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Glucocorticoids, frequently used anti-inflammatory and immunosuppressive agents, are associated with ocular hypertension and glaucoma. Endothelin-1 (ET-1) is also implicated in glaucoma pathology and optic neuropathy as its concentration is elevated in glaucoma patients and in animal models of glaucoma, and chronic administration of ET-1 produces damage to the optic nerve head in rats. Glucocorticoids have been reported to regulate the expression of ET-1 gene and ET receptors in the cardiovascular system. However in the eye, the interactions between glucocorticoids and endothelin have not yet been investigated, particularly as both glucocorticoids and ET-1 have been implicated in the regulation of intraocular pressure and contribute to glaucoma pathology. Therefore, the purpose of the investigations described herein was to determine the novel mechanisms that may be involved in the regulation of intraocular pressure by glucocorticoids through interactions with ET-1 and ET receptors in NPE cells, a source of ET-1, and in TM cells where both glucocorticoids and ET-1 effect aqueous humor outflow. The hypothesis was that ET-1 exacerbates the actions of glucocorticoids on TM cells and contributes to increased outflow resistance.

Furthermore, individual sensitivities to glucocorticoids differ considerably. About one in every three people in the general population is considered potential steroid responders while almost all primary open angle glaucoma (POAG) patients are steroid responders and develop ocular hypertension after ocular administration of glucocorticoids. The molecular mechanisms underlying the higher glucocorticoid responsiveness among POAG patients remain unknown. The glucocorticoid receptor beta isoform (hGR β) has become a candidate for glucocorticoid resistance in some diseases, especially in asthma, based on the reports of its negative activity. The purpose of this segment of the investigations was to test the hypothesis that glucocorticoid responsiveness was regulated by the expression of hGR β in TM cells.

We demonstrated that dexamethaosone (Dex), a synthetic glucocorticoid, increased ET-1 synthesis and release from human non-pigmented ciliary epithelial (HNPE) cells. Dex also suppressed ET_B receptor protein expression and attenuated ET-1 mediated increase in nitric oxide (NO) while Dex had no effect on ET_A receptor expression and ET_A receptor mediated intracellular Ca²⁺ mobilization in TM cells. The increase in the release of ET-1 from HNPE cells with a concomitant decrease of ET_B receptor protein expression and ET_B receptor mediated NO release by Dex in TM could result in an increase in the contraction and decrease in relaxation of trabecular meshwork thus reducing the intratrabecular space. Such actions by ET-1 may exacerbate Dex effects on the outflow pathway leading to increased outflow resistance and consequently elevated intraocular pressure that typically is associated with glucocorticoids.

We have also found a significant difference in hGR β levels among normal versus glaucomatous TM cell lines, with the POAG TM cell lines having lower hGR β receptor expression. This is coincidence with the fact that in the normal population, there is a low rate of glucocorticoid responders as compared to almost all POAG patients considered as glucocorticoid responders. Overexpression of hGR β in TM cells, produced by transfecting a hGR β expression construct, inhibited Dex-induced expression of myocilin,

a glaucomatous gene, supporting the contention that hGR β acts as a negative regulator of glucocorticoid activity. In addition, we studied the machinery of cytoplasm to nuclear transport of hGR β . We identified that a chaperon protein, hsp90, is a requirement for the nuclear translocation of hGR β .

In conclusion, we have described a novel-signaling pathway for glucocorticoids through the regulation of ET-1 and ET receptors in the anterior segment which have consequences on aqueous humor outflow. We have also demonstrated a possible molecular mechanism by which glucocorticoid responsiveness in POAG patients is achieved as a result of the low level of nuclear hGR β receptor isoform expression. Furthermore, we have, for the first time, identified hap90 as a chaperon protein for the translocation of hGR β from the cytoplasm to the nucleus.

MECHANISMS OF GLUCOCORTICOID – INDUCED OCULAR HYPERTENSION

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CHAPTER I

INTRODUCTION

Glaucoma

Glaucoma is the second leading cause of blindness in the world with a prevalence of approximate 66 million people worldwide.¹ Elevated intraocular pressure (IOP) remains one of the most important risk factors for the development of glaucomatous optic neuropathy.^{2, 3} While no cure exists for glaucoma, surgery and medial therapy to reduce the elevated IOP has been used to delay the progression of damage to the optic nerve. Of the many forms of glaucoma, primary open-angle glaucoma (POAG) is the most prevalent.⁴ POAG is associated with elevated IOP, which is due to impaired aqueous humor outflow and is correlated with morphologic and biochemical changes in the trabecular meshwork (TM),⁵ a main resistance in the aqueous humor outflow pathway. Although the actual mechanism responsible for optic nerve damage in POAG is unclear, POAG has a complex or multifactorial etiology and genetic factors have long been implicated in its pathophysiology. By application of molecular genetic techniques, the chromosomal locations of six genes that can independently cause POAG has been mapped (GLC1A, GLC1B, GLC1C, GLC1D, GLC1E and GLC1F), including a glaucoma gene, myocilin (GLC1A), located in chromosome 1.6 Myocilin was identified and detected in high amounts in the trabecular meshwork. Although the function of

myocilin remains unknown, mutations in the myocilin gene were shown to be associated with both juvenile and adult-onset POAG.⁶ In addition to localizing and identifying genes for specific types of glaucoma, researchers have begun to characterize the gene products and investigate the molecular mechanisms involved in glaucoma.

Glucocorticoids and Glaucoma

Glucocorticoids, important steroid hormones for treating a variety of ocular diseases and conditions, has gained notoriety due to its tendency to induce multiple side effects, including the development of ocular hypertention and glaucoma. Glucocorticoids appear to be associated with POAG. It has been reported that POAG patients have elevated levels of the endogeneous glucocorticoid, cortisol, in their blood^{7, 8, 9, 10, 11} and aqueous humor⁸ compared to non-glaucomatous subjects. The administration of glucocorticoids can cause ocular hypertention which is dependent on the potency, the dose and the duration of treatment of glucocorticoids.¹² Topical ocular administration of a potent glucocorticoid for 4-6 weeks can produce an elevated IOP in approximately 35% of the general population and 20% of responders, classified as high steroid responders, are more likely to eventually develop POAG.^{13, 14} In contrast to the normal population, almost all POAG patients are considered steroid responders.^{13, 15} Moreover glucocorticoid-induced glaucoma is similar in many ways to POAG including increasing outflow resistance and an increase in IOP.¹² Since the trabecular meshwork is located in the aqueous humor outflow pathway and plays a critique role in aqueous humor outflow, the effects of glucocorticoids on the trabecular meshwork have been studied for many years in either cell culture, whole explant organ culture system, perfusion human eye, or in vivo.

Glucocorticoids change the morphology and activity of trabecular meshwork, including reorganization of the cytoskeleton to form ordered cross-linked actin networks (CLANs),¹⁶ altered expression of extracellular matrix glycoprotein fibronectin¹⁷ and laminin,¹⁸ changes in extracellular metalloproteinase activity,^{19, 20} altered phagocytosis or migratory activities,^{16, 21} increase in cell adhesion molecules,²² and enhanced expression of myocilin, a glaucoma gene (*MYOC*).^{23, 24, 25} Overall glucocorticoids increase extracellular material deposits in trabecular meshwork, and subsequently increase outflow resistance and increase IOP.

Human Glucocorticoid Receptor Isoforms $GR\alpha$ and $GR\beta$

Glucocorticoids action on target tissue to elicit specific biological responses is dependent on the presence of glucocorticoid receptors.²⁶ The glucocorticoid receptor (hGR) has been detected in many ocular tissues, including trabecular meshwork.²⁷ The cloning of the full length human glucocorticoid receptor²⁸ predicted the existence of two receptor isoforms termed hGR α and hGR β , which differ only at the carboxyl terminus. Such findings are expected if the two hGR isoforms were formed via alternative splicing. Encio and Detera-Wadleigh²⁹ ascertained the genomic structure of human GR and confirmed that hGR α and hGR β originate from the same gene by alternative splicing. Based on these observations, it is clear that the human GR gene contains 10 exons, and alternative splicing of the hGR gene generates hGR α with exons of 1-8 and 9 α which translates into a 777 amino acid protein, whereas hGR β with exons of 1-8 and 9 β translates into a 742 amino acid protein. Hence hGR α and hGR β are identical through

amino acid 727 but diverge subsequently with hGRa having an additional 50 amino acids and hGR β an additional, nonhomologous 15 amino acids (see Figure 1).^{28, 29} Besides alternative splicing of human hGR, the hGR gene is subjected to alternative translation initiation from a downstream in-frame ATG codon, a potential alternative translation initiation site, which produces two forms of hGR, named hGR-A and hGR-B.³⁰ Because hGRa is predominantly expressed and is shown to be most abundant with ligand binding studies,²⁸ it has been the primary focus of subsequent research. As a result, hGRa expression, biochemical properties, and physiological function have been well characterized. hGRa belongs to the superfamily of steroid/thyroid/retinoic acid receptor proteins that function as ligand-dependent transcription Factors.²⁶ It is comprised of a unique amino-terminal region including a transactivation domain, a central DNA-binding domain, crucial for specific interaction of the receptor with DNA sequences containing glucocorticoid response elements (GRE) and a carboxyl terminus. The carboxyl terminus has the hormone-binding domain as well as sequences important for interaction with heat shock protein 90 (hsp90),³¹ nuclear translocation,³² receptor dimerization,³³ and transactivation.³⁴ The ability of both natural and synthetic glucocorticoids to elicit cellular responses is through hGRa. Upon hormone binding, hGRa regulates positively or negatively transcription. hGRa predominantly exists in the ctytoplasm and undergoes ligand-dependent translocation to the nucleus,^{32, 35, 36} where it binds to glucocorticoid response elements in the promoter regions of target genes and regulates gene expression. hGR α in the nucleus can also physically interact with other transcription factors, such as AP-1³⁷ and NF- κ B,³⁸ modulate gene expression apart from DNA binding. Moreover, the

<u>ALTERNATIVE SPLICING GENERATES GRα AND GRβ ISOFORMS</u></u>



Figure 1. GR α and GR β originate from the same GR gene which contains 10 exons. Alternative splicing of GR gene generated GR α with exons of 1-8 and 9 α which translated into 777 amino acid protein, where GR β with exons 1-8 and 9 β translated into 742 amino acid protein. Hence GR α and GR β are identical through amino acid 727, but then diverge with GR α having an additional 50 amino acid and GR β having an additional non-homologous 15 amino acids. It is these different amino acids in the carboxyl terminus which allow GR α but not GR β to bind to hormones and regulate gene expression. Besides the original initiation site, there is an internal ATG codon, which is a potential alternative translation initiation site for producing two isoforms of GR, named GR-A and GR-B.

actions of hGR α are known to vary among different cells due to variations in the concentration of many cellular modulatory factors, such as coactivators like SRC-1 or TIF2, corepressors like NcoR or SMRT, and heat shock protein HSP90 etc. In contrast to hGR α , the unique end of carboxyl terminal of hGR β influences several key biochemical properties that distinguish it from hGR α . It does not bind to glucocorticoids and lacks transcriptional activity by itself.²⁸, ³⁹ Currently the physiological significance of hGR β is not clear.

The Dominant Negative Activity of the hGR β Isoform

At the time Hamberger et al^{28} discovered hGR β , they found the hGR β protein did not bind to glucocorticoid analogues, and immunoblot analysis using polyclonal antibody directed against the human glucocortiocid receptor only recognized hGR α in most human and mouse cell lines. They concluded that the predominant physiological form of the glucocorticoid receptor is the hGR α . Little was known about hGR β until Bamberger et al^{40} found that mRNA of hGR β were expressed throughout the human body, and overexpression of hGR β in transfected COS cells disrupted the enhancing effects of hGR α on gene transcription. Oakley et al^{39} also observed that mRNA of hGR β is expressed in various human adult and fetal tissues. Their group found in transfected cell lines that hGR β did not bind glucocorticoids and antiglucocorticoids, was transcriptionally inactive on the glucocorticoid responsive element, and hGR β repressed the transcriptional activity of hGR α on the glucocorticoid responsive promoter.^{39, 41}

Although the concept of hGR β as a dominant negative inhibitor of hGR α activity remains controversial,⁴² there are increased reports that glucocorticoid insensitvity is associated with increased expression of hGRB, with the most extensive study in chronic asthma. Several investigators have found that peripheral blood mononuclear cells (PBMC) from patients with glucocorticoid-insensitive asthma have a decrease ability of their hGR to bind its glucocorticoid response elements.^{43, 44} Hamid et al⁴⁵ reported that airway cells PBMC from patients with glucocorticoid resistant asthma express significantly higher levels of hGR^β than the same cells from patients with glucocorticoidsensitive asthma, and GRB expression in glucocorticoid-insensitive asthma was particularly high in airway T cells. The inflammatory cells from patients with glucocorticoid-sensitive asthma had much higher ratio of hGRa/hGRB than from glucocorticoid-resistant asthma patients.⁴⁶ Increased expression of hGRB at night in PBMC from patients with nocturnal asthma was associated with decreased steroid responsiveness in nocturnal asthma.⁴⁷ Overall the amount of hGR^β was found to correlate with glucocorticoid resistance and therapy efficacy in asthma.⁴⁸ Besides research in asthma diseases, it has also been observed that hGRB was expressed much higher in peripheral lymphocytes from patients with steroid-resistant unlcerative colitis (UC) comparing with the steroid-sensitive UC patients.⁴⁹ High constitutive expression of $hGR\beta$ by human neutrophils prevented these cells from experiencing glucocorticoid-induced cell death.⁵⁰ Interestingly, mice are known to be deficient in the expression of hGR β ,⁵¹ when virally trnasduced hGRB cDNA into mouse hybridoma cells, the stable expression

of hGR β results in glucocorticoid insensitivity of these cells.⁵² Although the molecular mechanism underlying negative activity of hGR β is not known yet, formation of transcriptional impaired hGR α -hGR β heterodimers may be responsible for the antagonism.^{41, 52}

Glucocorticoid Receptor nuclear translocation

Glucocorticoid receptors, like other steroid receptors, are capable of shuttling between nuclear and cytoplasmic compartments.^{53, 54} hGRa undergoes hormone-dependent nuclear import in most cells,³⁵ and has served as a useful paradigm for cytoplasmic anchoring.⁵⁵ In the absence of glucocorticoids, GR α resides predominantly in the cytoplasm of cells as an oligomeric complex containing one molecule of receptor, and two molecules of heat shock protein 90 (hsp90) and often one molecule of hsp70, which directly bind to the receptor,^{55, 56} and one molecule of immunophilin either FKBP52. FKBP51, Cyp40, or PP5, which have tetratricopeptide repeat (TPR) domains interacting with hsp90.^{54, 57} Hsp90 and hsp70 are both required for glucocorticoid receptor complex assembly and for proper folding to the steroid-binding conformation.⁵⁸ It is generally accepted that once hormone binds to hGRa, receptors undergo conformational change and dissociate from Hsp90, Hsp70 and the TPR proteins, followed by nuclear translocation and binding to GRE to regulate gene transcription.^{59, 60, 54} However it is also found that the complex of hGRa and hsp90 is dynamic in the sense that assembly and disassembly occurs constantly,⁵⁶ and hGRa and hsp90 can move together from the

cytoplasm to the nucleus.⁶¹ A couple of observations suggested that the dynamic assembly and disassembly of GR-hsp90 heterocomplexes is required for receptor movement.^{62, 63, 64} hGRa has been found associated with microtubules,⁶⁵ and binding of GR-hsp90 to immunophilins is involved in both dynein interaction and hGR nuclear movement.^{66, 67, 68} The machinery of hGRa transportation to the nucleus has been suggested as a dynamic interaction of GR-hsp90-FKBP52 heterocomplexes and requiring the retrograde motor protein, dynein, to move it along microtubular tracks.⁶⁸ Recently, Davies et al⁶⁹ found that Dex binding switches GR-hsp90-FKBP51 to GR-hsp90-FKBP52 and recruits dynein, then GR-hsp90-FKBP52-dynein complex shuttles to the nucleus, and release GR into the nucleus (see Figure 2). While nucleocytoplasmic translocation of hGRa is becoming more and more clear, still nothing is known about hGRB translocation. Although Oakley et al⁷⁰ detected hGRB predominantly in the nucleus independent on glucocorticoid treatments, other groups identified that it also exists in the cytoplasmic fraction in some human original cells.^{71, 42} In addition, hGRβ can be associated with hsp90.^{41, 42} It is possible that the transport of hGR β also requires an association with hsp90. Since hGRa activation needs ligand binding to recruit adapter protein FKBP52 and motor protein dynein.^{68, 69} and hGRB does not bind to ligand.^{40, 39} the transport mechanism of hGR α and hGR β may be not exactly the same. However the stability of hGR^β interaction with hsp90 may impact upon the efficiency of receptor nuclear translocation and alter their subcellulular distribution.

MODEL OF THE INHIBITION OF hGRB ON hGRa



Figure 2. This model presents the translocation of hGR α and hGR β and formation of the transcriptional inactive heterocomplex of hGR α and hGR β in the trabecular meshowork cell. In the absence of hormone, hGR α is primarily located in the cytoplasm of the cells as an oligomeric complex containing hsp90 and immunophilin FKBP51. As the consequence of glucocorticoid binding, immunophilin FKBP52 interchanges with FBKP51 followed by concomitant recruitment of dynein, and then hGR α -hsp90-FKBP52-dynein complex associate with microtubules and translocates toward the nucleus and finally release of hGR α into the nucleus. However, hGR β is spontaneously transported and released into the nucleus along microtubular tracks. In the nucleus, hGR β competes with hGR α to form transcriptional inactive heterocomplex of hGR α -hGR β and inhibits or attenuates the ability of hGR α to regulate gene expression.

