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## ASSOCIATION BETWEEN SMAD3 GENE rs6494629 C/T POLYMORPHISM AND KNEE OSTEOARTHRITIS IN INDONESIAN POPULATION.

B MARPAUNG, OM SJAH

Division of Rheumatology, Department of Internal Medicine, Faculty of Medicine,  
Universitas Sumatera Utara, Medan, Indonesia

### ABSTRACT

**Background.** Osteoarthritis (OA) risk factors include older age, obesity, physical activity, trauma, female gender, and genetic factors. One of the genetic factors suspected to be involved in OA development is the Sma and Mad homologue 3 (SMAD3) polymorphism. Previous studies had examined the association between SMAD3 rs6494629 C/T polymorphism and risk of knee OA, unfortunately the results were controversial. The aim of this study was to evaluate the association between SMAD3 rs6494629 C/T polymorphism and knee OA in Medan, Indonesia.

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**Keywords:** Knee osteoarthritis, SMAD3 protein, polymorphism, TGF- $\beta$ , molecular epidemiology

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## INTRODUCTION

Osteoarthritis (OA) is the most common joint disease and the main cause of chronic pain and disability.<sup>1</sup> OA occurs most commonly in knee, hands, feet, and spine joints, and is relatively common in shoulder and hip joints. The prevalence of OA continues to increase due to population ageing. Risk factors for OA

include older age, obesity, physical activity, trauma, female gender, and genetic factors.<sup>2-7</sup>

One of the genetic factors suspected to be involved in OA development is the Sma and Mad homologue 3 (SMAD3) polymorphism.<sup>8</sup> SMAD3 protein is a member of SMAD family and it is encoded by the SMAD3 gene located on chromosome 15q21-22, including 9 exons and 8 introns.<sup>8,9</sup> SMAD3 protein is the most important medium in transforming growth factor- $\beta$  (TGF- $\beta$ )/Smad signal transduction.<sup>10,11</sup> The protein encoded

**Correspondence:** Blondina Marpaung, MD., Ph.D. Division of Rheumatology, Department of Internal Medicine, Faculty of Medicine, Universitas Sumatera Utara, Dr. Mansyur 5 Medan, Indonesia. Tel: +6281262186275. Email: [blondina@usu.ac.id](mailto:blondina@usu.ac.id)

by this gene forms the family of protein SMAD which is an intracellular molecule or protein associated with TGF- $\beta$  signalling pathways. SMAD3 expression has been postulated to play a role in OA development.<sup>12-14</sup> SMAD3 protein acts as a mediator that has the effect of inhibiting TGF- $\beta$  on chondrocyte maturation.<sup>15</sup> TGF- $\beta$  is thought to play a role in protecting against cartilage damage. The low levels of TGF- $\beta$  are associated with cartilage damage and OA progression.<sup>16</sup>

Previous studies had examined the relationship between SMAD3 rs6494629 C/T polymorphism and risk of knee OA, but with controversial results, which may be due to racial/ geographical differences in susceptibility of SMAD3 polymorphism to knee OA.<sup>17-22</sup> Hence, the aim of this study is to investigate the association between SMAD3 rs6494629 C/T polymorphism and knee OA in the Indonesian population.

## METHOD

### *Patient Selection*

This study was a prospective case control study on 80 consecutive knee OA patients recruited from the Rheumatology clinic at Adam Malik General Hospital, Medan, Indonesia between October 2017 and March 2018. One hundred healthy controls attending other clinics at the hospital, matched to age and gender were also recruited. Demographic data on age, gender, height and weight were collected, the latter two for calculation of body mass index (BMI). The diagnosis of knee OA was confirmed by clinical examination and Knee radiographs, which also fulfilled the criteria of the American College of Rheumatology.<sup>23</sup> The radiographic film evaluation was performed on anteroposterior and lateral radiographic views of the knee. Severity on the knee OA population was assessed using the Kellgren–Lawrence (K–L) grading scale.<sup>24</sup> OA was classified into mild (K–L grade 2), moderate (K–L grade 3), and

severe (K–L grade 4). Only patients with radiographic evidence of OA, defined as K–L score of  $\geq 2$ , were included in the study. Subjects with other etiologies of knee joint disorders such as rheumatoid arthritis, gouty arthritis, septic arthritis, post traumatic, or dysplasias were excluded. This study also included 100 age and sex-matched healthy control participants with no symptoms of joint disease (pain, swelling, tenderness, or restriction of movement) in whom standard radiograph of knee joints confirmed the absence of radiographical knee OA. Subjects in both groups with chronic diseases like cardiopulmonary disease, diabetes, hypertension, as well as tumor or autoimmune disease also were excluded. Written informed consent were obtained from all participants. This study was approved by the Institutional Review Board of Universitas Sumatera Utara.

