Medica Coverage Policy

Policy Name:	**Genetic Testing: Exome and Genome Sequencing for The Diagnosis of Genetic Disorders**
Medica Effective Date:	**January 01, 2025**

Important Information – Please Read Before Using This Policy

These services may or may not be covered by all Medica plans. Coverage is subject to requirements in applicable federal or state laws. Please refer to the member's plan document for other specific coverage information. If there is a difference between policy requirements and the member's plan document, the member's plan document will be used to determine coverage. With respect to Medicare, Medicaid, and other government programs, this policy will apply unless those programs require different coverage. Members may contact Medica Customer Service at the phone number listed on their member identification card to discuss their benefits more specifically. Providers with questions about this Medica coverage policy may call the Medica Provider Service Center toll-free at 1-800-458-5512.

Medica coverage policies are not medical advice. Members should consult with appropriate health care providers to obtain needed medical advice, care, and treatment.

OVERVIEW

Exome sequencing (ES) (also known as 'whole exome sequencing (WES)') involves sequencing and copy number variant (CNV) analysis of the portion of the genome that contains protein-coding DNA, which are termed exons. Together, all of the exons in a genome are known as the exome, which constitutes approximately 1% of the genome and is currently estimated to contain about 85% of heritable disease-causing variants.

Genome sequencing (GS) (also known as 'whole genome sequencing (WGS)') is a comprehensive method that sequences both coding and noncoding regions of the genome. GS has a greater ability to detect large deletions or duplications in protein-coding regions compared with ES, as well as the ability to detect variants that may be missed by ES, such as copy-number variants (CNV), mid-size insertions and deletions (ca. 10-500 bp), nucleotide repeat expansion mutations, deeper intronic mutations, structural variants(e.g., translocations, inversions), and variants that result in methylation defects and uniparental disomy. GS requires greater data analysis but less DNA preparation prior to sequencing.

ES and GS have been proposed for use in patients presenting with disorders and anomalies not immediately explained by standard clinical workup. Potential candidates for ES and GS include patients who present with a broad spectrum of suspected genetic conditions. GS has been shown to have a higher diagnostic yield compared to ES when used as a first line test.

ES reanalysis is often performed approximately 18 months to 2 years following initial, uninformative ES. Studies have shown that the diagnostic yield of ES reanalysis is comparable to performing GS after an uninformative ES.

Rapid exome sequencing (rES) and rapid genome (rGS) sequencing involves sequencing of the exome or genome, respectively, in an accelerated time frame. Preliminary results can typically be returned in less than 7 days, and a final report in less than two weeks. Studies suggest that the use of rES or rGS in acutely-ill infants, presenting with complex phenotypes that are likely rare genetic conditions, can identify a genetic diagnosis more quickly, allowing

clinicians and family members to change acute medical or surgical management options and end the diagnostic odyssey.

Trio testing is preferred whenever possible. Testing of one available parent is a valid alternative if both are not immediately available and one or both parents can be done later if needed. Exome sequencing or genome sequencing can reveal incidental findings or secondary findings. These findings are defined as results that are not related to the indication for undergoing the sequencing, but may be of medical value or utility. Disclosure of these findings has been a topic of intense debate within the medical genetics community. In 2013, ACMG published recommendations for reporting secondary findings that included a list of conditions to be included. The list currently includes 59 genes that confer highly-penetrant and medically actionable conditions.

Pre-test and post-test genetic counseling that facilitates informed decision-making, the possibility to identify secondary finding with the option to 'opt out' of receiving these results, elicits patient preferences regarding secondary and/or incidental findings if possible, and formulates a plan for returning such results before testing occurs is strongly advised.

If a genetic diagnosis is not found by ES or GS, periodic reanalysis of the previously obtained genomic sequence is recommended. Reevaluation can occur on the variant-level or case-level. Any variants identified and reported prior to the current ACMG variant classification standards should be reevaluated using the current ACMG standards.

POLICY REFERENCE TABLE

The tests and associated laboratories and CPT codes contained within this document serve only as examples to help users navigate claims and corresponding coverage criteria; as such, they are not comprehensive and are not a guarantee of coverage or non-coverage.

Use the current applicable CPT/HCPCS code(s). The following codes are included below for informational purposes only and are subject to change without notice. Inclusion or exclusion of a code does not constitute or imply member coverage or provider reimbursement.

NOTE: MN residents covered under Commercial Fully Insured/Self-insured (non-ERISA), Individual Family Business, Medicare or Medicaid Products:

Rapid whole genome testing will apply to Minnesota residents 21 years of age or younger who are receiving inpatient hospital services in an intensive care unit or a neonatal or high acuity pediatric care unit.

