

Glutathione S-transferase P1 (GSTP1) polymorphism in patients with chronic obstructive pulmonary disease

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Abstract

Background—Enzymes that contribute to the local detoxification in alveoli and bronchioles have an important role in the defence mechanism against tobacco smoke. It has been suggested that genetic susceptibility to smoking injury may confer a risk for the development of chronic obstructive pulmonary disease (COPD). The polymorphisms in glutathione S-transferase P1 (GSTP1), a xenobiotic metabolising enzyme, were investigated in patients with COPD.

Methods—Polymerase chain reaction (PCR) and restriction fragment length polymorphism (RFLP) were performed to genotype GSTP1 polymorphisms in exon 5 (Ile105Val) and exon 6 (Ala114Val). Blood samples were taken from 53 patients with COPD and 50 control subjects at the Tokyo University Hospital, the Juntendo University Hospital, and the Tokyo Kenbikyoin Clinic for use in the study.

Results—The proportion of GSTP1/Ile105 homozygotes was significantly higher in the patients with COPD than in the control subjects (79% vs 52%). The odds ratio for GSTP1/Ile105 homozygotes versus all other genotypes was 3.5 (95% CI 2.7 to 4.6) for COPD. Polymorphism at residue 114 of GSTP1 was not found in either group.

Conclusions—Genetic polymorphism of exon 5 of GSTP1 may be associated with COPD because the GSTP1/Ile105 genotype is predominantly found in COPD. It is suggested that the GSTP1/Ile105 genotype may be less protective against xenobiotics in tobacco smoke.

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Keywords: glutathione S-transferase P1 (GSTP1); polymorphism; chronic obstructive pulmonary disease; tobacco

Chronic obstructive pulmonary disease (COPD) is characterised by irreversible airflow limitation in the lungs.¹ Although COPD is now the 12th largest burden in the world, it is estimated that it will rise to be the fifth largest burden by 2020.²

Two major hypotheses on the cause of COPD and emphysema—namely, the protease-antiprotease hypothesis and the oxidant-antioxidant hypothesis—were put forward over 30 years ago.^{3,4} It is believed that xenobiotics, which include reactive epoxides and benzo(a)pyrene, are also involved in the

pathogenesis of COPD by their ability to inhibit antiproteases⁵ and promote cell and tissue damage in the lungs. The most important risk factor for the development of COPD is smoking. However, only 10–20% of chronic heavy smokers develop symptomatic COPD,^{6,7} which indicates that a difference in susceptibility to tobacco smoke injury must exist and may be related to genetic factors. Furthermore, a recent study suggested that familial factors other than protease inhibitors might influence the development of airflow obstruction and chronic bronchitis.⁸

Glutathione S-transferases (GSTs) consist of a superfamily of dimeric phase II metabolic enzymes that catalyse the conjugation of reduced glutathione with various electrophilic compounds. GSTs may play an important part in cellular defence by detoxifying various toxic substrates in tobacco smoke.⁹ GSTs are separated into the following classes: alpha (GSTA), mu (GSTM), pi (GSTP), theta, sigma, and kappa. GSTM is genetically polymorphic and it has been shown that deletion of a partial locus of this gene is associated with lung cancer and emphysema.¹⁰

Polymorphisms of GSTP1 have been reported—for example, isoleucine (Ile) 105 valine (Val) in exon 5, alanine (Ala) 114 valine (Val) in exon 6.¹¹ The activity of this enzyme is affected by substitution at position 105 which is located in the hydrophobic substrate binding site, and this has considerable effects depending on the type of chemical reaction.¹² Individuals with the 105Val allele have a higher risk of developing lung cancer than those with the 105Ile allele.¹³ However, it has recently been suggested that GSTP1/Val105 has a higher catalytic efficiency than GSTP1/Ile105 with regard to the metabolism of carcinogenic aromatic epoxides.¹⁴ In addition, GSTP1 is expressed more abundantly in alveoli, alveolar macrophages, and respiratory bronchioles than GSTM and other kinds of GSTs that are not expressed in the peripheral lungs.¹⁵

In this study we investigated whether the polymorphism of GSTP1 gene has an association with the development of COPD using a polymerase chain reaction (PCR) based genotyping assay to detect variant forms of GSTP1.