Endothelin-1 and Glaucoma

. A. 1

The endothelin (ET) family of peptides comprises mainly three isoforms, ET-1, -2, and -3.72 ET-1 and ET-3 are expressed in the eye, including iris, choroid, retina, optic nerve head, ciliary body, lens and corneal endothelium, and studies also show their presence in the aqueous and vitreous humors. ET-1, well known as a potent vasoactive peptide, may contribute to the etiology of glaucoma, as its concentration is elevated in the aqueous humor in POAG patients and in animal models of glaucoma.^{73, 74} Moreover, chronic administration of ET-1 can produce an optic neuropathy.⁷⁵ In the anterior segment, the non-pigmented ciliary epithelial cells have been shown to be a source for ET-1, as they endogenously synthesize and release ET-1.76, 77 ET-1 has also been shown to inhibit Na+/K+-ATPase and decrease aqueous humor formation.^{78, 79} Such effects could contribute to the functional response in the decrease IOP after intravitreal administration of ET as shown in rabbits.^{80, 81} In the classical model (Fig. 3), ET-1's action on the regulation of intraocular pressure is explained by paracrine effects on contractions of the ciliary muscle (CM) and trabecular meshwork (TM), with the net effect depending on which of the contractions dominate. For instance, in bovine eyes, the contraction of TM would reduce intratrabecular space and decrease aqueous humor outflow even in the presence of CM contraction. Since glucocorticoids cause changes in the morphology and activity of trabecular meshwork with concomitant increases in the deposition of extracellular matrix materials,⁸² the contraction of the TM in the presence of glucocorticoids could reduce the intertrabecular space and consequently increase outflow resistance and IOP as a maladaptation.

Anterior Chamber Actions of Endothelin-1



IOP Regulation

Figure 3. Several actions of endothelin-1 (ET-1) in regulating intraocular pressure are involved in the anterior chamber. Classic ET-1's action on the regulation of intraocular pressure is explained by paracrine effect on contractions of the ciliary muscle (CM) and trabecular meshwork (TM), with the net effect depending on which of the contractions dominate. For instance, in bovine eyes or glucocorticoid treated eyes, the contraction of TM would reduce intratrabecular space and decrease aqueous humor outflow even in the presence of CM contraction. In addition, ET-1 can also inhibit Na+/K+-ATPase in non-pigmented ciliary epithelium and decrease aqueous humor formation.

SPECIFIC AIMS

Glucocorticoids and endothelin-1 are both implicated in glaucoma pathology and optic neuropathy. In vascular smooth muscle cells and other cell types, glucocorticoids have been reported to increase ET-1 gene expression and regulate ET receptors.^{83, 84, 85, 86} However in the eye, the interactions between glucocorticoids and endothelin have not yet been investigated. The first part of this research project intends to address the interaction of endothelin with glucocorticoids in human non-pigmented ciliary epithelial (HNPE) cells, which have been shown to be a source for ET in the anterior chamber, and additionally in human TM, a main resistance in aqueous humor outflow pathway. Such studies would describe novel signaling pathways for glucocorticoids in the anterior segment and define consequences on aqueous humor outflow and possibly glaucoma pathology. Glucocorticoids can increase IOP, however this response is not consistent within the population. Approximately 90% of primary open angle glaucoma (POAG) patients respond to glucocorticoids with an increase in IOP following topical ocular administration of glucocorticoids, whereas only 35% of general population are referred as glucocorticoid responders.¹⁵ Little is known about the molecular basis underlying steroid responsiveness in glaucoma. It has been reported that glucocorticoid receptor β (hGR β) may be associated with glucocorticoid resistance in other diseases, especially in asthma.^{43, 44, 45, 46, 47, 48} The secondary part of this research project intends to investigate the potential role of hGRB in regulating glucocorticoid sensitvity in glaucoma. The hypothesis to test is that glucocorticoids upregulate endothelin-1 and regulate endothelin receptor subtypes in the anterior segment which contributes to the glucocorticoid-induced

ocular hypertension and that low expression of hGR β in glaucomatous TM leads to glucocorticoid sensitivity in glaucoma. The following specific aims will address these mechanisms.

- Aim 1: Determine the regulation of glucocorticoids on the release of ET-1 and the expression of ET receptors in HNPE cells.
 - 1.1 Quantitate the levels of mRNA expression of ET-1, ET_A and ET_B receptors in the presence and absence of dexamethasone treatment in cultured transformed human non-pigmented ciliary epithelial (HNPE) cells.
 - 1.2 Measure the amount of ET-1 peptide released and differential expression of ET_A and ET_B receptor protein in the presence and absence of dexamethasone in HNPE cells.
- Aim 2: Determine the effect of glucocorticoids on the expression of ET receptor subtypes in TM cells.
 - 2.1 Measure the regulation of mRNA expression of ET_A and ET_B receptors by dexamethasone in normal and glaucomatous TM cell lines.
 - 2.2 Measure changes in ET_A and ET_B receptor protein expression by dexamethasone in normal and glaucomatous TM cell lines.

- Aim 3: Measure the relative expression of hGR α and hGR β and their regulation by dexamethasone in various TM cell lines as well as determining the subcellular distribution of hGR β in normal and glaucomatous TM cell lines.
 - 3.1 Study the protein expression of hGR β in at least 3 normal and 3 glaucomatous primary TM cell lines in the presence or absence of dexamethasone.
 - 3.2 Further determine the subcellular distribution and the relative amounts of $hGR\beta$ between those 3 normal and 3 glaucomatous TM cell lines using immunofluorescence microscopy.
- Aim 4: Identify the mechanism of translocation of hGR β from the cytoplasm to the nucleus in TM cells and the inhibitory activity of hGR β in hGR α action on glaucoma gene expression or glaucoma phenotype formation.
 - 4.1 Determine if heat shock protein 90 (hsp90) is a chaperone for hGR β translocation from the cytoplasm to the nucleus.
 - 4.2 Determine if microtubules are involved in the translocation of hGR β from the cytoplasm to the nucleus.

4.3 Evaluate the role of hGR β in the regulation of glucocorticoid sensitivity in trabecular meshwork by determining if it inhibits the expression of a glaucoma marker gene.

EXPERIMENTAL DESIGN

Three individual experiments were designed to investigate specific aim I, II, III, and IV. These experiments are discussed in detail in chapters 2, 3, and 4. However, a brief description of the experimental rational and methodology is provided below.

Study # 1: We tested the hypotheses that glucocorticoids upregulate endothelin-1 and regulate endothelin receptor subtypes in non-pigmented ciliary epithelial cells. This study was conducted by comparing mRNA and protein levels of ET-1, ET_A, and ET_B receptors between dexamethasone treatments and vehicle control. This study allowed us to detect the novel cross-talk between endothelin-1 and glucocorticoids in the eye (*Zhang X*, *Krishnamoorthy RR*, *Prasanna G*, *Narayan S*, *Clark A*, *Yorio T*. *Dexamethasone regulates endothelin-1 and endothelin receptors in human non-pigmented ciliary epithelial (HNPE) cells. Exp Eye Res. 2003;76:261-72)*.

Study # 2: We tested the hypotheses that glucocorticoids regulate endothelin receptor subtypes in trabecular meshwork cells, which contribute to the glucocorticoid-induced ocular hypertention. This study was accomplished by measuring mRNA and protein levels of ET_A and ET_B receptors in normal and glaucomatous TM cells with or

without dexamethasone treatment conditions. We also evaluated the function of ET_A and ET_B receptors by measuring the mobilization of intracellular Ca²⁺ induced by ET-1 and ET-1-stimulated nitric oxide release respectively. These experimental designs were aimed to detect the novel signaling pathways for dexamethasone in the regulation of outflow resistance besides increasing the deposition of extracellular matrix materials in the trabecular meshwork (*Zhang X, Clark AF, and Yorio T. Interactions of Endothelin-1 with Dexamethasone in Primary Cultured Human Trabecular Meshwork Cells. Invest Ophthalmol Vis Sci. In Press)*.

Study # 3: We tested the hypotheses that glucocorticoid receptor β (hGR β) is a key component in regulating glucocorticoid responsiveness and that low expression of hGR^β in glaucomatous TM cells leads to glucocorticoid sensitivity in glaucoma. We focused on comparing the expression of $hGR\beta$ in several human normal and glaucomatous TM cell lines. Such study allowed us to observe the obvious differences in relative amount of hGR^β between normal and glaucomatous TM cells. This study also investigated the transport mechanism involving in moving hGR β from the cytoplasm to the nucleus, which may give rationale and explanations about the different nuclear amounts of hGRB as seen in normal and glaucomatous TM cells. Finally, in this study, we directly tested if hGR β could inhibit a glucocorticoid response by determining if overexpression of hGRB reduced dexamethaonse induction of myocilin, a well known glaucoma gene. Data from this study could provide the most direct evidence for the potential role of hGRβ in regulating glucocorticoid sensitivity in an *in vitro* model system (Zhang X, Clark AF, and Yorio T. Expression and Translocation of Glucocorticoid Receptor β and its Regulation of Glucocorticoid Responsiveness in Trabecular Meshwork Cells. To be sumitted).

METHODS

The methodology used in each investigation is described in detail in each of the chapters (II, III, and IV); however, it is appropriate to discuss these techniques briefly with respect to each specific aim.

Quantitative Polymerase Chain Reaction (QPCR)

QPCR was used to compare mRNA levels of ET-1, ET_A , and ET_B between Dex treatment and control in HNPE and TM cells. Total cellular RNA was isolated from cells using the Trizol B reagent (Life Technologies, Rockville, MD). cDNA was synthesized from total RNA from each sample using random primers and AMV Reverse Transcriptase (Promega, Madison, WI). QPCR amplification of each sequence was performed using SYBR Green PCR Core regents (PE Applied Biosystems, Foster City, CA) in a Cepheid Smart Cycler (Cepheid, Sunnyvale, CA). Quantification of relative RNA level was achieved using the comparative C_T method (as described in PE Biosystems User Bulletin#2: <u>http://docs.appliedbiosystems.com/pebiodocs/04303859.pdf</u>.

ET-1 Radioimmunoassay

Radioimmunoassay of ET-1 was performed to measure the ET-1 released in the culture media from HNPE cells in the presence or absence of Dex (100 nM) for 24 h. A

commercially available radioimmunoassay (RIA) kit for ET-1 (Peninsula Laboratories, Belmont, CA) was used according the manufacture's protocol. The sample ET-1 concentration was obtained from a standard curve.

Western Blot Analysis for ET_A and ET_B Receptors

In order to measure the expression of ET_A and ET_B receptors in HNPE and TM cells under Dex (100 nM) or control conditions, the plasma membrane fractions were isolated. Western Blot analysis was performed using primary rabbit polyclonal ET_A or ET_B antibodies (Alomone Labs, Jerusalem, Israel) respectively, and secondary horseradish peroxidase-conjugated anti-rabbit IgG (Amersham Pharmacia Biotech, Piscataway, NJ). The non-specific bands in the immunoblots for ET_A and ET_B receptors were identified by pre-incubating the anti- ET_A or anti- ET_B antibodies with their respective receptor peptides (Alomone Labs, Jerusalem, Israel).

[¹²⁵I]ET-1 Binding Assay

In order to verify and better quantify the ET receptor density changes by Dex (100 nM) for 24 h in HNPE cells, [¹²⁵I]ET-1 binding to its receptors was performed. First the plasma membrane fractions were isolated and [¹²⁵I]ET-1 (NEN Life Science Product. Inc., Boston, MA) binding to total ET receptors (ET_A and ET_B) was measured. Non-specific binding was defined as filter-bound radioactivity measured in the presence of unlabeled ET-1 (Sigma Chemical, St Louis, MO) before addition of [¹²⁵I] ET-1. The binding of ET_A receptor was determined by pre-treating with sarafatoxin S6C (Peninsula

Lab Inc. Belmont, CA), an ET_B agonist, to block the binding of $[^{125}I]ET-1$ to ET_B receptors. ET_B receptor binding was defined as the total specific $[^{125}I]ET-1$ binding minus the amount of ET_A receptor binding.

Measurement of Intracellular Ca²⁺ Mobilization

In order to determine whether ET_A receptor function was altered by Dex (100 nM) treatment for 72 h, ET-1 effects on intracellular calcium were measured using the Fura-2, AM fluorescent probe technique in both normal and glaucomatous TM cells under vehicle control and Dex treatment conditions. The intracellular $[Ca^{2+}]_i$ within single cells was measured with a Nikon fluorescent microscope using Imaging Metafluor software (Universal Imaging Co., West Chester, PA). ET-1 (100 nM) was added and changes in fluorescence ratios were recorded. BQ610 (Peninsula Lab Inc. Belmont, CA), an antagonist of ET_A receptor, was used at concentration of 1 μ M to determine whether ET-1 induced-Ca²⁺ mobilization was mediated through ET_A receptor.

Determination of Nitrite Accumulation in Culture Medium

In order to determine whether ET_B receptor function was altered by Dex (100 nM) treatment for 72 h in TM cells, the effect of Dex on ET-1-induced nitric oxide (NO) release was measured using a Griess colorimetric nitric oxide synthase assay kit. The concentration of Nitrite, the final oxidation product of NO in the culture medium, was calculated from a constructed nitrite standard curve. An ET_B receptor antagonist, BQ788 (Peninsula Lab Inc. Belmont, CA), was used to determine the role of ET_B receptor on NO release induced by ET-1.
Conventional or confocal Immunofluorescence Microscopy or Double Immunofluorescence Microscopy

Immunofluorescence microscopy was used to compare the relative amount of hGR^β between several normal and glaucomatous TM cell lines. and double immunofluorescence microscopy was used to detect the colocalization of hGR β with β tubulin or hsp90 in normal and glaucomatous TM cells. TM cells grown on subconfluence coverslips was fixed in 4% paraformaldehyde and permeabilized in 0.2% Triton X-100. Polyclonal rabbit anti-hGRβ antibody (Affinity PA3-514) and Alexa Fluor 594 goat anti-rabbit IgG (red fluorescence, Molecular Probe) was used to stain hGRB. For double imuunofluorescence, either primary rabbit anti-hGR β antibody + mouse antiβ-tubulin antibody (Santa Cruz sc-5274), or primary anti-hGRβ antibody + mouse antihsp90 antibody (Santa Cruz sc-13119) and secondary Alexa Fluor 594 goat anti-rabbit IgG + Alexa Fluor 488 goat anti-mouse IgG (green fluorescence, Molecular Probe) was used to stain either hGRB and B-tubulin or hGRB and hsp90. DAPI was used to define nuclear regions. Immunofluorescence was viewed under a Nikon Diaphot Fluorescence Microscope or Zeiss LSM-410 Confocal Scanning Laser Microscopy System.

Western Blot Analysis for $hGR\beta$ in Cytoplasmic and Nuclear Fractions

In order to confirm the subcellular distribution of hGR β in TM cells, cytosolic and nuclear fractions were isolated and Western Blot analysis was conducted to detect both

hGR α and hGR β in those isolated fractions. The effects of Dex (100 nM) in the subcellular distribution of hGR α and hGR β were also investigated.

Co-immunoprecipitation of hGR_β-hsp90 Complexes

In order to find out whether hGR β is physically associated with hsp90, Coimmunoprecipitation of hGR β -hsp90 complex was performed. First, we used mouse antihsp90 monoclonal antibody to immunoprecipitate hsp90 complexes and used anti-hGR β antibody to run immunoblotting to detect GR β , then we used anti-hGR β antibody to do immunoprecipitation and used anti-hsp90 antibody to perform immunoblotting to detect hsp90.

Transfection of TM cells with $hGR\beta$ expression vectors

To test the negative activity of hGR β , we transfected pCMX-hGR β , a hGR β expression vector, into TM cells and detected whether the overexpression of hGR β inhibited the induction of myocilin by Dex (100 nM). Transfection was conducted using CalPhosTM Mammalian Transfection Kit (BD Biosciences) and Western Blotting was performed to detect the myocilin expression using polyclonal anti-myocilin antibody.

