The Contribution of Genetic Architecture to the 10-Year Incidence of Age-Related Macular Degeneration in the Fellow Eye

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PURPOSE. To correlate a genetic risk score based on age-related macular degeneration (AMD) susceptibility genes with the risk of AMD in the second eye.

METHODS. This is a retrospective, open cohort study consisting of 891 unilateral AMD patients, who were followed for at least 12 months and recruited from three institutes. DNAs were genotyped using Illumina OmniExpress, HumanOmn1.5-8, and/or HumanExome. Survival analyses and Cox proportional hazard models were used to examine the association between 11 AMD susceptibility genes and the duration until second-eye involvement in 499 samples from Kyoto University, which were replicated in two other cohorts. Genetic risk score (GRS) was also evaluated.

RESULTS. The ARMS2 rs10490924 recessive model (hazard ratio [HR]meta = 2.04; Pmeta = 3.4 × 10^{-5}) and CFH rs800292 additive model (HRmeta = 1.77; Pmeta = 0.013) revealed significant associations with second-eye involvement. The dominant model of TNFRSF10A rs13278062, VEGFA rs945080, and CFI rs4698775 showed consistent effects across three datasets (I² = 0%; HRmeta = 1.46, 1.30, 1.51, respectively). The GRS using these five single nucleotide polymorphisms (SNPs) was also significantly associated (HRmeta [per score] = 2.42; P = 2.2 × 10^{-5}; I² = 0%). After 10 years from the first visit, the patients within the top 10% by GRS showed a 51% hazard rate, in contrast to 2.3% among patients within the lowest 10% by GRS.

CONCLUSIONS. We demonstrated that the GRS using ARMS2, CFH, TNFRSF10A, VEGFA, and CFI was significantly associated with second-eye involvement. Genetic risk has high predictive ability for second-eye involvement of AMD.

Keywords: age-related macular degeneration, genetics, second-eye involvement, bilateral AMD

Age-related macular degeneration (AMD) is a major cause of progressive, irreversible visual impairment among elderly populations in developed countries.1-5 Although the impairment of quality of life (QOL) is limited when AMD has been observed in a single eye, QOL will be severely damaged if the second eye is also affected by AMD.6-5 Thus, predicting second-eye involvement of AMD in unilateral cases is of great importance in the clinical setting. So far, while many population-based studies have investigated risk factors for AMD in the first eye, reporting age, cataract, education, sex, smoking, dietary intake, and soft drusen as possible risk factors as well as genetic risk,6-12 risk factors for AMD in the second eye have not been fully evaluated.13-16

In 2013, the largest genome-wide association study on AMD identified 19 AMD susceptibility loci,17 including 12 known loci.18-32 Some of these genes, together with other environmental factors, were proven to be good predictors for AMD development in the first eye by evaluating a prospective cohort with a mean follow-up of 6.5 years.13,14 On the other hand, to what extent these AMD susceptibility genes contribute to second-eye involvement is currently controversial. While cross-sectional evaluation14,33-36 and retrospective longitudinal analysis15 revealed genetic architecture associated with second-eye involvement, a Comparison of Age-related Macular Degeneration Treatment Trial (CATT) study group reported in their subanalysis of a prospective study that they could not find significant associations between the four AMD susceptibility...
genes CFH, ARMS2/HTRA1, and C3 and hazard rate of second-eye involvement.16 However, though the evidence in the prospective study is high, the CATT study is limited by a follow-up period of only 2 years, which might not be long enough to detect the differences across genotypes. In addition, only four single nucleotide polymorphisms (SNPs) were evaluated in the study. Considering the trend observed in the CATT study that risk allele carriers were more likely to develop AMD in their second eye, the impact of genetics on the second-eye involvement needs to be further evaluated.

In the current study, we conducted survival analysis according to the genotypes of 11 out of 19 recently reported AMD susceptibility genes whose associations with AMD have also been confirmed in the Asian population.

