples (NT) in one-way ANOVA with Dunnett's post hoc test.

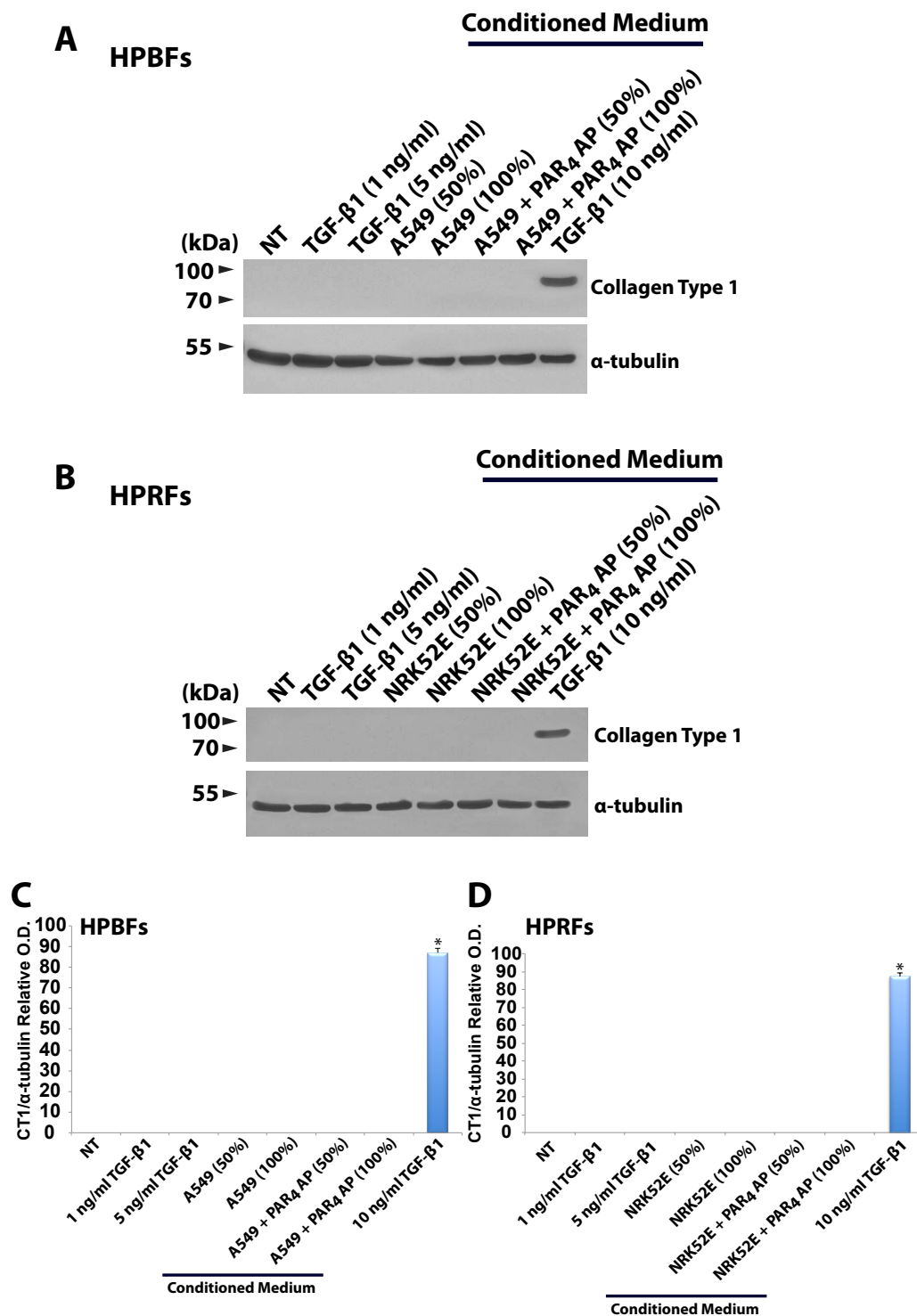


Figure 6.9: No Collagen Type 1 are detected by Western Blotting after Cultured with Different Conditioned Media. Quiescent (A) HPBFs or (B) HPRFs were cultured in the media as indicated for 24 h. Cell lysates were obtained and then subjected to SDS-PAGE followed by immunoblotting with antibodies against collagen type 1 and α -tubulin. α -tubulin was used as a loading control. Expected band sizes: collagen type I (~ 90 kDa) and α -tubulin (~ 52 kDa). (C & D) Results were quantitated and summarised in a bar chart, where optical densities were normalised to α -tubulin loading controls. Results are expressed as mean \pm SEM of three independent experiments. * indicates $p < 0.05$ compared with untreated samples (NT) in one-way ANOVA with Dunnett's post hoc test.

6.5 Discussion

The goal of this chapter was to examine the effects of different conditioned media on HPBF and HPRF proliferation. Under normal conditions, the damaged epithelium is able to repair itself rapidly. It has been demonstrated that immediately after injury, the epithelial cells at the edge of the damaged area de-differentiate, flatten and rapidly migrate on a provisional matrix to provide a covering layer over the denuded basement membrane, followed by the proliferation of new epithelial cells. The new epithelial layer is formed within 24 h after the injury (ERJEFÄLT and PERSSON, 1997a). Damage of epithelial cells release a number of pro-fibrotic mediators including TGF- β , TNF- α , PDGF, FGF and PGE₂ that influence fibroblast proliferation and migration, matrix production and remodelling (ERJEFÄLT and PERSSON, 1997b).

The lung epithelium is the primary site of lung inflammation and damage as well as the release of inflammatory mediators. Alterations in the structure and function of lung epithelial cells may affect the production of these mediators. Extensive lesion and changes in the airway wall architecture are commonly found in patients with respiratory infections, asthma, cystic fibrosis and chronic obstructive pulmonary disease (KNIGHT, 2001).

The normal airway is lined with a layer of pseudocolumnar epithelial cells (BREEZE and WHEELDON, 1977). During inflammatory respiratory disorders, extensive injury of airway epithelium occurs, with shedding of the epithelial cells in the bronchial and alveolar lumen. Inflammatory cells then release cytokines that damage the surface epithelium and underlying tissues as well as stimulate fibroblast proliferation (RAEBURN and WEBBER, 1994). Disruption of the integrity of the alveolar epithelium and slow re-epithelialisation of the denuded area are distinct pathologies in IPF and asthma (SELMAN *et al.*, 2001; HOLGATE *et al.*, 2006).