Coverage Criteria Sections	Example Tests (Labs)	Common CPT Codes	Common ICD Codes	Ref
Standard Exome Sequencing	Genomic Unity Exome Analysis - Proband (Variantyx)	81415	F70-F79, F80.0-F89, Q00.0-Q99.9, R56.9, R62.0, R62.50, R62.51, G40.909	1, 3, 5, 7, 8, 12, 13
	Genomic Unity Exome Analysis - Comparator (Duo or Trio) (Variantyx Inc.)	81416		
	XomeDx - Proband (GeneDx)	81415		
	Exome - Proband Only (Invitae)			
	XomeDx - Duo (GeneDx)	81415, 81416		
	XomeDX - Trio (GeneDx)			
	Exome - Duo (Invitae)			

Coverage Criteria Sections	Example Tests (Labs)	Common CPT Codes	Common ICD Codes	Ref
	Exome - Trio (Invitae)			
Reanalysis of Exome or Genome Sequencing Data	Exome Reanalysis (Ambry)	81417	F70-F79, F80-F89, Q00.0-Q99.9, R56.9, R62.0, R62.50, R62.51, G40.909	4, 9, 10, 12
	Whole Genome Reanalysis (ARUP)	81427		
Rapid Exome Sequencing	XomeDxXpress (GeneDx)	81415, 81416	F70-F79, F80-F89, Q00.0-Q99.9, R56.9, R62.0, R62.50, R62.51, G40.909	1, 3, 5, 6, 7, 8, 11, 12, 13
	ExomeNext-Rapid (Ambry)			
	PGxome RAPID Exome Test (PreventionGenetics, part of Exact Sciences)			
	STAT Whole Exome Sequencing (PerkinElmer Genomics)			
Standard Genome Sequencing	Genomic Unity Whole Genome Analysis - Proband (Variantyx Inc.)	0212U	F70-F79, F80-F89, Q00.0-Q99.9, R56.9, R62.0, R62.50, R62.51, G40.909	1, 3, 5, 7, 8, 11, 12, 13
	Genomic Unity® Whole Genome Analysis - Comparator (Variantyx Inc.)	0213U		
	GenomeSeqDx (GeneDx)	81425, 81426		
	TruGenome Trio (Illumina, Inc)			
	Whole Genome Sequencing (PerkinElmer Genomics)			
	MNGenome (MNG Laboratories)			
	Praxis Whole Genome Sequencing (Praxis Genomics LLC)	0265U		
Rapid Genome Sequencing	Rapid Whole Genome Sequencing (Rady Children's Institute for Genomic Medicine)	0094U	F70-F79, F80-F89, Q00.0-Q99.9, R56.9, R62.0, R62.50, R62.51, G40.909	2, 3, 6, 8, 11
	Rapid Whole Genome Sequencing, Comparator Genome (Rady Children's Institute for Genomic Medicine)	0425U		
	Ultra-Rapid Whole Genome Sequencing (Rady Children's Institute for Genomic Medicine)	0426U		
	STAT Whole Genome Sequencing (PerkinElmer Genomics)	81425, 81426		
	MNGenome STAT (Labcorp/MNG Laboratories)			

OTHER RELATED POLICIES

This policy document provides coverage criteria for exome and genome sequencing for the diagnosis of genetic disorders in patients with suspected genetic disorders and for population-based screening. Please refer to:

- ***Oncology: Molecular Analysis of Solid Tumors and Hematologic Malignancies*** for coverage criteria related to exome and genome sequencing of solid tumors and hematologic malignancies.
- ***Genetic Testing: Multisystem Inherited Disorders, Intellectual Disability, and Developmental Delay*** for coverage criteria related to diagnostic genetic testing performed after a child has been born.
- ***Genetic Testing: Prenatal and Preconception Carrier Screening*** for coverage criteria related to prenatal carrier screening, preimplantation genetic testing, or preconception carrier screening.
- ***Genetic Testing: Prenatal Diagnosis (via Amniocentesis, CVS, or PUBS) and Pregnancy Loss*** for coverage related to prenatal exome sequencing.
- ***Genetic Testing: General Approach to Genetic and Molecular Testing*** for coverage criteria related to exome and genome sequencing that is not specifically discussed in this or another non-general policy, including known familial variant testing.

