BRIEF COMMUNICATION

Genome sequencing in persistently unsolved white matter disorders


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Abstract

Genetic white matter disorders have heterogeneous etiologies and overlapping clinical presentations. We performed a study of the diagnostic efficacy of genome sequencing in 41 unsolved cases with prior exome sequencing, resolving an additional 14 from an historical cohort (n = 191). Reanalysis in the context of novel disease-associated genes and improved variant curation and annotation resolved 64% of cases. The remaining diagnoses were directly attributable to genome sequencing, including cases with small and large copy number variants (CNVs) and variants in deep intronic and technically difficult regions. Genome sequencing, in combination with other methodologies, achieved a diagnostic yield of 85% in this retrospective cohort.

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Cas Simons, Ryan J. Taft and Adeline Vanderver contributed equally to this work

Introduction

Next-generation sequencing (NGS) including both targeted gene panels and exome sequencing has become a central component of the diagnostic evaluation of individuals with a neurologic disorder of unknown origin. Exome sequencing has shown success in phenotypically diverse cohorts, including the leukodystrophies, a broad class of genetic disorders that affect the white matter of the central nervous system (CNS). Leukodystrophies are diverse in origin and highly heterogeneous in presentation and disease course, making diagnosis challenging. Until recently, the probability of obtaining a definitive molecular diagnosis was less than 50% over 5 years and despite increases of up to threefold in diagnostic efficacy, many cases remain unsolved. Previously, we reported on a cohort of 191 families with a suspected leukodystrophy, of which 71 were persistently unsolved despite targeted molecular and enzymatic testing and 19 were lost to follow-up. Trio-or-greater exome sequencing analysis resolved 42% (30/71) of unsolved cases, which, in combination with standard of care approaches, yielded a 77% overall diagnostic rate from 172 families available for testing. This was a substantial increase over the historical norms, but left at least 23% persistently unsolved.

Genome sequencing has the potential to detect a wide variety of variant types, including single-nucleotide variants and indels (out-performing exome sequencing in protein-coding regions), copy number variants (CNV), repeat expansions, and detection of pathogenic nonprotein-coding variation that is missed by other NGS approaches. We pursued genome sequencing on the remaining 41 persistently unsolved families to assess the potential value of genome sequencing diagnostics in a pediatric neurological disease cohort.

Methods

Recruitment

Affected individuals were referred to the Myelin Disorders Bioregistry Project (MDBP) for unsolved leukencephalopathy of presumed genetic etiology between 1 August 2009 to 31 July 2013, as previously described. The study had approval from the institutional review boards at collaborating institutions.

Clinical and neuroimaging descriptions are available on request. All individuals had abnormal white matter identified by neuroimaging, suggestive of a leukodystrophy. Symptom onset ranged from birth to 19 years. Ethnicities varied and included individuals of mixed and northern
European descent, as well as African American, Arabian,
African, Asian, and Latin American origin.1

**Genome sequencing and analysis**

Genome sequencing was performed at Illumina Inc., San
Diego on an Illumina 2000 using 2 x 125 nucleotide
paired-end reads. Dual analyses were run in parallel for
each sample. In one, reads were aligned to the reference
human genome (GRCh37) using the Burrows-Wheeler
Aligner (BWA) software package and pedigree informed
variant calling was performed using the GATK Haplo-
typeCaller v3.7.6. Variant annotation was performed using
Snpeff v4.3.m.7 This analysis used a custom variant anno-
tation and interpretation interface to identify possible
causal variants. In the other analysis, samples were pro-
cessed using the Illumina Secondary Analysis Software
v5.11.0 (Northstar v5 release), aligned to the reference
human genome (GRCh37). Candidate variants were iden-
tified using a custom-built variant interpretation engine.
In both analyses, variants were triaged and prioritized by
minor allele frequency, conservation, genotype, inheri-
tance, disease-association, consequence, and predicted
pathogenicity. Candidate splice-altering variants were vali-
dated using a minigene splicing assay (Appendix S1).8

**Assessment of Variants**

Putatively causal variants were assessed as per the Ameri-
can College of Medical Genetics (AGMC) guidelines.9
Cases with variants in known disease genes meeting the
ACMG criteria for pathogenic or likely pathogenic, and
whose clinical features were concordant with the estab-
lished gene–disease relationship (including magnetic reso-
nance imaging (MRI) patterns) were classified as resolved.
Candidate variants in potentially novel disease genes were submit-
ted to GeneMatcher.

