The American Journal of Human Genetics, Volume 98

Supplemental Data

Biallelic Mutations in GNB3 Cause

a Unique Form of Autosomal-Recessive

Congenital Stationary Night Blindness

Ajoy Vincent, Isabelle Audo, Erika Tavares, Jason T. Maynes, Anupreet Tumber, Thomas Wright, Shuning Li, Christelle Michiels, Christel Condroyer, Heather MacDonald, Robert Verdet, José-Alain Sahel, Christian P. Hamel, Christina Zeitz, Elise Héon, and GNB3 Consortium

Supplemental Data:

Supplemental Methods:

Whole exome sequencing and analysis pipeline:

Briefly, 2×100 bp paired end sequencing was done using the Illumina Hi-Seq 2500 platform after target enrichment of 3µg of genomic DNA using the Agilent SureSelect Human Exome Library V5 kit followed by an in house standardized pipeline analysis. Overall mean exon coverage in trio-1 was 87-111X with >20X target base coverage of 96-97%. Overall mean exon coverage in trio-2 was 68-131X with >20X base coverage of 92-97%. Sequence reads were trimmed, and subsequently aligned to the reference human genome (hg 19/GRCh 37) using Burrows-Wheelchair aligner.^{1; 2} PCR duplicate reads were removed (MarkDuplicates, Picard tools v.1.112) and local realignment was performed (GATK 3.2.2). GATK haplotype caller3.2.2 was used to annotate single nucleotide variants (SNVs) and insertions/deletions (indels).^{3;4} Only variants with minor allele frequency ≤ 0.01 reported in external and internal databases [NHLB] Exome Sequencing Project (ESP) Exome Variant Server; 1,000 genomes; dbSNP; Exome Aggregation Consortium (ExAC); and Complete Genomics (CG) control database (54 exomes)] were retained. Pathogenic prediction was performed using six different tools that included Polyphen-2, SIFT, mutation taster, combined annotation-dependent depletion Phred, and conservation values amongst PhyloP placental mammals and PhyloP 100-vertebrates.⁵⁻⁹

Supplemental Results:

Full-field electroretinogram (ERG):

The ERG assessments of families A and B were done at separate sites using comparable basic International Society for Clinical electrophysiology of Vision (ISCEV) protocols. The amplitude and implicit time data of standard ERG responses obtained from affected members are detailed in supplemental table (Table S3). The DA 0.01 ERG b-wave showed moderate (n=2; sib-ship from Family A) to severe (n=2; II-5 from Family A and proband from family B) amplitude reduction. The DA3.0 ERG showed normal a-wave and reduced b-wave in all four cases. The bright-flash DA10.0 ERG was electronegative (b/a <1) in all three tested individuals. These findings suggest partial (sib-ship; p.Lys57del/p.Trp339*) or severe rod ON-bipolar dysfunction (2 cases; p.Trp339*/p.Trp339*; p.Ser67Phe/ p.Ser67Phe). Flicker ERG (LA3.0 30Hz) showed normal amplitude and implicit-time in the sib-ship; delayed implicit-timing with near normal amplitudes were noted in two subjects (II-5, Family A, p.Trp339*/p.Trp339* and IV-3, Family B, p.Ser67Phe/p.Ser67Phe). The LA 3.0 single flash ERG results are detailed in the main text.

Cone phototransduction sensitivity (S_c) and Maximal amplitude (Rm_{p3}) measurement:

After pupil dilatation (right eye) and ten minute light adaptation, Case-II-5 (Family A) was tested using a series of four bright white flashes (25, 63, 157 and 241 cd.s.m⁻²) under a rod saturating (30.0 cd.m⁻²) background. Burian-Allen electrodes were used for the recording; at each step, five or more reproducible traces were averaged. Pupils measured 9mm after the testing. The cone sensitivity (S_c) and maximal cone photoreceptor amplitude (Rm_{p3}) were calculated as described.^{10; 11} In brief, equation 1 was fitted to the initial 12 ms of the waveforms obtained from the 4 flash intensities using a grid search algorithm.

$$P3(i,t) = \left\{ \frac{i \cdot s_c \cdot (t-t_d)^3}{i \cdot s_c \cdot (t-t_d)^3 + 1} \right\} \cdot Rm_{p3}$$
 (Equation 1)

