Discovery of URAT1 SNPs and association between serum uric acid levels and URAT1

Sung Kweon Cho,1 Soril Kim,2 Jae-Yong Chung,3 Sun Ha Jee2

ABSTRACT

Objectives: Human urate transporter 1 (URAT1) is a member of the organic anion transporter family (SLC22A12) that primarily regulates the renal tubular reabsorption of uric acid. This case–control study was designed to analyse whether hURAT1 might also be a candidate gene for hyperuricaemia or hypouricaemia.

Setting: We recruited 68 healthy volunteers and divided them into two groups: a normal uric acid group and a hyperuricaemia group. We analysed the sequence of the URAT1 gene and found five significant single nucleotide polymorphisms (SNPs). We then selected 900 male subjects from the 262 200 enrolled in the Korean Cancer Prevention Study-II (KCPS-II) cohort for further genetic analysis.

Participants: DNA samples from 36 individuals with normal uric acid (<4.5 mg/dL) and 32 individuals with hyperuricaemia (>8.5 mg/dL) were sequenced. Five significant SNPs (rs7929627, rs75786299, rs3825017, rs11602903 and rs121907892) were identified. We then chose 900 subjects from the KCPS-II cohort consisting of 450 subjects with normal uric acid (UA <4.5 mg/dL) and 450 subjects with hyperuricaemia (UA >8.7 mg/dL). The groups were matched by age, body mass index, metabolic syndrome and use of anti-hypertensive medication.

Primary outcome measures: We compared the OR of the incidence of hyperuricaemia by URAT1 genotype.

Results: The strongest association with hyperuricaemia was observed for rs7929627 (IVS7-103A/G) and rs3825017 (N82N) which showed an association with hyperuricaemia with ORs of 32.05 and 0.350, respectively. Individuals carrying the GATAG haplotype (n=32) showed the highest risk for hyperuricaemia with an OR of 92.23 (p=9.55×10−3).

Conclusions: These results indicate that five newly described SNPs in the hURAT1 gene are significantly associated with uric acid level (4-2008-0318 and 4-2011-0277).

INTRODUCTION

Uric acid is the final metabolic product of purine nucleotides in humans. An elevated level of serum uric acid is a risk factor for gout.1 Uric acid is produced primarily in the liver, and two-thirds of it is excreted via the kidney. A deficit in uric acid excretion results in hyperuricaemia, leading to diseases such as gout. On the other hand, an increase in uric acid excretion causes urolithiasis. The uric acid transport system of renal proximal tubules plays an important role in the determination of serum uric acid levels.2 Uric acid enters the proximal tubules in its anion form. In humans, uric acid is almost fully reabsorbed through the kidney; only 10% of filtered acid is secreted.2 Absence of the enzyme uricase and the presence of an effective renal anion transport system contribute to higher uric acid levels in humans than in other mammals.3 4 Uric acid serum level in the general population follows a normal distribution.1 The intake of purines or fructose may influence serum uric acid level. Genetic factors may explain the critical process of uric acid reabsorption and its role in hyperuricaemia. The heritability of uric acid serum concentration has previously been estimated to be 40–70%.5 6 Strong evidence of this can be seen in studies7 and segregation analysis in

