Research Article

Haplotypes of \textit{HTRA1} rs1120638, \textit{TIMP3} rs9621532, \textit{VEGFA} rs833068, \textit{CFI} rs10033900, \textit{ERCC6} rs3793784, and \textit{KCTD10} rs56209061 Gene Polymorphisms in Age-Related Macular Degeneration

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\textbf{Background.} To determine the impact of \textit{HTRA1} rs11200638, \textit{TIMP3} rs9621532, \textit{VEGFA} rs833068, \textit{CFI} rs10033900, \textit{ERCC6} rs3793784, and \textit{KCTD10} rs56209061 genotypes on the development of age-related macular degeneration (AMD) in the Lithuanian population.

\textbf{Methods.} A total of 916 subjects were examined: 309 patients with early AMD, 301 patients with exudative AMD, and 306 healthy controls. The genotyping of \textit{HTRA1} rs11200638, \textit{TIMP3} rs9621532, \textit{VEGFA} rs833068, \textit{CFI} rs10033900, \textit{ERCC6} rs3793784, and \textit{KCTD10} rs56209061 was carried out using the RT-PCR method.

\textbf{Results.} Our study showed that single-nucleotide polymorphisms rs3793784 and rs11200638 were associated with increased odds of early and exudative AMD, and the variant in \textit{KCTD10} (rs56209061) was found to be associated with decreased odds of early and exudative AMD development after adjustments for age and gender in early AMD analysis and after adjustments only for age in exudative AMD. The haplotype containing two minor alleles C-A and the G-A haplotype in rs3793784-rs11200638 were statistically significantly associated with an increased risk of exudative AMD development after adjustment for age, while the G-G haplotype showed a protective role against early and exudative AMD and the haplotype C-G in rs3793784-rs11200638 was associated with a decreased risk only of exudative AMD development.

\textbf{Conclusions.} Our study identified two markers, rs11200638 and rs3793784, as risk factors for early and exudative AMD, and one marker, rs56209061, as a protective factor for early and exudative AMD development. The haplotypes constructed of rs3793784-rs11200638 were found to be associated with AMD development, as well.

1. \textbf{Introduction}

Age-related macular degeneration (AMD) affects the macula (the central part of the retina) and is the most common cause of visual loss in persons over the age of 60 in developed countries \cite{1}. Population estimates have placed the prevalence of AMD approximately from 7% to 10% in adults aged 40-90 yrs. \cite{2-4}. The 10-year incidence of neovascular AMD is 4.1% in persons older than 75 years \cite{5}.

In 2002, there were 13.8% blind people due to AMD according to the data of the Lithuanian Medical Social Expertise Commission \cite{6}, and it takes second place after glaucoma \cite{6}.

AMD is a progressive eye disease that has been linked with several pathological factors, i.e., chronic oxidative stress, autophagy decline, and inflammation \cite{7-9}. However, the full etiology of AMD remains unclear and the treatment options are limited. AMD is a challenging disease to study from a genetic perspective too, because, unlike disorders that exhibit Mendelian inheritance patterns (where one gene and one mutation within that gene is responsible for the phenotype observed in a given family), the development and
severity of complex diseases like AMD are influenced by multiple factors. The high prevalence of the disease implies that there is more than one gene or environmental factor as well as interactions among these factors, which influence an individual's susceptibility to the disease [10].

Early AMD is usually asymptomatic. Early AMD is defined as the presence of drusen and retinal pigmentary abnormalities; late AMD includes dry AMD (geographic atrophy of the retinal pigmentary epithelium in the absence of neovascular AMD) or neovascular AMD (detachment of the retinal pigment epithelium, hemorrhages, and/or scars).