**Results**

Forty-one families that remained without a molecular eti-
ology after exome sequencing received genome sequencing
(Fig. 1A). The mean read depth in probands was 34X and
on average, 91% of the genome had coverage depth greater
than 20X (Appendix S1). Genome sequencing resulted in a
molecular diagnosis for 14 families (34%) (Table 1). Nine
diagnoses were achieved through improvements in variant
curation or novel disease-associated genes described since
the exome sequencing analysis. Five diagnoses were achieved
through identification of CNVs (three cases), deep intronic
variants (one case), and variants in techni-
cally difficult regions (one case). One case was considered
clinically resolved following multidisciplinary review.

Since our initial study, more than 1,200 new gene–dis-
ease relationships have been described, and studies have
shown increases of up to 10% in diagnostic yield with
reanalysis within 24–36 months.10 Reanalysis in the con-
text of recently published literature (and associated anno-
tation pipelines) allowed resolution of an additional eight
cases. These included a de novo missense variant in
H3F3B (OMIM:601058) (LD_0246),11 a hemizygous, syn-
onymous variant in AIFM1 (OMIM:300169) (LD_0500),12
and biallelic variants in HIKESHI (OMIM:614908)
(LD_0162),13 NXX6-2 (OMIM:605955) (LD_0527),14 and
SPATA5 (OMIM:613940) (LD_0808),15 all previously
associated with prominent white matter disease in multi-
ple affected individuals. Affected individuals in families
LD_0579 and LD_0587 had variants in genes previously
implicated in neurologic syndromes where improvements
in our analysis pipeline or improved phenotypic under-
stand permitted a diagnosis or prioritized a high confi-
dence candidate, in LICAM (OMIM:308840)16 and
KDM5C (OMIM:314690),17 respectively. White matter
abnormalities are a rare association with LICAM-related
disorder.16 LD_0587 has a clinical presentation with intel-
ductual disability, epilepsy, aggressive behavior, and
macrocephaly, all consistent features of KDM5C-related
disorder and is classified as clinically resolved but the
identified variant lacks definitive proof to be classified as
likely pathogenic or pathogenic.17 This case was not
included in overall numbers of definitively resolved cases
as this variant remains a variant of uncertain significance
per the ACMG criteria. Finally, causal nonprotein-coding
variants were identified in SNORD118 (OMIM:616663),
confirming a clinical diagnosis of leukoencephalopathy
with calcifications and cysts (OMIM:614561) in
LD_0807.18 SNORD118 variants were found as part of a
targeted cohort study and concomitantly found in our
genome sequencing cohort.18

In two individuals, genome sequencing revealed vari-
ants not identified on exome sequencing analysis due to
lack of variant annotation or stringent filtering. For
LD_0725, genome sequencing revealed a mitochondrial
DNA variant, m.3243A>G in MT-TL1 (OMIM:590050),
carried on 42% of reads in the affected individual and
15% of the maternal reads. This variant has been previ-
ously associated with mitochondrial encephalomyopathy,
lactic acidosis, and stroke-like episodes (MELAS
[OMIM:540000]). LD_0315 had biallelic variants in
DARS2 (OMIM:610956), associated with leukoen-
cephalopathy with brainstem and spinal cord involvement
and lactate elevation (LBSL [OMIM:611105]). An intronic
variant, c.228-21delTinsCC, p.(Arg76Serfs*5) that has
been shown to affect mRNA splicing of DARS2 with skip-
ing of exon 319 was found in trans with a previously
unreported missense variant, c.294G>T, p.(Glu98Asp).
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**Genome Sequencing in Persistently Unsolved White Matter Disorders**

**A**

Original Cohort = 191  
GS Cohort = 41

- 21% Unsolved  
- 16% ES Solved  
- 10% Excluded  
- 53% SoC  
- 27% SNV  
- 7% CNV  
- 2% mtDNA  
- 10% Candidates  
- 54% Unsolved

**B**

Exome Sequencing

**C**

Genome Sequencing  
GJC2 c.916_928dupGCCTCCGCCCCCG; p.Ala310fs

**D**

Normal Allele  
Duplicated Allele
Stringent variant filtering performed during the prior exome sequencing analysis excluded this intronic variant and precluded a diagnosis. To confirm the predicted splicing change of intronic and exonic variants based on SpliceAI annotations, we generated a minigene splicing reporter assay (Appendix S1), demonstrating each variant results in the skipping of exon 3 (Appendix S1).

