Chromosome Microarray Testing (Non-Oncology Conditions) (for North Carolina Only)

Policy Number: CSNCT0559.07
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Instructions for Use

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Related Policies
None

Application

This Medical Policy only applies to the State of North Carolina.

Coverage Rationale

Pre-test genetic counseling is strongly recommended in order to inform persons being tested about the advantages and limitations of the test as applied to a unique person.

Chromosome microarray testing using array comparative genomic hybridization (aCGH) and/or single-nucleotide polymorphism (SNP) array is proven and medically necessary for the following:

- Evaluation of an embryo/fetus in the following cases:
  - Intrauterine Fetal Demise or Stillbirth
  - Testing the products of conception following pregnancy loss
  - Individuals undergoing invasive prenatal testing (i.e., amniocentesis, chorionic villus sampling, or fetal tissue sampling)
- Evaluation of individuals with one or more of the following:
  - Autism spectrum disorder (ASD)
  - Isolated severe congenital heart disease
  - Multiple anomalies that are not specific to a Well-Delineated Genetic Syndrome and cannot be identified by a clinical evaluation alone
  - Developmental Delay/Intellectual Disability where a specific syndrome is not suspected
- Evaluation of biological parent or sibling of a fetus or child with an abnormal or equivocal finding on chromosome microarray testing results

Chromosome microarray testing using aCGH or SNP array is unproven and not medically necessary for all other populations and conditions due to insufficient evidence of efficacy.

Definitions

Developmental Delay: Developmental Delay may be used to describe children younger than 5 years of age who present with delays in the attainment of developmental milestones at the expected age (Moeschler and Shevell, 2014, reaffirmed 2019).

Intellectual Disability: A condition diagnosed before age 18 that includes below-average intellectual function and a lack of skills necessary for daily living (MedlinePlus, 2020).

Intrauterine Fetal Demise or Stillbirth: Fetal death at or after 20 weeks' gestation [American College of Obstetricians and Gynecologists (ACOG), Society of Maternal Fetal Medicine (SMFM), 2020, reaffirmed 2021].

Prenatal Diagnosis: A laboratory test performed on fetal deoxyribonucleic acid (DNA) or chromosomes before birth to determine if a fetus has a genetic or chromosomal disorder (ACOG, 2016a, reaffirmed 2023).

Well-Delineated Genetic Syndrome: A syndrome is a collection of recognizable traits or abnormalities that tend to occur together and are associated with a specific disease. Distinguishing characteristics, such as specific facial features or other physical traits, lab tests, or family history can be used to identify a genetic syndrome (Talking Glossary of Genomic and Genetic Terms, National Human Genome Research Institute, 2023). Examples of Well-Delineated Genetic Syndromes include but are not limited to: Down syndrome, Klinefelter syndrome, Marfan syndrome, neurofibromatosis type 1, osteogenesis imperfecta, Prader-Willi syndrome, Rett syndrome, trisomy 13 (Patau syndrome), Trisomy 18 (Edwards syndrome), Turner syndrome, and Williams syndrome.

Applicable Codes

The following list(s) of procedure and/or diagnosis codes is provided for reference purposes only and may not be all inclusive. Listing of a code in this policy does not imply that the service described by the code is a covered or non-covered health service. Benefit coverage for health services is determined by federal, state, or contractual requirements and applicable laws that may require coverage for a specific service. The inclusion of a code does not imply any right to reimbursement or guarantee claim payment. Other Policies and Guidelines may apply.

CPT Code	Description
*0156U	Copy number (e.g., intellectual disability, dysmorphology), sequence analysis
*0209U	Cytogenomic constitutional (genome-wide) analysis, interrogation of genomic regions for copy number, structural changes, and areas of homozygosity for chromosomal abnormalities
81228	Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of genomic regions for copy number variants, comparative genomic hybridization [CGH] microarray analysis
81229	Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of genomic regions for copy number and single nucleotide polymorphism (SNP) variants, comparative genomic hybridization (CGH) microarray analysis
*81349	Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of genomic regions for copy number and loss-of-heterozygosity variants, low-pass sequencing analysis
*81479	Unlisted molecular pathology procedure

Codes labeled with an asterisk (*) are not on the State of North Carolina Medicaid Fee Schedule and therefore may not be covered by the State of North Carolina Medicaid Program.

