Genetic networks in mouse retinal ganglion cells

Felix L. Struebing, Emory University
Richard K. Lee, University of Miami
Robert W. Williams, University of Tennessee
Eldon Geisert Jr, Emory University

Journal Title: Frontiers in Genetics
Volume: Volume 7, Number SEP
Publisher: Frontiers Media | 2016-09-28, Pages 169-169
Type of Work: Article | Final Publisher PDF
Publisher DOI: 10.3389/fgene.2016.00169
Permanent URL: https://pid.emory.edu/ark:/25593/rrvzq

Final published version: http://dx.doi.org/10.3389/fgene.2016.00169

Copyright information:
© 2016 Struebing, Lee, Williams and Geisert.
This is an Open Access work distributed under the terms of the Creative Commons Attribution 4.0 International License (https://creativecommons.org/licenses/by/4.0/).

Accessed March 1, 2020 12:18 AM EST
Genetic Networks in Mouse Retinal Ganglion Cells

Felix L. Struebing 1, Richard K. Lee 2, Robert W. Williams 3 and Eldon E. Geisert 1*

1 Department of Ophthalmology, Emory University School of Medicine, Atlanta, GA, USA, 2 Bascom Palmer Eye Institute, University of Miami Miller School of Medicine, Miami, FL, USA, 3 Department of Genetics, Genomics and Informatics, University of Tennessee Health Science Center, Memphis, TN, USA

Retinal ganglion cells (RGCs) are the output neuron of the eye, transmitting visual information from the retina through the optic nerve to the brain. The importance of RGCs for vision is demonstrated in blinding diseases where RGCs are lost, such as in glaucoma or after optic nerve injury. In the present study, we hypothesize that normal RGC function is transcriptionally regulated. To test our hypothesis, we examine large retinal expression microarray datasets from recombinant inbred mouse strains in GeneNetwork and define transcriptional networks of RGCs and their subtypes. Two major and functionally distinct transcriptional networks centering around Thy1 and Tubb3 (Class III beta-tubulin) were identified. Each network is independently regulated and modulated by unique genomic loci. Meta-analysis of publically available data confirms that RGC subtypes are differentially susceptible to death, with alpha-RGCs and intrinsically photosensitive RGCs (ipRGCs) being less sensitive to cell death than other RGC subtypes in a mouse model of glaucoma.

Keywords: retinal ganglion cells, gene regulatory networks, transcription factors, recombinant inbred strain, subtypes

INTRODUCTION

The retinal ganglion cell (RGC) is the final output neuron of the retina, projecting through the optic nerve to the brain, where it targets a number of functionally distinct areas: for visual perception, RGC axons travel to the lateral geniculate nucleus (Chalupa and Günhan, 2004); for the regulation of circadian rhythms, they pass through the suprachiasmatic nucleus (Guido et al., 2010); and for eye movements, a group of RGC axons terminates in the superior colliculus (Triplett et al., 2014); and for the pupillary light reflex, RCG axons terminate in the pretectal area (Young and Lund, 1998). Each of these areas receives input from distinct subtypes of RGCs with unique morphological and molecular signatures. At the present time, over 30 subtypes of RGCs (Baden et al., 2016) are estimated to exist. They all receive inputs from other types of retinal neurons (bipolar cells and amacrine cells), and most of them express similar groups of genes that may serve as general RGC markers (Raymond et al., 2008; Rodriguez et al., 2014). Identifying gene expression patterns in RGCs and their subtypes is currently an active area of research, as demonstrated by the discovery of new subtypes of ganglion cells based on gene expression (Macosko et al., 2015; Sanes and Masland, 2015).

The death of RGCs in glaucoma or after injury eventually leads to loss of vision (Templeton et al., 2009; Zode et al., 2011; Munguba et al., 2014; Nuschke et al., 2015). However, the susceptibility of RGC subtypes to death differs among the distinct subtypes. Some RGCs are resistant to injury, while others appear to be more sensitive to insult, indicating differential gene expression and response to injury among subtypes (Chang et al., 2013; Duan et al., 2015; Puyang et al., 2015). The present
study focuses on transcriptional networks within RGCs of the mouse, using gene expression data measured across 55 strains of recombinant inbred BXD mice (King et al., 2015) as well as the bioinformatic tools from GeneNetwork (Williams and Mulligan, 2012). The analysis begins by examining genes correlated with two relatively general RGC markers, Thy1 and Tubb3. Each of these markers forms a unique network of genes that appears to function independently across many of the RGC subtypes. These networks are functionally different to the point of having distinct transcription factor binding sites. Subtype-specific networks partially overlapping with the Thy1-network are also present. In a meta-analysis of previously published data from a microarray study of a mouse glaucoma model (Howell et al., 2011), we examine the differential effects of this disease state on transcriptional networks in RGC subtypes and confirm intrinsically photosensitive RGCs (ipRGCs) and alpha-RGCs as more resistant to cell death (Duan et al., 2015).