AEC in IPF secrete a number of cytokines, growth factors, proteases, surfactant proteins, adhesion molecules and matrix components, which may regulate the inflammatory and fibrotic response within the lung (KUWANO *et al.*, 2004). DNA damage or apoptosis of AEC has been reported in acute lung injury (BARDALES *et al.*, 1996) and IPF (KUWANO *et al.*, 1996; BARBAS-FILHO *et al.*, 2001). Epithelial cell damage and cell death during alveolitis induce the formation of gaps in the epithelial basement membranes. When the degree of lung injury is mild, damaged tissue will normally be repaired, whereas excess cell death may lead to irreparable lung damage and pulmonary fibrosis (KUWANO *et al.*, 2004). The migration of fibroblasts through these gaps into the alveolar space leads to intra-alveolar fibrosis (FUKUDA *et al.*, 1987). Hence, severe injury and impaired repair of AECs disturb normal epithelial-fibroblast interaction, causing proliferation of fibroblasts and eventually leading to pulmonary fibrosis (KUWANO *et al.*, 2004).

In the kidney, tubular damage and monocyte infiltration are two of the histopathological hallmarks of acute and chronic tubulointerstitial injury (GOOR *et al.*, 1994; WOLF, 1995). Extensive injury of tubules and excessive deposition of ECM in the tubular interstitium have been commonly described in patients with chronic kidney diseases (KUNCIO *et al.*, 1991). There is increasing evidence that tubular epithelial cell damage is involved in the events that promote interstitial fibrosis as approximately 80% of renal volume is occupied by tubules (EDDY, 1994).

A recent study has suggested that injured tubular epithelium plays a crucial role in renal fibrosis by responding to the injuries and amplifying the pro-fibrotic cytokines (WU *et al.*, 2013). The potential involvement of tubular epithelial cells in renal fibrosis is elucidated by the activation of inflammatory and fibrogenic signalling in renal tubules after injury (LIU,

2011). NF κ B signalling is activated in renal tubular epithelium in response to injuries, causing the release and production of inflammatory cytokines that initiate peritubular inflammation (MOLITORIS, 1999). Therefore, damage and death of proximal tubular cells are responsible for the pathophysiological and clinical aspects of kidney injury, and ultimately converge on common pathways that lead to progressive renal scarring.

Collectively, these findings show that epithelial cells might play an important role in the pathogenesis of organ injury and fibrosis by releasing cytokines that promote fibroblast proliferation. Thus, the effect of epithelial cell derived conditioned media on HPBFs and HPRFs were examined. TGF- β 1 promoted fibroblast proliferation in a dose dependent manner, showing a reliable positive control for fibroblast proliferation (**Figures 6.1A & 6.1B**). Although all three concentrations of TGF- β 1 induced fibroblast proliferation, 5 ng/ml TGF- β 1 had the most robust effect. The number of cells is slightly increased when treated with 10 ng/ml of TGF- β 1, indicating they have differentiated into myofibroblasts (supported by the α -SMA staining and Western blotting). Similar to the results in this study, STRUTZ *et al.* (2001) reported that TGF- β 1 caused a dose- and time- dependent induction of proliferation in human renal fibroblasts. They also demonstrated that TGF- β 1 induces fibroblast proliferation is largely mediated by FGF-2.

The results demonstrate that epithelial cell derived conditioned medium promotes fibroblast proliferation *in vitro* in a concentration dependent manner. Conditioned media derived from A549 and NRK52E cultures showed similar concentration dependent activities in both HPBFs and HPRFs (**Figures 6.2 & 6.3**). The number of fibroblasts decreased after the peak proliferative activity, suggesting that apoptosis of fibroblasts might occur. When the volume of epithelial cell derived conditioned medium increased, the volume of fibroblast growth medium in the culture

medium decreased, suggesting that there may be a lack of nutrients that is essential for the growth of fibroblasts. In contrast, the proliferative activity of both HPBFs and HPRFs did not significantly increase when cultured with HEK-PAR₄ cell-derived conditioned media when PAR₄ is not activated (**Figures 6.4**).

A few studies demonstrated that PARs are involved in cell proliferation (BERGER *et al.*, 2001a; TANAKA *et al.*, 2005; FURUHASHI *et al.*, 2008). However, the potential effects of PAR₄ activation on fibroblast proliferation have not been examined. Here, A549 and NRK52E cell-derived conditioned media when PAR₄ activated promoted a lower proliferative activity in HPBFs and HPRFs compared to the media when PAR₄ is not activated (**Figures 6.2 & 6.3**). In contrast, HEK-PAR₄ cell-derived conditioned media promoted higher proliferative activity in both HPBFs and HPRFs in cultures when PAR₄ is activated compared to those cultured in medium when PAR₄ is not activated.

Together, these results show that the conditioned media derived from A549 and NRK52E cultures promote higher proliferative activities when PAR₄ is not activated, whereas those derived from HEK-PAR₄ cultures promote higher proliferative activities when PAR₄ is activated. The reason behind this is not clear. While PAR₄ is expressed in all three cell lines, it is overexpressed in HEK-PAR₄ cells. It is possible that different mediators are being produced and released in different cell types. Different pro-fibrotic mediators have different actions on fibroblasts, for example, PDGF is a strong inducer of fibroblast proliferation (ROM *et al.*, 1988) whereas PGE₂ is a potent inhibitor for fibroblast proliferation (BITTERMAN *et al.*, 1986). Also, the amount of mediators produced and released could also be one of the factors that cause different proliferative activities in different cell types.

TGF- β 1 promotes the differentiation of fibroblasts into myofibroblasts

by increasing the expression of α -SMA and the formation of stress fibres (DESMOULIÈRE *et al.*, 1993; see **Chapter 3**). The addition of 10 ng/ml TGF- β 1 to the fibroblast cultures promoted the differentiation of HPBFs and HPRFs into myofibroblasts but not in the lower concentrations. These results were confirmed by immunofluorescent staining using anti- α -SMA antibody (**Figures 6.5**) and Western blotting using α -SMA and collagen type I antibodies (**Figures 6.8 & 6.9**). Also, none of the epithelial cell-conditioned media could differentiate the fibroblasts into myofibroblasts in these experiments (**Figures 6.6 & 6.7 & 6.8 & 6.9**). These findings suggest that fibroblasts that are proliferating (but not differentiating) do not express α -SMA and do not exhibit elevated levels of collagen synthesis. This is supported by the study demonstrated by GROTENDORST *et al.* (2004). They demonstrated that fibroblast proliferation, differentiation and collagen synthesis are induced by TGF- β via the connective tissue growth factor (CTGF)-dependent pathways. TGF- β and CTGF are coordinately expressed at sites of tissue repair and fibrosis (FRAZIER *et al.*, 1996; SHINOZAKI *et al.*, 1997). TGF- β -stimulated fibroblast proliferation and differentiation can be blocked with anti-CTGF antibodies, indicating that CTGF plays an important role in fibrotic disease (GROTENDORST *et al.*, 2004). However, CTGF alone is not responsible for determining whether cells respond to TGF- β by proliferation or differentiation. Rather, CTGF acts in conjunction with other growth factors such as epidermal growth factor (EGF) and insulin-like growth factor-2 (IGF-2) to control the events. In the presence of TGF- β , CTGF and EGF, cells undergo proliferation, whereas in the presence of TGF- β , CTGF and IGF-2, cells undergo differentiation (GROTENDORST *et al.*, 2004). Thus, when cells are stimulated with TGF- β , the factor controlling TGF- β to induce cell proliferation or myofibroblast formation is dependent on the presence of the other growth factors. Different concentration of TGF- β 1 present in the conditioned media will cause different concentration of pro-fibrotic mediators released and thus, causing different cellular responses.