AMD is a disease of multifactorial etiology, the development of which is determined by environmental and genetic risk factors. In addition to these factors, various single-nucleotide polymorphisms (SNPs) have been widely reported to be associated with AMD [11]. Genome-wide association studies (GWAS) have confirmed multiple AMD-associated loci. Recently, a large-scale GWAS with thousands of cases and controls reported several additional AMD-associated loci, including rs9621532 near the tissue inhibitor of metalloproteinase 3 (TIMP3) and the synapsin III (SYN3) region of chromosome 22q12.3 [11]. HTRA1, the third gene in the 10qa26, is highly conserved among species and has several variants that have consistently been found to be associated with AMD [12–18]. One of the most consistently AMD-associated variants is the SNP rs11200638, located within the putative HTRA1 promoter [15, 17–21]. As the lipid level has been implicated as a major risk factor in AMD [22, 23], GWAS analyze the associations between lipid-trait genes and AMD risk [24–26]. A recent study has shown that two intronic variants rs11066782 and rs11613718 in KCTD10 or potassium channel tetramerisation domain-containing 10 gene were associated with high-density lipoprotein cholesterol (HDL-C) concentrations and with coronary heart disease (CHD) risk [27], while rs2338104 in the KCTD10 gene located in chromosome 12q24 was associated with AMD development [28]. The other intronic variant, rs5620906 in KCTD10, was even related to the advanced AMD subtypes [29].

Today, it is known that the complement system is involved in the pathogenesis of AMD [30]. Therefore, different types of studies were performed to detect the association between CFI polymorphisms and AMD. Numerous researches have shown CFI gene’s role in AMD pathogenesis [31–35]. The CFI gene is located on chromosome 4q25 and encodes complement factor I (FI), which is an important component of the complement system. Factor I is composed of one light and one heavy polypeptide chains held together by disulfide bonds. These chains are encoded by the CFI gene. The light chain has a serine protease domain. The main function of factor I is to cleave C4b and inactivate C3 [36].

Another gene, the Excision Repair Cross-Complementing Group 6 (ERCC6) gene, which is located on human chromosome 10 at q11.23 and has 84,171 bases with 21 exons, may be also associated with AMD. Loss of function mutations in the ERCC6 cause the autosomal recessive disorder Cockayne syndrome, which includes a lot of severe physical and neurologic peculiarities, with premature aging and retinopathy as signs of the disease. These observations led to the hypothesis that oxidative DNA damage and insufficient DNA repair contribute to aging pathology, including AMD [37, 38].

Vascular endothelial growth factor A (VEGFA) is a member of the VEGF-related polypeptide family. VEGF plays a key role in increased vascular permeability, angiogenesis, cell growth, and migration of endothelial cells [39–42]. Therefore, it is believed that the polymorphism of the VEGFA gene rs833068 can be associated with AMD. Also, it may influence the visual outcomes in neovascular AMD [43, 44].

There have already been many SNPs analyzed that were known to be involved in lipid metabolism, tissue remodeling, and DNA damage mechanisms, and their associations with AMD development were revealed [45, 46].

We believe that selected SNPs and previously analyzed genetic molecular marker complexes are necessary for understanding, diagnosing, and forecasting AMD. Genetic biomarkers could be useful as biological markers of AMD diagnosis, progression, prognosis, and maybe treatment with anti-VEGF and could be adapted for practical work. While the association studies of these SNPs have not been conducted in both (early and exudative) AMD forms previously, we decided to involve patients with early and exudative AMD and compare the genetic differences between developments of early and exudative AMD.

Most studies focusing on certain molecular pathways involved in the AMD pathogenesis are done in Asian regions. As we know, allele frequencies are known to vary with latitude in different geographic regions which demands further researches to better understand risk factors of AMD development in the Lithuanian population.

Also, we believe that genetic variations combined with other risk factors or molecular changes can benefit physicians in creating personalized genetic therapies and/or lifestyle programs for increased-risk individuals in the future.