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CHAPTER II

DEXAMETHASONE REGULATES ENDOTHELIN-1 AND ENDOTHELIN RECEPTORS IN HUMAN NON-PIGMENTED CILIARY EPITHELIAL (HNPE) CELLS

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SUMMARY

Endothelin-1 (ET-1) lowers intraocular pressure (IOP) in animal models by regulating aqueous humor dynamics through both inflow and outflow mechanisms. Moreover, ET's concentration is elevated in glaucoma patients and in animal models of glaucoma. Glucocorticoid therapy often can lead to increase IOP in susceptible individuals including patients with primary open angle glaucoma (POAG). In this study, we examined the effects of dexamethasone (Dex), a frequently used anti-inflammatory glucocorticoid, on the synthesis and release of endothelin-1 and on the expression of endothelin receptors in human non-pigmented ciliary epithelial (HNPE) cells, an established source for ET-1 in the anterior chamber. As measured by ET-1 immunoreactivity, ET-1 was concentration-dependently increased following 24 hr Dex treatment, with a maximum concentration (100 nM) causing a 3-fold increase of ET-1 release. Western blot analysis of HNPE cells showed the expression of endothelin receptor A (ET_A) and endothelin receptor B (ET_B) with approximate molecular weights of 40 kDa. Dex treatment decreased ET_A receptor expression at all Dex doses, but upregulated ET_B receptors with 10 nM Dex having the greatest effect. Quantitative PCR demonstrated that Dex also increased the mRNA of pre-pro-ET-1 (ppET-1) and ET_B but decreased the mRNA of ET_A. RU486, a glucocorticoid receptor antagonist, was able to block Dex's actions on ET release and ET_B receptor expression, but did not block its action on ET_A receptor expression. Endothelin receptors were minimally expressed in HNPE cells as determined in binding experiments (B_{max}: ET_A 17, ET_B 25 fmol/mg membrane protein). However Dex treatment stimulated a dramatic increase in ET_B

receptor density while decreasing ET_A receptors (B_{max} : ET_A 11, ET_B 116 fmol/mg membrane protein). The regulation of endothelin and its receptors could be a novel mechanism associated with glucocorticoid's effects on intraocular pressure. The increase in ET-1 and disproportionate regulation in ET receptor expression by Dex could promote dysregulation in ET's mechanism on both inflow and outflow, thus affecting aqueous humor dynamics in the anterior chamber of the eye.

Key words: Dexamethasone, Endothelin-1, Endothelin Receptor A, Endothelin Receptor B, Ciliary Epithelium, Aqueous Humor Dynamics, Intraocular Pressure, Glucocorticoid Receptor, RU486

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INTRODUCTION

Glucocorticoids, potent immunosuppressants and anti-inflammatory agents, are associated with primary open-angle glaucoma (POAG). It has been reported that POAG patients have elevated levels of the endogenous glucocorticoid, cortisol, in their blood (Ray et al., 1977; Rozsival et al., 1981; Schwatz et al., 1987; McCarty and Schwartz, 1991) and aqueous humor (Rozsival et al., 1981). Over 90% of POAG patients, compared with 35% of general population, are considered glucocorticoid responders and produce an elevated intraocular pressure following topical ocular administration of glucocorticoids (Becker, 1965; Lewis et al., 1988). The ability of both natural and synthetic glucocorticoids to act on a target tissue and elicit specific responses is dependent on the presence of the glucocorticoid receptors, which function as ligand-dependent transcription factors (Evans, 1988). Classically the actions of glucocorticoids are mediated by the activated glucocorticoid receptor binding to glucocorticoid response elements in the targeted genes. The activated glucocorticoid receptor is also capable of binding other transcription factors and thereby regulating their function (Jonat et al., 1990; Samples et al., 1993; Ray and Prefontaine, 1994).

The effects of glucocorticoids on the trabecular meshwork have been studied as a model system to better understand the pathogenic mechanisms involved in ocular hypertension. Glucocorticoids affect aqueous humor outflow resistance through morphological and activity changes in trabecular meshwork, including alterations in cell size and cytoskeletal organization (Wilson et al., 1993; Clark et al., 1997), extracellular matrix production (Johnson et al., 1990; Steely et al., 1992), extracellular

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metalloproteinase activity (Samples et al., 1993; Snyder et al., 1993), phagocytosis (Johnson et al., 1997), cell adhesion molecules (McCartney et al., 1994; Underwood et al., 1999), and enhanced expression of the glaucoma gene, *MYOC* (Polansky et al., 1997; Clark et al., 2001). McCarty and Schwartz (1982) reported that rabbit iris-ciliary body contained high-affinity receptors for dexamethasone and the iris-ciliary body glucocorticoid receptor was present in nearly twice the concentration as compared to the rabbit liver receptor. Similarly the glucocorticoid receptor was also detected in human ocular tissues, including non-pigmented ciliary epithelium, trabecular meshwork, corneal epithelium and endothelium, and anterior lens epithelium (Strokes et al., 2000). The action of glucocorticoids on other ocular tissues may offer insight into glucocorticoid-induced ocular hypertension and its significance to glaucoma.

Endothelin-1 is also implicated in glaucoma pathology and optic neuropathy (Orgul et al., 1996; Cioffi and Sullivan, 1999; Yorio et al., 2002) as its concentration is elevated in glaucoma patients and in animal models of glaucoma (Noske et al., 1997; Kallberg et al., 2002). HNPE cells have been shown to be a source for ET, as they endogenously synthesize and release ET-1 (Lepple-Weinhues et al., 1992; Prasanna et al., 1998). Some of ET-1's action on the regulation of intraocular pressure can be explained by paracrine effects on the ciliary muscle and trabecular meshwork resulting in increased aqueous humor outflow (Erickson-Lamy et al., 1991), while autocrine effects have been linked to inhibition of Na⁺/K⁺-ATPase and a decrease in aqueous humor formation (Taniguchi et al., 1996; Prasanna et al., 2001). The diverse biological activities of ET-1 appear to be mediated through different receptor subtypes, ET_A and ET_B receptors (Pang and Yorio,

1997; Yorio et al., 2002). In the cardiovascular system, many factors influence ETreceptor expression profile, including actions of cytokines, growth factors, vasoactive agents, flow sheer stress (Rubanyi and Polokoff, 1994), chronic heart diseases (Zolk et al., 1999), and the action of glucocorticoids (Kanse et al., 1991; Roubert et al., 1993; Kato et al., 1995; Morin et al., 1998). Little is known of the interactions between glucocorticoids and endothelin in the eye. The current study focuses on the interaction of endothelin with glucocorticoids in cultured human non-pigmented ciliary epithelial (HNPE) cells.

MATERIAL AND METHODS

Cell Culture

SV-40 transformed human ciliary epithelial cells (HNPE: passage 15-30) (a gift of Dr. Miguel Coca-Prados) (Martin-Vasallo et al., 1989) were grown at 37° C and 5% CO₂ in Dulbecco's modified Eagle's medium (DMEM, Gibco, Grand Island, NY) supplemented with 10% fetal bovine serum and penicillin/streptomycin (Gibco, Grand Island, NY) and 44 mM NaHCO₃. For treatments, HNPE cells were grown on either 100 mm culture dishes or 6-well culture plates (35 mm diameter/well). The culture media was then changed to serum-free (SF) DMEM and treated for 24 hours with the glucocorticoid agonist, dexamethasone (dissolved in ethanol) (Sigma Chemical, St Louis, MO), at a final concentration range of 1 to 100 nM or with an equivalent volume of vehicle (ethanol). RU486 (dissolved in ethanol) (BIOMOL Research Labs, Inc., Plymouth Meeting, PA), an antagonist of the glucocorticoid receptor, was used at concentration of 1 μ M to block the

effect of dexamethasone in some of the experiments. The antagonist was added 30 minutes prior to the addition of dexamethasone.

Extraction and Measurement of ET-1 in the Culture Media

Endothelin-1 extraction and measurement were done according to the procedures described by Prasanna et al. (1998). HNPE cells were grown on 6-well cultured plates and treated with Dex (1, 10, 100 nM), RU486 (1 μ M) + Dex (100 nM), RU486 (1 μ M) or TNFa (10 nM) (Pepro Tech Inc. Rocky Hill, NJ) in 1 ml of SF-DMEM for 24 hours, and the culture media were collected after treatments. The medium samples were acidified with 1 ml of 1% trifluoroacetic acid (TFA: v/v in water) for 10 minutes, then applied to pre-treated Sep-Pak C₈ cartridges (125 Å; Waters Corp., Milford, MA). Elution was carried out by application of solvent A (40% methanol + 0.5% TFA; v/v) (2 × 1 ml) and solvent B (90% methanol + 0.5% TFA; v/v) (2×1 ml). The eluents (containing ET-1) in solvent B were then dried under a nitrogen stream. For measurement of endothelin-1 released in the culture media, a commercially available radioimmunoassay (RIA) kit for ET-1 was used (Peninsula Laboratories, Belmont, CA). Briefly, on the first day, the dried eluents were reconstituted with 200 µl of radioimmunoassay buffer, and 0.1 ml of rabbit anti-ET-1 was added to each 0.1 ml of reconstituted sample. Samples were stored overnight at 4°C. On the following day, the samples were treated with 0.1 ml of [¹²⁵I]ET-1 (10-15,000 cpm/tube) overnight at 4°C. On the third day, the samples were treated with 0.1 ml of goat anti-rabbit IgG serum and 0.1 ml of normal rabbit serum for 90 minutes, and then added to 0.5 ml of RIA buffer and centrifuged at 1700Xg for 20 minutes at 4°C.

The supernatant was aspirated and the remaining pellet was counted in a gamma counter. The sample ET-1 concentrations were obtained from a standard curve.

Membrane preparation and Western Blotting

The isolation of plasma membrane was performed as previously described (Dibas et al., 1996). HNPE cells grown to confluence on 100 mm dishes were washed and scraped in PBS buffer (0.2 g/l KCl, 8 g/l NaCl, 2.16 g/l Na₂HPO₄·7H₂O). After a brief centrifugation, the cells were resuspended in homogenization buffer (32 mM Tris-HCl, 16 mM sodium pyrophosphate, 1.6 mM EDTA, 0.8 mM EGTA, 0.64 mM NH₄ molybdate, add fresh 3.2 mM DTT) containing protease inhibitors (20 µg/ml leupeptin, 20 µg/ml aprotinin, 20 µg/ml soybean trypsin inhibitor and 40 µg/ml PMSF). The samples were quickly sonicated and the homogenate was centrifuged briefly to sediment unbroken cells and nuclei. The supernatant was centrifuged at 100,000Xg for 35 minutes at 4°C. The resultant pellet was dissolved in homogenization buffer containing proteinase inhibitors, Triton-X 100 (0.1%) and NP-40 (0.1%) by gently aspirating several times and incubating on ice for 30 minutes. Protein concentration of the membranes was determined using the BCA reagent and bovine serum albumin as the protein standard (Sigma Chemical, St Louis, MO). Membrane protein (60 µg) from HNPE was mixed with SDS-sample buffer (4X: 62.5 mM Tris, pH6.8, 0.1% (v/v) glycerol, 2% SDS, 0.05% 2-B mercaptoethanol and 0.005% (w/v) bromophenol blue), and incubated at 100°C for 5 minutes. SDS-PAGE was performed on 7.5% gels according to the procedures described by Laemmli (1970) using a Bio-Rad electrophoresis unit. Protein was then transferred to nitrocellulose membranes (Schleicher & Schuell Inc. Keene, NH) according to methods

of Towbin et al. (1979) in transfer buffer (192 mM Glysine, 20% methanol and 25 mM Tris pH 8.3) at room temperature overnight using Bio-Rad electrophoretic transfer unit. The blots were blocked in 10% non-fat milk in TBST buffer (10 mM Tris-HCl, 150 mM NaCl, and 0.05% Tween-20) for 1 hour before probing with a 1:200 dilution of rabbit polyclonal ET_A or ET_B antibodies (Alomone Labs, Jerusalem, Israel) for 1 hour. Nonspecific bands in the immunoblot for ETA and ETB receptors were identified by preincubating the anti-ET_A or anti-ET_B antibodies with their respective receptor peptides (Alomone Labs, Jerusalem, Israel) at a ratio of 1 µg peptide per 1 µg antibody at 37°C for 1 hr before probing blots. These receptor peptides are the fractions (about 1.8 kDa) of ET receptors and were used to produce these antibodies. Following this incubation period, the blots were washed 3X for 5 minutes each in10 ml of TBST, and probed with 1:10,000 dilution of horseradish peroxidase-conjugated anti-rabbit IgG (Amersham Pharmacia Biotech, Piscataway, NJ) for 30 minutes. After 3 washes with TBST, the blots were developed using an ECL kit (Amersham Pharmacia Biotech, Piscataway, NJ). Densitometric analysis of the bands was done using the Scion image analysis software (NIH). The quantification of band intensity is represented as a percentage to the value of its corresponding control band in the same membrane and the intensity for ET_A and ET_B are presented as a mean percentage in four separate experiments.

Membrane preparation and [¹²⁵I]ET-1 binding

The binding assay protocol was modified from Bolger et al. (1990) and the lab protocol of Dr. Masashi Yanagisawa (Department of Molecular Genetics, University of Texas Southwestern Medical Center, Dallas TX). HNPE cells were grown in 150 mm

culture dishes and homogenized in homogenization buffer containing proteinase inhibitors and centrifuged at 100,000Xg for 35 minutes as described previously. The supernatants were discarded and the pellets were resuspended in binding buffer (25 mM Hepes pH 7.4, 135 mM NaCl, 2.7 mM KCl, 1.8 mM CaCl₂, and 1.1 mM MgSO₄) containing protease inhibitors (5 µg/ml leupeptin, 5 µg/ml aprotinin, 5 µg/ml soybean trypsin inhibitor and 10 µg/ml PMSF) by gently aspirating. The homogenates were centrifuged at 100,000Xg for another 35 minutes. The supernatants were discarded and the pellets homogenized in binding buffer containing 0.7 µg/ml aprotinin and 1.6 µg/ml PMSF using a polytron stirrer (Talboys Engineering Corp., Emerson, NJ). Protein concentration was determined using the BCA protein assay, and the membrane faction concentration diluted in binding buffer to 1 μ g/ μ l. 50 μ g membrane protein was used for each binding reaction. [¹²⁵I]ET-1 (NEN Life Science Product. Inc., Boston, MA) binding was performed in polypropylene tube in a total assay volume of 100 µl containing 25 µl of [125I]ET-1 ranged from 0.025 to 2.4 nM, 50 µl of membrane faction, 25 µl of competition reagent or buffer at 37°C for 1 hour. Binding was terminated by adding 10 ml of cold wash buffer (10 mM Tris-HCl and 150 mM NaCl pH 7.4 at 4°C) and rapid vacuum filtration over glass fiber filters (No. 30, Schleicher & Schuell Keene, NH) presoaked with 1% w/v BSA. Filters were washed with 10 ml of wash buffer twice and the bound radioactivity was quantitated in a gamma counter. Non-specific binding was defined as filter-bound radioactivity measured in the presence of 1 µM unlabeled ET-1 (Sigma Chemical, St Louis, MO) before addition of $[^{125}I]$ ET-1. The binding of ET_A receptor was determined by pre-treating with 0.5 µM sarafatoxin S6C (Peninsula Lab Inc.

Belmont, CA), an ET_{B} agonist, to block the binding of [¹²⁵I]ET-1 to ET_{B} receptors. ET_{B} receptor binding was defined as the total specific [¹²⁵I]ET-1 binding minus the amount of ET_{A} receptor binding. Estimates of the equilibrium dissociation constant (Kd) and maximun number of binding sites (Bmax) were obtained using unweighted linear regression analysis of data transformed by the method of Scatchard (1949).

RNA isolation and Quantitative Polymerase Chain Reaction

Total cellular RNA was isolated from HNPE cells using the Trizol B reagent (Life Technologies, Rockville, MD). cDNA was synthesized from 5 µg of total RNA from each sample using random primers and AMV Reverse Transcriptase (Promega, Madison, WI) in a reaction volume of 50 µl at 42°C for 30 min. QPCR primers for ppET-1, ET_A and ET_B (Table 2) were designed from their respective cDNA sequence using GeneJockey II program (BioSOFT, Ferguson, MO). These primers are designed spanning different exons. B-actin served as an internal control to account for variability in the initial concentration and quality of the total RNA and in the conversion efficiency of the reverse transcription reaction. QPCR amplification of each sequence was performed with 2.5 µl of cDNA sample in a total volume of 25 µl using SYBR Green PCR Core regents (PE Applied Biosystems, Foster City, CA). QPCR reactions were performed for 50 cycles of denaturation at 94°C for 30 sec, annealing at 60°C (for β -actin and ET_A) or 58°C (for ppET-1 and ET_B) for 30 sec and extension at 72°C for 30 sec in an Cepheid Smart Cycler (Cepheid, Sunnyvale, CA). Immediately after the real-time PCR run, the melting curves were generated to detect the melting temperatures of the specific products (data not shown). The QPCR product purity was also confirmed by analyzing the QPCR products by 2% agarose gel electrophoresis. The authenticity of QPCR products were confirmed by DNA sequencing and a BLAST search of the sequence through NCBI (<u>http://www.ncbi.nim.nih.gov</u>) (data not shown). Quantification of relative RNA level was achieved by using the comparative C_T method (as described in PE Biosystems User Bulletin#2: <u>http://docs.appliedbiosystems.com/pebiodocs/04303859.pdf</u>.) QPCR data is presented as the mean percentage to the value of its corresponding untreated control in three separate experiments.

RESULTS

Dexamethasone Effects on ET-1 Concentrations

The effect of Dex on ET-1 release into the culture medium from HNPE cells was determined using a radioimmunoassay for ET-1 following cells treated with or without Dex. We used the cytokine TNF- α as a positive control, as we previously demonstrated that TNF- α increases ET-1 release in these cells (Prasanna et al., 1998). TNF- α treatment significantly elevated ET-1 concentration in the media as compared to that observed in control HNPE cells. Interestingly, 24 hr Dex treatment also increased ET-1 releasing into the media compared to control (Fig. 1A) (control (11 ± 1.5 pg/ml media/mg protein) = $100 \pm 14\%$; TNF- α = $361 \pm 38\%$; Dex 1 nM = $129 \pm 20\%$; Dex 10 nM = $294 \pm 30\%$; Dex 100 nM = $316 \pm 38\%$, Mean \pm S.E. of 9 experiments). Moreover, the Dex response was blocked by pretreatment with RU486 (1 μ M), a glucocorticoid receptor antagonist (Fig. 1B) (control = $100 \pm 14\%$; Dex 100 nM = $316 \pm 38\%$; RU486 + Dex 100 nM = $178 \pm$

33%; RU486 = $108 \pm 18\%$, Mean \pm S.E. of 9 experiments), suggesting Dex-treated ET-1 release was through glucocorticoid receptor activation.

