Junctional Adhesion Molecule-1 Is Upregulated in Spontaneously Hypertensive Rats
Evidence for a Prohypertensive Role Within the Brain Stem

Hidefumi Waki, Beihui Liu, Masao Miyake, Kiyoaki Katahira, David Murphy, Sergey Kasparov, Julian F.R. Paton

Abstract—Junctional adhesion molecule-1 (JAM-1) forms part of the tight junction between adjacent endothelial cells. Using microarray technology, we showed previously that JAM-1 was differentially expressed in the brain stem of spontaneously hypertensive rats compared with normotensive Wistar–Kyoto (WKY) rats. In this study, we quantified the expression of JAM-1 in the brain stem of spontaneously hypertensive rats and WKY rats and established whether any differential expression was confined to this region of the brain or was ubiquitous throughout the central nervous system and, indeed, the whole body. Because the nucleus tractus solitarii plays a pivotal role in arterial pressure regulation, we assessed whether JAM-1 in this region affects the chronic regulation of arterial pressure. Real time RT-PCR revealed that JAM-1 mRNA was upregulated in multiple regions of the brain and all of the peripheral vascular beds studied. In the nucleus tractus solitarii, the level of JAM-1 mRNA was significantly higher in both young (3-week–old, prehypertensive) and adult male spontaneously hypertensive rats (15 to 18 weeks old) than that of age-matched WKY rats (fold differences; prehypertensives: 1.01±0.06 versus 1.59±0.13; n=10; P<0.01; adult: 1.08±0.14 versus 2.86±0.57; n=10; P<0.01). After adenoviral-mediated expression of JAM-1 in the nucleus tractus solitarii of adult WKY rats (15 weeks old; n=6), systolic pressure was increased from 120±4 to 132±4 mm Hg (P<0.01). Our data suggest that JAM-1 expression in the spontaneously hypertensive rat is upregulated throughout the body compared with the WKY rat and that this is not secondary to the hypertension. When JAM-1 is expressed in the nucleus tractus solitarii, it raises arterial pressure, suggesting a novel prohypertensive role for this protein within the brain stem. (Hypertension. 2007;49:1-7.)

Key Words: hypertension • brain stem • inflammation • baroreflex control • adhesion molecules

Essential hypertension is a complex polygenic trait with underlying genetic components, many of which remain unknown. Unmasking these genes may provide novel information about blood pressure regulation and could be potential future targets for therapeutic intervention. This is pertinent, because 50% of patients with hypertension on antihypertensive medication continue to have elevated levels of blood pressure (www.heartstats.org).1 Despite accumulating evidence that gene expression profiles are altered in essential hypertension,2,3 prohypertensive genes remain unclear. One confounding factor is that hypertension itself induces changes in gene expression as a secondary effect.

We are exploring the role of the autonomic nervous system in the etiology of hypertension. It is documented that human essential hypertension is associated with a high level of sympathetic nerve activity in humans.4–6 Grassi6 postulated that neurogenic hypertension is maintained by sympathetic overactivity and that this may even be causative. Consistent with that viewpoint, Smith et al5 have shown sympathetic overactivity in white coat hypertensive subjects. Furthermore, in a rat model of hypertension (the spontaneously hypertensive rat [SHR]), sympathetic nerve activity is also substantially elevated relative to Wistar–Kyoto (WKY) rats.7,8 It thus appears that the sympathetic nervous system may play a key role in the manifestation of hypertension in both humans and animal models. Although numerous brain stem regions can control sympathetic nerve activity, the nucleus of the solitary tract (NTS) is one of the key central regions playing a role in the regulation of both the set point of arterial pressure,9–11 as well as baroreflex gain control, a feedback mechanism essential for homeostatic regulation of arterial pressure.10,12,13 A preliminary cDNA microarray experiment14 suggested several differentially expressed genes in the NTS between SHR and their progenitor strain, the WKY rat. One of them
was junctional adhesion molecule (JAM)-1. This gene was upregulated in both adult and juvenile (prehypertensive) SHRs and, hence, not secondary to the high blood pressure. JAM-1 is a member of the immunoglobulin superfamily of adhesion molecules that form tight junctions between adjacent endothelial cells and, therefore, form a part of the blood–brain barrier.15,16 JAM-1 has other functions, such as promotion of leukocyte-endothelial adhesion and subsequent inflammation.17 This might be important, because leukocyte accumulation within the systemic circulation was deemed to be a contributing factor for the hypertension in the SHR because of enhanced hemodynamic resistance.18 In addition, JAM-1 is also a risk factor for both atherosclerosis and atherothrombosis,17,19 both of which can be related to hypertension.20