The systems genetics and bioinformatics approach used in the present study demonstrates how signatures of RGCs and their subtypes can be extracted from a complex neural tissue such as the retina.

RESULTS

RGC Markers Segregate into Two Major Correlation Networks

The present study examines the correlation of gene expression in the retina across the BXD recombinant inbred strain set to define gene networks active in RGCs. The BXD strain set is derived from two parental strains, the C57BL/6J mouse and the DBA/2J mouse. Natural variation in gene expression across strains can be used to identify co-regulated genes with a similar expression pattern, allowing for the construction of genetic networks (Williams et al., 2001; Geisert et al., 2009; Templeton et al., 2013a; Keeley et al., 2014).

The data used in this study consist of whole retinal samples collected from 55 BXD strains. They can be found on www.geneNetwork.org under the identifier “DoD Retina Normal Affy MoGene 2.0 ST (May15) RMA Gene Level”. Two features of this dataset enhance the quality of the analysis: The first is that the retina is a tissue that can be consistently isolated with minimal contamination by other tissues. The second is the quality of the RNA with an average RNA Integrity Score of 9.43 and a standard error of 0.037 across the 220 samples isolated for this dataset.

The analysis began with two well-characterized markers for RGCs, Thy1 and Tubb3, as they both exhibited substantial variability in mRNA expression levels across BXD strains (Figure 1). Expression of Thy1 ranged from 10.39 in BXD42 to 11.45 in BXD15 (this data is presented on a log2 scale and the difference in expression is equivalent to an over 2-fold change). A similar variability in gene expression was observed for Tubb3, with expression levels ranging from 9.68 (BXD6) to 10.74 (BXD2). When correlations for Thy1 and Tubb3 were made across all microarray data, both produced a highly correlated group of genes. For Thy1, the top 100 correlates had an absolute r-value (Pearson) greater than 0.89 (Bonferroni-adjusted p < 1e-12) and the top 2000 correlates all had an absolute r-value greater than 0.77 (adj. p < 1e-8). If we examine the Pearson correlation values above 0.60, which corresponds to an adjusted p-value of 0.02, then Thy1 has a total of 8596 correlates. This tightly correlated list of genes forms a potential network, and indicates that the genes in this network are co-regulated across the BXD strains (King et al., 2015). Within the list of the top 2000 Thy1-correlates, we found several other well-characterized RGC markers, including Rbfox3 (producing NeuN, Neuronal Nuclei), Pou4f1 (producing BRN3A), and Pou4f2 (producing BRN3B) (Table 1). Interestingly, the Thy1 correlate list did not contain other known RGC markers, including Tubb3.

For Tubb3, the top 100 genes had an absolute r value greater than 0.71 (adj. p < 1e-6), and the top 2000 genes showed values greater than 0.52 (adj. p = 0.12) and did not contain Thy1, Pou4f1, Pou4f2, or Rbfox3. This was also true for the 1387 correlates with Pearson r > 0.60 (equal to a significant Bonferroni-adjusted p-value of 0.02). However, other RGC markers were present in the Tubb3 correlation list, including the newly described Rbpm5 (RNA binding protein with multiple splicing) as well as Calb2 (Calcium binding 2) and Chrrn6 (Cholinergic receptor nicotinic alpha 6).

These two networks are relatively independent, with minimal overlap. When examining the correlates of the Thy1-network relative to the Tubb3-network, only one gene is shared within their top 100 correlates (1%), 31 genes (1.55%) are present in the top 2000 correlates, and 51 genes (0.05%) are in common with the 9982 genes found in both the Thy1 (8596 genes) and the Tubb3 (1386 genes) correlation lists with a Pearson correlation above 0.6.

The basis for the segregation of genes into two distinct networks is illustrated by plotting the correlations for combinations of genes from both networks. In Figure 2, the expression of Thy1, Pou4f1, Tubb3, and Rbpm5 across BXD strains is displayed in scatterplots. These plots demonstrate the tight correlation for Thy1-Pou4f1 (Figure 2A) and Tubb3-Rbpm5 (Figure 2C). They further show the lack of correlation between Thy1 and Tubb3 (Figure 2B) as well as Tubb3 and Pou4f1 (Figure 2D). The presence of additional RGC markers in the correlation lists of Thy1 and Tubb3 together with the minimal overlap of genes indicated the presence of at least two RGC-specific transcriptional networks in mouse RGCs.

Since we selected Thy1 and Tubb3 to serve as primary RGC markers for this analysis based upon literature evidence, we wondered if an alternative unbiased approach would validate our findings. As an independent examination of these networks, we performed weighted gene correlation network analysis (WGCNA) on the whole microarray dataset (Langfelder and Horvath, 2008). This method relies on unsupervised clustering of co-expressed genes across all of the BXD RI strains into so-called modules or eigengenes and thus represents an unbiased approach to test the assumption that Thy1- and Tubb3- networks exist independently from each other. WGCNA created 18 modules of co-expressed genes. Module #1 contained 1741 of the top 2000 Thy1 correlates, whereas only 131 genes from the top 2000 modules.
**FIGURE 1** RNA expression across the BXD RI strain set for *Thy1* (left) and *Tubb3* (right) with the means and standard errors. There was an approximately 2-fold difference in mean expression levels for both genes. This data is given as raw expression values on a log$_2$ scale +8.