HCPCS Code	Description
S3870	Comparative genomic hybridization (CGH) microarray testing for developmental delay, autism spectrum disorder and/or intellectual disability

Diagnosis Code	Description
F70	Mild intellectual disabilities

Diagnosis Code	Description
F71	Moderate intellectual disabilities
F72	Severe intellectual disabilities
F73	Profound intellectual disabilities
F78.A1	SYNGAP1-related intellectual disability
F78.A9	Other genetic related intellectual disability
F79	Unspecified intellectual disabilities
F80.0	Phonological disorder
F80.1	Expressive language disorder
F80.2	Mixed receptive-expressive language disorder
F80.4	Speech and language development delay due to hearing loss
F80.81	Childhood onset fluency disorder
F80.82	Social pragmatic communication disorder
F80.89	Other developmental disorders of speech and language
F80.9	Developmental disorder of speech and language, unspecified
F81.0	Specific reading disorder
F81.2	Mathematics disorder
F81.81	Disorder of written expression
F81.89	Other developmental disorders of scholastic skills
F81.9	Developmental disorder of scholastic skills, unspecified
F82	Specific developmental disorder of motor function
F84.0	Autistic disorder
F84.3	Other childhood disintegrative disorder
F84.5	Asperger's syndrome
F84.8	Other pervasive developmental disorders
F84.9	Pervasive developmental disorder, unspecified
F88	Other disorders of psychological development
F89	Unspecified disorder of psychological development
H93.25	Central auditory processing disorder
N96	Recurrent pregnancy loss
O02.1	Missed abortion
O02.89	Other abnormal products of conception
O03.4	Incomplete spontaneous abortion without complication
O03.9	Complete or unspecified spontaneous abortion without complication
O09.511	Supervision of elderly primigravida, first trimester
O09.512	Supervision of elderly primigravida, second trimester
O09.513	Supervision of elderly primigravida, third trimester
O09.519	Supervision of elderly primigravida, unspecified trimester
O09.521	Supervision of elderly multigravida, first trimester
O09.522	Supervision of elderly multigravida, second trimester
O09.523	Supervision of elderly multigravida, third trimester
O09.529	Supervision of elderly multigravida, unspecified trimester
O26.20	Pregnancy care for patient with recurrent pregnancy loss, unspecified trimester
O26.21	Pregnancy care for patient with recurrent pregnancy loss, first trimester
O26.22	Pregnancy care for patient with recurrent pregnancy loss, second trimester
O26.23	Pregnancy care for patient with recurrent pregnancy loss, third trimester

Diagnosis Code	Description
O28.0	Abnormal hematological finding on antenatal screening of mother
O28.1	Abnormal biochemical finding on antenatal screening of mother
O28.2	Abnormal cytological finding on antenatal screening of mother
O28.3	Abnormal ultrasonic finding on antenatal screening of mother
O28.4	Abnormal radiological finding on antenatal screening of mother
O28.5	Abnormal chromosomal and genetic finding on antenatal screening of mother
O28.8	Other abnormal findings on antenatal screening of mother
O28.9	Unspecified abnormal findings on antenatal screening of mother
O35.0XX0	Maternal care for (suspected) central nervous system malformation in fetus, not applicable or unspecified
O35.0XX1	Maternal care for (suspected) central nervous system malformation in fetus, fetus 1
O35.0XX2	Maternal care for (suspected) central nervous system malformation in fetus, fetus 2
O35.0XX3	Maternal care for (suspected) central nervous system malformation in fetus, fetus 3
O35.0XX4	Maternal care for (suspected) central nervous system malformation in fetus, fetus 4
O35.0XX5	Maternal care for (suspected) central nervous system malformation in fetus, fetus 5
O35.0XX9	Maternal care for (suspected) central nervous system malformation in fetus, other fetus
O35.1XX0	Maternal care for (suspected) chromosomal abnormality in fetus, not applicable or unspecified
O35.1XX1	Maternal care for (suspected) chromosomal abnormality in fetus, fetus 1
O35.1XX2	Maternal care for (suspected) chromosomal abnormality in fetus, fetus 2
O35.1XX3	Maternal care for (suspected) chromosomal abnormality in fetus, fetus 3
O35.1XX4	Maternal care for (suspected) chromosomal abnormality in fetus, fetus 4
O35.1XX5	Maternal care for (suspected) chromosomal abnormality in fetus, fetus 5
O35.1XX9	Maternal care for (suspected) chromosomal abnormality in fetus, other fetus
O35.2XX0	Maternal care for (suspected) hereditary disease in fetus, not applicable or unspecified
O35.2XX1	Maternal care for (suspected) hereditary disease in fetus, fetus 1
O35.2XX2	Maternal care for (suspected) hereditary disease in fetus, fetus 2
O35.2XX3	Maternal care for (suspected) hereditary disease in fetus, fetus 3
O35.2XX4	Maternal care for (suspected) hereditary disease in fetus, fetus 4
O35.2XX5	Maternal care for (suspected) hereditary disease in fetus, fetus 5
O35.2XX9	Maternal care for (suspected) hereditary disease in fetus, other fetus
O35.8XX0	Maternal care for other (suspected) fetal abnormality and damage, not applicable or unspecified
O35.8XX1	Maternal care for other (suspected) fetal abnormality and damage, fetus 1
O35.8XX2	Maternal care for other (suspected) fetal abnormality and damage, fetus 2
O35.8XX3	Maternal care for other (suspected) fetal abnormality and damage, fetus 3
O35.8XX4	Maternal care for other (suspected) fetal abnormality and damage, fetus 4
O35.8XX5	Maternal care for other (suspected) fetal abnormality and damage, fetus 5
O35.8XX9	Maternal care for other (suspected) fetal abnormality and damage, other fetus
O36.4XX0	Maternal care for intrauterine death, not applicable or unspecified
O36.4XX1	Maternal care for intrauterine death, fetus 1
O36.4XX2	Maternal care for intrauterine death, fetus 2
O36.4XX3	Maternal care for intrauterine death, fetus 3
O36.4XX4	Maternal care for intrauterine death, fetus 4
O36.4XX5	Maternal care for intrauterine death, fetus 5
O36.4XX9	Maternal care for intrauterine death, other fetus
P02.9	Newborn affected by abnormality of membranes, unspecified

