Reproducible Porcine Model of Thoracic Aortic Aneurysm

Shaina R. Eckhouse, MD; Christina B. Logdon, MVT; J. Marshall Oelsen, BS; Risha K. Patel, BS; Allison D. Rice, BS; Robert E. Stroud, MS; W. Benjamin Wince, MD; Rupak Mukherjee, PhD; Francis G. Spinale, MD, PhD; John S. Ikonomidis, MD, PhD; Jeffrey A. Jones, PhD

Background—Thoracic aortic aneurysms (TAAs) develop secondary to abnormal aortic extracellular matrix remodeling, resulting in a weakened and dilated aortic wall that progressed to rupture if left unattended. Currently, no diagnostic/prognostic tests are available for the detection of TAA disease. This is largely driven by the lack of a large animal model, which would permit longitudinal/mechanistic studies. Accordingly, the objective of the present study was to establish a reproducible porcine model of aortic dilatation, which recapitulates the structural and biochemical changes observed during human TAA development.

Methods and Results—Descending TAAs were induced in Yorkshire pigs (20–25 kg; n=7) through intra-adventitial injections of collagenase (5 mL, 0.35 mg/mL) and periadventitial application of crystalline CaCl₂ (0.5 g). Three weeks after TAA induction, aortas were harvested and tissue was collected for biochemical and histological measurements. A subset of animals underwent MRI preoperatively and at terminal surgery. Results were compared with sham-operated controls (n=6). Three weeks after TAA induction, aortic luminal area increased by 38±13% (P=0.018 versus control). Aortic structural changes included elastic lamellar degradation and decreased collagen content. The protein abundance of matrix metalloproteinases 3, 8, 9, and 12 increased in TAA tissue homogenates, whereas tissue inhibitors of metalloproteinases 1 and 4 decreased.

Conclusions—These data demonstrate aortic dilatation, aortic medial degeneration, and alterations in matrix metalloproteinase/tissue inhibitors of metalloproteinase abundance, consistent with TAA formation. This study establishes for the first time a large animal model of TAA that recapitulates the hallmarks of human disease and provides a reproducible test bed for examining diagnostic, prognostic, and therapeutic strategies.

Key Words: animal models ▪ aortic diseases ▪ aneurysm ▪ cardiovascular disease ▪ remodeling

A thoracic aortic aneurysm (TAA) is defined as a localized dilatation to a diameter >1.5x normal in the supradiaphragmatic aorta.¹⁻³ TAA development is influenced by a series of interrelated mechanisms that result in weakened aortic wall and gross dilatation progressing to rupture if left untreated.¹⁻⁴ Alarming, there are no diagnostic or prognostic tests currently available for detecting and tracking TAA disease. Typically, a TAA is diagnosed incidentally during a routine physical examination or during the workup of another medical issue.¹⁻³ Furthermore, current therapeutic options are limited to high-risk open surgical repair or endovascular stent grafting, which is often constrained by the anatomic location of the TAA and is associated with procedure- and device-related complications. Even with surgical treatment, these approaches do not directly target the underlying cellular and molecular mechanisms that drive TAA development.

