Association of Genetic Variants With Response to Anti–Vascular Endothelial Growth Factor Therapy in Age-Related Macular Degeneration

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IMPORTANCE Visual acuity (VA) outcomes differ considerably among patients with neovascular age-related macular degeneration (nAMD) treated with anti–vascular endothelial growth factor (VEGF) drugs. Identification of pharmacogenetic associations may help clinicians understand the mechanisms underlying this variability as well as pave the way for personalized treatment in nAMD.

OBJECTIVE To identify genetic factors associated with variability in the response to anti-VEGF therapy for patients with nAMD.

DESIGN, SETTING, AND PARTICIPANTS In this multicenter genome-wide association study, 678 patients with nAMD with genome-wide genotyping data were included in the discovery phase; 1380 additional patients with nAMD were genotyped for selected common variants in the replication phase. All participants received 3 monthly injections of bevacizumab or ranibizumab. Clinical data were evaluated for inclusion/exclusion criteria from October 2014 to October 2015, followed by data analysis from October 2015 to February 2016. For replication cohort genotyping, clinical data collection and analysis (including meta-analysis) was performed from March 2016 to April 2017.

MAIN OUTCOMES AND MEASURES Change in VA after the loading dose of 3 monthly anti-VEGF injections compared with baseline.

RESULTS Of the 2058 included patients, 1210 (58.8%) were women, and the mean (SD) age across all cohorts was 78 (7.4) years. Patients included in the discovery cohort and most of the patients in the replication cohorts were of European descent. The mean (SD) baseline VA was 51.3 (20.3) Early Treatment Diabetic Retinopathy Study (ETDRS) score letters, and the mean (SD) change in VA after the loading dose of 3 monthly injections was a gain of 5.1 (13.9) ETDRS score letters (ie, 1-line gain). Genome-wide single-variant analyses of common variants revealed 5 independent loci that reached a P value less than 10 × 10−5. After replication and meta-analysis of the lead variants, rs12138564 located in the CCT3 gene remained nominally associated with a better treatment outcome (ETDRS letter gain, 1.7; β, 0.034; SE, 0.008; P = 1.38 × 10−5). Genome-wide gene-based optimal unified sequence kernel association test of rare variants showed genome-wide significant associations for the C10orf88 (P = 4.22 × 10−3) and UNC93B1 (P = 6.09 × 10−3) genes, in both cases leading to a worse treatment outcome. Patients carrying rare variants in the C10orf88 and UNC93B1 genes lost a mean (SD) VA of 30.6 (17.4) ETDRS score letters (ie, loss of 6.09 lines) and 26.5 (13.8) ETDRS score letters (ie, loss of 5.29 lines), respectively, after 3 months of anti-VEGF treatment.

CONCLUSIONS AND RELEVANCE We propose that there is a limited contribution of common genetic variants to variability in nAMD treatment response. Our results suggest that rare protein-altering variants in the C10orf88 and UNC93B1 genes are associated with a worse response to anti-VEGF therapy in patients with nAMD, but these results require further validation in other cohorts.

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Advanced age-related macular degeneration (AMD) is a leading cause of blindness in elderly individuals. The most vision-impairing type of advanced AMD is neovascular AMD (nAMD), which is responsible for the majority of visual acuity (VA) loss caused by this disease. Currently, the most effective treatment for nAMD is intravitreal injections of anti–vascular endothelial growth factor (VEGF) antibodies. Although this treatment has resulted in dramatic improvements in VA for many patients with nAMD, a high degree of variability in treatment response has been observed; approximately 10% of patients with nAMD show a decline in VA of at least 15 Early Treatment Diabetic Retinopathy Study (ETDRS) score letters (ie, 3 lines) on the letter chart despite treatment.