*Tubb3* correlates were assigned to this module. The majority of the *Tubb3* correlates belonged to modules #4 ($n = 279$), #5 ($n = 886$), and #6 ($n = 327$), none of which contained any of the *Thy1* correlates. This minor overlap in module affiliation between genes of both networks reaffirms our finding that the *Thy1* - and *Tubb3*-network function individually.
To define the genomic location of upstream modulators for both the Thy1- and the Tubb3-network, we examined interval maps for the 7 RGC marker genes found in both correlation lists (Thy1, Rbfox3, Pou4f2, Pou4f1, Tubb3, Calb2, and Rbpms). When we investigated each marker’s signature quantitative trait locus (QTL), we found that Thy1, Rbfox3, Pou4f2, and Pou4f1, had similar interval maps. The same was true for Tubb3, Calb2, and Rbpms. To further investigate this phenomenon, we plotted multiple interval maps as heat maps for each marker and its 20 highest correlated genes (Figure 3). In these heat maps, rows correspond to the QTL curve of a single correlated gene plotted across the entire genome. Two color gradients were used to characterize differential expression between strains: A yellow to red gradient identified a transcript whose expression was higher in strains with a B haplotype (allele origin from C57BL/6J), whereas a green to blue gradient represented a transcript whose expression was higher in strains with the D haplotype (allele origin from DBA/2J). The linkage significance (LRS or LOD-score) increased with color intensity. In other words: A deeply colored vertical line characterized a genomic locus that may contain a regulatory element responsible for the differential expression of these genes.

These bands are thought to identify a genomic locus modulating the expression of the genes in the network across the BXD RI strains. Likely candidates for modulating gene expression include transcription factors, micro RNAs or long noncoding RNAs (Geisert et al., 2009; Templeton et al., 2013b; Williams and Auwerx, 2015). Since the analysis is only correlational in nature, we cannot exclude the possibility that loci for individual networks do not have regulatory roles, as they could just be co-regulated with the other identified networks. When comparing heat maps for both networks, no overlap in patterns was observed. Thus, the RGC marker genes segregated into two independently regulated gene networks. From here on, we will refer to these networks as the Thy1-network and the Tubb3-network. This is an arbitrary nomenclature, mirroring the most prominent RGC marker for each of both networks. For the Thy1-network, the strongest modular signature was localized at the distal end of Chromosome 1. For members of the Tubb3-network, the most prominent genomic signature was on mid-distal Chromosome 13. Several candidate genes exist in those loci; a comprehensive analysis is attached as Supplemental Material (Supplemental Tables 1, 2).

There are three potential scenarios that would allow two specific genetic networks to exist within a single cell population. The first is that the mRNA levels of each marker differ across the entire retina. The second explanation is that their mRNA expression levels differ in specific RGC subtypes, leading to unique expression of each protein within each RGC subtype. The third potential mechanism involves differences in the percentage of each of the RGC subtypes from strain to strain. To further examine this, we immunostained retinas with THY1 and Class III beta tubulin. In these retinal whole mounts, the more than 90% of labeled cells were double-labeled of RGCs were both THY1- and Class III beta tubulin- positive (Figure 4), indicating that the two markers are co-localized and expressed in the same cell. Despite their protein co-expression, their mRNA level may differ from cell to cell. When examining the double stained cells, the intensity of each stain varies from ganglion cell to ganglion cell. Some cells had approximately equal labeling for THY1 and Class III beta tubulin.
tubulin, while in other cells THY1 staining was more intense than Class III beta tubulin. In a few cells, the labeling of Class III beta tubulin was more intense. It also appeared that some cells were labeled by only one of the two markers. Thus, even though both markers are co-expressed in many RGCs, their expression levels do not consistently correlate with each other, corroborating that their expression is independently regulated.

Since multiple subtypes of RGCs are known to exist, one could predict that there are also multiple genetic networks within each of these subtypes. We compiled an extended list of RGC markers from the literature. This list consisted of 17 proteins and their respective genes, 6 of which are known to be relatively specific for a single RGC subtype (Table 1).

Calculating the correlation in expression across the BXD RI strain set and displaying these relations in a network graph revealed that indeed two major network hubs formed around Thy1 and Tubb3 based on the highest correlations surrounding these two markers (Figure 5). The only significant connection between Thy1 and Tubb3 existed through 2 of their respective correlates, Slc17a6 (VGLUT2), and ChRNA6. Except for Hoxd10 (a marker of ON-directionally selective RGCs), all the other RGC markers had a direct connection to either Thy1 or Tubb3.

**Functional Differences of RGC Networks**

Following the identification of two gene networks related to normal RGC function, we asked whether both networks had any functional differences.