Effects of Dexamethasone on ET_A and ET_B Receptor Protein Expression

HNPE cells have been shown to be a source for ET-1 (Prasanna et al., 1998; Lepple-Weinhues et al., 1992), however ET receptor expression has been less examined. In order to investigate ET receptor expression under control and Dex treatment conditions, we carried out Western Blotting. Western blot analysis revealed that both ETA and ETB receptors are present in HNPE cells. Anti-ETA recognized two bands with the sizes of approximate 60 kDa and 40 kDa (Fig. 2A), and ET_A receptor peptide was able to block the recognition of the 40 kDa band, but was unable to block recognition of the 60 kDa band (Fig. 2B). Anti-ET_B recognized two bands with one of 50 kDa and one at approximately 40 kDa (Fig. 2D), and the ET_B receptor peptide completely blocked the lower band, but was unable to block the top band (Fig. 2E). The top bands (60 kDa or 50 kDa) therefore were being recognized as nonspecific bands by anti-ET_A or anti-ET_B antibody. The ET_A and ET_B receptor sizes were approximately 40 kDa with ET_B slightly smaller than ETA. These molecular weights are similar to the sizes described by the manufacturer of the anti- ET_A and anti- ET_B antibodies (Alomone Labs).

Treatment with Dex for 24 hours produced a concentration-dependent decrease in the protein levels of the ET_A receptors (Fig. 2C, lanes 2,3,4), but significantly increased the protein levels of the ET_B receptors at 10 nM Dex (Fig. 2F, lane 3). RU486 treatment did not block Dex -induced alteration of protein expression of the ET_A (Fig. 2C, lane 5), but completely blocked Dex action on ET_B receptor expression (Fig. 2F, lane 5). It was interesting that RU486 alone decreased ET_A receptor expression at high concentration RU486 100 nM and 1 μ M (Fig. 2H, lanes 4,5).

Endothelin Receptor Binding Characteristics in HNPE Cells Treated with Dex

In order to verify and better quantify the ET receptor density changes, [¹²⁵I]ET-1 binding to its receptors was performed in HNPE cells. Competition [¹²⁵I]ET-1 binding experiments found that 1µM ET-1 was able to block all of the [¹²⁵I]ET-1 binding to its ET receptors (data was not shown). Therefore we used 1 µM ET-1 to determine nonspecific binding. Since Western blot analysis found 10 nM Dex appeared to consistently influence both ET_A and ET_B receptor expression, we used the 10 nM Dex dose to investigate Dex's effect on ET receptor density in these binding experiments. Under control conditions, HNPE cells appear to have a relatively low ET binding activity (total ET receptor 41 \pm 0.81, ET_A 17 \pm 0.5, ET_B 25 \pm 0.36 fmol/mg membrane protein, mean \pm SE of 4 experiments). However, the total ET receptor density increased following 10 nM Dex treatment with the largest component of the increase attributed to the increases in ET_B receptor density (total ET receptor 126 ± 17, ET_A 11 ± 1.9, ET_B 116 ± 16 fmol/mg membrane protein, mean \pm SE of 4 experiments) (Fig. 3). Table 1 summarizes the effect of 10 nM Dex on ET binding. Dex treatment did not significantly change the affinity of ET-1 for the ET_A receptor (control 0.63 \pm 0.05 versus Dex 0.49 \pm 0.1 nM, mean \pm SE of 4 experiments), but significantly modified the affinity of ET-1 binding to the total ET receptor population (control 1.14 ± 0.08 versus Dex 4.25 ± 0.16 nM, mean \pm SE of 4 experiments), which could reflect the predominant changes that occurred in the ET_B receptor.

Dexamethasone Effects on mRNA Expression of prepro-ET-1, ET_A and ET_B receptors in HNPE Cell

Since there were protein expression changes in ET-1, ET_A and ET_B receptors following Dex treatment, we next determined if Dex treatment also regulated the mRNA expression of ET-1 and its receptors. We carried out Quantitative PCR (QPCR) analysis for ppET-1, ET_A and ET_B receptors. Dex treatment for 24 hours significantly increased the mRNA levels of ppET-1 at 10 nM and 100 nM Dex (Fig 4A, lanes 3,4), but decreased the mRNA amount of the ET_A receptor in a concentration-dependent manner (Fig 4B, lanes 2,3,4), while significantly increasing the mRNA levels of the ET_B receptor with 10 nM Dex having the greatest effect (Fig 4C, lanes 3, 4). RU486 at 1 μ M completely blocked the Dex effects on the ppET-1 and ET_B receptor (Fig 4A and C, lane 5), but not on the ET_A receptor (Fig 4B, lane 5). RU486 alone also decreased the mRNA levels of the ET_A receptor (Fig 4B, lane 6).

DISCUSSION

Treatment of HNPE cells with dexamethasone (Dex), a potent synthetic glucocorticoid, caused a concentration-dependent increase in ET-1 mRNA and peptide levels. A maximal three fold stimulation of ET-1 release in the medium was observed at a dose of 100 nM Dex for 24 hrs, similar in magnitude to the induction seen with TNF α (10 nM) reported by our laboratory (Prasanna et al., 1998). RU486, an antagonist of glucocorticoids, has been shown to block glucocorticoid regulation of pre-pro-ET-1 mRNA and ET-1 release (Calderon et al., 1994; Morin et al., 1998). In the current study,

the stimulationary action of Dex on HNPE cell was blocked by the co-incubation of RU486 (1 μ M), showing an involvement of glucocorticoid receptors in this response of ET-1.

How glucocorticoids regulate ET-1 expression is not clear. The actions of glucocorticoids can be mediated by the activated glucocorticoid receptor binding to glucocorticoid response elements in the targeted genes or binding other transcription factors and thereby regulating their function (Jonat et al., 1990; Samples et al., 1993; Ray Prefontaine, 1994). Alternatively, glucocorticoid responses and may involve glucocorticoid receptor activation of a primary response gene whose gene product in turn secondarily activates other genes (Gotoh et al., 1997; Shepard et al., 2001). The basal transcription level of the ET-1 encoding gene depends on two critical regions in its promoter: a GATA motif and an AP-1 consensus (Lee et al., 1990). There has been no report of a glucocorticoid response element for the ET-1 promoter. Interestingly, the GATA family members have a highly homologous DNA binding domain that contains two zinc fingers reminiscent of those of the glucocorticoid receptor (Omichinski, et al., 1993; Raich and Romeo, 1993). It has also been reported that glucocorticoid receptors bind a member of GATA family and interfere with its function before any interaction with DNA (Chang et al., 1993). Glucocorticoid receptors may indirectly regulate ET-1 gene expression by interacting with GATA family members. Recently some other transcription factors such as Vezf1/DB1, hypoxia-induced factor (HIF-1) were also demonstrated to be able to activate the transcription of ET-1 (Aitsebaomo et al., 2001; Kakinuma et al., 2001; Yamashita et al., 2001). The induction of (HIF)-1 alpha in heart

failure as an adaptation against impaired energy metabolism alternatively causes an elevation of cardiac ET-1 gene expression (Kakinuma et al, 2001). Whether there is a novel molecular mechanism of up-regulation of ET-1 as an adaptation in response to Dex treatment in HNPE cells is unknown. Glucocorticoids have been reported to increase ET-1 gene expression in vascular smooth muscle cells (Morin et al., 1998) and in bronchial epithelial cells (Aubert et al., 1997), and also stimulate ET-1 peptide secretion (Kato et al., 1995; Roubert et al., 1993; Kanse et al., 1991). In the present study, we demonstrated that Dex treatment for 24 hrs increased both ET-1 mRNA and peptide levels. Further experiments are needed to delineate the pathways that may be involved in the response to Dex treatment in HNPE cells.

Both quantitative PCR and Western blot analysis indicated that Dex concentrationdependently decreased the ET_A receptor but increased the ET_B receptor with 10 nM Dex having the greatest effect. RU486 has been shown to reverse the effect of glucocorticoids on ET receptor numbers in vascular smooth muscle cells (Provencher et al., 1995). In this study, RU486 blocked Dex's effects on the ET_B but not ET_A receptor expression. It also appears that RU486 may function as a partial agonist, as it had its own action on ET_A receptor expression. In fact, RU486, a classical antagonist for both progesterone and glucocorticoid receptors, interferes with steroid-mediated activation, but often confers an agonist activity to steroid receptors (Beck et al., 1993; Sartorius et al., 1994; Liu et al., 2002). Recently, it has been reported that RU486 can exhibit partial agonist activity and the N terminus of glucocorticoid receptor is a critical determinant for RU486-mediated agonist activity (Schulz et al., 2002). Shepard et al. (2001) also reported that RU486 functions as a partial agonist at myocilin/TIGR expression in trabecular meshwork cells. Such observations are important in evaluating the responses seen with glucocorticoids in the presence of RU486, and could account for the inability of RU486 to block Dexmediated decrease in ET_A receptors.

ET-1 has been known to regulate its biological effects using two subtype receptors, the ET_A and ET_B receptors (Pang and Yorio, 1997; Yorio et at., 2002). Both subtypes are present in the ciliary body (Ripodas et al., 1998). In this study, we observed the expression of both mRNAs and proteins for ET_A and ET_B receptors in isolated HNPE cells. The ET_A and ET_B receptor proteins had molecular weights of appoximately 40 kDa, although ET_B receptors were slightly smaller than ET_A receptors. Using an autoradiography technique, Ripodas (1998) reported that ciliary body ETA and ETB receptors had molecular weights of 52 kDa and 34 kDa and suggested that the 34 kDa band is a proteolytic degradation product of the 52 kDa band. We also identified immunoreactive bands at about 60 kDa or 50 kDa using anti-ET_A or ET_B receptor antibodies respectively. However, labeling of these higher molecular weight bands was not blocked by the addition of competing soluble ET_A and ET_B receptor peptides, demonstrating the upper bands in the immunoblots were non-specific antibody binding. There have been numerous reports of different molecular weights for ETA and ETB receptors that range between 50 kDa and 70 kDa (Kondoh et al., 1990; Shannon and Hale, 1994; Freedman et al., 1997; Kurokawa et al., 1997), but other investigators have shown ET receptors with similar apparent molecular weights to what we have found (between 30 and 40 kDa) (Masuda et al., 1989; Bednar et al., 1991; Takasuka et al.,

1994). The apparent differences in reported molecular weights could be attributed to the source of antibody, species or tissue specificity, post-translation modification, result of difference *in vivo* proteolytic processing, or ultimately the result of the inaccuracy inherent in the estimation of the molecular weight of membrane proteins by SDS-PAGE.

[¹²⁵I]ET-1 binding experiments supported Western Blot analysis data in that Dex treatment regulated ET_A and ET_B receptor expression. HNPE cells had a much lower density of ET receptors, but had a similar binding affinity for ET-1 as compared to that found in other tissues (Bolger et al., 1990). Dex treatment did not change the receptor affinity but dramatically increased ET_B receptor density while decreasing ET_A receptor density. Sarafatoxin S6C, a specific agonist for the ET_B receptor, was able to compete for $[^{125}I]ET-1$ binding to the ET_B receptor. The remaining $[^{125}I]ET-1$ binding sites appeared to be ET_A receptors. Although there have been some reports about another endothelin receptor subtype, ET_C receptors (Karne et al., 1993), the ET_C receptor appears to be specific for ET-3 and is only been reported in amphibians (Karne et al., 1993). The high affinity binding of $[^{125}I]ET-1$ seen in this study strongly suggests that ET_A and ET_B receptors are responsible for this binding. The observations that ET_A receptors were down-regulated, but ET_B receptors were up-regulated by Dex demonstrate that additional mechanisms for ET receptor regulation exist besides agonist-induced homologous receptor down-regulation. Indeed glucocorticoids and chronic heart failure have been reported to induce the regulation of ET receptors in addition to a regulation of ET-1 (Zolk et al., 1999; Borcsok et al., 1998). Although the magnitudes were different, both Western Blotting and ligand binding experiments showed a similar trend in Dex's regulation of ET_A and ET_B receptors. Those differences in the magnitude may be attributed to different sensitivities of both techniques and the extent of the extraction of membrane proteins for Western Blotting.

Changes in ET receptor expression and concomitant increases in ET-1 release by Dex could contribute to the Dex response in ocular tissues. In normal situations, increases in ET-1 in the anterior segment may have beneficial effects by contracting ciliary smooth muscle (Wiederholt, 1998) and increasing aqueous humor outflow (Erickson-Lamy et al., 1991) while inhibiting Na⁺, K⁺-ATPase in non-pigmented ciliary epithelial cells through ET_B receptors and decreasing aqueous humor formation (Prasanna et al., 2001). Such effects could contribute to the functional response in the decrease in IOP after intravitreal administration of ET (Sugiyama et al., 1995; Granstam et at., 1991). However in the presence of dexamethasone, there are changes in the morphology and activity of trabecular meshwork with concomitant increases in the deposition of extracellular matrix materials (Wordinger and Clark, 1999). The increase in synthesis and release of ET-1 from non-pigmented ciliary epithelial cells and contraction of ciliary smooth muscle by ET-1 in attempt to reduce IOP could also contract the trabecular meshwork and reduce the intertrabecular space and consequently increase outflow resistance and IOP as a maladaptation. Although ET_B receptors could play a role in clearance of ET-1 (Paasche et al., 2001; Bremnes et al., 2000), ET-1 has been shown to increase inducible NO synthase 2 and NO concentration in ocular tissues (Prasanna et al., 2000), which can have a further damaging effect on the eye (Neufeld, 1999). Such changes in ET receptor densities and

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the increase in ET release could thus play a role in Dex-induced ocular hypertention and glaucoma, however this awaits further experimentation.

In conclusion, we have described a novel signaling pathway for dexamethasone in HNPE cells that regulates the release of ET-1 and the expression of ET receptors. Such actions could have consequences on aqueous humor inflow/outflow and intraocular pressure that are associated with endothelin and/or glucocorticoids.

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FIGURE 1. Effects of dexamethasone (Dex) and RU486, a glucocorticoid receptor antagonist, on endothelin-1 (ET-1) release from HNPE cells. ET-1 released into the culture media from HNPE cells grown in 6-well plates was measured using radioimmunoassay (RIA). A) HNPE cells were treated with no Dex (control), 1 nM, 10 nM, 100 nM Dex for 24 hrs. Tumor necrosis factor- α (TNF- α ; 10 nM) was used as a positive control. B) HNPE cells were treated 24 hrs with no Dex (control), 100nM Dex, 1 μ M RU486 + 100 nM Dex, or 1 μ M RU486. HNPE cells were pre-treated with 1 μ M RU486 for 30 minutes before the addition of 100 nM Dex. ET-1 released in control cells corresponded to 11.2 ± 1.5 pg / ml media / mg protein and was taken as 100 % (n = 9). * Denotes statistical significance of mean % ET-1 released from Dex treatments versus that of control and ** denotes statistical significance of mean % ET-1 released from RU486 + Dex treatment versus that of Dex as determined by One-way ANOVA and Student-Newman-Keuls multiple comparison test at p < 0.05.

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1 nM Dex

10 nM Dex

10 nM TNFa

B



FIGURE 2. Effects of dexamethasone (Dex) and RU486 on the protein expression of ET_A and ET_B receptors in HNPE cells as determined by Western Blotting. Panels A-F, HNPE cells were treated for 24 hours with: control (lane 1); 1 nM Dex (lane 2); 10 nM Dex (lane 3); 100 nM Dex (lane 4); 1 µM RU486 + either 100 nM Dex (Fig. 3A and 3B lane 5) or 10 nM Dex (Fig. 3D and 3E lane 5); 1 µM RU486 (lane 6); Panels G-H, HNPE cells were treated for 24 hours with: control (lane 1); RU486 1 nM (lane 2); 10 nM (lane 3), 100 nM (lane 4) and 1 μ M (lane 5). Western blot analysis of ET_A receptor without (Fig. 3A), and with pre-incubation with ET_A receptor blocking peptide (Fig. 3B). Western blot analysis for ET_{B} receptor without (Fig. 3D), and with pre-incubation with ET_{B} receptor blocking peptide (Fig. 3E). Western Blotting for ET_A without pre-incubation with ET_A receptor blocking peptide (Fig. 3G). Both ET_A and ET_B can be detected as protein bands approximately 40 kDa. Densitometric analysis of the bands was done using the Scion image analysis software (NIH). The quantification of band intensity is represented as a percentage to the value of its corresponding control band in the same membrane and the intensity for ET_A (Fig. 3C), ET_B (Fig. 3F) and ET_A (Fig. 3H) are presented as a mean percentage in four separate experiments. *Denotes statistical significance of mean % ET receptor density from Dex or RU486 treatments versus that of control and ** denotes statistical significance of mean % of ET_B receptor density from RU486 + Dex treatments versus that of Dex treatment as determined by One-way ANOVA and Student-Newman-Keuls multiple comparison test at p < 0.05.

