

## ORIGINAL ARTICLE

**ASSOCIATION OF THE MMP7 –181A>G PROMOTER  
POLYMORPHISM WITH EARLY ONSET OF  
CHRONIC OBSTRUCTIVE PULMONARY DISEASE**

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**ABSTRACT**

Chronic obstructive pulmonary disease (COPD) is characterized by decreased air flow and is associated with abnormal chronic inflammation in the airways and extensive tissue remodeling. Matrix metalloproteinase-7 (MMP7) is produced primarily by the epithelium of many organs, including the lungs. A functional MMP7 –181A>G (rs11568818) promoter polymorphism influences the binding of nuclear regulatory proteins modulating the transcription of the gene. In this study, we genotyped 191 patients with COPD for *MMP7* –181A>G single nucleotide polymorphism (SNP) and 215 control subjects using the polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) method and explored the role of that polymorphism as a risk factor for COPD. There were no differences in the genotype and allele distribution of the *MMP7* –181A>G SNP between the COPD patients and control groups ( $p = 0.341$  and  $p = 0.214$ ). However, the carriers of the G allele (AG and GG genotypes), appeared to develop COPD significantly earlier than those with the AA genotype ( $61.01 \pm 10.11$  vs.  $64.87 \pm 9.00$  years,  $p = 0.032$ ). When the genotype distribution was studied only in the groups of patients ( $n = 76$ ) and controls ( $n = 106$ ) younger than 60 years, we found significantly higher frequency of the carriers of the G allele in COPD patients than in the controls, determining about a 3-fold higher risk for COPD [odds ratio (OR) –3.33, 1.36-8.14,  $p = 0.008$  for GG, and

OR = 2.91, 1.38-6.13,  $p = 0.005$  for AG+GG]. Based on our results, the *MMP7* –181A>G promoter variant may influence early development of COPD. This effect could be attributed to the increased production of the enzyme resulting in enhanced airway wall protein degradation and injury.

**Keywords:** Age; Chronic obstructive pulmonary disease (COPD); Matrix metalloproteinase-7 (MMP7); Polymorphisms; Risk.

**INTRODUCTION**

Chronic obstructive pulmonary disease (COPD) is a preventable and treatable disease with some significant extrapulmonary effects that may contribute to its severity in individual patients. Its pulmonary component is characterized by airflow limitation that is not fully reversible. The airflow limitation is associated with an abnormal inflammatory response of the lung to noxious particles or gases [1].

Smoking is one of the main risk factors for COPD, but since not all smokers develop COPD, as well as the fact that the disease often develops in middle age, it is suggested that other factors may play a role in the pathogenesis such as genetic factors [2]. Inhalation of cigarette smoke, organic and/or inorganic dust, chemical agents and particle matters increase the risk of developing COPD. The presence of these irritants, may lead to chronic inflammation and structural changes in the lung due to repeated injury and repair [3]. Pathological changes characteristic for COPD are found in the proximal airways, peripheral airways, lung parenchyma and pulmonary vasculature [4].

One of the main roles of the epithelial cells is to provide a barrier against pathogens and to release antimicrobial products. By producing chemoattractants and adhesion molecules, epithelial cells contribute to the migration of the inflammatory cells to injury sites [5,6]. Epithelial

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damage is an important characteristic of several pulmonary diseases including COPD. Numerous enzymes, proteins and peptides are involved in the process of tissue repair and remodeling [7].

The matrix metalloproteinases (MMPs) family is composed of more than 25 zinc-dependent proteases that cleave the extracellular matrix and cell-surface proteins to regulate wound healing, physiological angiogenesis and immune response [8]. Matrix metalloproteinases can activate and increase the bioavailability of a variety of non matrix proteins, including cytokines, chemokines, receptors and antimicrobial peptides [5,9]. Matrilysin 1 (MMP-7), unlike many MMPs, is expressed by non injured, non inflamed mucosal epithelia in most adult human tissues (7). Besides extracellular matrix (ECM) components, MMP-7 processes cell surface molecules such as pro-defensin, Fas-ligand, pro-tumor necrosis factor (TNF), and E-cadherin [10,11].