MATERIALS AND METHODS

The current study is a multicenter, retrospective, open cohort study, which was approved by the Institutional Review Board at Kyoto University Graduate School of Medicine, Fukushima Medical University, and Kobe City General Hospital, and all study conduct adhered to the tenets of the Declaration of Helsinki. Written informed consent was obtained from each patient who was genotyped.

Subjects and Phenotyping

All subjects were recruited from a Kyoto AMD cohort that consisted of 1576 unrelated neovascular AMD patients who were genome scanned. These samples were collected from all over Japan, mainly Kyoto University Hospital (Kyoto samples), Fukushima Medical University (Fukushima samples), and Kobe City General Hospital (Kobe samples). Comprehensive ophthalmic examinations were conducted on all patients; these included dilated fundus examination, fluorescein angiography, and indocyanine angiography. The diagnosis of exudative AMD was made by retinal specialists according to the International Classification System for age-related maculopathy37 as we previously described.31 Patients with the following conditions were excluded from the study subjects: high myopia (spherical equivalent ≤ −6.00 diopters [D]), geographic atrophy or drusen only, and an old lesion without a clear diagnosis of AMD.

For the discovery stage, we selected participants as follows. (1) Quality control (QC) using genotype call rate (details are described in genotyping section) excluded 21 patients, resulting in 1555 patients left. (2) Eight hundred ninety patients who visited Kyoto University Hospital were selected in order to access their detailed charts. (3) A total of 499 patients who visited Kyoto University Hospital were selected resulting in 1555 patients left. (2) Eight hundred ninety patients who visited Fukushima samples (n = 263) and Kobe samples (n = 129). Results of the Cox regression analyses were meta-analyzed using the inverse-variance method. To evaluate the heterogeneity of the associations across three datasets, we also calculated I² value. The hereditary models that showed consistent effects across all three datasets, namely, were selected for the final models. A P value less than 0.05 was considered statistically significant. These statistical analyses were conducted using R software ver. 3.02 (http://www.r-project.org/; in the public domain). CRAN package “survival” was applied.

Genetic Risk Score

We computed genetic risk scores (GRS) using the five genotypes of five genes, which were consistently associated with an AMD-free period across three datasets, namely, ARMS2 rs10490924 (A69S), CFH rs800292 (I62V), TNFRSF10A rs13278062, VEGFA rs943080, and CFI rs4698775 (see Results section for detail). First, we constructed a Cox proportional hazard regression model including these five SNPs at once within Kyoto samples. We employed a recessive model for ARMS2, an additive model for CFH, and a dominant model for others. As such, we coded the genotypes as follows: risk
of the second eye, while marginal associations were observed in the second eye. These results showed that 39.8% of the patients who were homozygous for ARMS2 rs10490924 developed AMD in their second eye within 10 years, and 27.4% of the patients who were homozygous for CFH rs800292 did not develop AMD. Since only one patient was homozygous for C2/CFB rs429608 or APOE rs4420635, we evaluated these two SNPs in a recessive model (i.e., risk homozygous versus others). Similarly, C3 rs2241394 was evaluated in a recessive model (i.e., nonrisk homozygous versus others). The P values of the log-rank tests are displayed in each plot.

Table 2 shows the results of the Cox proportional hazard model for all the hereditary models for the 11 SNPs after adjustment for age at first visit and sex. Strong to modest effects were observed in all hereditary models of ARMS2, CFH, and C2/CFB, six of which yielded a P value of less than 0.05. An additional six associations also showed modest (i.e., odds ratio [OR] \( \geq 1.3 \)) effects, with a P value of less than 0.5: CETP recessive model, VEGFA dominant model, TNFRSF10A dominant model, CFI dominant model, and ADAMTS9 additive and recessive models. These associations were further evaluated using two independent Japanese cohorts. Although none of the associations yielded a P value of less than 0.05 in the replication cohorts, possibly due to sample size, six associations of five genes showed consistent effects across all the three datasets with an \( F \) value of 0% in meta-analysis, namely, the ARMS2 recessive model, CFH additive and recessive model, VEGFA dominant model, TNFRSF10A dominant model, and CFI dominant model (Table 3). The P value for proportional hazard assumption testing was <0.05 only in the dominant model of rs13278062 in the evaluation of Kobe samples (Supplementary Table S2).