TAA development is multifactorial and results in degeneration of the aortic wall structure and composition, in part because of extracellular matrix (ECM) remodeling. One mechanism that drives the pathological ECM remodeling process is the dysregulation of the matrix metalloproteinases (MMPs) and their endogenous tissue inhibitors of metalloproteinases (TIMPs).¹,³,⁸,¹⁰,¹¹ In the normal aorta, a stoichiometric balance exists between MMPs and TIMPs, keeping MMP activity tightly regulated. However, in TAA disease, this balance is disrupted, favoring increased proteolysis and leading to pathological remodeling of the aortic ECM. A second driving force in TAA development occurs because of alterations in the cellular constituents within the aortic wall. In clinical TAA specimens, infiltration of inflammatory cells, in combination with the apoptotic loss of smooth muscle cells, contributes significantly to changes in aortic structure and function.¹²⁻¹⁶
To further understand these changes and the mechanisms driving them, a murine model of TAA has been established, in which the application of CaCl$_2$ to the periadventitial surface of the descending thoracic aorta resulted in progressive aortic dilatation and aortic wall remodeling, recapitulating key hallmarks of human aneurysmal disease.$^{12-23}$ Importantly, this model of TAA demonstrated alterations in the protein abundance of MMPs and TIMPs, favoring pathological ECM remodeling and the emergence of a fibroblast-derived myofibroblast population concomitant with a loss of medial smooth muscle cells.$^{22,23}$ Although the murine model is advantageous for studying specific cellular and molecular mechanisms that influence TAA development, the physiological, anatomic, and functional differences of the mouse aorta limit the translation of these findings to human application. Thus, it is important to bridge the gap between the extensive work performed in murine models and direct clinical application in humans$^{24}$ through the development of a clinically relevant large animal model of TAA that will permit mechanistic and targeted therapeutic interventions. Therefore, the objective of the present study was to establish a reproducible porcine model of aortic dilatation, which recapitulates the structural and biochemical changes observed in clinical disease.

**Methods**

**Chronic Instrumentation**

Yorkshire pigs (n=7, castrated males; weight, 20–25 kg; HamBone Farms, Orangeburg, SC) underwent sedation with intramuscular ketamine (22 mg/kg), placement of an intravenous cannula in an ear vein, and endotracheal intubation followed by an initiation of mechanical ventilation. A stable plane of anesthesia was maintained with isoflurane (2%, 3 L/min O$_2$; Baxter Healthcare Corp, Deerfield, IL), and a maintenance infusion of intravenous fluids (10 mL/kg, lactated Ringers) was begun. A postero lateral left thoracotomy was performed based on the fourth intercostal space, and the proximal descending thoracic aorta was dissected from the surrounding tissue. The hemiayzygos vein and 2 to 3 sets of the cranial-most intercostal arteries were ligated and divided where appropriate, creating an ≈1 cm area of isolated descending thoracic aorta centered on a line passing through the apex of the heart. Low-dose type II bacterial collagenase (5 mL, 0.35 mg/mL in saline with 0.1 mol/L CaCl$_2$; Catalog No. LS004176, Worthington Biochemical Corp, Lakewood, NJ) was circumferentially injected intra- adventitially into the vascular wall of the isolated region. A piece of absorbable gelatin sponge (Gelfoam; Pharmacia Corp, Kalamazoo, MI) was cut to fit and positioned under the mobilized aortic region. Dry powdered CaCl$_2$ (0.5 g, 0.75 mol/L equivalent, Catalog No. C5080, Sigma-Aldrich Chemical Company, St. Louis, MO) was then circumferentially applied to the adventitial surface of the isolated segment of aorta. The Gelfoam was then wrapped around the aorta, enclosing the area of CaCl$_2$, application, to minimize irritation to the lung and heart. The chest was closed in layers, and the animals were allowed to recover. Results were compared with referent control animals (n=6) that did not receive collagenase injections or CaCl$_2$ powder. All animals were treated and cared for in accordance with the National Institutes of Health Guide for the Care and Use of Laboratory Animals (Revised, 1996), and all protocols were approved by the Medical University of South Carolina’s Institutional Animal Care and Use Committee.

**Aortic Tissue Harvest**

At the time of terminal surgery (n=6, 3 weeks after TAA induction), the animals were sedated (diazepam, 200 mg PO), and isoflurane anesthesia was induced (5%, 1.5 L/min O$_2$). A median sternotomy was performed, and the ascending, arch, and descending aorta were harvested. The treatment region was carefully excised and cut into segments that were subsequently used for histological and biochemical analysis.

