Genetic association and gene-gene interaction of HAS2, HABP1 and HYAL3 implicate hyaluronan metabolic genes in glaucomatous neurodegeneration

Kaustuv Basu\textsuperscript{a}, Abhijit Sen\textsuperscript{b}, Kunal Ray\textsuperscript{c}, Ilora Ghosh\textsuperscript{a}, Kasturi Datta\textsuperscript{a,}\textsuperscript{*} and Arijit Mukhopadhyay\textsuperscript{d,}\textsuperscript{*}

\textsuperscript{a}Biochemistry Laboratory, School of Environmental Sciences, Jawaharlal Nehru University, New Delhi, India
\textsuperscript{b}Dristi Pradip, Jodhpur Park, Kolkata, India
\textsuperscript{c}Molecular and Human Genetics Division, CSIR-Indian Institute of Chemical Biology, Kolkata, India
\textsuperscript{d}Genomics and Molecular Medicine, CSIR-Institute of Genomics and Integrative Biology, Delhi, India

Abstract. Hyaluronan (HA) plays a significant role in maintaining aqueous humor outflow in trabecular meshwork, the primary ocular tissue involved in glaucoma. We examined potential association of the single nucleotide polymorphisms (SNPs) of the HA synthesizing gene – hyaluronan synthase 2 (HAS2), hyaluronan binding protein 1 (HABP1) and HA catabolic gene hyaluronidase 3 (HYAL3) in the primary open angle glaucoma (POAG) patients in the Indian population. Thirteen tagged SNPs (6 for HAS2, 3 for HABP1 and 4 for HYAL3) were genotyped in 116 high tension (HTG), 321 non-high tension glaucoma (NHTG) samples and 96 unrelated, age-matched, glaucoma-negative, control samples. Allelic and genotypic association were analyzed by PLINK v1.04; haplotypes were identified using PHASE v2.1 and gene-gene interaction was analyzed using multifactor dimensionality reduction (MDR) v2.0. An allelic association (rs6651224; \(p = 0.03; \) OR: 0.49; 95% CI: 0.25–0.94) was observed at the second intron (C \(\rightarrow\) G) of HAS2 both for NHTG and HTG. rs1057308 revealed a genotypic association (\(p = 0.03\)) at the 5’ UTR of HAS2 with only HTG. TCT haplotype (rs1805429 – rs2472614 – rs8072363) in HABP1 and TTGA and TTGA (rs2285044 – rs3774753 – rs1310073 – rs1076872) in HYAL3 were found to be significantly high (\(p < 0.05\)) both for HTG and NHTG compared to controls. Gene-gene interaction revealed HABP1 predominantly interacts with HAS2 in HTG while it associates with both HYAL3 and HAS2 in NHTG. This is the first genetic evidence, albeit from a smaller study, that the natural polymorphisms in the genes involved in hyaluronan metabolism are potentially involved in glaucomatous neurodegeneration.

Keywords: Hyaluronan, HAS2, HABP1, HYAL3, SNP, POAG

1. Introduction

Glaucoma is a neurodegenerative disorder, caused by retinal ganglion cell (RGC) death, atrophy and axon degeneration, with or without elevated intra-ocular pressure [1]. It is the second largest cause of blindness after cataract affecting more than 80 million people worldwide [2]. Primary open angle glaucoma (POAG) is the major sub-type accounting for more than 50% of the total disease burden [3]. POAG can be sub-divided into two sub-types, high tension glaucoma (HTG) and nor-
mal tension glaucoma (NTG). Under normal situation, during aqueous humor outflow in the anterior chamber, the fluid exits through the trabecular meshwork (TM) and reaches into Schlemm’s canal and aqueous veins. If the TM passage gets blocked, the outflow mechanism is disturbed resulting into elevated intra ocular pressure (IOP) leading to HTG [4]. NTG is usually classified when the RGC death occurs in absence of an elevated IOP [5].

In POAG, the extracellular matrix (ECM) alters in the retina interrupting cell-cell and cell-ECM interactions and eventually causes RGC death by apoptosis. Extensive remodeling of ECM components including collagen I and IV, transforming growth factor-β2 (TGF-β2), matrix metalloproteinase (MMP-1), hyaluronan (HA) and chondroitin sulphate are reported in glaucomatous eye [6]. Being a high molecular weight mucopolysaccharide, HA is reported to act as a filter in the TM controlling aqueous humor flow and protecting the anterior chamber from shrinkage. Along with other glycosaminoglycans (GAGs), it is deposited on the trabecular wall reducing the flow channel diameter. Relatively small amounts of HA (0.06 mg/ml) and larger amounts of chondroitin sulphate (0.78 mg/ml) are speculated to be instrumental in aqueous flow resistance in the POAG TM, thus eventually increasing pressure on the retinal ganglion cells and optic nerve and finally lead to glaucoma [7]. A change in its normal distribution pattern has also been reported in several other parts of the eye in POAG [8]. Decrease in aqueous humor outflow resistance by hyaluronidase perfusion illustrates the importance of HA in glaucoma [9]. These observations along with high viscosity and ROS scavenging potentials have made HA a very important component in glaucoma research [10,11].

