Angiotensin II Receptor Subtypes in the Skeletal Muscle Vasculature of Patients With Severe Congestive Heart Failure

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Background—Vascular remodeling occurs in the skeletal muscle of patients with severe congestive heart failure (CHF); this remodeling is mediated in part by increased activity of the renin-angiotensin system. Animal models suggest that in the vasculature, angiotensin II receptor type 2 (AT2-R) expression may be upregulated in pathological states associated with vascular remodeling. The therapeutic effects of an AT1-R antagonist may, therefore, be in part due to increased plasma angiotensin II levels, which stimulate AT2-R. However, whether AT2-R is expressed in the skeletal muscle vasculature of patients with severe CHF is unknown.

Methods and Results—The steady-state transcript levels of the AT1-R and AT2-R genes were analyzed by reverse transcription–polymerase chain reaction in RNA samples prepared from the skeletal muscle of 12 patients with severe CHF (V˙ O₂, 10 mL · kg⁻¹ · min⁻¹) and 5 age-matched healthy subjects who underwent vastus lateralis biopsies. Human fetal skeletal muscle RNA served as a positive control for the expression of AT1-R and AT2-R gene transcripts. Transcripts from the AT1-R gene were detected readily in all samples. In contrast, transcripts from the AT2-R gene were only detected in fetal skeletal muscle samples and could not be detected in the skeletal muscle vasculature of healthy subjects or that of CHF patients, who were treated with either angiotensin-converting enzyme inhibitors or AT1-R antagonists.

Conclusions—The AT2-R gene is not expressed in the skeletal muscle of patients with CHF. In the absence of detectable AT2-R gene transcripts, the AT2-R pathway is unlikely to contribute to the effects of AT1-R antagonists on the skeletal muscle vasculature in patients with severe CHF. (Circulation. 2000;102:2210-2213.)

Key Words: angiotensins \( \bullet \) receptors \( \bullet \) heart failure \( \bullet \) muscle, skeletal
Methods

Study Population

Twelve patients with New York Heart Association class IV CHF and 5 age-matched healthy subjects participated in the study. The patient group included 4 women and 8 men whose age, left ventricular ejection fractions, and peak VO₂ averaged 62±6 years, 24±6%, and <10 mL·kg⁻¹·min⁻¹, respectively. The cause of CHF was ischemic cardiomyopathy in 10 patients and nonischemic cardiomyopathy in 2. Medical therapy consisted of ACE inhibitors (lisinopril, n=4; fosinopril, n=3; 40 mg/d) or AT1-R antagonists (160 mg/d valsartan, n=5), furosemide (mean dose, 114±40 mg/d), and digoxin in all patients, long-acting oral nitrate preparations in 10 patients, and β-adrenergic blockers in 2 patients. The control group consisted of 5 sex- and age-matched healthy subjects who had a peak VO₂ of >30 mL·kg⁻¹·min⁻¹. The Ethical Review Board of the Albert Einstein College of Medicine approved the study. All patients gave written informed consent before the study.

Muscle Biopsies

Biopsies of the vastus lateralis muscle 15 cm above the patella were performed using a needle biotome (Bard). A sample of the vastus lateralis muscle taken from a 23-week-old fetus was provided by the Albert Einstein College of Medicine Tissue Bank. All samples were immediately plunged in liquid nitrogen and transferred to a freezer, where they were kept at −80°C until analysis.

RNA Isolation and Reverse Transcription–Polymerase Chain Reaction Analysis of Skeletal Muscle Samples

Each tissue sample was transferred to a 6-mL polypropylene tube containing 1 mL of Trizol (Gibco/BRL) and was homogenized with a hand-held tissue tearer (Biospec Products). Extracted RNA was isolated by isopropanol precipitation. After the nucleic acids were washed in 70% ethanol, they were resuspended in distilled water and the DNA was removed by digestion with 1 U of RQI RNAse-free DNase (Promega Corp) for 10 minutes at 37°C. The concentration of purified RNA was determined by optical density and then diluted to 0.125 μg/μL. Each RNA sample (0.5 μg) was reverse-transcribed at 37°C for 90 minutes in a 20-μL reaction containing 100 pmol of the random hexamer pdN6 (Pharmacia) and 40 U of murine leukemia virus reverse transcriptase (Gibco/BRL).