In conclusion, this study provides preliminary results which support the idea that epithelial cell injury promotes proliferation of fibroblasts, an event that is thought to be involved in the pathogenesis of fibrosis. These experiments indicate that conditioned media derived from confluent epithelial cell cultures (when cell death starts to occur) contain factors which can stimulate fibroblast proliferation but not differentiation. However, due to time constraints, the mediators present in the conditioned media that promote the fibroblast proliferation were not identified in this chapter. Hence, additional studies are needed to address this, which could be done by using the commercially available enzyme-linked immunosorbent assay (ELISA) kits.

Chapter 7

General Discussion and Future Work

7.1 General Discussion

The interactions of fibroblasts, ECM production and the role of cytokines released in the fibrogenesis have been thought to contribute to the pathogenesis of fibrotic diseases. Incorporating the findings presented in this thesis and the published literature within the field, **Figure 7.1** demonstrates the possible events that might occur as a consequence of tissue injury (See below).

The hypothesis of this thesis is that 'PAR₄ is expressed in both lung and renal fibroblasts and PAR₄ activating peptide and cathepsin G can induce apoptosis in fibroblasts via PAR₄-dependent and independent mechanism'.

The data presented in this thesis indicate that: first, both HPBFs and HPRFs do not endogenously express PAR₄; second, CG and trypsin induce apoptosis in HPBFs and HPRFs PAR₄ independently and PAR₄ AP induces apoptosis in HEK- PAR₄ cells via PAR₄ signalling pathway. Hence, the above hypothesis has to be rejected.

The findings in this research are outlined below.

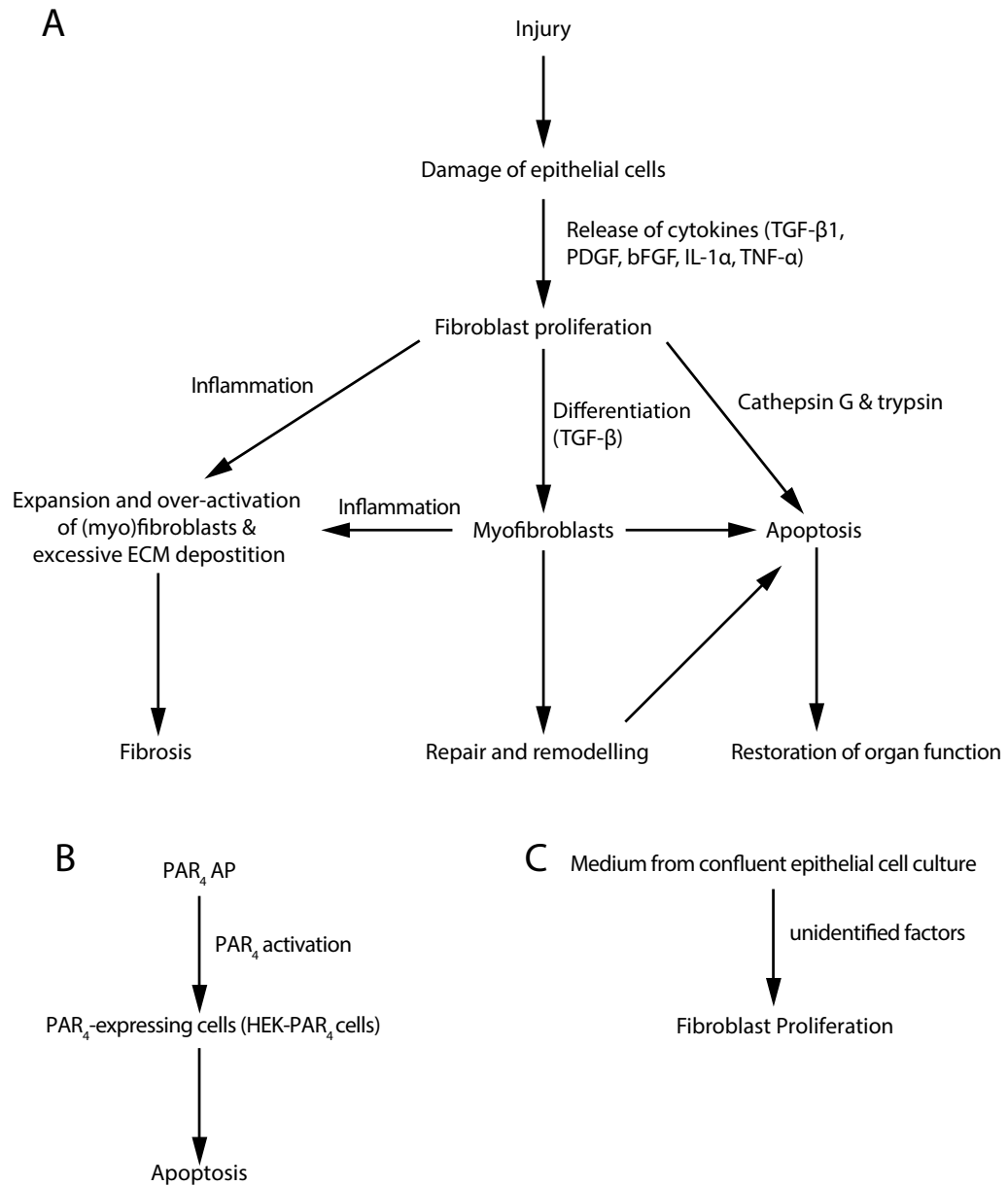


Figure 7.1: A Schematic Illustration Summarising the Main Findings in this Thesis (A) Damaged epithelial cells release a number of pro-fibrotic mediators that regulate fibroblast proliferation, matrix production and remodelling. Cathepsin G and trypsin were found to induce apoptosis in two types of fibroblasts, HPBFs and HPRFs, where endogenous PAR₄ expression was not detected. (B) When treated with PAR₄ AP, apoptosis was induced in PAR₄-expressing HEK293 cells. (C) Conditioned medium derived from confluent epithelial cell culture could induce the proliferation of HPBFs and HPRFs. The cellular and molecular factors contained in the conditioned medium which contributed to this proliferation effect remain to be identified. See text for details.