**Aortic Histological Measurements**

Two independent tissue segments from each aorta (n=6 TAA, n=6 control; separated by ≈1.0 cm) were fixed in 10% formalin for 48 hours at 4°C, followed by 70% ethanol for 24 hours at 4°C. The pair of fixed tissue sections was then paraffin-embedded on end, and 5-µm-thick cross sections were cut and mounted on glass slides. The tissue sections were then deparaffinized and stained with hematoxylin and eosin (general structure), Verhoeff-Van Gieson (elastic architecture), and picrosirius red (collagen fibers). Microscopic images of aortic tissue sections were visualized on a Zeiss Axioskop 2 microscope (Carl Zeiss MicroImaging, Thornwood, NY) using a 63x/1.4 Plan-NEOFluAR objective and acquired using an Axioscam MRC color charge-coupled device camera connected to a computer running AxioVision (v4.7). All subsequent image analysis was performed using SigmaScanPro v5.0 (SPSS, Chicago, IL). Collagen and elastin content was determined from the digitized images as a percentage of total tissue area in a minimum of 5 random high-power fields from each aortic section for each pig using computer-assisted morphometric methods. The number of elastic lamellae was counted from Verhoeff-Van Gieson–stained sections.

Cellular constituents within the aortic media were identified and quantified using immunohistochemical techniques with antibodies that recognized cell type–specific marker proteins.$^{22}$ Tissue sections on slides were incubated in a citrate buffer for 30 minutes for antigen retrieval. The tissue sections were then incubated in blocking solution (3% BSA in Tris-buffered saline wash solution) for 2 hours at room temperature, followed by overnight incubation at 4°C with cell type–specific primary antibodies diluted in blocking solution. Cell type–specific antisera were used to identify the following: (1) fibroblasts (goat anti–discoidin domain receptor 2 [DDR2], 1:100; SC-7555; Santa Cruz Biotechnology, Santa Cruz, CA); (2) smooth muscle cells/myofibroblasts (rabbit anti–smooth muscle myosin heavy chain 2 [Myh11], 1:100; ab53219; Abcam, Cambridge, MA); (3) smooth muscle cells/myofibroblasts (rabbit anti–α-smooth muscle actin [α-SMA], 1:100; ab2547; Abcam); and (4) smooth muscle cells (rabbit anti-desmin, 1:20; DR8281; Sigma-Aldrich, St. Louis, MO). The slides were then washed with PBS and incubated in 3% H$_2$O$_2$/PBS for 30 minutes at room temperature to block endogenous peroxidase activity. The sections were then incubated with primary antibody species-specific peroxidase-conjugated species-appropriate secondary antibodies (VectaStain, Vector Laboratories, Burlingame, CA). Positive immune reactions were visualized by incubating the sections with 0.05% diaminobenzidine, which formed a brown precipitate on reaction with the peroxidase enzyme. Serial sections were used for negative controls and were processed in the same fashion but without the addition of the primary antisera. The number of positively stained cells was counted from a minimum of 5 digitized images of high-power fields from each aortic section for each pig.

To calculate the aortic luminal cross-sectional area, 4 sections from 2 separate aortic segments of the treatment region were digitized (8 total sections per animal). The luminal area was digitally filled in, and area measurements were made using a calibrated (1 cm²/1 cm² area) digital caliper. The measured aortic luminal area for each of the 8 sections was then averaged to calculate a mean aortic luminal area per aorta. A mean for each sample group, TAA group and control group, was then calculated, and the results were expressed as a percent change from control.