Diagnosis Code	Description
P95	Stillbirth
Q20.1	Double outlet right ventricle
Q20.2	Double outlet left ventricle
Q20.3	Discordant ventriculoarterial connection
Q20.4	Double inlet ventricle
Q20.5	Discordant atrioventricular connection
Q20.6	Isomerism of atrial appendages
Q20.8	Other congenital malformations of cardiac chambers and connections
Q20.9	Congenital malformation of cardiac chambers and connections, unspecified
Q21.0	Ventricular septal defect
Q21.1	Atrial septal defect
Q21.2	Atrioventricular septal defect
Q21.3	Tetralogy of Fallot
Q21.4	Aortopulmonary septal defect
Q21.8	Other congenital malformations of cardiac septa
Q21.9	Congenital malformation of cardiac septum, unspecified
Q22.0	Pulmonary valve atresia
Q22.1	Congenital pulmonary valve stenosis
Q22.2	Congenital pulmonary valve insufficiency
Q22.3	Other congenital malformations of pulmonary valve
Q22.4	Congenital tricuspid stenosis
Q22.5	Ebstein's anomaly
Q22.6	Hypoplastic right heart syndrome
Q22.8	Other congenital malformations of tricuspid valve
Q22.9	Congenital malformation of tricuspid valve, unspecified
Q23.0	Congenital stenosis of aortic valve
Q23.1	Congenital insufficiency of aortic valve
Q23.2	Congenital mitral stenosis
Q23.3	Congenital mitral insufficiency
Q23.4	Hypoplastic left heart syndrome
Q23.81	Bicuspid aortic valve
Q23.82	Congenital mitral valve cleft leaflet
Q23.88	Other congenital malformations of aortic and mitral valves
Q23.9	Congenital malformation of aortic and mitral valves, unspecified
Q24.0	Dextrocardia
Q24.1	Levocardia
Q24.2	Cor triatriatum
Q24.3	Pulmonary infundibular stenosis
Q24.4	Congenital subaortic stenosis
Q24.5	Malformation of coronary vessels
Q24.6	Congenital heart block
Q24.8	Other specified congenital malformations of heart
Q24.9	Congenital malformation of heart, unspecified
Q87.86	Kleefstra syndrome
Q89.7	Multiple congenital malformations, not elsewhere classified