Strengths and limitations of this study

- This study provides new understanding of asymptomatic hyperuricaemia observed during clinical trial screenings or regular medical checkups.
- This study was well powered and well controlled: 900 subjects selected from the Korean Cancer Prevention Study-II cohort, were divided into a hyperuricaemia group (n=450) and a normal group (n=450), and matched for age, body mass index, metabolic syndrome and use of anti-hypertensive medication.
- The result of this study is limited to healthy Korean subjects with hyperuricaemia.
- Longitudinal and disease-course studies are needed to evaluate the relevance of URAT1 SNPs in gout and other metabolic diseases.
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10 identi
et al
SNP, we validated the
dL (0.076 µmol/L) and 32 with uric acid levels above
Korean subjects (36 with uric acid levels below 4.5 mg/
study, we conducted full direct sequencing in 68 healthy
of URAT1 with serum uric acid in Korean subjects. In this
not found in German or Czech Caucasians subjects.16 17
mutation, W258X for hypouricaemia, and other
hypouricaemia-related SNPs in Japanese patients, were
It is well known that W258X (rs121907892) is associated
It
families.8 Kottgen et al9 recently reported that 28 genetic
loci could explain the observed 6% variance in uric acid in
European Caucasian subjects. The most influential
loci, as one might expect, encode proteins involved in
secretion and renal filtration of uric acid. Since Enomoto
et al10 identified the urate transporter in the human
kidney (URAT1, encoded by SLC22A12), a urate–anion
exchanger localised on the apical side of the proximal
tubule, many genome-wide association studies (GWAS)
and target SNP studies have found significant polymorph-
isms in different ethnic groups.11–15 The most frequent
mutation, W258X for hypouricaemia, and other
hypouricaemia-related SNPs in Japanese patients, were
not found in German or Czech Caucasians subjects.16 17
It is well known that W258X (rs121907892) is associated
with hypouricaemia in Korean individuals.12 Recently, a
high frequency of SLC22A12 variants (c.1245_1253del
c.1400C>T; 1.87% and 5.56%, respectively) which
contribute to renal hypouricaemia was reported in the
Roma population.18 Our aim was to clarify the association
of URAT1 with serum uric acid in Korean subjects. In this
study, we conducted full direct sequencing in 68 healthy
Korean subjects (36 with uric acid levels below 4.5 mg/
Dl (0.076 µmol/L) and 32 with uric acid levels above
8.5 mg/dL (0.14 µmol/L)). After selection of a tagging
SNP, we validated the five significant URAT1 SNPs in 900
men chosen from the Korean Cancer Prevention Study-II
(KCPS-II) cohort.

MATERIALS AND METHODS
Discovery of URAT1 variants by direct sequencing
Sixty-eight male genomic DNA samples were selected
from healthy individuals from the DNA bank of
Severance hospital, Seoul, Korea (4-2008-0318) taking
into account uric acid level (36 subjects with levels below
4.5 mg/dL (0.076 µmol/L) and 32 subjects with levels
above 8.0 mg/dL (0.13 µmol/L)). Ethics approval was
obtained from Severance institutional review board and
all participants provided informed consent. The health
status of each individual was evaluated by routine physical
examination and laboratory tests. Participants were
divided into two groups: a normal uric acid group that
included hypouricaemic individuals, and a hyperuricae-

dma group. To identify genetic variants of URAT1, the
entire 5802 bp URAT1 gene including the coding region,
flanking intronic sequences and 3′UTR region was ampli-
fied and sequenced using an automated genetic analyzer
(Applied Biosystems, Foster City, California, USA).
Haplotype assembly was performed using the programme
Haplovie (V.4.2; developed by the Broad Institute,
Cambridge, Massachusetts, USA). Nucleotide location
numbers were assigned from the translational start site
(GenBank accession number: AB071863).

SNP selection
Study-specific association analyses for sequencing the
data of the 68 subjects were performed using linear
regression for uric acid, assuming an additive genetic
model. For uric acid, the covariates were age and body
mass index (BMI). Excluding SNPs of less than 1% allele frequency, we selected eight SNPs as tagging SNPs
with high linkage disequilibrium (LD) (r²>0.8). Among
these eight SNPs, five URAT1 SNPs significant for uric
acid were selected as candidate SNPs for the replication
cohort.

Data collection of replication cohort
The KCPS-II cohort consisted of 262 200 participants
who were given routine health examinations at health
promotion centres in South Korea from 1994 to 2012.
Baseline data were collected by trained interviewers.
Information on socio-demographic factors, health status
and lifestyle was included in the questionnaires. A
general health examination was performed at the same
time. Standing height, body weight and waist circumfer-
ence were measured with participants wearing light
indoor clothing and without shoes. BMI was calculated
as weight in kilograms divided by height in metres
squared. For each individual, blood was drawn after at
least 8 h of fasting for whole blood and serum samples.
Uric acid, creatinine, triglyceride, total cholesterol, low
density lipoprotein (LDL) cholesterol, high density lipo-
protein (HDL) cholesterol and blood glucose levels
were measured using an Hitachi-7600 analyzer. Nine
hundred male subjects were selected from the KCPS-II
cohort according to the following criteria: (1) 450 sub-
jects with a uric acid level below 4.1 mg/dL (normal

group including hypouricaemia) and 450 subjects with a
uric acid level above 8.7 mg/dL (hyperuricaemia
group); and (2) age, BMI and subjects with metabolic
syndrome or taking anti-hypertensive drugs were equally
distributed into the two separate groups. All 900 subjects
agreed to provide DNA samples (4-2011-0277). To opti-
mise the effect of the URAT1 SNPs, other factors affect-
ing uric acid were balanced between the two groups.