Early identification of patients with poor treatment response is a critical step in optimizing AMD treatment. Patients classified as nonresponders based on an absence of VA improvement after anti-VEGF injections might have better outcomes with higher frequency of dosing along with regular monitoring, although, to our knowledge, there is no definitive proof of this at this time. Also, alternative therapies with the potential for longer action are currently being developed for nAMD, and it is possible that other therapeutic options will become available. Therefore, establishing which factors are involved in treatment response variability could aid in the stratification of patients for the best treatment regime or therapeutic option.

Using the resources of the International AMD Genomics Consortium (IAMDGC) and additional nAMD cohorts treated with anti-VEGF therapy, we performed a multicenter genome-wide association study to (1) evaluate in a hypothesis-free approach the association of common genetic variants with VA treatment response to anti-VEGF therapy in patients with nAMD and (2) evaluate the cumulative association of rare protein-altering variants with VA treatment response to anti-VEGF therapy in patients with nAMD. Identification of pharmacogenetic associations can help to identify underlying causal genes and mechanisms and suggest potential new drug targets and might be used as robust biomarkers for precision medicine.

Methods

Study Cohorts

Retrospective data collection for patients included in the discovery and replication cohorts was carried out in multiple clinics (Table 1). The discovery cohort included patients with nAMD who were evaluated as part of the International AMD Genomics Consortium (IAMDGC) project. All groups collected data according to Declaration of Helsinki principles. Study participants provided informed written consent, and protocols were reviewed and approved by local ethics committees. The inclusion criteria for all study center patients can be found in the eMethods in the Supplement. Information about sex, age at first injection, and baseline VA before anti-VEGF treatment and after 3 monthly injections (within 2 weeks) was collected. Visual acuity was collected in ETDRS letters or Snellen eye chart and was transformed into logMAR for analysis.

Exome Array Genotyping and Quality Control

DNA samples from patients included in the discovery cohort were uniformly genotyped with a custom-modified HumanCoreExome array (Illumina) by the IAMDGC at the Center for Inherited Disease Research, Baltimore, Maryland. Genotype quality control and imputation were performed with the IAMDGC, as has been previously detailed. Principal components analysis (PCA) was performed, and only individuals of European descent, based on the PCA, were included in the analysis. The first 2 informative PCA eigenvalues (PC1 and PC2), which account for genetic variation in data coming from shared ancestry, were additionally used as covariates to adjust for population stratification. Identity-by-descent analysis was performed using PLINK version 1.9 and samples with a relatedness score (PI-HAT) greater than 0.25 were excluded.

Treatment Outcome Measurement

The outcome measure was a functional response defined as the change in VA after treatment, which was defined as the initial VA before treatment subtracted from the final VA after 3 anti-VEGF injections, and was analyzed as a continuous variable. The change in VA distributions (logMAR) was evaluated for normal distribution among each study cohort, and outliers (detected using the labeling rule; mean within 3 SDs) were adapted to mean within 2 SDs.

Genome-Wide Analyses of Common Variants

Variants with imputation quality scores (R²) greater than 0.6 and minor allele frequencies (MAF) of 0.05 or greater were included in the common variant analysis. Genome-wide single-variant association analyses using the change in VA as the testing variable were performed and included the first 2 ancestry principal components (PC1 and PC2), baseline VA, and age at first injection as covariates via a quantitative linear regression model (linear Wald testing) using the qIm package in the EPACTS (Efficient and Parallelizable Association Container Toolbox) software version 3.2.6 (http://genome.sph.umich.edu).
Table 1. Demographics and Clinic Characteristics of the Discovery and Replication Cohorts

