

# SEX-SPECIFIC CARDIAC REMODELING AND FUNCTIONAL RECOVERY: INSIGHTS INTO PROTEOMIC MECHANISMS

Doctoral dissertation

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## Introduction

Cardiovascular disease remains the leading global cause of death, imposing immense economic strain. Men and women diverge early in cardiac development through chromosomal and epigenetic mechanisms, further shaped by lifelong hormonal environments. These differences translate into distinct clinical phenotypes: women experience myocardial infarction and obstructive coronary disease later, but suffer higher early mortality. Sex-specific remodeling patterns are also evident. After infarction, males typically develop dilatation and eccentric hypertrophy, whereas females favour concentric geometry and stable scarring. In pressure-overload states, men progress toward classic systolic failure, while women more often develop HFpEF-like phenotypes with preserved ejection fraction but increased stiffness. Fibrosis, metabolic reprogramming, and immune signalling also differ by sex at transcriptomic and proteomic levels. Cardiac remodeling itself encompasses inflammatory activation, matrix degradation, fibrosis, hypertrophy, and eventual deterioration or—if afterload is relieved—reverse remodeling. Yet reverse remodeling

responses vary widely, implying underlying molecular determinants such as sex steroids, whose influences on mitochondrial function, calcium handling, fibrosis, and apoptosis remain incompletely mapped. Proteomics offers a high-resolution view of these processes, surpassing genomics and transcriptomics by capturing functional protein networks. Advances in high-resolution MS, TMT multiplexing, and bioinformatic pipelines now allow quantification of thousands of cardiac proteins, but few studies integrate these datasets with load-independent haemodynamics. This thesis addresses these gaps using complementary rodent models—diffuse ischaemic injury via isoproterenol and pressure overload via aortic banding and debanding—combined with pressure–volume analysis, steroid-omics, and deep proteomics.

## Objectives

This study aims to (1) characterize early sex-specific functional and proteomic changes in a rat model of isoproterenol induced myocardial ischemia; (2) analyse steroid-hormone profiles in ischemic female rats and determine their impact on cardiac function; (3) assess how sex influences reverse remodeling using a standardized aortic banding–debanding model; and (4) identify molecular and functional markers that quantify reverse remodeling and predict outcomes. Overall, the goal is to define the mechanisms by which biological sex shapes ventricular adaptation, supporting the development of sex-aware cardioprotective strategies.

## Methods

This study complied with EU Directive 2010/63/EU and NIH animal-care guidelines. All procedures were approved by the relevant ethical committees in Hungary and Germany and followed ARRIVE guidelines.

**Myocardial ischemia study:** Young adult Wistar rats were assigned to sex-matched control and ischemic groups. Ischemia was induced by two daily subcutaneous injections of isoproterenol (85 mg/kg), while controls received saline. Cardiac function was assessed 48 h later using pressure–volume (PV) analysis.

**Aortic banding–debanding study:** Prepubertal Sprague–Dawley rats underwent abdominal aortic banding (AB) or sham surgery. A 22-gauge needle standardized the constriction across sexes. Only rats with confirmed pressure overload (systolic BP  $\geq 180$  mmHg) were included. After 6 weeks, subsets underwent debanding surgery and were followed to week 12. Ten experimental groups covered sham, AB, and DB conditions in both sexes.

**Echocardiography:** Serial imaging with a Vevo 2100 system measuring diameters, wall thicknesses, and left ventricular (LV) mass.