In this study, we limited our study to genes in biological pathways relevant to AMD pathogenesis, including the complement system regulation (CFI) [36], extracellular matrix deposition and angiogenesis (HTRA1) [12], increased vascular permeability (VEGFA) [39], or degradation of the extracellular matrix (TIMP3) [11]. We also included SNPs in the gene associated with lipid metabolism (KCTD10) [27] and in the ERCC6 gene associated to DNA damage caused by the oxidative stress and leading to the loss of protein function in aging pathology [38].

Furthermore, allele frequencies are known to vary with latitude depending on the region; for this reason, we aimed to determine associations between the HTRA1 rs1120638, TIMP3 rs9621532, VEGFA rs833068, CFI rs10033900, ERCC6 rs3793784, and KCTD10 rs56209061 gene polymorphisms and the development of AMD in the Lithuanian population.

2. Materials and Methods

Our study was conducted in the Department of Ophthalmology, Hospital of Lithuanian University of Health Sciences, and in the Laboratory of Ophthalmology, Neuroscience Institute, Lithuanian University of Health Sciences.
The study was approved by the Ethics Committee for Biomedical Research, Lithuanian University of Health Sciences (No. BE-2/13). All subjects provided written informed consent in accordance with the Declaration of Helsinki.

### 2.1. Controls and Patients with Age-Related Macular Degeneration Group Formation.

A total of 916 subjects were examined, including patients with early AMD (n = 309), patients with exudative AMD (n = 301), and healthy controls (n = 306) (Table 1).

The control group consisted of subjects who had no ophthalmologic pathology on examination and who agreed to take part in this study. Also, according to the age of AMD patients, only subjects older than 55 years old were involved in the control group to avoid the age effect in our study.

AMD patients were not eligible for enrollment in the study if they had (i) unrelated eye disorders, e.g., high refractive error, cloudy cornea, lens opacity (nuclear, cortical, or posterior subcapsular cataract) except for minor opacities, keratitis, acute or chronic uveitis, glaucoma, or diseases of the optic nerve; (ii) systemic illnesses, e.g., diabetes mellitus, malignant tumors, systemic connective tissue disorders, chronic infectious diseases, or conditions following organ or tissue transplantation; and (iii) ungraded color fundus photographs resulting from obscuration of the ocular optic system or because of fundus photograph quality.

The ophthalmological evaluation, DNA extraction, and genotyping used in our research were described in previous studies [47, 48].

### 2.2. Statistical Analysis.

Statistical analysis was performed using the SPSS/W 20.0 software (Statistical Package for the Social Sciences for Windows Inc., Chicago, Illinois, USA). Data are expressed as absolute numbers with percentages. Frequencies of the genotypes are expressed in percentages.

Hardy-Weinberg analysis was performed to compare the observed and expected frequencies of CFI rs10033900, ERCC6 rs3793784, VEGFA rs833068, HTRA1 rs11200638, TIMP3 rs9621532, and KCTD10 rs56209061 using the $\chi^2$ test in all groups. The distribution of CFI rs10033900, ERCC6 rs3793784, VEGFA rs833068, HTRA1 rs11200638, TIMP3 rs9621532, and KCTD10 rs56209061 in the early and exudative AMD and control groups was compared using the $\chi^2$ test or the Fisher exact test. Binomial logistic regression analysis was performed to estimate the impact of genotypes on early and exudative AMD development. Odds ratios and 95% confidence intervals are presented.

For multiple comparisons of the SNPs studied, we used a significance value corrected by the Bonferroni approach. This adjustment was done for CFI rs10033900, ERCC6 rs3793784, VEGFA rs833068, HTRA1 rs11200638, TIMP3 rs9621532, and KCTD10 rs56209061 resulting in a “corrected” significance threshold of $\alpha = 0.008$ (0.05/6, since we analyzed 6 different SNPs) for genetic data.

Haplotype analysis was restricted to polymorphisms located on the same chromosome, the haplotype rs3793784-rs11200638. Estimation of the haplotype frequencies and haplotype association tests for the haplotypes with frequencies of at least 5% was carried out using PLINK software version 1.07 [49]. Linkage disequilibrium (LD) analysis was assessed by $D'$ and $r^2$ measures.

