REVIEW

STAT5a/b contribute to sex bias in vascular disease: A neuroendocrine perspective

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ABSTRACT. Previous studies have elucidated a neuroendocrine mechanism consisting of the hypothalamus (growth hormone releasing hormone, GHRH) – pituitary (growth hormone, GH) – STAT5a/b axis that underlies sex-biased gene expression in the liver. It is now established that male vs female patterned secretion of GHRH, and thus of circulating GH levels ("pulsatile" vs "more continuous" respectively), leading to differently patterned activation of PY-STAT5a/b in hepatocytes results in sex-biased gene expression of cohorts of hundreds of downstream genes. This review outlines new data in support of a STAT5a/b-based mechanism of sex bias in the vascular disease pulmonary hypertension (PH). Puzzling observations in PH include its 2-4-fold higher prevalence in women but a male-dominance in many rodent models, and, paradoxically, inhibition of PH development by estrogens in such models. We observed that conditional deletion of STAT5a/b in vascular smooth muscle cells (SMC) in mice converted the male-dominant model of chronic hypoxia-induced PH into a female-dominant phenotype. In human idiopathic PH, there was reduced STAT5a/b and PY-STAT5 in cells in late-stage obliterative pulmonary arterial lesions in both men and women. A juxtaposition of the prior liver data with the newer PH-related data drew attention to the hypothalamus-GH-STAT5 axis, which is the major target of estrogens at the level of the hypothalamus. This hypothesis explains many of the puzzling aspects of sex bias in PH in humans and rodent models. The extension of STAT5-anchored mechanisms of sex bias to vascular disease emphasizes the contribution of central neuroendocrine processes in generating sexual dimorphism in different tissues and cell types.

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ABBREVIATIONS. 2-ME, 2-methoxyestradiol; 5-HT, 5-hydroxytrptamine; BCL6, B-cell lymphoma protein 6; BMP, bone morphogenetic protein; BMPR2, BMP receptor 2; CYP, cytochrome P450 enzymes; E2, estradiol-17 β ; EC, endothelial cells; eNOS, endothelial nitric oxide synthase; GH, growth hormone; IPAH, idiopathic pulmonary arterial hypertension; MCT, monocrotaline; MCTP, monocrotaline pyrrole; PASMC, pulmonary artery smooth muscle cells; PH, pulmonary hypertension; RVH, right ventricular hypertrophy; RVSP, right ventricular systolic pressure; RV/S+LV, ratio of wet weights of right ventricle to that of septum plus left ventricle; SERT, serotonin transporter; SMC, smooth muscle cells

INTRODUCTION

Men and women and men have clear differences in prevalence of vascular disease.^{1,2} As examples, the prevalence of hypertension, atherosclerosis and coronary artery disease is higher in men than in women.^{1,2} However, as a converse example, the prevalence of pulmonary hypertension $(PH)^{a}$ is 2-4-fold higher in women than in men, even though after diagnosis, women have a better outcome than men.³⁻⁶ In many rodent models of arterial remodeling after vascular injury (femoral artery cuffing or common carotid artery ligation) or chronic hypoxia-induced PH males show more extensive vascular remodeling than females. $6-19$ In these models the administration of estrogens [estradiol-17 β (E2) or 2-methoxyestradiol (2-ME)] is typically protective.^{6,16-19} This produces the apparently paradoxical situation that in a disease like PH, while women have a higher prevalence than men, the typical rodent models of PH (chronic hypoxia or monocrotaline administration) show a male dominance and E2 administration inhibits the latter. $6,16-19$ This dichotomy between humans and rodents, and, more generally, the varied differences in sex bias^b between men and women in vascular disease prevalence and models of vascular injury remain incompletely understood.^{6,16-20} Indeed, it has been especially perplexing to understand the different sex-bias observations in similar vascular disease situations in different species. As examples, understanding the differences between sex bias in PH in humans compared to PH in rodent models, or even in understanding the differences between models of PH in the rat compared to the mouse (e.g. monocrotaline is efficient in producing PH in the male rat, but not in the mouse) has been a challenge. $6,16-20$ Thus far, the main mechanistic focus of various studies to understand these situations has been to focus almost exclusively on the direct effects of E2 or other sex hormones on vascular cells. As examples, there is an extensive literature on the effects of E2 on increasing the function of eNOS in endothelial cells, the ability of E2 to stimulate vascular smooth muscle cell proliferation, and to inhibit the trafficking of vasorelevant receptors such as BMPR2 (bone morphogenetic receptor 2) to the cell surface.6,21-28 However, these studies of direct effects of sex hormones on vascular cells, taken together, have been unable to explain the many disparate sex bias observations in a vascular disease such as PH in humans and different rodent species.

