Genetic Testing of Mitochondrial Disorders

Policy Number: AHS – M2085	Prior Policy Name and Number, as applicable: N/A
Initial Effective Date: June 1, 2023	Current Effective Date: June 1, 2023
Line(s) of Business: HMO; PPO; QUEST Integration; Medicare; FEP	Precertification: Required

I. Policy Description

Mitochondrial disease refers to a heterogeneous group of disorders caused by dysfunctional mitochondria, the organelles responsible for oxidative phosphorylation within the cell. Mitochondrial diseases are classified according to the primary genetic defect, including those affecting respiratory chain proteins or ancillary proteins, mitochondrial RNA translation defects, inner membrane lipid defects, mutations causing depletion of mitochondrial DNA, or mutations to mitochondrial dynamics. Tissues with high energy demands, such as brain, heart, and skeletal muscle, are most affected by mitochondrial diseases. As a result, mitochondrial encephalopathy and cardiomyopathy are the most prominent manifestations.

II. Indications and/or Limitations of Coverage

Application of coverage criteria is dependent upon an individual's benefit coverage at the time of the request

1) Genetic testing to confirm the diagnosis of a mitochondrial disorder (Eg. Mitochondrial Encephalomyopathy, Lactic Acidosis, and Stroke-like episodes (MELAS), Myoclonic Epilepsy and Ragged-Red-Fibers (MERRF), Chronic Progressive External Ophthalmoplegia (CPEO), Kearns-Sayre syndrome, Leigh syndrome) **MEETS COVERAGE CRITERIA** as an alternative to muscle biopsy when clinical signs and symptoms are consistent with a specific mitochondrial disorder, but the diagnosis cannot be made with certainty without genetic testing.

2) In patients strongly suspected of having a mitochondrial disorder without symptomology associated with a specific mitochondrial condition, genomic sequencing and large deletion detection of the entire mitochondrial genome with heteroplasmy detection **MEETS COVERAGE CRITERIA**.

3) Quantification of mitochondrial DNA (mtDNA) in tissue to diagnose mtDNA depletion syndromes **MEETS COVERAGE CRITERIA.**

4) Genetic counseling for mitochondrial disorder genetic testing **MEETS COVERAGE CRITERIA**. It is RECOMMENDED but is NOT REQUIRED.

The following does not meet coverage criteria due to a lack of available published scientific literature confirming that the test(s) is/are required and beneficial for the diagnosis and treatment of a patient's illness.

5) Combination testing of mitochondrial genome testing with whole-exome sequencing (WES) with intronic variants testing and regulatory variants testing, sometimes referred to as whole exome plus testing, including but not limited to Genomic Unity ® Exome Plus Analysis, **DOES NOT MEET COVERAGE CRITERIA**.

6) Combination testing of mitochondrial genome testing with whole-genome sequencing (WGS) with intronic variants testing and regulatory variants testing, sometimes referred to as Genomic Unity ® Whole Genome Analysis, **DOES NOT MEET COVERAGE CRITERIA**.

7) Genetic testing for mitochondrial disorders **DOES NOT MEET COVERAGE CRITERIA** in all other situations.

III. Scientific Background

Mitochondrial diseases are generally inherited and present with an elaborate genetic makeup. Several different types of mitochondrial diseases and resulting ailments exist which include "mitochondrial encephalomyopathy, lactic acidosis, and stroke-like episodes (MELAS), myoclonic epilepsy and ragged-red-fibers (MERRF), chronic progressive external ophthalmoplegia (CPEO), Kearns-Sayre syndrome (KSS), neuropathy, ataxia, and retinitis pigmentosa (NARP), maternally inherited Leigh syndrome (MILS), and Leber hereditary optic neuropathy (LHON)." These diseases can be caused by mutations in either nuclear DNA (nDNA) or mitochondrial DNA (mtDNA); many different mitochondrial disease mutations have been identified, but clinical symptoms are extremely variable and may even differ between patients carrying the same mtDNA mutation. Symptoms present in several areas of the body, including the central nervous system, cardiovascular system, gastrointestinal system, endocrine system, and neuromuscular system. Clinical differences depend on age of onset, affected organ or tissue, and disease progression. Phenotypic variability and severity can create challenges when diagnosing affected patients.

Pathogenic variants in more than 300 genes have been associated with mitochondria-related disorders. For example, infantile onset of mitochondrial diseases with multiple mitochondrial respiratory chain defects result from mutation(s) in the Required for Meiotic Nuclear Division protein 1 (*RMND1*) gene. Further, a pathogenic variant in the ubiquinone biosynthesis protein (*COQ4)* gene has been affiliated with mitochondrial disease development. Patients with mutations in the NADH dehydrogenase mitochondrial (*MT-ND1* and *NDUF)* genes share phenotypic and genotypic correlations in Leigh Syndrome. The individual symptoms are nonspecific, and symptom patterns can overlap considerably. As a result, a patient often cannot be easily classified into one particular syndrome.

Previously, the prevalence of mitochondrial diseases was considered low. With the advent of advanced genetic analysis tools, numerous studies now report a higher incidence of mitochondrial-associated mutations. A meta-analysis of the prevalence of the three primary mtDNA mutations that cause LHON in Europe shows a prevalence of approximately 1:45,000. A longitudinal study in Sweden reports an incidence of mitochondrial encephalomyopathies, in general, at 1:11,000, and an incidence of infantile mitochondrial myopathy with cytochrome C oxidase deficiency at 1:51,000. The authors conclude that "mitochondrial encephalomyopathies are relatively common neurometabolic disorders in childhood." A 2015 study in the United Kingdom reports that "the total prevalence of adult mitochondrial disease, including pathogenic mutations of both the mitochondrial and nuclear genomes (≈1 in 4,300), is among the commonest adult forms of inherited neurological disorders." An Australian study estimates a "minimum birth prevalence of 13.1/100 000 or 1/7634 for respiratory chain disorders with onset at any age."

