



Manifestations of gene expression profiles in human right atrial myocardium caused by mechanical stretch

Ryusuke Suzuki^{1,4} · Masaki Morishima⁴ · Chisato Nakada³ · Shinji Miyamoto² · Katsushige Ono⁴

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Abstract

This investigation was aimed to identify gene profiles in human atrial myocardium in response to chronic mechanical stretch. Right atrial appendages from 21 patients were divided into 2 groups based on the size of right atrial volume. The microarray DATA analyses differentially identified 335 genes (> 2.0-fold, corrected $P < 0.05$) including “functionally unknown genes”. This study identified 26 up-regulated genes (natriuretic peptide B, G protein subunit gamma 13, thyroid stimulating hormone beta, etc.) and 23 down-regulated genes (oligodendrocyte transcription factor 1, carbonic anhydrase 12, etc.), which could be responsible for chronic stretch-mediated structural remodeling in the atrium.

Keywords Atrial stretch · Gene expression profile · DNA microarray · STRING analysis

Introduction

In cardiac physiology, preload is the amount of sarcomere stretch experienced by cardiomyocytes at the end of ventricular filling during diastole. In cardiac pathophysiological conditions, for instance, the case of dilated cardiomyopathy, the muscle walls of the heart become stretched and thin, so they cannot contract properly to pump blood around the body. In general, mechanical forces are able to activate hypertrophic growth of cardiomyocytes in the overloaded

ventricular myocardium [1]. Mechanical stretch also can be an important trigger for various arrhythmias; enlargement of atrial size is highly associated with the occurrence of atrial fibrillation, and reduced atrial size may be important in preventing atrial fibrillation [2]. In vice versa, atrial fibrillation is often associated atrial dilation with pathologically increased cardiomyocyte stretch. However, the mechanisms by which stretch creates a substrate for atrial fibrillation remain unclear. Once initiated, atrial fibrillation alters atrial electrical and structural properties that promote its maintenance and recurrence, which is named “atrial remodeling” [2]. Atrial remodeling refers to structural and functional changes in the atrial myocytes in response to internal or external stimuli caused by atrial fibrillation. In this context, analyses of atrial myocardium with atrial fibrillation may not be suitable for study on cellular mechanisms for onset of atrial fibrillation, because altered cellular signals may not be the mechanisms for atrial fibrillation but be the consequences caused by atrial fibrillation [2]. Although several studies have revealed changes of gene expression profiles in the atrium caused by atrial fibrillation, virtually nothing is known about whole (gene and exon-level) transcriptome response to stretched human cardiomyocytes independently of the presence of atrial fibrillation [3, 4]. In this regard, we characterized comprehensive studies of mechanically stretch-induced gene expression changes in human atrial myocardium in the absence of atrial fibrillation.

Ryusuke Suzuki, and Masaki Morishima have contributed equally to this work.

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✉ Katsushige Ono
ono@oita-u.ac.jp

¹ Department of Cardiovascular Surgery, Japanese Red Cross Kumamoto Hospital, Kumamoto, Kumamoto, Japan

² Department of Cardiovascular Surgery, Oita University School of Medicine, Yufu, Oita, Japan

³ Department of Molecular Pathology, Oita University School of Medicine, Yufu, Oita, Japan

⁴ Department of Pathophysiology, Oita University School of Medicine, 1-1 Idaigaoka, Hasama, Yufu, Oita 879-5593, Japan