In this study, we have quantified the level of JAM-1 gene expression in the brain stem of SHR relative to WKY rats using real-time RT-PCR and assessed JAM-1 expression in other regions of the brain, as well as numerous peripheral tissues. Our findings indicate that, in the SHR brain (including NTS), expression of JAM-1 mRNA is increased and shifted toward a transcript containing an extended 3′ untranslated region (3′UTR); this effectively leads to higher levels of immunoreactive JAM-1 protein. Importantly, chronic overexpression of JAM-1 in the NTS of WKY rats using viral gene transfer raised arterial pressure supporting a novel prohypertensive role for this protein.

**Methods**

Procedures were carried out according to the United Kingdom Home Office Guidelines on Animals (Scientific Procedures) Act of 1986. The animals were housed individually, allowed normal rat chow and drinking water ad libitum, and kept on a 12-hour light/12-hour dark cycle.

**Differential Gene Expression in the SHR and WKY Rats**

**Extraction of RNA**

Both 3- (SHR, n=10; WKY, n=10) and 15- to 18-week-old (SHR, n=10; WKY, n=10) male rats were humanely killed by cervical dislocation. Regions of the brain (cerebellum, cerebral cortex, NTS, paraventricular nuclei, rostral ventrolateral medulla, and supraoptic nuclei) and internal organs (eg, liver, lung, kidney, spleen, skeletal muscle, and heart) were dissected (or punched if brain) rapidly from each animal and homogenized in 400 μL of TRIZol reagent (Invitrogen). To avoid contamination with genomic DNA, the RNA samples were treated with RNase-free DNase I (Roche Diagnostics GmbH). RNA purity was verified by performing PCR on samples not treated with reverse transcriptase.

**Quantitative RT-PCR**

β-Actin, JAM-1, JAM-3, intercellular adhesion molecule-1 (ICAM-1), and vascular cell adhesion molecule-1 genes were tested in this study; primer details are available in an online data supplement at http://hyper.ahajournals.org. For JAM-1, 2 different sets of primers were used (for the coding part of the transcript, nucleotides 430 to 652 or 500 to 600 m from midline, and 500 to 600 μm below the dorsal surface of the medulla). Each injection was made over 1 minute. To avoid postsurgical cardiovascular effects, animals were allowed to recover for 5 days before blood pressure data were sampled. Data analysis was performed using the Hey-Presto system23 on the day before NTS microinjection of virus and on days 5 to 7 and 14 after microinjections. On these days, arterial pressure was measured continuously for 5 minutes every hour from 9:00 AM until 8:05 AM on the following day. Heart rate (HR) was derived from the interpulse interval. Averaged systolic blood pressure (SBP) and HR were calculated. The spontaneous cardiac baroreflex gain (sBRG) was also determined from spontaneous changes in SBP and HR as described previously.22,23

**Data Analysis**

Group data were expressed as mean±SEM. To evaluate time-dependent effects of JAM-1 expression, we used 2-way repeated-measures ANOVA and the Scheffe test for multiple comparisons of cardiovascular variables across time and between different groups. A paired/ unpaired t test was also used for comparisons between 2 groups. Differences were considered significant if P<0.05.

