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. 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 population and its natural history is to enlarge an average of 0.14 cm per year. 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 1990s has led to the discovery and understanding of genetic and molecular mechanisms of TAAD. To date, variants in 37 genes have been associated with TAAD (Table 1; Fig. 1). These genes explain approximately 30% of the familial nonsyndromic

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
Table 1  Genes associated with syndromic and nonsyndromic thoracic aortic aneurysm and/or dissection, associated vascular characteristics, and size criteria for elective surgical intervention (any gene newly reported during the past year to be associated with TAAD is highlighted in red)

<table>
<thead>
<tr>
<th>Gene</th>
<th>Protein Description</th>
<th>Mode of inheritance</th>
<th>Animal model for vascular phenotype?</th>
<th>Gene Protein Animal model leading to vascular phenotype?</th>
<th>Associated clinical characteristics of the vasculature</th>
<th>Ascending aorta size (cm) for surgical intervention</th>
</tr>
</thead>
<tbody>
<tr>
<td>ACTA2</td>
<td>Smooth muscle α-actin</td>
<td>AD</td>
<td>Yes</td>
<td>AAT6</td>
<td>Multisystemic smooth muscle dysfunction</td>
<td>4.5–5.0</td>
</tr>
<tr>
<td>COL5A1</td>
<td>Collagen 5 α1 chain</td>
<td>No</td>
<td>Yes</td>
<td>COL5A1</td>
<td>Marfan syndrome, classic Type I</td>
<td>5.0–5.5</td>
</tr>
<tr>
<td>COL5A2</td>
<td>Collagen 5 α2 chain</td>
<td>Partially f</td>
<td>No</td>
<td>FBN1</td>
<td>Marfan syndrome, classic Type II</td>
<td>5.0–5.5</td>
</tr>
<tr>
<td>COL5A3</td>
<td>Elastic microfibril interfascicule 1</td>
<td>No</td>
<td>Partially k</td>
<td>COL5A3</td>
<td>Marfan syndrome, classical Type I</td>
<td>5.0–5.5</td>
</tr>
<tr>
<td>LTBPI</td>
<td>Latent TGF-β binding protein 1</td>
<td>No</td>
<td>Partially n</td>
<td>LTBPI</td>
<td>Marfan syndrome, classical Type II</td>
<td>5.0–5.5</td>
</tr>
<tr>
<td>LTBPI2</td>
<td>Latent TGF-β binding protein 2</td>
<td>No</td>
<td>Partially m</td>
<td>LTBPI2</td>
<td>Marfan syndrome, classical Type II</td>
<td>5.0–5.5</td>
</tr>
<tr>
<td>MAS2A</td>
<td>Methionine adenosyltransferase II α</td>
<td>No</td>
<td>Partially l</td>
<td>MAS2A</td>
<td>Marfan syndrome, classical Type II</td>
<td>5.0–5.5</td>
</tr>
<tr>
<td>MRP5</td>
<td>Macrophage-associated glycoprotein 2</td>
<td>No</td>
<td>Partially j</td>
<td>MRP5</td>
<td>Marfan syndrome, classical Type II</td>
<td>5.0–5.5</td>
</tr>
</tbody>
</table>