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Discovery Phase (n = 678)</th>
<th>Replication Phase (n = 1380)</th>
<th>Total (n = 2058)</th>
</tr>
</thead>
<tbody>
<tr>
<td>No. of patients</td>
<td>155</td>
<td>220</td>
<td>375</td>
</tr>
<tr>
<td>Age at first injection, mean (SD), y</td>
<td>76.9 (7.2)</td>
<td>79.6 (7.0)</td>
<td>78.3 (7.1)</td>
</tr>
<tr>
<td>Female, %</td>
<td>91 (58.7)</td>
<td>89 (61.0)</td>
<td>180 (72.3)</td>
</tr>
<tr>
<td>Baseline VA, mean (SD)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>logMAR</td>
<td>0.657 (0.367)</td>
<td>0.598 (0.407)</td>
<td>0.624 (0.398)</td>
</tr>
<tr>
<td>ETDRS score letters</td>
<td>52.2 (18.4)</td>
<td>55.1 (28.1)</td>
<td>53.7 (23.2)</td>
</tr>
<tr>
<td>Snellen eye chart</td>
<td>20/100</td>
<td>20/250</td>
<td>20/100</td>
</tr>
<tr>
<td>Change in VA after 3 mo, mean (SD)</td>
<td>0.051 (0.274)</td>
<td>0.106 (0.301)</td>
<td>0.082 (0.273)</td>
</tr>
<tr>
<td>ETDRS score letters</td>
<td>2.6 (13.7)</td>
<td>5.3 (19.2)</td>
<td>4.3 (13.9)</td>
</tr>
<tr>
<td>Lines gained or lost</td>
<td>0.5</td>
<td>0.6</td>
<td>0.8</td>
</tr>
</tbody>
</table>

Abbreviations: BRAMD, Comparing the Effectiveness of Bevacizumab to Ranibizumab in Patients with Exudative Age-Related Macular Degeneration trial cohort; ETDRS, Early Treatment Diabetic Retinopathy Study; EUGENDA, European Genetic Database study cohort; IVAN, Alternative Treatments to Inhibit VEGF in Age-related Choroidal Neovascularisation trial cohort; VA, visual acuity.

a ETDRS score letter equivalents were calculated in the following manner: ETDRS score letters = 85 – (logMAR/0.02).
b Change in VA was calculating by subtracting VA after 3 months of treatment from baseline VA.
Genotyping and Association Analyses in Replication Cohorts

The lead variants of the loci that reached the threshold for suggestive significance were selected for genotyping in independent replication cohorts. These included single-nucleotide polymorphisms rs241692 (FHIT), rs12138564 (CCT3), rs13002976 (LOC105373426), rs242939 (CRHRI), and rs2237435 (INHBA).

Genotyping in the replication phase was performed using either KASP genotyping assay (LGC Group) or MassARRAY System with iPLEX chemistry (Agena Bioscience), depending on the center performing the genotyping. All variants fell within Hardy-Weinberg equilibrium measures.

The association analysis in the replication cohort was performed in the same manner as the discovery cohort, except for the inclusion of PCA as covariates. The results of all cohorts were combined in a meta-analysis. Subsequently, an overall meta-analysis of the discovery and replication phase was performed.

Gene-Based Analysis of Rare Variants

We performed gene-based analyses using the optimal unified sequence kernel association test as implemented in EPACTS. Rare and low-frequency (MAF < 0.05) protein-altering variants (ie, missense, nonsense, or affecting canonical splice sites) were included in the analysis. Imputed variants were only included if the imputation quality (R²) was 0.8 or greater. Association tests were adjusted for age, baseline VA, and the first 2 ancestry principal components, and a sensitivity analysis adjusting for 10 ancestry principal components was additionally performed. To account for multiple testing, the Bonferroni procedure was applied. The summary statistics for each single variant were extracted from a comparable single-variant analysis using EPACTS.

Results

Characteristics of the Study Cohorts

We collected demographic and VA treatment response information for 2058 patients with nAMD who received anti-VEGF therapy. In the discovery phase, 678 patients from 5 different cohorts were genotyped with exome arrays by the IAMDGC and used for genome-wide association analyses on common and rare variants. In the replication phase, 1380 individuals from 6 different cohorts were genotyped for common variants identified in the discovery study.