Differences were considered statistically significant when $P < 0.008$.

### 3. Results

A total of 916 subjects were examined, including patients with early AMD (n = 309), patients with exudative AMD (n = 301), and healthy controls (n = 306) (Table 1).

We performed the Hardy-Weinberg equilibrium (HWE) testing among the control group subjects, and the analysis showed that the distribution of the genotypes of all SNPs in the control group did not deviate from HWE (Table 2).

In this study, we analyzed six SNPs in the early AMD, exudative AMD, and control groups and found statistically significant differences in the genotype distribution of ERCC6 rs3793784, HTRA1 rs11200638, and KCTD10 rs56209061 in early and/or exudative AMD groups compared to the control group (Table 3). Also, it was found that the allele A at
rs11200638 was more frequent in early AMD patients than in controls (0.35 vs. 0.28, \( P = 0.005 \)) as well as in the exudative AMD group compared to controls (0.54 vs. 0.28, \( P < 0.001 \)); the A allele at rs56209061 was statistically significantly less frequent in the early AMD group than in the control group (0.07 vs. 0.13, \( P < 0.001 \)) and in the exudative AMD group compared to controls (0.08 vs. 0.13, \( P = 0.006 \)) (Table 3).

Binomial logistic regression was performed to evaluate the impact of SNPs on early and exudative AMD development. It revealed that the genotype CC at rs3793784 was associated with 2-fold increased odds of early AMD development under the recessive model (\( \text{OR} = 2.007; \ 95\% \ 	ext{CI}: 1.255-3.209; \ P = 0.004 \)) (Table 4). The allele A at rs11200638 was also associated with increased odds of early AMD development under the additive model (\( \text{OR} = 1.387; \ 95\% \ 	ext{CI}: 1.096-1.755; \ P = 0.007 \)) (Table 4). The rs56209061 polymorphism was associated with decreased odds of early AMD development: the GA genotype revealed decreased odds of early AMD under the codominant and overdominant models (\( \text{OR} = 0.471; \ 95\% \ 	ext{CI}: 0.307-0.724; \ P < 0.001 \)), as well as each A allele at rs56209061 under the additive model (\( \text{OR} = 0.491; \ 95\% \ 	ext{CI}: 0.332-0.726; \ P < 0.001 \)) (Table 4).

Binomial logistic regression in the exudative AMD and control groups were adjusted for age because patients with exudative AMD were statistically significantly older than control subjects. The genotype CC at rs3793784 was associated with increased odds of exudative AMD development under the codominant and recessive models (\( \text{OR} = 2.271; \ 95\% \ 	ext{CI}: 1.333-3.870; \ P = 0.003 \) and \( \text{OR} = 2.427; \ 95\% \ 	ext{CI}: 1.483-3.970; \ P < 0.001 \)), respectively. The rs11200638 AA
genotype was associated with increased odds of exudative AMD development under the codominant and recessive models (OR = 8.683; 95% CI: 5.090-14.810; P = <0.001 and OR = 5.146; 95% CI: 3.174-8.344; P = <0.001, respectively), as well as the AA+GA under the dominant model (OR = 3.701; 95% CI: 2.569-5.332; P = <0.001) and the GA genotype under the codominant model (OR = 2.603; 95% CI: 1.761-3.846; P = <0.001) (Table 5). Also, each A allele at rs11200638 was associated with increased odds of exudative AMD development under the additive model (OR = 2.876; 2.230-3.709; P = <0.001) (Table 5). The associations of the rs56209061 polymorphism with exudative AMD development were found under the additive model (OR = 0.583; 95% CI: 0.394-0.863; P = 0.007) (Table 5).

Unfortunately, no associations of the VEGFA rs833068 were found with early or exudative AMD development in the Lithuanian population.