A Neuroendocrine Mechanism (Hypothalamus-GH-STAT5) Underlying Sex-Biased Gene Expression in the Liver

There are a series of relevant and critical insights pertaining to mechanisms determining sex-biased gene expression in the liver that have not quite percolated into the vascular disease literature.²⁹ The pharmacologic issue driving extensive studies of sex bias in liver gene expression was the difference between men and

women (and male vs female animals) to metabolize administered xenobiotics. Thus a major focus of these studies was the sex-biased expression of individual members of the P450 cytochrome (CYP) enzyme family that metabolize medications. It was observed that, in the rat, CYP2A2, 2C11 and 3A2 were male-biased, but 2C12 female-biased, with 2C6 expressed in both sexes.²⁹⁻³⁵ There were species-specific differences: CYP3A subfamily was male-biased in rats, but female-biased in humans and mice.²⁹⁻³⁵ Administration of estrogens or testosterone into rodents, respectively "feminized" or "masculinized" CYP enzyme expression.²⁹ As in most of the vascular biology literature today, investigators in liver-gene expression in the early 1970s considered this sex-biased expression to be mainly the result of direct effects of sex hormones (estrogens and testosterone) on the hepatocyte.³⁶

A critical discovery in 1973 by Colby et al.³⁷ was the observation that the feminizing effect of an injection of E2 into a rat or a mouse on sex-biased liver gene expression was indirect and had an absolute dependence on the pituitary. This has since been extensively confirmed - the feminizing effects of exogenously administered E2 or the masculinizing effects of testosterone on sex-biased gene expression in the liver are blocked by hypophysectomy.^{29,38-48} The major target of injected E2 (and other sex hormones) is the hypothalamus, in particular the arcuate nucleus.⁴⁹⁻⁵⁴ [Note that there is no blood-brain barrier at the arcuate nucleus and additional "circumventricular" regions in the brain.] As subsequently elucidated in detail by Waxman et al and other investigators in the last 2 decades a neuroendocrine mechanism of sex-bias, operating through an axis consisting of the arcuate nucleus-growth hormone releasing hormone (GHRH)-growth hormone (GH) signal transducer and activator of transcription 5 (STAT5) accounts for sex-biased expression of >1000 genes in the liver, and other tissues of the body.29,46-59 The generation of sexual dimorphism at the level of the hypothalamus results from the male vs female patterned secretion of GHRH and corresponding patterns of GH secretion $(Fig. 1)$.^{29,30,60-66} This has been extensively confirmed in mice, rats and humans (Fig. 2 is an example of human data).^{29,30,60-66} Circulating GH levels in the male (M) are referred to as "pulsatile" (2-4 peaks per day) with very low interpulse levels; in the female (F) there is a higher frequency of pulses $(>7$ peaks/day) with significant interpulse levels,

FIGURE 1. Mean plasma GH levels in female and male rats, 45 and 90 days old, sampled at 30 min intervals for a 6-h period. The number of animals in each group is shown in parenthesis. Vertical lines represent the SEM. Adapted from Edén (1979) with permission of The Endocrine Society.⁶⁰

thus this is called "more continuous" (Figs. 1 and 2). This results in M vs F patterned activation of PY-STAT5a/b in the distal tissues (Fig. 3) and downstream of that a major cascade of sex-specific gene expression of $>1,000$ genes.^{29,67} Even when assayed at a single timepoint in humans (in the morning after fasting) the median value of serum GH levels was 80- 120 fold higher in women than in men.⁶⁶ This is a higher sexual dimorphism ratio than that for E2 (ratio: 2.2 female bias) or testosterone (ratio: 14 male bias) observed in the same sera.⁶⁶

Mice, rats and humans have quantitative differences in the respective male vs female patterns of circulating $GH.²⁷$ (Figs. 1 and 2). Human males show GH pulses of high magnitude, with very low interpulse levels; however, women show a more continuous level of GH 100-fold higher than in the male (Fig. 2).^{30,60-66} In contrast, male rats show discrete pulses approximately every 3-4 hr with little or no circulating GH detectable during the interpulse interval.³⁰ (Fig. 1). In female rats, the pulses are more frequent, the pulse heights are lower and the interpulse levels are higher. 30 (Fig. 1). Male mice also have a pulsatile pattern; female mice have a pattern that tends to have a higher frequency

FIGURE 2. Sex-bias in circulating GH levels in male and female humans. Panels A and B: representative profiles of plasma GH levels showing that both men and women have pulsatile GH levels, but there is a higher overall level of GH in women. Adapted from Winer et al (1990) with permission of The Endocrine Society.⁶¹

but with low interpulse levels. 62 Thus a difference between female humans and female rodents (rat or mouse) is in the much higher continuous GH levels in women compared to female rodents.(Figs. 1 and 2).

