Genes Associated with Thoracic Aortic Aneurysm and Dissection: 2019 Update and Clinical Implications

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Introduction

This review presents an annual update to the article “Genes Associated with Thoracic Aortic Aneurysm and Dissection: Update and Clinical Implications” originally published in 2017 and updated in 2018 in AORTA.1,2 We have updated the list of genes with identified genetic variants predisposing individuals to a thoracic aortic aneurysm or dissection (TAAD) in ►Table 1, and the recommendation for individualized surgical interventions for specific genetic mutations is presented in ►Fig. 1.

Thoracic aortic aneurysm (TAA) affects 1% of the general population3 and its natural history is to enlarge an average of 0.14 cm per year.4 Prior to often lethal dissection or rupture, TAs are usually asymptomatic. However, if identified and treated with appropriate blood pressure control and surgical intervention, life expectancy is improved.

Report of inherited TAAD in the 1990s5 has led to the discovery and understanding of genetic and molecular mechanisms of TAAD.6 To date, variants in 37 genes have been associated with TAAD (►Table 1; ►Fig. 1). These genes explain approximately 30% of the familial nonsyndromic

Thoracic aortic aneurysm is a typically silent disease characterized by a lethal natural history. Since the discovery of the familial nature of thoracic aortic aneurysm and dissection (TAAD) almost 2 decades ago, our understanding of the genetics of this disorder has undergone a transformative amplification. To date, at least 37 TAAD-causing genes have been identified and an estimated 30% of the patients with familial nonsyndromic TAAD harbor a pathogenic mutation in one of these genes. In this review, we present our yearly update summarizing the genes associated with TAAD and the ensuing clinical implications for surgical intervention. Molecular genetics will continue to bolster this burgeoning catalog of culprit genes, enabling the provision of personalized aortic care.

Abstract

Thoracic aortic aneurysm is a typically silent disease characterized by a lethal natural history. Since the discovery of the familial nature of thoracic aortic aneurysm and dissection (TAAD) almost 2 decades ago, our understanding of the genetics of this disorder has undergone a transformative amplification. To date, at least 37 TAAD-causing genes have been identified and an estimated 30% of the patients with familial nonsyndromic TAAD harbor a pathogenic mutation in one of these genes. In this review, we present our yearly update summarizing the genes associated with TAAD and the ensuing clinical implications for surgical intervention. Molecular genetics will continue to bolster this burgeoning catalog of culprit genes, enabling the provision of personalized aortic care.