### 3.1. Haplotype Associations with AMD

In this section, we performed an association analysis between the risk of early and exudative AMD and the haplotypes of rs3793784-rs11200638. The r² values were 0 and 0.003 in early AMD and exudative AMD analyses, respectively; for the haplotype block, D' values were 0.008 and 0.056 in early AMD and exudative AMD analyses, respectively, which shows that rs3793784 and rs11200638 are in weak linkage disequilibrium.

The haplotype containing two minor alleles C-A in rs3793784-rs11200638 and the G-A haplotypes were...
Table 6: Haplotypes associated with AMD.

<table>
<thead>
<tr>
<th>Single-nucleotide polymorphisms</th>
<th>Haplotype</th>
<th>Frequency (cases)</th>
<th>Frequency (controls)</th>
<th>Chi square</th>
<th>Degree of freedom</th>
<th>P value*</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Early AMD</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>rs3793784-rs11200638</td>
<td>C-A</td>
<td>0.1343</td>
<td>0.1014</td>
<td>9.554</td>
<td>1</td>
<td>0.051</td>
</tr>
<tr>
<td></td>
<td>G-A</td>
<td>0.2196</td>
<td>0.1771</td>
<td>3.485</td>
<td>1</td>
<td>0.054</td>
</tr>
<tr>
<td></td>
<td>C-G</td>
<td>0.2569</td>
<td>0.2586</td>
<td>0.004</td>
<td>1</td>
<td>0.943</td>
</tr>
<tr>
<td></td>
<td>G-G</td>
<td>0.3892</td>
<td>0.4629</td>
<td>6.840</td>
<td>1</td>
<td>0.007</td>
</tr>
<tr>
<td><strong>Exudative AMD</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>rs3793784-rs11200638</td>
<td>C-A</td>
<td>0.2371</td>
<td>0.1069</td>
<td>36.30</td>
<td>1</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td></td>
<td>G-A</td>
<td>0.3077</td>
<td>0.1716</td>
<td>30.97</td>
<td>1</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td></td>
<td>C-G</td>
<td>0.1765</td>
<td>0.2530</td>
<td>10.55</td>
<td>1</td>
<td>&lt;0.001</td>
</tr>
<tr>
<td></td>
<td>G-G</td>
<td>0.2787</td>
<td>0.4685</td>
<td>46.75</td>
<td>1</td>
<td>&lt;0.001</td>
</tr>
</tbody>
</table>

*P value adjusted for age in exudative AMD analysis; P values < 0.008 indicated in bold are statistically significant.

statistically significantly associated with an increased risk of exudative AMD development after adjustment for age (Table 6), while the G-G haplotype showed the protective role against both early and exudative AMD and the haplotype C-G in rs3793784-rs11200638 was associated with a decreased risk only of exudative AMD development (Table 6).

4. Discussion

Different genes may be responsible for AMD development, and various AMD clinical subtypes may be found in our practice [10]. In our research, we analyzed the HTRA1 rs1120638, TIMP3 rs9621532, VEGFA rs833068, CFI rs10033900, ERCC6 rs3793784, and KCTD10 rs56209061 genotype effects on AMD development in the Lithuanian population.