Demographic information and clinical parameters of the study cohorts are described in Table 1. The mean change in VA after the loading dose of 3 monthly injections for all patients included in the study was 0.101 logMAR, which corresponded to a gain of 5.1 ETDRS score letters (ie, 1 line gain), and the mean change varied by cohort (Table 1). Age and VA at baseline have been the factors most consistently described as influencing change in VA after anti-VEGF treatment. This was also true for the total patient population and in most of the individual cohorts (eTable 1 in the Supplement). Therefore, these variables were included as covariates in all our subsequent analyses.

Association of rs12138564 in the CCT3 Gene With Response to Anti-VEGF Therapy

In the discovery phase, we performed genome-wide single-variant association analyses on the change in VA after 3 monthly anti-VEGF injections. Linear regression models were conducted on 6089769 quality-controlled common variants (MAF ≥ 0.05).

We identified a total of 111 variants with suggestive significance level (P < 10⁻⁵) (Figure 1A; eFigure in the Supplement). Consecutive conditional analysis revealed that these variants were distributed across 5 different loci, for which the lead variants were rs12138564, rs13002976, rs241692, rs2237435, and rs242939 (Table 2). The details of the associations per cohort are presented in eTable 2 in the Supplement.

In the replication phase, the lead variants of the 5 associated loci were analyzed in 6 independent cohorts of patients with nAMD treated with anti-VEGF therapy, which comprised a total of 1380 patients. The results of the discovery and replication phase were combined in an overall meta-analysis of 11 cohorts, including 2058 patients with nAMD (Table 2; eTable 2 in the Supplement). The association of single-nucleotide polymorphism rs12138564 with functional treatment response remained nominally significant, showing a positive association of the minor allele with treatment outcome (β, 0.034; SE, 0.008; P = 1.38 × 10⁻⁶) (Table 2; eTable 2 in the Supplement). Single-nucleotide polymorphism rs12138564 is located in intron 8 of the CCT3 gene (Figure 1B). The other 4 lead variants did not replicate, and their association was lost after the meta-analysis of the discovery and replication cohorts (Table 2; eTable 2 in the Supplement).

The heterozygous rs12138564 GT genotype group showed an increased improvement in VA after anti-VEGF treatment compared with the reference GG genotype group (P = .008), and the homozygous TT group showed the largest improvement (P = .002). The GG genotype group showed a mean improvement in VA of 0.079 logMAR or approximately 4 ETDRS score letters (ie, 0.79 lines gained), the GT group, 0.118 logMAR or approximately 6 ETDRS score letters (ie, 1.18 lines gained), and the TT group, 0.150 logMAR or approximately 7.5 ETDRS score letters (ie, 1.5 lines gained) (Figure 1C).

Additionally, variants shown to be associated with treatment response in previous studies were not associated.
with VA treatment outcome at genome-wide or suggestive significance levels \( (P < .003 \text{ [ie, .05 / 18]}) \) in this study (eTable 3 in the Supplement). We also analyzed 52 AMD-associated variants reported by the largest AMD case-control genome-wide association study (GWAS) performed so far.\(^2\) None of the 47 variants present in 1 or more of our study cohorts were found to be associated with VA response at either a suggestive significance level \( (P < .001 \text{ [ie, .05 / 47]}) \) nor at the genomewide significance level (eTable 4 in the Supplement).

**Association of Rare Variants in C10orf88 and UNC93B1 With Response to Anti-VEGF Therapy**

Using the rare variation content of the IAMDGC exome array, we analyzed the cumulative association of rare proteinaltering variants with nAMD functional treatment response. We performed gene-based optimal unified sequence kernel association tests\(^2\) of quality-controlled variants with an MAF < 0.05. A total of 58,414 protein-altering variants classified as missense, nonsense, or affecting canonical splice sites distributed in a total of 14,788 genes were included in the analysis.