Barca et al. (2020) evaluated the phenotypic and molecular characteristic of 666 participants in the North American Mitochondrial Disease Consortium (NAMDC) aiming to better understand mitochondrial diseases in North America. Multisystemic disorder was the most common diagnosis (113 participants), compared to classical mitochondrial syndrome. Leigh syndrome (97 participants) and

MELAS (71 participants) were the most frequent classical syndromes. Pathogenic variants in mtDNA, with the most common variants being *POLG1* and *PDHA1*, were more common than pathogenic gene variants.

The figure below gives examples of classical phenotype mitochondrial diseases along with the clinical features and molecular genetics associated with each disorder.

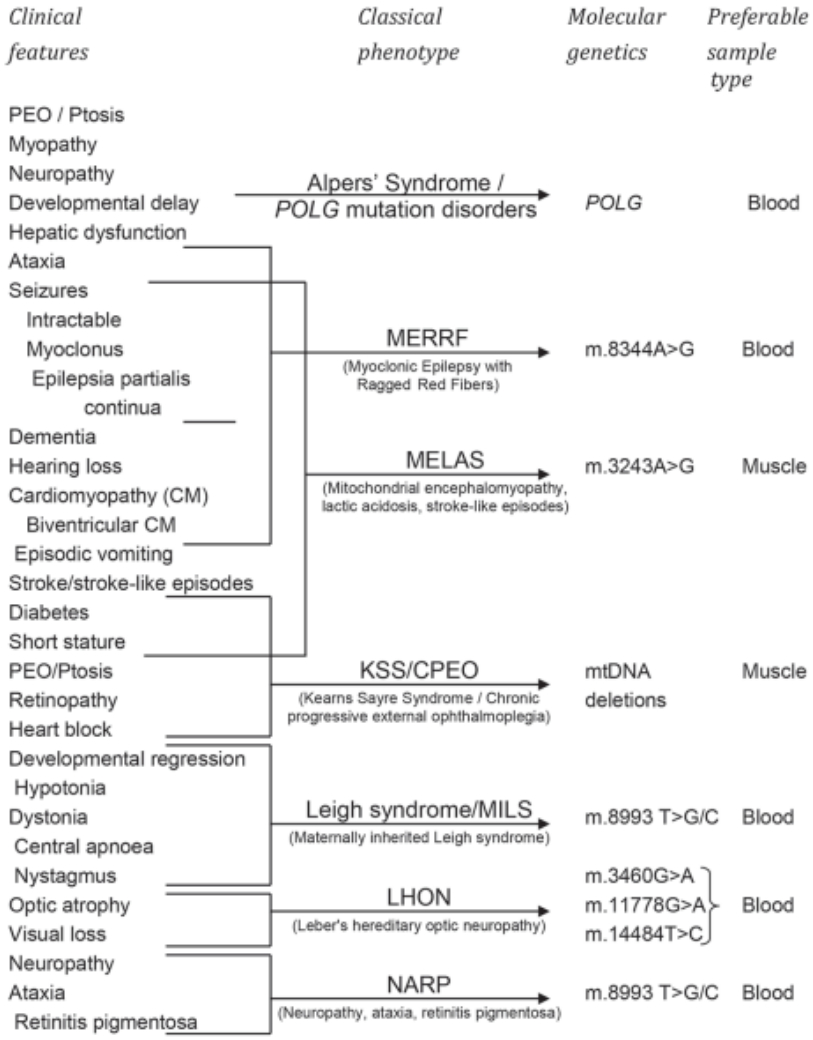


Figure 1. Algorithm for mitochondrial mutation analysis. Key clinical features, although not specific for each disease, can be used to select pertinent genetic tests and hence improve the efficiency of the analysis process.

The evaluation and diagnostic approach for a mitochondrial disorder varies according to age, clinical phenotype, and presumed inheritance pattern. Biochemical testing is indicated for patients who do not have a clear clinical picture of one specific disorder. Measurement of serum lactic acid is often used as a screening test, but the test is neither sensitive nor specific for mitochondrial disorders. "Identifying causative mutations underlying mitochondrial dysfunction is the ultimate gold standard for the

diagnosis. Two mitochondrial diseases (MNGIE and coenzyme Q10 deficiency) are particularly important to identify because of potential treatments."

Clinical Utility and Validity

Clinical utility is high for confirming the diagnosis of mitochondrial disorders in people who have clinical features consistent with a specific mitochondrial disease. In these patients, a positive result on genetic testing can avoid a muscle biopsy and eliminate the need for further clinical workup. Additionally, genetic testing may impact reproductive decision making when a defined mitochondrial disease is present in the family that is severe enough to cause impairment and/or disability. If genetic testing is used in this situation, there will be a decreased risk of a mitochondrial disorder in the offspring. Such testing includes whole-exome sequencing, whole-genome sequencing, and whole mitochondrial sequencing.

The most common first-line diagnostic test for a mitochondrial disease is massively parallel sequencing (MPS), also known as Next-Generation Sequencing (NGS); other accepted methods included targeted panels, whole-exome sequencing (WES) and whole-genome sequencing (WGS). Broad-based exome sequencing has been considered the first-line diagnostic tool for primary mitochondrial disease (PMD) (McCormick, Zolkipli-Cunningham, & Falk, 2018), and other researchers have used WES in tandem with rapid mitochondrial genome (mtDNA) sequencing for diagnoses.

Whole-exome sequencing is likely to increase the detection rate but will also increase the rate of identifying a variant of uncertain significance (VUS). In one study from the U.K., 53 patients who had biochemical evidence of a mitochondrial disorder, but were negative on genetic testing of the primary mitochondrial disorder mutations, underwent whole exome sequencing. Probable pathogenic mutations causative of a mitochondrial disorder were identified in 28 patients (53%), and an additional four patients had variants that were possibly pathogenic. "False negative rates vary by genomic region; therefore, genomic testing may not be as accurate as targeted single gene testing or multigene molecular genetic testing panels. Most laboratories confirm positive results using a second, well-established method."