7.1.1 PAR Expression Characterised in HPBFs and HPRFs and transformation of fibroblasts into myofibroblasts

In this thesis, the use of human primary fibroblasts has provided a realistic understanding of cellular responses, compared to results obtained from immortalised cell lines. However, the major limitations when using human primary fibroblasts is the variabilities from donor to donor and the potential changes in phenotype with each passage. Here, both HPBFs and HPRFs were characterised by the positive expression of two fibroblast makers prolyl 4-hydroxylase and vimentin, confirming their fibroblastic nature. In addition, cells were only used between passage 2 and 5 in order to keep characteristics as consistent as possible. Without LPS stimulation, PAR₁, PAR₂ and PAR₃ are present in the HPBFs and only PAR₁ and PAR₂ are present in the HPRFs. The difference of PAR family expression in HPBFs and HPRFs may be due to the different origins of the fibroblasts used. There was no significant difference in PAR expression between different cultures of HPBFs or HPRFs. Contradictory to the findings of

this study, earlier reports showed LPS reproducibly induced expression of functional PAR₄ in HPBFs (RAMACHANDRAN *et al.*, 2007). In this study, experimental data inconsistently showed that LPS induced PAR₄ expression in HPBFs. PAR₄ expression was induced in some cases but in most cases, no PAR₄ was detected (presented in **Chapter 3**). These different observation may be to the differences in the anatomical location of the tissues. Even within a single tissue, fibroblasts are not a homogenous population and exist as sub-sets of cells (FRIES *et al.*, 1994). Also, there are a number of factors that could influence the PAR expressions on fibroblast include age, sex, smoking habit or pathological changes *in situ* prior to isolation for the experiments, all of which could have affected the fibroblast phenotype. Since most experiments were repeated at least five times, it is likely that the results are robust.

The differentiation of fibroblasts to myofibroblasts is the key event in wound healing and remodelling processes. TGF- β 1 is one of the most investigated profibrotic cytokines. Its critical role in tissue remodelling has been well recognised and *in vitro* studies have shown that it enhances myofibroblast differentiation of fibroblasts (THANNICKAL *et al.*, 2003; SERPERO *et al.*, 2006). In this study, the protein levels of collagen type I and α -SMA for TGF- β 1-treated fibroblasts were significantly higher than that for untreated fibroblasts, demonstrating the transformation of fibroblasts to myofibroblasts (presented in **Chapter 3**).

7.1.2 CG inhibit PAR₄ Activation

In **Chapter 4 and 5**, HEK293 cells with functional PAR₄ expression were successfully established (termed HEK-PAR₄). The effects of PAR₄ AP (AYPGQV) and CG on HEK-PAR₄ cells in intracellular calcium mobilisation were different. HEK-PAR₄ cells activated by PAR₄ AP resulted in a brisk rise in intracellular calcium whereas intracellular calcium

mobilisation did not change when stimulated with CG. These differences in the effect of PAR₄ AP and CG imply that CG does not activate PAR₄. Indeed, A549 cells, the human alveolar epithelial cells that endogenously expressed PAR₄, also failed to be activated by CG. The experimental evidence implicating PAR₄ cleavage as the mechanism mediating CG in fibroblasts is more questionable. Data obtained in **Chapter 5** demonstrated that expression of human PAR₄ confers responsiveness to PAR₄ AP but not to CG. The further observation that CG-treated HEK-PAR₄ cells elicit a reduced response to the stimulatory actions of PAR₄ AP suggests that CG might cleave PAR₄ at the ECL2 domain and cause PAR₄ to be unresponsive to the PAR₄ AP. In addition, CUMASHI *et al.* (2001) demonstrated that CG did not trigger aggregation in murine platelets and SABRI *et al.* (2003b) also demonstrated that human PAR₄ conferred responsiveness to thrombin and PAR₄ AP but not to CG. These studies and experimental data reported herein demonstrate that CG acts independently of PAR₄. Together this suggests that CG does not proteolytically activate PAR₄ and raise doubts that CG contributes to the PAR₄ cleavage.

These results are in contrast to the experimental evidence by SAMBRANO *et al.* (2000) which demonstrated that CG is a strong agonist for PAR₄ in human platelets. This difference was likely due to the cell specific differences in post-translational processing of PAR₄. For example, a few studies demonstrated that the extent of glycosylation of receptor is important for receptor expression, stability and activation (see **Chapter 4 Discussion**) (BRASS *et al.*, 1992; NAKAYAMA *et al.*, 2003; XIAO *et al.*, 2011).

7.1.3 CG and Trypsin Induce Apoptosis Independently of PAR₄

The effect of CG on apoptosis of fibroblasts would be particularly vital in areas of interstitial inflammation, where neutrophil infiltration leads to fibroblast proliferation and ECM accumulation. In addition, the important regulatory role of PARs in both normal and inflammatory states emphasises the need to investigate further the relationship between PARs and the proteases that modulate their activities. Understanding the complicated network of extracellular proteases and PARs on lung and renal fibroblasts may reveal promising pharmaceutical targets for the treatment of fibrotic diseases in lung and kidney.

Targeting specific cell types with apoptotic agents represents a major challenge in therapeutic intervention for fibrotic diseases such as IPF and renal fibrosis. Apoptosis is one of several mechanisms involved in the development of fibrosis and the complexity of interactions between these different mechanisms remains far from being solved. This study provides evidence that CG and trypsin can induce apoptosis in lung and renal fibroblasts in concentration dependent fashion (see **Chapter 5**). CG and trypsin induced pronounced morphologic changes in lung and renal fibroblasts without PAR₄ expression. In addition, there was no significant difference in the percentage of apoptotic cells between empty vector control and HEK-PAR₄ cells when treated with CG, suggesting PAR₄ expression is not required for CG to trigger apoptosis. The mechanisms underlying the cellular actions of CG are still incompletely understood. Hence, further studies are required to investigate the downstream signalling pathway activated by CG.

7.1.4 PAR₄-dependent induction of apoptosis

As presented in **Chapter 5**, PAR₄ AP is able to trigger higher percentage of apoptosis in HEK-PAR₄ cells compared to empty vector control, suggesting that apoptosis can also be mediated by PAR₄ signalling. Although PAR₄ is not endogenously expressed in HPBFs and HPRFs (**Chapter 3**), it might be present in other types of fibroblasts. Thus, it would be worth determining the expression of PAR₄ in other fibroblasts and if PAR₄ activation by PAR₄ AP or other agonists could induce apoptosis.

Interestingly, coagulation Factor Xa and PAR₁ AP have been reported to induce apoptosis in some cancer cell lines (BORENSZTAJN *et al.*, 2007; BORENSZTAJN and SPEK, 2008). Importantly, PAR₄ was detected in about 55% of malignant samples (see Review by ELSTE and PETERSEN (2010)). It is currently unclear whether the effect of PAR₄ activation on apoptosis is specific to the PAR₄-expressing HEK293 cells. This question could be answered by testing the effect of the same PAR₄ AP in another PAR₄-expressing cell line. Hence, if it is true that activation of PAR₄ would contribute to apoptosis in different cell lines, and given that PAR₄ is present in several cancer cells, careful evaluation of the molecular mechanism underlying apoptosis induction via PAR₄ activation might also benefit the drug development to treat certain cancers.