In order to facilitate this analysis, we grouped genes with a similar heat map pattern belonging to the same network into one "synthetic trait" using principal component analysis. These "synthetic traits" provide for more robust functional network analysis than a single marker gene, and they can be used to generate correlation lists specific to a group of genes by reducing...
FIGURE 3 | RGC markers segregate into two major correlation networks. For each of the general RGC markers on the right, the eQTL curve for the 20 highest correlated genes was plotted as a heat map. In these, the LRS/LOD score is given in pseudocolors: A yellow to red gradient identifies a transcript whose expression is higher in strains with a B haplotype at that locus (allele origin from C57BL/6J), whereas a green to blue gradient represents a transcript whose expression is higher in strains with the D haplotype (allele origin from DBA/2J). There are several strong and sharp trans-bands extending across Thy1, Rbfox3, Pou4f2, and Pou4f1, such as on distal Chromosome 1 or 13. There are also trans-bands extending across Tubb3, Calb2, and Rbpms on mid Chr. 13 and proximal Chr. 14. No overlap is present between the genes separated by the black line, indicating that RGC markers segregate into two major independently regulated gene networks. The panel on the right lists genes that are found in more than one of the top 20 correlations. For example, Arhgap44 is present in the 20 highest correlates for both Thy1 and Pou4f1.

FIGURE 4 | Maximum intensity projections of confocal z-stacks taken from retinal whole-mounts showing the co-localization of THY1 (A) and Class III beta-tubulin (B) in the retinal ganglion cell layer from a C57BL/6 mouse. Most cells were double-stained for both RGC markers (C), but some cells only expressed Class III beta-tubulin (arrowhead) or THY1 (arrow). Furthermore, the staining intensity was different across cells, and some cells had large somata and were more intensely stained than others (large arrowhead in “merge”). Staining with the secondary antibodies only did not result in unspecific fluorescence (data not shown). Scale bar in C = 100 µm.

the dimensionality of the data (Yin et al., 2012; Vanderlinden et al., 2013; Graybeal et al., 2014).

The synthetic trait for the Thy1-network was constructed using Thy1 and its direct correlates Rbfox3, Pou4f1, and Pou4f2, while the Tubb3-network was constructed using Tubb3, Calb2, and Rbpms. When we compared the correlations of these networks using WebGestalt-based gene ontology (GO) analysis (Wang et al., 2013), each of the two synthetic traits was enriched in genes with very different molecular and cellular functions. The Thy1-network was significantly enriched in genes involved in neuron development, synaptic transmission, cation transmembrane transporter activity and voltage-gated channel activity (adj. p < 0.0000001 for all), strongly indicating that this network was highly neuron-specific (Supplemental Figure S1). Some examples of the genes associated with neuronal development and synaptic transmission included: Tnr, NeuroD2, L1cam, Syn2, Grn4, and Gabbr1 (see Supplemental Table 3 for the whole list). A close examination of the highest (r > 0.9) correlates...
also revealed that at least 6 genes (Gsk3a, Srgap1, Arhgap44, Ncdn, L1cam, and Lrrc4b) were functionally associated with neurite outgrowth.

The Tubb3 synthetic network contained genes that were associated with completely different biological functions (Supplemental Figure S2). Several members of the tubulin family of proteins were at the top of the correlation list, such as Tubg2, Tubda4a, Tubg1, Tubb5, and Tuba1b. Gene Ontology analysis revealed enrichment in GO terms “guanyl nucleotide binding” and “protein polymerization” (both with adj. p < 0.001), including the genes Rab11b, Bab8a, Tufm, Rab11b, Arf6, and Rab4b. The highest correlates of the Tubb3 synthetic trait were two genes encoding proteins from the Rab family (Rab15 and Rab4b).

**Distinct Groups of Transcription Factor Binding Sites Are Associated with the Two RGC networks**

Since the Thy1- and the Tubb3-network were functionally enriched for distinct GO terms, we asked if this difference would be reflected in their transcription factor binding site (TFBS) distribution. We searched the promoter sequences for genes in the Thy1-network using the TRANSFAC FMatch algorithm (Matys et al., 2006) for over-represented TFBS in comparison to the Tubb3-network and vice versa (Tables 2a,b). Genes of the Thy1-network were ~4 times more enriched in TFBS for p53 and Dec1, two master regulators of cell cycle progression (Qian et al., 2012). The Thy1-network was also more enriched in TFBS for PPAR gamma and estrogen receptor alpha as well as effectors SP1 and AP1. In contrast, the promoters of genes in the Tubb3-network were significantly enriched in TFBS of developmental origin, such as Pax6, Six6, proteins of the Sox and Oct family, as well as Pou4f1.

**Genomic Regulation of Subtype-Specific RGC Markers**

Since our analysis revealed two distinct molecular networks governing normal RGC function, we hypothesized that subtype-specific RGC markers would contain regulatory signatures from either one or both RGC networks.