One of our evaluated genes, HTRA1, has been shown to be associated with an increased risk of wet AMD in the Chinese population [50]. Our study is also in agreement with this, and we found that the HTRA1 rs1120638 minor allele was associated with the increased odds of both early and exudative AMD development. It is known that the HTRA1 gene encodes a serine protease expressed in RPE and drusen. The protein appears to regulate the degradation of extracellular matrix proteoglycans and works in conjunction with other extracellular matrix degradation enzymes (i.e., collagenases and metalloproteinases). HTRA1 also binds to and inhibits the transformation of growth factor-beta (TGF-β), a factor known to play a crucial role in extracellular matrix deposition and angiogenesis [12, 51]. Therefore, it is possible that HTRA1 may play a role in the regulation of the Bruch’s membrane and the growth of vessels into the RPE. One study has concluded that the HTRA1 SNP rs1120638 is the most likely causal variant of AMD at the 10q26 locus among the Han Chinese population and estimated the combined population attributable risk for CFH and HTRA1 alleles to be 75% [12]. Recently, rs2284665 in ARMS2/HTRA1 has also been identified as affecting the growth of CNV in AMD [52]. Overall, variants of ARMS2/HTRA1 genes confer a major risk of the development of AMD. Tang et al. in meta-analysis have summarized a strong evidence of the association between the HTRA1 -512G>A polymorphism and AMD and indicated a codominant model of action [53]. The higher levels of HTRA1 expression in RPE cells have been proven by a group of scientists as well [54]. Most recently, a study has reported a significant association between AMD and a haplotype containing both the ARMS2 indel and the HTRA1 promoter rs11200638 variant [18]. This is not surprising given that variants of both HTRA1 and ARMS2 are in high linkage disequilibrium [13, 55], and we go in agreement with all these studies talking about the significant role of HTRA1 in AMD development.

While many other studies have proven the association between TIMP3 rs9621532 and AMD, we did not reveal any significant results in our population. TIMP3 is a senescence protein that regulates extracellular matrix remodeling and is highly expressed in RPE [56]. Mutations in TIMP3 were implicated in Sorsby’s fundus dystrophy (SFD), an autosomal dominant disorder featuring accumulation of macular drusen and progression to CNV and retinal degeneration [57–60]. The increased TIMP3 protein in Bruch’s membrane and drusen of AMD eyes has also been correlated with AMD disease pathology [61]. TIMP3 serves as an extracellular ligand for VEGFR-2 and thus directly regulates angiogenesis [62]. Most importantly, the TIMP3 protein increases in intensity only in older individuals [63], and significantly elevated TIMPs were also detected in Bruch’s membrane of AMD patients with respect to age-matched controls [61]. The enhanced expression of TIMP3 could prevent ECM remodeling and contribute to the thickening of Bruch’s membrane with lower integrity because of changes in the homeostatic balance of turnover, which is precisely what is observed in AMD [61]. The study done by Ardeljan et al. has characterized its phenotypic influence on AMD using three independent study cohorts: case-control studies from the National Eye Institute Clinical Center (NEI, n = 397) and the Age-Related Eye Disease Study (n = 523) as well as a nested case-control study from the Blue Mountains Eye Study (BMES, n = 852). Their data suggest that rs9621532 carriers have a lower risk of developing nAMD, potentially because of the decreased transcription of TIMP3. The authors state that the association is still noteworthy and may actually be indicative of an important functional variant [64]. This group of
scientists has found that rs9621532 carriers have a lower risk of developing nAMD [64]; however, in our study of the Lithuanian population, we did not find statistically significant results of the rs9621532 being associated with AMD development, even when we included quite a big group of subjects: 309 patients with early AMD, 301 patients with exudative AMD, and 306 healthy controls.

KCTD10 is a member of the polymerase delta-interacting protein 1 (PDIP1) gene family [65], which consists of 3 members, PDIP1, KCTD10, and TNAIP1 [66–69]. It has been found that KCTD10 can be induced by TNF-α and interact with PCNA and the small subunit (p50) of DNA polymerase δ [68]. A promoter analysis has shown that KCTD10 can be regulated by transcription factors [69]. There has even been a novel transcription factor ETV1 identified, which is unique to gastrointestinal stromal tumors (GISTs), suggesting that KCTD10 functions as a tumor suppressor protein [70]. While the exact functions of KCTD10 in mammalian development are not clear, the studies have revealed that KCTD10 is highly expressed in the human heart, skeletal muscle, and placenta, with evidence that KCTD10 may play a role in the development of the neuroepithelium of the neural tube and dorsal root ganglion [68]. KCTD10 can also be associated with DNA synthesis and cell proliferation [71], suggesting that this protein may play an important role in tissue development [67, 69]. Also, a recent study has shown that the minor alleles at rs11066782 and rs11613718 in KCTD10 were associated with higher HDL-C concentrations and a lower CHD risk in the Chinese population [26]. A meta-analysis has been performed to reveal the impact of KCTD10 rs2338104 on AMD development, and results showed a statistical significance only in African Americans and Mexican Americans (P < 0.05) [27]. In another meta-analysis, the distribution of an effective allele at rs56209061 was compared between GA vs. CNV and showed the relation to advanced AMD subtypes [28]. Unfortunately, these associations did not survive corrections for multiple testing [27, 28]. In our study, we revealed opposite results; when comparing with other scientists’ groups [27, 28], we found statistically significant associations of the rs56209061 with early and exudative AMD development, considering minor allele A at rs56209061 as a protective marker for early and exudative AMD.