Keywords

► genetics
► thoracic aortic aneurysm
► aortic dissection

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<tr>
<td>ACTA2</td>
<td>Smooth muscle α-actin</td>
<td>Yes20</td>
<td>+</td>
<td>+</td>
<td>AA1T + multisystemic smooth muscle dysfunction + MYH5</td>
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<td>4.5-5.012,25</td>
<td>AD</td>
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<tr>
<td>ARH1</td>
<td>Ariadne RBR E3 ubiquitin protein ligase 153</td>
<td>No</td>
<td>+</td>
<td>+</td>
<td>FTA1</td>
<td>Aortic and intracranial aneurysm15</td>
<td>Standard</td>
<td>Unknown</td>
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<td>BGN</td>
<td>Biglycan</td>
<td>Yes26</td>
<td>+</td>
<td>–</td>
<td>Meester-Loeys syndrome</td>
<td>ARD, TAAD, pulmonary artery aneurysm, IA, arterial tortuosity27</td>
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<td>COL1A2</td>
<td>Collagen 1 α2 chain</td>
<td>No</td>
<td>+</td>
<td>–</td>
<td>EDS, arthrochalasia Type (VIIb) + cardiac valvular type</td>
<td>Borderline aortic root enlargement22,28</td>
<td>Standard</td>
<td>AD + AR</td>
<td>130060 225320</td>
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<tr>
<td>COL5A1</td>
<td>Collagen 5 α1 chain</td>
<td>Yes29,30</td>
<td>+</td>
<td>–</td>
<td>EDS, vascular Type (IV)</td>
<td>TAAD, early aortic dissection1, visceral arterial dissection, vessel fragility, IA1,31</td>
<td>5.0-32</td>
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<td>COL5A2</td>
<td>Collagen 5 α2 chain</td>
<td>No27</td>
<td>+</td>
<td>–</td>
<td>EDS, classic Type I</td>
<td>ARD, rupture/dissection of medium-sized arteries33-36</td>
<td>Standard</td>
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<td>EMILIN1</td>
<td>Elastin microfibril interfacer 1</td>
<td>No</td>
<td>+</td>
<td>–</td>
<td>CTD and peripheral neuropathy</td>
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<td>FBN1</td>
<td>Fibrillin-1</td>
<td>Yes35-40</td>
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<td>+</td>
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<td>5.025,51</td>
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<td>FN1A</td>
<td>Filamin A</td>
<td>Yes33.54</td>
<td>+</td>
<td>–</td>
<td>Periventricular nodular heterotopia and otopalatal-todigital syndrome</td>
<td>Aortic dilatation/aneurysms, peripheral arterial dilatation,55 PDA, IA,56 BAV</td>
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<td>FOXE3</td>
<td>Forkhead box 3</td>
<td>Yes67</td>
<td>–</td>
<td>+</td>
<td>AA1T1</td>
<td>TAAD (primarily Type A dissection)32</td>
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<td>HCN4</td>
<td>Hyperpolarization-activated cyclic nucleotide-gated potassium channel 4</td>
<td>No</td>
<td>–</td>
<td>+</td>
<td>Noncompaction cardiomyopathy, bradycardia, and mitral valve disease</td>
<td>Ascending aortic dilation18</td>
<td>Standard</td>
<td>AD</td>
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<td>LOX</td>
<td>lysyl oxidase</td>
<td>Yes39-62</td>
<td>–</td>
<td>+</td>
<td>AA1T0</td>
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<td>LTBPII</td>
<td>Latent TGF-β binding protein</td>
<td>No3,10</td>
<td>+</td>
<td>–</td>
<td>Aortic dilatation with associated musculoskeletal findings</td>
<td>TAAD13</td>
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<td>Yes6,32</td>
<td>+</td>
<td>–</td>
<td>Dental anomalies and short stature</td>
<td>TAAD, AAA, visceral and peripheral arterial aneurysms14</td>
<td>Standard</td>
<td>AR</td>
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<td>MAT2A</td>
<td>Methionine adenosyltransferase II α</td>
<td>No163</td>
<td>–</td>
<td>+</td>
<td>FTA1</td>
<td>Thoracic aortic aneurysms, BAV63</td>
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<td>MFAP5</td>
<td>Microfibril-associated glycoprotein 2</td>
<td>Partially5,64</td>
<td>–</td>
<td>+</td>
<td>AA1T9</td>
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<td>Associated clinical characteristics of the vasculature</td>
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<td>–</td>
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<td>AAT4</td>
<td>TAAD, early aortic dissection, PDA, CAD, peripheral vascular occlusive disease, carbid IA</td>
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<td>–</td>
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<td>PRAG1</td>
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<td>–</td>
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<td>ROR2D4</td>
<td>Roundabout guidance receptor 4</td>
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<td>–</td>
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<td>SLC2A10</td>
<td>Glucose transporter 10</td>
<td>No</td>
<td>–</td>
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<td>SMAD2</td>
<td>No</td>
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<td>SMAD3</td>
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<td>LDS Type III</td>
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<td>SMAD4</td>
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<td>TIMP3</td>
<td>Tissue inhibitors of matrix metalloproteinase 3</td>
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<td>BAV/TAAD</td>
<td>Standard</td>
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<td>TIMP1</td>
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<td>–</td>
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<td>TGFβ2</td>
<td>TGF-β2</td>
<td>Yes</td>
<td>+</td>
<td>+</td>
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<td>TGFβ3</td>
<td>TGF-β3</td>
<td>No</td>
<td>+</td>
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<td>LDS Type V</td>
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<td>TGFβR1</td>
<td>TGF-β receptor type I</td>
<td>Yes</td>
<td>+</td>
<td>+</td>
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<td>4.0–4.5, 51, 39</td>
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Abbreviations: AAA, abdominal aortic aneurysm; AAT, aortic aneurysm, familial thoracic; AD, autosomal dominant; AOV, aortic valve disease; AR, autosomal recessive; ARD, aortic root dilatation; AVM, arteriovenous malformation; BAV, bicuspid aortic valve; CAD, coronary artery disease; CTD, connective tissue disease; CVD, cerebrovascular disease; EDS, Ehlers-Danlos syndrome; FTAAD, familial thoracic aortic aneurysm; FTAA, familial thoracic aortic aneurysm and/or dissection; HHT, hereditary hemorrhagic telangiectasia; IA, intracranial aneurysm; JP, juvenile polyposis; LDS, Loes-Dietz syndrome; MYMY, moyamoya disease; OMIM, Online Mendelian Inheritance in Man; PDA, patent ductus arteriosus; SVAS, supravalvular aortic stenosis; TGF, transforming growth factor; TAAD, thoracic aortic aneurysm and/or dissection; TGFB, TGF-β receptor; XL, X-linked dominant.
Note: It is important to note that since mutations in many of these genes are rare and have only recently been implicated in TAAD, there is a lack of adequate prospective clinical studies. Therefore, it is difficult to establish threshold diameters for the intervention of TAAs, and each individual must be considered on a case by case basis, taking into account the rate of change in aneurysm size (>0.5 cm per year is considered rapid), any family history of aortic dissection at diameters <5.0 cm, and the presence of significant aortic regurgitation, which are all indications for early repair if present; A + symbol in the syndromic TAAD column indicates that mutations in the gene have been found in patients with syndromic TAAD (same for the nonsyndromic TAAD column). A − symbol in the syndromic TAAD column indicates that mutations in the gene have not been found in patients with syndromic TAAD (same for the nonsyndromic TAAD column); A reference is provided for each of the associated vascular characteristics not reported in the OMIM entry for that gene.