Expanded panels are defined as panels that include more genes than are associated with any specific disorder. When these panels are used in individuals with nonspecific signs and symptoms that are not consistent with a "classic" presentation of a mitochondrial disorder, the probability of finding a pathogenic mutation is considerably less. Conversely, the likelihood of a false-positive result and the number of VUS (a variant of uncertain significance) may be substantially increased. Table 1, below, lists examples of commercially available expanded genetic panels for mitochondrial disorders.

Table 1. Examples of Commercially Available Expanded Genetic Panels for Mitochondrial Disorders

Laboratory	Lab Test or Panel	Number of Genes Included on Panel
Gene Dx® (Gaithersburg, MD)	MitoXpanded Panel (GeneDX, 2021b)	~1800
	Combined Mito Genome Plus Mito Focused Nuclear Gene Panel (GeneDX, 2021a)	202

Transgenomic® (New Haven, CT)	Nuclear Mitome Test (Transgenomic, 2011)	>400
ARUP® (Salt Lake City, UT)	Mitochondrial Disorders Panel (ARUP, 2021)	>150
Baylor® Miraca Genetics Laboratories (Houston, TX)	Mitome Nuclear Genes (BMGL, 2015)	164
Medical Neurogenetics® (Atlanta, GA)	Mitochondrial Genome Sequencing & Deletion Analysis (Medical Neurogenetics, 2021)	>300

Wood et al. (2019) compared the mtDNA sequencing results of the long-read sequencing technology Oxford Nanopore Technologies (ONT) MinION to the Illumina MiSeq, a next generation sequencing platform. A total of 12 patients participated in this study (three healthy controls and nine with known mtDNA deletion disorders). Both of these next-generation sequencing methods were more efficient than LR-PCR and/or Southern Blotting; further, MinION proved to be just as accurate as the Illumina MiSeq in this study, successfully identifying all mtDNA deletions. This tool may assist in making the mitochondrial disease diagnostic process more efficient and cost effective in the future.

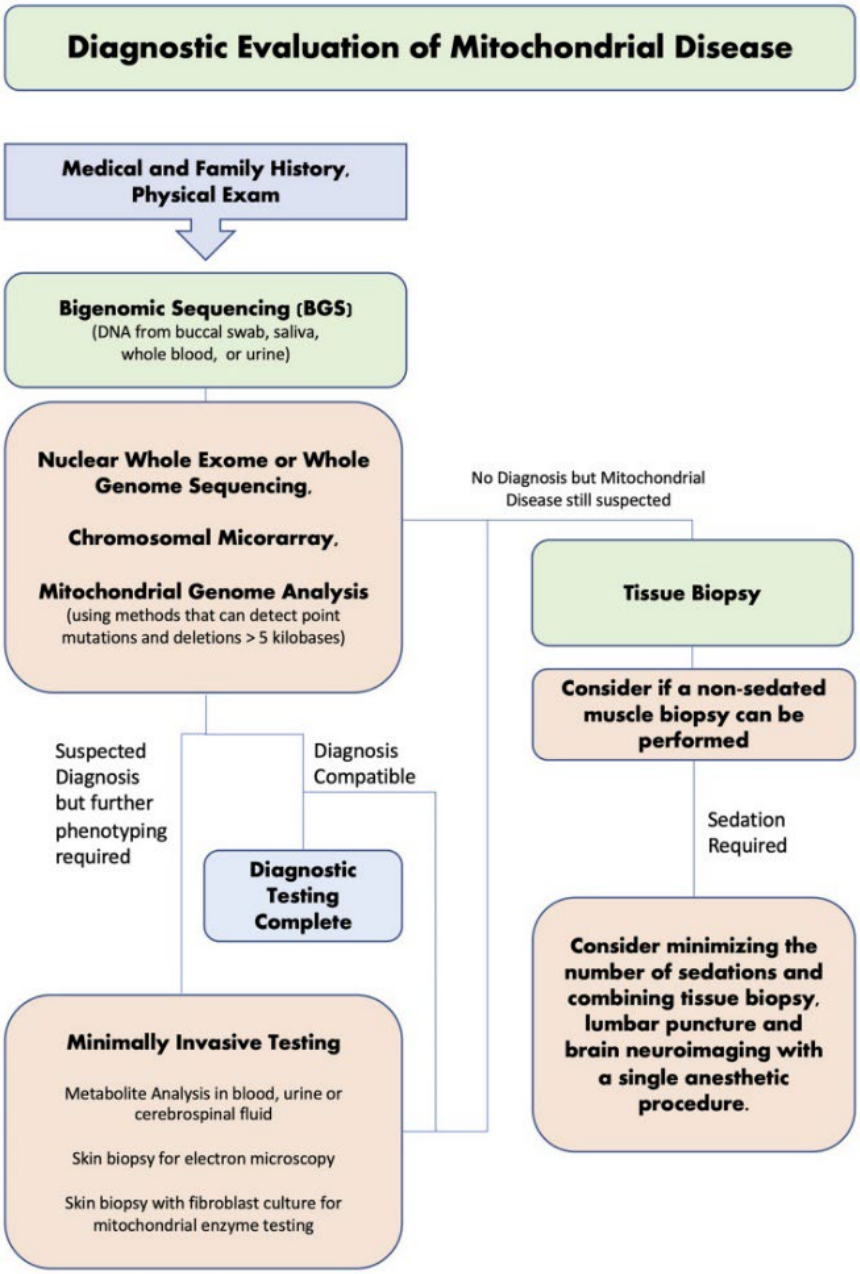
Wagner et al. (2019) researched the effectiveness of exome sequencing (ES) for mitochondrial disease diagnostics; data was used from 2111 clinical cases. The researchers stated that "ES identified known pathogenic mtDNA point mutations in 38 individuals, increasing the diagnostic yield by nearly 2%. Analysis of mtDNA variants by ES had a high recall rate (96.2 ± 5.6%) and excellent precision (99.5 ± 2.2%) when compared to the gold standard of targeted mtDNA next generation sequencing. (Wagner et al., 2019)." These results suggest that ES should be considered as a diagnostic tool for both nDNA and mtDNA testing.