The Cox proportional hazard model, including five genes at once, provided single-SNP \( \beta \) coefficient for each gene (Table 4), and we computed the GRS based on these values as indicated in the Methods section (Table 5). Figure 2 illustrates a Kaplan-

### Table 1. Baseline Characteristics of the Study Subjects

<table>
<thead>
<tr>
<th>Item</th>
<th>Kyoto</th>
<th>Fukushima</th>
<th>Kobe</th>
</tr>
</thead>
<tbody>
<tr>
<td>n</td>
<td>499</td>
<td>265</td>
<td>129</td>
</tr>
<tr>
<td>Sex, male:female</td>
<td>348:151</td>
<td>197:66</td>
<td>89:40</td>
</tr>
<tr>
<td>Age at the first visit, y*</td>
<td>72.2 ± 8.2</td>
<td>72.1 ± 8.2</td>
<td>71.6 ± 8.6</td>
</tr>
<tr>
<td>Follow-up period, mo†</td>
<td>55.5 (36.0, 83.0)</td>
<td>63.0 (43.0, 84.0)</td>
<td>67.0 (52.0, 95.0)</td>
</tr>
<tr>
<td>Number of events</td>
<td>54, 10.8%</td>
<td>22, 8.4%</td>
<td>6, 4.6%</td>
</tr>
</tbody>
</table>

* Mean ± standard deviation are described.
† Median (1st quantile, 3rd quantile) are displayed.

Table 2. Hazard Ratio After an Adjustment for Sex and Age at the First Visit Using the Cox Proportional Hazard Model

<table>
<thead>
<tr>
<th>Gene</th>
<th>SNP</th>
<th>Chr</th>
<th>Position</th>
<th>Effect Allele EAF</th>
<th>Additive Model</th>
<th>Dominant Model</th>
<th>Recessive Model</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>HR per Allele (95% CI)</td>
<td>P</td>
<td>HR (95% CI)</td>
</tr>
<tr>
<td>ARMS2</td>
<td>rs10490924</td>
<td>10</td>
<td>124214488</td>
<td>T</td>
<td>1.63 (1.06–2.50)</td>
<td>0.025</td>
<td>1.70 (0.74–3.87)</td>
</tr>
<tr>
<td>CFH</td>
<td>rs800292</td>
<td>1</td>
<td>19664223</td>
<td>G</td>
<td>2.10 (1.15–3.81)</td>
<td>0.016</td>
<td>3.71 (0.51–27.1)</td>
</tr>
<tr>
<td>C2/CFB</td>
<td>rs429608</td>
<td>6</td>
<td>31930462</td>
<td>G</td>
<td>0.94 (0.43–2.10)</td>
<td>0.22</td>
<td>0.85 (0.43–1.67)</td>
</tr>
<tr>
<td>C3</td>
<td>rs2241394</td>
<td>19</td>
<td>66852936</td>
<td>G</td>
<td>0.95 (0.49–2.00)</td>
<td>0.91</td>
<td>0.96 (0.49–1.92)</td>
</tr>
<tr>
<td>APOE</td>
<td>rs4420638</td>
<td>19</td>
<td>45242946</td>
<td>T</td>
<td>1.13 (0.44–2.87)</td>
<td>0.80</td>
<td>—</td>
</tr>
<tr>
<td>CETP</td>
<td>rs3764261</td>
<td>16</td>
<td>56995324</td>
<td>A</td>
<td>0.87 (0.50–1.50)</td>
<td>0.61</td>
<td>0.73 (0.39–1.38)</td>
</tr>
<tr>
<td>VEGFA</td>
<td>rs943080</td>
<td>6</td>
<td>43826627</td>
<td>T</td>
<td>1.04 (0.67–1.62)</td>
<td>0.86</td>
<td>1.44 (0.51–4.08)</td>
</tr>
<tr>
<td>TNFRSF10A</td>
<td>rs13278062</td>
<td>8</td>
<td>23082971</td>
<td>T</td>
<td>1.14 (0.74–1.75)</td>
<td>0.55</td>
<td>1.39 (0.72–2.68)</td>
</tr>
<tr>
<td>CFI</td>
<td>rs4698775</td>
<td>4</td>
<td>11059047</td>
<td>G</td>
<td>0.24 (0.17–1.84)</td>
<td>0.58</td>
<td>1.48 (0.80–2.72)</td>
</tr>
<tr>
<td>TGFB1</td>
<td>rs534353</td>
<td>9</td>
<td>10190836</td>
<td>T</td>
<td>1.02 (0.67–1.54)</td>
<td>0.94</td>
<td>0.85 (0.43–1.67)</td>
</tr>
<tr>
<td>ADAMTS9</td>
<td>rs6795735</td>
<td>5</td>
<td>64705365</td>
<td>T</td>
<td>1.83 (0.84–4.00)</td>
<td>0.13</td>
<td>—</td>
</tr>
</tbody>
</table>