The production of the enzyme is highly up-regulated by injury or exposure to bacteria, stimulating cell migration and coordinating the inflammatory response [12-14]. Thus, MMP-7 participates in the processes of defense, repair and inflammation.

In the promoter of the gene of MMP-7 an A>G transition has been identified as a functional polymorphism (MMP7 -181A>G; rs11568818). The polymorphism has been shown to modulate transcriptional activity by influencing the binding of nuclear regulatory proteins. The G allele has greater basal transcriptional activity than the A allele in *in vitro* experiment in the human monocyte/macrophage cell line U937 [15]. The nuclear proteins bind with higher affinity to the G allele than to the A allele, resulting in significant increase in promoter activity [16,17].

So far, there are only very limited studies concerning the role of MMP-7 and its genetic variants in lung diseases such as lung cancer [18], pneumoconiosis [19], bronchiolitis obliterans syndrome (BOS) in patients after lung transplantation [20], and idiopathic pulmonary fibrosis (IPF) [21]. Concerning COPD, there was only one report showing increased serum level of MMP-7 in patients exposed to biomass and tobacco smoke compared with non smoking healthy controls, and the levels were negatively correlated with spirometric index of lung function (FEV1 %pr.) [22]. However, there has only been one study exploring the functional variants of MMP-7 in the development of COPD [23].

In this respect we aimed to evaluate the possible role of the MMP7 -181A>G promoter polymorphism as predisposing factor for COPD in a population from the region of Stara Zagora, Bulgaria.

## MATERIAL AND METHODS

**Patients and Controls.** We have genotyped 191 patients with COPD and 215 healthy volunteers or individuals unaffected by lung or cancer diseases. The inclusion criteria for COPD were as follows: age higher than 40 years; forced expiratory volume in one second (FEV1) of <80.0%; forced expiratory volume in one second (FEV1)/forced vital capacity (FVC) ratio of  $\leq 70.0\%$ ; FEV1 reversibility after inhalation of 400  $\mu\text{g}$  Salbutamol of <12.0%.

In both groups, the age of inclusion in the study and smoking status were noted; in the patients' group: age of diagnosis, the spirometric indexes, duration and the stages of the disease (GOLD stages) were also reported. The available demographic and clinical data are presented in Table 1. Informed consent was obtained from patients and controls before the beginning of the study.

**DNA Isolation and Genotyping.** Genomic DNA was isolated from 0.2 mL of whole blood using a commercial kit for isolation of genomic DNA from blood (GenElute™ Mammalian Genomic DNA Miniprep Kit, Sigma-Aldrich, St. Louis, MO, USA).

The genotyping for the MMP7 -181A>G (rs11568818) was performed by the polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP)-based method. The final volume of each reaction was 15  $\mu\text{L}$ , containing 0.5 U Dream Taq Polymerase (Fermentas, Waltham, MA, USA), 1.5  $\mu\text{L}$  10  $\times$  PCR buffer (with 1.5 mM MgCl<sub>2</sub>), 0.6  $\mu\text{L}$  dNTPs (Sigma-Aldrich) in a final concentration of 200  $\mu\text{M}$  for each of the four dNTPs, 0.3  $\mu\text{L}$  of each primer in concentration of 20 pmol/ $\mu\text{L}$  (MMP7F: 5'-TGG TAC CAT AAT GTC CTG AAT G-3'; MMP7R: 5'-TCG TTA TTG GCA GGAAGC ACACAA TGAATT-3') and distilled water to the end volume.

The temperature profile of the PCR reactions included primary denaturing of the template DNA for 3 min. at 94°C, followed by 30 cycles of denaturation for 30 seconds at 94°C, annealing for 30 seconds at 53.6°C and polymerization for 30 seconds at 72°C. The PCR reaction was terminated by a final extension for 5 min. at 72°C.

The restriction reaction was performed with 5U *EcoRI* in final volume of 5  $\mu\text{L}$  for 16 hours at 37°C. The obtained restriction products were analyzed by 4.0% agarose gel stained with ethidium bromide. The results were documented by the Gel documentation system (Syngene; Synoptics Ltd., Cambridge, Cambridgeshire, UK).