It needs emphasis that a major signaling mechanism activated by GH in target tissues is the Jak2-STAT5a/b pathway (Fig. 3A). 29,67 Thus the regulation of gene expression by GH (activation or repression) is mediated by lowlevel activation of PY-STAT5 in M vs F patterns.^{29,67} (Fig. 3A). This patterned PY-STAT5 activation, in combination with other transcription factors (HNF4, HNF6, C/EBP), transcriptionally activated or repressed cohorts of hundreds of genes in hepatocytes. Cascades of downstream gene expression included regulation by STAT5-mediated patterned activation of master transcription repressors or activators such as BCL6 and $Cux2^{29,57-59,67}$ This generates a cascade of sex-biased gene expression but without the direct effect of any steroid sex hormone (Fig. 3B). Parenthetically, STAT5a and STAT5b are ubiquitous 90 kDa cytoplasmic proteins that are 96% related to each other and are derived from adjacent genes at the STAT5a/b locus in both mouse and man.^{29,67} STAT5a and STAT5b have overlapping as well as some discrete functions.^{29,67} Of the 7 STAT transcription factors, STAT5a and STAT5b are the only ones implicated in mediating sex-biased gene expression.^{29,67}

Waxman and colleagues, and others, have shown in detailed studies (29,67 and citations

FIGURE 3. Schematics illustrating concepts of how male (pulsatile) vs female (more continuous) patterns of circulating GH elicit patterned activation of PY-STAT5 in the rat liver (Panel A), and thus sex-biased gene expression (Panel B). Schematics adapted from Waxman and O'Connor (2006) with permission of The Endocrine Society.⁶⁷

therein) that sex-biased expression of genes by GH-STAT5 activation in the hepatocyte depends on a "dynamical" signaling process that involves multiple activation and inactivation cycles (frequency as in "pulsatile" or "continuous"), differences in magnitude of signal strength ("level" of GH), the rates of these changes (different slopes) resulting in different rates of association of different transcription regulatory proteins (including PY-STAT5a/b) at the level of the chromatin encompassing different genes (Fig. 3). It is these differences in signal strength, frequency, slopes of the activation and inactivation reactions, and in co-associated proteins that lead to different chromatin conformations (active or inactive for RNA transcription) in the DNA context of different genes. The net result is a cellular phenotype driven by the GH-STAT5 axis consisting of the sex-biased expression of hundreds of genes differently in different species (Fig. 3). This patterned activation of cells includes longer-lived chromatin remodeling at the respective male and female-specific genes in that respective male-derived hepatocytes were more responsive to the male pulsatile pattern of GH in culture, and female-derived less so.^{29,33}

Different aspects of the specific GH patterns affect sex-biased expression of the same genes differently in different species.³¹⁻³⁵ As an example the CYP3A subfamily is male-biased in rats, but female-biased in mice and humans.^{29,31-35} We note that CYP3A has been shown to be induced by GH through $STAT5$ ⁶⁸ and in an issue relevant to pulmonary hypertension, it is the CYP3A subfamily of enzymes that convert the injected inactive monocrotaline (MCT) to the bioactive monocrotaline pyrrole (MCTP) in male rats, $69,70$ Thus it is no surprise that MCT administration into a male rat produces PH more efficiently than in the female. $6,17$

Sex Bias and STAT5a/b in Vascular Disease

We mentioned earlier that in rodents aortic remodeling after a balloon injury or pulmonary arterial remodeling after exposure to chronic hypoxia was more pronounced in males,

although the mechanisms have not been eluci $data.\overline{6}$ ⁻¹⁵ In vascular smooth muscle cells (SMCs), PY-STAT5b has been identified as a transcription factor which facilitates growth and motility, and neointima formation in response to thrombin, PDGF and arterial injury.^{21-25,71-74} Suppression of activation of PY-STAT5b signaling in the vessel wall reduced balloon injury-induced neointima formation.73 Remarkably, that hypophysectomy in the male rat markedly impaired arterial remodeling after aortic balloon injury due to reduced vascular SMC proliferation and myointima formation, was reported in $1978⁷⁵$ and confirmed,⁷⁶ but the mechanisms remained to be elucidated. It is now known that GH promotes vascular SMC proliferation and migration, and is required for normal vascular reactivity and remodeling.77-80 Indeed, the prevalence of systemic hypertension is 20-50% in patients with acromegaly (in whom the plasma GH levels are high) due to "stiffer arteries."77-80 Nevertheless, the issue of the GH-STAT5 axis contributing to sex bias in vascular remodeling has received little attention.

