МОНГОЛ УЛСЫН БОЛОВСРОЛ, СОЁЛ, ШИНЖЛЭХ УХААН, СПОРТЫН ЯАМ АНАГААХЫН ШИНЖЛЭХ УХААНЫ ҮНДЭСНИЙ ИХ СУРГУУЛЬ



МӨНХЗОРИГИЙН ЭНХБИЛЭГ

# УУШГИНЫ АРХАГ БӨГЛӨРӨЛТ ӨВЧНИЙ ҮЕД *TGFB1*, *MMP9* ГЕНИЙН ПОЛИМОРФИЗМЫГ СУДАЛСАН ДҮН

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# ТОВЧ ХУРААНГУЙ

**Түлхүүр үг:** Уушгины архаг бөглөрөлт өвчин, *TGFB1, MMP9,* нэг нуклеотидын полиморфизм

**Сэдвийн нэр:** Уушгины архаг бөглөрөлт өвчний үед *TGFB1, MMP9* генийн полиморфизмыг судалсан дүн

**Үндэслэл:** УАБӨ үүсэх эрсдэлт хүчин зүйлд агаарын бохирдол, амьдралын хэв маяг, тамхидалт зэрэг гадаад орчны хүчин зүйлс нөлөөлдөг. 2015 оны судалгаагаар дэлхийн даяар 329 сая хүн УАБӨ-өөр өвчилсөн байдаг. Нөгөө талаас УАБӨ үүсэхэд хувь хүний бие махбодын онцлог, уушгины гаж хөгжил, хөгшрөлт, удамшлын хүчин зүйл зэрэг нөлөөлж байна. Тухайлбал, *TGFB1* генийн rs1800470 полиморфизмын гомозигот CC /C+869T/ генотиптэй өвчтөнүүдийн цусны ийлдсэнд TGFβ1 уургийн идэвхөндөр байдаг нь тогтоожээ. Мөн MMP9 генийн rs3918242 полиморфизмын гомозигот TT генотиптэй үед MMP9 уураг их хэмжээтэй байдаг гэсэн судалгаа байдаг. TGFβ1 болон MMP9 уургийн хэмжээ нэмэгдсэнээр УАБӨ-ний үед жижиг бронхи болон альвеолын хананд фиброз үүсэлт нэмэгдэж сорвижилт бий болсноор альвеолын тэлэх чадвар алдагдаж, уушгины агаарын хийн солилцоо буурч, УАБӨ-өөр өвчлөх эрсдэл нэмэгддэг байна.

**Хэрэглэгдэхүүн ба арга зүй:** Судалгаанд хяналтын бүлэгт 100, тохиолдлын бүлэгт 100 хүнийг хамруулсан. *TGFB1* генийн rs1800470 полиморфизмыг ПГУ-д суурилсан огтлогдсон хэрчмийн уртын полиморфизмын (RFLP-Restriction Fragment Length Polymorphism) аргаар олшруулж, бүтээгдэхүүнийг *MspA1I* гэсэн өвөрмөц рестрикцийн эсгэг ашиглан зүсэж, үр дүнг 2.8%-ийн агарозын гельд гүйлгэн тодорхойлсон. Цусны сийвэн дэх MMP-9 уургийн концентрацыг хүний MMP9 уураг илрүүлэх цомог ашиглан тодорхойлсон. Статистик боловсруулалтыг Microsoft Excel, STATA 13.0 программ ашиглан гүйцэтгэсэн.

**Үр дүн:** Бидний судалгааны үр дүнгээр *TGFB1* генийн rs1800470 полиморфизмын лейцин, пролин аллелийн давтамж судалгааны бүлгүүдэд ач холбогдол бүхий ялгаатай, гомозигот лейцин генотип нь тохиолдлын бүлэгт өндөр давтамжтай (OR=2,43; 95% ИИ 1,08-5,46; p=0.02) байгаа нь УАБӨ-д бага зэргийн эрсдэлт нөлөөтэй байлаа. Харин цусны сийвэн дэх MMP9 уургийн түвшин бүлгүүдэд харьцуулалт хийхэд статистик ач холбогдол бүхий ялгаа илэрсэнгүй.

**Дүгнэлт:** Бидний судалгааны үр дүнгээр *TGFB1* генийн rs1800470 полиморфизм УАБӨ үүсэх эрсдэл нөлөөтэй байж болзошгүйг харуулж байна. Мөн *MMP9* генийн rs3918242 полиморфизм УАБӨ-д эрсдэлт нөлөөгүй байлаа.

# ABSTRACT

**Keywords:** COPD, Transforming growth factor beta-1, polymorphism, *TGFB1, MMP9*

**Title:** The result of *TGFB1* and *MMP9* gene polymorphism in patients with COPD

**Background:** A COPD is globally distributed disease and increasing due to air pollution, life style, and smoking. As of 2015 COPD affected 329 million people or nearly 5.8 percent of the global population. An environmental and internal factors lead to develop COPD. As an example of internal factor CC homozygote of rs1800470 polymorphism (*TGFB1* gene) can increase serum TGF-β1 in patients, increasing alveolar and bronchial fibrosis, alveolar destruction and reduced air ventilation.

**Objective:** To investigate rs1800470 polymorphism of *TGFB1* gene and rs3918242 polymorphism of *MMP9* gene in COPD

**Materials and methods:** We involved 100 patients with COPD and 100 healthy individuals for the case–controls study. Restriction fragment length polymorphism (RFLP) analysis was performed to determine the rs1800470 polymorphism in exon 1 of the *TGB1* gene. The PCR products were digested with *MspA1I* restriction enzyme. The restricted DNA fragments were electrophoresed on a 2.5% agarose gel. The total MMP9 concentration in the serum samples was measured by using the human MMP-9 immunoassay (ELISA; R&D system Inc). Statistical analyses were performed using Microsoft Excel and STATA 13.0 software.

**Results:** Our result showed that there was significant association between rs1800470 polymorphism of *TGFB1* gene and an increased risk of COPD. Allele frequencies of Leu and Pro were significantly different between the two groups ($p<0.05$). Genotype frequency of the homozygote Leu/Leu polymorphism in COPD patients was significantly different from healthy control. COPD patients group with the CC (OR=2.43; 95% CI 1.08-5.46; p=0.024) genotype had a higher frequency of COPD. Serum concentration of MMP-9 was not significantly higher in COPD patients than in control subjects.

**Conclusion:** The *TGFB1* gene polymorphism might be one of the genetic factors that make these patients more susceptible to the risk of COPD development than healthy subject. However rs3918242 polymorphism of MMP couldn't be the causative variable of COPD.

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