Where i = intensity (log scotopic trolands), t = time (ms), $S_c = \text{Sensitivity} (td \cdot s^{-1} \cdot \sec^{-3})$, $t_d = time$ delay (ms) and $\text{Rm}_{p3} = \text{maximal cone photoreceptor amplitude } (\mu V)$. To determine t_d , waveforms from the control subjects were fitted allowing all 3 parameters (S_c , Rm_{p3} and t_d) to vary; modal

value of t_d (2.2 ms) was then used to fit all control and patient data. Case II-5 had Rm_{p3} of -97µV (Normal Range: ⁷74 - ¹103 µV); S_c was reduced $[log(S_c)] = 0.83$ (Normal Range: 1.59 – 2.17).

Filtering Steps	Total Vari			
	Case III -2	Case II-5	Shared Genes	
Total Variants	95,306	93,262		
Coding sequence and splicing Variants	21,496	20,201		
Non-synonymous Coding Variants and splicing Variants	9,721	9,632		
Variants with Allele frequency ≤ 0.01 in public databases	515	461		
Genes with ≥ 2 variants	42 genes	30 genes	Shared Genes 13 genes (18 variants) 6 genes (11 variants) 6 genes (11 variants) 1 gene (1 variant)	
	(73 variants)	(48 variants)	(18 variants)	
Genes remaining after removal of homozygous variants in	33 genes	22 genes	6 genes	
affected, if present in homozygous state in unaffected	(64 variants)	(40 variants)	(11 variants)	
parents				
Genes remaining after removal of heterozygous variants in	32 genes	21 genes	6 genes	
affected, if present in homozygous state in unaffected	(62 variants)	(38 variants)	(11 variants)	
parents				
Genes remaining after removal of homozygous or	32 genes	10 genes	1 gene (1	
compound heterozygous variants shared between Case II-5	(62 variants)	(18 variants)	variant)	
(affected) and Case II-4 (unaffected sibling of II-5)			GNB3	

Supplemental Table 1: The filtering steps used in the analysis of WES data from Family A

Supplemental	Table 2:	Summary	of the clir	nical phenc	type in	the two	families
11		J		1	2 I		

Family	Case (Sex, Age) Mutation	BCVA RE: LE	Refractive Error RE:LE	Color Vision	CS RE:LE	Visual Field	Comment
	III-2 (M, 7yr)	20/25:	+2.25/-0.75 x 30°:	Normal RG & BY	1.50:	I4e target – 105° BE	Night-blindness since childhood
	p.Lysdel57/p.Trp339*	20/30	+2.00/-0.75 x 20°	(HRR)	1.50	III4e target – 130° BE	
	III-1 (M, 13yr)	20/25:	Plano: Plano	Normal RG & BY	1.65:	I4e target – 100° BE	Asymptomatic
А	p.Lysdel57/p.Trp339*	20/25		(HRR)	1.80	III4e target – 125° BE	
	II-5 (F, 48yr)	20/30:	-1.50/-1.00 x 70°:	Mild RG deficit,	1.35:	I4e target – 100° BE	Night-blindness since childhood,
	p.Trp339*/p.Trp339*	20/25	-1.50/-1.50 x 90°	Normal BY (HRR)	1:35	III4e target – 130° BE	Photophobia – recent
В	IV-3 (F, 65yr)	20/25:	+2.50/-4.50 x 95°:	Normal (saturated	NA	IIIc target – 120° RE	Night blindness since childhood; photophobia
	p.Ser67Phe/p.Ser67Phe	20/25	+2.50/-5.00 x 75°	D15); Moderate BY		IIIc target – 115° LE	since thirties; Late onset (55 years) cerebellar
				deficit (unsaturated			ataxia and peripheral neuropathy of
				D15			undetermined etiology

Abbreviations: RE - right eye; LE - left eye; BE - both eyes; BCVA - best-corrected visual acuity; CS - contrast sensitivity; HRR -

Hardy Rand Rittler; RG – red-green; BY – blue-yellow; NA – not available; GVF – Goldmann visual fields.