We identified 2 genes associated with VA treatment response at a genome-based genome-wide significance level \( (P < 3.38 \times 10^{-6} \text{ [ie, .05 / 14788]}) \); chromosome 10 open reading frame 88 \( (C10orf88; P = 4.22 \times 10^{-7}) \) and unc-93 homologue B1 \( (UNC93B1; P = 6.09 \times 10^{-7}) \); carriers of rare variants in these genes showed worse VA response compared with non-carriers (Table 3; Figure 2A). Sensitivity analysis adjusting for 10 ancestry principal components showed comparable results \( (C10orf88; P = 2.24 \times 10^{-7} \text{; } UNC93B1; P = 1.65 \times 10^{-7}) \). Patients who did not carry a rare variant in either \( C10orf88 \) or \( UNC93B1 \) gained on average 0.109 logMAR or 5.5 ETDRS score letters (ie, 1.0 line gained) of VA after treatment. In contrast, the mean change in VA after treatment for carriers of rare variants in \( C10orf88 \) was a loss of 0.609 logMAR or 30.6 ETDRS score letters (ie, 6.09 lines). The carriers of rare variants in \( UNC93B1 \) showed a substantial decrease in VA after treatment as well, losing on average 0.529 logMAR or 26.5 ETDRS score letters (ie, 5.29 lines) (Figure 2B).

All variants included in the burden tests for these 2 genes had a high imputation quality score \( (R^2) \) of 1 and showed the same direction of the association. For \( C10orf88 \), 3 rare protein-altering variants were included; 2 led to an amino acid change \( (c.412G\rightarrow A; \text{ p.Glu138Lys} \text{ and } c.827T\rightarrow C; \text{ p.Ile276Thr}) \) and 1 variant introduced a stop codon \( (c.1258C\rightarrow T; \text{ p.Gln420*}) \). The p.Glu138Lys (rare allele count = 3; \( P = 4.96 \times 10^{-4} \)) and p.Ile276Thr (rare allele count = 3; \( P = 2.33 \times 10^{-5} \)) variants individually showed a nominal association with worse response to treatment. The variant p.Gln420* was present in only 1 individual and did not show an association at the singlevariant level \( (P = .12) \). The variants p.Glu138Lys and p.Gln420* had a combined annotation-dependent depletion score greater than 20, which indicates that they are among the 1% most deleterious substitutions in the human genome (eTable 5 in the Supplement).

Two variants contributed to the burden of the \( UNC93B1 \) gene, both leading to an amino acid change \( (c.385C\rightarrow A; \text{ p.Leu129Ile} \text{ and } c.626C\rightarrow T; \text{ p.Pro209Leu}) \). Both variants indi-

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**Table 3**

<table>
<thead>
<tr>
<th>Locus plot of rs12138564</th>
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<tbody>
<tr>
<td><strong>A</strong> Manhattan plot</td>
</tr>
<tr>
<td><strong>B</strong> Locus plot of single-nucleotide polymorphism rs12138564</td>
</tr>
<tr>
<td><strong>C</strong> Change in VA after treatment</td>
</tr>
</tbody>
</table>

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A, Manhattan plot of genome-wide association study for common variants in a discovery cohort \( (n = 678) \). The blue line indicates the suggestive significance threshold \( (P < 5 \times 10^{-3}) \). B, Locus plot of single-nucleotide polymorphism rs12138564 in the CCTJ3 gene. The light blue line and right y-axis show the observed recombination rate. C, Visual acuity (VA) change after 3 months of treatment stratified by rs12138564 genotypes in discovery and replication cohorts. The black bars indicate the mean change in VA of the beehive cluster.