Legati et al. (2016) suggest a two-tiered approach to genetic testing where targeted NGS is used first in cases of suspected mitochondrial disorders followed by WES in patients who have inconclusive results. "Importantly, WES on selected cases has unraveled the presence of pathogenic mutations in genes encoding non-mitochondrial proteins (e.g. the transcription factor E4F1), an observation that further expands the intricate genetics of mitochondrial disease and suggests a new area of investigation in mitochondrial medicine."

Pronicka et al. (2016) suggest that whole-exome sequencing (WES) is a better diagnostic tool than NGS. A total of 113 pediatric Polish patients participated in this study; variants were identified in both nDNA and mtDNA. WES was able to identify "likely causative mutations" in 67 patients, with 50.5% of all detected genetic changes novel variants; further, "In 47 patients, changes in 31 MD-related genes (*ACAD9, ADCK3, AIFM1, CLPB, COX10, DLD, EARS2, FBXL4, MTATP6, MTFMT, MTND1, MTND3, MTND5, NAXE, NDUFS6, NDUFS7, NDUFV1, OPA1, PARS2, PC, PDHA1, POLG, RARS2, RRM2B, SCO2, SERAC1, SLC19A3, SLC25A12, TAZ, TMEM126B, VARS2*) were identified."

In a study by Kerr et al. (2020), 390 patients were recruited and tested for mitochondrial disease (MD) through traditional diagnostic pathways (metabolite analysis, tissue neuropathology and respiratory chain enzyme activity) and new diagnostic approaches (next generation sequencing (NGS) and nuclear whole exome sequencing (nWES)). Testing through traditional diagnostic methods resulted in a mitochondrial diagnosis in 115 out of 390 patients (29.50%). In comparison, 116 out of 390 patients

were recruited for NGS, which identified 36 patients (31%) with a mitochondrial diagnosis. To confirm diagnosis, patients were further tested through nuclear whole exome sequencing (nWES), which provided a secondary diagnosis in "two cases who already had a pathogenic variant in mtDNA, and a revised diagnosis (*GLUL*) in one case that had abnormal pathology but no pathogenic mtDNA variant". nWES also identified a mitochondrial diagnosis in one patient who tested negative from NGS. The author offers a diagnostic evaluation strategy, as shown in the figure below, and recommends that "a non-invasive, bigenomic sequencing (BGS) approach (using both a nWES and optimized mtDNA analysis to include large deletions) should be the first step in investigating for mitochondrial diseases. There may still be a role for tissue biopsy in unsolved cases or when the diagnosis is still not clear after NGS studies" (Kerr et al., 2020).



Another study clearly demonstrates the heterogeneity of genetic mutations causing mitochondrial disorders. Of the 142 patients with childhood-onset mitochondrial disorders, researchers "identified 37 novel mutations in known mitochondrial disease genes and 3 mitochondria-related genes (*MRPS23*, *QRSL1*, and *PNPLA4*) as novel causative genes." These researchers utilized whole mtDNA and exome and chromosomal aberration analysis approaches to "enhance the ability to identify pathogenic gene mutations in patients."

A study by Fang et al. (2017) recruited 141 children with suspected mitochondrial disorders and used NGS to identify genetic characteristics. Forty children were gene confirmed with a known mitochondrial disease; 62.5% of those cases were due to a mtDNA mutation and 37.5% due to a nDNA mutation. This study found the most prevalent disorders to be Leigh Syndrome and MELAS.

Spath et al. (2021) studied parallel preimplantation genetic testing (PGT) for mtDNA disease and aneuploidy on four patients at risk of transmitting mtDNA disease. Aneuploidy is the condition of having an abnormal number of chromosomes. "Half of the embryos tested were shown to be aneuploid (16/33)." Notably, not all the participants had the same mtDNA mutations. Patients A and D had a m.8993T>G mutation; mutations were detected in embryo biopsies from Patient A but not Patient B. Patient C had a m.10191T.G mutation, no mutations were detected in embryo biopsies from Patient C. Patient D had a m3243A>G mutation, mutations were detected in embryo biopsies from Patient D. Patients A and D displayed somatic heteroplasmy for mtDNA mutations, "heteroplasmic women had a higher incidence of affected embryos than those with undetectable somatic mutant mtDNA but were still able to produce mutation-free embryos." The authors concluded that "strategies providing a combination of PGT for mtDNA disease and aneuploidy may be advantageous compared with approaches that consider only mtDNA."

Wu et al. (2021) evaluated the cost-efficiency and cost-benefit of genomic sequencing for children presenting clinical indications of mitochondrial diseases compared to the conventional diagnosis pathway in Australia. The authors used a decision tree model approach and a discrete-event simulation approach on data from 78 pediatric-onset patients. The conventional diagnosis pathway refers to a diagnostic workup including metabolic, imaging, and histopathological investigations, and genetic testing. Genomic sequencing was less costly and more effective than conventional care. The authors concluded that "genomic sequencing is cost-saving relative to traditional investigative approaches, while enabling more diagnoses to be made in a timely manner, offering substantial personal benefits to children and their families."

Farahvash et al. (2021) did a case study on two siblings with mitochondrial neurogastrointestinal encephalopathy disease (MNGIE). The two patients experienced gastrointestinal and cachexia symptoms for years and underwent numerous exploratory tests and surgeries which did not improve their condition. Eventually, the patients were diagnosed with MNGIE following genetic testing for the TYMP gene. The authors concluded that "MNGIE diagnosis is important to establish to avoid unnecessary invasive testing for gastrointestinal, ophthalmological, and neurological symptoms and to ensure patients receive appropriate nutritional and genetic counselling."