Table 1 continued...
<table>
<thead>
<tr>
<th>Gene</th>
<th>Protein</th>
<th>Animal model leading to vascular phenotype?</th>
<th>Syndromic TAAD</th>
<th>Nonsyndromic FTAAD</th>
<th>Associated disease/syndrome</th>
<th>Associated clinical characteristics of the vasculature</th>
<th>Ascending aorta size (cm) for surgical intervention</th>
<th>Mode of inheritance</th>
<th>OMIM</th>
</tr>
</thead>
<tbody>
<tr>
<td>MYH11</td>
<td>Smooth muscle myosin heavy chain</td>
<td>Partially</td>
<td>–</td>
<td>+</td>
<td>AAT4</td>
<td>TAAD, early aortic dissection, PDA, CAD, peripheral vascular occlusive disease, carotid IA</td>
<td>4.5–5.25,67</td>
<td>AD</td>
<td>132900</td>
</tr>
<tr>
<td>MYLK</td>
<td>Myosin light chain kinase</td>
<td>No</td>
<td>–</td>
<td>+</td>
<td>AAT7</td>
<td>TAAD, early aortic dissection, AAA, coronary artery aneurysm/dissection, aortic tortuosity, small vessel CVD</td>
<td>4.5–5.25,68</td>
<td>AD</td>
<td>613780</td>
</tr>
<tr>
<td>NOTCH1</td>
<td>NOTCH1</td>
<td>Partially</td>
<td>–</td>
<td>+</td>
<td>AOV1</td>
<td>BAV/TAAD</td>
<td>Standard AD</td>
<td>AD</td>
<td>109730</td>
</tr>
<tr>
<td>PRAG1</td>
<td>Type I CMA-dependent protein kinase</td>
<td>No</td>
<td>–</td>
<td>+</td>
<td>AAT8</td>
<td>TAAD, early aortic dissection, AAA, coronary artery aneurysm/dissection, aortic tortuosity, small vessel CVD</td>
<td>4.5–5.25,67</td>
<td>AD</td>
<td>615436</td>
</tr>
<tr>
<td>ROBO4</td>
<td>Roundabout guidance receptor 4</td>
<td>Yes</td>
<td>–</td>
<td>+</td>
<td>BAV</td>
<td>BAV/TAAD</td>
<td>Standard AD</td>
<td>AD</td>
<td>607528</td>
</tr>
<tr>
<td>SLC2A10</td>
<td>Glucose transporter 10</td>
<td>No</td>
<td>–</td>
<td>–</td>
<td>Shprintzen-Goldberg syndrome</td>
<td>ARD, arterial tortuosity, pulmonary artery dilation, other (splenic) arterial aneurysms</td>
<td>Standard AD</td>
<td>AD</td>
<td>182212</td>
</tr>
<tr>
<td>SMA2</td>
<td>SMAD2</td>
<td>No</td>
<td>–</td>
<td>–</td>
<td>Unidentified CTD with arterial aneurysm/dissections</td>
<td>ARD, ascending aortic aneurysms, vertebral/cerebral aneurysms and dissections, AAA</td>
<td>Standard AD</td>
<td>AD</td>
<td>Unassigned</td>
</tr>
<tr>
<td>SMA3</td>
<td>SMAD3</td>
<td>Partially</td>
<td>–</td>
<td>+</td>
<td>LDS Type III</td>
<td>ARD, TAAD, early aortic dissection, AAA, arterial tortuosity, other arterial aneurysms/dissections, IA</td>
<td>4.0–4.225,31</td>
<td>AD</td>
<td>613795</td>
</tr>
<tr>
<td>SMA4</td>
<td>SMAD4</td>
<td>Yes</td>
<td>+</td>
<td>–</td>
<td>JP/HHT syndrome</td>
<td>ARD, TAAD, AVMs, IA</td>
<td>Standard AD</td>
<td>AD</td>
<td>175050</td>
</tr>
<tr>
<td>SMA6</td>
<td>SMAD6</td>
<td>No</td>
<td>–</td>
<td>+</td>
<td>AOV2</td>
<td>BAV/TAAD</td>
<td>Standard AD</td>
<td>AD</td>
<td>602931</td>
</tr>
<tr>
<td>TIMP3</td>
<td>Tissue inhibitors of matrix metalloproteinase 3</td>
<td>No</td>
<td>–</td>
<td>–</td>
<td>AOVVD</td>
<td>BAV/TAAD</td>
<td>Standard XLD</td>
<td>XLD</td>
<td>188826</td>
</tr>
<tr>
<td>TIMP1</td>
<td>Tissue inhibitors of matrix metalloproteinase 1</td>
<td>No</td>
<td>–</td>
<td>–</td>
<td>AOVVD</td>
<td>BAV/TAAD</td>
<td>Standard XLD</td>
<td>XLD</td>
<td>305370</td>
</tr>
<tr>
<td>TGB2</td>
<td>TGF-β2</td>
<td>Yes</td>
<td>+</td>
<td>+</td>
<td>LDS Type V</td>
<td>ARD, TAAD, arterial tortuosity, other arterial aneurysms, BAV</td>
<td>4.5–5.25,67</td>
<td>AD</td>
<td>614816</td>
</tr>
<tr>
<td>TGB3</td>
<td>TGF-β3</td>
<td>No</td>
<td>+</td>
<td>–</td>
<td>LDS Type V</td>
<td>ARD, TAAD, AAA/dissection, other arterial aneurysms, IA</td>
<td>Standard AD</td>
<td>AD</td>
<td>615582</td>
</tr>
<tr>
<td>TGRB1</td>
<td>TGF-β receptor type 1</td>
<td>Yes</td>
<td>+</td>
<td>+</td>
<td>LDS Type I + AAT5</td>
<td>TAAD, early aortic dissection, AAA, arterial tortuosity, other arterial aneurysms/dissection, IA, PDA, BAV</td>
<td>4.0–4.525,51,51</td>
<td>AD</td>
<td>609192</td>
</tr>
<tr>
<td>TGRB2</td>
<td>TGF-β receptor type II</td>
<td>Yes</td>
<td>+</td>
<td>+</td>
<td>LDS Type II + AAT3</td>
<td>TAAD, early aortic dissection, AAA, arterial tortuosity, other arterial aneurysms/dissection, IA, PDA, BAV</td>
<td>4.0–4.525,51,51</td>
<td>AD</td>
<td>610168</td>
</tr>
</tbody>
</table>