FIGURE 2

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FIGURE 3. Effect of dexamethasone (Dex 10 nM) on ET receptor density as determined by saturation plot of [¹²⁵I]ET-1 binding. Non-specific binding was determined by adding 1 μ M of ET-1. Quantitation of ET_A and ET_B receptors was determined by sarafatoxin S6C (500 nM), an ET_B selective agonist. HNPE cells were treated for 24 hours with or without Dex (10 nM). 50 μ g membrane protein was used for each binding reaction. * Denotes statistical significance of mean of ET receptor density from Dex treatment versus that of control in four experiments as determined by One-way ANOVA and Student-Newman-Keuls multiple comparison test at p<0.01.

FIGURE 3

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TABLE 1

Summary of the Binding Results of ET-1 in Control and Dexamethasone treatment in HNPE cells

	Receptor Density (B _{max})	Kd (nM)	
	(fmol/mg membrane protein)		
Control			
Total ET Receptor	41 ± 0.81	1.14 ± 0.08	
ETA	17 ± 0.50	0.63 ± 0.05	
ETB	25 ± 0.36	а.	
Dexamethasone 10 nM	2	±	
Total ET Receptor	126 ± 17 *	$4.25 \pm 0.16^{\dagger}$	
ET_A	11 ± 1.9 *	0.49 ± 0.10	
ETB	116 ± 16 [§]	8 8 1	

NOTE: Estimates of the equilibrium dissociation constant (Kd) and maximum number of binding sites (B_{max}) were obtained using unweighted linear regression analysis. Statistic significance was determined by one-way ANOVA and Student-Newman-Keuls multiple comparison test. Values are expressed as mean \pm S.D. (n = 4). For receptor density, * p < 0.01 control ET receptor versus Dex ET receptor, * p < 0.01 control ET_A versus Dex ET_A, * p < 0.01 control ET_B versus Dex ET_B. For Kd, [†]p < 0.001 control ET receptor.

FIGURE 4. Dexamethasone effects on the mRNA expression of prepro-ET-1, ET_A and ET_B receptors in HNPE cells as determined by quantitative PCR. HNPE cells were treated for 24 hours with: vehicle control (lane 1); 1 nM Dex (lane 2); 10 nM Dex (lane 3); 1 μ M RU486 + 100 nM Dex (Fig 4A and B, lane 5) or 1 μ M RU486 + 10 nM Dex (Fig 4C, lane 5); 1 μ M RU486 (lane 6). β -actin was used as an internal control. QPCR data is presented as the mean percentage of mRNA levels to the value of its corresponding control in three separate experiments. * Denotes statistical significance of mean % ppET-1 or ET receptor mRNA from Dex or RU486 treatment versus of control and ** denotes statistical significance of mean % from RU486 + Dex treatments versus that of Dex treatment as determined by One-way ANOVA and Student-Newman-Keuls multiple comparison test at p<0.05.

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TABLE 2

- 21

Quantitative PCR Primer Sequences and Expected Product Sizes

Gene	Sense	Anti-Sense	Spacing
ppET-1*	TATCAGCAGTTAGTGAGAGG	CGAAGGTCTGTCACCAATGTGC	180 bp
ET _A	GTTGAACAGAAGGAATGGCAGC	ATTCACATCGGTTCTTGTCC	181 bp
ET _B	TCACTGTGCTGAGTCTATGTGC	AGCAGATTCGCAGATAACTTCC	206 bp
β -actin	TGTGATGGTGGGGAATGGGTCAG	TTTGATGTCACGCACGATTTCC	514 bp

NOTE: *ppET-1 represents pre-pro-endothelin-1.



FIGURE 4

- 3 -

CHAPTER III

INTERACTIONS OF ENDOTHELIN-1 WITH DEXAMETHASONE IN PRIMARY CULTURED HUMAN TRABECULAR MESHWORK CELLS

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Abstract

<u>Purpose:</u> Aqueous humor endothelin-1 (ET-1) concentrations are increased in patients with primary open-angle glaucoma (POAG) as well as in animal models of glaucoma. Glucocorticoids have also been associated with glaucoma as topical administration of glucocorticoids can increase intraocular pressure by increasing outflow resistance in the trabecular meshwork (TM) in some individuals. Recently, we have shown that dexamethasone (Dex), a synthetic glucocorticoid, can increase ET-1 release from human non-pigmented ciliary epithelial cells (HNPE), a source for aqueous ET-1. In the current study we address the downstream interaction of ET-1 with Dex in target TM cells, an action which may alter outflow resistance.

<u>Methods</u>: A normal primary human TM cell line (NTM) and a TM cell line (GTM) derived from a glaucomatous patient were used. These cells were treated with vehicle or Dex. The mRNA levels of prepro-ET-1, endothelin receptor A (ET_A), and endothelin receptor B (ET_B) were measured by quantitative RT-PCR (QPCR). The protein expression of ET_A and ET_B receptors were investigated by Western blotting using polyclonal anti-ET_A and anti-ET_B antibodies respectively on plasma membrane fractions. Intracellular Ca²⁺ ([Ca²⁺]_i) mobilization mediated by ET-1 was measured using the Fura-2, AM fluorescent probe technique as an index of ET receptor function. ET-1-stimulated nitric oxide release was measured using a Griess colorimetric nitric oxide synthase assay kit.

<u>Results:</u> Both normal and glaucomatous cultured TM cells expressed prepro-ET-1 mRNA less abundantly compared to HNPE cells, and Dex treatment had no effect on the mRNA

expression of the ET-1 gene. TM cells expressed mRNA of ET_A receptors as detected by QPCR, whereas the ET_B message was not clearly delineated. Western blot analysis showed that both ET_A and ET_B receptor proteins were present. The ET_A receptor was linked to calcium mobilization as ET-1 produced an increase in intracellular calcium release and this increase was blocked with a selective ET_A receptor antagonist. Dex failed to induce any change in the expression of the ET_A receptor in both normal and glaucomatous TM cells, and this was supported by a lack of a Dex's effect on the ET-1 induced calcium response. However, Dex treatment diminished ET_B receptor protein expression as well as produced a decrease in ET-1-stimulated nitric oxide (NO) release, a response mediated by ET_B receptors in TM cells.

<u>Conclusion</u>: The Dex-induced increase in ET-1 release from HNPE cells coupled to the downstream Dex-induced specific suppression of ET_B receptor protein expression and declines in ET-1 mediated increase in NO release in TM cells could increase contraction and decrease relaxation of TM and contribute to the declines in conventional aqueous humor outflow and increases in intraocular pressure that are seen with glucocorticoids.

Key Words: Endothelin-1, Endothelin Receptor A, Endothelin Receptor B, Trabecular Meshwork, Dexamethaonse, Calcium, Nitric Oxide, Outflow Resistance

INTRODUCTION

Glaucoma is commonly associated with elevated intraocular pressure (IOP) as seen in POAG, which results primarily from pathological changes in the aqueous humor outflow pathway. Endothelin-1, a potent vasoactive peptide, may contribute to the etiology of POAG, as aqueous ET-1 concentrations are increased in POAG¹ and in animal models of glaucoma.² Moreover, chronic administration of ET-1 can produce an optic neuropathy³, ^{4, 5} and ET-1 has been proposed as a contributor of glaucoma pathophysiology.⁶ In the anterior segment, HNPE cells have been shown to be a source for aqueous ET-1, as they endogenously synthesize and release ET-1.^{7, 8}

Endothelin-1 has a variety of physiological and/or pathophysiological ocular functions depending on the receptor subtype present and the tissue involved. There are two major classes of endothelin receptors, ET_A and ET_B , which have been cloned and characterized in mammalian species.^{9, 10} Most commonly, ET_A mediates ET-1-induced increase in intracellular calcium $[Ca^{2+}]_i^{11}$ and vasoconstriction,¹² while ET_B mediates vasodilation apparently through increases in NO production.¹³ ET_B receptors are also involved in the clearance of circulating ET-1.^{14, 15, 16, 17} Although it has been reported that ET-1 elicited $[Ca^{2+}]_i$ transients,¹⁸ the expression and regulation of ET receptors in the trabecular meshwork as well as the downstream signaling events relating to outflow regulation are incompletely understood.

Glucocorticoids, potent immunosuppressants and anti-inflammatory agents, are associated with primary open-angle glaucoma (POAG). It has been reported that POAG patients have elevated levels of the endogenous glucocorticoid, cortisol, in their blood¹⁹, ^{20, 21} and aqueous humor.¹⁹ Ocular administration of glucocorticoids produce an elevated intraocular pressure in some subjects.^{22,23} It has been well established that glucocorticoids change the morphology and activity of trabecular meshwork, including altering cell size and cytoskeletal organization,^{24, 25} increasing extracellular matrix production,^{26, 27} decreasing extracellular metalloproteinase activity,²⁸ and enhancing expression of a glaucoma gene, *MYOC*.^{29, 30} Overall, glucocorticoids increase extracellular matrix material deposition in the trabecular meshwork and subsequently increase outflow resistance and IOP. Recently we have shown that glucocorticoids can increase ET-1 release from HNPE cells³¹ and the HNPE cells may represent the cell source for ET-1 in the aqueous. A novel signaling pathway for glucocorticoids involving ET-1 may be implicated in the increase in outflow resistance by glucocorticoids. We therefore investigated whether the down-stream actions of ET-1 on the target TM cells were affected by glucocorticoids.

MATERIAL AND METHODS

Cell Culture

A primary normal human TM cell line (NTM) from a 79 years old normal white male donor, and a primary glaucomatous human TM cell line (GTM) from a 79 years old POAG white male donor were used. These cells were isolated and propagated as previously described.^{24, 25, 27, 30} The cells were grown at 37°C and 5% CO₂ in Dulbecco's modified Eagle's medium (DMEM, Gibco, Grand Island, NY) supplemented with 10% fetal bovine serum and penicillin/streptomycin/Glutamine (Gibco, Grand Island, NY) and '44 mM NaHCO₃. For experiment protocols, TM cells were grown confluent either on 100 mm culture dishes, 6-well culture plates (35 mm diameter/well), or 24-well culture plates (15 mm diameter/well). The culture media was then changed to 5% FBS DMEM and treated for 72 hours with an equivalent volume of vehicle (ethanol) or the glucocorticoid agonist, dexamethasone (dissolved in ethanol) (Sigma Chemical, St Louis, MO), at a final concentration of 100 nM. RU486 (BIOMOL Research Labs, Inc., Plymouth Meeting, PA) (1 μ M), an antagonist of glucocorticoids receptors, was used in some experiments. HNPE cells and astrocytoma cells U373 MG were used as positive controls for ET-1 or ET-receptor expression.

RNA isolation and Quantitative Polymerase Chain Reaction

Total cellular RNA isolation and QPCR were performed as previously described.³¹ QPCR primers for human ppET-1, ET_A, ET_B, S15, and myocilin (Fisher-Scientific Genosys, TX) are shown in Table 1. The constitutively expressed "housekeeping" gene S15, a small ribosomal subunit protein, was served as an internal control. Myocilin gene expression was used as an index of a glucocorticoid response. Myocilin primer pairs and QPCR amplification were designed according to Shepard et al.³² The authenticity of QPCR products was confirmed by DNA sequencing and a BLAST search of the sequence through NCBI (<u>http://www.ncbi.nim.nih.gov</u>) (data not shown). Quantification of relative RNA concentrations was achieved by using the comparative C_T method (as described in PE Biosystems User Bulletin#2:

http://docs.appliedbiosystems.com/pebiodocs/04303859.pdf.)

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Plasma membrane isolation and Western Blotting analysis

The isolation of plasma membranes and Western Blotting were performed as previously described.³¹ Briefly after Dex treatment, plasma membrane fractions were isolated from both NTM and GTM cells. Protein concentration was determined using bicinchoninic acid reagent (BCA). Western blotting for ET_A and ET_B receptors was performed using polyclonal anti- ET_A or anti- ET_B antibodies respectively, with secondary horseradish peroxidase-conjugated donkey anti-rabbit IgG, and visualized using an enhanced chemiluminescence (ECL) system. Non-specific bands in the immunoblots were indentified by pre-inbubating the anti- ET_A or anti- ET_B antibodies was accomplished using the Scion image analysis software (NIH).

Measurement of intracellular Ca²⁺ mobilization

Dynamic video imaging was used to measure intracellular Ca^{2+} within single cells following a previously described method.³³ Both NTM and GTM cells were grown on 25-mm diameter converslips (Fisher Scientific, PA) inserted in 6-well culture plates. After washing three times with KRB buffer (in mM: 115 NaCl, 2.5 CaCl₂, 1.2 MgCl₂, 24 NaHCO₃, 5 KCl, 5 glucose, and 25 HEPES, pH 7.4), cells were incubated with 3 μ M fura-2, AM dye (Molecular Probes, Eugene, OR) in KRB buffer at 37°C for 30 min. Following this incubation period, cells were washed three times and were maintained in KRB buffer at 37°C. The intracellular [Ca²⁺]_i was measured with a Nikon fluorescent microscope using Imaging Metafluor software (Universal Imaging Co., West Chester, PA) and fluorescence signal ratios at 340/380 nm exitation wave lengths were collected every 5 secs. ET-1 (100 nM) was added to the buffer and changes in fluorescence ratios were recorded. BQ610 (Peninsula Lab Inc. Belmont, CA), an antagonist of ET_A receptor, was used at concentration of 1 μ M to determine whether ET-1 induced-Ca²⁺ mobilization was mediated through ET_A receptor. The antagonist was added 30 minutes prior to the addition of ET-1. In order to convert fluorescent ratios to calcium concentrations, maximum and minimum ratios of fluorescence were obtained by applying 1 μ M calcium ionophore, 4-Bromo-A23187 (Calbiochem, CA), and 5 mM EGTA, respectively. The intracellular Ca²⁺ concentration ([Ca²⁺]_i) was then calculated by using the Grynkiewicz equation.³⁴

Determination of nitrite accumulation in culture medium

* *

Following treatment with Dex for 72 hrs, confluent NTM cells grown on 24-well culture plates were shifted to serum-free (SF) DMEM with 250 μ l SF-DMEM each well, supplied with 100 nM Dex and additional 100 nM ET-1. After this 24 hour incubation, culture media were collected and NO was measured as nitrite, the final oxidation breakdown product of nitric oxide (NO) released into the culture medium using Griess colorimetric nitric oxide synthase assay kit (Calbiochem, San Diego, CA) according to the manufacture's protocol. Nitrite concentration in the culture medium was calculated from a constructed nitrite standard curve. An ET_B receptor antagonist, BQ788 (Peninsula Lab Inc. Belmont, CA) 1 μ M, was added 30 minutes prior to the addition of ET-1 to determine the role of ET_B receptor on NO release induced by ET-1.

RESULTS

The mRNA Expression of prepro-ET-1, ET_A and ET_B receptors in NTM and GTM Cells

QPCR revealed that both normal and glaucomatous TM cells express prepro-ET-1 message, however the prepro-ET-1 mRNA level was apparently much lower in TM cells than that in HNPE cells (Fig. 1). Dex (100 nM) produced a significant increase in mRNA levels of prepro-ET-1 in HNPE cells while it had no effect on prepro-ET-1 mRNA levels in TM cells (Fig. 1)

Both NTM and GTM cells expressed abundant mRNA of ET_A receptors and Dex (100 nM) had no effect on the mRNA expression of ET_A receptors, although these cells responded to Dex (100 nM) by significantly increasing myocilin mRNA expression (Fig. 2). ET_B receptor message expression was not detected in both NTM and GTM cells under either control, Dex (100 nM), or a serum free overnight condition, while as expected, ET_B receptor mRNA was present in positive control cells tested, including brain astrocytoma and HNPE cells (data not shown).

Effects of Dexamethasone on ET_A and ET_B Receptor Protein Expression in NTM and GTM Cells

Since there was mRNA expression of ET_A receptors while ET_B receptor mRNA was not detected, we next determined if TM cells expressed ET_A and ET_B receptor proteins and if their levels were under the regulation by Dex. Western blot analysis revealed that both ET_A and ET_B receptor proteins were present in NTM and GTM cells. Anti- ET_A antibody recognized an approximately 43 kDa band (Fig. 3A and 3D), and ET_A receptor peptide completely blocked the recognition of this band (Fig. 3B and 3E). Therefore this 43 kDa protein was the ET_A receptor. Treatment with Dex for 72 hours did not alter protein levels of the ET_A receptor (Fig. 3C and 3F).

Anti-ET_B antibody recognized three bands sized approximately 80 kDa, 65 kDa and 38 kDa (Fig. 4A and 4D). Competing ET_B peptide was able to completely block the recognition of only the lowest band while the other bands remained (Fig 4B and 4E). Therefore, the high molecular weight bands appear to be nonspecific bands, and the protein recognized with a size of 38 kDa is the ET_B receptor. Dex treatment for 72 hours significantly decreased the protein levels of ET_B receptors in both NTM and GTM cells (Fig. 4C and 4F). Treatment with RU486 (1 μ M), an antagonist of glucocorticoid receptors, did not block Dex-induced decrease of ET_B receptor protein and interestingly, RU486 alone, showed partial agonist activity as itself also decreased ET_B receptor amount (Fig. 4G and 4H).