**MMP/TIMP Measurements**

**Immunoblotting**

Aortic tissue (n=6 TAA, n=6 control) was transferred to cold extraction/homogenization buffer (buffer volume 1:6 wt/vol) containing 10 mMmoldL cacodylic acid pH 5.0, 0.15 mol/L NaCl, 10 mMmoldL ZnCl$_2$, 1.5 mMmoldL Na$_2$EDTA, and 0.01% Triton X-100 (vol/vol) and homogenized using the Qiagen TissueLyser (Qiagen). The homogenate was...
centrifuged (800g, 10 minutes, 4°C), and 10 μg of the supernatant was loaded on a 4% to 12% bis-tris gradient gel and fractionated by electrophoresis. The proteins were then transferred to nitrocellulose membranes (0.45 μm, Bio-Rad) and incubated in anti-serum (MMP-1, MMP-3, MMP-7, MMP-8, MMP-12, MMP-13, MT1-MMP, TIMP-1, TIMP-2, TIMP-3, and TIMP-4; see online-only Data Supplement and Table I in the online-only Data Supplement for details) diluted in 5% nonfat dry milk/PBS. Species-specific secondary peroxidase-conjugated antibody was then applied (1:5000, 5% nonfat dry milk/PBS), and signals were detected with a chemiluminescent substrate (Western Lighting Chemiluminescence Reagent Plus; Perkin Elmer) and recorded on film. Band intensity was quantified using Gel-Pro Analyzer software (version 3.1.14, Media Cybernetics Inc, Silver Spring, MD) and reported as a percent change from unoperated reference control homogenates.

Gelatin Zymography

The relative abundance of MMP-2 and MMP-9 was assessed in aortic tissue homogenates (n=6 TAA, n=6 control) by gelatin zymography. Aortic homogenates (10 μg protein) were fractionated on a non-denaturing 10% polyacrylamide gel containing 0.1% (wt/vol) gelatin (Invitrogen Corporation, Carlsbad, CA). The gels were then equilibrated and incubated in zymogram developing buffer (Invitrogen) for 18 hours at 37°C. After staining with 0.5% Coomassie Brilliant Blue (2 hours, room temperature), the gels were destained to reveal regions of gelatin clearance. The relative abundance of MMP-2 (as verified by a recombinant MMP-2 standard) was then determined by densitometry using the Gel-Pro Analyzer software.

Computations and Data Analysis

Statistical analyses were performed using the STATA statistical software package (Statacorp version 8.2, College Station, TX). For each comparison, the distribution of continuous variables was tested using the Shapiro–Wilk normality test. All continuous variables were found to be normally distributed within each group. The values for luminal area, wall thickness, collagen-to-elastin ratio, the number of elastic lamellae, and the number of cells per high-power fields from histology sections (stained with DDR2, Myh11, desmin, and α-SMA) were compared between TAA and control animals using a 2-tailed, 2-sample mean comparison test. The percent change in relative protein abundance as determined by Western blotting was examined using a 2-tailed 1-sample mean comparison test versus control (normal aorta set to a value of 100). Pairwise correlation analysis was performed to examine the relationships between MMP and TIMP abundance versus aortic luminal area. All results are presented as means±SEM, and P<0.05 were considered statistically significant.