Our interest in the functions of STAT5 species (both unphosphorylated U-STAT5 and Tyrphosphorylated PY-STAT5) in vascular biology and sex bias arose several years ago from the discovery that U-STAT5a/b and STAT5a-GFP associated with the endoplasmic reticulum (ER) and Golgi apparatus in pulmonary arterial endothelial and smooth muscle cells. $81,82$ siRNA mediated knockdown of U-STAT5a/b in vascular cells (a) produced a remarkable cystic ER/ lunate nucleus phenotype, and (b) inhibited trafficking of the tsO45 VSV-G-GFP glycoprotein, and vasorelevant receptors such as BMPR2 to the cell surface. $81,82$ Moreover, the inhibition of intracellular trafficking of BMPR2 to the cell surface by siRNA-mediated knockdown of STAT5a/b was combinatorially exacerbated by estradiol-17 β (E2).⁸² These observations, and
the data of Waxman and colleagues implicating the data of Waxman and colleagues implicating STAT5 in mediating sex bias in liver gene expression, $29,67$ led us to ask whether STAT5 might underlie the sex bias seen in a vascular disease such as PH.

Our approach⁸³ to test the hypothesis relating sex and STAT5a/b in vascular remodeling has been to develop novel mice lines which have a conditional vascular smooth musclespecific deletion of the floxed STAT5a/b locus using the $SM22\alpha$ -Cre method [heterozygous] $SM22\alpha$ -Cre, STAT5a/b fl/wt (designated "+/-") and homozygous $SM22\alpha$ -Cre, STAT5a/ b fl/fl (designated " $-/-$ ")]. In such mice both the adjacent STAT5a and STAT5b were deleted in SMCs, especially vascular SMCs.⁸³ In contrast to endothelial-cell-specific STAT5a/b knockout mice (produced using the Tie2-Cre approach) which have microcytic anemia and are difficult to maintain postnatally, 54 the SMC-specific $STAT5a/b+/-$ and $-/-$ knockout mice were fertile and viable.⁸³

For our initial studies in these conditional SMC:STAT5a/b knockout mice, we focused on the sex-biased response to chronic hypoxia. It is well known that in the wt mouse chronic hypoxia typically triggers a male-dominant pulmonary arterial remodeling with female mice showing less extensive changes.6,16-19 Hypoxia has been shown to activate PY-STAT5 in cancer cells in culture.⁸⁴ We observed that although male and female mice had equal levels of STAT5a/b expression in pulmonary arterial walls in lung sections and in isolated PASMCs,⁸³ mice subjected to chronic hypoxia showed a sex-bias in the level of PY-STAT5 activation in the pulmonary arterial walls greater level of activation in the female than in the male (Fig. 4). An investigation of the effect of conditional STAT5a/b knockout on PH induced by chronic hypoxia revealed that the male dominance was abrogated in the hypoxic $STAT5a/b$ +/- and -/- mice (Figs. 5 and 6).⁸³ Overall, female $STAT5a/b +/-$ and $-/$ developed the greatest increase in right ventricular systolic pressure (RVSP), in right ventricular hypertrophy (RVH) and in pulmonary arterial remodeling (Figs. 5 and 6).⁸³ Additionally, knockout males also had more severe PH than wt males (Fig. 6). These data provided the first evidence implicating STAT5a/b in the sexual dimorphism observed in a vascular disease process. At the cellular level this increased severity of PH in hypoxic STAT5a/b knockout mice involved marked hypertrophy of SMCs in the pulmonary arterial tunica media.⁸³

The effects of a knockout of STAT5a/b in vascular SMCs likely extend beyond the

FIGURE 4. Sex-biased activation of PY-STAT5a/b in pulmonary arterial walls in wild-type mice after 7 weeks of chronic hypoxia (expt. as in Fig. 6). At the conclusion of the experiment in Fig. 6, quantitative immunofluorescence was used to evaluate levels of PY-STAT5a/b in the arterial walls of pulmonary arterial segments in sections of lungs using methods previously described (83) . *P <0.05 in comparisons between hypoxia and normoxia groups of the 2 sexes; and also in the male vs female hypoxia comparison; scale bar $=$ 50 μ m.