Hyaluronan, the unbranched complex polysaccharide is synthesized by hyaluronan synthase in the plasma membrane and degraded by the action of hyaluronidase [12,13]. HAS2, located on chromosome 8q24.12 is principally responsible for polymerization of high molecular weight of HA (up to $2 \times 10^6$ Da) and plays a vital role in tissue expansion and developmental growth influenced by growth factors, cytokines and hormones and also reported to synthesize HA in perineuronal net in the central nervous system [14,15]. During glaucoma TGF-β concentration increases in aqueous humor and in vitro study shows the HAS2 isomer is maximally upregulated in response to TGF-β [16]. Hyaluronidase is used exogenously to reduce HA and chondroitin sulfate concentration on glaucomatous trabecular wall to maintain normal aqueous outflow [17,18]. HYAL3, located on chromosome 3p21.3 is expressed in brain [19] and retina (our unpublished data) having role in HA catabolism, although the gene has not been explored much [13]. Hyaluronan mediates its multifunctional activity by interacting with a family of proteins named hyaladherin [20]. One of the members of hyaladherin is hyaluronan binding protein 1 (HABP1) isolated and characterized from our laboratory [21]. The gene encoding HABP1 was identified from human fibroblast cDNA expression library and reported to be localized on human chromosome 17p13.3 [22]. Sequence analysis confirms its multifunctional nature due to its identity with globular head of C1q and p32, the protein co-purified with splicing factor SF2, but its function was unknown [23]. HABP1 is represented as a synonym of C1QBp/p32 in the human genome database.

With this background, we wanted to evaluate the possible association of single nucleotide polymorphisms (SNPs) of genes involved in crucial steps of HA metabolism in glaucomatous neurodegeneration. We selected HAS2 to represent the synthesis of HA, HABP1 to represent the binding partner (hyaladherin) of HA and HYAL3 to represent hyaluronidase. Our study is the first to report association of these genes in POAG and implicate the role of HA in the disease process.

2. Materials and methods

2.1. Selection of the study subjects

For the case-control study, the genomic DNA samples were recruited from a large ethnic group speaking Indo-European language from the eastern part of India. The inclusion and exclusion criteria were used as previously reported [24]. Briefly, patients having IOP above or below 21 mmHg coupled with damaged visual field and/or optic disc cupping were included in the study. Patients with ocular hypertension but no visual field defect were excluded. Further, we divided the POAG cohort into HTG and non-HTG (NHTG) subgroups. The NHTG group is not formally classified as NTG because for practical reasons we could not evaluate IOP at multiple time-points which are critical for clinical confirmation. These patients did not have any record of an IOP $> 21$ mm Hg (without medication or surgery) and hence classified as non-HTG patients. The “unrelated” control samples we used for the association study were tested negative for both IOP and the visual field changes and were matched for gender, ethnicity and age.
Schematic representation of HAS2 gene with selected SNPs

Fig. 1. The hyaluronan synthesizing gene HAS2 is associated with HTG: Panel (A) shows a schematic representation of the genomic region of HAS2 with selected SNPs marked with arrow. Black boxes represent the exonic regions (E) of the gene. Panel (B) depicts the frequency variation of the minor allele (G) of rs6651224 in the HTG patients compared to the controls. The histogram shows protective allelic association in HTG patients. Panel (C) shows difference of genotypic frequency of GG in the HTG patients with respect to controls for rs1057308 (HAS2). The data were presented as the mean ± SD.

2.2. Selection of SNPs

In the present study, 13 tagged SNPs (rs3910552, rs1057308, rs4302848, rs11992999, rs6651224 and rs2385924 of HAS2 (Fig. 1A); rs8072363, rs2472614 and rs1805429 of HABP1 (Fig. 2A); rs1076872, rs13100173, rs3774753 and rs2285044 of HYAL3 (Fig. 3A)) were selected using CEU as a reference population, with minor allele frequency (MAF) cut-off at 0.1 and the r² ≥ 0.8. Tagged SNPs (tSNP) reported in Caucasian (CEU) populations in HapMap database got priority as the previous study [25] suggests SNPs in CEU population are portable to Indian populations.