Association analysis
After ensuring demographic similarity between the two
groups (table 1), we estimated the effects of five signifi-
cant URAT1 SNPs on uric acid as an OR using a multi-

variate binary logistic regression method. BMI, systolic
blood pressure, diastolic blood pressure, total chol-
esterol, triglyceride, fasting glucose, LDL cholesterol, HDL
cholesterol and creatinine are included as covariates.
Pearson’s χ² test was used to calculate the allelic risk
of hyperuricaemia. The data were analysed using SPSS
software V.18 (SPSS, Chicago, Illinois, USA). In general,
p values of <0.05 were considered statistically significant,
but we used adjusted p values based on the Bonferroni
correction when we performed multiple statistical tests
simultaneously.

Haplotype association analysis
Haplotype imputation by expectation maximisation was
performed in PLINK to produce the most likely

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haplotype calls. These data were then used to perform a BMI, systolic blood pressure, diastolic blood pressure, total cholesterol, triglyceride, fasting glucose, LDL cholesterol, HDL cholesterol and creatinine-adjusted logistic regression in PLINK, producing ORs and p values.

Locus-specific hyperuricaemia genetic risk score and correlation with uric acid level

We used the simple count method to calculate the genetic risk score (GRS) of five URAT1 SNPs. In case of loss-of-function URAT1 polymorphism, a score of 3 was assigned to those homozygous for the reference allele, 2 to heterozygotes, and 1 to those homozygous for the loss-of-function allele. In case of gain-of-function URAT1 polymorphism, 1 was assigned to those with the reference allele, 2 to heterozygotes, and 3 to those homozygous for the gain-of-function allele. In this study the GRS ranges from 3 to 15. Subjects were divided into four groups of 225 each based on GRS score, from low to high. The GRS distribution of the four groups was: 0<GRS<5.0, 5.0≤GRS<6.0, 6.0≤GRS<7.0 and 7.0≤GRS. Where the hyperuricaemia group and the normal group had the same GRS, we estimated the incremental GRS quintile effect on hyperuricaemia versus the normal ratio with reference to the Q1 group. The attenuation of the association of GRS of the hyperuricaemia group versus the normal group in a balanced demographic sampling from the cohort suggests a causal association between URAT1 SNPs and uric acid.19

RESULTS

URAT1 SNP discovery and association analysis with uric acid

Whole sequencing of URAT1 was performed in 68 male Korean subjects, divided into a hyperuricaemia group and a normal control group (including hypouricaemia). Sequencing revealed 26 SNPs in the URAT1 gene (table 2). Our study is the first to identify one SNP in the promoter region (c.-46G>A) and three non-coding variants (c.506+32T>C, c.662-18C>G and c.1395-105C>T) of URAT1. Excluding mono call error, we conducted a correlation analysis of 26 URAT1 SNPs with uric acid (data not shown). We plotted 19 URAT1 SNPs, excluding SNPs of less than 1% allele frequency. From 19 SNPs, we selected eight SNPs as tagging SNPs with high LD (r2>0.8). The eight SNPs are rs11602903, rs7929627, rs476037, rs373337426, rs75786299, rs148845071, rs3825017 and...
rs121907892. rs11602903 represents rs974313, rs825016, rs825018, rs524023, rs11251825, rs1529909, rs2021860 and rs799496. rs7929627 represents rs11291837 and rs7932775. rs76037 represents rs3832794. Five tagging SNPs (rs7929627, rs75786299, rs825017, rs11602903 and rs121907892) significantly associated with uric acid were selected for replication.