### *SMAD3 rs6494629 C/T*

Genomic DNA was extracted from whole blood collected in ethylenediamine tetraacetic acid (EDTA) tubes from knee OA and control groups using the standard isothiocyanate guanidine (GTC) extraction method and/or the QIAamp DNA Blood Mini Kit (Qiagen, Hilden, Germany). Single nucleotide polymorphism (SNP) in the SMAD3 gene, rs6494629 C/T was determined using the polymerase chain reaction (PCR)-restriction fragment length polymorphism (RFLP) method.<sup>25</sup> Amplification reaction was performed with 200 ng of genomic DNA in a 50- $\mu$ l PCR mixture using 10 pmol of each primer, 0.25 mM each deoxyribonucleoside triphosphate (dNTP) (Qiagen), 1 U HotStar Taq polymerase (Qiagen) and  $\times 1$  PCR buffer (containing 1.5  $\mu$ M magnesium chloride; Qiagen). The PCR primers used for SMAD3 rs6494629 C/T polymorphisms were 5'-CATCTTTCCTCCTGGCCATA-3' (forward) and (5'-CTTAGCGAAGGAAACCAGCA-3' (reverse). The PCR cycle conditions consist of an initial denaturation step at 95°C for 15 min, followed by 35 cycles at 94°C for 30 s, 55.6°C for 60 s

and 72°C for 60 s, with an extension at 72°C for 10 min. Ten µl of PCR product [430 base pairs (bp) in length] was digested with 1 µl HpaII (Fermentas/Fisher Scientific, UK) at 37°C for 15 min, separated on a 2.5% agarose gel and visualized with ethidium bromide staining under ultraviolet light. HpaII digestion of the PCR product yielded 155 and 275 bp for allele C and 399 bp for the undigested allele T. Randomly selected patients were analysed by direct sequencing, using an ABI PRISM Sequencer (Applied Biosystems) to confirm the accuracy of the method.

### Statistical Analysis

Total knee OA subjects had met minimum sample size of the estimation sample calculation. Case and control groups were divided into two groups based on age  $\leq$  50 years and  $>$  50 years to determine association between SMAD3 gene polymorphism and knee OA in younger and older age group. Data analysis was performed through simple logistic regression using SPSS 22nd version (SPSS Inc., Chicago). A value of  $p < 0.05$  with 95% confidence interval was considered statistically significant.

### RESULTS

Case and control groups were homogeneous by age and sex. BMI was significantly higher in cases than control group. Majority of cases (93.75%) were patients with mild to moderate (K-L grade 2-3) OA (Table 1).

There was no significant association between SMAD3 gene rs6494629 C/T polymorphism and knee OA in cases as compared to controls (Table 2). However, when the cases and controls were divided into two groups based on age  $\leq$  50 years and  $>$  50 years, there was a significant association between SMAD3 gene rs6494629 C/T polymorphism and knee OA in the younger age groups ( $\leq$ 50 years), particularly cases with TT genotype and T allele were at higher risk for developing knee OA (TT genotype, OR 2.54; T allele, OR 1.71). However this association did not appear in the  $>$  50 years age group (Table 3).

### DISCUSSION

SMAD protein is a family of intracellular protein that acts as a signal transduction for TGF- $\beta$ , from cell membrane to nucleus.<sup>14</sup> Low SMAD3 increased bone morphogenetic protein signaling and accelerated chondrocytes differentiation.<sup>26</sup> TGF- $\beta$  can regulate MMP through SMAD3 protein levels during the OA progression process.<sup>27</sup> Van der Kraan et al reported that TGF- $\beta$  might regulate the differentiation of chondrocytes that were important for OA. TGF- $\beta$  has an anabolic effect on chondrocytes through SMAD3 gene signals that play a role for synovial joint homeostasis.<sup>28</sup> TGF- $\beta$  is important for maintaining the cartilage. Low TGF- $\beta$  is associated with increased risk of OA.<sup>29,30</sup>

The occurrence of OA is influenced by genetic factors. SMAD3 gene polymorphisms

**Table 1. Baseline characteristics in knee OA patients and controls**

Variable	Cases	Controls	P
Age (years)	53.8 $\pm$ 6.8	54.3 $\pm$ 6.2	0.837
Gender			
Female	45 (56.3%)	56 (56%)	0.973
Male	35 (43.7%)	44 (44%)	
Body mass index	26.2 $\pm$ 4.4	24.1 $\pm$ 3.5	<0.001
Kellgren-Lawrence grading			
2	39 (48.8%)	-	
3	36 (45%)	-	
4	5 (6.2%)	-	

**Table 2. Association between SMAD3 gene rs6494629 C/T polymorphism and knee OA**

Genotype/ Allele	Knee OA n (%)	Control n (%)	Total n (%)	p	OR (95% CI)
TT	17 (68)	8 (32)	25 (100)	0.055	1.72 (1.01 -2.49)
CT	34 (43)	45 (57)	79 (100)	0.671	1.03 (0.71-1.5)
CC	29 (38.2)	47 (61.8)	76 (100)		1 (ref.)
TT+CT	51 (49)	53 (51)	104 (100)	0.320	1.15 (0.82-1.61)
CC	29 (38.2)	47 (61.8)	76 (100)		1 (ref.)
TT	17 (68)	8 (32)	25 (100)	0.056	1.5 (1.05-2.15)
CT+CC	63 (40.6)	92 (59.4)	155 (100)		1 (ref.)
Allele T	68 (52.7)	61 (47.3)	129 (100)	0.078	1.41 (0.98 – 1.56)
Allele C	92 (39.8)	139 (60.2)	231 (100)		1 (ref.)