Chr, chromosome; EAF, effect allele frequency.
* Risk allele for age-related macular degeneration set to the effect allele.
FIGURE 1. Kaplan-Meier curves based on the genotype of each gene in the discovery stage and the corresponding P value of the Cox proportional hazard model without adjustment are displayed. (A) Significant differences were observed for ARMS2 A69S (rs10490924) genotypes. Homozygous patients (TT genotype; blue) had a 39.8% hazard rate after 10 years from their first visit. Red represents the GT genotype, while black represents the GG genotype. (B) Marginal differences were observed among CFH I62V (rs800292) genotypes. Homozygous patients (GG genotype; blue) had a 27.4% hazard rate after 10 years from their first visit. Red represents the GA genotype, while black represents the AA genotype. (C) The difference between VEGFA rs943080 TT or TC genotypes (red) and the CC genotype (black) was not statistically significant. (D) The difference between TNFRSF10A rs13278062 GT or TT genotype (red) and GG genotype (black) was not statistically significant. (E) The difference between CFI rs4698775 GG or GT genotype (red) and the TT genotype (black) was not statistically significant.
<table>
<thead>
<tr>
<th>Gene</th>
<th>Model</th>
<th>HR (95% CI)</th>
<th>P</th>
<th>EAF, effect allele frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>ARMS2</td>
<td>Dominant</td>
<td>1.38 (0.39–4.87)</td>
<td>0.80</td>
<td>—</td>
</tr>
<tr>
<td>CFH</td>
<td>Additive</td>
<td>2.10 (0.75–5.81)</td>
<td>0.016</td>
<td>46.9%</td>
</tr>
<tr>
<td>C2/CFB</td>
<td>Additive</td>
<td>0.43 (0.21–0.90)</td>
<td>0.025</td>
<td>54.4%</td>
</tr>
<tr>
<td>CETP</td>
<td>Recessive</td>
<td>1.74 (0.53–5.65)</td>
<td>0.36</td>
<td>—</td>
</tr>
<tr>
<td>rs943080</td>
<td>Dominant</td>
<td>1.44 (0.51–4.08)</td>
<td>0.49</td>
<td>—</td>
</tr>
<tr>
<td>VEGFA</td>
<td>Dominant</td>
<td>1.39 (0.72–2.78)</td>
<td>0.20</td>
<td>—</td>
</tr>
<tr>
<td>TNFRSF10A</td>
<td>Dominant</td>
<td>1.48 (0.80–2.72)</td>
<td>0.21</td>
<td>—</td>
</tr>
<tr>
<td>CFI</td>
<td>Additive</td>
<td>1.83 (0.84–4.00)</td>
<td>0.13</td>
<td>46.9%</td>
</tr>
<tr>
<td>ADAMTS9</td>
<td>Recessive</td>
<td>1.80 (0.84–3.94)</td>
<td>0.16</td>
<td>56.6%</td>
</tr>
</tbody>
</table>

