SEXUAL DIMORPHISM IN RENAL ANGIOTENSIN RECEPTORS GENE EXPRESSION: SEX CHROMOSOME COMPLEMENT INVOLVEMENT

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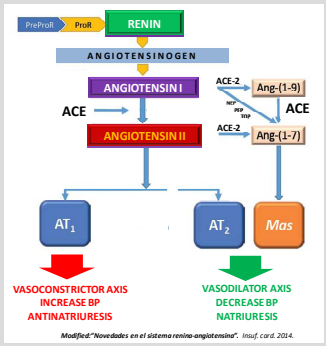
INTRODUCTION

The process of biological sex differentiation involves genetic and hormonal developmental steps.

Clinical and basic findings indicate that the angiotensinergic system differentially regulates hydroelectrolyte and cardiovascular responses in male and female.

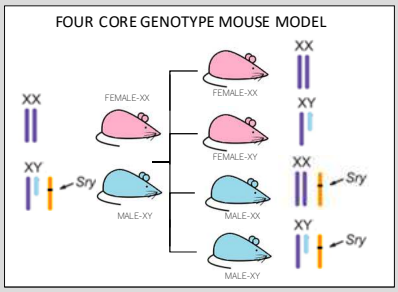


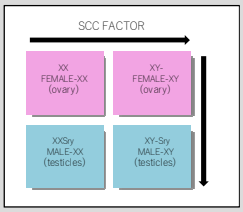
Studies have demonstrated major gender differences in the way males and females respond to stimulation and inhibition of the RAS (Renin Angiotensin System) under physiological and pathophysiological circumstances .

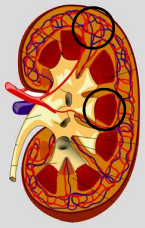
The pressor response to angiotensin II (ANG II) is attenuated in females compared with males what highlights the importance of studying basal kidney RAS complements involved in blood pressure regulation and in the development of hypertension which is also sexually dimorphic.

Considering that the kidney plays an important role in regulating the blood pressure and our previous evidence that suggests a modulatory gene expression effect of sex chromosome complement (SCC) on angiotensinergic receptors in the brain, **this study aimed to define whether sex chromosome complement may differentially modulate sex differences in renal basal ANG II and ANG-(1-7) receptor expression.**

METHODS







· Kidney were removed and RNA was isolated from punches of specific medulla and cortex.

-RNA concentration was quantified a NanoDrop 2000 UV-Vis Spectrophotometer.

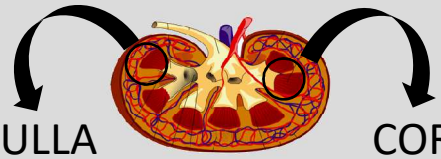
-Agtr1a and Agtr2 gene expression were determined in the Step One Real-Time equipment (Applied Biosystems), using Power SYBR Green Real-time PCR Master Mix and Mas1 gene expression was determined with SYBR Green Real-time PCR Master Mix.

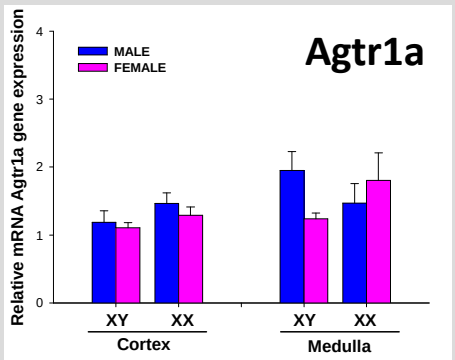
- The relative quantification was determined by the ΔΔCt method ($\Delta Ct = Ct_{unknown} - Ct_{reference\ gene}$). For each sample, the Ct was determined and normalized to the average of the housekeeping gene.

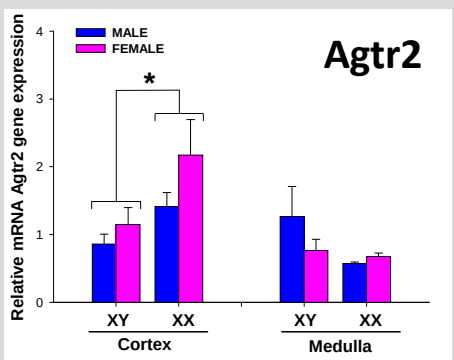
STATISTICAL ANALYSIS

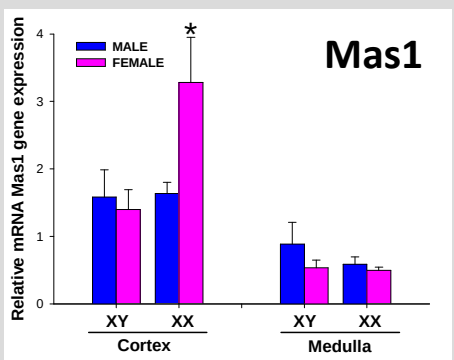
Relative gene expression data were subjected to a 2-way mixed ANOVA with gonadal sex (male/female) and SCC (XY/XX) as independent factors. Results were expressed as group mean (M) ± standard error (SE) whit error probability was set at 0.05.

RESULTS

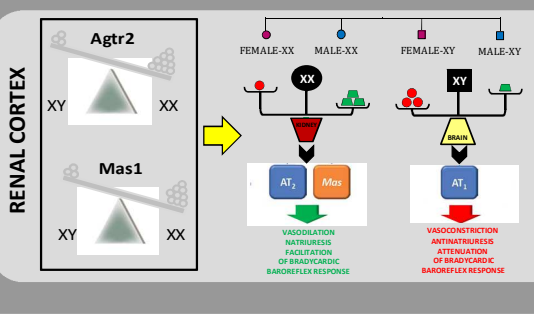








Relative mRNA expression of angiotensin type 1a (Agtr1a), 2 (Agtr2) and Mas (Mas1) receptors at the renal cortex and medulla. Bar graphs show relative Agtr1a, Agtr2 and Mas1 mRNA gene expression in gonadectomized Male-XY and Male-XX [blue bars] and in Female-XY and Female- XX mice [pink bars]. Values are mean ± SE, n=4/group.



CONCLUSION

These results, in agreement with our brain data (SCC effect at the Area Postrema), reveal a modulatory effect of SCC on AT2 and Mas gene expression with an enhancement of the vasodilator and natriuretic arm of RAS in XX-SCC mice; that may underlie sex differences in the regulation of arterial pressure.

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