FIGURE 5. Abrogation of the male dominance of PH in the chronic hypoxia model in mice with heterozygous $SM22$ -Cre, $STAT5a/b+/-$ deletion (7 weeks' of hypoxia; n= 5 per group). Panel A, RVSP; Panel B, RVH; Panels C, PA remodeling in terms of wall thickness; Panel D: PA remodeling in terms of SMA-positive vessels; Panel E, Van Gieson's elastin staining. Scale bar = 45 μ m). *P $<$ 0.05. Adapted from Sehgal et al (2014). 83

pulmonary circulation. Although, the male and female SMC:STAT5a/b-/- mice had similar systolic, diastolic and mean blood pressures as respective wt mice, 83 "resistance" arteries such as second-order mesenteric arteries isolated from the knockout mice were 10-100-fold less responsive to vasodilation by acetylcholine (Fig. 7). Whether there is a STAT5-dependent sex bias in the mesenteric artery vasodilation response to acetylcholine is as yet unclear.

Reduced of STAT5a/b in SMCs in Vascular Lesions in Human Idiopathic Arterial Pulmonary Hypertension (IPAH)

Quantitative immunofluorescence analyses showed a marked reduction of STAT5a/b and of PY-STAT5 in SMCs in obliterative vascular lesions in lung sections derived from both male and female patients with late-stage IPAH, albeit with some variations between patients and in lesions in the same patient (Fig. 8).^{20,83} We have previously reported changes in the organization of the endoplasmic reticulum (ER)-associated proteins atlastin-3 (ATL3) and reticulon-4 (RTN4) (also called NogoB) in vascular ECs and SMCs following siRNA-mediated knockdown of $STAT5a/b$.⁸¹ Thus we evaluated expression of ATL3 and RTN4 in cells in IPAH lesions. Expression of ATL3 was markedly reduced but that of RTN4 was increased.⁸³ These data, taken together with our previous observations of an increase in Golgi apparatusassociated tether giantin and SNARE Vti1a in such cells, 85 point to the occurrence of ER stress and of changes in intracellular trafficking in cells in such obliterative arterial lesions.

We then investigated the expression of a known STAT5-dependent gene target in such

FIGURE 6. Female mice develop the severest PH in response to chronic hypoxia after homozygous S M22-Cre, STAT5a/b-/- deletion (7 weeks' of hypoxia; n= 5 per group). Panel A, RVSP; Panel B, RVH; Panels C, PA remodeling in terms of wall thickness; Panel D: PA remodeling in terms of SMA-positive vessels; Panel E, Van Gieson's elastin staining. Scale bar = 45 μ m). *P < 0.05. Adapted from Sehgal et al $(2014).^{83}$

lesions – the master transcription repressor BCL6. Waxman and colleagues have shown that BCL6 expression is driven by the GH-STAT5 axis in hepatocytes (male-biased in the liver), that the DNA binding motifs of STAT5 and BCL6 are very similar, and that BCL6 can repress STAT5 expression.57-59 The data obtained showed a marked reduction of BCL6 in cells in obliterative IPAH lesions (Fig. 8). 20,83 This loss of BCL6 is consistent with the overall thinking about IPAH pathogenesis today in that (a) it is known that genetic deletion of *BCL6* in mice results in a hypercytokine production state which includes pulmonary vasculitis, $86-88$ and (b) that several investigators have proposed that the PH disease process involves localized pulmonary vascular inflammation.⁸⁹⁻⁹² Thus, a reduction in BCL6 in cells in obliterative lesions of IPAH (Fig. 8) is consistent with development of a localized proinflammatory state. However, lung sections from both men and women with IPAH showed reduced BCL6 expression, perhaps because the sections available were from patients with latestage disease (Fig. 8).^{20,83}

In considering sex bias in the pathogenesis of PH in humans (and in rodent models) we need to keep in mind 2 separate issues. First is the contribution of intact levels of STAT5a/b and PY-STAT5 as part of the GH-STAT5 axis in the early stages of the disease to mediating sex bias in humans (the 2-4-fold higher prevalence in women than in men) and in rodent models (typically male-dominance with, paradoxically, inhibition of PH by E2). Second is loss of STAT5a/b, PY-STAT5 and BCL6 in the late stages of IPAH in both men and women. These two issues get combined in the hypoxic

FIGURE 7. Resistance arteries (second-order mesenteric arteries) are "stiffer" in mice with homozygous SM22-Cre, STAT5a/b-/- deletion. The phenotypes of isolated pressurized (80 mm Hg) resistance arteries derived from groups of male and female wt and mutant mice were evaluated in terms of the vasorelaxation response to acetylcholine (Ach) using methods as in ref.¹¹² and expressed as % change in peripheral diameter (% PD)(pooled data from $n = 4$ per group; mean \pm SE). *P $<$ 0.05 comparing respective wt and knockout groups (pooling both sexes) by ANOVA.