**Hemodynamics:** A microtip conductance catheter

measured LV-PV loops. Load-independent indices were obtained during transient IVC occlusion.  $\tau$  (Tau) was derived using the Glantz method. After measurements, hearts were excised, perfused, and weighed; HW/TL was calculated. Histology: LV sections were stained with H&E and picosirius red. Necrosis and fibrosis were quantified using QuPath and ImageJ. qRT-PCR: LV RNA was isolated, reverse-transcribed, and normalized to GAPDH. Steroid hormone profiling: Serum steroids were quantified by HPLC–MS. Western blot: Proteins were extracted, separated by SDS-PAGE, transferred, probed with antibodies, and normalized to GAPDH. Proteomics: ISO samples underwent TMT-labeling. LC–MS/MS data were processed with MaxQuant or FragPipe, with MSstatsTMT for quantification, batch correction, and imputation. Statistics: Normality testing preceded ANOVA, t-tests, or nonparametric tests as appropriate. Proteomic differential expression used limma with FDR correction. MixOmics enabled PLS-DA and sPLS-DA. LASSO identified LV parameters most strongly linked to protein abundance. GO enrichment used clusterProfiler; network and subnetwork analyses were performed with STRING and MCODE.

## Results

ISO induced comparable myocardial necrosis in both sexes, with increased HW/TL but unchanged collagen content. Mortality was higher in males. Functionally, males showed a marked fall in MAP, SW, EF and PRSW, indicating impaired systolic performance, whereas females primarily developed diastolic dysfunction with higher  $\tau$ , LVEDP and EDPVR. Proteomics (2,224 proteins) revealed: females upregulated more proteins—particularly cytoskeletal, contractile, ECM-repair and inflammatory mediators—while males showed stronger downregulation of mitochondrial and metabolic enzymes. Western blots confirmed sex-specific induction of VASP and OPN in females. In F-Isch animals, 2-hydroxyestrone strongly correlated with PRSW,  $\tau$ , dP/dtmin and HW/TL. GO analysis linked 2-OHE1 and estradiol to fatty acid oxidation and oxidative phosphorylation. In the AB-DB study, males consistently exhibited larger LV mass, chambers, CD, and higher myh7/myh6 ratios, while females displayed higher LVESP, Ea, ESPVR and shorter  $\tau$ . Under pressure overload, males showed greater decline in contractility and worse diastolic function by week 12.

Debanding induced robust reverse remodeling in both sexes—reducing LVmass, HW/TL, CD, nppa and myh7/myh6—but fibrosis regressed more in females. Proteomics (2,348 proteins) showed similar pressure overload-induced changes in both sexes, dominated by downregulated lipid-catabolic pathways. After unloading, females nearly normalized their proteome, particularly restoring fatty acid oxidation, whereas males retained substantial residual alterations. sPLS-DA, DE analysis and GO mapping confirmed sex-specific inflammatory (female) vs. cytoskeletal/translation (male) signatures. Reanalysis identified  $\tau$  as the functional parameter most strongly linked to proteomic remodeling (842 proteins).  $\tau$ -associated proteins spanned energy metabolism, sarcomeric renewal, RNA processing and stress signalling. ROC analysis identified  $\tau$ -linked proteins (e.g., GSTK1, COQ9, TMOD4, SORBS2, NRAP) with AUC>0.85 for detecting active remodeling. Network analysis revealed tightly interconnected  $\tau$ -driven modules, and transcription-factor mapping highlighted MAX, MYC, ATF3, MAFF and IRF1 as key regulators.

## Conclusions

This work compared male and female rat hearts across diffuse ischemia, pressure-overload hypertrophy, and reverse remodeling, integrating load-independent PV metrics with deep TMT-proteomics. Early isoproterenol-induced injury was largely sex-neutral, but females preserved contractility by up-regulating contractile, cytoskeletal, and chaperone proteins, whereas males showed greater metabolic suppression and lower mechano-energetic efficiency. Females exhibited transient diastolic stiffening linked to enriched ECM-repair signatures. Steroidomics identified 2-hydroxyestrone as a key predictor of better female functional recovery through enhanced mitochondrial and fatty-acid-oxidation pathways. In pressure-overload unloading, both sexes regressed hypertrophy similarly, though females showed greater collagen resorption, while males displayed stronger rebound due to worse baseline function. Across models, the relaxation constant  $\tau$  most closely tracked proteomic remodeling, yielding a protein panel that sensitively detects active cardiac remodeling.

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