**Statistical Analyses.** Statistical analyses were performed using the Statistical Package for the Social Sciences (SPSS), version 16.0 for Windows (SPSS Inc., Chicago, IL, USA). Continuous variables were analyzed for

**Table 1.** Demographic and clinical data of patients with chronic obstructive pulmonary disease and controls.

Characteristics	Patients with COPD (%)	Controls (%)	p Value
Number	191	215	
males	146 (76.4)	109 (50.7)	<0.001 <sup>a</sup>
females	45 (23.6)	106 (49.3)	
Age (years) at inclusion in the study median (range)	67 (36-88)	59 (18-80)	<0.001 <sup>b</sup>
Age (years) at diagnosis of the disease median (range)	64 (30-86)	–	
Smoking status	<i>n</i> = 186	<i>n</i> = 164	<0.001 <sup>a</sup>
non-smokers	54 (29.0)	97 (59.0)	
ex-smokers	89 (48.0)	25 (15.0)	
current smokers	43 (23.0)	42 (26.0)	
FEV1 %pr (mean ± SD) (range)	50.60 ± 14.10 (15-79)	93.40 ± 11.90 (82-114)	<0.001 <sup>b</sup>
FEV1/FVC % (mean ± SD) (range)	61.1 ± 8.6 (27.1-70.0)	80.4 ± 7.2 (76.3-93.0)	<0.001 <sup>b</sup>
COPD staging (GOLD 2009)			
stage II (moderate)	102 (55.0%)	–	
stage III (severe)	73 (39.0)	–	
stage IV (very severe)	11 (67.0)	–	

COPD: chronic obstructive pulmonary disease; SD: standard deviation.

<sup>a</sup> Determined by the  $\chi^2$  test.

<sup>b</sup> Determined by the Mann-Whitney U test.

normality of the distribution using the Kolmogorov-Smirnov test (One-Sample Kolmogorov-Smirnov D-Test in SPSS, version 16; SPSS Inc.). When the level of significance in this test was lower than 0.05 ( $p < 0.05$ ), the hypothesis for normal distribution was rejected. The continuous variables with normal distribution were compared between two or more independent groups by the Student *t*-test or one-way analysis of variance (ANOVA) test with least significant difference (LSD) *post hoc* analysis, while those with an abnormal distribution were analyzed with the Mann-Whitney U or Kruskal-Wallis tests. The frequencies of distribution in the contingency tables were analyzed using  $\chi^2$  test, or Fisher's exact test, when needed. The odds ratio (OR) and 95% confidence interval (95% CI) were calculated by binary logistic regression with age and sex as covariates. The Hardy-Weinberg equilibrium (HWE) was calculated by an inter-active calculation tool for  $\chi^2$  tests of goodness of fit

and independence [24]. Factors with a *p* value of  $< 0.05$  were considered to be statistically significant.

## RESULTS

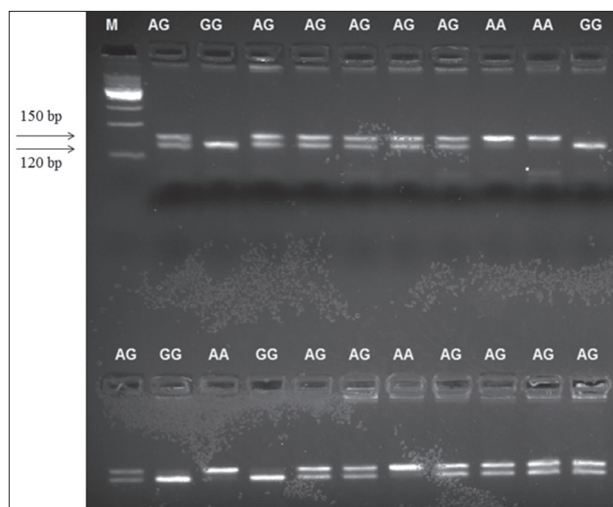
The PCR product amplified with the primers for *MMP7* –181A>G was 150 bp in length. The *EcoRI* digestion resulted in 150 bp for the AA genotype, 150, 120 and 30 bp for the AG genotype, and 120 and 30 bp for the GG genotype (Figure 1).