Genotype associations and allelic associations
We examined the relationship between the five selected URAT1 SNPs and hyperuricaemia incidence in the discovery and replication stage of this study (table 3). All five selected SNPs showed a significant (p<0.05) association with uric acid level in the discovery stage (data not shown). In the replication stage, it was observed that subjects heterozygous or homozygous for rs7929627 were more likely to be hyperuricaemic than those in the control group (OR=3.32, 95% CI 4.51 to 9.11, p=1.12×10⁻⁸). Subjects heterozygous or homozygous for rs7929627, rs75786299 and rs3825017, and is associated with a gain-of-function mutation (p=0.035; OR=1.48). Haplotype GGTAG contains two gain-of-function SNPs, rs7929627 and rs3825017, and is associated with a significantly increased incidence of hyperuricaemia (p=0.011; OR=1.64). Haplotype GATAG contains three gain-of-function SNPs, rs7929627, rs75786299 and rs3825017, and is associated with a significantly increased incidence of hyperuricaemia (p=92.23). Haplotype AGCAA contains one loss-of-function SNP, rs121907892, and is associated

Haplotype association analysis
We performed logistic regression analysis to evaluate the association between the incidence of hyperuricaemia and haplotype of the five selected SNPs with reference to the AGCG AGCAG haplotype. Haplotype AGCAG SNPs are rs7929627, rs75786299, rs825017, rs11602903 and rs121907892. Haplotype GGCAG contains one gain-of-function SNP, rs7929627, and is associated with a significantly increased incidence of hyperuricaemia (p=0.035; OR=1.48). Haplotype GGTAG contains two gain of function SNPs, rs7929627 and rs3825017, and is associated with a significantly increased incidence of hyperuricaemia (p=0.011; OR=1.64). Haplotype GATAG contains three gain-of-function SNPs, rs7929627, rs75786299 and rs3825017, and is associated with a significantly increased incidence of hyperuricaemia (p=92.23). Haplotype AGCAA contains one loss-of-function SNP, rs121907892, and is associated

Table 2 Frequency of URAT1 genetic variations in Korean subjects

<table>
<thead>
<tr>
<th>rs number</th>
<th>Variant</th>
<th>Amino acid substitution</th>
<th>Minor allele frequency</th>
<th>rs number</th>
<th>Variant</th>
<th>Amino acid substitution</th>
<th>Minor allele frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>Promoter variants</td>
<td></td>
<td></td>
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<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>rs11602903</td>
<td>c.-788A&gt;T</td>
<td>0.265</td>
<td>rs559946</td>
<td>c.-424C&gt;T</td>
<td>0.265</td>
<td></td>
<td></td>
</tr>
<tr>
<td>rs524023</td>
<td>c.-764C&gt;T</td>
<td>0.265</td>
<td>rs3825018</td>
<td>c.-220A&gt;G</td>
<td>0.265</td>
<td></td>
<td></td>
</tr>
<tr>
<td>rs9734313</td>
<td>c.-718C&gt;T</td>
<td>0.265</td>
<td>–</td>
<td>c.-46G&gt;A</td>
<td>0.007</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Coding variants</td>
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<td></td>
<td></td>
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</tr>
<tr>
<td>rs3825017</td>
<td>c.246C&gt;T</td>
<td>0.224</td>
<td>rs121907893</td>
<td>c.650C&gt;T</td>
<td>0.007</td>
<td></td>
<td></td>
</tr>
<tr>
<td>rs3825016</td>
<td>c.258C&gt;T</td>
<td>0.265</td>
<td>rs121907892</td>
<td>c.774G&gt;A</td>
<td>0.44</td>
<td></td>
<td></td>
</tr>
<tr>
<td>rs11231825</td>
<td>c.426T&gt;C</td>
<td>0.265</td>
<td>rs7932775</td>
<td>c.1309T&gt;C</td>
<td>0.427</td>
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<tr>
<td>rs121907892</td>
<td>c.774G&gt;A</td>
<td>0.044</td>
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<td></td>
</tr>
</tbody>
</table>

Data were obtained from DNA samples from 68 unrelated Korean individuals. The position of the variant is based upon the translational start site.
Table 3  Allele association of five tagged SNPs in the normal group and hyperuricaemia group in the replication cohort

