MUTATION ANALYSIS IN SMAD2, TGFβ2, AND SMURF2 GENES IN PATIENTS WITH THORACIC AORTIC ANEURYSM AND DISSECTION

ANALISIS MUTASI GEN SMAD2, TGF\(\beta\)2, DAN SMURF2 PADA PASIEN DENGAN THORACIC AORTIC ANEURYSM AND DISSECTION





THESIS

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ABBREVIATIONS

ACTA2 Actin Smooth Muscle Alpha 2

BAV Bicuspid Aortic Valve

COL3A1 Collagen type 3 Alpha 1

ECM Extracellular Matrix

EDS Ehler-Danlos Syndrome

FBN1 Fibrillin 1

FTAAD Familial Thoracic Aortic Aneurysm and Dissection

HRM High Resolution Melting

LAP Latency Associate Propeptide

LDS Loeys-Dietz Syndrome

LLC Large Latent Complex

LTBP Latent TGFβ Binding Protein

MFS Marfan Syndrome

MMP Matrix Metalloproteinase

MYH11 Myosin Heavy Chain 11

MYLK Myosin Light Chain Kinase

PDA Patent Ductus Arteriosus

SLC Small Latent Complex

SMAD Mothers against decapentaplegic

SMURF2 Smad Ubiquitination Regulatory Factor 2

TAA Thoracic Aortic Aneurysms

TAAD Thoracic Aortic Aneurysms and Dissection

TGFβ Transforming Growth Factor Beta

TGFβR Transforming Growth Factor Beta Receptor

VSMC Vascular Smooth Muscle Cell

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ABSTRACT

Background: Thoracic aortic aneurysm and dissection (TAAD) is one of 15^{th} most leading cause of the death in USA and of the silent killer in the world. Several genes associated with TAAD have been recognized, i.e. *FBN1*, *ACTA2*, *TGF\betaR1*, *TGF\betaR2*, *MYH11*, *MYLK* and *SMAD3*. However, many cases of familial TAAD have not been found for the mutation in those genes. The other genes that might be had association with TAAD are *SMAD2*, *TGF\beta2* and *SMURF2*.

Methods: Three hundred sixty five patients with TAAD and related disorders, who did not carry any mutation in FBN1, $TGF\beta R1$, $TGF\beta R2$, ACTA2 and MYH11 were included. Mutation screening of the gene variants in SMAD2, $TGF\beta 2$ and SMURF2 were done by using high resolution melting (HRM) technique. The aberrant sample patterns on the curve analysis then were sequenced. Confirmation of the mutation was done by comparing the HRM curves between patients and the healthy control. The pathogenicity potency of the mutation was predicted by using mutation prediction software SIFT and align GVGD, which integrated in Alamut software. Phosphorylation/glycosylation site was predicted by YinOYang software.

Results: Three patients were found to carry SMAD2 mutation, i.e., c.6_8del, c.1346T>C, c.1369G>A. One mutation, c.1369G>A was predicted to increase phosphorylation, and the other mutations predicted to loss of phosphorylation/glycosylation site. All of the SMAD2 mutations were not found in the control. One patient was found to carry nonsense mutation of $TGF\beta2$, c.547C>T (Gln183X). Two missense mutation of $TGF\beta2$, c.272G>A and c.703C>G were found in four patients and have been registered in SNP databases with frequency less than 1%. All mutations in SMAD2 and $TGF\beta2$ were predicted to be pathogenic. No mutation was found in SMURF2 gene.

Conclusion: Three novel mutations were found in SMAD2 gene and one novel mutation was found in $TGF\beta2$ in TAAD patients who did not carry any mutation in FBN1, $TGF\beta R1$, $TGF\beta R2$, ACTA2 and MYH11.

Keywords: Thoracic aortic aneurysm and dissection, mutation, SMAD2, $TGF\beta2$, SMURF2

ABSTRAK

Latar belakang: Thoracic aortic aneurysm and dissection (TAAD) adalah satu dari 15 teratas penyebab kematian di Amerika Serikat dan merupakan silent killer di dunia. Beberapa gen yang berkaitan dengan TAAD sudah dikenali yaitu FBN1, ACTA2, $TGF\beta R1$, $TGF\beta R2$, MYH11, MYLK dan SMAD3. Namun, pada banyak kasus TAAD familial tidak ditemukan mutasi pada gen-gen tersebut. Gen lain yang kemungkinan berkaitan dengan TAAD adalah SMAD2, $TGF\beta 2$ dan SMURF2.

Metode: Sampel DNA diambil dari 365 pasien TAAD dan penyakit terkait, yang tidak memiliki mutasi di gen *FBN1*, *TGFβR1*, *TGFβR2*, *ACTA2* dan *MYH11*. Skrining mutasi gen pada *SMAD2*, *TGFβ2* dan *SMURF2* dilakukan dengan teknik *high resolution melting* (*HRM*). Sampel dengan pola berbeda pada analisa kurva dilakukan sekuensing. Konfirmasi mutasi dilakukan dengan membandingkan kurva HRM antara pasien dan kontrol sehat. Potensi patogenitas mutasi diprediksi dengan software SIFT dan *align* GVGD, yang tergabung dalam software Alamut. Situs fosforilasi/glikosilasi diprediksi dengan software YinOYang.

Hasil: Mutasi c.6_8del, c.1346T>C, c.1369G>A pada gen *SMAD2* ditemukan pada 3 pasien yang berbeda. Mutasi c.1369G>A diprediksi meningkatkan fosforilasi dan dua mutasi lainnya kehilangan situs fosforilasi/glikosilasi. Semua mutasi *SMAD2* tidak ditemukan pada kontrol. Mutasi c.547C>T (Gln183X) pada gen $TGF\beta2$ ditemukan pada satu pasien. Dua mutasi pada gen $TGF\beta2$, c.272G>A dan c.703C>G ditemukan pada empat pasien dan telah terdaftar di database SNP dengan frekuensi kurang dari 1%. Semua mutasi pada *SMAD2* dan $TGF\beta2$ tersebut diprediksikan patogenik. Tidak ditemukan mutasi pada gen *SMURF2*.

Kesimpulan: Tiga mutasi novel ditemukan pada gen SMAD2 dan satu mutasi novel ditemukan pada gen $TGF\beta2$ pada pasien TAAD yang tidak memiliki mutasi pada gen FBN1, $TGF\beta R1$, $TGF\beta R2$, ACTA2 dan MYH11.

Kata kunci: *Thoracic aortic aneurysm and dissection*, mutasi, *SMAD2*, *TGFβ2*, *SMURF2*