COVERAGE CRITERIA

STANDARD EXOME SEQUENCING

I. Standard exome sequencing (81415, 81416, 0214U, 0215U), with trio testing when possible, is considered **medically necessary** when:

A. The member has not previously had genome sequencing, **AND**

B. Alternate etiologies have been considered and ruled out when possible (e.g., environmental exposure, injury, infection, isolated prematurity), **AND**

C. Clinical presentation does not fit a well-described syndrome for which single-gene or targeted multi-gene panel testing is available, **AND**

D. The member's personal and family histories have been evaluated by a Medical Geneticist, Genetic Counselor or an Advanced Practice Nurse in Genetics (APGN), **AND**

E. The member meets at least one of the following clinical findings:

1. The member has unexplained epilepsy diagnosed at any age, **OR**
2. The member has global developmental delay or intellectual disability with onset prior to age 18 years, **OR**
3. The member was diagnosed with at least one congenital anomaly (functional and/or structural), **OR**
4. The member has at least **TWO** of the following:

a) Bilateral sensorineural hearing loss of unknown etiology, **OR**

b) Symptoms of a complex neurological disorder (e.g., dystonia, hemiplegia, spasticity, epilepsy, myopathy, muscular dystrophy), **OR**

c) Family history suggestive of a genetic etiology, including consanguinity, **OR**

d) Clinical or laboratory findings suggestive of an inborn error of metabolism, **OR**

e) Autism, **OR**

f) Severe neuropsychiatric condition (e.g., schizophrenia, bipolar disorder, Tourette syndrome, self-injurious behavior, reverse sleep-wake cycles), **OR**

g) Period of unexplained developmental regression (unrelated to epilepsy or autism).

II. Repeat standard exome sequencing (81415, 81416, 0214U, 0215U) is considered **investigational**.

III. Standard exome sequencing (81415, 81416, 0214U, 0215U) is considered **investigational** for all other indications, including screening asymptomatic/healthy individuals for genetic disorders.

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REANALYSIS OF EXOME OR GENOME SEQUENCING DATA

I. Reanalysis of exome or genome sequencing data (81417, 81427) is considered **medically necessary** when*:

A. The member had exome or genome sequencing at least 18 months ago, **OR**

B. The member's phenotype has expanded to include clinical findings** that were not present at the time of the initial exome or genome sequencing analysis, **AND**

1. Results of prior exome or genome sequencing do not explain these new clinical findings.

II. Reanalysis of exome or genome sequencing data (81417, 81427) is considered **investigational** for all other indications.

*If reanalysis of exome data is not possible, see the genome sequencing criteria for additional coverage information.

**See Standard Exome Sequencing or Standard Genome Sequencing criteria for qualifying clinical findings.

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RAPID EXOME SEQUENCING

I. Rapid exome sequencing (rES) (81415, 81416), with trio testing when possible, is considered **medically necessary** when:

A. The member is an acutely-ill infant (12 months of age or younger), **AND**

B. The member has not previously had genome sequencing, **AND**

C. Alternate etiologies have been considered and ruled out when possible (e.g., environmental exposure, injury, infection, isolated prematurity), **AND**

D. Clinical presentation does not fit a well-described syndrome for which rapid single-gene or targeted multi-gene panel testing is available, **AND**

E. The member's personal and family histories have been evaluated by a Medical Geneticist, Genetic Counselor or an Advanced Practice Nurse in Genetics (APGN), **AND**

F. The member meets at least one of the following clinical findings:

1. The member has unexplained epilepsy, **OR**
2. The member has global developmental delay, **OR**
3. The member was diagnosed with at least one congenital anomaly (functional and/or structural), **OR**
4. The member has at least **TWO** of the following:
   a) Bilateral sensorineural hearing loss of unknown etiology, **OR**
   b) Symptoms of a complex neurological disorder (e.g., dystonia, hemiplegia, spasticity, myopathy, muscular dystrophy), **OR**
   c) Family history suggestive of a genetic etiology, including consanguinity, **OR**
   d) Clinical or laboratory findings suggestive of an inborn error of metabolism, **OR**
   e) Severe neuropsychiatric condition (e.g., schizophrenia, bipolar disorder, Tourette syndrome, self-injurious behavior, reverse sleep-wake cycles), **OR**
   f) Period of unexplained developmental regression (unrelated to epilepsy or autism).

II. Rapid exome sequencing (rES) (81415, 81416) is considered **investigational** for all other indications, including screening asymptomatic/healthy individuals for genetic disorders.

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STANDARD GENOME SEQUENCING

I. Standard genome sequencing (81425, 81426, 0212U, 0213U, 0265U), with trio testing when possible, is considered **medically necessary** when:

A. Alternate etiologies have been considered and ruled out when possible (e.g., environmental exposure, injury, infection, isolated prematurity), **AND**

B. Clinical presentation does not fit a well-described syndrome for which single-gene or targeted multi-gene panel testing is available, **AND**

C. The member's personal and family histories have been evaluated by a Medical Geneticist, Genetic Counselor or an Advanced Practice Nurse in Genetics (APGN), **AND**

D. The member meets at least one of the following clinical findings:

1. The member previously had uninformative exome sequencing (ES), **AND**
   a) ES reanalysis is not possible, **OR**
2. The member has unexplained epilepsy diagnosed at any age, **OR**
3. The member has global developmental delay or intellectual disability with onset prior to age 18 years, **OR**