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Table 2. Single-Variant Association Analyses of 5 Lead Variants in the Discovery and Replication Phases

<table>
<thead>
<tr>
<th>Chromosome</th>
<th>Position (n = 678)</th>
<th>Lead Variant</th>
<th>MA</th>
<th>Gene</th>
<th>Discovery Phase</th>
<th>Replication Phase</th>
<th>Total Phase</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>P Value</td>
<td>P Value</td>
<td>P Value</td>
</tr>
<tr>
<td>1</td>
<td>156 291 600</td>
<td>rs12138564</td>
<td>T</td>
<td>CCT3</td>
<td>5.74 × 10⁻⁷</td>
<td>0.019 (0.009)</td>
<td>0.029</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>0.034 (0.008)</td>
<td>1.38 × 10⁻⁵</td>
</tr>
<tr>
<td>2</td>
<td>10 678 538</td>
<td>rs13002976</td>
<td>G</td>
<td>NOL10</td>
<td>1.21 × 10⁻⁶</td>
<td>0.009 (0.008)</td>
<td>0.265</td>
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<tr>
<td></td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td>0.009 (0.008)</td>
<td>0.219</td>
</tr>
<tr>
<td>3</td>
<td>60 410 187</td>
<td>rs241692</td>
<td>G</td>
<td>FHIT</td>
<td>4.46 × 10⁻⁷</td>
<td>-0.023 (0.017)</td>
<td>0.187</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>0.011 (0.016)</td>
<td>0.493</td>
</tr>
<tr>
<td>7</td>
<td>41 731 051</td>
<td>rs2237435</td>
<td>A</td>
<td>INHBA</td>
<td>6.58 × 10⁻⁶</td>
<td>0.015 (0.009)</td>
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<td>0.005 (0.008)</td>
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<tr>
<td>17</td>
<td>43 805 579</td>
<td>rs242939</td>
<td>C</td>
<td>CRHR1</td>
<td>2.25 × 10⁻⁶</td>
<td>-0.021 (0.017)</td>
<td>0.214</td>
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<tr>
<td></td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td>0.020 (0.014)</td>
<td>0.162</td>
</tr>
</tbody>
</table>

Abbreviation: MA, minor allele.

* Chromosomal position according to the NCBI RefSeq hg19 human genome reference assembly.

Table 3. Gene-Based Analysis of Rare Variants on Response to Anti-Vascular Endothelial Growth Factor Therapy in Neovascular Age-Related Macular Degeneration

<table>
<thead>
<tr>
<th>Gene</th>
<th>Chromosome</th>
<th>Chromosomal Position</th>
<th>No. of Rare Variants</th>
<th>Value β (SE) (n = 2058)</th>
<th>RAC</th>
<th>P Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>C10orf88</td>
<td>10</td>
<td>124 692 082 to 124 712 511</td>
<td>3</td>
<td>-0.128 (0.027)</td>
<td>7</td>
<td>4.22 × 10⁻⁷</td>
</tr>
<tr>
<td>UNC93B1</td>
<td>11</td>
<td>67 765 163 to 67 770 499</td>
<td>2</td>
<td>6.09 × 10⁻⁷</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Abbreviation: RAC, rare allele count.

* Chromosome and chromosomal position according to the NCBI RefSeq hg19 human genome reference assembly.

Discussion

We have undertaken a multicenter pharmacogenetic study of patients with nAMD and performed both GWAS of common variants and a gene-based analysis for the cumulative effect of rare variants. We evaluated the role of genetic variation on the change in VA after the loading dose of 3 monthly injections. Visual acuity is the most relevant outcome measure for patients, as it directly influences their quality of life.49

Our GWAS for common variants had 80% power to detect variants of moderate effects, explaining at least 6.2% of the variance in treatment response.50 However, no single-variant associations were found at the genome-wide significance level, suggesting a limited association of individual common variants with treatment outcome. We identified the variant rs12138564, located in intron 8 of the CCT3 gene, to be suggestive associated with treatment response after replication analysis, and therefore, this variant may merit further investigation in alternative cohorts.