Standard = surgical intervention at 5.0–5.5 cm; Early aortic dissection = dissection at aortic diameters <5.0 cm.

Individuals with MYLK and ACTA2 mutations have been shown to have aortic dissections at a diameter of 4.0 cm.23,68 There are no data to set threshold diameters for surgical intervention for EDS Type IV.31 The Canadian guidelines recommend surgery for aortic root sizes of 4.0–5.0 cm and ascending aorta sizes of 4.2–5.0 cm, though these patients are at high risk of surgical complications due to poor quality vascular tissue.92 There are limited data concerning the timing of surgical intervention for LDS Type IV. However, there has been a case of a Type A aortic dissection at an aortic diameter <5.0 cm,87 hence the recommended threshold range of 4.5–5.0 cm.

Current U.S. guidelines recommend prophylactic surgery for LDS Types I and II at ascending aortic diameters of 4.0–4.2 cm.25,51 However, the European guidelines state that more clinical data are required.33 Patients with TGFBR2 mutations have similar outcomes to patients with FBN1 mutations once their disease is diagnosed,93 and the clinical course of LDS 1 and 2 does not appear to be as severe as originally reported.91,94,95 Therefore, medically treated adult patients with LDS 1 or 2 may not require prophylactic surgery at ascending aortic diameters of 4.0–4.2 cm.21 Individuals with TGFBR2 mutations are more likely to have aortic dissections at diameters <5.0 cm than those with TGFBR1 mutations.91,95 A more nuanced approach proposed by Jondeau et al utilizing the presence of TGFBR2 mutations (vs. TGFBR1 mutations), the co-occurrence of severe systemic features (arterial tortuosity, hypertelorism, wide scarring), female gender, low body surface area, and a family history of dissection or rapid aortic root enlargement, which are all risk factors for aortic dissection, may be beneficial for LDS 1 and 2 patients to avoid unnecessary surgery at small aortic diameters.91 Therefore, in LDS 1 or 2 individuals without the above features, Jondeau et al maintain that 4.5 cm may be an appropriate threshold, but females with TGFBR2 mutations and severe systemic features may benefit from surgery at 4.0 cm.91