Effects of Dexamethasone on ET-1-mediated Intracellular Calcium Mobilization

To determine whether ET_A receptor function was altered by Dex treatment, ET-1 effects on $[Ca^{2+}]_i$ were measured in both NTM and GTM cells under vehicle control and Dex treatment conditions. As expected, primary TM cells produced a significant increase in $[Ca^{2+}]_i$ in response to 100 nM ET-1, and this response showed a typical biphasic phenotype with a transient spike followed by a sustained plateau (Fig. 5A and 5D). This plateau was still maintained even after ET-1 was removed (data not shown). The initial rise in $[Ca^{2+}]_i$ peaked at Ca^{2+} concentrations well over 1 μ M while baseline levels were

initially below 100 nM (see Table 2). Dex (100 nM) treatment for 72 hours did not alter ET's Ca^{2+} response phenotype in both NTM and GTM cells (Fig. 5B and 5E), and Dex did not change the basal levels of $[Ca^{2+}]_i$ nor the ET-1-induced peak response in $[Ca^{2+}]_i$ in these TM cells. Pre-incubation with BQ610, an antagonist of ET_A receptors, completely blocked ET-1 mediated $[Ca^{2+}]_i$ mobilization (Fig. 5C). This indicated that ET-1 mediated $[Ca^{2+}]_i$ mobilization occurred through activation of ET_A receptors in TM cells.

Effects of Dexamethasone on ET-1-induced Nitric Oxide Release from NTM cells

In order to determine whether the decrease of ET_B receptor amount by Dex caused a similar decrease in functional response in TM cells, the effect of Dex on ET-1-induced nitric oxide (NO) release was measured. A Griess colorimetric assay was used to detect the nitrite (the final oxidation product of NO) in culture medium. ET-1 (100 nM) significantly elevated nitrite concentrations in medium compared to that observed in control cells without ET-1 treatment, and BQ 788 1 μ M, an ET_B receptor antagonist, completely blocked the elevation of nitrite by ET-1 (Fig. 6). This indicated that ET-1 mediated NO release occurred through activation of ET_B receptors in TM cells. Dex (100 nM) alone did not alter NO release compared to the vehicle control; however, Dex treatment significantly decreased the ET-1 mediated NO release compared to cells without Dex treatment. This was consistent with the finding that Dex decreased ET_B receptor expression in TM cells (as reported above) and that ET-1 stimulated NO release by activating ET_B receptors.

DISCUSSION

It was postulated that aqueous ET-1 could have consequence on the down-stream Dex effects on TM since it is known that ET-1 could contract TM and TM contraction increases outflow resistance while TM relaxation increases outflow facility.^{35, 36} However it was not known if TM cells express ET-1 or if Dex treatment stimulates ET-1 expression. In this study, QPCR was able to detect weak prepro-ET-1 mRNA expression in both NTM and GTM cells. Dex treatment did not change prepro-ET-1 mRNA expression in these TM cells. Compared to TM cells, HNPE cells expressed about four fold higher basal levels of prepro-ET-1 mRNA in control cells, and Dex treatment caused a further three fold increase of prepro-ET-1 message. Upon Dex (100 nM) treatment, HNPE cells expressed over 10 fold higher levels of prepro-ET-1 mRNA compared to TM cells. We propose that NPE cells are the source of aqueous humor ET-1 and that released ET-1 may have downstream actions in TM. The finding that Dex treatment also enhanced ET-1 expression and release suggests that ET-1 may mediate Dex effects on target tissues such as TM cells.

ET-1 has diverse biological activities through different receptor subtypes, ET_A and ET_B receptors.^{6, 37} Although ET-1 has significant actions on the regulation of IOP,³⁸ functional ET receptor expression in trabecular meshwork, a tissue regulating outflow resistance, is not certain. Previously, ET_A receptor mRNA but not ET_B receptor message in TM cells was identified by RT-PCR.¹⁸ Presently, only ET_A receptor mRNA was detected by QPCR, whereas the ET_B receptor message was not clearly delineated.

However, Western blot analysis showed that both ET_A and ET_B receptor proteins were present. The reason for this apparent difference between message and protein could be due to the finding that ET_B mRNA has a short intracellular half-life as the 3' noncoding region contains an AUUUA motif implicated in selective destabilization of mRNA.¹⁰ The finding that ET_B receptor expression was not readily detected could reflect instability of the ET_B mRNA in TM cells.

Western blotting revealed that the ET_A receptor protein had a molecular weight of 43 kDa, whereas the ET_B receptor was slightly less than 40 kDa. Previously we found ET_A and ET_B receptors had similar molecular weights in HNPE cells.³¹ There have been numerous reports of different molecular weights for ET_A and ET_B receptors that range between 30 - 70 kDa.^{39, 40, 41, 42, 43} The ET_A gene has a single transcreption start site, whereas the murine and bovine ET_B gene has been reported to have alternative transcriptional initiation sites.^{44, 45} An ET_B splice variant from alternative RNA splicing was identified in various human tissues.⁴⁶ Moreover, a metalloproteinase cleavage site was also identified in the ET_B protein sequence.⁴⁷ Overall, the apparent differences in reported molecular weights could be attributed to the source of antibodies, species or tissue specificity, post-translation modification, different proteolytic processing, or ultimately the result of inaccuracy inherent in the estimation of the molecular weight of membrane proteins by SDS-PAGE.

QPCR and Western blot analysis demonstrated that 100 nM Dex treatment for three days did not alter ET_A receptor mRNA and protein levels. In contrast, Dex treatment decreased ET_B receptor protein levels. There are several mechanisms that could account

for the effect of glucocorticoids on the regulation and expression of ET_B target gene. Activated glucocorticoid-receptor complex can either bind to the glucocorticoid response element in target genes to regulate the transcription of these genes, or perhaps interfering with other transcription factors, such as NF- κ B and AP-1, and thereby preventing the actions of these transcription factors.⁴⁸ Some other glucocorticoid responses may involve glucocorticoid receptor activation of a primary response gene whose gene product in turn secondarily activates other genes.³² However the precise mechanism of glucocorticoid regulation of ET_B receptor expression remains unclear. There is also very little information available on the regulation of endothelin receptor gene expression. Therefore, further experiments are needed to delineate the pathways that may be involved in the regulation of ET_B receptor expression by Dex in TM cells.

RU486 was unable to block Dex's effects on the ET_B receptor protein. It also appears that RU486 may function as a partial agonist, as it had its own action on ET_B receptor protein level. In fact, RU486, a classical antagonist for both progesterone and glucocorticoids receptors, interferes with steroid-mediated activation but often confers an agonist activity to steroid receptors.^{49, 50, 51} RU486 could also function as a partial agonist in TM cells and HNPE cells.^{31, 32} This partial agonist activity may explain the inability of RU486 to block Dex-mediated decrease in ET_B receptors.

ET-1 can mediate intracellular calcium $[Ca^{2+}]_i$ and contraction of trabecular meshwork³⁵ via ET_A receptors.¹⁸ This was supported by the finding that the ET_A receptor antagonist, BQ610, completely blocked this calcium mobilization. Dex treatment had no effects on ET_A mRNA and protein levels as detected by QPCR and Western Blotting, and

Dex also did not alter the function of ET_A receptors because both the baseline and ET-1induced peaked increase of $[Ca^{2+}]_i$ was similar under Dex treatment and control conditions. This normal function of ET_A receptors is important in considering Dex's effect on aqueous humor outflow, particularly since Dex increases ET-1 release from HNPE cells and ET-1 targets normally functioning ET_A receptors on TM cells. Such as action could cause more intensive contraction of the TM.

The finding that TM cells expressed not only ET_A receptors but also ET_B receptors suggested a complex regulation function. ET_B receptors most commonly regulate vasodilatation or relaxation.⁵² The signaling pathway coupled to ET_B receptors has been linked to nitric oxide (NO) production. ET-1 activates endothelial nitric oxide synthase (eNOS) and hence NO production via ET_B receptors in vascular endothelial cells.¹³ ET-3 increases retinal blood flow through activation of $ET_{\rm B}$ receptors, which also is dependent on NO production.⁵³ ET-1 and ET-3 also enhance inducible nitric oxide synthase (iNOS) expression, and this is mediated by ET_B receptors in glial cells.⁵⁴ TM cells have been shown to express different isoforms of NOS and produce NO.55, 56, 57 Presently we determined that the ET_B receptors were linked to NO production in NTM cells. We were able to detect basal levels of NO production in NTM cell culture media and showed that 100 nM ET-1 markedly increased NO release. An ET_B receptor antagonist BQ788 completely blocked this stimulation of NO by ET-1. These findings indicated that ET-1induced NO release is mediated by ET_B receptors. Dex treatment decreased the ET_B receptor protein level and also reduced ET-1-induced NO release, further implicating ET_B in ET-1-induced NO release in TM cells. There are several reports that NO donors could ****

relax trabecular meshwork and lower IOP.^{58, 59, 60} This decrease of ET_B receptor level and subsequent decrease of ET-1-induced release of NO by Dex could reduce NO mediated relaxation of TM. Moreover, ET_B receptors are known to mediate ET-1 clearance.^{14, 15, 16,} ¹⁷ The decrease of ET_B receptors in TM cells by Dex could also potentiate ET-1-mediated contraction of TM via ET_A receptors.

In conclusion, Dex-induced specific suppression of ET_B receptor protein expression and declines in ET-1 mediated increase in NO levels in TM cells with the concomitant increase of ET-1 release from HNPE cells by Dex could increase contraction and decrease relaxation of trabecular meshwork and reduce the intratrabecular space. This may exacerbate Dex effects on the outflow pathway leading to increased outflow resistance and consequently elevated intraocular pressure.

Acknowledgements

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Legends to figures:

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Fig. 1. The mRNA expression of prepro-ET-1 in NTM and GTM cells as determined by QPCR.

(A) HNPE cells were used as positive controls and treated for 24 hours with vehicle control (lane 1); 1 nM Dex (lane 2); 10 nM Dex (lane 3); 100 nM Dex (lane 4). NTM cells vehicle control (lane 5); 100 nM Dex (lane 6); GTM cells vehicle control (lane 7); and 100 nM Dex (lane 8). S15 was used as an internal control. (B) QPCR data are presented as the mean \pm SEM % to the vehicle control value of HNPE cells. Experiments were repeated three times for each culture cell line. * Denotes statistical significance from Dex treatment vs from vehicle control in HNPE cells and ** denotes statistical significance from vehicle control or Dex treatment in TM cells vs from vehicle control in HNPE cells as determined by One-way ANOVA and Student-Newman-Keuls multiple comparison test at p < 0.05.

Table 1

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Quantitative PCR Primer Sequences and Expected Product Sizes

ppET-1*TATCAGCAGTTAGTGAGAGGCGAAGGTCTGTCACCAATGTGC180 bp ET_A GTTGAACAGAAGGAATGGCAGCATTCACATCGGTTCTTGTCC181 bp ET_B TCACTGTGCTGAGTCTATGTGCAGCAGATTCGCAGATAACTTCC206 bpMyocilinGCCCATCTGGCTATCTCAGGCTCAGCGTGAGAGGCTCTCC82 bpS15TTCCGCAAGTTCACCTACCCGGGCCGGCCATGCTTTACG361 bp	

NOTE: *ppET-1 represents pre-pro-endothelin-1.

Fig. 1



Fig. 2. Effects of dexamethasone on the mRNA expression of ET_A receptors in NTM and GTM cells as determined by quantitative PCR.

(A)-(C) NTM cells. (D)-(F) GTM cells. QPCR data are presented as the mean \pm SEM % of mRNA levels of ET_A or myocilin from Dex treatment to the respective vehicle control values. * Denotes statistical significance of mean \pm SEM % of myocilin from Dex treatment vs from control using student's t-test (p < 0.001). Experiments were repeated three times for each culture cell line.

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Fig. 3. Effects of dexamethasone on the protein expression of ET_A receptors in NTM and GTM cells as determined by Western Blotting. (A)-(C) NTM cells. (D)-(F) GTM cells. Western blot analysis of ET_A receptor using anti- ET_A receptor antibody without (A and D) and with pre-incubation with ET_A receptor peptide (B and E). The quantification of band intensity (C and F) is represented as mean \pm SEM % to the value of its corresponding vehicle control band in the same blot. There was no statistically significant difference as determined by student's t-test in three repeated experiments for each culture cell line.





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Fig. 4. Effects of dexamethasone on the protein expression of ET_B receptors in NTM and GTM cells as determined by Western Blotting. (A)-(C) NTM cells. (D)-(F) GTM cells. (G)-(H) the effects of RU486 on the action of Dex in ET_B receptor amount in NTM Cells. Western blot analysis of ET_B receptor using anti- ET_B receptor antibody without (A, D and G) and with pre-incubation with ET_B receptor peptide (B and E). The quantification of band intensity (C, F and H) is represented as mean \pm SEM % to the value of its corresponding vehicle control band in the same blot. * Denotes statistical significance from Dex and/or RU486 treatment vs from Dex treatment as determined by student's t-test or One-way ANOVA and Student-Newman-Keuls multiple comparison test (p \leq 0.001). Experiments were repeated three times for each culture cell line.

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Fig. 4

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Fig. 5. Effects of dexamethasone on ET-1-mediated intracellular Ca^{2+} mobilization in NTM and GTM cells. NTM cells treated with vehicle (A) or 100 nM Dex (B). NTM cells pre-incubated with ET_A receptor antagonist, BQ610 1 μ M (C). GTM cells treated with vehicle (D) or 100 nM Dex (E).

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Fig. 5



Time (min)

Time (min)

Table 2

Cell Line / Treatments		Baseline	Peak	Number of Cells
		(Mean ± SEM nM)	(Mean ± SEM nM)	(n)
NTM	Control	87.08 ± 9.45	1157.03 ± 164.67 *	51
NTM	Dex	73.54 ± 7.37	1183.34 ± 204.37 *	50
GTM	Control	45.70 ± 5.16	1295.64 ± 211.76 *	20
GTM	Dex	44.81 ± 6.98	1230.11 ± 218.71 *	20
NTM	BQ610	21.31 ± 2.60	23.16 ± 2.95	13

Summary of ET-1(100 nM) Mediated [Ca²⁺]_i Peak Response in TM Cells

NOTE: * Statistic significance was determined by t-test at p<0.001 between baseline and ET-1 induced peak level.

Fig. 6. Effects of dexamethasone on ET-1-induced nitric oxide release from NTM cells.

Data are represented as mean \pm SEM μ M of nitrite released in culture medium. * Denotes statistical significance from vehicle control + ET-1 (100 nM) treatment vs that from vehicle control, ** denotes statistical significance from vehicle control + BQ788 (1 μ M) + ET-1 (100 nM) vs that from vehicle control + ET-1 (100 nM), and *** denotes statistical significance from Dex + ET-1 (100 nM) treatment vs that from vehicle control + ET-1 (100 nM) as determined by One-way ANOVA and Student-Newman-Keuls multiple comparison test (p < 0.05) in three repeated experiments on NTM cells.



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CHAPTER IV

EXPRESSION AND TRANSLOCATION OF GLUCOCORTICOID RECEPTOR β AND ITS REGULATION OF GLUCOCORTICOID RESPONSIVENESS IN TRABECULAR MESHWORK CELLS

Xinyu Zhang, Abbot F. Clark, and Thomas Yorio

(To be submitted)

Abstract

Glucocorticoids (GC) can increase aqueous humor outflow resistance via morphological and biochemical changes in the trabecular meshwork (TM) that typically result in an increase in intraocular pressure (IOP). Glucocorticoids have also been associated with primary angle glaucoma (POAG), however individual sensitivities to open glucocorticoids differ considerably. About one in every three people in the general population is considered as a potential steroid responder while almost all POAG patients are steroid responders. The molecular mechanisms responsible for glucocorticoid sensitivities are unknown. The human glucocorticoid receptor (hGR) gene undergoes alternative splicing and generates two protein isoforms: a cytoplasmic alpha form (hGRa), which functions as a ligand-dependent transcription factor to regulate gene expression, and a beta isoform (hGR β), which does not bind ligands and has been shown to attenuate hGR α action. We detect hGR β not only in the cytoplasm but also in the nucleus in different TM cell lines. Most normal TM cell lines have relatively high amounts of hGR β expression, especially in the nuclear region compared to glaucomatous TM cell lines. Moreover, overexpression of hGR β in TM cells attenuates the induction of myocilin by dexamethaonse (Dex) treatment supporting the conclusion that hGRB acts as a negative regulator of hGRa activity. As detected by coimmunoprecipitation, hGRB can complex with heat shock protein 90 (hsp90). Interestingly, in the TM cells, which have high amount of hGR β in the nucleus, hsp90 is also concentrated in the nucleus. When hGRß is overexpressed in TM cells, both hGRß and hsp90 accumulate in the nucleus, and 17AAG (17-allylamino, 17-demethoxygeldanamycin, a geldanamycin derivative), an inhibitor of hsp90, blocks this nuclear accumulation of hGR β and hsp90. Taken together, our results suggest that glucocorticoid responsiveness in TM cells is regulated by the expression of hGR β in TM cells, and Hsp90 is a chaperon protein for nuclear transport of hGR β .

Introduction

Glaucoma is the second leading cause of blindness in the world¹ and primary open angle glaucoma (POAG) is the most prevalent form of glaucoma that is generally associated with an elevated intraocular pressure (IOP).^{2, 3} Glucocorticoids (GCs), potent immunosuppressants and anti-inflammatory reagents, are also associated with POAG.^{4, 5,} Glucocorticoids change the morphology and biochemical activity of trabecular 6 meshwork, including reorganize cytoskeletal structure,^{7, 8, 9} increase extracellular matrix production;^{10, 11, 12, 13} alter extracellular metalloproteinase activity;^{14, 15} increase cell adhesion molecules:¹⁶ and enhance the expression of myocilin, a glaucoma gene.^{17, 18} Overall, glucocorticoids increase extracellular material deposition in trabecular meshwork and subsequently increase outflow resistance with a subsequent increase in IOP. However, individual sensitivities to glucocorticoids differ considerably. POAG patients have a much higher prevalence of glucocorticoid responsiveness than do normal subjects, with almost all POAG patients being considered GC responders, compared with one third of the normal population.¹⁹ The molecular basis for the variance in GC responsiveness is unknown.