2.3. Genotyping

Genotyping was carried out in The Centre for Genomic Application (TCGA, New Delhi, India), using MALDI-TOF based chemistry on the Sequenom platform. The multiplexed assays for the mentioned SNP IDs were designed using the assay design software provided by the Massarray platform. The primers were synthesized at the oligo facility in TCGA. For accuracy of the genotyping data, 10% of the samples were duplicated.

2.4. Data analysis

Initially as a quality check step Hardy-Weinberg Equilibrium was tested (p < 0.05) for the genotypes by Fisher’s Exact Test using PLINK v1.04 version [26] (http://pngu.mgh.harvard.edu/~purcell/plink). Minimum minor allele frequency was kept at 0.01. On the basis of these quality control criteria, three SNPs of HAS2 (rs2385924, rs11992999 and rs3910552) were filtered out and case-control association study was carried forward using the remaining 10 SNPs. For association analysis, allelic and genotypic frequencies were compared by chi-square test having one and two degrees of freedom, respectively. For test of association a p-value of less than 0.05 was considered significant. Haplotypes and their frequencies were analyzed from phase-unknown genotype data by using the PHASE version 2.1 [27]. In order to check for gene-gene interaction, multifactor dimensionality reduction (MDR) ver 2.0 was used based on the principle of non-parametric and genetic model-free alternative to logistic regression [28]. The data were presented as the mean ± SD. An unpaired Student’s t-test was used to compare the data obtained.
A Schematic representation of HABP1 with selected SNPs

B HABP1 - TCT Haplotype frequency in POAG patients and controls

Fig. 2. Risk haplotype of hyaluronan binding gene HABP1 for POAG: Panel (A) shows a schematic representation of the genomic region of HABP1 with selected SNPs marked with arrow. Black boxes represent the exonic regions (E) of the gene. Panel (B) depicts the variation in the frequency of TCT haplotype of HABP1 in HTG and NHTG patients compared to the controls. The histogram represents significant association ($p < 0.05$) of TCT haplotype in both categories of POAG patients.

A Schematic representation of HYAL3 with selected SNPs

B HYAL3 - TTGA and TTAG Haplotype frequency in HTG and NHTG patients compared to the controls

Fig. 3. Haplotypic association of hyaluronan catabolic gene HYAL3 in POAG: Panel (A) represents a cartoon of HYAL3 gene with the selected tagged SNPs. Black boxes represent the exonic regions (E) of the gene. Panel (B) depicts the frequency variation of TTGA and TTAG haplotypes of HYAL3 in the HTG (red) and NHTG (green) patients compared to the controls (blue). The data shows the haplotypes are significantly associated with both HTG and NHTG. (Colours are visible in the online version of the article; http://dx.doi.org/10.3233/DMA-2012-0915)
Table 1
Allelic association of the hyaluronan metabolic genes with POAG in Indian population

<table>
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<th>Gene</th>
<th>SNP</th>
<th>Minor Allele frequency</th>
<th>Chi-square</th>
<th>p-value</th>
<th>OR</th>
<th>95% C.I.</th>
<th>Type of glaucoma</th>
<th>Remark</th>
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3. Results and discussion

In this study we explored the role of genetic variations in three genes, involved in HA metabolism, for glaucomatous neurodegeneration by case-control study. We genotyped 437 POAG patients (116 HTG & 321 non-HTG) and 96 glaucoma-negative controls followed by haplotypic and allelic association analyses.

3.1. The hyaluronan synthesizing gene, HAS2 is associated with HTG

rs6651224 (C>G) located in intron-II of HAS2 showed significant association (chi square: 4.63; p-value: 0.03; OR: 0.49; 95% CI: 0.25–0.94) with the HTG patients. The frequency of the minor ‘G’ allele in the cases was significantly less than that in controls (0.08 vs 0.16), implicating its protective role in HTG [Fig. 1B(i)]. In NHTG group the variant showed the same trend but was not significant (p = 0.08; OR = 0.65; 95% CI: 0.39–1.06) (Table 1). Another variation in HAS2 rs1057308 (A>G), located at 5’ UTR (exon 1) showed significant genotypic (GG) association with the HTG patients (Chi square; 7.18; p-value: 0.02). The higher frequency of GG (0.17) in the HTG with respect to the control groups (0.068) implicates a higher risk conferred by this genotype for HTG patients in the study population (Fig. 1C(ii)). We could not observe any association of this variant (p = 0.18) in NHTG group. Interestingly, rs1057308 is also located in the intergenic sequence of the natural antisense of HAS2 (HAS2AS) complimentary to the 5’ UTR of HAS2. HAS2AS is reported to hinder the hyaluronan synthesizing function of HAS2 [29]. rs1057308 can potentially alter the function of HAS2AS consequently altering the regulation of hyaluronan synthesis. As mentioned earlier, if produced in larger quantities, the HA polysaccharide deposits on the TM wall and may eventually elevate IOP by blocking the aqueous humor outflow [7].