7.1.5 Conditioned Medium Derived from Epithelial Cell Culture Promotes Fibroblast Proliferation

Apoptosis can be detrimental or beneficial, depending on the cell type, the circumstances and the timing. For example, the stimulation of apoptosis in fibroblasts and myofibroblasts in the fibrotic disease can be beneficial because they are the key effector cells in fibrosis that produce excessive ECM. However, excessive epithelial cell apoptosis could lead to barrier

collapse and a deficit of anti-fibrotic mediators. The major function of the epithelium was thought to act as a physical barrier, but recent studies indicate that it has the capacity to modulate a variety of inflammatory processes through the production and release of inflammatory cytokines including TGF- β , TNF- α , and IL-1, -6, and -8. Some of these cytokines play important roles in fibroblast proliferation, myofibroblast differentiation and collagen production. Thus, in order to manipulate apoptosis therapeutically, the cell-type specificity and location of apoptosis must be considered.

This thesis demonstrates that conditioned media derived from confluent epithelial cell cultures (when cell death started to occur) contained factors sufficient to stimulate fibroblast proliferation but not differentiation. The conditioned media derived from A549 and NRK52E cultures promoted higher proliferative activities when there is no PAR₄ activated whereas HEK- PAR₄ cells promoted higher proliferative activities with PAR₄ activated (**Chapter6**). This study supports the concept that epithelial cell injury promotes the proliferation of fibroblasts. This finding is consistent with the previous findings demonstrated by NAKAMURA *et al.* (1995). They demonstrated that the bronchial epithelial cell-conditioned medium increased the number of fibroblasts in a serum-free culture system in a concentration dependent manner. However, due to time constraints, this chapter did not directly assess the mediators present in the conditioned media that promote the fibroblast proliferation, thus the contribution of mediators to the fibroblast growth stimulatory activity in the conditioned media could not be confirmed in this study.

7.2 Future Work

Under normal wound healing, myofibroblasts disappear from the repaired wound site via programmed cell death. Persistence of myofibroblasts likely depends on a variety of mediators released from the resident or infiltrating cells and causes hypertrophic scarring and fibrosis (RAMOS *et al.*, 2006). Furthermore, myofibroblasts are resistant to apoptosis under pathological conditions. Therefore, strategies that promote myofibroblast apoptosis may highlight effective therapies for the treatment of fibrotic disease.

Future work will be aimed at elucidating the mechanisms of cell apoptosis mediated by CG, trypsin and PAR₄ AP. Hence, the molecular mechanism upstream of caspase-3 should be investigated to identify whether the cell death is derived from the TNF/death receptor pathway (i.e. probe for caspase-8) or the mitochondrial pathway (i.e. probe for caspase-9 or cytochrome) .

Findings in this study also lead to the prediction that CG and trypsin induce anoikis (cell detachment dependent apoptosis) of lung and renal fibroblasts. CG-induced cell death of rat cardiomyocytes has been reported (SABRI *et al.*, 2003b). Mechanisms of anoikis have not been fully characterised but an ECM/integrin-focal adhesion kinase (FAK) pathway is known to play a central role, with loss of constitutive adhesion signalling by FAK being one of the early events (SCHALLER, 2001). Western blot analysis using lysates from agonist treated cells could be performed to study whether CG and trypsin could affect the phosphorylation activity of FAK. If FAK activity is affected, this would suggest that CG- and trypsin-induced cell death is cell detachment dependent.

Furthermore, the ability of CG and trypsin to stimulate the activities of MAP kinases ERK1/2, JNK and p38-MAP kinase over a series of concentrations and time points could be assessed by Western blotting using

antibodies against phosphorylated (activated) signalling proteins. In addition, the P13K/Akt signalling pathway is also known as a major pathway for cell survival (DATTA *et al.*, 1999) and cleavage of Akt by activated caspases disables this cell survival signalling pathway (ROKUDAI *et al.*, 2000). Therefore, degradation of Akt following CG or trypsin treatment could be assessed using Western blotting. All these experiments should be performed alongside the apoptosis experiments.

For PAR₄ driven apoptosis responses, it is plausible that the mechanism of cell death might mimic that reported for PAR₁ in bronchial epithelial cells (i.e. mitochondrial pathway) (SUZUKI *et al.*, 2005). Similar to those experiments proposed for CG and trypsin above, activation of one or more of the three major MAP kinases (ERK1/2, JNK and p38-MAP kinases) induced by PAR₄ should be investigated. MAP kinase inhibitors could be used to assess which of these MAP kinases plays a role in the PAR₄ induced cell death.

Finally, it would be interesting to determine the cytokines or mediators that are present in the conditioned media. This could be done by using the commercially available enzyme-linked immunosorbent assay (ELISA) kits. The developments made in these areas have important clinical implications. However, several questions need to be considered before cytokine or antibody therapy can be effectively applied clinically. These include safety issues, dosage, treatment regimens and effective delivery systems. Furthermore, the majority of research has focused on targeting single mediator. It is likely that the combinations of cytokines and antibodies, or other agents such as protease inhibitors, will be more beneficial.

7.3 Conclusion

In conclusion, fibroblast activation, proliferation and apoptosis represent a useful experimental system for understanding the general biological processes of repair and remodelling after tissue injury. Continued exploration along the line of this thesis may ultimately shed lights on new therapies for fibrotic diseases based on pharmacological of apoptosis.