The remaining five cases were resolved due to the identification of variants not typically identifiable by exome sequencing. The first is related to a region that is technically difficult to assess. Biallelic variants were identified in LD_0617 in GJC2 (OMIM:608803), causative of Pelizaeus-Merzbacher-like disease (PMLD [OMIM:608804]). A 13bp paternally inherited duplication, c.916_928dupGCCTCCGCCCCCG, p.Ala310fs in GJC2, was previously undetected by exome sequencing due to a lack of coverage in this region.1 (C) The duplication lies in the middle of a 110 nucleotide block of a ~95% GC-rich region and was identified in the affected individual and father on genome sequencing, where it is indicated by a green rectangle. (D) Sanger chromatogram confirming the presence of the c.916_928dupGCCTCCGCCCCCG variant in the LD_0617 proband. The duplicated sequence is indicated in red with the second copy in LD_0617 bold and underlined.

Genome sequencing CNV analysis provided a diagnosis in three affected individuals (Table 1). LD_0498 was found to have an X-linked 396kb duplication covering ARX (OMIM:300382), previously associated with a broad spectrum of neuroimaging abnormalities and early infantile epileptic encephalopathy (OMIM:308350). LD_0671 was found to harbor a 21kb de novo deletion encompassing a region in chromosome 2 covering SATB2 (OMIM:608148), previously associated with Glass syndrome (OMIM:612313).23

Discussion

Of the original 191 families examined in this cohort, 101 received a definitive diagnosis using enzymatic, biochemical, or single gene molecular approaches (53%). Nineteen families were subsequently lost to follow-up, leaving 71 families able to be tested by NGS. Thirty nine cases were solved by exome sequencing,1 and in this study, genome sequencing established a diagnosis in an additional 14 families yielding a 20% improvement, and an overall diagnostic efficacy of NGS of genome or exome sequencing increased to 44/71 (62%) and in total resolution of 145/172 (84%) of the original testable cohort.

Reanalysis by genome sequencing also led to the identification of variants in recently described disease genes AIFM1, HIKESHI, H3F3B, NKX6-2, SPATA5, and genes missed in the previous analysis (LI1CAM). This is consistent with multiple recent studies that have shown increases of up to 10% in diagnostic yield with reanalysis within 24–36 months.10 Improvements in variant annotation and filtering detected variants in mitochondrial DNA and intronic regions proximal to captured exons. It is expected that these would have been identified on exome sequencing if performed with current testing modalities.

Genome sequencing findings improved the overall diagnostic yield in this cohort by ~11% (5/44 cases solved by NGS), through the detection of variants in GC-rich regions, deep intronic variants, and CNVs. As sequencing assays and associated informatic pipelines improve, some of these variant types may be detected by exome sequencing. In our exome analysis, however, these variants were not found due to limitations of either sequencing or analysis, some of which will be difficult to overcome due to
<table>
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<th>Family ID</th>
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<th>Current Age</th>
<th>Initial Age</th>
<th>Gene</th>
<th>Zygosity</th>
<th>Variant (GRCh37) &amp; Transcript ID</th>
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<td>H3F3B</td>
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<td>c.365G&gt;T, G</td>
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<td>8 Y</td>
<td>NX6-2</td>
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<td>c.606delG, insTA Lys202fs</td>
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<td>N/A</td>
<td>0.0000</td>
<td>N/A</td>
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<td>PS1, PM2</td>
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<td>LD_0807</td>
<td>F</td>
<td>17 Y</td>
<td>12 Y</td>
<td>SWORID118</td>
<td>Het. (n)</td>
<td>c.1969 +115_1969+116delAG</td>
<td>Pro658Serfs*24</td>
<td>N/A</td>
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<td>LD_0393</td>
<td>F &amp; M</td>
<td>N/A</td>
<td>N/A</td>
<td>CSF1R</td>
<td>Hom.</td>
<td>c.1946 +1, 115, 1969 +116delAG</td>
<td>N/A</td>
<td>N/A</td>
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<td>F</td>
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<td>1 Y</td>
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<td>c.288-2 TdelTinsCC</td>
<td>N/A</td>
<td>N/A</td>
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<td>2 Y</td>
<td>GC2</td>
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<td>Deceased</td>
<td>KIKESH</td>
<td>Het.</td>
<td>c.160G&gt;T, Val54Leu</td>
<td>N/A</td>
<td>N/A</td>
<td>0.0000</td>
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<td>Likely pathogenic</td>
<td>PS1, PS3, PP3, PP4</td>
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<td>5 M</td>
<td>L1CAM</td>
<td>Het. (m)</td>
<td>c.1103T&gt;A, Ile368Asn</td>
<td>N/A</td>
<td>N/A</td>
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<td>18 M</td>
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<td>c.554G&gt;A, Gly185Glu</td>
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<td>N/A</td>
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<td>PS1, PS3, PP3, PP4</td>
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<td>9 M</td>
<td>KDM3C</td>
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<td>N/A</td>
<td>N/A</td>
<td>0.0000</td>
<td>N/A</td>
<td>Likely pathogenic</td>
<td>PS1, PS3, PP3, PP4</td>
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(Continued)
limitations of the assay (e.g. GC-rich regions) or the ability of exome to accurately detect large genomic alterations in single cases.