Our data on genetic association of HAS2 with POAG is supported by the previous observation on upregulation of HAS2 both in transcriptional as well as in translational level in bovine trabecular meshwork under treatment of the growth factors, TGF-beta and PDGF-BB simulating glaucomatous condition in vitro [16], implicating probable role of HAS2 in glaucomatous neurodegeneration.

3.2. A risk haplotype of hyaluronan binding gene HABP1 for both HTG and NHTG

In HABP1, the frequency of TCT haplotype (rs1805429, rs2472614, rs8072363) was significantly higher in both HTG and NHTG patients (p < 0.05) compared to matched controls (0.16 in HTG, 0.18 in NHTG vs. 0.09 in controls), indicating that this is a risk haplotype for POAG (Fig. 2B). Our present observation on
Table 2

<table>
<thead>
<tr>
<th>Gene</th>
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<th>Frequency (%)</th>
<th>Haplotype association</th>
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The association of haplotype of HABP1 in POAG is strongly supported by a recent report on significant up-regulation and synaptic relocalization of the complement component 1q (C1q) in adult retina during early stage of glaucoma [30] as well as the protective nature of mutant C1qa in glaucomatous mice model [31]. As mentioned earlier, C1q is one of the important ligands of the multifunctional HABP1 [23,32], implicating its role in glaucoma. In addition, in a recent report, HABP1 has been found interacting with Forkhead Box C1 (FOXC1), which is principally responsible for axenfeld-rieger malformations in human with reports of glaucoma as a secondary complication [33]. HABP1 is predominantly cytoplasmic and its nuclear domain co-localizes with FOXC1 and helps in its transcription activation. Mutation (p.Phe112Ser) in FOXC1 disturbed its interaction with HABP1 that might eventually lead to eye disease [34]. Thus, our observation corroborating with these reports justifies the probable involvement of HABP1 in glaucomatous neurodegeneration. This can be independent through both FOXC1 and C1q or they might be working in synergy.

3.3. Hyaluronan catabolic gene HYAL3 represents two risk haplotypes for both HTG and NHTG

Four SNPs were selected (rs2285044, rs3774753, rs1310073, and rs1076872) from HYAL3 in the present study. As depicted in Fig. 3C, TTAG and TEGA, the two major haplotypes were found to be significantly over represented (p < 0.05) in both HTG and NHTG compared to controls [(TTAG: HTG, 26.29%; NHTG, 24.75%; Controls, 16.43%) and (TEGA: HTG, 47.84%; NHTG, 49.03%; Controls, 34.93%)] (Table 2).

3.4. Gene-gene interaction network of hyaluronan metabolic genes in glaucoma

We explored possible interactions between the genotypes using a regression approach and observed HABP1 plays an important role in both HTG and NHTG. In HTG, it interacts only with HAS2, not with HYAL3 while in NHTG it associates with both of them. We observed AA of rs1057308 (HAS2) significantly co-occur more (p < 0.01) with TC of rs1805429 (HABP1) and CC of rs2472614 (HABP1) in HTG patients (8.62%) compared to controls (3.12%) (Fig. 4A). The same three SNPs as above in HAS2 and HABP1 with GG, TT and CG genotypes, respectively, co-occur with significantly higher frequency in HTG samples compared to normal individuals (4.31% vs 1.04%, p < 0.01) [data not shown]. This indicate that the two loci in HABP1, rs1805429 and rs2472614 are interacting in a dominant fashion (both one type homozygote and heterozygote co-occur more in HTG patients) via rs1057308 (HAS2) independent of its genotype (both AA and GG shows interaction). Interestingly, when TT of rs1805429
Fig. 4. Gene-gene interaction of hyaluronan synthesizing gene, HAS2 and hyaluronan binding gene, HABP1 in high tension glaucoma. In panel (A) MDR output shows AA of rs1057308 (HAS2) significantly co-occur (p < 0.01) with TC of rs1805429 (HABP1) and CC of rs2472614 (HABP1) in higher frequency in HTG patients (8.62%) compared to controls (3.12%) implicating risk interaction for HTG. Panel (B) shows significant co-occurrence (p < 0.001) of CC of rs6651224 (HAS2) and AT of rs4302848 (HAS2) with TT of rs1805429 (HABP1) and CG of rs2472614 (HABP1) in higher frequency in normal individuals (11.45%) in comparison to the HTG group (3.44%) implicating a protective interaction for HTG. The black bars represent distributions of cases (left) and controls (right). For each gene-gene interaction panel, in the left numbers above bars represent the numbers of cases and controls while in the right percentage is represented. In top row, high-risk cells are indicated by dark colour, low-risk cells by light colour, and empty cells by no colour. Case-control pairs marked with circle are magnified in the histogram and represented according to the frequency of co-occurrence.