<table>
<thead>
<tr>
<th>SNP amino acid change (rs number)</th>
<th>Genotype</th>
<th>Normal uric acid group</th>
<th>High uric acid group</th>
<th>Allele frequency</th>
<th>Allele OR (95% CI)</th>
<th>p Value</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>UA &lt;4.5 mg/dL (&lt;0.076 µmol/L)</td>
<td>UA &gt;8.5 mg/dL (&gt;0.14 µmol/L)</td>
<td>Control</td>
<td>Case</td>
<td></td>
</tr>
<tr>
<td>Discovery stage</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>IVS7-103A/G (rs7929627)</td>
<td>AA</td>
<td>17</td>
<td>7</td>
<td>0.32</td>
<td>0.53</td>
<td>2.37 (1.18 to 4.76)</td>
</tr>
<tr>
<td></td>
<td>AG</td>
<td>14</td>
<td>16</td>
<td>0.015</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>GG</td>
<td>5</td>
<td>9</td>
<td>1.09 (1.01 to 1.17)</td>
<td>0.016</td>
<td></td>
</tr>
<tr>
<td>IVS3+11A/G (rs75786299)</td>
<td>GG</td>
<td>36</td>
<td>27</td>
<td>0.08</td>
<td>1.09 (1.01 to 1.17)</td>
<td>0.016</td>
</tr>
<tr>
<td></td>
<td>GA</td>
<td>0</td>
<td>5</td>
<td>0.83</td>
<td>1.09 (1.01 to 1.17)</td>
<td>0.016</td>
</tr>
<tr>
<td>N82N (rs3825017)</td>
<td>CC</td>
<td>27</td>
<td>13</td>
<td>0.13</td>
<td>0.31</td>
<td>3.13 (1.30 to 7.52)</td>
</tr>
<tr>
<td></td>
<td>CT</td>
<td>9</td>
<td>17</td>
<td>0.09</td>
<td>0.31</td>
<td>0.915 (0.853 to 0.983)</td>
</tr>
<tr>
<td></td>
<td>TT</td>
<td>0</td>
<td>2</td>
<td>0.45</td>
<td>0.31</td>
<td>0.915 (0.853 to 0.983)</td>
</tr>
<tr>
<td>-788A/T (rs11602903)</td>
<td>AA</td>
<td>15</td>
<td>21</td>
<td>0.34</td>
<td>0.19</td>
<td>0.452 (0.204 to 1.003)</td>
</tr>
<tr>
<td></td>
<td>AT</td>
<td>18</td>
<td>10</td>
<td>0.45</td>
<td>0.19</td>
<td>0.452 (0.204 to 1.003)</td>
</tr>
<tr>
<td></td>
<td>TT</td>
<td>3</td>
<td>1</td>
<td>0.45</td>
<td>0.19</td>
<td>0.452 (0.204 to 1.003)</td>
</tr>
<tr>
<td>W258X (rs121907892)</td>
<td>GG</td>
<td>30</td>
<td>32</td>
<td>0.09</td>
<td>0.31</td>
<td>0.915 (0.853 to 0.983)</td>
</tr>
<tr>
<td></td>
<td>GA</td>
<td>6</td>
<td>0</td>
<td>0.45</td>
<td>0.19</td>
<td>0.452 (0.204 to 1.003)</td>
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<td>AA</td>
<td>0</td>
<td>0</td>
<td>0.45</td>
<td>0.19</td>
<td>0.452 (0.204 to 1.003)</td>
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<tr>
<td>Replication stage</td>
<td></td>
<td></td>
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<td></td>
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<tr>
<td>IVS7-103A/G (rs7929627)</td>
<td>AA</td>
<td>236</td>
<td>119</td>
<td>0.27</td>
<td>0.48</td>
<td>2.56 (2.10 to 3.12) (R: A)</td>
</tr>
<tr>
<td></td>
<td>AG</td>
<td>188</td>
<td>228</td>
<td>0.27</td>
<td>0.48</td>
<td>2.56 (2.10 to 3.12) (R: A)</td>
</tr>
<tr>
<td></td>
<td>GG</td>
<td>26</td>
<td>103</td>
<td>0.27</td>
<td>0.48</td>
<td>2.56 (2.10 to 3.12) (R: A)</td>
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<tr>
<td>IVS3+11A/G (rs75786299)</td>
<td>GG</td>
<td>449</td>
<td>419</td>
<td>&lt;0.01</td>
<td>0.03</td>
<td>32.07 (4.37 to 235.44) (R: G)</td>
</tr>
<tr>
<td></td>
<td>GA</td>
<td>1</td>
<td>31</td>
<td>0.03</td>
<td>0.25</td>
<td>2.29 (1.78 to 2.93) (R: C)</td>
</tr>
<tr>
<td>N82N (rs3825017)</td>
<td>CC</td>
<td>345</td>
<td>254</td>
<td>0.13</td>
<td>0.25</td>
<td>2.29 (1.78 to 2.93) (R: C)</td>
</tr>
<tr>
<td></td>
<td>CT</td>
<td>96</td>
<td>168</td>
<td>0.13</td>
<td>0.56</td>
<td>2.29 (1.78 to 2.93) (R: C)</td>
</tr>
<tr>
<td></td>
<td>TT</td>
<td>9</td>
<td>28</td>
<td>0.13</td>
<td>0.56</td>
<td>2.29 (1.78 to 2.93) (R: C)</td>
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<tr>
<td>-788A/T (rs11602903)</td>
<td>AA</td>
<td>136</td>
<td>122</td>
<td>0.42</td>
<td>0.20</td>
<td>0.350 (0.284 to 0.432) (R: A)</td>
</tr>
<tr>
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<td>AT</td>
<td>253</td>
<td>136</td>
<td>0.42</td>
<td>0.20</td>
<td>0.350 (0.284 to 0.432) (R: A)</td>
</tr>
<tr>
<td></td>
<td>TT</td>
<td>161</td>
<td>122</td>
<td>0.42</td>
<td>0.20</td>
<td>0.350 (0.284 to 0.432) (R: A)</td>
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<tr>
<td>W258X (rs121907892)</td>
<td>GG</td>
<td>282</td>
<td>450</td>
<td>0.19</td>
<td>0.01</td>
<td>0.447 (0.242 to 0.72) (R: G)</td>
</tr>
<tr>
<td></td>
<td>GA</td>
<td>164</td>
<td>0</td>
<td>0.19</td>
<td>0.01</td>
<td>0.447 (0.242 to 0.72) (R: G)</td>
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<tr>
<td></td>
<td>AA</td>
<td>4</td>
<td>0</td>
<td>0.19</td>
<td>0.01</td>
<td>0.447 (0.242 to 0.72) (R: G)</td>
</tr>
</tbody>
</table>