IV. Guidelines and Recommendations

Mitochondrial Medicine Society

The Mitochondrial Medicine Society published the following consensus recommendations on genetic testing for mitochondrial disorders:

1. "Massively parallel sequencing/NGS of the mtDNA genome is the preferred methodology when testing mtDNA and should be performed in cases of suspected mitochondrial disease instead of testing for a limited number of pathogenic point mutations.
2. Patients with a strong likelihood of mitochondrial disease because of a mtDNA mutation and negative testing in blood, should have mtDNA assessed in another tissue to avoid the possibility of missing tissue-specific mutations or low levels of heteroplasmy in blood; tissue-based testing also helps assess the risk of other organ involvement and heterogeneity in family members and to guide genetic counseling.
3. Heteroplasmy analysis in urine can selectively be more informative and accurate than testing in blood alone, especially in cases of MELAS due to the common m. 3243A>G mutation.
4. mtDNA deletion and duplication testing should be performed in cases of suspected mitochondrial disease via NGS of the mtDNA genome, especially in all patients undergoing a diagnostic tissue biopsy.
    a. If a single small deletion is identified using polymerase chain reaction–based analysis, then one should be cautious in associating these findings with a primary mitochondrial disorder.
    b. When multiple mtDNA deletions are noted, sequencing of nuclear genes involved in mtDNA biosynthesis is recommended.
5. When a tissue specimen is obtained for mitochondrial studies, mtDNA content (copy number) testing via real-time quantitative polymerase chain reaction should strongly be considered for mtDNA depletion analysis because mtDNA depletion may not be detected in blood.
    a. mtDNA proliferation is a nonspecific compensatory finding that can be seen in primary mitochondrial disease, secondary mitochondrial dysfunction, myopathy, hypotonia, and as a by-product of regular, intense exercise.
6. When considering nuclear gene testing in patients with likely primary mitochondrial disease, NGS methodologies providing complete coverage of known mitochondrial disease genes is preferred. Single-gene testing should usually be avoided because mutations in different genes can produce the same phenotype. If no known mutation is identified via known NGS gene panels, then whole exome sequencing should be considered."

The Mitochondrial Medicine Society also commented on the set of mtDNA depletion syndromes, which are "characterized by a significant reduction in mtDNA copy number in affected tissues". They note that diagnosis of these conditions "requires quantification of mtDNA content, typically in affected tissue, with identification of a significant decrease below the mean of normal age, gender, and tissue-specific control when normalized to nDNA tissue content". Since NGS of the mtDNA genome does not identify mtDNA content, a separate quantitative real-time polymerase chain reaction must be used.

The Mitochondrial Medicine Society in 2017 released their guidelines regarding patient care standards. Within this set of guidelines, they state, "Pregnancy in mitochondrial disease also elicits the concern of transmission of a genetic disorder. Appropriate preconception genetic counseling and discussion of options of prenatal testing are needed. A fetus affected by mitochondrial disease may also be at higher risk for prenatal morbidity. Finally, premature ovarian failure is a feature of several mitochondrial disorders and affected women should be referred for assisted reproductive technologies if they wish to have children."

Association for Clinical Genomic Science (ACGS)

The ACGS published guidelines for the genetic testing strategies for diagnostic and familial testing, variant interpretation and reporting, and prenatal diagnosis and reproductive options. The guidelines report the minimal level of testing recommended for the most common diagnostic referrals, listed below, noting possible further testing with nuclear DNA testing and whole mtDNA sequencing for all phenotypes.

- Phenotype: ataxia, possible diagnosis of late-childhood or adult-onset peripheral neuropathy, pigmentary retinopathy (NARP) or mitochondrial myopathy, encephalopathy, lactic acidosis, and stroke-like episodes (MELAS). Minimum level of testing for: m.8993T>G p.(Leu156Arg), m.8993T>C p.(Leu156Pro)(*MT-ATP6*), m.3243A>G (*MT-TL1*).
- Phenotype: cardiomyopathy, familial hypertrophic cardiomyopathy with maternal inheritance. Minimum level of testing for: m.4300A>G (*MT-TI*), m.3243A>G (*MT-TL1*)
- Phenotype: diabetes mellitus and sensorineural hearing loss. Minimum level of testing for: m.3243A>G (*MT-TL1*), m.3243A>G (*MT-TL1*).
- Phenotype: encephalopathy/seizures with lactic acidosis, possible diagnosis of mitochondrial myopathy, encephalopathy, lactic acidosis, and stroke-like episodes (MELAS) or infantile onset subacute relapsing encephalopathy, cerebellar and brain stem signs (MILS). Minimum level of testing for: m.3243A>G, (*MT-TL1*), m.8993T>G p.(Leu156Arg), m.8993T>C p.(Leu156Pro), (*MT-ATP6*).
- Phenotype: non-syndromic sensorineural hearing loss, particularly if onset following aminoglycoside exposure. Minimum level of testing for m.1555A>G (*MT-RNR1*).
- Phenotype: Kearns-Sayre syndrome Onset, below the age of 20 years, PEO and pigmentary retinopathy with one of either cardiac conduction block, cerebrospinal fluid protein concentration greater than 100 mg/dL, or cerebellar ataxia. Minimum level of testing for: large-scale mtDNA rearrangements (single and multiple deletions), m.3243A>G (*MT-TL1*).
- Phenotype: Leber hereditary optic neuropathy, optic atrophy, childhood or midlife (adult onset) acute or subacute painless bilateral central vision loss. Minimum level of testing for: m.3460G>A p.(Ala52Thr) (*MT-ND1*), m.11778G>A p.(Arg340His) (*MT-ND4*), m.14484T>C p.(Met64Val) (*MT-ND6*).
- Phenotype: mtDNA depletion syndrome, neonatal or infantile hepatocerebral, myopathic, encephalomyopathic or neurogastrointestinal presentations; may also include growth failure, lactic acidosis, and hypoglycemia. Minimum level of testing for: mtDNA copy number analysis.
- Phenotype: myoclonic epilepsy, myoclonus, seizures; cerebellar ataxia; myopathy. Minimum level of testing for: m.8344A>G (*MT-TK*), m.3243A>G (*MT-TL1*).
- Phenotype: Pearson syndrome, sideroblastic anemia of childhood; Pancytopenia; Exocrine pancreatic failure. Minimum level of testing for: large-scale mtDNA rearrangements.
- Phenotype: progressive external ophthalmoplegia (PEO), ptosis, typically adult-onset ptosis, paralysis of the extraocular muscles (ophthalmoplegia), oropharyngeal weakness, and variably severe proximal limb weakness. Minimum level of testing for: large-scale mtDNA rearrangements (single and multiple deletions, m.3243A>G (*MT-TL1*).
- Phenotype: stroke-like episodes, typically before age 40 years. Minimum level of testing for: m.3243A>G (*MT-TL1*).