Results

Surgical induction of TAA was uneventful with minimal perioperative complications (Table II in the online-only Data Supplement). At 3 weeks after TAA induction, aortic dilatation was evident on gross examination. None of the TAA-induced animals experienced aortic rupture before terminal surgery. Dilatation started within the region of induction and would typically extend 1 to 2 cm beyond the distal-most point of the treatment region. Significant wall thinning was grossly observed in aortic cross sections in all TAA-induced animals versus referent controls (Figure 1A). Aortic luminal area, calculated from histological sections, increased by 38±13% (P=0.018) in TAA-induced animals compared with referent controls (intra-assay coefficient of variation [CV]: TAA=12.2%; control=12.2%; interassay CV: TAA=16.6%; control=3.1%; Figure 1B). To confirm aortic dilatation in vivo, the descending thoracic aorta was examined, and aortic diameter measurements were made using an MRI scanner (Siemens Magnetom Trio 3T, Germany). ECG-gated 2-dimensional dark-blood turbo spin-echo images, acquired during a single breath-hold in a ventilated animal, were obtained under physiological hemodynamic loading conditions in 1 animal before surgical induction of TAA and at 4 weeks after TAA induction. In this animal, aortic diameter was increased by 63.3% over the preinduction baseline value at 4 weeks after TAA induction (n=6) and compared with referent controls (n=6). Aortic diameter increased by 38±13% (P=0.018 vs control). MRI of the descending thoracic aorta before (top) and at 4 weeks after TAA induction (bottom). Short-axis views (left) and sagittal views (right) were recorded at 4 weeks after TAA induction. Aortic diameter was measured at the widest part of the aneurysm (17.8 mm) and demonstrated a 63.3% increase over preinduction baseline (10.9 mm), obtained in the same animal.
At the molecular level, the protein abundance of the ECM proteases (MMPs) and their endogenous inhibitors (TIMPs) was measured (Figure 4A–4C). The abundance of active MMP-2, MMP-3, MMP-8, MMP-9, MMP-12, and MT1-MMP was increased in TAA specimens versus referent controls, although no changes in MMP-1, MMP-7, or MMP-13 were observed. Conversely, the abundance of TIMP-1 and TIMP-4 was decreased compared with referent controls, whereas no changes in TIMP-2 or TIMP-3 were observed. Pairwise correlation analysis revealed direct significant relationships between aortic luminal area and active MMP-2 abundance ($r=0.6149; P=0.033$) or MT1-MMP abundance ($r=0.5696; P=0.053$). Furthermore, a trend toward an inverse relationship between aortic luminal area and TIMP-4 ($r=-0.5403; P=0.086$) was observed but failed to reach statistical significance. Immunoblotting revealed that no residual type II bacterial collagenase was detectable within the aortic tissue by the time of terminal study (Figure 4C).

**Discussion**

TAAs develop secondary to abnormal ECM remodeling, where alterations in the activity of MMPs and their endogenous inhibitors (TIMPs) favor increased proteolysis, facilitating aortic wall thinning and dilatation. Although numerous studies have been performed in wild-type and genetically modified murine models of TAA and in clinical specimens obtained at the time of surgical intervention, the lack of a large animal model of TAA has limited the ability to perform serial mechanistic (serum/plasma testing) and interventional (device) studies at key points during TAA formation and progression. Thus,
the objective of the present study was to establish a reproducible porcine model of aortic dilatation that progresses to TAA and to determine whether and to what degree the cellular and structural changes in the ECM would recapitulate the clinical disease phenotype. The unique findings of the present study were 2-fold. First, this experimental methodology resulted in the reproducible dilatation of the descending thoracic aorta within 3 weeks after TAA induction. Second, changes in aortic wall structure, cellular content, and protein abundance of MMPs and TIMPs in this porcine model were consistent with the hallmarks of clinical TAA disease. Therefore, this large animal model of aortic dilatation may provide a reproducible test bed in which the development of diagnostic, prognostic, and therapeutic strategies can be examined for this devastating disease.

TAAs form and progress through a multifactorial process involving both cellular and extracellular mechanisms. This process induces changes in the ECM composition and structure during a prolonged period of time and results in connective tissue degeneration and elastic fiber fragmentation within the aortic wall. Initiation and expansion of a descending TAA involve both hemodynamic factors, such as high blood pressure correlating to increased aortic wall tension and enhanced localized proteolysis within the aortic wall, leading to a weakening of the structural framework. Together, these changes result in reduced aortic resilience and compliance and enhance the propensity for catastrophic aortic rupture.