SMC: $STAT5a/b$ –/– mouse model in which (a)the sex bias is reversed, and (b) females get more severe disease than males. What downregulates STAT5a/b levels in IPAH lesions in late stage disease in both men and women remains to be understood.

Reduced STAT5a/b in Hypertrophic PASMC Lines Isolated From IPAH **Patients**

The above immunofluorescence data derived from lung sections of IPAH patients showing reductions in STAT5a/b obliterative lesion raised the question whether cells derived from lung vessels of IPAH patients might also show such reductions. A corollary question was whether vascular cells with reduced STAT5 derived from IPAH patients might display cell hypertrophy and organellar changes. Cell imaging studies of the primary PASMC lines derived from female controls and IPAH patients showed that 9 out of 9 control SMC lines consisted of small cells, while 7 out of 11 IPAH SMC lines consisted of enlarged hypertrophic cells, with markedly enlarged Golgi apparatus (displayed using either anti-giantin or ant-Vti1a antibodies).83 Western blot analyses showed a correlation between the cluster of these hypertrophic SMC lines and reduced STAT5a expression (using the kmeans cluster statistic).⁸³ Thus, low STAT5 expression clustered with cell hypertrophy, and enlarged Golgi apparatus in female IPAHderived SMC lines in a multi-parameter pattern (not enough numbers of male-derived lines were available for study). These data provided further evidence for the involvement of a loss of STAT5 in the pathogenesis of PH.

A Neuroendocrine Perspective (Hypothalamus-GH-STAT5) of Sex Bias in PH

The previous literature about how the hypothalamus-GH-STAT5 axis underlies sex bias in liver gene expression, juxtaposed with the new data on the role of STAT5 in determining sex bias in hypoxic PH in a mouse model, and the puzzling sex-bias questions in the PH literature provides us with an opportunity to suggest a synthesis of these different lines of research. (Fig. 9; a more detailed synthesis is in ref. 20).

Why is prevalence of IPAH higher in women than in men? On average, women have 80-120 fold higher levels of circulating GH than FIGURE 8. Representative immunofluorescence images showing coordinate reductions in STAT5a/b, PY-STAT5 and BCL6 in obliterative pulmonary arterial lesions in male and female patients with late-stage IPAH compared to control arterial walls (white arrows). The patient numbers correspond to the listing in Supplemental Table 2 in ref. 83. Scale bar = 50 μ m.

men.66 Moreover this is in a more continuous pattern than in men (Fig. 2).^{20,29,61} It is known that GH promotes vascular smooth muscle cell proliferation and migration, and is required for normal vascular reactivity and modeling.77-80 We propose that these 80-120-fold higher levels and a more continuous pattern of GH, and thus activation of different sets of cell-cycle, celL-proliferation and cell-migration regulatory genes, 29 is why IPAH is more prevalent in women than men. (Fig. 9).

What is the relevant difference between a female human and a female rodent underlying differences in sex bias in PH? There are quantitative differences in patterns of circulating GH in males and females in mice, rats and humans resulting in the same gene being regulated differently in terms of sex-specificity in the 3 species (Figs. 1, 2 and 3)(discussed in detail in cies (**Figs. 1, 2** and **3**)(discussed in detail in refs).^{20,29,67} The major relevant difference between female humans and female rodents is in the much higher continuous GH levels in women compared to female rodents (Fig. 2). Thus expression of P450 CYP 3A subfamily genes is male-biased in the rat, $30,31$ but femalebiased in humans.³⁴

Is there really an estrogen paradox? We have suggested above that the basis for why women get more IPAH than men may be related to the 80-120-fold higher GH levels and not so much E2.⁶⁶ In animal models, typically in male rodents, E2 would be protective by targeting

FIGURE 9. The GH-STAT5-BCL6 neuroendocrine axis as it relates to sex-bias in the initiation and progression of the pathogenesis of pulmonary hypertension.

the hypothalamus directly. $49-54$ Thus, as has been shown in the liver literature, E2 would "feminize" GH patterns changing the male pattern of expression in rodents to a female pattern (Fig. 1). Therefore the apparent paradox can be explained by involving GH in human IPAH, and by the direct targeting of the hypothalamus by E2 (Fig. 9). 20,83

Why is the MCT model male-biased in the rat?^{6,16,17} Downstream of the GH/STAT5 axis is the sex-specific expression of P450 CYP3A subfamily members.^{29,30,31,34} STAT5 is the transcription factor that upregulates CYP3A.29,68 and it is the CYP3A subfamily enzymes that metabolize MCT to its active MCTP. $69,70$ In the rat this is male-biased but is female-biased in mouse and humans. $29-31,34$ Thus, a single injection of MCT efficiently induces PH in the male rat. However, MCT does not readily produce PH in the female mouse either suggesting the occurrence of additional inter-species differences.