Wenstrup et al found that mice heterozygous for an inactivating mutation in Col5a1 exhibit decreased aortic compliance and tensile strength compared with wild type mice.96 In an earlier paper, Park et al illustrated that mice heterozygous for a null allele in Col5a2 exhibited increased aortic compliance and reduced tensile strength compared with wild type mice.97

Todorovic et al showed that LTBP1 plays an important role in cardiac and bone development. Knockout mice displayed interrupted aortic arch, patent truncus arteriosus, hyperplastic semilunar valves, and atrial septal defects. However, aortic measurements were not reported.10

Guo et al showed that the knockout mice have larger aortic roots and ascending aortas than wild type, however, no aneurysms or dissections were reported.10

Guo et al found that the knockdown of MAT2AA in zebrafish led to defective aortic arch development.93

Combs et al demonstrated that MAFAP2 and MAFAP5 double knockout (MAFAP2 −/−; MAFAP5 −/−) mice exhibit age-dependent aortic dilation, though this is not the case with MAFAP5 single knockout mice.98

Koenig et al recently found that Notch1 haploinsufficiency exacerbates the aneurysmal aortic root dilation in a mouse model of MFS and that Notch1 heterozygous mice exhibited aortic root dilation, abnormal smooth muscle cell morphology, and reduced elastic laminae.100

Doyle et al found that knockdown of paralogs of mammalian SKI in zebrafish led to craniofacial and cardiac anomalies, including failure of cardiac looping and malformations of the outflow tract.101

Tan et al demonstrated that SMAD3 knockout mice only have developed aortic aneurysms with angiotensin II-induced vascular inflammation, though the knockout mice did have medial dissections evident on histological analysis of their aortas and exhibited aortic dilation relative to wild type mice prior to angiotensin II infusion.78

Cavallaro et al demonstrated that Madh6, which encodes SMAD6, mutant mice exhibited defects in cardiac valve formation, outflow tract septation, vascular tone, and ossification but no aneurysm development was observed.104

Gahlin et al showed that Mdx mice exhibited defects in cardiac valve formation, outflow tract septation, vascular tone, and ossification but no aneurysm development was observed.104

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TAAD. These genes encode proteins of the extracellular matrix, vascular smooth muscle cell contractile unit, or transforming growth factor β (TGF-β)-signaling pathways and thus are essential to the structure and maintenance of the aortic wall.

During 2018, several important studies were published that have enhanced our understanding of the pathogenesis of TAAD. Gould et al performed whole-exome sequencing (WES) and targeted sequencing on 736 individuals with bicuspid aortic valve (BAV), non-syndromic ascending aortic aneurysm (AscAA), and 376 controls. In 13 (1.8%) of the affected individuals a heterozygous ROBO4 mutation was identified, including two variants that segregated with disease among two affected families. ROBO4 is well expressed in vascular endothelial cells and plays a role in endothelial barrier function. In this study, its expression was found to be diminished in the resected aorta sample of an affected individual with AscAA. To further test their hypothesis that ROBO4 variants lead to the disruption of endothelial performance at a cellular level, thus altering vascular permeability, the authors cultured human aortic endothelial cells and either silenced ROBO4 or expressed ROBO4 variants. They confirmed that ROBO4 abnormalities did indeed induce endothelial barrier dysfunction. Lastly, the authors created homozygous ROBO4 knockout mice and a knock-in mouse with an ROBO4 splice donor site mutation; the affected mice presented with a mix of aortic valve dysfunction (BAV and/or aortic regurgitation or stenosis) and AscAA, confirming their suspicion that a heterozygous mutation in ROBO4 can lead to a nonsyndromic presentation of BAV/AscAA.