The genotype distribution in both controls and patients did not deviate from HWE ( $p = 0.998$  and  $p = 0.999$ ). After statistical processing of the data, we found no differences in the genotype and allele distribution of the *MMP7* –181A>G polymorphism between COPD patients and controls ( $p = 0.341$  and  $p = 0.214$ ) (Table 2). In the group of patients, there was no association between the genotype

**Table 2.** Genotype and allele frequencies of the *MMP7* –181A>G gene polymorphism in patients with chronic obstructive pulmonary disease and controls.

<i>MMP7</i> –181A>G	Patients		Controls		OR (95% CI)	p Value
	<i>n</i> = 191	Frequency	<i>n</i> = 215	Frequency		
<b>Genotype frequency</b>						
AA	43	0.225	54	0.251	1.0 (referent)	
AG	99	0.518	119	0.554	1.465 (0.826-2.598)	0.243
GG	49	0.257	42	0.195	1.045 (0.647-1.687)	0.903
AG+GG	148	0.775	161	0.749	1.154 (0.731-1.823)	0.562
<b>Allele frequency</b>						
–181 A	185	0.484	227	0.528	1.0 (referent)	
–181 G	197	0.516	203	0.472	1.191 (0.904-1.569)	0.232

OR: odds ratio; 95% CI: 95% confidence interval.



**Figure 1.** Agarose gel for visualization of the PCR-RFLP products and *MMP7*–181A>G genotyping.

and gender ( $p = 0.358$ ), smoking habit ( $p = 0.587$ ), stage of the disease ( $p = 0.924$ ) or spirometric indexes for lung function (for FEV1:  $p = 0.598$  and for FEV1/FVC:  $p = 0.3$ , Kruskal-Wallis test). Association of the *MMP*-7 G allele with severity of COPD was also not found ( $p = 0.876$ ).

However, the carriers of the G allele (AG and GG genotypes) appeared to develop COPD significantly early compared to those with the AA genotype ( $61.01 \pm 10.11$  vs.  $64.87 \pm 9.00$  years,  $p = 0.032$ , Student *t*-test). When the genotype distribution was studied only in the patients ( $n = 76$ ) and controls ( $n = 106$ ) younger than 60 years, significant difference was found. The frequency of the carriers of the G allele (AG and GG genotypes), was higher in COPD patients than in controls, showing a 3-fold higher risk for the development of COPD before the age of 60 years (Table 3).

## DISCUSSION

A common feature of COPD is the chronic inflammation in the airways and the development of extensive tissue remodeling during the course of the disease process [25]. The matrix metalloproteinases are a family of zinc-containing enzymes with proteolytic activity against a wide range of extracellular proteins [10]. Under normal physiological conditions, the activities of MMPs are precisely regulated at the level of transcription, activation of the precursor zymogens and inhibition by endogenous inhibitors [26]. Due to their activity, MMPs participate in many physiological and pathological processes in the body such as development, involution, inflammation, tumor growth, and repair [27,28].

Matrix metalloproteinases play an important role in the turnover of almost all extracellular matrix molecules and thus, participate in the pathogenesis of COPD [22,29]. An A>G substitution in the promoter of the *MMP7* gene has been shown to affect the promoter activity, as the G allele determines higher basal transcriptional activity *in vitro* in human monocyte/macrophage cell line U937 [15]. In this study, we did not find any significant difference in geno-type and allele distribution when we studied the entire COPD patient and control groups. However, the carriers of the G allele (AG and GG genotypes) appeared to develop COPD significantly early compared to those with the AA genotype. Moreover, the G allele determines about a 3-fold higher risk for COPD before the age of 60 years.

So far, only one study has been found in the literature exploring the role of *MMP7* –181A>G (rs11568818) in COPD. In the study of Mogulkoc *et al.* [23], the *MMP*-7 AA genotype has been found to be associated with an increased risk of COPD. On the contrary, in our study we found no association of the A allele with COPD, which might be explained by the difference in Bulgarian and

**Table 3.** Genotype and allele and genotype frequencies of the *MMP7* –181A>G gene polymorphism in the patients with chronic obstructive pulmonary disease and controls younger than 60 years.