4. The member was diagnosed with at least one congenital anomaly (functional and/or structural), **OR**
5. The member has at least **TWO** of the following:
    a) Bilateral sensorineural hearing loss of unknown etiology, **OR**
    b) Symptoms of a complex neurological disorder (e.g., dystonia, hemiplegia, spasticity, epilepsy, myopathy, muscular dystrophy), **OR**
    c) Family history suggestive of a genetic etiology, including consanguinity, **OR**
    d) Clinical or laboratory findings suggestive of an inborn error of metabolism, **OR**
    e) Autism, **OR**
    f) Severe neuropsychiatric condition (e.g., schizophrenia, bipolar disorder, Tourette syndrome, self-injurious behavior, reverse sleep-wake cycles), **OR**
    g) Period of unexplained developmental regression (unrelated to epilepsy or autism).

II. Repeat standard genome sequencing (81425, 81426, 0212U, 0213U, 0265U) is considered **investigational**.

III. Standard genome sequencing (81425, 81426, 0212U, 0213U, 0265U) is considered **investigational** for all other indications, including screening asymptomatic/healthy individuals for genetic disorders.

Note: When genome sequencing is performed, the mitochondrial genome is assumed to be included as a part of the analysis.

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RAPID GENOME SEQUENCING

Minnesota law requires coverage of rapid whole genome sequencing (rWGS) testing for patients 21 years of age and younger with a complex or acute illness of unknown etiology. Patient must be receiving inpatient hospital services in an intensive care unit or a neonatal or high acuity pediatric care unit.

Additional information regarding coverage requirements for rWGS testing services is available on the Minnesota Legislature, Office of the Revisor of Statutes, section 62A.3098, subdivisions 1 to 3 and 6 at: https://www.revisor.mn.gov/statutes/cite/62A.3098

I. Rapid genome sequencing (rGS) (81425, 81426, 0094U, 0425U, 0426U), with trio testing when possible, is considered **medically necessary** when:

A. The member is an acutely-ill infant (12 months of age or younger), **AND**

B. Alternate etiologies have been considered and ruled out when possible (e.g., environmental exposure, injury, infection, isolated prematurity), **AND**

C. Clinical presentation does not fit a well-described syndrome for which rapid single-gene or targeted multi-gene panel testing is available, **AND**

D. The member's personal and family histories have been evaluated by a Medical Geneticist, Genetic Counselor or an Advanced Practice Nurse in Genetics (APGN), **AND**

E. The member meets at least one of the following clinical findings:

1. The member has unexplained epilepsy, **OR**
2. The member has multiple congenital abnormalities (functional and/or structural) affecting unrelated organ systems, **OR**

3. The member has epileptic encephalopathy, **OR**
4. The member has at least **TWO** of the following:
    a) Abnormality affecting at least one organ system, **OR**
    b) Symptoms of a complex neurological condition (e.g., dystonia, hemiplegia, spasticity, epilepsy, hypotonia, myopathy, muscular dystrophy, global developmental delay, intellectual disability), **OR**
    c) Family history suggestive of a genetic etiology, including consanguinity, **OR**
    d) Laboratory findings suggestive of an inborn error of metabolism, **OR**
    e) Abnormal response to standard therapy.

II. Rapid genome sequencing (rGS) (81425, 81426, 0094U, 0425U, 0426U) is considered **investigational** for all other indications, including screening asymptomatic/healthy individuals for genetic disorders.

Note: When genome sequencing is performed, the mitochondrial genome is assumed to be included as a part of the analysis.

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PRIOR AUTHORIZATION

Prior authorization is not required. However, services with specific coverage criteria may be reviewed retrospectively to determine if criteria are being met. Retrospective denial may result if criteria are not met.

DEFINITIONS

1. **Exome Sequencing (ES)**: A genomic technique for sequencing all of the protein-coding regions of genes in the genome (also known as the exome).
2. **Genome Sequencing (GS)**: A genomic technique for sequencing the complete DNA sequence, which includes protein coding as well as non-coding DNA elements.
3. **Trio Testing**: Testing of the child and both biological/genetic parents, which increases the chances of finding a definitive diagnosis while reducing false-positive findings.
4. **Congenital anomalies:** According to ACMG, congenital anomalies are multiple anomalies not specific to a well-delineated genetic syndrome. These anomalies are structural or functional abnormalities usually evident at birth, or shortly thereafter, and can be consequential to an individual's life expectancy, health status, physical or social functioning, and typically require medical intervention.
5. **Global Developmental delay:** An individual that is slow-to-meet or not reaching milestones in the expected way for a child's age in at least two of the areas of development (communication, gross/fine motor, cognition, social-emotional, or adaptive skills)
6. **Intellectual disability (ID):** Defined by the DSM-V as an individual who meets all of the following:
    a. Deficits in intellectual functions, such as reasoning, problem solving, planning, abstract thinking, judgment, academic learning, and learning from experience, confirmed by both clinical assessment and individualized, standardized intelligence testing.

b. Deficits in adaptive functioning that result in failure to meet developmental and sociocultural standards for personal independence and social responsibility. Without ongoing support, the adaptive deficits limit functioning in one or more activities of daily life, such as communication, social participation, and independent living, across multiple environments, such as home, school, work, and community.

c. Onset of intellectual and adaptive deficits during the developmental period.