**Results**

**Quantitative Comparison of JAM-1 Gene Expression in WKY Rats and SHRs**

In WKY rats using 50 cycles of PCR, we failed to amplify the JAM-1 mRNA transcript containing 3′UTR (nucleotides 1145 to 1385 in BC065309; JAM-1/1145 to 1385) in the rostral ventrolateral medulla, supraoptic nuclei, cerebellum, liver, and heart. In contrast, expression was evident in the same tissues of the SHR (Figure 1 and 2). However, the JAM-1/1145 to 1385 transcript was detectable in the paraventricular nuclei, cerebral cortex, lung, kidney, spleen, and skeletal muscle of WKY rats but was clearly less abundant than that present in the SHR (Figures 1 and 2). Using real-time RT-PCR, we confirmed that the threshold cycle of β-actin of these tissues was the same between SHRs and WKY rats, indicating that the total RNA concentration in each sample was identical (data not shown). Because of its role in central control of arterial...
It was notable that the threshold cycle of NTS of both young and adult WKY rats. In contrast, it was regard to JAM-1/1145 to 1385, we failed to amplify it in the respect to SHRs, 1.01 \( \pm \) 0.06 versus 1.59 \( \pm \) 0.13 respectively, \( n = 10 \) for each strain, \( P < 0.01 \); young WKY rats and SHRs, 1.01 \( \pm \) 0.06 versus 1.59 \( \pm \) 0.13 respectively, \( n = 10 \) for each strain, \( P < 0.01 \); Figure 3). With regard to JAM-1/1145 to 1385, we failed to amplify it in the NTS of both young and adult WKY rats. In contrast, it was present in the NTS of SHRs in both young and adult animals (Figure 3). It was notable that the threshold cycle of \( \beta \)-actin was the same between the 2 strains of rats (Figure 3), indicating that the total RNA concentration in each sample was identical.

**Quantitative Comparison of the Levels of JAM-1 Gene Expression in the NTS of WKY Rats and SHRs**

In the NTS, the level of JAM-1 mRNA transcript representing the protein-coding sequences (JAM-1/430 to 652) was significantly higher in both young and adult SHRs compared with age-matched WKY rats (adult WKY rats and SHRs: 1.08 \( \pm \) 0.14 versus 2.86 \( \pm \) 0.57, respectively, \( n = 10 \) for each strain, \( P < 0.01 \); young WKY rats and SHRs, 1.01 \( \pm \) 0.06 versus 1.59 \( \pm \) 0.13 respectively, \( n = 10 \) for each strain, \( P < 0.01 \); Figure 3). Comparing it with other vascular adhesion molecules. However, in both young and adult WKY rats and SHRs, there were no differences in the level of JAM-3, ICAM-1, and vascular cell adhesion molecule-1 gene expression in the NTS (see the data supplement), suggesting that the upregulation of JAM-1 in the SHR was specific.

**Adenoviral Expression of JAM-1 in the NTS of the WKY Rat**

We next tested for any functional impact of JAM-1 expression on arterial pressure regulation. With JAM-1 being upregulated in the NTS of the SHR (compared with WKY rats), we decided to overexpress it in the NTS of WKY rats. Before viral injection, baseline levels of SBP, HR, and sBRG remained elevated compared with control levels (ie, pretransfection levels (361 \( \pm \) 10 bpm; sBRG, \(-1.99 \pm 0.13 \) bpm/mm Hg; Figure 5)). Five to 7 days after injection of the Ade-CMV-JAM-1, SBP significantly increased (control data above; 7 days after viral transduction: 132 \( \pm \) 4 mm Hg; \( P < 0.01 \)), whereas no changes were found in the SBP of the Ade-CMV-eGFP group (control data above; 7 days after viral transduction: 121 \( \pm \) 3 mm Hg). The average maximum increment of SBP occurred between 5 and 7 days and was 16.2 \( \pm \) 2.8 mm Hg; this value was significantly higher than that in the Ade-CMV-eGFP group (4.7 \( \pm \) 2.9 mm Hg; \( P < 0.05 \)). In contrast, HR was significantly decreased, whereas sBRG did not change 5 to 7 days after viral transduction in the Ade-CMV-JAM-1 group (7 days after viral transduction: HR, 311 \( \pm \) 8 bpm, \( P < 0.01 \); sBRG, \(-2.34 \pm 0.27 \) bpm/mm Hg, \( P \) value not significant; Figure 5).}

**Comparison of Levels of JAM-3, ICAM-1, and Vascular Cell Adhesion Molecule-1 Gene Expression in the NTS of WKY Rats and SHRs**

With the heightened mRNA of JAM-1 in the NTS of the SHRs, we ascertained the specificity of the differential expression by comparing it with other vascular adhesion molecules. However, in both young and adult WKY rats and SHRs, there were no differences in the level of JAM-3, ICAM-1, and vascular cell adhesion molecule-1 gene expression in the NTS (see the data supplement), suggesting that the upregulation of JAM-1 in the SHR was specific.

**Immunocytochemical Evidence for JAM-1 Presence in the NTS of SHRs and WKY Rats**

Although in the commissural NTS some JAM-1 immunoreactivity was detectable in WKY rats, it was clearly lower compared with the SHRs in all 6 of the rats studied (compare Figure 4A with 4B). Moreover, in the SHRs but not WKY rats, JAM-1 was extensively colocalized with RECA-1, a marker for endothelial cells consistent with JAM-1 expression in endothelium (Figure 4C).