In the present study, the combination of intra-adventitial injections of low-dose type II bacterial collagenase and peri-adventitial exposure to CaCl₂ powder was used to induce experimental TAAs in swine. The study demonstrated that this treatment protocol reproducibly induced a process that resulted in the dilatation of the descending thoracic aorta, consistent with that of aneurysm formation. When aortic geometry was assessed, either by examination of aortic intraluminal area from histological sections (demonstrating an ≈40% increase in intraluminal area at 3-week post-TAA induction) or cross-sectional diameter at the widest part of the aneurysm measured by MRI (demonstrating an ≈60% increase in diameter at 4-week post-TAA-induction), both measurements confirmed significant aortic dilatation. This increase in dilatation was accompanied by significant thinning of the aortic wall, resulting from the fragmentation of elastin, and a decrease in the number of intact elastic lamellar units. Furthermore, in addition to the loss of elastin content, the ratio of collagen to the hallmarks of clinical TAA disease. Therefore, this large animal model of aortic dilatation may provide a reproducible test bed in which the development of diagnostic, prognostic, and therapeutic strategies can be examined for this devastating disease.

To date, no large animal model of TAA has been described. Conversely, several large animal models (rabbit, swine) have previously been developed for the study of abdominal aortic aneurysms. Although there have been variable results with regard to the amount of aortic dilatation achieved, porcine models of abdominal aortic aneurysms using pancreatic elastase have demonstrated collagen and elastic degradation, with an associated increase in MMP production. In a rabbit model of abdominal aortic aneurysms, adventitial application of CaCl₂ along with a high cholesterol diet and the induction of adventitial inflammation, caused a doubling of the aortic diameter in 3 weeks. However, because of the regional heterogeneity between the thoracic and abdominal aorta, great caution should be taken when interpreting results from experimental models of abdominal aortic aneurysms with regard to the thoracic aorta and TAA disease. Variations in embryonic cellular origin, atherosclerotic burden, degree of inflammatory infiltration, protease profiles, and vessel mechanics complicate direct comparisons. Thus, the present study built on...
these past experiences to develop a reproducible model of TAA in swine.

It is now widely accepted that changes in aortic vascular structure and geometry occur during TAA development and are mediated, in part, by alterations in the abundance of a family of ECM proteolytic enzymes, the MMPs, and their endogenous tissue inhibitors, the TIMPs. The TIMPs bind to the MMPs in a 1:1 stoichiometric ratio and inhibit MMP activity. Under normal conditions, MMP and TIMP abundance is balanced; however, in the presence of TAA, this balance is disrupted in favor of proteolysis. Previous studies, from our group and others, using clinical TAA specimens have demonstrated this imbalance, leading to enhanced proteolysis. For example, Wilson et al demonstrated that MMP-8 abundance was increased, whereas TIMP-1 abundance was decreased. Similarly, Koullias et al demonstrated that the ratio of MMP-9 to TIMP-1 abundance was increased in TAA versus control specimens, suggesting that the aneurysm was in an enhanced proteolytic state. The present study demonstrated a general increase in MMP abundance, which was accompanied by a general decrease in TIMP abundance. This suggests an overall shift in the stoichiometric balance between these key mediators, favoring a more proteolytic phenotype. Furthermore, significant relationships between aortic luminal area and the increase in MMP abundance (MMP-2 and MT1-MMP) were identified, and an inverse trend was identified in relation to the decrease in TIMP abundance (TIMP-4). Together, these data suggest that elevated proteolysis likely drives aneurysm development in this model.