were reported to be associated with OA development, but these results were controversial.<sup>17-22</sup> Gene polymorphisms are strongly influenced by ethnicity so they showed different results. The study of Valdes in Europe showed SMAD3 polymorphism rs6494629C/T rs266335G/A, rs12901499A/G, and rs2289263A/C were significantly associated with knee OA, but only rs12901499A/G was associated with hip OA.<sup>18</sup> A study by Zhang et al and Liying et al in Chinese population and Sharma et al in India found that SMAD3 rs12901499 polymorphism was responsible for the occurrence of knee OA.<sup>20,22,31</sup> Kang et al in China showed that patients with TT gen-

otype and T allele of rs12102171, GG genotype and G allele of rs2289263 polymorphisms significantly increased the risk of having OA compared to control group.<sup>8</sup> However, Su et al in Taiwan reported no association of SMAD3 polymorphism (rs6494629 C/T and rs12901499A/G) and knee OA.<sup>19</sup> The GG genotype of rs12901499 might lower the risk of developing knee OA compared with the AA genotype.<sup>22</sup> On the contrary Sharma et al in India and Liying et al in northeastern China showed that SMAD3 rs12901499 polymorphism, GG and GA genotype, were significantly associated with the knee OA.<sup>20,31</sup>

**Table 3. Association between SMAD3 gene rs6494629 C/T polymorphism and knee OA by age group**

Genotype/ Allele	Knee OA n (%)	Control n (%)	Total n (%)	p	OR (95% CI)
<b>Age ≤50 years</b>					
TT	9 (90)	1 (10)	10 (100)	0.001*	3.6 (1.64 -7.91)
CT	17 (40.5)	25 (59.5)	42 (100)	0.234	1.62 (0.7-3.76)
CC	5 (25)	15 (75)	20 (100)		1 (ref.)
TT+CT	26 (50)	26 (50)	52 (100)	0.055	2 (0.89-4.48)
CC	5 (25)	15 (75)	20 (100)		1 (ref.)
TT	9 (90)	1 (10)	10 (100)	0.002*	2.54 (1.71-3.76)
CT+CC	22 (35.5)	40 (64.5)	62 (100)		1 (ref.)
Allele T	35 (56.5)	27 (43.5)	62(100)	0.005*	1.71 (1.17 – 2.5)
Allele C	27 (32.9)	55 (67.1)	82 (100)		1 (ref.)
<b>Age &gt;50 years</b>					
TT	8 (53.3)	7 (46.7)	15 (100)	0.469	1.24 (0.71 -2.18)
CT	17 (45.9)	20 (54.1)	37 (100)	0.769	1.07 (0.68-1.7)
CC	24 (42.9)	32 (57.1)	56 (100)		1 (ref.)
TT+CT	25 (48.1)	27 (51.9)	52 (100)	0.691	1.02 (0.72-1.53)
CC	24 (42.9)	32 (57.1)	56 (100)		1 (ref.)
TT	8 (53.3)	7 (46.7)	15 (100)	0.840	0.94 (0.49-1.78)
CT+CC	41 (44.1)	52 (55.9)	93 (100)		1 (ref.)
Allele T	33 (49.3)	34 (50.7)	67 (100)	0.442	1.13 (0.83 – 1.53)
Allele C	65 (43.6)	84 (56.4)	149 (100)		1 (ref.)

\*p&lt;0.05



In this study found that there was no significant association between SMAD3 gene rs6494629 C/T polymorphism and knee OA. Although subgroup analysis of age showed positive association between this SNP and knee OA risk in the younger age groups ( $\leq 50$  years). Patients with TT genotype and T allele were at risk for developing knee OA ( $p < 0.05$ ), but this association appeared in the  $\leq 50$  years age group. Our findings suggest that the role of SMAD3 rs6494629 genotypes with TT genotype and T allele may play a significant role in knee OA in younger patients but not in older patients ( $> 50$  years) where other comorbidities and environmental factors such as obesity, lack of physical activity, bone density, and trauma may contribute to the development of OA.

The limitations of our study include the small sample size which might make our study underpowered, as well as this study was not assess the role of SMAD3 rs6494629 C/T polymorphism against the expression of TGF- $\beta$ . This study was a hospital-based case-control study, and selection bias might happened.

## CONCLUSION

SMAD3 gene rs6494629 C/T polymorphism, predisposes to development of OA in younger age groups, whereas knee OA in older age was more influenced by other factors. Further studies are necessary to examine other SNPs that may affect the occurrence of knee OA and also identify the association of this polymorphism with other joints such as hip OA and spine OA.

**Competing Interests:** The authors have declared no conflict of interests present.

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