Why do female mice overexpressing the serotonin transporter (SERT) or the S100 calcium-binding protein S100A4/mts1 or the dexfenfluramine-administered mice, but not male mice, develop modest PH after 5 months? $93-97$ Although increased serotonin (5-HT) has been implicated in the pathogenesis of $PH₁⁹³⁻⁹⁷$ the mechanistic focus has largely been on direct effects of 5-HT on pulmonary vascular tissues. We note that it is already known that the PH-causing anorexigens fenfluramine, aminorex, phentermine and

fluoxetine increase 5-HT in the hypothalamus.⁹⁸⁻¹⁰¹ and that fenfluramine blunted GH responsiveness to GHRH. 102 Additionally, it is already known that PY-STAT5 signaling in the hypothalamus is involved in regulating appetite and sex-biased changes in body weight. 103 It has been shown already that 5-HT suppresses STAT5 expression and PY-STAT5 activation,¹⁰⁴ and 5-HT-receptor and dopaminergic D1, D2 receptor antagonists also inhibit PY-STAT5 activation (e.g., pimozide). $105,106$ We suggest that consideration of mechanisms in such models also include the central effects of 5-HT at the level of the hypothalamus and the arcuate nucleus, and sex-specific changes in the patterns of GH secretion and STAT5 activation. The femalebiased PH in these circumstances is likely generated at the level of the hypothalamus.

Why is there no sex bias in the hypoxia-SU5416 model? $6,18$ SU5416 (Sugen) has been described in the PH literature as an inhibitor of receptor 2 for vascular endothelial growth factor (VEGF R2)(6 and citations therein). However, it has been shown already that SU5416 inhibits activation of PY-STAT5. 107 The inhibition by SU5416 of PY-STAT5 activation [and of additional receptor tyrosine kinases^{108,109}] suggests why this model does not show a sex bias.

We emphasize that from our perspective, outlined in Figure 9, we specifically combine both central neuroendocrine mechanisms with peripheral tissue-level mechanisms in the pathogenesis of a vascular disease such as PH.

Discovering Sex-Biased and STAT5- Dependent Gene Expression Patterns in Vascular Cells

Investigations of sex bias and its GH-STAT5-dependence in liver gene expression using global unbiased microarray analyses of expressed RNA have established an important paradigm – the different expression patterns include cohorts of hundreds of genes that are male- or female-biased, that are upor down-regulated after hypophysectomy, that are up- or downregulated upon GH administration into hypohysectomized mice, and that are up- or down-regulated in hepatocytes from mice with a liver-specific $STAT5a/b-/-$ knockout, or those that are sex-biased but unaffected by any of these manipulations $(Fig. 3).^{29,67}$ Moreover, in each of these instances, while there are some genes that are coordinately affected similarly in males and females (e.g. reduction of $SOCS2$ expression after $STAT5a/b-/$ knockout in males and females), the cohorts of the affected genes in males and females are largely different. The important point in this paradigm is that sex-bias determinism through the GH-STAT5 axis at the level of peripheral tissues resides in changes in patterns of gene expression of cohorts of hundreds of genes (comprising transcription factors, growth factors and cytokines, intracellular trafficking mediators, cell adhesion molecules, and proteins that regulate cell proliferation, the cell cycle and apoptosis) and not just one or a few "mediators." Thus this paradigm is different from the reductionist approach of most investigators who ask for identification of changes in one or a few genes, and expect that to account for the development of sex-biased phenotypes in different tissues. Moreover, such patterns of sex-biased GH-STAT5-driven gene expression patterns are likely to be different in different tissue types in a particular species, and also different in the same tissue type in different species.