7. **Exome sequencing (ES) reanalysis** may not be possible in some situations. Sequencing platforms may have changed substantially enough that the performing lab can no longer use the data from the original ES in their pipeline. Specifically, ES reanalysis may not be possible if there have been improvements in technology/chemistry (e.g., new methods for DNA capture and/or sequencing), bioinformatics advancements, or there is new information regarding the genetic etiology of a condition that could explain the patient's clinical features and would not have been able to be detected by the previous exome sequencing.

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BACKGROUND AND RATIONALE

Standard Exome Sequencing

American College of Medical Genetics and Genomics (ACMG)

In 2021, ACMG (Manickam, 2021) published an evidence-based clinical practice guideline on exome and genome sequencing for pediatric patients with congenital anomalies or intellectual disability, which included the following:

- "We strongly recommend ES and GS as a first- or second-tier test… for patients with one or more congenital anomalies prior to one year of age, or for patients with intellectual disability/developmental delay with onset prior to 18 years of age. (p. 2031)
- "Isolated autism without ID or congenital malformation is formally out of scope for this recommendation but evaluation of exome/genome studies is ongoing." (p. 2034)

In 2020, ACMG (Malinowski, et al) released a systematic evidence-based review), which "provide[d] indirect evidence of the clinical and personal utility of ES/GS for patients with CA/DD/ID and their family members, noting that a "change in clinical management" resulted in over half of the patients examined as a result of their ES/GS results. (p. 1001)

In 2022, ACMG (Li, et al) released a clinical practice resource for the clinical evaluation of hearing loss published, which states that first-line genetic testing for individuals with exam findings that suggest a syndromic hearing loss etiology may include a variety of tests, including genome sequencing, depending on clinical presentation. For individuals without physical findings that suggest a syndromic hearing loss etiology, they recommend a tiered approach, starting with comprehensive hearing loss gene panel testing unless a more specific genetic etiology is evident for which targeted testing is appropriate. (p. 1400)

National Society for Genetic Counselors

The National Society for Genetic Counselors (NSGC) released a position statement (2013, updated 2020, reaffirmed 2023) stating the following in regard to secondary and incidental findings in genetic testing:

> "The National Society of Genetic Counselors strongly advises pre-test counseling that facilitates informed decision-making, elicits patient preferences regarding secondary and/or incidental findings if possible, and formulates a plan for returning such results before testing occurs"

The National Society of Genetic Counselors (NSGC) published evidence-based practice guidelines for individuals

with unexplained epilepsy (Smith et al, 2022). The NSGC recommendations are as follows (p. 4):

- Individuals with unexplained epilepsy should be offered genetic testing, without limitation of age.
- Multi-gene, comprehensive testing, such as exome sequencing, genome sequencing or a multigene panel as a first-tier test is strongly recommended.

Patient-Centered Laboratory Utilization Guidance Services

In the PLUGS July 2023 guidelines entitled "Genomic Sequencing for Rare Disease," the following clinical criteria are recommended for exome sequencing and genome sequencing.

"Exome sequencing or genome sequencing (ES/GS) is considered medically necessary when ALL of the following criteria are met:

1. The etiology of the patient's features is not known, and a genetic etiology is considered a likely explanation for the phenotype, based on one of the following…
    a. Epilepsy of unexplained etiology with onset at any age, OR
    b. Confirmed bilateral sensorineural hearing loss of unknown etiology and panel testing is unrevealing, OR
    c. Intellectual disability, following formal assessment by a developmental pediatrician or neurologist, defined as moderate/severe/profound by Diagnostic and Statistical Manual of Mental Disorders (DSM-5) criteria, diagnosed by 18 years of age, OR
    d. Global developmental delay, following formal assessment by a developmental pediatrician or neurologist, defined as significant delay in younger children, under age five years, in at least two of the major developmental domains: gross or fine motor; speech and language; cognition; social and personal development; and activities of daily living, OR
    e. Multiple congenital anomalies affecting unrelated organ systems, OR
    f. At least TWO of the following criteria are met:
        i. Abnormality affecting at minimum a single organ system
        ii. Autism
        iii. Severe neuropsychiatric condition (e.g., schizophrenia, bipolar disorder, Tourette syndrome, self-injurious behavior, reverse sleep-wake cycles)
        iv. Symptoms of a complex neurological condition (e.g., dystonia, hemiplegia, spasticity, hypotonia, myopathy, muscular dystrophy)
        v. Family history strongly suggestive of a genetic etiology, including consanguinity
        vi. Period of unexplained developmental regression (unrelated to epilepsy or autism)
        vii. Laboratory findings suggestive of an inherited metabolic disorder
2. Alternate etiologies have been considered and ruled out, when possible (e.g., MRI abnormalities/brain malformations, environmental exposure, injury, infection, isolated prematurity), AND
3. Clinical presentation does not fit a well-described syndrome for which more targeted testing is available." (p. 7)