European Academy of Neurology (EAN)

Regarding genetic testing for mitochondrial encephalopathy, lactic acidosis and stroke-like episodes (MELAS), the EAN recommends “Urgent genetic testing for MELAS should be considered in patients presenting with suspected SLE [stroke-like episode]. Search for the m.3243A>G variant (in urine where possible) and, if m.3243A>G variant is negative, POLG sequencing is required. Muscle biopsy should be

considered after excluding m.3243A>G and POLG variants." The EAN also notes that valproic acid is "contraindicated, mainly in patients with POLG variants."

MNGIE International Network

The MNGIE [Mitochondrial neurogastrointestinal encephalomyopathy] International Network recommended *TYMP* sequencing to confirm a MNGIE diagnosis. If a variant of unknown significance or a wild-type variant is found, the Network recommends biochemical testing of thymidine (dThd) and deoxyuridine levels to determine thymidine phosphorylase (TP) activity. The Network also remarks on several treatment options (both short- and long-term), which focus on restoring the biochemical balance of the patient.

V. State and Federal Regulations, as applicable

DISCLAIMER: If there is a conflict between this Policy and any relevant, applicable government policy for a particular member [e.g., Local Coverage Determinations (LCDs) or National Coverage Determinations (NCDs) for Medicare and/or state coverage for Medicaid], then the government policy will be used to make the determination. For the most up-to-date Medicare policies and coverage, please visit the Medicare search website: http://www.cms.gov/medicare-coveragedatabase/overview-and-quick-search.aspx. For the most up-to-date Medicaid policies and coverage, visit the applicable state Medicaid website.

A search of the FDA database on 10/13/2021 using the terms "mtDNA" and "mitochondrial disease" yielded 0 results. Many labs have developed specific tests that they must validate and perform in house. These laboratory-developed tests (LDTs) are regulated by the Centers for Medicare and Medicaid (CMS) as high-complexity tests under the Clinical Laboratory Improvement Amendments of 1988 (CLIA '88). As an LDT, the U. S. Food and Drug Administration has not approved or cleared this test; however, FDA clearance or approval is not currently required for clinical use.

VI. Important Reminder

The purpose of this Medical Policy is to provide a guide to coverage. This Medical Policy is not intended to dictate to providers how to practice medicine. Nothing in this Medical Policy is intended to discourage or prohibit providing other medical advice or treatment deemed appropriate by the treating physician.

Benefit determinations are subject to applicable member contract language. To the extent there are any conflicts between these guidelines and the contract language, the contract language will control.

This Medical Policy has been developed through consideration of the medical necessity criteria under Hawaii's Patients' Bill of Rights and Responsibilities Act (Hawaii Revised Statutes §432E-1.4), or for QUEST Integration members under Hawaii Administrative Rules (HAR 1700.1-42), generally accepted standards of medical practice and review of medical literature and government approval status. HMSA has determined that services not covered under this Medical Policy will not be medically necessary under Hawaii law in most cases. If a treating physician disagrees with HMSA's determination as to medical necessity in a given case, the physician may request that HMSA reconsider the application of the medical necessity criteria to the case at issue in light of any supporting documentation.

Genetic testing is covered for level 1 or 2A recommendations of the National Comprehensive Cancer Network (NCCN and in accordance with Hawaii's Patients' Bill of Rights and Responsibilities Act (Hawaii Revised Statutes §432E-1.4) or for QUEST members, the Hawaii Administrative Rules (HAR 1700.1-42).

VII. Evidence-based Scientific References

Akesson, L., Eggers, S., Chong, B., Hunter, M., Krzesinski, E., Brown, N., . . . Lunke, S. (2019). Rapid mitochondrial genome (MTDNA) sequencing: facilitating rapid diagnosis of mitochondrial diseases in paediatric acute care. *51*, 118–S119. Retrieved from https://www.pathologyjournal.rcpa.edu.au/article/S0031-3025(18)31004-3/abstract

ARUP. (2021, 06/04/2018). Mitochondrial Disorders Panel (mtDNA and Nuclear Genes). Retrieved from https://ltd.aruplab.com/Tests/Pub/3001959

Barca, E., Long, Y., Cooley, V., Schoenaker, R., Emmanuele, V., DiMauro, S., . . . Hirano, M. (2020). Mitochondrial diseases in North America: An analysis of the NAMDC Registry. *Neurol Genet, 6*(2), e402. doi:10.1212/nxg.0000000000000402

BMGL. (2015, 08/03/2015). MITOCHONDRIAL DNA (mtDNA) TEST REQUISITION. Retrieved from https://www.bcm.edu/research/medical-genetics-labs/index.cfm?pmid=26409

Chinnery, P. F. (2014). Mitochondrial Disorders Overview. In M. P. Adam, H. H. Ardinger, R. A. Pagon, S. E. Wallace, L. J. H. Bean, K. Stephens, & A. Amemiya (Eds.), *GeneReviews((R))* (Vol. 2014 update). Seattle (WA): University of Washington, Seattle

University of Washington, Seattle. GeneReviews is a registered trademark of the University of Washington, Seattle. All rights reserved.