Methods

The patient group consisted of 53 men with COPD diagnosed by pulmonary function tests (FEV₁/FVC <70%) and chest radiography who presented at the Tokyo University Hospital and the Juntendo University Hospital. Their serum

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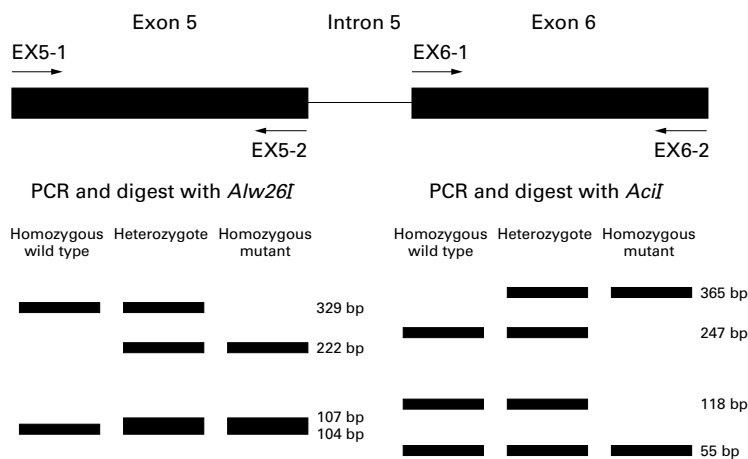


Figure 1 PCR based genotyping assays for GSTP1 polymorphism. Top panels show arrangement of exons 5 and 6. Lower panels show fragment patterns expected in individuals homozygous or heterozygous for GSTP1 polymorphisms.

α_1 -antitrypsin levels were within the normal range (mean (SE) 254.0 (7.4) mg/dl (range 159–391)). Blood samples from 50 control healthy subjects were obtained from the Health Check Division at the Tokyo Kenbikyoin Clinic.

All the patients were diagnosed as having COPD according to the guideline of the European Respiratory Society and the definition of COPD given by Fletcher and Pride.^{16, 17} The diagnosis was based on the signs and symptoms, pulmonary function tests (including forced expiratory volume in one second (%FEV₁), residual volume (RV)/total lung capacity (TLC), carbon monoxide transfer factor (TLCO)) under stable conditions (not at the time of exacerbation of the disease), and chest radiography (including CT scan). There were no patients with asthma included in the COPD group; 75% of the patients were receiving methylxanthine and 66% inhaled anticholinergic agents; 25% received inhaled β adrenergic agonist and inhaled corticosteroid,

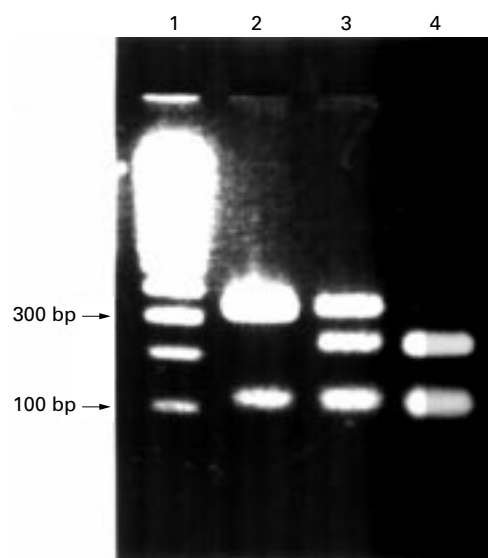


Figure 2 Representative electrophoresis gels with band visualisation in exon 5 polymorphism of GSTP1 showing only larger diagnostic bands. Lane 1, 100–1000 bp DNA ladder (the difference of each band is 100 bp); lane 2, homozygous mutant; lane 3, heterozygote; lane 4, homozygous wild type.

of which 15% received an oral β adrenergic agonist and less than 10% received oral prednisone. To remove the effects of sex differences and to match the smoking history, all control subjects were male and were current smokers free from pulmonary disease with normal pulmonary function test results. None of the control subjects had family members affected by COPD.

Genomic DNA was extracted from whole blood using the QIAamp Blood Kit (QIAGEN Inc, California, USA).

Because GSTP1 has been known to have two genetic polymorphisms in exon 5 and exon 6, two separate PCR assays were used to detect the two polymorphisms as follows: guanine to adenine transition in exon 5 changes Ile105 to Val, and transition of cytosine to thymidine in exon 6 changes Ala114 to Val at the protein level. The PCR and restriction fragment length polymorphism (RFLP) studies were performed using methods described by Watson *et al*¹⁸ with a slight modification.