**Figure 1.** Endogenous JAM-1 gene expression in various brain regions of SHRs and WKY rats. JAM-1 3’UTR-containing transcript (nucleotides 1145 to 1385 in GeneBank entry BC065309) was highly expressed in the supraoptic nuclei (SON), paraventricular nuclei (PVN), rostral ventrolateral medulla (RVLM), cerebellum, and cerebral cortex of SHR. In contrast, JAM-1/1145 to 1385 expression was observed only in the PVN and cerebral cortex of WKY, but the level of expression was lower than that in SHR. Note nonspecific bands in samples from SON of WKY rats.

**Figure 2.** Comparison of endogenous JAM-1 gene expression in different organs of SHR and WKY rats. JAM-1 3’UTR-containing transcript (nucleotides 1145 to 1385) was highly expressed in the liver, lung, kidney, spleen, skeletal muscle (s. muscle), and heart of SHRs, whereas in WKY rats the level of expression was lower and could be clearly detected in only lung, kidney, spleen, and skeletal muscle.
Location of NTS Sites Transduced With Ad-CMV-JAM-1 and AdV-CMV-eGFP

JAM-1 immunoreactivity was elevated after Ad-CMV-JAM-1 transduction compared with endogenous JAM-1 immunoreactivity (Figure 4). Numerous NTS cells including glia and blood vessels were immunopositive for JAM-1 on day 7 of posttransduction (Figure 4). In contrast, JAM-1 immunoreactivity in Ad-CMV-eGFP rats (data not shown) was equivalent to control (naïve rats) as depicted in Figure 4A. Moreover, based on the localization of JAM-1 immunoreactivity and eGFP expression, highly comparable NTS regions were transduced with both viruses. These regions spanned $-13.8$ to $-14.6$ mm relative to Bregma (ie, 400 μm rostral and caudal to calamus scriptorius), 300 to 800 μm from midline and 400 to 800 μm below the dorsal surface of the medulla.

Discussion

We have demonstrated that expression of JAM-1 mRNA is elevated in multiple organs in the SHR compared with WKY rat. In the brain stem (as exemplified in the NTS) JAM-1 protein is localized in endothelial cells, and the level of expression is higher quantitatively in the SHR compared with WKY rats. To
assess the functional consequence of heightened JAM-1 expression in the NTS, we used an adenovirus to chronically overexpress JAM-1 in this brain stem structure of normotensive WKY rats and found that this produces hypertension, consistent with a prohypertensive role of JAM-1.

JAM-1 Expression: SHRs Versus WKY Rats

With regard to the JAM-1/1145 to 1385 transcript, we found that the level of this transcript in WKY varied between organs, whereas it was present in all of the organs analyzed in the SHR. Regarding the NTS, JAM-1/1145 to 1385 transcript was not detectable in WKY rats, whereas it was clearly present in the SHR. This indicates that, in the SHR, JAM-1 mRNA is spliced differently to WKY rats. In the NTS (and other brain areas studied), it appears to have an extended 3’ UTR, a known feature present on many translationally efficient mRNAs. Alternatively, it is possible that the WKY transcripts lack 5’ UTR because of differences in the transcription termination mechanism. When primers for the protein-coding part of JAM-1 mRNA were used (JAM-1/430 to 652), the transcript could be clearly identified in the NTS of WKY rats, although the level of expression was much lower than that of SHRs (see Figure 3). These results suggest that in normotensive WKY rats, a significant fraction of JAM-1 mRNA lacks 3’ UTR sequences, annotated in GeneBank BC065309 entry, making it unstable and effectively reducing the amount of JAM-1 mRNA available for protein expression. Furthermore, processing of JAM-1 mRNA is shifted toward the 3’ UTR-containing transcript in many brain regions and bodily organs in the SHR compared with the WKY rat. JAM-1 is one of the proteins that forms the tight junction in both endothelial cells and some types of epithelial cells. Our immunocytochemistry data demonstrated that JAM-1 protein in the brain stem (as exemplified in NTS) is abundantly expressed in endothelial cells where the level of expression is higher in SHRs compared with WKY rats. Importantly, JAM-1 expression in the SHR is not secondary to hypertension, because prehypertensive SHRs also showed a high level of JAM-1 gene expression, at least in NTS.