The CFI gene spans 63 kb and is composed of 13 exons, of which the first 8 are responsible for the heavy chain and the last 5 for the light chain encoding. The light chain contains the serine protease domain [35]. The CFI gene’s function is to encode the complement factor I. This factor plays a major role in the complement system. It is expressed by hepatocytes, macrophages, lymphocytes, endothelial cells, and fibroblasts. The complement factor I serum protease plays a major role in the complement system as a C3b and C4b inactivator. Under the presence of cofactors H and C4-binding protein, the complement factor I regulates the complement cascade activation via cleaving the alpha-chains of complement components C4b and C3b. This way, it prevents the assembly of C3 and C5 convertase enzymes [72]. The complement system and CFI have been connected in the pathogenesis of AMD. First, studies that have shown an association between CFI SNPs and AMD were described by Fagerness et al. A case-control association study for advanced AMD has been performed to identify new regions of the gene of interest. As a result, this research has demonstrated the CFI rs10033900 association with AMD in a Caucasian cohort [30]. Other studies have confirmed this connection and have also shown the CFI rs10033900 gene polymorphism correlation with AMD in different cohorts [30–34]. For example, Ennis et al. have shown the CFI region and AMD susceptibility in a UK cohort [31]. Kondo et al. have indicated the association of the rs10033900 gene polymorphism with the C allele in a Japanese cohort [32]. There have been publications of the link between CFI rs10033900 and AMD in two independent cohorts from England and Scotland and also in the Han Chinese population [33, 34]. In our study, we did not determine any associations between CFI rs10033900 and AMD development in the Lithuanian population, and the results are in conflict with those of other studies.

We identified the homozygous carriers of the allele C of ERCC6 rs3793784 as a risk factor for early and exudative AMD, and we are in agreement with other studies [32, 40, 49]. Another study [32] has shown that ERCC6 may be functionally implicated in the etiology of AMD. They reported that AMD-affected donor eyes had a 50% lower ERCC6 expression than healthy donor eyes (P = 0.018) [32]. A number of studies have also elucidated that a single-nucleotide polymorphism (SNP) in the ERCC6 promoter regulatory region (rs3793784) was moderately associated with AMD [40, 73]. Combining our data with those of the literature, we hypothesized that the AMD-related reduced transcriptional activity of ERCC6 expression may be caused by diverse, small, and heterogeneous genetic and/or environmental determinants.