Darin, N., Oldfors, A., Moslemi, A. R., Holme, E., & Tulinius, M. (2001). The incidence of mitochondrial encephalomyopathies in childhood: clinical features and morphological, biochemical, and DNA abnormalities. *Ann Neurol, 49*(3), 377-383.

Dimmock, D. P., & Lawlor, M. W. (2017). Presentation and Diagnostic Evaluation of Mitochondrial Disease. *Pediatr Clin North Am, 64*(1), 161-171. doi:10.1016/j.pcl.2016.08.011

Fang, F., Liu, Z., Fang, H., Wu, J., Shen, D., Sun, S., . . . Shen, Y. (2017). The clinical and genetic characteristics in children with mitochondrial disease in China. *Sci China Life Sci, 60*(7), 746-757. doi:10.1007/s11427-017-9080-y

Farahvash, A., Kassardjian, C. D., & Micieli, J. A. (2021). Mitochondrial Neurogastrointestinal Encephalopathy Disease: A Rare Disease Diagnosed in Siblings with Double Vision. *Case Rep Ophthalmol, 12*(1), 174-181. doi:10.1159/000514098

GeneDX. (2021a, 03/2018). MITOCHONDRIAL GENE TABLE. Retrieved from https://www.genedx.com/Resources/Downloads/Resources%20and%20Forms/TRF-Files/TRF_Neuro.pdf

GeneDX. (2021b, 05/2018). MITOXPANDED PANEL GENE LIST. Retrieved from https://www.genedx.com/Resources/TIS-Files/TIS-J809.pdf

Gorman, G. S., Schaefer, A. M., Ng, Y., Gomez, N., Blakely, E. L., Alston, C. L., . . . McFarland, R. (2015). Prevalence of nuclear and mitochondrial DNA mutations related to adult mitochondrial disease. *Ann Neurol, 77*(5), 753-759. doi:10.1002/ana.24362

Hatakeyama, H., & Goto, Y. (2016). Concise Review: Heteroplasmic Mitochondrial DNA Mutations and Mitochondrial Diseases: Toward iPSC-Based Disease Modeling, Drug Discovery, and Regenerative Therapeutics. *Stem Cells, 34*(4), 801-808. doi:10.1002/stem.2292

Hirano, M., Carelli, V., De Giorgio, R., Pironi, L., Accarino, A., Cenacchi, G., . . . Zeviani, M. (2020). Mitochondrial neurogastrointestinal encephalomyopathy (MNGIE): Position paper on diagnosis, prognosis, and treatment by the MNGIE International Network. *J Inherit Metab Dis*. doi:10.1002/jimd.12300

Horvath, R., & Chinnery, P. (2019). *Diagnostic Approach to Mitochondrial Diseases*.

Kerr, M., Hume, S., Omar, F., Koo, D., Barnes, H., Khan, M., . . . Khan, A. (2020). MITO-FIND: A study in 390 patients to determine a diagnostic strategy for mitochondrial disease. *Molecular Genetics and Metabolism*. doi:https://doi.org/10.1016/j.ymgme.2020.08.009

Kohda, M., Tokuzawa, Y., Kishita, Y., Nyuzuki, H., Moriyama, Y., Mizuno, Y., . . . Okazaki, Y. (2016). A Comprehensive Genomic Analysis Reveals the Genetic Landscape of Mitochondrial Respiratory Chain Complex Deficiencies. *PLoS Genet, 12*(1), e1005679. doi:10.1371/journal.pgen.1005679

Legati, A., Reyes, A., Nasca, A., Invernizzi, F., Lamantea, E., Tiranti, V., . . . Zeviani, M. (2016). New genes and pathomechanisms in mitochondrial disorders unraveled by NGS technologies. *Biochim Biophys Acta, 1857*(8), 1326-1335. doi:10.1016/j.bbabio.2016.02.022

Lightowlers, R. N., Taylor, R. W., & Turnbull, D. M. (2015). Mutations causing mitochondrial disease: What is new and what challenges remain? *Science, 349*(6255), 1494-1499. doi:10.1126/science.aac7516

Ling, T.-k., Law, C.-y., Ko, C.-h., Fong, N.-c., Wong, K.-c., Lee, K.-l., . . . Lam, C.-w. (2019). A common COQ4 mutation in undiagnosed mitochondrial disease: a local case series. *51*, S112–S113. Retrieved from https://www.pathologyjournal.rcpa.edu.au/article/S0031-3025(18)30982-6/abstract

Mancuso, M., Arnold, M., Bersano, A., Burlina, A., Chabriat, H., Debette, S., . . . Markus, H. S. (2020). Monogenic cerebral small-vessel diseases: diagnosis and therapy. Consensus recommendations of the European Academy of Neurology. *Eur J Neurol, 27*(6), 909-927. doi:10.1111/ene.14183

Mascialino, B., Leinonen, M., & Meier, T. (2012). Meta-analysis of the prevalence of Leber hereditary optic neuropathy mtDNA mutations in Europe. *Eur J Ophthalmol, 22*(3), 461-465. doi:10.5301/ejo.5000055

Mavraki, E., Labrum, R., Sergeant, K., Alston, C. L., Woodward, C., Smith, C., . . . Fratter, C. (2020). BEST PRACTICE GUIDELINES FOR THE MOLECULAR DIAGNOSIS OF MITOCHONDRIAL DISEASE.

McCormick, E. M., Zolkipli-Cunningham, Z., & Falk, M. J. (2018). Mitochondrial disease genetics update: recent insights into the molecular diagnosis and expanding phenotype of primary mitochondrial disease. *Curr Opin Pediatr, 30*(6), 714-724. doi:10.1097/mop.0000000000000686

Medical Neurogenetics, L. (2021). Mitochondrial Genome Sequencing + Deletion Analysis. Retrieved from https://mnglabs.labcorp.com/tests/MOL189/mitochondrial-genome-sequencing-deletion-analysis

Meyers, D. E., Basha, H. I., & Koenig, M. K. (2013). Mitochondrial cardiomyopathy: pathophysiology, diagnosis, and management. *Tex Heart Inst J, 40*(4), 385-394.