Because the harvest of clinical TAA tissue specimens is restricted to the time of surgical intervention, information regarding mechanisms that contribute to TAA formation and progression has been severely limited. As such, in vivo studies have been confined to murine models of TAA in an effort to explore the mechanisms involved in the formation and progression of disease. With respect to TAA disease, the murine models replicate many of the structural and biochemical hallmarks seen in clinical specimens. For example, histological characterization of a murine model of TAA demonstrated a decrease in the number of lamellae within the aortic wall and progressive disruption of the elastic architecture with progressive dilatation and increased wall stiffness, as calculated by the ratio of total collagen area to total elastin. In addition to structural changes, murine models of TAA have provided evidence that changes in MMP and TIMP abundance occur concomitantly with the progression of TAA disease. Transgenic studies demonstrated the importance of several MMPs and TIMPs in the process of ECM proteolysis, leading to aortic dilatation. Specifically, in mice deficient for TIMP-1, TAA development was accelerated compared with wild-type animals, whereas in mice deficient for MMP-9, TAA development was attenuated. Importantly, studies of TAA progression in MMP-9 reporter mice demonstrated that MMP-9 gene promoter activation was localized to fibroblasts within the aortic wall, suggesting that fibroblast cell lineage may play an important role in TAA formation and progression. This was supported by a recent study demonstrating that, concurrent with the apoptotic loss of aortic smooth muscle cells, there was an increase in fibroblasts and fibroblast-derived cells after TAA induction. Cell type–specific marker measurements were made for fibroblasts (DDR2), smooth muscle cells (desmin), and myofibroblasts (α-SMA and Myh11) within aortic tissue sections after TAA induction. Interestingly, DDR2 and Myh11 concomitantly increased, whereas desmin decreased, and α-SMA remained unchanged. Taken together, these data suggested that, in addition to the geometric and structural changes induced during TAA development, dynamic changes in aortic cellular constituents also occur. These changes are characterized by the emergence of a fibroblast-derived myofibroblast population, positive for DDR2, Myh11, and α-SMA, concurrent with a decrease in desmin-positive aortic smooth muscle cells. Importantly, these alterations in the cellular constituents likely play an integral role in TAA formation and progression, by mediating changes in protease abundance and ECM protein production.

In the present study, the cellular constituents were measured in aortic tissue sections from pigs 3 weeks after TAA induction and demonstrated increased staining for DDR2 and Myh11, concomitant with decreased staining for desmin and α-SMA. These results suggested that the changes in aortic cellular constituents during TAA development in pigs may also be mediated, in part, by the formation of fibroblast-derived myofibroblasts, capable of directing the ECM remodeling process. Thus, this porcine model of TAA may be useful in further elucidating the mechanisms of cellular phenotype change and the role of fibroblast-derived cells in mediating aneurysm formation and progression.

The present study is not without limitations. First, because of the lack of a reproducible noninvasive method for measuring aortic diameter at baseline (before surgical TAA induction), a referent control group was used to establish normal intraluminal areas, as well as biochemical outcomes. Second, the change in aortic intraluminal area was measured at 3 weeks after TAA induction on fixed histological sections. These measurements may actually under-represent the change in maximal aortic diameter observed after TAA induction. The use of MRI provides a high-resolution method for anatomic measurements in live animals. When used in this study, MRI demonstrated that aortic dilatation increased by >60% at 4 weeks after TAA induction compared with baseline measurements obtained from the same animal before TAA induction. Third, because aortic measurements were obtained after terminal surgery at a single time point after TAA induction (3 weeks), whether and to what degree aortic dilatation progresses over time remain to be determined and will be addressed in future studies. Fourth, as previously identified in the mouse TAA model, CaCl2 can induce significant lung injury. To improve on previous methods, dry CaCl2 powder (0.75 mol/L equivalent) was applied to the periadventitial surface of the thoracic aorta and wrapped in gel foam to segregate the CaCl2-treated aorta from the lungs. Although at terminal procedure it was identified that the left lung was strongly adherent to the operative region, no lung necrosis or other gross changes were noted. All animals within the present study remained normoxic throughout the time course of the study as measured by pulse oximetry (data not shown). Finally, although significant relationships exist between aortic size and changes in MMP/TIMP abundance,
causality cannot be assumed; future studies intervening in the proteolytic pathway will be required.

These limitations notwithstanding, the present study demonstrated the creation of a novel and reproducible model of TAA development in swine, which recapitulates the structural, histological, and biochemical changes attributed to human TAA disease. The use of this model will be highly valuable for device and serial blood testing and may provide insight into potential new diagnostic, prognostic, and therapeutic approaches for this serious disease.

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