Belanger, et al

A review of the evaluation of children with global developmental delay and intellectual disability by Belanger et al (2018) defines global developmental delay (GDD) as the following:

- Significant delay (at least 2 standard deviations below the mean) in at least two developmental domains (gross or fine motor, speech/language, cognition, social/personal or activities of daily living. (p. 404)

Reanalysis of Exome or Genome Sequencing Data

Tan, et al

A study from 2020 examined data from 58 unsolved cases referred for any indication to evaluate the systematic reanalysis of singleton exome sequencing (ES). The authors performed a reanalysis at multiple timepoints following initial testing, and ultimately suggest that an interval of greater than 18 months from the original report may be optimal for reanalysis. (p. 1)

Alfares, et al

This study from 2018 compared the detection rates of whole-exome sequencing (WES) and whole-genome sequencing (WGS) in a clinical setting. The study included 108 patients with negative array CGH and negative or inconclusive WES results. WGS was performed on all patients, and the results of the study showed that 30% of the positive cases identified by WGS could be identified by reanalyzing WES raw data, and WGS achieved an only 7% higher detection rate. (p. 1328) The paper concluded that, although WGS is a more powerful tool than WES, in this study, "we showed that WGS has additional, but limited, clinical utility compared with reanalyzing WES data, and until the cost of WGS approximates that of WES, reanalyzing WES raw data is recommended before performing WGS." (p. 1333)

American College of Medical Genetics

A statement from ACMG (Deignan, 2019) included considerations for case-level exome re-analysis, which include the following:

- Significant improvements have been made to bioinformatics handling of the data (alignment/variant calling and/or the automated filtering processes)
- Updated clinical and family history information, which may result in the identification of additional variants that are associated with the indication(s) for testing. (p. 1269)

Patient-Centered Laboratory Utilization Guidance Services

The PLUGS July 2023 guidelines entitled "Genomic Sequencing for Rare Disease" state the following regarding reanalysis of exome or genome sequencing data:

"Periodic reanalysis of previously obtained exome or genome sequence has the potential for additional diagnostic yield because of expanding variant databases, as well as periodic novel gene discovery and publication. A review of twenty-seven peer-reviewed articles revealed a median new diagnosis rate via reanalysis of 15% and median reanalysis timeframe of 22 months. The authors suggest that an interval of greater than 18 months from the original report may be optimal for reanalysis." (p. 3)

The guidelines also state: "Re-analysis of previously obtained exome or genome sequence has the potential for additional diagnostic yield because of expanding variant databases, as well as periodic novel gene discovery and publication. Re-analysis could be considered prior to additional genomic sequencing, particularly if there has been onset or identification of additional symptoms that broadens the clinical phenotype assessed during the original ES/GS analysis…" (p. 8)

Rapid Exome Sequencing

American College of Medical Genetics and Genomics (ACMG)

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In 2022, ACMG (Li, et al) released a clinical practice resource for the clinical evaluation of hearing loss published, which states that first-line genetic testing for individuals with exam findings that suggest a syndromic hearing loss etiology may include a variety of tests, including genome sequencing, depending on clinical presentation. For individuals without physical findings that suggest a syndromic hearing loss etiology, they recommend a tiered approach, starting with comprehensive hearing loss gene panel testing unless a more specific genetic etiology is evident for which targeted testing is appropriate. (p. 1400)

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Patient-Centered Laboratory Utilization Guidance Services

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1. The etiology of the patient's features is not known, and a genetic etiology is considered a likely explanation for the phenotype, based on one of the following…
    a. Epilepsy of unexplained etiology with onset at any age, OR
    b. Confirmed bilateral sensorineural hearing loss of unknown etiology and panel testing is unrevealing, OR
    c. Intellectual disability, following formal assessment by a developmental pediatrician or neurologist, defined as moderate/severe/profound by Diagnostic and Statistical Manual of Mental Disorders (DSM-5) criteria, diagnosed by 18 years of age, OR
    d. Global developmental delay, following formal assessment by a developmental pediatrician or neurologist, defined as significant delay in younger children, under age five years, in at least two