Ng, Y. S., Alston, C. L., Diodato, D., Morris, A. A., Ulrick, N., Kmoch, S., . . . McFarland, R. (2016). The clinical, biochemical and genetic features associated with RMND1-related mitochondrial disease. *J Med Genet, 53*(11), 768-775. doi:10.1136/jmedgenet-2016-103910

O'Brien, M., Cryan, J., Brett, F., Howley, R., & Farrell, M. (2014). Ten years on: genetic screening for mitochondrial disease in Ireland. *Clin Neuropathol, 33*(4), 279-283. Retrieved from https://www.ncbi.nlm.nih.gov/pubmed/?term=Ten+years+on%3A+genetic+screening+for+mitochondrial+disease+in+Ireland

O'Ferrall, E. (2019). Mitochondrial myopathies: Clinical features and diagnosis. *UpToDate.* Retrieved from https://www.uptodate.com/contents/mitochondrial-myopathies-clinical-features-and-diagnosis

Parikh, S., Goldstein, A., Karaa, A., Koenig, M. K., Anselm, I., Brunel-Guitton, C., . . . Chinnery, P. F. (2017). Patient care standards for primary mitochondrial disease: a consensus statement from the Mitochondrial Medicine Society. *Genetics in medicine : official journal of the American College of Medical Genetics, 19*(12). doi:10.1038/gim.2017.107

Parikh, S., Goldstein, A., Koenig, M. K., Scaglia, F., Enns, G. M., Saneto, R., . . . DiMauro, S. (2015). Diagnosis and management of mitochondrial disease: a consensus statement from the Mitochondrial Medicine Society. *Genetics in medicine : official journal of the American College of Medical Genetics, 17*(9), 689-701. doi:10.1038/gim.2014.177

Pronicka, E., Piekutowska-Abramczuk, D., Ciara, E., Trubicka, J., Rokicki, D., Karkucinska-Wieckowska, A., . . . Ploski, R. (2016). New perspective in diagnostics of mitochondrial disorders: two years' experience with whole-exome sequencing at a national paediatric centre. *J Transl Med, 14*(1), 174. doi:10.1186/s12967-016-0930-9

Schon, E. A., DiMauro, S., & Hirano, M. (2012). Human mitochondrial DNA: roles of inherited and somatic mutations. *Nat Rev Genet, 13*(12), 878-890. doi:10.1038/nrg3275

Skladal, D., Halliday, J., & Thorburn, D. R. (2003). Minimum birth prevalence of mitochondrial respiratory chain disorders in children. *Brain, 126*(Pt 8), 1905-1912. doi:10.1093/brain/awg170

Sofou, K., de Coo, I. F. M., Ostergaard, E., Isohanni, P., Naess, K., De Meirleir, L., . . . Darin, N. (2018). Phenotype-genotype correlations in Leigh syndrome: new insights from a multicentre study of 96 patients. *J Med Genet, 55*(1), 21-27. doi:10.1136/jmedgenet-2017-104891

Spath, K., Babariya, D., Konstantinidis, M., Lowndes, J., Child, T., Grifo, J. A., . . . Wells, D. (2021). Clinical application of sequencing-based methods for parallel preimplantation genetic testing for mitochondrial DNA disease and aneuploidy. *Fertil Steril, 115*(6), 1521-1532. doi:10.1016/j.fertnstert.2021.01.026

Taylor, R. W., Pyle, A., Griffin, H., Blakely, E. L., Duff, J., He, L., . . . Chinnery, P. F. (2014). Use of whole-exome sequencing to determine the genetic basis of multiple mitochondrial respiratory chain complex deficiencies. *Jama, 312*(1), 68-77. doi:10.1001/jama.2014.7184

Thompson, K., Collier, J., Glasglow, R., Robertson, F., Pyle, A., Blakely, E., . . . Taylor, R. W. (2019). Recent advances in understanding the molecular genetic basis of mitochondrial disease. Retrieved from https://onlinelibrary.wiley.com/doi/full/10.1002/jimd.12104

Transgenomic, I. (2011). Transgenomic, Inc. Launches Best-in-Class Next-Generation Sequencing Test for Nuclear Mitochondrial Disorders at the 2011 United Mitochondrial Disease Foundation Meeting. *PR Newswire*. Retrieved from https://www.prnewswire.com/news-releases/transgenomic-inc-launches-best-in-class-next-generation-sequencing-test-for-nuclear-mitochondrial-disorders-at-the-2011-united-mitochondrial-disease-foundation-meeting-123996704.html

Wagner, M., Berutti, R., Lorenz-Depiereux, B., Graf, E., Eckstein, G., Mayr, J. A., . . . Wortmann, S. B. (2019). Mitochondrial DNA mutation analysis from exome sequencing-A more holistic approach in diagnostics of suspected mitochondrial disease. *J Inherit Metab Dis, 42*(5), 909-917. doi:10.1002/jimd.12109

Wood, E., Parker, M., Dunning, M., Hesketh, S., Wang, D., Pink, R., & Fratter, C. (2019). Clinical long-read sequencing of the human mitochondrial genome for mitochondrial disease diagnostics. Retrieved from https://www.biorxiv.org/content/10.1101/597187v1.full

Wu, Y., Balasubramaniam, S., Rius, R., Thorburn, D. R., Christodoulou, J., & Goranitis, I. (2021). Genomic sequencing for the diagnosis of childhood mitochondrial disorders: a health economic evaluation. *Eur J Hum Genet*. doi:10.1038/s41431-021-00916-8

VIII. Policy History

Policy approved by Medical Directors	9/20/2022
Policy approved at UMC	12/16/2022
Policy effective	6/1/2023
Updated Lines of Business	12/18/2023