We did not find any of the previously reported variants12,31-48,51 to be associated with functional response. This may be because of differences between the studies in response definition and patient population in terms of disease stage and other environmental factors or because of spurious findings. However, our results support the notion that none of the previously identified genetic markers are individually strong determinants of overall functional treatment response. Furthermore, we also did not find an association for any of the 52 AMD-associated variants reported in the largest AMD GWAS performed so far.22

The rare variant burden test revealed 2 genes associated with primary functional response at a genome-wide level: C10orf88 and UNC93B1. Therefore, these genes merit further evaluation in other large replication cohorts. The function of C10orf88 is still uncharacterized, and therefore the biological link to treatment response in nAMD is unclear. It has been suggested that common variants in C10orf88 are associated with vitamin D levels, although it cannot be excluded that the effect might be driven by the neighboring gene, ACADSB.52 Additionally, C10orf88 is expressed at low levels in the retina and retinal pigment epithelium/chorioid.53 UNC93B1 is involved in the innate and adaptive immune response by regulating toll-like receptor signaling.54-58 Therefore, our results may point toward an immune component in treatment response in AMD.

Carriers of rare variants (MAF ≤ 1%) in the C10orf88 and UNC93B1 genes lost on average 6.09 and 5.29 lines of vision, respectively, on the ETDRS letter chart. The association of rare variants with VA outcome after treatment was very large, making these findings potentially relevant for the clinical practice.59 Large changes in VA after treatment are rare; however, they are seen in clinical practice and clinical trials.19,20,60,61 For example, in the Alternative Treatments to Inhibit VEGF in Age-related Choroidal Neovascularisation clinical trial data set included in this study,19,20 5.7% of patients lost 15 or more EDTRS
Figure 2. Gene-Based Analysis of Rare Variants on Response to Anti-Vascular Endothelial Growth Factor (VEGF) Therapy in Neovascular Age-Related Macular Degeneration

A. Manhattan plot of genes analyzed in gene-based rare variant test. The horizontal line indicates the genome-wide significance level ($P < 3.38 \times 10^{-6}$ [ie, 0.05/14788]). B. Visual acuity (VA) change after 3 months of treatment stratified by noncarriers as well as carriers of rare variants in C10orf88 and UNC93B1. Comparisons are conducted using the optimal unified sequence kernel association test. The black bars indicate the mean change in VA.

**A**

B. Change in VA after treatment

No Rare Variant C10orf88 Rare Variant UNC93B1 Rare Variant

P = 6.09 \times 10^{-7}
P = 4.22 \times 10^{-7}

**B**

Changes in VA after 3 mo of Anti-VEGF Therapy, logMAR

-1.5 0 0.5 1 1.5

-1.5 0 0.5 1 1.5

A, Manhattan plot of genes analyzed in gene-based rare variant test. The horizontal line indicates the genome-wide significance level ($P < 3.38 \times 10^{-6}$ [ie, 0.05/14788]). B, Visual acuity (VA) change after 3 months of treatment stratified by noncarriers as well as carriers of rare variants in C10orf88 and UNC93B1. Comparisons are conducted using the optimal unified sequence kernel association test. The black bars indicate the mean change in VA.

**Limitations**

This study had limitations. Whether our findings on the functional response can be related to an anatomical response remains to be further investigated. We chose this time interval because 3 loading injections are administered widely in contrast to the follow-up treatment, which is variable per clinic, and its effect on VA outcomes. Most patients show the most improvement in their VA after the first 3 monthly injections; thus, this time interval can be predictive of a longer-term response. Moreover, long-term treatment response is likely to be affected by nonadherence to treatment protocols. However, patients may improve after the 3-month time point, and therefore the effect of the identified genetic variants on secondary or long-term response would need to be evaluated. We investigated the treatment response to bevacizumab or ranibizumab therapy in a combined analysis. Future studies will require an evaluation of the association of these genetic variants and treatment outcome after aflibercept treatment, as this drug is now routinely used in the clinical setting for nAMD treatment. The anatomical changes, such as retinal or subretinal hemorrhage, retinal pigment epithelium tears, and increase in macular thickness, may account for severe VA loss ($\geq 15$ ETDRS letters). Information on such factors was not available in this study; therefore, follow-up studies are needed to investigate if these variants are associated with anatomical variables after anti-VEGF treatment in nAMD. Another limitation is that 4 of 6 carriers of rare variants in the C10orf88 gene and all carriers of rare variants in the UNC93B1 gene were from the Jerusalem cohort. Therefore, this finding may be related to the genetic nature of that specific population.