Appendix

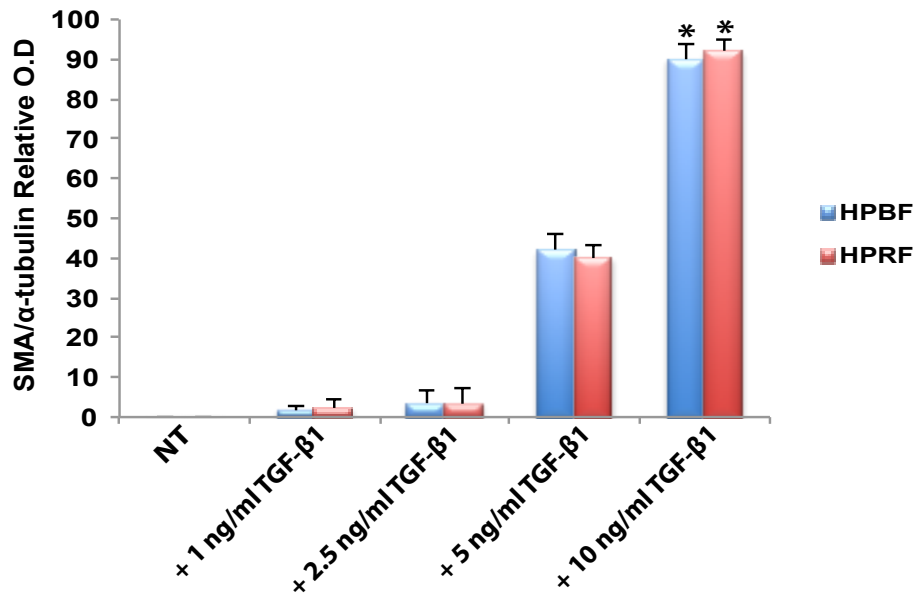


Figure A.1: Optimisation of the TGF- β concentration in the Induction of α -SMA. Quiescent HPBFs and HPRFs were stimulated with different concentration of TGF- β 1 under serum free conditions for 24 h. Cell lysates were obtained and then subjected to SDS-PAGE followed by immunoblotting with antibodies against α -SMA and α -tubulin. Results were quantitated and summarised in a bar chart, where optical density was normalised against the α -tubulin. Results are expressed as mean \pm SEM of three independent experiments. * indicates $p < 0.05$ compared with no treatment control (no TGF- β 1 added) in one-way ANOVA with Dunnett's post hoc test.

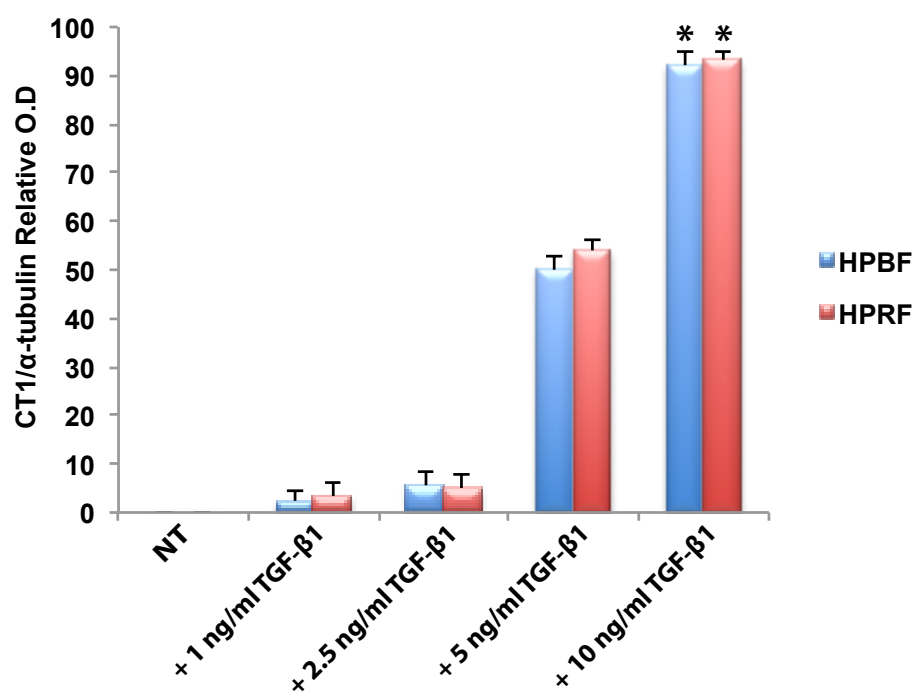


Figure A.2: Optimisation of the TGF- β concentration in the Induction of Collagen Type 1 expression. Quiescent HPBFs and HPRFs were stimulated with different concentration of TGF- β 1 under serum free conditions for 24 h. Cell lysates were obtained and then subjected to SDS-PAGE followed by immunoblotting with antibodies against collagen type 1 and α -tubulin. Results were quantitated and summarised in a bar chart, where optical density was normalised against the α -tubulin. Results are expressed as mean \pm SEM of three independent experiments. * indicates $p < 0.05$ compared with no treatment control (no TGF- β 1 added) in one-way ANOVA with Dunnett's post hoc test.