Thus, we generated heat maps of the highest correlates of each subtype-specific marker (Cartpt2, Jam2, Kcng4, Opn4, Spp1, and Hoxd10, see Figure 5). This comprehensive analysis revealed that two pairs of genes were regulated in a similar fashion: Cartpt and Jam2 as well as Kcng4 and Opn4 showed very similar heat maps to each other. When we compared the heat maps...
for these 4 subtype-specific markers, we found that some of their bands were at identical loci as bands observed in the Thy1-network (Figure 6). While Cartpt/Jam2 had the distinct band from distal Chromosome 1, Kcng4/Opn4 shared a band on distal Chromosome 13. It was also noticed that the allelic distribution of correlates for Cartpt/Jam2 seen as a blue line on distal Chromosome 1 was diametrical to the original Thy1-correlates, where the line was mostly yellow-red (see Figure 3). This simply implies that the top 20 correlates of Cartpt and Jam2 are in fact correlated inversely to Cartpt or Jam2 itself, whereas the top 20 correlates of Thy1 are positively correlated to Thy1 itself.

**Overlap of Correlates of Subtype-Specific Markers with the Thy1-network and the Tubb3-network**

When we took the top 2000 correlates (an arbitrary cut-off) of each of the six subtype specific markers (Cartpt, Jam2, Kcng4, Opn4, Hoxd10, and Spp1) and examined the distributions of these markers across the Thy1- and the Tubb3-networks, we were able to see the relative interplay between these networks (Table 3). For Spp1 and Hoxd10, the majority of the overlap was seen with genes from the Tubb3-network. The picture was quite different for the remaining subtype-specific markers. For Cartpt, Opn4, Kcng4, and Jam2, the overlap was dominated by similarities with the Thy1-network. This analysis was also conducted using only the genes with a Pearson correlation value above 0.6 (adj. \( p < 0.02 \)) and it displayed a similar trend (Table 3). Taken together these data indicate that each of the RGC subtypes has a unique interplay with the Thy1- and the Tubb3-networks. The dramatic differences in overlap between correlates may reflect the differential expression of the Thy1- and Tubb3-networks in different RGC subtypes. These relationships can also be seen in the network map (Figure 5).

### Susceptibility of RGC Marker Genes to Glaucomatous Nerve Damage

The identification of RGC subtypes has raised the question whether or not there is a difference in susceptibility to nerve damage, subsequent cell survival, or axon regeneration. In order to test this hypothesis on a transcriptional level, we used publicly available microarray data generated from DBA/2J glaucomatous eyes (Howell et al., 2011) and correlated glaucoma severity score (GSS) with expression levels of RGC markers (Figure 7). As expected, expression levels of all general RGC markers decreased as nerve damage increased (implicated by the negative correlation between GSS and RGC markers in Figure 7, dashed blue line). This was also the case for two subtype-specific markers, Jam2 and Cartpt. Interestingly, expression levels of markers for alpha-RGCs (Kcng4 and Spp1) and ipRGCs (Opn4) did not correlate to GSS (cutoff \( r < 0.6 \)), suggesting that these two RGC subtypes are differentially susceptible to nerve damage.

### DISCUSSION

Using the DoD CDMRP Retina expression microarray dataset to examine correlates of known RGC markers across the BXD RI strain set, this study revealed two distinct gene networks regulating normal RGC function. Detecting these transcriptional networks with high statistical power required tissue from 55 RI strains with 4 biological replicates per strain. The bioinformatic tools on GeneNetwork allowed us to extract gene networks from a complex structure such as the mouse retina (Geisert et al., 2009; Keeley et al., 2014). Interestingly, almost all of the general RGC markers described in the literature (see Table 1) selectively group with one of two genetic networks, the Thy1-network or the Tubb3-network. Both Thy1 (Barnstable and Drager, 1984) and Tubb3 (Snow and Robson, 1994) are believed to be generalized markers for RGCs. Nonetheless, these markers segregate into two distinct genetic networks. Two scenarios could explain the biological basis of correlated genes that are co-regulated in BXD RI mice: (I) differences in cell number of each RGC subtype across the BXD strains, or (II) differences in gene expression within individual RGC subtypes (Geisert et al., 2009; Keeley et al., 2014). Currently, we are not able to explain these differences.
FIGURE 6 | Heat maps for RGC subtype-specific marker genes. Cartpt/Jam2 share the trans-band on distal Chromosome 1 with the Thy1-network, whereas Kcng4/Opn4 share the Thy1-network trans-band from Chromosome 13. There is no obvious overlap of trans-bands with either network for Hoxd10. For Spp1, no obvious trans-bands can be appreciated, suggesting that this gene is not part of a transcriptional network in its normal state.