Our study lends support to a previous study that suggested that currently up to 80% of white matter disorders may be able to be solved. Notably, no recurring diagnoses were made in the current cohort of \( n = 41 \), and only a minority across all tiers of NGS testing (20%) were associated with canonical leukodystrophy genes. These data indicate that only a fraction of affected individuals would achieve a diagnosis using targeted testing approaches, including panels of classically defined leukodystrophy genes now in widespread use. An established diagnostic workflow for laboratory and genetic testing in combination with MRI pattern recognition suggests that if initial biochemical and enzymatic testing is not confirmatory and if the MRI does not fit an established leukodystrophy, broad-based NGS testing should be implemented. Our data support this approach, favoring genome sequencing over exome sequencing.

**Acknowledgments**

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<th>Family ID</th>
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<th>Current Age</th>
<th>Age at Initial MRI</th>
<th>Known Syndrome (OMIM)</th>
<th>Genotype</th>
<th>Allele Frequency</th>
<th>Total Allele Frequency</th>
<th>Known Syndrome (OMIM)</th>
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<td>M</td>
<td>11</td>
<td>Y</td>
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<td>11</td>
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<td>Y</td>
<td>396,991</td>
<td>Het.</td>
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<td>N/A</td>
<td>ARX, POLA1, PCYT1B</td>
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<td>N/A</td>
<td>Glass Syndrome (OMIM:612313)</td>
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Los Reyes, Bennet Lavenstein, Brendan Lanpher, Gerhard Kurleman, Dan Miller, Amirah Khouzam, Vani Rajan, Erin Ramos, Shimul Chowdhury, Tina Hambuch, Kelin Ru, Greg Baillie, Sean Grimmond, Ljuba Caldivic, Joe Devaney Miriam Bloom, Sarah Evans, Jennifer Murphy, and Nathan McNeill for providing care to the affected individuals and families, referral to the Myelin Disorders Bioregistry Project, or previous contributions to this longstanding project.

Conflict of Interest

BRL, ED, AG, VG, and RJT are/were employees of Illumina, Inc. Nemours receives revenue from diagnostic testing performed in the Nemours Molecular Diagnostics Laboratory. GB has received compensation for traveling to meetings and advisory boards from Ionis, Shire/Takeda, Actelion Pharmaceuticals and Children’s Hospital of Philadelphia. She served on the scientific advisory board for Ionis (2019) and has received research grants from Shire/Takeda and Bluebird Bio. AV receives support from Shire, Gilead, Eli Lilly and Illumina for research activities. Otherwise the authors report no conflict of interest.

Author Contributions

GH, BRL, CS, RJT, and AV designed and managed the project and wrote the manuscript. JC, AT, MW, EMJ, YJC, SF, HRW, ID, EB, NM, NIW, TEMA, SMK, CT, GMH, LG, and SI provided functional analysis of variants and confirmation of variants and contributed to figures. BRL, SJB, CS, and RJT contributed bioinformatics expertise. GH, BRL, AP, JLS, GB, RS, MSvdK, GB, CS, RJT, and AV performed analysis of or provided consultation for cases from the manuscript. All authors reviewed the manuscript.

References


Supporting Information

Additional supporting information may be found online in the Supporting Information section at the end of the article.

Appendix S1. A supplemental text PDF file is provided which includes methods and results for the minigene splicing reporter assay used in the case of LD_0315 (Section 1) and sequencing coverage achieved for proband samples (Table S2). Case reports are for each of the 41 families with diagnoses associated with single-nucleotide variants and small insertion-deletion events (Section 2), copy number variants (Section 3), or remaining unsolved after genome sequencing and analysis (Section 3). The supplemental text of the original study can be found at: https://imb.uq.edu.au/download/Vanderver_AON_2016_case_reports.pdf