Family	Case (Age/ Age Range)	Eye	DA 0.01 b-wave Amp	DA 3.0 a-wave Amp	DA 3.0 b-wave Amp	DA 3.0 b:a	DA 10.0 b:a	LA 3.0 a-wave IT	LA 3.0 a-wave Amp	LA 3.0 b-wave IT	LA 3.0 b-wave Amp	LA 30 Hz IT	LA 30 Hz Amp
	III-2 (11yr)	RE	73	183	214	1.17	0.94	17	48	31	179	29	237
		LE	58	186	228	1.23	0.89	16	42	31	180	NA	NA
	III-1 (13yr)	RE	68	165	208	1.26	0.98	17	56	31	165	29	210
А		LE	59	181	233	1.28	NA	NA	NA	NA	NA	29	149
	II-5 (48yr)	RE	0	252	179	0.71	0.73	24	36	36	86	35	86
В	IV-3 (65yr)	RE	0	173	139	0.80	NA	31	100	49	96	33	88
		LE	0	158	126	0.80	NA	34	93	49	79	NA	NA
Control (No	ormal Range)	EI	161 - 430	172 - 440	296 - 652	1.36 - 2.98	1.33 - 2.07	14 - 17	25 - 62	27 - 30	119 - 232	25 - 29	89 - 184

Supplemental Table 3: Detailed Electroretinogram phenotype in the two families

Abbreviations: RE - right eye; LE - left eye; EI - either eye (only one eye data was included); DA - dark adapted; LA - light adapted; $Amp - amplitude (\mu V)$; IT - implicit time (ms); NA - not available.

Supplemental References:

- 1. Bolger, A.M., Lohse, M., and Usadel, B. (2014). Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics 30, 2114-2120.
- 2. Li, H., and Durbin, R. (2010). Fast and accurate long-read alignment with Burrows-Wheeler transform. Bioinformatics 26, 589-595.
- 3. DePristo, M.A., Banks, E., Poplin, R., Garimella, K.V., Maguire, J.R., Hartl, C., Philippakis, A.A., del Angel, G., Rivas, M.A., Hanna, M., et al. (2011). A framework for variation discovery and genotyping using next-generation DNA sequencing data. Nature genetics 43, 491-498.
- McKenna, A., Hanna, M., Banks, E., Sivachenko, A., Cibulskis, K., Kernytsky, A., Garimella, K., Altshuler, D., Gabriel, S., Daly, M., et al. (2010). The Genome Analysis Toolkit: a MapReduce framework for analyzing next-generation DNA sequencing data. Genome research 20, 1297-1303.
- Adzhubei, I.A., Schmidt, S., Peshkin, L., Ramensky, V.E., Gerasimova, A., Bork, P., Kondrashov, A.S., and Sunyaev, S.R. (2010). A method and server for predicting damaging missense mutations. Nature methods 7, 248-249.
- 6. Kumar, P., Henikoff, S., and Ng, P.C. (2009). Predicting the effects of coding non-synonymous variants on protein function using the SIFT algorithm. Nature protocols 4, 1073-1081.
- Kircher, M., Witten, D.M., Jain, P., O'Roak, B.J., Cooper, G.M., and Shendure, J. (2014). A general framework for estimating the relative pathogenicity of human genetic variants. Nature genetics 46, 310-315.
- 8. Schwarz, J.M., Cooper, D.N., Schuelke, M., and Seelow, D. (2014). MutationTaster2: mutation prediction for the deep-sequencing age. Nature methods 11, 361-362.
- 9. Pollard, K.S., Hubisz, M.J., Rosenbloom, K.R., and Siepel, A. (2010). Detection of nonneutral substitution rates on mammalian phylogenies. Genome research 20, 110-121.
- 10. Hood, D.C., and Birch, D.G. (1995). Phototransduction in human cones measured using the alphawave of the ERG. Vision research 35, 2801-2810.
- 11. Birch, D.G., Hood, D.C., Locke, K.G., Hoffman, D.R., and Tzekov, R.T. (2002). Quantitative electroretinogram measures of phototransduction in cone and rod photoreceptors: normal aging, progression with disease, and test-retest variability. Arch Ophthalmol 120, 1045-1051.