Both the Thy1- and the Tubb3-networks contained large groups of genes that were consistent with a neuronal phenotype. However, they were each enriched in distinct functional roles. The Thy1-network appeared to be functionally involved in neuronal development and maintenance, as well as axon guidance. Some of the highest correlates of this network (Gsk3a, Srgap1, Arhgap44, Ncdn, L1cam, and Lrc4b) were all previously reported to affect dendrite or axon pathfinding and outgrowth (Schwaibold and Brandt, 2008; Cherry et al., 2011; Ip et al., 2011; Galic et al., 2014). Therefore, this network could be directly involved in RGC process extension, potentially including dendrites and axons projecting to the brain. Furthermore, the network was enriched in transmembrane ion transporters. This included several calcium- and sodium-gated channel subunits, all of which have been previously localized to RGCs (Lipton and Tauck, 1987; Farrell et al., 2014).

The Tubb3-network contained genes that differed in function from those of the Thy1-network. The biological processes enriched in this group included protein polymerization and organic substrate metabolic processes. Under molecular processes, the Tubb3-network was enriched for GTP binding proteins and GTPase activity, two mechanisms known to be essential for cellular transport involving the cytoskeleton (Roychowdhury and Rasenick, 2008; Schappi et al., 2014). The highest two correlates of the Tubb3-network were Rab15 and Rab4b, two G-proteins that are known to play an important role in endosome formation and vesicle movement along actin and tubulin networks (Zuk and Elferink, 2000; Falk et al., 2014). Several other genes in this list were associated with intracellular trafficking, such as sorting nexin 32 (Snx32, a molecule that links transport vesicles to dynactin (Wassmer et al., 2009), vesicle associated membrane protein 1 (Vamp1, a SNARE protein important for linking vesicles to the target membrane; Hasan et al., 2010), Pigu (a GPI anchor protein; Guo et al., 2004), and Tmem9 (part of the lysosomal membrane; Kveine et al., 2002). These genes were highly correlated with and specific to the Tubb3-network.

These findings suggest that the Tubb3-network is functionally associated with cytoskeleton and vesicle transport in RGCs. Since neurons are known for the significant amount of cytoskeletal proteins necessary to maintain dendritic and axonal integrity (Koene, 2015), it can be hypothesized that the Tubb3-network is involved in maintenance of these structural elements.

Taken together, this analysis indicates that each network has distinct molecular functions and that both of these networks can exist independently within a single RGC.

To distinguish between these two potential explanations. Our analysis also revealed that these networks have unique biological functions.

Frontiers in Genetics | www.frontiersin.org 9 September 2016 | Volume 7 | Article 169
The functional differences between networks were mirrored by the transcription factor binding site (TFBS) analysis for promoters of their respective genes. Members of the Thy1-network showed significant enrichment in TFBS for proteins regulating cell cycle, growth and apoptosis (Tu et al., 2013).

<table>
<thead>
<tr>
<th>Subtype Marker</th>
<th>Top 2000</th>
<th>Total Overlap (of 4000)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cartpt</td>
<td>1022</td>
<td>54</td>
</tr>
<tr>
<td>Jam2</td>
<td>382</td>
<td>25</td>
</tr>
<tr>
<td>Kcnq4</td>
<td>326</td>
<td>241</td>
</tr>
<tr>
<td>Opn4</td>
<td>713</td>
<td>185</td>
</tr>
<tr>
<td>Hoxd10</td>
<td>10</td>
<td>19</td>
</tr>
<tr>
<td>Spp1</td>
<td>29</td>
<td>756</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Subtype Marker</th>
<th>Pearson r &gt; 0.6</th>
<th>Total Overlap (of 9982)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cartpt</td>
<td>2482</td>
<td>0</td>
</tr>
<tr>
<td>Jam2</td>
<td>1030</td>
<td>3</td>
</tr>
<tr>
<td>Kcnq4</td>
<td>886</td>
<td>207</td>
</tr>
<tr>
<td>Opn4</td>
<td>1086</td>
<td>56</td>
</tr>
<tr>
<td>Hoxd10</td>
<td>4</td>
<td>17</td>
</tr>
<tr>
<td>Spp1</td>
<td>13</td>
<td>9</td>
</tr>
</tbody>
</table>

For the top table, the top 2000 correlates of both networks served as comparison, whereas a Pearson r cutoff of >0.6 was chosen for the lower table, corresponding to a Bonferroni-corrected value of p < 0.02.

Genes belonging to the Tubb3-network, however, showed an over-representation of TFBS for transcription factors known to establish cell fate decisions during development, particularly in later stages. Proteins such as OTX1, PAX6, SIX6, or POU4F1 belonged to the latter group (Zagozewski et al., 2014). Pou4f1 was not originally found in the correlates of the Tubb3-network, which might seem surprising. A possible explanation for this is that the Thy1-network, which correlates well with the expression of Pou4f1 across the BXD strains, acts upstream of the Tubb3-network. In a developmental sense, this could suggest that members of the Thy1-network establish expression of Pou4f1, which can then bind to members of the Tubb3-network to influence their transcription. Because Pou4f1 was originally not found to be part of the Tubb3-network but the Thy1-network instead, we hypothesize here that basic cell cycle tasks such as survival decisions are managed by members of the Thy1-network, while members of the Tubb3-network regulate the fine-tuning of RGC development, possibly even influencing subtype commitments.