For polymerase chain reaction (PCR), 2 μL of each reverse transcription (RT) product was used in a 20-μL reaction containing 1.5 mM MgCl₂, 1.0 mM of each primer, 200 μM of each deoxynucleoside triphosphate, and 0.1 μL of α³²P-dCTP as a tracer, when applicable. Fetal skeletal muscle RNA served as a positive control for the expression of AT1-R and AT2-R gene transcripts. The integrity of all RNA samples was analyzed by amplifying transcripts for smooth muscle α-actin, β-actin, von Willebrand factor, and GAPDH. Mock reactions that lacked only the RT enzyme were conducted for all samples to exclude the presence of products derived from genomic DNA. Primer sequences are shown in the Table.¹⁻¹⁵

Each PCR was initiated with a 2-minute denaturing incubation at 95°C and finished with a 10-minute extension at 72°C. The number of cycles was 45 for AT2-R and 35 for all other genes; cycles were performed as follows: 30 seconds at 94°C, 1 minute at 58°C, and 1 minute at 72°C. Products were analyzed using 1.5% agarose or 5% polyacrylamide gel electrophoresis. To test the sensitivity of the assay, RT-PCR was performed using serial dilutions of the RNA from the vastus lateralis muscle of a 23-week-old fetus. The RNA was diluted 1:10, 1:100, and 1:1000 in dCTP-treated RNAse-free H₂O. To ensure an equal total amount of RNA in each sample (0.5 μg), the diluted samples were supplemented with RNA extracted from human whole blood (not expressing the AT2-R gene). Samples were reverse-transcribed and amplified by PCR using incorporated α³²P-dCTP as a tracer. All selected primers amplified CDNA at the expected sizes. Restriction enzyme analysis confirmed that the desired targets had been amplified.

Results

Total RNA was purified from the skeletal muscle of healthy individuals or CHF patients and used in PCR reactions to determine the presence of specific transcripts. As a positive control for AT1-R and AT2-R, RNA was also derived from a fetal sample of skeletal muscle because both genes are expressed at this stage of development.² The PCR conditions used were not designed necessarily to be quantitative but rather to ensure very high sensitivity for detecting relatively low transcript levels. Transcripts encoding AT1-R, von Willebrand factor, and GAPDH were detected readily, as expected, in all samples; some examples are shown in Figure 1. The GAPDH product is derived from a highly expressed housekeeping gene and serves as a positive control for general RNA integrity; products were also detected similarly in all samples using primers specific for smooth muscle α-actin or β-actin (data not shown). The von Willebrand factor gene is a specific marker for endothelial cells, and it was analyzed here to demonstrate the presence of vascular tissue in each of the biopsied samples.

![Figure 1](https://circ.ahajournals.org/content/120/11/2211/F1.large.jpg)

Figure 1. Representative examples of RT-PCR products detecting expression of AT1-R, von Willebrand factor (VWF), and GAPDH in skeletal muscle of patients with severe CHF and healthy controls. FT indicates fetal skeletal muscle; NL, skeletal muscle from normal control; ARB, skeletal muscle sample from patient treated with AT1-R antagonist; and ACEI, skeletal muscle sample from patient treated with ACE inhibitor.
Discussion

In the rat vasculature, the AT2-R gene is expressed at low levels in the aorta and can be detected by autoradiography throughout the aortic wall, with higher levels reported in the microcirculation of the skeletal muscle. In the adult rat skeletal muscle microcirculation, AT2-Rs were localized using anti–AT2-R antibodies to the endothelial cells, vascular smooth muscle cells, fibroblasts, mast cells, macrophages, and pericytes. The AT2-R gene is expressed in endothelial cells derived from the spontaneous hypertensive rat coronary arteries but not in endothelial cells derived from bovine aorta or porcine peripheral arteries.

The expression of AT2-R in the adult rat skeletal muscle vasculature is in apparent contrast to normal human adults. The AT2-R gene is highly expressed during fetal development, but its products decrease rapidly after birth and, in the adult, they are restricted to the adrenals, uterus, ovary, lung, heart, and specialized nuclei in the brain. In human primary cell cultures, AT2-R transcripts are found in coronary endothelial cells using RT-PCR, but the receptors are not detected by radioligand assay in vascular smooth muscle cells from the renal artery. In the human kidney, AT2-R expression was localized using in situ hybridization to the medial layer of the interlobular arteries. In the failing heart, AT2-R expression is unchanged or upregulated, whereas AT1-R expression levels are decreased. The present data indicate that the AT2-R gene is not re-expressed in the skeletal muscle vasculature of subjects who are diagnosed by peak oxygen uptake as severe CHF patients.