The first isolation and cloning of the human glucocorticoid receptor described two distinct isoforms termed hGR α and hGR β , which were formed via alternative splicing and differed only at their carboxyl termini.²⁰ hGR α predominantly exists in the cytoplasm and undergoes ligand-dependent translocation to the nucleus,^{21, 22, 23} where it regulates transcription of hormone-sensitive genes. In contrast, hGR β is predominantly located in the nucleus, does not bind to glucocorticoids and antiglucocorticoids and lacks

transcriptional activity by itself.^{20, 24} In addition, hGR β main action appears to be in its ability to attenuate the gene transcription regulation of hGR α .^{25, 24, 26, 27} The increased expression of hGR β has been shown to be associated with glucocorticoid resistance in some diseases,^{28, 29, 30, 31} with an extensive study in asthma.^{32, 33, 34, 35, 36} Glucocorticoid receptors are capable of shuttling between cytoplasmic and nuclear compartments.^{37, 38} Upon binding of a glucocorticoid, hGR α is translocated from the cytoplasm to the nucleus along microtubular tracks, requiring an association with heat shock protein 90 (hsp90), immunophilin, and the motor protein dynein.^{39, 40} hGR β can also complex with hsp90.^{26, 41} However, no information is available concerning the translocation of hGR β .

In the present study, we investigate the potential role of hGR β in regulating glucocorticoid sensitivity in glaucoma. We demonstrate there is significant difference of expression of hGR β between TM cell lines derived from normal subjects and that from POAG patients, consistent with the considerably different glucocorticoid sensitivity between these two groups. We also directly evaluated the negative activity of hGR β in inhibiting the induction of myocilin, a glaucoma gene, by dexamethasone. Finally, we demonstrated, for the first time, that hsp90 is a chaperon for the nuclear import of hGR β .

Materials and Methods

Cell Culture. Eleven human TM cell lines were generated as previously described.^{10, 42,} ⁴³ Four primary normal TM cell lines (SNTM, SNTM153-00, SNTM302-00, NTM33902) and a stable transformed TM cell line (HTM-5) were derived from donors (ages 79 year, 58 year, 77 year, 6 day, and 18 year old respectively) with no reported history of glaucoma. The five primary glaucomatous TM cell lines (GTM956-99, SGTM152-99, GTM602-02, GTM626-02, GTM554-99) and a stable transfromed TM cell line (HTM-3) were derived from donors (ages 75, 79, 94, 78, 80, and 72 year old respectively) with a documented history of POAG. Early passages of TM cells were grown to confluence on 100 mm culture dishes or glass coverslips in 37° C and 5% CO₂ in DMEM (Gibco) supplemented with 10% FBS and penicilin/streptomycin/glutamate (Gibco) and 44 mM NaHCO₃. The effect of glucocorticoids on the hGR α and hGR β receptors in TM cells was examined by addition of 100 nM dexamethasone (Dex, Sigma Chemical) for 3 days in 5% FBS DMEM.

Western Blot Analysis. The cytoplasmic and nuclear fractions were isolated as described previously.³⁹ SDS-PAGE was performed on 4-15% gradient gels (Bio-RAD). Membranes were then incubated with polyclonal anti-hGR SC-1003 (Santa Cruz) or anti-hGR β PA3-514 (Affinity Bioreagents) at a dilution of 1:200 or 1:500 respectively. Membranes were also incubated with monoclonal anti-histone1 (Santa Cruz) at 1: 200 dilution as a control for separation of cytoplasmic and nuclear fractions. Immunoreactivity was detected by using enhanced chemiluminescence (ECL, Amershem Pharmacia).

Immunocytochemistry. TM cells were grown on glass coverslips to confluence, then fixed in 4% paraformaldehyde for 30 min, permeabilized in 0.2% Triton X-100 for 15 min, and incubated in 0.2M glycine for 30 min. After blocking for 20 min with 5% bovine serum albumin + 5% normal goat serum, these cells were incubated overnight at 4° C with either anti-hGR β alone, or anti-hGR β + anti-hsp90, or anti-hGR β + anti- β tubulin (Santa Cruz). Subsequently, the cells were treated for 1 h with either Alexa Fluor 594 goat anti-rabbit IgG (Molecular Probe), or Alexa Fluor 594 goat anti-rabbit IgG + Alexa Fluor 488 goat anti-mouse IgG (Molecular Probe) at a dilution of 1:200. Finally the cells were incubated with 300 nM DAPI to stain nuclear regions. Images were viewed under a Nikon Diaphot Fluorescence Microscope and image analysis was performed using image analysis software Scanalytics IPLab. For confocal microscopy, Alexa Fluor 633 goat anti-rabbit IgG was used instead of Alexa Fluor 594 goat anti-rabbit IgG. Confocal immunofluorescence was performed using Zeiss LSM-410 Confocal Scanning Laser Microscope System.

Coimmunoprecipitation. Immunoprecipitation of hGR β -hsp90 complex for cytoplasmic and nuclear fractions of TM cells was performed according to the methods described previously (Oakley, 1999). First anti-hsp90 antibody was used to immunprecipitate and anti-hGR β antibody was used in immunoblotting, then we used the same protocol but reverse the sequence of antibody administration by using anti-hGR β to run immunoprecipitation and using anti-hsp90 to perform immunoblotting.

Human GR β Constructs and Transfection. hGR β expression plasmid pCMX-hGR β was prepared by modifying the plasmid pCMX-hGR α , which was initially modified from plasmid pCMX.⁴⁴ hGR α expression plasmid pCMX-hGR α was made using PCR to amplify hGR α cDNA with adding Asp718 site to 5' and Bam HI site to 3' and cloning this cDNA into Asp718/Bam HI sites of pCMX. hGR β expression plasmid pCMX-hGR β

was generated using PCR of the hGR β receptor specific sequence with adding EcoRI site to 5' and Bam HI site to 3' and inserting this fragment into EcoRI/Bam HI sites of pCMX-hGR α . Identity of the inserted cDNA was confirmed by sequencing. Confluent TM cells were transfected using calcium phosphate reagent according to the manufacture's recommendations (BD Biosciences). Cells were switched to serum-free media 24 h post-transfection and cytoplasmic and nuclear lysates were isolated for Western Blotting for hGR β , hsp90 or myocilin. In some experiments, the cells were imaged for hGR β and hsp90 under confocal microscopy after transfection.

17AAG Treatment. For the study of nuclear translocation of hGRβ, Normal HTM-5 cells were transfected with hGRβ as stated above. 17AAG (17-allylamino, 17-demethoxygeldanamycin)⁴⁵ (gift from Dr. Thomas Mueller, Kosan Biosciences, Inc.), an inhibitorof hsp90 was added at a final concentration of 1 μ M during transfection and post-transfection. Cells underwent immunocytochemistry analysis as stated above for hGRβ and hsp90 using confocal microscopy.

RESULTS

Expression of glucocorticoid receptor isoforms hGR α and hGR β in cultured TM cell lines. Almost all known effects of glucocorticoids are mediated via the hGR α glucocorticoid receptor. The trabecular meshwork appears to be the main target of glucocorticoids in inducing ocular hypertension. It is known that trabecular meshwork cells express the glucocorticoid receptor (hGR),⁴⁶ however the isoforms of hGR have not

been specified in TM cells. To address this question, we examined the expression of hGR α and hGR β in the cytoplasmic and the nuclear fractions of several cultured primary and transformed TM cell lines. Western Blotting only detected histone 1 in the nuclear fractions (Fig. 1) indicating we got clear separation of cytoplasmic and nuclear fractions. Both normal and POAG TM cell lines expressed hGR β proteins as detected as a 90 kDa doublet protein by epitope-specific hGR β protein in both cytoplasmic and nuclear fractions (Fig. 1). 100 nM Dex treatment for 72 h did not change the amount of hGR β receptor expression. This data also demonstrated that the hGR β isoform is not susceptible to hormone-induced down-regulation and persists in the cells despite glucocorticoid administration.

Western Blot analysis also detected the hGR α receptor protein at a molecular weight of 95 kDa in both normal and POAG TM cell lines. 100 nM Dex treatment caused hGR α translocation from the cytoplasmic to the nuclear fractions and also time-dependent homologous down-regulation of hGR α (Fig. 2).

Differential expression of hGR β between normal and glaucomatous TM cell lines. Glucocorticoid responsiveness varies with a far higher prevalence among POAG patients than among normal subjects.¹⁹ The molecular mechanism underlies the higher GC responsiveness among POAG patients is unknown. hGR β has become a candidate for glucocorticoid resistance in some diseases, especially in asthma ⁴⁷ based on the reports of its negative activity.^{24, 25, 26, 27} We compared the expression and subcellular distribution of hGR β between normal TM cell lines and POAG TM cell lines. Immunocytochemisty detected hGR β staining in both the cytoplasm and the nucleus, and 100 nM Dex treatment for 72 h had no effect on the expression of hGR β in all these normal and POAG TM cell lines (Fig. 3, Fig. 4). However, four among the five normal TM cell lines (SNTM, HTM-5, SNTM302-00, and SNTM153-00) had relatively high amount of hGR β staining and more concentrated in the nuclear regions, except one normal TM cell line (NTM334-02, 6 day old), which had low immunoreactivity of hGR β in the nucleus. Whereas all POAG TM cell lines (GTM956-99, HTM-3, SGTM152-99, GTM602-02, GTM626-02, GTM554-99) expressed low amount of hGR β , particularly lower in the nucleus. These immunostaining data indicated that most POAG TM cell lines had a lower expression of hGR β , especially in the nucleus compared to normal TM cell lines.

Inhibitory effect of hGR β on Dex-induced expression of myocilin. Since POAG TM cell lines had a relatively low expression of hGR β , which is consistent with high sensitivity to glaucocorticoids among POAG patients, we directly tested the effect of overexpression of hGR β in the expression of a glaucomatous gene, myocilin, which can be induced by Dex treatment. Transfected HTM-5 cells with pCMX-hGR β increased the immunostaining of hGR β as detected by confocal microscopy (Fig. 5A and 5B). This data showed that transfection with pCMX-hGR β could overexpress hGR β in HTM-5 cells and again, demonstrated the specificity of hGR β antibody. Western Blot analysis also detected the increase in the amount of nuclear hGR β after transfection with the hGR β expression vector, while Dex treatment for 72 h did not change the amount of hGR β detected (Fig. 5C). Whereas, 100 nM Dex treatment for 72 h significantly induced

the expression of myocilin in the cytoplasmic fractions, and this induction was inhibited by overexpression of hGR β (Fig. 5C).

The association of hGR β with microtubules. Conventional immunofluorescence staining of hGR β using anti-hGR β antibody in SNTM (normal) cells showed a fibrous distribution nature in the cytoplasm (Fig. 6A). It seems that the hGR β receptor aligns itself with the cytoskeleton structure in these SNTM cells, whereas the immunostaining of hGR β in SGTM152-99 (glaucomatous) cells showed a punctuate pattern (Fig. 6B). Further study of the cytoplasmic distribution pattern of hGR β was performed by using a conventional immunofluorescence double staining for hGR β (red) and β -tubulin (green). The staining of hGR β was closely associated and in some points, colocalized with microtubule tracks in both SNTM cells (Fig. 7A) and SGTM152-99 cells (Fig. 7B). The punctuate staining of cytoplasmic hGR β in SGTM 152-99 could reflect the low expression of hGR β in this glaucomatous TM cell line. The association of hGR β with microtubules could play a role in the transport of hGR β to the nucleus.

The chaperon effects of hsp90 in nuclear transportation of hGR β . Since hsp90 is known to be involved in the translocation of hGR α from the cytoplasm to the nucleus,^{39, 48, 49, 50} and hGR β is identical with hGR α through most sequences except the last 27 amino acids,⁵¹ we were interested in the role of hsp90 in the cytoplasm to the nuclear transport of hGR β . Using SNTM (normal) cells, co-immunoprecipitation studies of hGR β using anti-hGR β antibody demonstrated that hsp90 was associated with hGR β as Western Blot analysis using anti-hsp90 was able to detect hsp90 protein in the nuclear

fraction (Fig. 8A). In addition, when reversed the sequence of antibodies, immunoprecipitation of hsp90, using anti-hsp90 antibody, was able to precipitate hGR β as the immunoblot was able to detect hGR β protein following immunoprecipitation (Fig. 8B). These data supported that hGR β could complex with hsp90.

Confocal microscopy detected a high amount of hGRB staining in the nucleus in SNTM (normal) cells (Fig. 9A). Interestingly, hsp90 also accumulated in the nucleus (Fig. 9B) and both hGR β and hsp90 colocalized in the nucleus of these normal TM cells (Fig. 9C). In contrast, SGTM1529-99 (glaucomatous) cells had a much lower nuclear staining of hGR_β (Fig. 9D), and consequently, hsp90 was also lower in the nucleus (Fig. 9E) and there was not much colocalization of hGR β and hsp90 in the nucleus in this POAG TM cells (Fig. 9F). Furthermore, transfection of HTM-5 cells with a pCMXhGR β vector produced a hGR β overexpression and accumulation of hGR β in the nucleus in these TM cells (Fig. 10A). Consequently, hsp90 was also concentrated and colocalized with hGR β in the nucleus in the cells which overexpressed hGR β , but not in the cells which were not transfected (Fig. 10B and 10C). This coincidence of nuclear localization of hGR β and hsp90 and changes in their co-expression following hGR β transfection suggested that hsp90 associates with hGRB and is most likely the nuclear transport chaperon of hGRβ.

17AAG is an hsp90 inhibitor, which binds to hsp90 and inhibits hsp90 association with client proteins. Such as action by 17AAG simultaneously leads to degradation of these client proteins⁴⁵. As reported above, HTM-5 cells transfected with pCMX-hGR β

caused accumulation of both hGR β and hsp90 in the nucleus in these cells which overexpressed hGR β (Fig. 11A, B and C). However 1 μ M 17AAG treatment completely blocked the nuclear import of hGR β in these HTM-5 cells transfected with hGR β expression vector. This data confirmed that hsp90 was a chaperon protein for the cytoplasm to the nuclear transport of hGR β .

Discussion

The molecular basis of variable glaucocorticoid sensitivities as pertaining GCinduced ocular hypertention is poorly understood. There are some reports that hGRB has a negative activity to glucocorticoid-regulated response^{24, 25, 26, 27} and hGR β becomes a potential candidate for GC-resistance in asthma.⁴⁷ We detected that hGR^β was expressed in cultured normal and POAG TM cell lines. Although the amino acid sequences of hGR α and hGR β isoforms are identical except the carboxyl termini,²⁰ the anti-hGR β antibody we used was specific for hGR β , because this antibody only recognized protein bands with a molecular weight of 90 kDa, the size of hGR β , and unlike hGR α , this receptor protein did not undergo ligand-dependent nuclear translocation and homologous down-regulation of receptors. Furthermore, when we transfected TM cells with an hGRß expression vector, this antibody was able to detect the overexpression of hGRB in these transfected cells. By using 4-15% gradient gels, we were able to detect the doublets of hGRß pretein. The double bands of hGRß protein would be due to an alternative translation site for the GR gene.⁵²

By using two different techniques, Western Blotting and immunocytochemisty, we localized hGR β in the cytoplasm and the nucleus in cultured primary and transformed TM cell lines. Some cell strains had high amount of hGR β in the nucleus, while others had hGR β staining in the cytoplasm but lower in the nucleus. Previous reports as to the subcellular localization of hGR β have been varied. Oakley RH et al ⁵³ showed that hGR β was located in the nucleus, however other groups^{54, 41} reported that hGR β is present in the cytoplasm. The apparent differences in reported subcellular distribution of hGR β could be attributed to tissue specificity, differential expression regulation, variable intracellular stability, or variance in nuclear transportation efficiency. In the current study, both cytoplasmic and nuclear hGR β was detected and that the amount present in the nucleus can be influenced by overexpression.

The striking finding in this study was the significant difference of the hGR β amount among normal versus glaucomatous cell lines. POAG TM cell lines had lower hGR β receptor expression than normal TM cell lines. This is coincidence with the fact that in the normal population, there is a low rate of GC responders as compared to almost all of the POAG patients considered as GC responders.¹⁹ These results suggest that low expression of hGR β could lead to glucocorticoid sensitivity in TM cells. In order to directly test that the amount of hGR β can regulate glucocorticoid responsiveness, we generated a hGR β expression vector pCMX-hGR β and increased cellular hGR β amount in TM cells by transfecting this construct, followed by detecting the induction of myocilin expression after challenging these TM cells with dexamethsone. Although

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mutant myoclin is associated with POAG,⁵⁵ the function of myocilin in trabecular meshwork remains unknown. The myocilin gene is known to be upregulated by glucocorticoids, like Dex, and can be used as an index of glucocorticoid responsiveness. We found that higher levels of hGR β could indeed act to negatively regulate the activity of hGR α , as overexpression of hGR β inhibited Dex-induced myocilin expression in TM cells. Our studies, therefore, identify a possible molecular mechanism by which glucocorticoid responsiveness is achieved as a result of the low level of the negative isoform receptor hGR β .