p Value is determined by Pearson's $\chi^2$ test in the allele analysis. R, reference allele.
with the absence of hyperuricaemia. Haplotype AGCTA contains two loss-of-function SNPs, rs11602903 and rs121907892, and is associated with the absence of hyperuricaemia. Haplotypes AGCTG and GGCTG were not significantly different from the reference haplotype.

**Gout GRS association**

A simple GRS was calculated to determine the cumulative effect of the URAT1 SNPs. In each set, the incidence of hyperuricaemia was significantly higher than the GRS of the control group (Q1) (table 4). We found a correlation between GRS and incidence of hyperuricaemia (Q1 vs Q2, Q1 vs Q3 and Q1 vs Q4: OR=4.00, \( \text{p} = 2.00 \times 10^{-6} \); OR=5.78, \( \text{p} = 4.50 \times 10^{-10} \); and OR=15.62, \( \text{p}=1.94 \times 10^{-25} \), respectively).

**DISCUSSION**

We found significant uric acid-related URAT1 SNPs that differed between hyperuricaemic and normal or hypouricaemic subjects. Five selected SNPs from the discovery stage showed a significant association with uric acid in the 900 replication cohort subjects. In the haplotype analysis, the OR for the incidence of hyperuricaemia was gradually increased when an individual carried one gain-of-function SNP, two SNPs or three SNPs (OR=1.48, 1.64 and 92.23 respectively). On the other hand, the OR decreased when an individual had one loss-of-function SNP or two such SNPs (OR=0.86 and 0, respectively). Finally, we investigated the effect of URAT1 on uric acid levels using GRS analysis (table 4).

Founder mutation rs121907892 showed the strongest association with hyperuricaemia in our study. In the replication cohort, the uric acid level in individuals homozygous (AA) for rs121907892 was 1.85±0.17 mg/dL (0.031 ±0.0029 µmol/L), while the uric acid of subjects homozygous (AA) for rs121907892 was below 2 mg/dL (0.034 µmol/L). Interestingly, Korean subjects with the rs11602903 allele were at an increased risk for hyperuricaemia, whereas Graessler et al reported that the AA genotype of rs11602903 in German subjects was associated with reduced renal uric acid excretion (OR=1.8, 95% CI 1.129 to 2.993, \( \text{p}=0.0139 \) for fractional excretion of uric acid). Decreased renal uric acid excretion implies increased URAT1 activity, which should correlate with higher uric acid levels. Considering the difference in allele frequency in the two ethnic groups, the risk associated with the allele is comparable. Li et al, studying a Chinese population, showed that people with the rs11602903 allele had an increased incidence of hyperuricaemia. Our tagging SNP, rs7929627, a SNP in intron 7, is genetically identical to rs7932775, a SNP in exon 8. Han Chinese individuals carrying rs7932775 were at increased risk for hyperuricaemia. A recent report on a Caucasian Czech population did not show any significant difference in serum uric acid level associated with rs7932775. Since our replication set focused instead on rs7929627, it is difficult to explain this discrepancy between studies in Caucasian and Asian populations. Further investigation is needed.