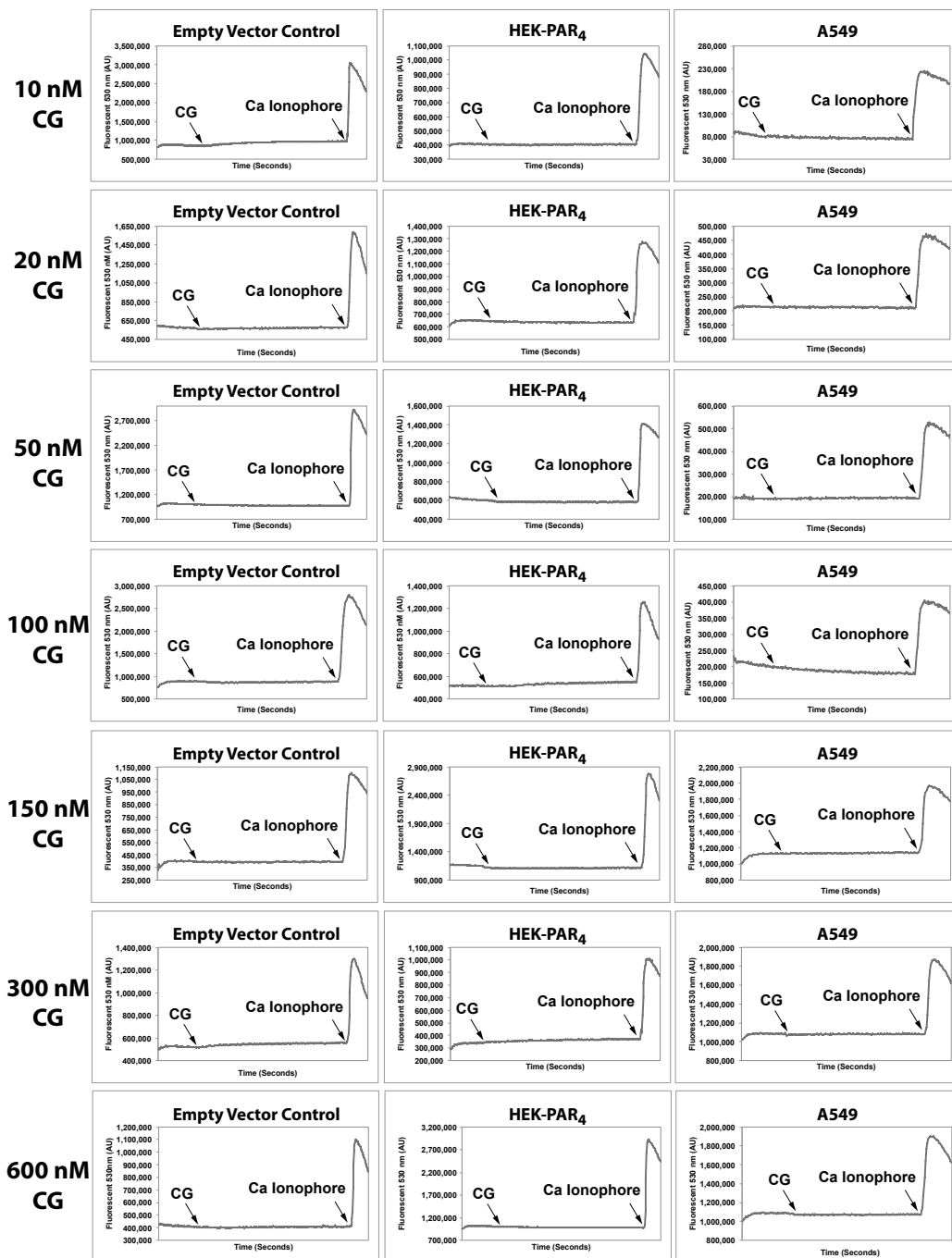


Figure A.3: Optimisation of the Concentrations of CG in Calcium Mobilisation Assay. Cells at 70-85% confluence in 75 cm² flasks were harvested and incubated with Fluo-3 AM at room temperature for 25 min. Cells were then washed and resuspended in calcium assay buffer. Functional PAR₄ activities were assessed by treating the cells with different concentrations of CG as indicated. An increase in fluorescence (E530) monitored by fluorescence spectrophotometer is indicative of calcium mobilisation. Arrows indicate the time when test agonists were added. These results represent data from three independent experiments.

At Room Temperature

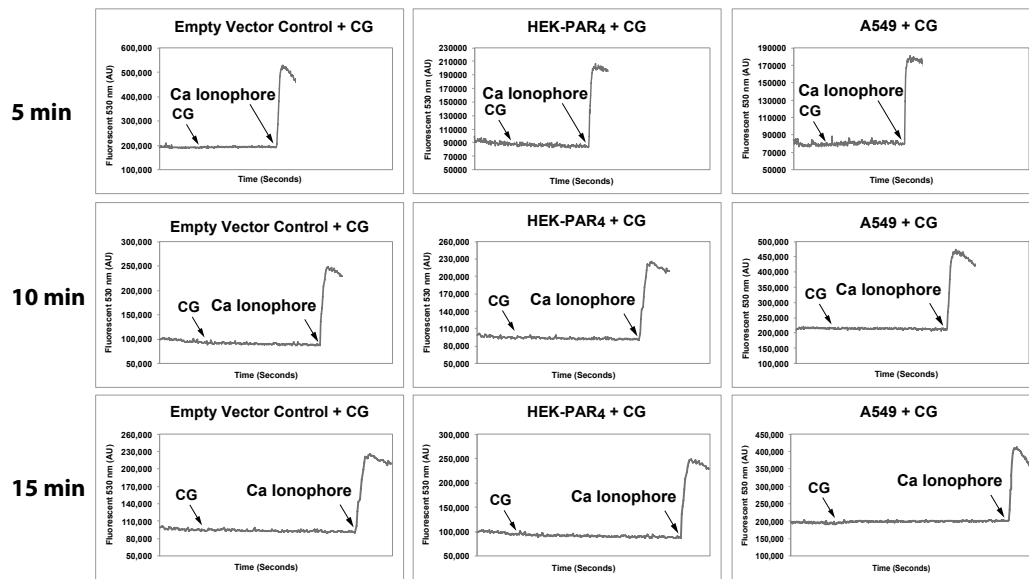


Figure A.4: Optimisation of the action of CG in Various Incubation Time at Room Temperature. Cells at 70-85% confluence in 75 cm² flasks were harvested and incubated with Fluo-3 AM at room temperature for 25 min. Cells were then washed and resuspended in calcium assay buffer. Functional PAR₄ activities were assessed by treating the cells with CG for 5, 10 and 15 min at room temperature. An increase in fluorescence (E530) monitored by fluorescence spectrophotometer is indicative of calcium mobilisation. Arrows indicate the time when test agonists were added. These results represent data from three independent experiments.

At 37°C

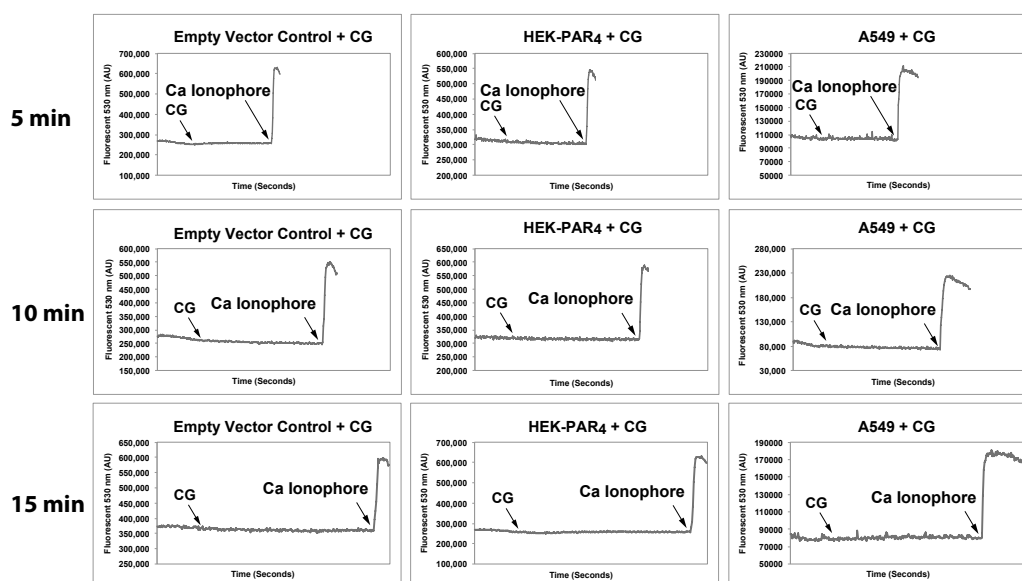


Figure A.5: Optimisation of the action of CG in Various Incubation Time at 37°C. Cells at 70-85% confluence in 75 cm² flasks were harvested and incubated with Fluo-3 AM at room temperature for 25 min. Cells were then washed and resuspended in calcium assay buffer. Functional PAR₄ activities were assessed by treating the cells with CG for 5, 10 and 15 min at 37°C. An increase in fluorescence (E530) monitored by fluorescence spectrophotometer is indicative of calcium mobilisation. Arrows indicate the time when test agonists were added. These results represent data from three independent experiments.