The identification of neuronal subtypes has gained a considerable amount of attention in neuroscience across a variety of scientific disciplines (Hoshino, 2012; Russ and Kaltschmidt, 2014). This is especially the case for RGC subtypes (Kay et al., 2011; Dhande et al., 2013; Sanes and Masland, 2015). The establishment of transgenic mouse models has recently transformed the field, and new paradigms are starting to emerge. For example, it is becoming increasingly evident that RGC subtypes seem to be differentially susceptible to nerve injury to the point of having different chances of survival or regeneration (Kay et al., 2011; Dhande et al., 2013; Pérez de Sevilla Müller et al., 2014; Duan et al., 2015; Sanes and Masland, 2015). In order to develop new therapeutic approaches to nerve regeneration,
it may be necessary to tease apart the transcriptional programs of injury-susceptible and non-susceptible RGC subtypes.

When we investigated the heat maps of subtype-specific gene correlates, we found that two pairs—Kcnq4/Opn4, or Jam2/Cartpt—showed similarity to two different heat map bands from the Thy1-network. Kcnq4 marks alpha-RGCs, while Opn4 marks ipRGCs, and these two subtypes were recently found to be most resistant to optic nerve crush (Pérez de Sevilla Müller et al., 2014; Duan et al., 2015). Since the regulatory pattern of those two gene pairs was very similar based on heat map analysis of their co-varying genes, it would be interesting to systematically investigate if these upstream modulatory loci are responsible for increased neuronal survival or regeneration. Bioinformatic analysis of RGC marker susceptibility to glaucomatous nerve damage supported the notion that alpha-RGCs and ipRGCs were also most resistant to neurodegeneration. The decrease in mRNA expression of alpha-RGC markers (Kcnq4, Spp1) and ipRGC markers (Opn4) did not correlate with GSS (a visual grading scale for optic nerve axon damage), whereas the overwhelming majority of RGC markers did.

Interestingly, the discovery of Spp1 marking a particular RGC subtype had only been made after crush injury to the optic nerve in a mouse model (Pérez de Sevilla Müller et al., 2014; Duan et al., 2015). In this study, it was found that alpha-RGCs secreting Osteopontin (the protein made from the gene Spp1) were most resistant to optic nerve crush among all RGC subtypes, and that this protective effect was due to Osteopontin. We were not able to identify putative upstream modulatory loci for this gene due to the lack of distinct trans-QTL bands. This suggests that Spp1 is part of a genetic network that needs to be activated by neuronal injury before it can be co-regulated in a more RGC-specific way. This phenomenon has been observed elsewhere for other genes following retinal injury (Templeton et al., 2013b).

In summary, we have identified multiple loci modulating RGC function in the BXD mouse strain set, and we have provided in silico evidence for the differential susceptibility of RGC subtypes to neurodegeneration and cell death. One caveat of this study is the fact that the performed analysis is only a correlative one. Proving a biological cause will require experimental manipulation of the mentioned genes and examination of the effects in vivo or in vitro. Nevertheless, our findings enhance the understanding of the RGC’s normal transcriptome, as they are the first to describe gene regulatory networks for some of their subtypes. They may serve others and us as a reference for future studies on RGC subtype identification and their susceptibility to injury.

**MATERIALS AND METHODS**

**Animals**

All of the procedures involving mice were approved by IACUC at Emory University and adhered to the ARVO Statement for the Use of Animals in Research.

**Microarray Datasets**

Two microarray datasets were used in this project as part of a comprehensive meta-analysis.

(i) The Department of Defense (DoD) Normal Retina Database (May2015). This is the most comprehensive retina microarray dataset and creation is described in King et al. (2015). The DoD Normal Retina Dataset consists of 222 microarrays from 55 different strains BXD mice, the parental strain C57BL/6J, the parental strain DBA/2J and an F1 cross.

(ii) The Howell et al. (2011), DBA/2J Glaucoma Retina M430 2.0 (Sep11) RMA database. This dataset consists of retinal tissue dissected from 40 DBA/2J mouse eyes at 10.5 months of age showing varying levels of RGC damage due to naturally occuring glaucoma in this mouse strain (as graded by visual inspection of the optic nerve). Twenty eyes served as negative controls. The generation of this dataset is described in Howell et al. (2011).

All of the used datasets are publicly accessible through www.genenetwork.org.

**Statistical Analysis and Plot Generation**

GeneNetwork provided the platform for correlation analysis, principal component generation, and linkage analysis. In general, datasets were queried for gene symbols, downloaded from GeneNetwork, and additional analysis was performed in R whenever necessary. P-values mentioned in relation to Pearson’s coefficient throughout this paper are based on pairwise comparisons. All p-values were Bonferroni-adjusted for 36,012 genes, which is equal to the number of genes captured from the loci showing trans-bands. For a cis-QTL considered to be a good candidate gene, it should fulfill three conditions: (i) be expressed above background, (ii) correlate well with the trait used to create the trans-bands, and (iii) have a nucleotide variation that alters either protein structure or other regulatory elements (such as promoters or enhancers). These lists are appended as Supplemental Tables.