Under certain conditions endothelial JAM-1 shows a transmembrane luminal orientation thereby protruding into the bloodstream. With its leukocyte binding site (via a leukocyte function-associated antigen-1), JAM-1 is known to cause leukocyte adhesion. In addition, JAM-1 can activate platelet aggregation. In this context, it is curious that leukocyte adhesion and platelet aggregability are enhanced in both the SHRs and humans with essential hypertension. All of these abnormalities can cause accumulation of these cells leading to release of inflammatory mediators, atherosclerosis, and athero-

**Figure 5.** JAM-1 overexpression in the NTS of WKY rats raises arterial pressure. Five days after NTS injection of Ad-CMV-JAM-1, SBP was elevated significantly in WKY rats. This remained above control levels for the 14-day observation period. HR was transiently decreased, whereas sBRG was unaffected. In the Ade-CMV-eGFP group, all of these parameters were unaffected by viral transduction except for HR on day 5. *P < 0.05, **P < 0.01, and ***P < 0.001 compared before and after Ad-CMV-JAM-1 transduction. ##P < 0.01 compared before and after Ad-CMV-eGFP transduction. $P < 0.05 compared with Ad-CMV-eGFP transduction.
Possible Mechanisms by Which JAM-1 in NTS Elevates Arterial Pressure

Our findings show that high level of JAM-1 expression at the level of NTS can cause hypertension in WKY rats. The question of how this arises comes about. We have recently described that adenoviruses with the human CMV promoter drive extremely low levels of gene expression in most NTS neurons. On the other hand, these vectors clearly transduce local vasculature. Based on evidence that JAM-1 can cause leukocyte and platelet adhesion in the peripheral circulation, it was necessary to assess whether this could occur within the brain after inducing JAM-1 overexpression. The data that we present suggest that, at least in NTS, JAM-1 can induce leukocyte binding (see the data supplement). It remains unclear what, if any, effect this would have on NTS neurons impinging on downstream neuronal networks controlling sympathetic activity. Nevertheless, these results raise the intriguing and novel possibility that there is a link between high levels of leukocyte/platelet adhesion in the brain stem and excessive levels of sympathetic nerve activity. Thus, once adhered to the endothelium, leukocytes (and platelets) release both cytokines and reactive oxygen species, such as superoxide. These are established products from such cells and are known to activate a sympathetic vasocmotor system with a general inflammatory reaction.

Perspectives

We have revealed that there is widespread JAM-1 expression in the SHR compared with the WKY rat. Increased JAM-1 protein expression in brain stem structure(s) regulating arterial pressure, such as the NTS, could contribute to hypertension. It remains to be established whether a similar scenario applies to other brain regions of the SHR, such as the circumventricular organs, hypothalamus, and rostral ventrolateral medulla, and also peripheral tissues, such as the kidney and heart, and how this may contribute to hypertension.

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Disclosures

None.
References


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Methods

Method for Immunohistochemistry

Animals (SHR, n=6; WKY, n=18; both strains were 15 to 18 weeks old) were humanely killed by cervical dislocation. The brainstem was removed, fixed with 4% paraformaldehyde for at least 24 h, and transferred to phosphate buffered saline (PBS) containing 30% sucrose. Serial sections (40 µm) through NTS were obtained using a freezing microtome. The sections were rinsed in PBS, put in 10% serum with 0.3% Triton X-100 for 15 minutes at room temperature, rinsed again and incubated with an JAM-1 antibody, sc-17427, (Santa Cruz Biotechnology, dilution: 1:200 in PBS with 1% serum and 0.3% Triton X-100). After overnight incubation at 4°C, the sections were rinsed in PBS and incubated with biotinylated horse anti-goat IgG (1:500 dilution, Vector Laboratories, UK) for 1 hour. The sections were rinsed and then incubated in streptavidin conjugated Alexa-Fluor 488 (1:500 dilution, Molecular Probes, USA) for 1 hour. Finally, sections received a PBS wash before mounting in Vectashield (Vector Laboratories). Sections were photographed using a Leica TCS-NT scanning laser confocal microscope. In order to determine the cell types expressing JAM-1, we used double labelling fluorescence immunohistochemistry with an endothelial cell marker (RecA1, Abcam plc, UK). A leukocyte marker - W3/25 anti-rat CD4 monoclonal antibody (kindly received from Dr S.M. Nicholls, Ophthalmology, Bristol Eye
Hospital, Bristol UK, dilution: 1:200 in PBS with 1% serum and 0.3% Triton X-100) was also used to identify leukocyte adhesion within the NTS of WKY and SHR (See Supplemental Data IV).