**TABLE 5.** Effect of Genetic Risk Score on Second-Eye Involvement of AMD Determined Using the Cox Proportional Hazard Model

<table>
<thead>
<tr>
<th>Gene</th>
<th>Model</th>
<th>Genetic Risk Score, per 1 Point</th>
</tr>
</thead>
<tbody>
<tr>
<td>Kyoto samples</td>
<td>1.81</td>
<td>10^{-4}</td>
</tr>
<tr>
<td>Fukushima samples</td>
<td>2.22</td>
<td>10^{-5}</td>
</tr>
<tr>
<td>Kobe samples</td>
<td>2.12</td>
<td>—</td>
</tr>
</tbody>
</table>

**DISCUSSION**

Since bilateral AMD severely impairs QOL,4–5 second-eye AMD development is a great concern for clinicians treating patients with unilateral AMD. Bilateral advanced disease was evaluated previously for 5 number of genes. There are few studies that suggest genetic effects on second-eye involvement. In the current study, we demonstrated that GRS calculated using five AMD susceptibility genes, that is, ARMS2, CFH, TNFRSF10A, VEGFA, and CFI, were significantly associated with second-eye involvement, and patients with low GRS values had low hazard rates in contrast to the high hazard rates observed among patients with high GRS.

Though there are studies regarding AMD bilaterality,44–46 studies evaluating the association between genetics and incidence of bilateral involvement among unilateral late AMD.
patients are scarce. So far, several cross-sectional studies have reported the association of \textit{CFH} and \textit{ARMS2/HTRA1} with bilateral early or late AMD. For \textit{CFH}, Despriet et al.\textsuperscript{47} reported that patients homozygous for the Y402H variant had a higher OR for bilateral late AMD (OR, 17.93; 95% confidence interval [CI], 9.00–35.70) than unilateral late AMD (OR, 6.58; 95% CI, 3.47–12.48), while the Blue Mountain Eye Study and Los Angeles Latino Eye Study reported the association of \textit{CFH} Y402H with bilateral involvement of early AMD, but not late AMD.\textsuperscript{33,35} In the study by Despriet et al.,\textsuperscript{47} OR of bilateral involvement comparing AMD patients with risk homozygous at \textit{CFH} Y402H to those with nonrisk homozygous was 17.93/6.58 = 2.72, which is relatively lower than the current HR of 1.77 × 1.77 = 3.13. For \textit{ARMS2/HTRA1}, three groups, including the one that analyzed Age-Related Eye Disease Study (AREDS) data, showed its association with bilateral late AMD.\textsuperscript{14,34,36} In contrast to \textit{CFH}, previously reported ORs for \textit{ARMS2/HTRA1}, though they varied from each other (i.e., ranging from 1.23 to 3.27), showed a stronger association with bilateral AMD.

\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{figure2.png}
\caption{Kaplan-Meier curves based on the genetic risk score (GRS) values calculated using the genotypes of \textit{ARMS2}, \textit{CFH}, \textit{TNFRSF10A}, \textit{VEGFA}, and \textit{CFI} are displayed. (A) The diagram shows a Kaplan-Meier curve using the Kyoto samples (n = 499). Each line represents patients with the top 10% GRS values (blue), patients with lowest 10% GRS (black), and others (red). After 10 years from their first visit, patients with GRS values in the top 10% had a 51.0% hazard rate, in contrast to 2.3% among patients with GRS values in the lowest 10%. (B) The diagram shows a Kaplan-Meier curve using the Fukushima samples (n = 265). Each line represents patients with top 25% GRS values (blue), patients with lowest 25% GRS values (black), and others (red). After 10 years from their first visit, patients with GRS values in the top 10% had a 27.6% hazard rate, in contrast to the 1.7% rate among patients with GRS values in the lowest 10%.
}
\end{figure}