of the major developmental domains: gross or fine motor; speech and language; cognition; social and personal development; and activities of daily living, OR
   e. Multiple congenital anomalies affecting unrelated organ systems, OR
   f. At least TWO of the following criteria are met:
      i. Abnormality affecting at minimum a single organ system
      ii. Autism
      iii. Severe neuropsychiatric condition (e.g., schizophrenia, bipolar disorder, Tourette syndrome, self-injurious behavior, reverse sleep-wake cycles)
      iv. Symptoms of a complex neurological condition (e.g., dystonia, hemiplegia, spasticity, hypotonia, myopathy, muscular dystrophy)
      v. Family history strongly suggestive of a genetic etiology, including consanguinity
      vi. Period of unexplained developmental regression (unrelated to epilepsy or autism)
      vii. Laboratory findings suggestive of an inherited metabolic disorder
2. Alternate etiologies have been considered and ruled out, when possible (e.g., MRI abnormalities/brain malformations, environmental exposure, injury, infection, isolated prematurity), AND
3. Clinical presentation does not fit a well-described syndrome for which more targeted testing is available." (p. 7)

Rehm et al (2023)

A 2023 paper by Rehm et al demonstrated that exome and genome sequencing had a significantly lower VUS rate (22.5%) compared to multigene panels (32.6%). (p. 5 and 6)

Kingsmore SF, Cakici JA, Clark MM et al. 2019

The NSIGHT2 study, a prospective randomized, controlled, blinded trial (RCT) in acutely ill infants, found that 24% of infants undergoing rapid exome sequencing had genetic disease. They conclude that diagnostic testing in infants with diseases of unknown etiology, rapid genomic sequencing, including rapid exome sequencing can be performed as a first tier test in infants with diseases of unknown etiology at time of admission to ICUs. In unstable infants and in those whom a genetic diagnosis was likely to impact immediate management, rapid genomic sequencing had optimal analytic and diagnostic performance by virtue of shortest time to results. (p. 725)

Belanger, et al

A review of the evaluation of children with global developmental delay and intellectual disability by Belanger et al (2018) defines global developmental delay (GDD) as the following:

- Significant delay (at least 2 standard deviations below the mean) in at least two developmental domains (gross or fine motor, speech/language, cognition, social/personal or activities of daily living. (p. 404)

Standard Genome Sequencing

American College of Medical Genetics and Genomics (ACMG)

In 2021, ACMG (Manickam, et al) published an evidence-based clinical practice guideline on exome and genome sequencing for pediatric patients with congenital anomalies or intellectual disability , which included the following:

- "We strongly recommend ES and GS as a first- or second-tier test… for patients with one or more congenital anomalies prior to one year of age, or for patients with intellectual disability/developmental delay with onset prior to 18 years of age." (p. 2031)
- "Isolated autism without ID or congenital malformation is formally out of scope for this recommendation but evaluation of exome/genome studies is ongoing." (p. 2034)

In 2020, ACMG (Malinowski et al) released a systematic evidence-based review (Malinowski, 2020), which "provide[d] indirect evidence of the clinical and personal utility of ES/GS for patients with CA/DD/ID and their family members, noting that a "change in clinical management" resulted in over half of the patients examined as a result of their ES/GS results. (p. 1001)

In 2022, ACMG (Li et al) released a clinical practice resource for the clinical evaluation of hearing loss published, which states that first-line genetic testing for individuals with exam findings that suggest a syndromic hearing loss etiology may include a variety of tests, including genome sequencing, depending on clinical presentation. For individuals without physical findings that suggest a syndromic hearing loss etiology, they recommend a tiered approach, starting with comprehensive hearing loss gene panel testing unless a more specific genetic etiology is evident for which targeted testing is appropriate. (p. 1400)

National Society for Genetic Counselors

The National Society for Genetic Counselors (NSGC) released a position statement (2013, updated 2020, reaffirmed 2023) stating the following in regard to secondary and incidental findings in genetic testing:

> "The National Society of Genetic Counselors strongly advises pre-test counseling that facilitates informed decision-making, elicits patient preferences regarding secondary and/or incidental findings if possible, and formulates a plan for returning such results before testing occurs."

The National Society of Genetic Counselors (NSGC) published evidence-based practice guidelines for individuals with unexplained epilepsy (Smith et al, 2022). The NSGC recommendations are as follows (p. 4):

- Individuals with unexplained epilepsy should be offered genetic testing, without limitation of age.
- Multi-gene, comprehensive testing, such as exome sequencing, genome sequencing or a multigene panel as a first-tier test is strongly recommended.

Patient-Centered Laboratory Utilization Guidance Services

In the PLUGS July 2023 guidelines entitled "Genomic Sequencing for Rare Disease," the following clinical criteria are recommended for exome sequencing and genome sequencing.