**Method for power spectral analysis of HR and SBP variability**

Power spectral analysis of SBP and HR variability was performed using a fast Fourier transform (FFT) algorithm as described by us recently\(^1\). The magnitude of power was integrated in the very low-frequency (VLF) band (0-0.27 Hz), the low-frequency (LF) band (0.27-0.75 Hz) and the high-frequency (HF) band (0.75–3.3 Hz)\(^1\). The HF power of HR variability, the ratio of LF to HF (LF:HF) of HR variability and the LF + VLF power of SBP variability were analyzed on the day before NTS microinjection of virus and on the 7\(^{th}\) day after microinjections. We assumed that the HF power of HR variability is mediated by cardiac parasympathetic tone whereas the LF:HF of HR variability is an index of cardiac sympathetic tone\(^2\). Similarly, the LF + VLF power of SBP variability is, in part, mediated by vasomotor sympathetic tone\(^3\).
References


**Legends**

**Figure S1.** Leukocyte marker (W3/25) shows leukocyte accumulation in the NTS capillaries of hypertensive rats demonstrating a high immune environment. Immunohistochemistry indicated endogenous leukocyte accumulation in the capillaries of the medulla including the NTS of SHR but not WKY rats (A). Following JAM-1 expression in WKY rats (which was normally devoid of leukocytes) leukocyte adhesion was evoked. Importantly, immunoreactivity for leukocytes was not found in control WKY in which adenovirus expressing eGFP had been injected previously (B). This suggested that the leukocyte adhesion was due to JAM-1 expression and not related to the presence of the adenovirus and is consistent with the leukocyte adhesion property of JAM-1.

**Figure S2.** Expression of JAM-1 at the level of the NTS alters autonomic cardiovascular activity.

Seven days post viral transduction with Ade-CMV-JAM-1 the LF + VLF power of SBP variability was significantly increased (from 7.32 ± 0.22 to 8.01 ± 0.29 mmHg², p<0.05) indicative of raised sympathetic activity. In contrast, no changes were found in this variable in WKY rats transduced with Ade-CMV-eGFP. Seven days post viral transduction with Ade-CMV-JAM-1 both the LF:HF and HF power of HR variability were significantly
increased (LF:HF of HR variability: from 0.25 ± 0.01 to 0.29 ± 0.02, p<0.05; HF power of HR variability: from 14.2 ± 0.9 to 19.6 ± 1.5 bpm², p<0.05). 

*p<0.05 compared before and after Ad-CMV-JAM-1 transduction. #p<0.05 compared before and after Ad-CMV-eGFP transduction.
**Table S1. Primer details used for quantitative RT-PCR**

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<th>Accretion No.</th>
<th>Primers/product details</th>
<th>Amplification size</th>
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<td></td>
<td>reverse: GTACTCCTGCTTGCTGATCCAC</td>
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*This set of primers was used with primers for VCAM-1 and ICAM-1*
Table S2. JAM-3, ICAM-1 and VCAM-1 gene expression (fold differences) in the NTS of WKY and SHR

<table>
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<th>SHR</th>
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<tr>
<td>ICAM-1</td>
<td>1.01±0.05 (n=10)</td>
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<td>VCAM-1</td>
<td>1.04±0.10(n=10)</td>
<td>1.19±0.09(n=10)</td>
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<tr>
<td>YOUNG</td>
<td></td>
<td></td>
</tr>
<tr>
<td>JAM-3</td>
<td>1.02±0.10(n=6)</td>
<td>1.06±0.06(n=5)</td>
</tr>
<tr>
<td>ICAM-1</td>
<td>1.02±0.10(n=6)</td>
<td>1.20±0.15(n=5)</td>
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<tr>
<td>VCAM-1</td>
<td>1.02±0.09(n=6)</td>
<td>0.89±0.07(n=5)</td>
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</table>

Expression of target genes relative to β-actin gene in each sample were derived using the comparative \(2^{-\Delta\Delta CT}\) method. Fold differences were calculated against the average of age-matched WKY. For JAM-3, ICAM-1 and VCAM-1 gene expression, no significant differences were found between WKY and SHR.
Figure S1
Figure S2