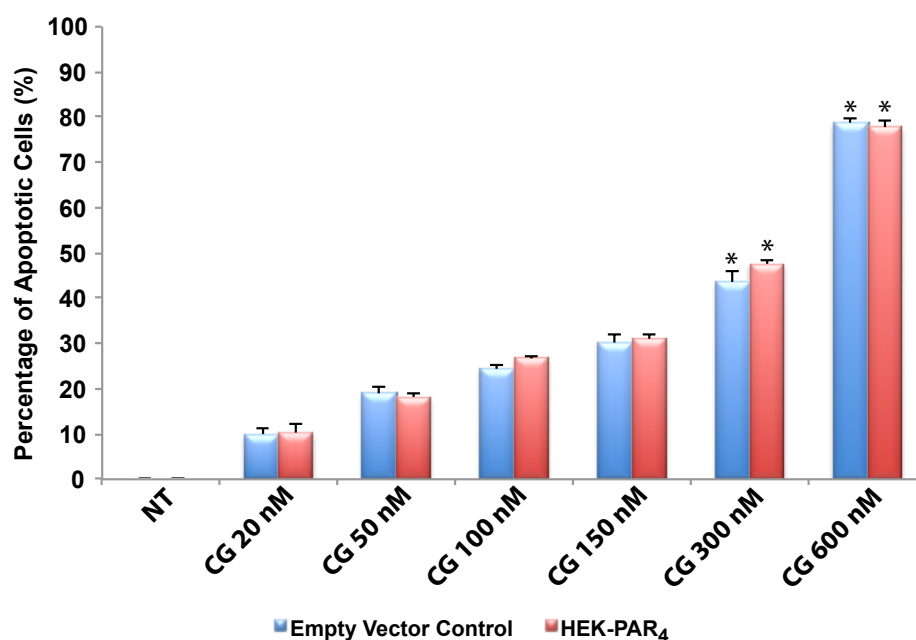


Figure A.6: Optimisation of the concentrations of CG in the Induction of Cell Apoptosis. Cells at 70-85% confluence in 6-well plate were quiesced and treated with different concentrations of the CG for 24 h. The cells were then incubated with FITC-conjugated Annexin V and propidium iodide in the dark. Binding of Annexin V/PI to empty vector control and HEK-PAR₄ cells that were exposed to different concentrations of CG was evaluated by flow cytometry. Results are expressed as percentage of apoptotic cells, presented as the mean \pm SEM of three independent experiments. * indicates $p < 0.05$ compared with NT in one way ANOVA with Dunnett's post hoc test. ** indicates $p < 0.05$ between empty vector control and HEK-PAR₄ Cells in one way ANOVA with Bonferroni post hoc test.

Abbreviations

A549	Adenocarcinomic human alveolar basal epithelial cell
ACT	α 1-antichymotrypsin
AEC	Alveolar epithelial cell
AKI	Acute kidney injury
AP	Activating peptide
Apaf-1	Apoptotic protease-activating factor 1
APS	Ammonium persulphate
ATP	Adenosine-5'-triphosphate
Bcl-2	B cell lymphoma-2
BICD1	Bicaudal D homolog 1
bFGF	Basic fibroblast growth factor
BMP	Bone morphogenic protein
bp	Base pair
BSA	Bovine serum albumin
CAB	Calcium assay buffer
CAM	Cell adhesion molecule
cAMP	Cyclic adenosine monophosphate
CBB	Coomassie brilliant blue
cDNA	Complementary DNA
CG	Cathepsin G
CKD	Chronic kidney disease
CTFG	Connective tissue growth factor
DAB	3,3'-diaminobenzinetetrahydrochloride

DAG	Diacylglycerol
DEPC	Diethylpyrocarbonate
DMEM	Dulbecco's modified Eagle's medium
DMSO	Dimethyl sulfoxide
DNA	Deoxyribonucleic acid
dNTP	Deoxynucleotide tri-phosphate
ECL2	Extracellular loop 2
ECL	Enhanced chemiluminescence
ECM	Extracellular matrix
ED-A	Ectodysplasin-A
EDTA	Ethylene diamine tetraacetic acid
EGF	Epidermal growth factor
EGFP	Enhanced green fluorescent protein
EGTA	Ethylene glycol tetraacetic acid
ELISA	Enzyme-linked immunosorbent assay
EMT	Epithelial-mesenchymal transition
EndoMT	Endothelial-mesenchymal transition
ERK	Extracellular signal-regulated kinase
FACS	Fluorescence-activated cell sorting
FAK	Focal adhesion kinase
FasL	Fas ligand
FBS	Foetal bovine serum
FGF	Fibroblast growth factor
FITC	Fluorescein isothiocyanate
Fluo-3 AM	Fluo-3 acetoxymethyl ester
GM-CSF	Granulocyte-macrophage colony-stimulating factor
GPCR	G protein-coupled receptor
GRK	G protein-coupled receptor kinase
GTP	Guanosine triphosphate
H ₂ O ₂	Hydrogen peroxide
HEK293	Human embryonic kidney 293 cell

HEPES	4-(2-hydroxyethyl)piperazine-1-ethanesulfonic acid
hPAR ₄	Human PAR ₄
HPBF	Human primary bronchial fibroblast
HPRF	Human primary renal fibroblast
HRP	Horseradish peroxidase
IFN	Interferon
IGF-2	Insulin-like growth factor
IL	Interleukin
InsP3	Inositol 1,4,5-triphosphate
IPF	Idiopathic pulmonary brosis
JNK	Jun amino-terminal kinase
kb	kilobase
kDa	kilo Dalton
LAP	Latency-associated peptide
LN-CAP cells	Androgen-sensitive human prostate adenocarcinoma cells
LPS	Lipopolysaccharide
MAPK	Mitogen-activated protein kinase
mRNA	Messenger RNA
NC	Negative control
NFkB	Nuclear Factor-KappaB
NRK52E	Normal rat kidney epithelial cell
nt	Nucleotide
PAGE	Polyacrylamide gel electrophoresis
PAR	Proteinase-activated receptor
PAK	p21 activated kinase
PBS	Phosphate buffered saline
PBS-T	Phosphate buffered saline with Tween-20
PCR	Polymerase chain reaction
PDGF	Platelet-derived growth factor
PGE ₂	Prostaglandin E ₂
PI	Propidium iodide

PIPES	1,4-Piperazinediethanesulfonic acid
PI3	Phosphatidylinositol 3
PKC	Protein kinase C
PLC	Phospholipase C
PMSF	Phenylmethylsulfonyl fluoride
PMN	Polymorphonuclear leukocytes neutrophil
POMC	Pro-opiomelanocortin
PS	Phosphatidylserine
RA	Rheumatoid arthritis
rDNase	Recombinant DNase
ROS	Reactive oxygen species
RNA	Ribonucleic acid
RNases	Ribonucleases
RPMI	Roswell Park Memorial Institute
RT-PCR	Reverse transcription PCR
SDS-PAGE	Sodium dodecyl sulfate polyacrylamide gel electrophoresis
SEM	Standard error of the mean
SMA	Smooth muscle actin
SNX1	Sorting nexin 1
TAE	Tris-acetate-EDTA
TBS	Tris-buffered saline
TBS-T	Tris-buffered saline with Tween-20
TBS-Tx	Tris-buffered saline with Triton X-100
TEMED	N,N,N',N'-tetramethylethylenediamine
TGF	Transforming growth factor
TNF	Tumour necrosis factor
UV	Ultra violet

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