**Gene Ontology Analysis**

GO analysis was performed using WebGestalt (Wang et al., 2013). The top 500 genes of each network were used to compile a gene list and duplicates were removed. GO term enrichment was calculated using Affymetrix MouseGene 2.0 ST probe set IDs against a background dataset from the same chip. GO trees are appended as expanded view data. All p-values presented in the GO analysis are corrected for multiple comparisons using the Bonferroni method.

**Candidate Gene Analysis**

A list of candidate genes for putative upstream modulators of both networks was created by extracting genes with cis-QTLs from the loci showing trans-bands. For a cis-QTL considered to be a good candidate gene, it should fulfill three conditions: (i) be expressed above background, (ii) correlate well with the trait used to create the trans-bands, and (iii) have a nucleotide variation that alters either protein structure or other regulatory elements (such as promoters or enhancers). These lists are appended as Supplemental Tables.
Transcription Factor Binding Site Analysis

Gene lists including the top 500 correlated genes in each network were compiled, duplicates were removed, and uploaded to BIOBASE. The TRANSFAC FMatch algorithm was used to search for overrepresented neuron-specific transcription factor binding sites in the gene lists using the “best supported promoter” model for each gene (Matys et al., 2006). As a background dataset for both networks, the opposite network was chosen. Resulting p-values were Bonferroni-adjusted. The enrichment window for a gene’s promoter was chosen to be −5000 to +100 bp of its best supported transcription start site. “Minimize false positives” was selected as cut-off method. The TRANSFAC data version was 2016.2, and only high-quality matrices were used for the analysis.

WGCNA Analysis

Weighted gene network analysis was performed using the WGCNA package in the R environment (Langfelder and Horvath, 2008). A soft thresholding power of 10 was used to calculate the adjacency matrix based on the criterion of scale-free topology (Zhang and Horvath, 2005). Modules were identified using the following parameters for the blockwiseModules function: minimum module size of 100, merge cut height of 0.25, and maximum block size of 2000. The top 2000 correlates of Thyl and Tubb3 were then each merged with their module affiliation by Affymetrix Probe Set ID and the resulting list was checked for overlaps.

Immunohistochemistry

Two 60 day-old Thy1-CFP C57BL/6 transgenic mouse (Jax identifier B6.Cg-Tg(Thy1-CFP)23Jrs/J) were deeply anesthetized with a mixture of 13 mg/kg of xylazine and 87 mg/kg of ketamine and intracardially perfused with 0.9% saline followed by 4% paraformaldehyde. Retinas were dissected and flat-mounted on glass slides following a standard protocol. Retinas were blocked in 4% bovine serum albumin in PBS overnight. One retina was stained with anti-TUJ1 (a gift from Anthony Frankforter, dilution 1:1000) and anti-GFP (Invitrogen, 1:500) antibodies overnight and then labeled with appropriate Alexa Fluor-conjugated secondary antibodies. One retina served as negative secondary antibody control (data not shown). High-resolution Z-stacks were captured on a Nikon confocal microscope with the Nikon C1 software throughout the entire ganglion cell layer only. Z-stacks were collapsed using Fiji (Schindelin et al., 2012) and the whole image was adjusted for contrast and brightness using Adobe Photoshop.

ACCESSIBILITY OF DATA

The data presented in this article is publicly available under www.genenetwork.org and can be downloaded under http://genenetwork.org/webqtI/main.py?FormID=sharinginfo&GN_AccessionId=709.

AUTHOR CONTRIBUTIONS

FS, EG provided the initial design of the study. FS performed experiments and bioinformatic analyses with assistance from EG, FS, EG wrote the paper with input from RW and RL. RW supplied the datasets through the GeneNetwork platform and is responsible for its maintenance. RL has provided intellectual framework for this project as part of an ongoing collaborative effort between his laboratory and the laboratories of EG, RW.

ACKNOWLEDGMENTS

This work was supported by DoD CDMRP Grant W81XWH1210255 from the USA Army Medical Research & Materiel Command and the Telemedicine and Advanced Technology (to EG), NIH Grant R01EY017841 (to EG), Vision Core Grant P30EY006360 (to P. Michael Iuvone), and Unrestricted Funds and a Stein Innovation Award from Research to Prevent Blindness (to the Ophthalmology Department at Emory University, the University of Tennessee Health Science Center, and the Bascom Palmer Eye Institute, University of Miami Miller School of Medicine). FS is supported by the institutional training grant T32EY00792-30 (to P. Michael Iuvone). The authors would like to thank Rebecca King for technical assistance with the retinal flat mounts and Dr. John Nickerson for his comments on the manuscript.

SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: http://journal.frontiersin.org/article/10.3389/fgene.2016.00169

REFERENCES