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; FTAAD, familial thoracic aortic aneurysm and/or dissection; HHT, hereditary hemorrhagic telangiectasia; IA, intracranial aneurysm; JP, juvenile polyposis; LDS, Loeys-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; TGFBR, TGF-β receptor; XLD, X-linked dominant.
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2019 Update on the Genetics of TAAD

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

There are no data to set threshold diameters for surgical intervention for EDS Type IV. However, there are limited data concerning the timing of surgical intervention for LDS Type IV. In this entity, there has been a case of a Type A aortic dissection at an aortic diameter < 5.0 cm.

Wenstrup et al found that mice heterozygous for an inactivating mutation in Col5a1 exhibit decreased aortic compliance and tensile strength relative to wild type mice.

Individuals with MYLK and ACTA2 mutations have been shown to have aortic dissections at a diameter of 4.0 cm.

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.

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 to avoid unnecessary surgery at small aortic diameters.

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In a recent study, Park et al demonstrated that Col5a2 haploinsufficiency increased the incidence and severity of AAA and led to aortic arch ruptures and dissections in an angiotensin II-induced aneurysm mouse model.

Patients with TGFBR2 mutations have similar outcomes to patients with FBN1 mutations once their disease is diagnosed, and the clinical course of LDS 1 and 2 does not appear to be as severe as originally reported.

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. Individuals with TGFBR2 mutations are more likely to have aortic dissections at diameters < 5.0 cm than those with TGFBR1 mutations.

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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 (ARHI1) have been observed in patients with early-onset or familial TAAD. ARHI1 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. Corbit et al. demonstrated that Turner syndrome patients with putatively-deleterious mutations in TIMP3 are associated with a greater incidence of BAV and TAA than the patients without TIMP3 variants. Hemizygosity for coincident TIMP1/TIMP3 variants, synergistically increased the risk for BAV and TAA, due to TIMP1’s functional redundancy with TIMP3.

Numerous mutations of the myosin light chain kinase (MYLK) gene have been associated with TAAD. Shalata et al. have identified an additional MYLK missense mutation in a single pedigree. Myosin light chain kinase phosphorylates 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 RAP1GDS1 gene and known to be involved in the contraction of vascular smooth muscle cell (VSMC). Using a heterozygous SmgGDS+/− mouse model, since the complete knockout (SmgGDS−/−) was embryologically 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+−/+ mice, the mice had less aortic growth and fewer aortic ruptures, suggesting that SmgGDS could be used as a biomarker or a therapeutic agent.

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. With our greater understanding of the genetics of the individuals affected with TAAD and their specific genetic mutations or susceptibility variants, we can provide a personalized aortic care, tailoring surgical recommendations for each patient depending on their individual genetic profiles. Because most families that have multiple affected members with TAAD have not had known genetic variants identified in the aortopathy genes, we expect many new genes harboring variants for TAAD will be discovered in the foreseeable future and thereby enhance our genetic dictionary. Furthermore, it is important to remind ourselves that every disease-causing mutation starts out as a variant of unknown significance (VUS). Only after extensive functional studies it is possible to confidently state that a VUS is a disease-causing mutation. Such work requires multidisciplinary collaboration.

We will continue to report annual updates regarding the “TAAD genetic dictionary” with updates to the Table and Figure below and provide suggested surgical intervention criteria for each identified mutation.

Funding
None.

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

Acknowledgment
None.

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