Although rs3825017 was not significantly associated with uric acid levels in the Chinese study, it showed a strong association in our study (OR=2.29, 95% CI 1.78 to 2.93, \( \text{p}=3.44 \times 10^{-11} \)). Because the population size of the present study was much larger, it is likely that we observed real effects that would not otherwise have been statistically significant. rs75786299 is the SNP most strongly associated with hyperuricaemia in our study (OR=32.07, 95% CI 4.37 to 235.44, \( \text{p}=3.44 \times 10^{-11} \)). Because of its low allelic frequency (1.8% in Korean subjects), this SNP was not identified by any previous GWAS study. Further functional study is needed to confirm our results, although Lee et al investigated the prevalence of hypouricaemia and its association with two URAT1 SNPs (W258X and T217M). This may be explained by population selection as we did not recruit patients with nephrolithiasis and low uric acid. Further study is needed to investigate patients with nephrolithiasis and low uric acid to demonstrate consistency with the previous report. Second, we could not evaluate all of the significant SNPs from the discovery stage. Since coverage of our five tagged SNPs is in the high LD region (\( r^2 = 0.8 \)), other SNPs might show different results in the replication stage. However, we are confident that these five selected SNPs convincingly illustrate an association of URAT1 with uric acid level in Korean subjects. Third, our study results have not been confirmed in patients with gout or nephrolithiasis. A logical next step is to investigate URAT1 SNP association with gout and nephrolithiasis.

We conclude that the haplotype association of our five selected URAT1 SNPs with hyperuricaemia has a potential predictive benefit. We found the hyperuricaemia related variant in the combined analysis (GATAAG; OR=92.23, \( \text{p}=0.0096 \)), which is associated with a high risk of gout in Korean subjects. We also found the hypouricaemic related variant (AGCTA), which is associated with a high risk for nephrolithiasis. To validate a

### Table 4 Adjusted ORs and 95% CIs for the hyperuricaemia group versus the normal group ratio by genetic risk score (GRS) of URAT1 SNP among 900 subjects

<table>
<thead>
<tr>
<th>GRS quartile</th>
<th>OR</th>
<th>95% CI</th>
<th>( p ) Value</th>
<th>( p ) For trend</th>
</tr>
</thead>
<tbody>
<tr>
<td>Q1</td>
<td>1.00</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Q2</td>
<td>4.00</td>
<td>2.26 to 7.08</td>
<td>( 2.00 \times 10^{-6} )</td>
<td></td>
</tr>
<tr>
<td>Q3</td>
<td>5.78</td>
<td>3.33 to 10.04</td>
<td>( 4.50 \times 10^{-10} )</td>
<td>1.18 \times 10^{-31}</td>
</tr>
<tr>
<td>Q4</td>
<td>15.62</td>
<td>9.32 to 26.19</td>
<td>( 1.94 \times 10^{-25} )</td>
<td></td>
</tr>
</tbody>
</table>
genetic marker for future risk prediction for gout or nephrolithiasis, a large data association study is required that investigates the prevalence of our SNPs in gout patients or subjects who have had kidney stones.

**Contributors** SKC, J-YC, SHJ: participated in research design; SKC, SK: conducted the study; SKC, SK, J-YC: performed data analysis; SKC, SK, J-YC, SHJ: wrote or contributed to the writing of the manuscript.

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**Competing interests** None declared.

**Patient consent** Obtained.

**Ethics approval** Severance hospital institutional review board approved this study.

**Provenance and peer review** Not commissioned; externally peer reviewed.

**Data sharing statement** No additional data are available.

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Discovery of URAT1 SNPs and association between serum uric acid levels and URAT1

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