Latent transforming growth factor binding proteins (LTBP), a family of extracellular matrix glycoproteins, have been shown to play a significant role in TGF-β regulation. LTBP1, in particular, can bind to fibrillin-1 and inactivate TGF-β. Quiñones-Pérez et al described a case series involving a three-generation family with TAA found to have a chromosome 2p22.3-p22.2 deletion involving LTBP1, amongst other genes. Despite multiple genes being involved in the deletion, LTBP1 was considered the likely culprit given its relationship to TGF-β. In addition to TAA, the affected individuals displayed additional features of Marfan syndrome (MFS) and Loeys-Dietz syndrome, even though none of them met the criteria for diagnosis.

Mutations of the latent TGF-β binding protein-3 (LTBP3) gene have been associated with TAAD in a WES study of 271 individuals from unrelated families with heritable thoracic aortic disease (multiple affected family members) without a known genetic etiology for aortopathy. In this study, compound heterozygous variants in one family and a homozygous insertion/deletion variant in LTBP3 in a second family were identified. Sequencing of 338 additional individuals with non-syndromic TAAD found nine additional heterozygous LTBP3 rare variants. The authors also demonstrated that LTBP3 knockout mice manifested enlarged aortic roots and ascending aortas compared with wild type mice. These findings demonstrate that individuals with LTBP3 are at increased risk for TAAD, in addition to the already established risk for skeletal and dental abnormalities.

Rare mutations in the Parkin-like E3 ubiquitin ligase Ariadne-1 (ARHI) have been observed in patients with early-onset or familial TAAD. ARHI encodes a protein of the LINC (linker of nucleoskeleton and cytoskeleton), a protein complex essential for anchoring myocyte nuclei to the cytoskeleton. Aortic tissues from patients with these mutations exhibit affected nuclear morphology in vascular smooth muscle cells.
It is well known there is an increased risk for BAV and TAA among individuals with Turner syndrome, although the precise etiology has thus far remained elusive. Corbitt et al. demonstrated that Turner syndrome patients with putatively-deleterious mutations in \textit{TIMP3} are associated with a greater incidence of BAV and TAA than the patients without \textit{TIMP3} variants. Hemizygosity for coincident \textit{TIMP1/ TIMP3} variants, synergistically increased the risk for BAV and TAA, due to \textit{TIMP1}'s functional redundancy with \textit{TIMP3}.

Numerous mutations of the myosin light chain kinase (\textit{MYLK}) gene have been associated with TAAD. Shalata et al. have identified an additional \textit{MYLK} missense mutation in a single pedigree. Myosin light chain kinase phosphoralytes myosin regulatory light chains to facilitate actin-myosin generation of contraction. The mutation was shown to be functional, reducing kinase activity.

Insights to the pathogenesis of TAAD are as important as identifying TAAD variants. Nogi et al. found the protein expression of small GTP-binding protein GDP dissociation stimulator (SmgGDS) in aortic smooth muscle cells was decreased in TAAD patients compared with controls. SmgGDS is encoded by the \textit{RAP1GDS1} gene and known to be involved in the contraction of vascular smooth muscle cell (VSMC). Using a heterozygous SmgGDS\textsuperscript{+/−} mouse model, since the complete knockout (SmgGDS\textsuperscript{−/−}) was embryonically lethal, they observed that the downregulation of SmgGDS was causing "pathological phenotype changes in VSMC" via the angiotensin-II pathway. Furthermore, they demonstrated that when SmgGDS was overexpressed in the SmgGDS\textsuperscript{−/+}, the mice had less aortic growth and fewer aortic ruptures, suggesting that SmgGDS could be used as a biomarker or a therapeutic agent.

\textbf{Conclusion}

Advances in 2018 have increased our understanding of the pathogenesis of TAAD. The number of genes with genetic variants or mutations associated with TAAD has increased from 29 in our original 2017 report to 37 in this 2019 update. Advances in genetic techniques and bioinformatics tools have enabled rapid progress in the genetic and molecular understanding of TAA. As the cost for genome sequencing decreases, we anticipate accelerating progress. We will continue to report annual updates regarding the "TAA genetic dictionary" with updates to the Table and Figure below and provide suggested surgical intervention criteria for each identified mutation.

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\textbf{Conflict of Interest}

The authors declare no conflict of interest related to this article.

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