Briefly, the assay for the exon 5 variant uses the primer pair EX5-1 (5'-GTAGTTTGCC CAAGGTCAAG-3' starting at 2306 bp in GSTP1 complete code, GDB accession number X08058) and EX5-2 (5'-AGCCACCTGAGG GGTAAG-3' starting at 2721 bp). PCRs were carried out using the program temperature control system PC-800 (Astec, Tokyo, Japan). 100 ng of genomic DNA was added to a mixture containing 11 pmol of each primer, 0.5 U AmpliTaq Gold with 1.5 μ l 10 \times PCR buffer (containing 25 mM MgCl₂) and 1.5 μ l of 10 \times dNTPmix (Perkin-Elmer Applied Biosystems Division, California, USA) in a final volume of 15 μ l. The "auto-hot start" was used to prevent non-specific priming in the first cycle of PCR. Following an initial denaturation step at 95°C for 12 minutes, 15 cycles of PCR were performed (denaturation at 95°C for 30 seconds, annealing at 58°C for 30 seconds, elongation at 72°C for 60 seconds), followed by 25 cycles of amplification (denaturation at 95°C for 30 seconds, annealing at 55°C for 30 seconds, elongation at 72°C for 60 seconds) and one cycle of elongation at 72°C for five minutes. The PCR products were digested for two hours at 37°C with five units of *Alw26I* (Fermentas Inc, Vilnius, Lithuania).

The assay for the exon 6 variant was performed with the primer pair EX6-1 (5'-GGGAGCAAGCAGAGGAGAAT-3' at 3402 bp) and EX6-2 (5'-CAGGTTGTAGT CAGCGAAGGAG-3'). Following an initial denaturation step at 95°C for 12 minutes, 40 cycles of PCR were carried out (denaturation at 95°C for 30 seconds, annealing at 62°C for 30 seconds, and elongation at 72°C for 60 seconds) followed by one cycle of elongation at 72°C for five minutes. The PCR products were digested for two hours at 37°C with 5 units of *AclI* (New England BioLabs Inc, Massachusetts, USA). All the digests were electrophoresed on a gel with 3.5% Ultrapure Agarose (GibcoBRL, Maryland, USA) containing ethidium bromide. These assays are illustrated in fig 1 and the actual bands electrophoresed are shown in fig 2.

Table 1 Basic characteristics of the COPD and control groups

	COPD (n=53)	Control (n=50)
Age (years)	68.7 (9.4)	56.7 (4.1)
Pack years	50.4 (4.2)	42.9 (1.9)
%VC	90.3 (2.8)	102.0 (1.5)
FEV ₁ /FVC (%)	44.7 (1.6)	80.2 (0.6)
%FEV ₁	46.7 (2.3)	96.4 (1.5)

All values are mean (SE).

VC = vital capacity; FEV₁ = forced expiratory volume in one second; FVC = forced vital capacity.

ANALYSIS OF DATA

The difference in allele distribution and frequency in each group was examined by the χ^2 test, with the Fisher exact test where appropriate. Age, smoking index expressed as pack years (number of packs of tobacco smoked per day \times number of years smoked) and values of pulmonary function tests in the two groups were compared using the unpaired Student's *t* test. These analyses were performed using the StatView J-4.5 application program (SAS Institute Inc, North Carolina, USA). *p* values of <0.05 were considered statistically significant. All values are represented as mean (SE).

Results

Age, smoking history, and the results of pulmonary function tests of the two groups are shown in table 1. The difference in the mean tobacco consumption between the COPD patients and the control subjects was not significant. The mean (SE) FEV₁/FVC of the COPD group was approximately 50% lower than the control group (44.7 (1.6)% vs 80.2 (0.6)%).

The results of genetic polymorphism in exons 5 and 6 of GSTP1 are summarised in table 2. In exon 5 105Ile homozygote was the predominant genotype in each group; 105Val homozygosity is very uncommon in the Japanese population and in the present study only two individuals with this homozygote were found in the control group. 105Ile genotype was significantly more frequent in the COPD group than in control group (0.90 and 0.74, respectively). The odds ratio for GSTP1/Ile105 homozygotes versus all other genotypes was 3.5 (95% CI 2.7 to 4.6) for COPD. However, in exon 6 the 114Ala allele was found in both the COPD and control groups, and the 114Val allele was not found in either group.

Discussion

Chronic tobacco smoking is the major risk factor for the development of COPD, but only a relatively small proportion of smokers actually

develop airway obstruction. Genetic factors are related to this susceptibility and include genes regulating the protease-antiprotease and oxidant-antioxidant interactions. It has recently been suggested that genetic polymorphisms of cytochrome P450,¹⁹ microsomal epoxide hydrolase (mEPHX),²⁰ and tumour necrosis factor- α ²¹ may be associated with emphysema or COPD. In this report the contribution of gene encoding xenobiotic enzymes which metabolise the tobacco constituents has been investigated.