Importantly, the similar level of von Willebrand factor and smooth muscle α-actin transcripts measured in all samples (and detected easily in both fetal and adult skeletal muscle samples) indicates that the endothelial and smooth muscle cell compartment was not under-represented in the biopsy samples. Because endothelial cells are the primary site of AT2-R expression, this control provides confidence that the experiments are not biased by cell-type differences among samples.

Forced overexpression of the AT2-R gene in transgenic mice is sufficient to offset a AT1-R–mediated vasoconstrictive and pressor effect through an endothelium-dependent mechanism. AT2-R–mediated vasodilation is caused by paracrine effects of bradykinin liberated from vascular smooth muscle cells, which leads to the activation of the endothelial bradykinin type 2 receptor–mediated nitric oxide/cGMP system. However, AT2-R gene expression could not be detected in the skeletal muscle vasculature of adult controls or patients with severe CHF treated with ACE inhibitors or AT1-R antagonists. The RT-PCR assay was performed on serial dilutions of the positive-control fetal skeletal muscle RNA. To ensure an equal amount of total RNA in each sample, RT-PCR was performed on serial dilutions of the positive-control fetal skeletal muscle RNA. To ensure an equal amount of total RNA in each sample (0.5 μg), the diluted samples were supplemented with RNA extracted from human whole blood (not expressing the AT2-R gene but positive for control transcripts such as GAPDH; data not shown). Using ethidium bromide staining of the RT-PCR products, the transcripts were detected readily in fetal skeletal muscle RNA samples diluted 10-fold (Figure 2).

To increase the level of sensitivity, PCR reactions were amplified in the presence of trace α32P-dCTP, and products were analyzed by phosphorimage analysis after polyacrylamide electrophoresis. As shown in Figure 3, AT2-R gene transcripts were measurable in fetal skeletal muscle samples diluted at least 100-fold, but they could not be detected in undiluted skeletal muscle RNA from normal subjects or CHF patients. Therefore, we confirm that AT2-R gene expression is restricted to fetal-stage skeletal muscle and conclude that the gene is not re-expressed in CHF patients, even at 1/100 this level.
sensitive enough to detect AT2-R gene expression easily in a 1:100 dilution of fetal skeletal muscle RNA. The lack of expression of the AT2-R gene in the skeletal muscle vasculature indicates that direct vasodilatation resulting from AT2-R activation by increasing levels of circulating angiotensin II is unlikely to contribute to the relaxing effects of AT1-R blockade on the skeletal muscle beds.

The purpose of this study was to evaluate the expression of AT2-R at the transcriptional level. It would be interesting to confirm the lack of AT2-R at the level of protein or signaling activity. Unfortunately, because of the limiting size of biopsy material in this clinical study, it was not feasible to investigate the presence of AT2-R using ligand binding or Western blotting assays. However, considering that the highly specific and sensitive RT-PCR assay was negative for AT2-R mRNA in skeletal muscle samples, the presence of protein without RNA is unlikely.

The absence of AT2-R in the skeletal muscle vasculature of patients with CHF is compatible with the recent observation that AT1-R antagonism with losartan does not seem to offer added benefits over ACE inhibition with captopril. In summary, the AT2-R gene is not re-expressed in the skeletal muscle vasculature of patients with CHF and severely decreased peak aerobic capacity. In the absence of detectable AT2-R gene transcripts, the AT2-R pathway is unlikely to contribute to the effects of AT1-R antagonists on the skeletal muscle vasculature of patients with severe CHF.

References

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_Circulation_. 2000;102:2210-2213
doi: 10.1161/01.CIR.102.18.2210

_Circulation_ is published by the American Heart Association, 7272 Greenville Avenue, Dallas, TX 75231
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Print ISSN: 0009-7322. Online ISSN: 1524-4539

The online version of this article, along with updated information and services, is located on the World Wide Web at:
http://circ.ahajournals.org/content/102/18/2210