(HABP1) and CG of rs2472614 (HABP1) were observed together with CC of rs6651224 (HAS2) and AT of rs4302848 (HAS2), the co-occurrence revealed putative protective effect for HTG (3.44% vs 11.45% in controls, p < 0.05). The results are depicted in Fig. 4B.

The overall interaction map from the gene-gene interaction analysis shows, rs1805429 of HABP1 is the common member in both the best-fit protective and risk genetic interactions in HTG (Fig. 5). In this model, information gained about case-control status from knowledge about genotypes at one or more SNPs is measured by removal of entropy. The interaction map shows that rs6651224 of HAS2 has the strongest synergistic binding with rs1805429 (8.98% of the total entropy). This observation corroborates with the protective allelic association data of rs6651224. On the other hand, interaction between rs1057308 of HAS2 and rs1805429 has the maximum synergistic interaction (3.22% of the total entropy) potentially at-risk for HTG patients. We hypothesize that rs1805429 of HABP1 may influence the effect of rs1057308 (present in both HAS2 and HAS2-AS), to hinder the normal activity of natural antisense, and thus induces over-production of hyaluronan implying indirect role of the polymorphism (rs1805429) in aetiology of HTG. Interestingly, the locus rs2472614 of HABP1 reveals a detrimental interaction with HAS2 in HTG but it indicates beneficial interaction with HAS2 and HYAL3 in NHTG. This might lead to discovery of biological cross-talk between these molecules in the disease pathology.

Our present results indicate that the HA metabolic genes are involved in glaucomatous neurodegeneration probably by two different routes. In both, HTG and NHTG, hyaluronan binding protein (hyaladherin)
Hyaluronan is a major component of the human eye, predominantly present in vitreous humor [35] and also in the aqueous humor, conjunctiva, corneal stroma, iris, optic nerve etc [8,36]. Due to its viscous nature, the vitreous fluid has the potential to absorb shock and thus prevent trauma to the eye. It also plays an important role in optic nutrient transportation and ocular wound healing [8] and acts as a temporary matrix during the initial phase of wound healing in the corneal stroma. Together with its different binding protein partners (hyaladherin) like CSPG2/Versican, SPACR and SPACRCAN, HA helps in retinal development and retinal physiology [37]. It is reported, after the 5th decade of life, eyes usually stop producing HA leading to several eye problems like poor vision, dry eyes and floaters [38]. In diseases like macular degeneration, retinitis pigmentosa and glaucoma, its level is altered [39,40]. Accumulation of HA due to upregulation of choroidal HAS2 is thought to play important role in stromal swelling during recovery from myopia [41]. Interestingly, in another recent study myopia has been indicated as a risk factor for POAG [42]. Modulation in expression of HA-binding proteins like CD44 and CSPG2/Versican has been reported in glaucoma [43,44]. Inspite of excess-synthesis of HA on TM [7], its concentration was found decreased in aqueous humor in POAG patients in a different study [39]. In primary angle closure glaucoma (PACG), SPACR was upregulated in iris [45].

Since our observations along with other published works justify the importance of HA metabolism in the biological process of glaucoma and this field has not yet been explored much, in the present study we carefully ignored rigorous statistical correction so that any important signal might not get lost due to marginal association. It is advisable to further check the associations in large cohorts. Our present study on evaluating the association of genetic variants in the genes involved in HA metabolism provides the first genetic support to the earlier reports about the important role of HA and related genes in glaucomatous neurodegeneration. Interestingly, our results suggest that their involvement in the disease process might be via different routes for HTG and NHTG. Further studies on this area would provide more insight into these preliminary but important observations and, if proven, might provide new clues to disease management and therapy.

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