We have studied the genotype distribution of polymorphisms at positions 105 and 114 in GSTP1, an enzyme involved in protection against xenobiotics in the lung. The 105Ile genotype was found more frequently in the COPD group than in the control group, and the odds ratio for homozygotes of 105Ile was 3.5. The allele frequency of 105 amino acid of the control group is reported to be more similar to Taiwanese subjects than to Caucasians.¹⁸ The activity of this enzyme is influenced by substitutions in position 105 which is located in the hydrophobic substrate binding site. The effect of this polymorphism varies with the type of chemical reaction—for example, in reactions of Michael addition, nucleophilic addition and epoxide conjugation, and catalytic activity of GSTP1.¹² Although individuals with the 105Val allele have a higher risk of developing lung cancer than those with the 105Ile allele,¹³ it was also recently suggested that GSTP1/Val105 has a higher catalytic efficiency than GSTP1/Ile105 for carcinogenic aromatic epoxides.¹⁴ These findings therefore suggest that GSTP1 might catalyse the detoxification of some xenobiotics in the tobacco smoke and that this reaction might be also catalysed by GSTM, mEPHX, and cytochrome P4501A1, but not by glutathione peroxidase. In addition, GSTP1 differs from other GSTs in not having glutathione peroxidase activity.²² Epoxides can be detoxified principally by GSTs or epoxide hydrolases, and these have been reported to be associated with emphysema.²⁰

Furthermore, gene expression of GSTP1 in alveoli, alveolar macrophages, and respiratory bronchioles is more abundant than of GSTM and other GSTs which are not expressed in the lung.¹⁵ It is therefore possible that GSTP1 may play an important role in local detoxification of xenobiotics such as mEPHX in the lung.

Although exposure to tobacco smoke can alter the expression of some xenobiotic metabolising enzymes, Watson *et al* found no apparent relationship between smoking history

Table 2 Distribution of exon 5 and exon 6 polymorphism of GSTP1 genotypes in COPD and control groups

	Number of individuals (% of group)			Odds ratio (95% CI) for homozygotes of wild type	Major allele frequency
	Homozygous wild type	Heterozygote	Homozygous mutant		
Exon 5 polymorphism (Ile105Val)					
Control group	26 (52%)	22 (44%)	2 (4%)	1	0.74
COPD group	42 (79%)*	11 (21%)	0 (0%)	3.5 (2.7 to 4.6)	0.90
Exon 6 polymorphism (Ala114Val)					
Control group	50 (100%)	0 (0%)	0 (0%)		1.00
COPD group	53 (100%)	0 (0%)	0 (0%)		1.00

**p* = 0.009.

and 1-chloro-2,4-dinitrobenzene (CDNB) activity, which reflects the activity of the GSTs, in lung tissue. They also reported that individuals with the 105Val allele tended to have lower CDNB activity in the lung tissue of non-smokers, former smokers, and current smokers than those with the 105Ile allele, although the difference was not statistically significant.¹⁸

Tobacco smoke contains about 4000 substrates including carcinogenic agents and other possible causative agents of COPD such as volatile aldehydes and hydrogen cyanide.²³ GSTP1 prevents the inhibition of embryonic retinoic acid synthesis by aldehydes of lipid peroxidation.²⁴ It was also found recently that normal alveoli were restored by treatment with retinoic acid in elastase induced experimental emphysema.²⁵ In contrast, it has also been reported that retinoic acid treatment increased GSTP1 gene expression significantly in MGR3 cells, a human glioblastoma multiform cell line.²⁶ It is therefore also possible that the preventive role of GSTP1 in the development of COPD may be explained by its interaction with retinoic acid.

In this study the 114Val allele was not found in either group of subjects. If this allele exists in the Japanese population it is very rare and is therefore not an important contributing factor in the development of COPD in the Japanese population.

In summary, we have shown that the 105Ile genotype in exon 5 of GSTP1 might be associated with the pathogenesis of COPD. In terms of the number of subjects examined, this study is a preliminary work and a further study using a larger population is needed to clarify the association of the exon 5 polymorphism of the GSTP1 gene with individual susceptibility to development of COPD. Furthermore, in addition to the possible link between mEPHX and emphysema, investigation of the function of other xenobiotic enzymes such as GSTP1 may provide more insight to the pathogenesis of emphysema or COPD in smokers.

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