Although there are intensive studies and many new findings on the nuclear translocation of hGR α ,^{39, 40, 56, 57, 58} the nuclear import of hGR β is completely unknown. Currently we demonstrated that the cytoplasmic distribution of hGR β was closely associated with microtubules in both normal and glaucomatous TM cell lines. This suggested that microtubules may play a role in the cytoplasmic to the nuclear translocation of hGR β .

We also identified a chaperon protein, hsp90, as a requirement for the cytoplasmic to nuclear translocation of hGR β . Several findings support this mechanism. We found that in the normal TM cell line SNTM, which had a high level of hGR β in the nucleus, hsp90 was also concentrated in the nuclear region, while in the glaucomatous TM cell line SGTM152-99, hGR β and hsp90 were both present at lower concentration in the nucleus. Transfection with the hGR β construct in HTM-5 cells caused the overexpression and accumulation of hGR β protein in the nucleus that also leaded to an increase in hsp90

level in the nucleus in these transfected HTM-5 cells. Most importantly, 17AAG, an inhibitor of hsp90, which blocks the binding of client proteins to hsp90 and prevents chaperon activity as well as promoting the degradation of client proteins,⁴⁵ completely blocked the accumulation of hGR β in the nucleus in these transfected HTM-5 cells. Interestingly there was also a decrease in the accumulation of hGRB in the cytoplasm. This could be attributed to the degradation of hGRB in the cytosol under 17AAG treatment. The data indicated that accessibility of hGRB to hsp90 was required for the nuclear import of hGR β . Although like hGR α ,³⁹ the nuclear transportation of hGR β needs the association with hsp90, the transport machinery for hGR α or hGR β may be not exactly same because the hGR α undergoes hormone-dependent nuclear translocation but hGRB transports to the nucleus independent on hormones.²⁰ Further experiments are needed to delineate other components that may be involved in the regulation of the cytoplasm to nuclear translocation of hGR β .

In conclusion, we have demonstrated a possible molecular mechanism by which glucocorticoid responsiveness is expressed in individuals susceptible to increase IOP following steroid therapy. The mechanism is related to the relative expression of the hGR β isoform in the nucleus of TM cells. Furthermore, we have, for the first time, identified hap90 as a chaperon protein for the translocation of hGR β from the cytoplasm to the nucleus.

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FIGURE 1. Western Blot analysis of hGR β in cytoplasmic and nuclear fractions from normal and glaucomatous TM cell lines in the presence and absence of Dex treatment. Immunoblot of hGR β isoforms is performed by using an isoform-specific polyclonal antibody. TM cells were treated with 100 nM Dex or control vehicle for 72 h. Hela cell lysate was used as a positive control. Histone 1 was used as a nuclear marker. (A) Normal TM cell lines. (B) Glaucomatous TM cell lines.

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FIGURE 2. Western Blot analysis detecting the translocation of hGR α after Dex treatment for normal and glaucomatous TM cell lines using a polyclonal antibody against general GR. TM cells were treated with control vehicle or 100 nM Dex for 1, 2, 3, 4, 5 days, respectively as indicated.

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FIGURE 3. Immunocytochemistry analysis of hGR β expression and distribution in normal TM cell lines. TM cells were treated with 100 nM Dex or control vehicle for 72 h. The negative control staining for hGR β was performed using the rabbit pre-immune serum. The red color represents hGR β staining and blue color is DAPI staining for nuclear regions.

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FIGURE 4. Immunocytochemistry analysis of hGR β expression and distribution in glaucomatous TM cell lines. TM cells were treated with 100 nM Dex or vehicle control for 72 h. The negative control staining for hGR β was performed using rabbit preimmune serum. The red color represents hGR β staining and blue color is DAPI staining for nuclear regions.



FIGURE 5. Verification of the hGR^β antibody recognizing the hGR^β protein and detecting the effect of increased expression of hGRB on Dex-induced expression of mvocilin in transfected HTM-5 cells. Confocal microscopy detecting (A) Immunostaining of GR^β in HTM-5 cells transfected with control empty vector pCMX, (B) Immunostaining of GRB in HTM-5 cells transfected with GRB expression vector pCMX-GRB. (C) Western Blot detecting the expression of hGRB in the nuclear fraction and myocilin in the cytoplasmic fraction in transfected HTM-5 cells treated with control or 100 nM Dex in 5% FBS- DMEM for 72 h. Cells were transfected with pCMX and treated with vehicle control (lane 1), or Dex (lane 2), or transfected with pCMX-hGR^β and treated with Dex (lane 3). Histone 1 was used as a control for Western Blot for nuclear fraction and β -tubulin was used as a cytoplasmic fraction Western Blot control.

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FIGURE 6. Illustration of hGR β subcellular distribution pattern in the cytoplasm. (A) SNTM (normal), (B) SGTM152-99 (glaucomatous) cells were cultured to confluence without any treatment followed by fixation and precessing for immunocytochemisty as describe in Materials and Methods. Immunoreactivity was visualized under conventional immunofluorescence microscopy. Red color represents hGR β staining and blue is DAPI staining for nucleus.

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FIGURE 7. Double immunofluorescence microscopy detection of hGR β and β -tubulin. (A) SNTM (normal), (B) SGTM152-99 (glaucomatous) cells were cultured to confluence without any treatment followed by fixation and double immunostaining for hGR β (red) and β -tubulin (green) as described in Materials and Methods, to detect the association of hGR β with microtubules. Blue color is DAPI staining for nucleus. Immunostaining was viewed under conventional immunofluorescence microscopy.



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FIGURE 8. Coimmunoprecipitation of hGR β and hsp90 to detect a hGR β -hsp90 complex. SNTM (normal) cells were treated with Dex for 72 h followed by preparation of cytoplasmic and nuclear extracts. Coimmunopredipitation was performed as described in Materials and Methods. (A) Immunoprecipitation was carried by using hGR β antibody and the pellets of immunprecipitation were resolved by Western Blotting analysis using hsp90 antibody. (B) Immnoprecipitation was performed by using an hsp90 antibody and Western Blotting was used to detect hGR β using hGR β antibody. Hela cell lysates (Santa Cruz) was used positive control for Western Blott analysis.

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FIGURE 9. Double immunofluorescence microscopy detection of hGR β and hsp90. TM cells were cultured to confluence without any treatment followed by fixation and double immunostaining for hGR β (red) and hsp90 (green) to detect the colocalization of hGR β with hsp90. (A) hGR β staining in SNTM (normal) cells. (B) hsp90 staining in SNTM cells. (C) Overlay staining of hGR β and hsp90 in SNTM cells. (D) hGR β staining in SGTM152-99 (glaucomatous) cells. (E) hsp90 staining in SGTM152-99 cells. (F) Overlay staining hGR β and hsp90 in SGTM152-99 cells. Immunostaining was viewed under confocal microscopy (Bar —— stands for 60 μ M).

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FIGURE 9.



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FIGURE 10. Confocal microscopy and Western Blot analysis of hGR β and hsp90 in HTM-5 cells transfected with pCMX-GR β . HTM-5 cells were transfected with hGR β expression vector pCMX-GR β followed by fixation and double immunostaining or isolation of nuclear fractions for Western Blotting analysis for colocalization of hGR β and hsp90. In HTM-5 transfected with pCMX-GR β , (A) hGR β staining (red), (B) hsp90 staining (green), (C) Overlay staining of hGR β and hsp90. (D) Western Blot analysis for hGR β and hsp90 in nuclear fractions of HTM-5 transfected with pCMX (lane 1) and pCMX-hGR β (lane 2). Histone 1 was used as a Western Blot control for the nuclear fraction (Bar ______ stands for 15 μ M).

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FIGURE 11. Effect of hsp90 on translocation of hGR β from the cytoplasm to the nucleus in HTM-5 cells transfected with pCMX-GR β . HTM-5 cells were transfected with hGR β expression vector pCMX-GR β and treated with an hsp90 inhibitor, 17AAG, for 20 h as described in Materials and Methods. Followed by fixation and double immunostaining for hGR β and hsp90, cells were visualized under confocal microscopy to detect nuclear accumulation of hGR β and hsp90. In HTM-5 cells transfected with pCMX-GR β , (A) hGR β staining (red), (B) hsp90 staining (green), (C) Overlay staining of hGR β and hsp90. In HTM-5 transfected with pCMX-GR β and treated with 17AAG, (D) hGR β staining (red), (E) hsp90 staining (green), (F) Overlay staining of hGR β and hsp90 (Bar ______ stands for 60 μ M).



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CHAPTER V

CONCLUSIONS

The purpose of this dissertation was to investigate the mechanisms of glucocorticoid-induced ocular hypertention. This study design was necessary to ascertain not only the responses of glucocorticoids in the anterior segment associated with regulation of intraocular pressure but also to define the key element of control mechanisms that trigger glucocorticoid responsiveness in primary open-angle glaucoma (POAG) patients. Previous studies addressing pathological responses to glucocorticoids have been studied only in trabecualr meshwork. We examined the glucocorticoid responsiveness in both human non-pigmented ciliary epithelial (HNPE) cells and trabecular meshwork (TM) cells and determined if there was cross-talk between glucocorticoids and endothelin-1 (ET-1) as both glucocorticoids and ET-1 are implicated in glaucoma pathology. In addition, for over forty years, it has remained unknown as to what aspects of the control system were responsible for the glucocorticoid responsiveness in POAG patients. We investigated the potential role of the glucocorticoid receptor beta (hGR^β) isoforms as a possible contributor of the glucocorticoid responsiveness in TM cells based on the reports of its negative activity and suspected function in glucocorticoid resistance in some other diseases.

In general, the results obtained from the three related studies delineated in this dissertation support the following interpretation of the principal findings that occur in intraocular pressure regulation after glucocorticoid administration.

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The first investigation demonstrated that ET-1 was concentration-dependently increased following 24 h dexamethasone (Dex) treatment, with a maximum concentration (100 nM) causing a 3-fold increase of ET-1 release from cultured HNPE cells. Dex treatment also changed ET receptor expression with a decrease in ET_A receptors while increasing ET_B mRNA and protein expression. As HNPE cells are a source for aqueous humor ET-1 and ET-1 can act in an autocrine fashion to regulate aqueous humor formation in HNPE cells as well as targeting the down-stream TM in regulating aqueous humor outflow, ET-1 could have consequences on aqueous humor inflow and outflow in glaucoma as well as ocular hypertension seen with glucocorticoid therapy.

The second investigation demonstrated that Dex decreased ET_B receptor protein expression in both normal and glaucomatous TM cells and attenuated ET-1 mediated increase in nitric oxide (NO) release through ET_B receptors in TM cells, while having no effect on ET_A receptor expression and ET-1 mediated intracellular Ca²⁺ mobilization through ET_A receptors. Dex-induced specific suppression of ET_B receptor expression and decline in ET-1 mediated increase in NO levels in TM cells with a concomitant increase of ET-1 release from HNPE cells could result in enhanced contraction response and decrease in relaxation of trabecular meshwork, hence reducing the intratrabecular space. Such actions by ET-1 may exacerbate Dex effects on the outflow pathway leading to increased outflow resistance and consequently elevated intraocular pressure. Collectively, these studies suggest a novel signaling pathway for glucocorticoids in the anterior segment in regulation of aqueous humor outflow in part through their interactions with ET-1 and ET receptors (Figure 1). In these investigations, we also observed that RU486 - - -



Figure 1. A novel signaling pathway for glucocorticoids in the anterior segment in the regulation of intraocular pressure (IOP). Glucocorticoids increase endothelin-1 (ET-1) release from non-pigmented ciliary epithelial (NPE) cells with the concomitant suppression of endothelin B (ET_B) receptors and decline in nitric oxide (NO) release from trabecular meshwork (TM) cells. Such effects would increase contraction and decrease relaxation of trabecular meshwork and reduce the intratrabecular space. ET-1 thus may exacerbate glucocorticoid effects on the outflow pathway leading to increased outflow - resistance and consequently elevated intraocular pressure.
function as an glucocorticoid antagonist in those Dex response that resulted in enhanced expression whereas it was unable to block these Dex effects that resulted in decreased gene expression. In fact, RU486 acted as a partial agonist as itself produced a decrease in gene expression. The reason for this difference may be explained by the study that RU486 can recruit gene regulatory factors to an RU486-GR α receptor complex, and consequently limit the activities of these regulatory factors in the expression of their target genes. Additional studies need to be done to determine these mechanisms.

In the third investigation, we detected that most normal TM cell lines had relatively high amounts of hGRB expression, especially in the nucleus compared to POAG TM cell lines. This is coincidence with the fact that in the normal population, there is a low rate of glucocorticoid responders as compared to almost all of the POAG patients. Moreover, overexpression of hGRB in TM cells attenuated Dex-induced expression of myocilin, a glaucomatous gene. Therefore, our studies identify a possible molecular mechanism by which glucocorticoid responsiveness in POAG patients is achieved as a result of the low level of the negative isoform receptor hGR β (Figure 2). Interestingly, in the TM cells, which have high amount of hGR β in the nucleus, heat shock protein 90 (hsp90) was also concentrated in the nuclear regions, while in the glaucomatous TM cells, both hGRB and hsp90 were present at lower concentrations in the nucleus. Transfection with hGRB construct in TM cells caused the overexpression and accumulation of hGR^β protein in the nucleus that also led to an increase in hsp90 expression in the nucleus in these transfected TM cells. Most directly, 17AAG, an inhibitor of hsp90, which blocks the binding of - client proteins to hsp90, completely blocked the accumulation of hGRβ and hsp90 in the

nucleus in these transfected TM cells. These studies suggest that hsp90 is a requirement for transport of hGR β from the cytoplasm to the nucleus. Therefore, we have, for the first time, identified that hsp90 as a chaperon protein for the cytoplasm to nuclear translocation of hGR β .

In summary, we have described a novel signaling pathway for glucocorticoids in anterior segments in regulation of intraocular pressure (IOP) through interaction with ET-1 and ET receptors. We have also identified that glucocorticoid responsiveness in TM cells is regulated by the expression of hGR β in TM cells, and hsp90 is a chaperon protein for the nuclear translocation of hGR β . The enhanced effects of ET-1 on TM cells by glucocorticoids coupled with an enhanced glucocorticoids responsiveness in glaucoma patients may explain the ocular hypertension seen with glucocorticoids therapy in POAG patients.

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<u>A Possible Molecular Mechanism Regulating</u> <u>Glucocorticoid Responsiveness in TM Cells</u>



Figure 2. Glucocorticoid responsiveness pertaining to steroid-induced glaucoma is regulated by the expression of hGR β in trabecular meshwork (TM) cells. In normal TM cells, high amount of negative hGR β attenuates hGR α actions leading to glucocorticoid non-responsiveness, while in primary open-angle glaucoma patients, lower level of hGR β attributes to enhanced glucocorticoid responsiveness.

CHAPTER VI

PROPOSAL OF FURTHER RESEARCH

Although the research presented in this dissertation provided several striking new findings regarding the mechanisms of glucocorticoid-induced ocular hypertension and glucocorticoid reponsiveness, many questions remain unanswered. For example, how do TM cell lines differentially regulate the expression of hGR β ? Can hGR β , after overexpression, directly block steroid-induced ocular hypertension in an eye perfusion system? What are the other components, besides hsp90, required for the translocation of hGR β from the cytoplasm to the nucleus? Listed below are several future investigations:

1) To test the hypothesis that the expression levels of the splicing factor or factors in TM cell lines are controls for creating hGR β from GR pre-mRNA. hGR α and hGR β isoforms are created from the same pre-mRNA transcript via alternative splicing. Different cell types can have very different ratios of hGR α to hGR β . The factor or factors that control alternative splicing of GR pre-mRNA are of great importance. The family of serine-arginine-rich proteins known as SR proteins are major components for constitutive or alternative splicing processing in eukaryotic genes. Recently, a SR protein, SRp30 (serine-arginine-rich protein p30), has been reported to be necessary for alternative splicing of the GR pre-mRNA to create mRNA encoding hGR β in neutrophils.¹ To test

this hypothesis, an investigation should be designed to detect the expression of SRp30 in normal and glaucomatous TM cell lines to determine if the expression of SRp30 is coincident with the expression of hGR β receptor proteins. Further experiments could be conducted to detect the expression level of hGR β receptor protein by altering the SRp30 expression in an *in vitro* TM cell system.

2) In the current investigations, we observed that overexpression of hGR β inhibited the Dex-induced expression of myocilin. Although mutant myocilin is implicated in POAG, the function of myocilin remains unknown. A better way to exam the potential role of hGR β in regulating glucocorticoid responsiveness in glaucoma is to directly test if hGR β blocks the increase in intraocular pressure, which is seen following glucocorticoid administration. This experiment could be conducted by transferring adenovirus-mediated hGR β gene into the isolated anterior segment in eye perfusion system, followed by a challenge with dexamethasone and measurement of intraocular pressure.

3) The efficiency of transport of hGR β from the cytoplasm to the nucleus may be associated with the nuclear accumulation and stability of hGR β in TM cells. Hsp90 was identified, for the first time, as a chaperon protein for nuclear import of hGR β in the current investigations. Some other components may also be required for this retrograde nuclear transport. Several immunophilins and the motor protein dynein are involved in the nuclear translocation of hGR α . An investigation should be carried to determine the nuclear transport machinery of hGR β , mainly targeting on immunophilins and motor proteins. These experiments could be conducted using the procedures for hsp90 described in Chapter IV, including immunocytochemistry, co-immunoprecipitation, and the use of inhibitors.

Reference:

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