<i>MMP7</i> –181A>G	Patients		Controls		OR (95% CI)	<i>p</i> Value	OR (95% CI)	<i>p</i> Value
	<i>n</i> = 76	Frequency	<i>n</i> = 106	Frequency				
<b>Genotype frequency</b>								
AA	11	0.145	35	0.330	1.0 (referent)		1.0 (referent)	
AG	43	0.566	50	0.471	2.736 (1.252-5.962)	<b>0.016<sup>a</sup></b>	4.742 (1.426-15.768)	<b>0.011<sup>a</sup></b>
GG	22	0.289	21	0.198	3.333 (1.363-8.148)	<b>0.008<sup>a</sup></b>	3.194 (0.862-11.830)	0.082
AG+GG	65	0.855	71	0.670	2.913 (1.380-6.133)	<b>0.005<sup>a</sup></b>	4.122 (1.318-12.890)	<b>0.015<sup>a</sup></b>
<b>Allele frequency</b>								
–181 A	65	0.428	120	0.566	1.0 (referent)	–	–	–
–181 G	87	0.572	92	0.434	1.746 (1.147-2.657)	<b>0.009<sup>a</sup></b>	–	–

OR: odds ratio; 95% CI: 95% confidence interval.

<sup>a</sup> The bold *p* values denote that there is a statistical difference.

Turkish populations (*e.g.*, age, smoking, diagnosis, *etc.*).

It has been shown that the same variant is not a risk factor for IPF, but influences the plasma level of MMP-7 in patients, as carriers of the AA genotype had higher concentrations than carriers of other genotypes [21]. *MMP7*-181A>G has shown no association with the risk for lung cancer [18]. However, an increased risk for development of bronchiolitis obliterans syndrome has been reported for carriers of the AA genotype in patients after lung transplantation [20].

In COPD patients, the serum levels of MMP-7, as well as of some other MMPs, MMP-1 and MMP-9, has been found to be significantly higher in exposed to biomass and tobacco smoke when compared with unexposed healthy controls. Moreover, the levels of those enzymes have been found in negative correlation with the lung function indexes ( $FEV_1$  %pr) [22].

Matrilysin 1 has also been reported to associate with moderate panlobular emphysema as well as with severe and moderate centrilobular emphysema [30]. Matrilysin 1 efficiently cleaves the basement membrane protein entactin, which bridges laminin and collagen type IV, and suggested a potentially important role for MMP-7 in the disruption of basement membranes by inflammatory cells [31]. Matrilysin 1 is produced by the epithelium of several uninjured, uninfamed tissues, such as lung, liver and breast. Except in intact tissues, matrilysin is expressed in migrating epithelium in injured airways [5].

It has been shown that MMP-7 mediates shedding of E-cadherin from alveolar epithelium during progression of bleomycin-induced pulmonary fibrosis [7]. In specimens of emphysema, strong immunoreactive signal for matrilysin protein has been detected in epithelial cells lining damaged alveoli, especially in cells bordering denuded epithelium [6]. The higher promoter activity of the G allele may contribute to ongoing epithelial activation by mediating persistent shedding of the E-cadherin ectodomain, altering cell-cell interactions. By cleaving the Fas ligand, matrilysin can regulate apoptosis and it may promote local coagulation by cleaving tissue factor pathway inhibitor [31]. Altogether, these data suggest that the carriers of the G allele may lead to disruption of ECM and cell-cell interactions, impairment of the process of tissue repair or fibrosis, and thus, to early development of COPD.

In conclusion, the results of our study suggest that *MMP7*-181A>G (rs11568818) promoter polymorphism might affect the risk for COPD, as the carriers of the G allele (AG and GG genotypes) could be considered as predisposing factors for early onset of COPD. This effect could be attributed to the increased production of the enzyme resulting in enhanced airway wall protein degradation and

injury due to its direct ability for ECM degradation. In this respect, the latter suggestion is warranted to be proven by analyzing the possible association of genotypes with serum MMP-7 levels in patients with COPD.

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**Declaration of Interest.** The authors report no conflicts of interest. The authors alone are responsible for the content and writing of this article.

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