**Conclusions**

Our multicenter GWAS suggests that the variability in primary functional treatment outcome in nAMD is probably not explained by large effects of common variants. However, our results suggest that rare genetic variants may have large effects on treatment outcome after 3 monthly anti-VEGF injections; these results require further validation in other cohorts.
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Association of Genetic Variants With Response to Anti-VEGF Therapy for AMD


A dozen years ago, the world changed for patients with neovascular age-related macular degeneration (nAMD) because of the introduction of the anti–vascular endothelial growth factor factor therapy (VEGF) agents ranibizumab and bevacizumab.¹,² For the first time, treatments were available that not only prevented loss of visual acuity but also improved vision for most patients. The outcomes found through 1 to 2 years of treatment were in stark contrast to the dismal course of untreated eyes and eyes treated with the modestly beneficial treatments available before 2005 (thermal laser, photodynamic therapy with verteporfin, or intraocular injection of pegaptanib).³

However, visual acuity outcomes and structural changes associated with anti-VEGF treatment vary tremendously among patients. While mean change in visual acuity after 3 injections is about 1 line of improvement on the Early Treatment Diabetic Retinopathy Study chart, some patients lose as many as 5 lines, and others gain as much as 6 lines of visual acuity.¹,³,⁴ Factors such as the level of visual acuity at presentation and the age of the patient influence response to treatment, but together with other baseline predictors, these account for 10% or less of the variability in change in visual acuity scores.⁵,⁶

Several single-nucleotide polymorphisms (SNPs) in multiple genes are associated strongly with the prevalence of the early or late stages of age-related macular degeneration (AMD).⁷ Many ophthalmologists and scientists wondered whether these SNPs were also associated with varying responses to anti-VEGF treatment. However, data analyses conducted by several research groups⁸ have failed to identify strong, reproducible associations between treatment response and these SNPs or between treatment response and a high number of other SNPs, including those associated with the VEGF signaling pathway.

In this issue of JAMA Ophthalmology, Lorés-Motta et al⁹ report on the results of a large (approximately 2000 patients) genome-wide association study (GWAS) from an international collaboration of clinical and genetic investigators. They examined more than 6 gene variants and, using appropriate methods for evaluating pharmacogenetic associations, identified 3 gene variants that were associated with treatment response in patients treated for 3 months with ranibizumab or bevacizumab. Importantly, the association of these variants with treatment response was identified in 1 group of patients and then replicated in a second, independent group of patients. Such replication increases the probability that the associations are real; however, replication in other groups of patients would solidify the findings.

One relatively common variant, rs12138564, located in the C10orf88 gene, was associated with a modest benefit in treatment response (approximately 0.5 lines of visual acuity beyond the typical improvement of 1 line).⁵ In contrast, rare variants of 2 genes, C10orf88 and UNC93B1, were associated with extraordinarily large mean decreases in visual acuity (5 or more lines).

Understanding the function of C10orf88 and UNC93B1 may help in understanding the actions of VEGF and anti-VEGF agents in nAMD in the future. Lorés-Motta et al⁹ tell us, to that date, the function of C10orf88 is uncharacterized, but that UNC93B1 regulation is involved in the regulation of toll-like receptor (TLR) signaling, implicating an immune component to treatment response. Whether the poor response to treatment in these patients is because of a virulent form of nAMD or resistance to anti-VEGF agents remains to be determined. The importance of the identification of these 2 rare variants to current clinical management is limited by the fact that they are indeed rare. Only 7 of 2058