\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{figure3.png}
\caption{Color fundus photography (first column), fluorescein angiography (second column), indocyanine green angiography (third column), and optical coherence tomography (fourth column) images of a 78-year-old female whose genetic risk score was 0.21 (rs10490924, GT; rs800292, AA; rs943080, CC; rs79037040, TT; rs4698775, TT). (A) At the first visit, age-related macular degeneration was observed in her left eye, while no lesion was found in her right eye. Visual acuity was 20/20 in the right eye and 20/50 in the left eye. (B) Even after 7.7 years from her first visit, no lesion had been found in her right eye.
}
\end{figure}
In addition to ARMS2 and CFH, we confirmed consistent effects of VEGFA, TNFRSF10A, and CFI on second-eye involvement across three cohorts. The GRS values calculated from these five genes were significantly associated with second-eye involvement after adjustment for age and sex. Patients with low GRS values were less likely to develop AMD in their second eye for their age (Fig. 3), while patients with high GRS values tended to develop AMD in their second eye earlier for their age (Fig. 4). It is surprising that as many as 51.0% of patients with higher GRS values will develop AMD in their second eye within 10 years from their first visit. What is more important is the low hazard rate among patients with lower GRS values. These patients rarely develop AMD in their second eye, with a hazard rate within 10 years from their first visit ranging from 1.7% to 2.3%. Considering that patients with nonrisk homozygous ARMS2 or CFH had a hazard rate of 10% to 20% (Figs. 1A, 1B), the predictive ability of GRS was considerably higher than that of any single SNP genotype. Though AMD is becoming controllable due to the progress of anti-VEGF treatment, its long-term prognosis is not necessarily good. Since bilateral involvement of AMD severely impairs patients’ QOL, we might need to perform more intense treatment to maintain visual capacity of the first eye and frequent follow-up for the early detection of second-eye involvement, especially for the patients with high risk of second-eye involvement.

Although this study has strengths due to its relatively large sample size, repeated replication using three cohorts, and comprehensive evaluation of AMD susceptibility SNPs, it does have limitations. First, it is retrospective. As most of the participants underwent treatment in each institute, the response to the treatment might be associated with loss to follow-up, which is a possible cause of selection bias. However, currently, it is controversial whether the AMD susceptibility genes are associated with the response to treatment. As such, we cannot assume that genetics are associated with loss to follow-up. Since noninformative selection does not cause bias, we cannot say that this retrospective study is biased by selection. Secondly, the follow-up intervals were different, which might have caused a delay in the diagnosis of the second-eye involvement. However, since second-eye involvement directly affects patient QOL, they would voluntarily visit the doctor if it occurs. Thus, delay in the diagnosis would not have affected the results much. Third, the current study did not
employ nongenetic factors, such as smoking status and macular status, within the model. Including these factors would further increase predictive ability. However, since evaluation of environmental factors was beyond the scope of this study, whose aim was to correlate genetic risk and second-eye involvement, this should be explored in the future studies. Lastly, the sample size is still a limitation. Though we included a relatively large number of patients, analysis using more samples would allow us to detect more susceptibility genes. It would also allow us to conduct reliable genome-wide survival analysis.

In conclusion, we demonstrated that AMD susceptibility genes were significantly associated with second-eye involvement using a large number of Japanese unilateral AMD patients across three independent longitudinal cohorts. The difference in hazard rates between patients with high GRS and low GRS values was considerable. By considering other environmental risk factors, the current approach may bring substantial benefits to real-world practice in the future.

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