Unfortunately, we found no associations between our last evaluated variant in the VEGFA gene (rs833068) and early or exudative AMD development in the Lithuanian population. On the other hand, VEGFA has been reported as a predisposing gene to AMD. A recent meta-analysis investigating the genetic susceptibility of AMD has demonstrated that VEGFA rs943080 is in a strong linkage disequilibrium (LD) with rs4711751 (r² = 1.0 in 1000 Genomes CEU data), which is significantly associated with advanced AMD [43]. There was nominal evidence found of a replication in the same direction as the initial study for VEGFA rs943080 (P < 0.05) [74]. While some studies found significant VEGF impact on AMD development [75–80], others showed opposite results [81]. For example, a study from Spain proved that VEGFA or VEGFR genes are not associated with the different AMD subtypes. A group of scientists states that further studies in different populations, and with a larger cohort of patients, are needed to confirm these results [81]. Oszajca et al. conducted a case-control study of 200 Polish patients with recognized AMD (dry and wet) who were compared to 100 healthy controls, and they proved that the CC genotype for VEGF +936C/T markedly increases the risk of age-related macular degeneration but does not influence its progression [75]. Also, a Chinese study confirmed the importance of VEGF on AMD [76]. An Indian study found associations with neovascular AMD for an SNP near VEGFA (rs4711751) (OR = 0.64, 95% CI 0.54 to 0.77, P = 10⁻⁷) [77].
An Italian study involved a cohort of 1976 subjects, including 976 patients affected with exudative AMD and 1000 control subjects. This analysis revealed that VEGFA was significantly associated with AMD susceptibility. The multivariate analysis showed that age, smoking, dietary habits, and sex, together with the genetic variants, were significantly associated with AMD in our population [78]. A review also described that VEGFA was significantly associated with the risk of AMD in the Italian cohort [79]. Finally, a genome-wide single variant analysis of 16,144 advanced AMD patients and 17,832 controls of European ancestry was performed, and it found that the VEGFA rs943080 T/C genotype was highly associated with AMD \( (P = 1.1 \times 10^{-14}) \) [80].

Different genotype distributions can be explained by controversial results in different populations. One genotype may be protective in one population, while the same genotype may increase a likelihood of disease development in another population. Wang et al. confirmed that some gene polymorphisms might be significant in the East Asian population but not in the European population [81]. Gaedigk et al. also confirm that the allele frequencies also differ in different populations: in an Ashkenazi Jewish and European cohort, a CYP2D6*4 allele is the highest, while in an East Asian cohort, it is the lowest [82].

AMD is a disease of multifactorial etiology. Its development is determined not only by genetic but also by modified and unmodified environmental risk factors. Overall, the most important pathogenetic mechanisms causing the development of AMD are the formation of drusen, local inflammation, and neovascularization. But it is still not clear why in some patients early AMD may remain early AMD for all life without any or with very insignificant progression, while in others, it may progress to late AMD (exudative or atrophic forms). The rs3793784 and rs11200638 SNPs and the haplotypes constructed from these two SNPs could be used as biomarkers for the progression of early AMD towards the exudative AMD form, because there were associations found between both early and exudative AMD forms and rs3793784 and rs11200638; however, it is necessary to follow our patients to assess the development and/or progression of AMD. Also, functional studies should be performed to confirm SNP variants as biomarkers for any diagnosis.

5. Conclusions

Our study identified two markers (HTRA1 rs11200638 and ERCC6 rs3793784) as risk factors for early and exudative AMD and one marker (KCTD10 rs56209061) as a protective factor for early and exudative AMD development.

The haplotypes constructed of rs3793784-rs11200638 were found to be associated with AMD development, as well.

5.1. Strengths and Limitations. Some limitations of this study have to be acknowledged: first, we did not perform functional studies to confirm the associations between SNPs and AMD development; second, the sample size of control subjects was relatively small; any other environmental risk factors were not included in our study.

The strengths of our study include a thorough clinical examination of the patients: all the patients were consulted by a general practitioner, and patients with malignant tumors, rheumatoid diseases, and end-stage liver or renal diseases and other systemic infectious and noninfectious diseases were excluded from the study as well.

Abbreviations

- AMD: Age-related macular degeneration
- SNPs: Single-nucleotide polymorphisms
- RPE: Retinal pigment epithelium
- BrM: Bruch’s membrane
- GA: Geographic atrophy.

Data Availability

Data will be provided in case a request is made by editors, reviewers, or scientists.

Conflicts of Interest

The authors declare no conflict of interest.

Authors’ Contributions


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Disease Markers


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