"Exome sequencing or genome sequencing (ES/GS) is considered medically necessary when ALL of the following criteria are met:

1. The etiology of the patient's features is not known, and a genetic etiology is considered a likely explanation for the phenotype, based on one of the following…
    a. Epilepsy of unexplained etiology with onset at any age, OR
    b. Confirmed bilateral sensorineural hearing loss of unknown etiology and panel testing is unrevealing, OR
    c. Intellectual disability, following formal assessment by a developmental pediatrician or neurologist, defined as moderate/severe/profound by Diagnostic and Statistical Manual of Mental Disorders (DSM-5) criteria, diagnosed by 18 years of age, OR
    d. Global developmental delay, following formal assessment by a developmental pediatrician or neurologist, defined as significant delay in younger children, under age five years, in at least two of the major developmental domains: gross or fine motor; speech and language; cognition; social and personal development; and activities of daily living, OR
    e. Multiple congenital anomalies affecting unrelated organ systems, OR
    f. At least TWO of the following criteria are met:
        i. Abnormality affecting at minimum a single organ system
        ii. Autism

iii. Severe neuropsychiatric condition (e.g., schizophrenia, bipolar disorder, Tourette syndrome, self-injurious behavior, reverse sleep-wake cycles)
iv. Symptoms of a complex neurological condition (e.g., dystonia, hemiplegia, spasticity, hypotonia, myopathy, muscular dystrophy)
v. Family history strongly suggestive of a genetic etiology, including consanguinity
vi. Period of unexplained developmental regression (unrelated to epilepsy or autism)
vii. Laboratory findings suggestive of an inherited metabolic disorder

2. Alternate etiologies have been considered and ruled out, when possible (e.g., MRI abnormalities/brain malformations, environmental exposure, injury, infection, isolated prematurity), AND
3. Clinical presentation does not fit a well-described syndrome for which more targeted testing is available." (p. 7)

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Rapid Genome Sequencing

Patient-Centered Laboratory Utilization Guidance Services

In the PLUGS June 2022 guidelines entitled "Rapid Genome Sequencing," the following clinical criteria are recommended for coverage for "acutely-ill individuals" who meet "ALL of the following criteria":

"1. The etiology of the patient's features is not known and a genetic etiology is considered a likely explanation for the phenotype, based on one of the following:

a) Multiple congenital abnormalities affecting unrelated organ systems, OR

b) Epileptic encephalopathy, OR

c) TWO of the following criteria are met:

- abnormality affecting at minimum a single organ system
- symptoms of a complex neurological condition (e.g., dystonia, hemiplegia, spasticity, epilepsy, hypotonia, myopathy, muscular dystrophy, global developmental delay, intellectual disability)
- family history strongly suggestive of a genetic etiology, including consanguinity
- laboratory findings suggestive of an inborn error of metabolism
- abnormal response to standard therapy

2. Alternate etiologies have been considered and ruled out when possible (e.g., MRI abnormalities/brain malformations, environmental exposure, injury, infection, isolated prematurity), AND

4. rGS is more efficient and economical than the separate single-gene tests or panels that would be recommended based on the differential diagnosis (e.g., genetic conditions that demonstrate a high degree of genetic heterogeneity)..." (p. 3 and 4)

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The National Society for Genetic Counselors (NSGC) released a position statement (2013, updated 2020, reaffirmed 2023) stating the following in regard to secondary and incidental findings in genetic testing:

> "The National Society of Genetic Counselors strongly advises pre-test counseling that facilitates informed decision-making, elicits patient preferences regarding secondary and/or incidental findings if possible, and formulates a plan for returning such results before testing occurs."

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- Individuals with unexplained epilepsy should be offered genetic testing, without limitation of age.
- Multi-gene, comprehensive testing, such as exome sequencing, genome sequencing or a multigene panel as a first-tier test is strongly recommended.

Kingsmore SF, Cakici JA, Clark MM et al. 2019

This report is from the NSIGHT2 study, a prospective randomized, controlled, blinded trial (RCT) in acutely ill infants, primarily from the NICU, PICU, and CVICU at Rady Children's Hospital, San Diego (RCHSD) to compare the effectiveness and outcomes between rWGS and rWES, with analysis as singleton probands and familial trios. The inclusion criteria for the 1,248 ill infants defined the maximum age at the time of admission as four months. They found that 24% of infants undergoing rapid exome sequencing had genetic disease. They conclude that diagnostic testing in infants with diseases of unknown etiology, rapid genomic sequencing, including rapid exome sequencing can be performed as a first tier test in infants with diseases of unknown etiology at time of admission to ICUs. In unstable infants and in those whom a genetic diagnosis was likely to impact immediate management, rapid genomic sequencing had optimal analytic and diagnostic performance by virtue of shortest time to results. (p. 725)

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Note: Medica uses the genetic testing clinical criteria developed by Concert Genetics, an industry-leader in genetic testing technology assessment and policy development.

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