The availability of mice with SMC-specific $STAT5a/b-/-$ deletion allows for the derivation of primary PASMC and aortic SMC lines from males and females and an investigation of sex- and STAT5-specific patterns of gene expression using global unbiased RNA microarray or RNA sequencing approaches. Similarly, the availability of primary human PASMC lines derived from IPAH patients (females in this instance) with low STAT5 expression and corresponding control lines with high STAT5 allows for a similar investigation of STAT5-biased patterns of gene expression. The identification of BCL6 as a master transcription factor downstream of STAT5 in sex determinism hepatocytes by Waxman and colleagues, $57-59$ suggests the possibility that derivation of mice with SMC-specific deletion of BCL6, singly or in combination with STAT5a/b, may also lead to mice that have lost the male-dominant PH phenotype after exposure to chronic hypoxia. Such studies are likely to be informative with respect to the pathogenesis of the human disease in that we observed a marked decrease in BCL6 in SMCs in obliterative arterial lesions in IPAH (Fig. 8). The nestin-Cre-STAT5a/b-/- mice already developed by Lee et al. 103 which have deletion of STAT5a/b in the central nervous system including the hypothalamus provide a substrate to directly test the role of the hypothalamus in sex bias in the chronic hypoxia model as proposed in Figure 9 (STAT5 and PY-STAT5 are the relevant transcription factors in the hypothalamus that regulate appetite, sexual dimorphism of body weight, and insulin resistance). 103

We note that GH and STAT5 are involved in vascular SMC proliferation, motility and remodeling after injury, $71-75,77-80$ and that transgenic male mice overexpressing bovine GH developed hypertension between 5 and 6 months of age, independent of their bodyweight.¹¹⁰ This hypertension then persisted long-term.¹¹⁰ Such observations, together with our data in Figure 7, implicate the GH-STAT5 axis in systemic vascular biology. The extent to which the GH-STAT5 axis contributes to sex bias in systemic vascular remodeling remains an open question, but one that can now be addressed using the conditional SMC-specific $STAT5a/b-/-$ mice.

Conclusions

Fifty years ago Frantz and Rabkin reported observing markedly higher plasma GH levels in fasting ambulatory women than in men. 111 They also observed that administration of an estrogen (diethylstilbestrol) to men (diethylstilbestrol) to men "feminized" the pattern of circulating GH, and postulated that this was due to an effect of estrogen on the pituitary or higher centers. Over the next several decades these seminal observations led to the development of the neuroendocrine perspective of sex-biased liver gene expression anchored in hypothalamus-GH-STAT5 mediated mechanisms. These mechanisms, elucidated in great detail by numerous investigators, have now proven useful in understanding puzzling sex-bias issues in the pathogenesis of the vascular disease pulmonary hypertension in humans and rodent models. A critical insight transposed into vascular biology from the prior liver literature is that exogenously administered estrogens (and other sex hormones) affect sex-biased gene expression in peripheral tissues by affecting neuronal cells in the hypothalamus, and thus "feminizing" (or "masculinizing") the pattern of GH secretion. This is an insight missing from the vascular biology literature. The focus of sex-bias studies in vascular biology thus far has almost exclusively been on the direct effects of sex hormones on vascular cells. The inclusion of the neuroendocrine GH-STAT5 pathways in considering sexual dimorphism in human disease and in rodent models broadens our mechanistic perspective of how sex and gender bias comes about. Part of this broadening of perspective includes the appreciation that the generation of a net sex-biased phenotype in a particular cell type in a particular species involves changes in the expression and function of cohorts of hundreds of genes through STAT5-anchored mechanisms, but also inclusive of STAT5-independent mechanisms. The paradigm at hand is one in which STAT5 transcription factors, in association with other cell-type-specific transcription factors, are transient activators or repressors of the expression of large cohorts of genes in different patterns depending upon the dynamical

properties of GH-STAT5 activation such that the same pathways can contribute to both inhibiting or enhancing a particular disease process depending upon sex and species, and the particular pulmonary hypertension circumstance. The novel neuroendocrine concept, for the moment, is that the GH-STAT5 axis connects sexual dimorphism phenotype at the level of peripheral vascular tissues to mechanisms at the level of the hypothalamus.

DISCLOSURE OF POTENTIAL CONFLICTS OF INTEREST

No potential conflicts of interest were disclosed.

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NOTES

^a Some investigators use the phrase "pulmonary arterial hypertension (PAH)" to generically encompass the human disease and rodent models. Others use the phrase "pulmonary hypertension (PH)" as the generic term and reserve "pulmonary arterial hypertension (PAH)" for different forms of the human disease [such as idiopathic pulmonary arterial hypertension (IPAH) or hereditary pulmonary arterial hypertension (HPAH)]. In this essay we follow the second approach, and use PH as the generic term.

^bThe phrase "sex bias" refers to biological differences, while the phrase "gender bias" refers to behavioral and congnitive differences. Thus "sex bias" is appropriate throughout this article.

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