Diagnosis Code	Description
Q89.8	Other specified congenital malformations
Q89.9	Congenital malformation, unspecified
Q90.0	Trisomy 21, nonmosaicism (meiotic nondisjunction)
Q90.1	Trisomy 21, mosaicism (mitotic nondisjunction)
Q90.2	Trisomy 21, translocation
Q90.9	Down syndrome, unspecified
Q91.0	Trisomy 18, nonmosaicism (meiotic nondisjunction)
Q91.1	Trisomy 18, mosaicism (mitotic nondisjunction)
Q91.2	Trisomy 18, translocation
Q91.3	Trisomy 18, unspecified
Q91.4	Trisomy 13, nonmosaicism (meiotic nondisjunction)
Q91.5	Trisomy 13, mosaicism (mitotic nondisjunction)
Q91.6	Trisomy 13, translocation
Q91.7	Trisomy 13, unspecified
Q92.0	Whole chromosome trisomy, nonmosaicism (meiotic nondisjunction)
Q92.1	Whole chromosome trisomy, mosaicism (mitotic nondisjunction)
Q92.2	Partial trisomy
Q92.5	Duplications with other complex rearrangements
Q92.61	Marker chromosomes in normal individual
Q92.62	Marker chromosomes in abnormal individual
Q92.7	Triploidy and polyploidy
Q92.8	Other specified trisomies and partial trisomies of autosomes
Q92.9	Trisomy and partial trisomy of autosomes, unspecified
Q93.0	Whole chromosome monosomy, nonmosaicism (meiotic nondisjunction)
Q93.1	Whole chromosome monosomy, mosaicism (mitotic nondisjunction)
Q93.2	Chromosome replaced with ring, dicentric or isochromosome
Q93.3	Deletion of short arm of chromosome 4
Q93.4	Deletion of short arm of chromosome 5
Q93.7	Deletions with other complex rearrangements
Q93.51	Angelman syndrome
Q93.52	Phelan-McDermid syndrome
Q93.59	Other deletions of part of a chromosome
Q93.81	Velo-cardio-facial syndrome
Q93.82	Williams syndrome
Q93.88	Other microdeletions
Q93.89	Other deletions from the autosomes
Q93.9	Deletion from autosomes, unspecified
Q95.2	Balanced autosomal rearrangement in abnormal individual
Q95.3	Balanced sex/autosomal rearrangement in abnormal individual
Q99.8	Other specified chromosome abnormalities
Q99.9	Chromosomal abnormality, unspecified
R48.0	Dyslexia and alexia
R62.0	Delayed milestone in childhood
R62.50	Unspecified lack of expected normal physiological development in childhood
R62.51	Failure to thrive (child)

Diagnosis Code	Description
R62.59	Other lack of expected normal physiological development in childhood
R89.8	Other abnormal findings in specimens from other organs, systems, and tissues
Z14.1	Cystic fibrosis carrier
Z14.8	Genetic carrier of other disease
Z36.0	Encounter for antenatal screening for chromosomal anomalies
Z37.1	Single stillbirth
Z37.3	Twins, one liveborn and one stillborn
Z37.4	Twins, both stillborn
Z37.60	Multiple births, unspecified, some liveborn
Z37.61	Triplets, some liveborn
Z37.62	Quadruplets, some liveborn
Z37.63	Quintuplets, some liveborn
Z37.64	Sextuplets, some liveborn
Z37.69	Other multiple births, some liveborn
Z37.7	Other multiple births, all stillborn
Z87.74	Personal history of (corrected) congenital malformations of heart and circulatory system

Description of Services

Genetic counseling is strongly recommended prior to chromosome microarray testing [also called chromosome microarray analysis (CMA)] in order to inform persons being tested about the advantages and limitations of the test as applied to their unique situation. CMA includes array comparative genomic hybridization (aCGH) and/or single-nucleotide polymorphism (SNP) array (Levy and Wapner, 2018).

Chromosome abnormalities are a well-established cause of congenital anomalies, dysmorphic features, Developmental Delay (DD), Intellectual Disability (ID), and other neurodevelopmental disorders. There are two types of CMA that are used for the detection of chromosomal abnormalities: aCGH and SNP array. These tests analyze multiple sequences of deoxyribonucleic acid (DNA) by identifying deletions and duplications across the genome simultaneously. The chromosomal microarray may be targeted in nature, assaying certain regions of the genome known to be associated with a specific syndrome or phenotype, and/or may be genome-wide (Shaffer et al., 2007). Currently, most clinical applications of CMA are being investigated for the diagnosis of chromosomal abnormalities in fetuses and newborns, and in children with developmental disorders. For diagnostic prenatal testing, CMA requires an invasive procedure (e.g., amniocentesis or chorionic villous sampling) to collect fetal cells.

SNP array testing and aCGH are used for the detection of genomic copy number variations (CNVs). CNVs are alterations that include deletion and/or duplication of one or more sections of DNA. This method allows the detection of chromosome imbalances that can provide more information than is detected by conventional chromosome analysis [e.g., standard karyotype or fluorescence hybridization (FISH)]. The aCGH approach detects CNVs of a DNA sequence in an individual by comparing it to a control. The SNP array approach detects CNVs by using DNA probes that are specific to a single base pair site in the genome. The copy number is quantified by either hybridization of the individual's DNA and control DNA (aCGH) or comparison of the individual's DNA to a control reference DNA sequence (SNP array). Areas of unequal hybridization (aCGH) or differences between an individual and reference DNA (SNP array) signify a DNA alteration, such as, large deletions or duplications. CNVs may be benign, with no effect on clinical phenotype, or may be pathogenic and result in a variety of phenotypic abnormalities (Kearney et al., 2011). If a CNV of unknown clinical significance is detected, a genomic database is used to determine if the abnormality has been previously reported and if it has been associated with a benign or proposed pathogenic condition. The disadvantages of CMA include the detection of variants of unknown clinical significance, false positive results that will require further testing and the inability to detect certain chromosomal abnormalities such as balanced rearrangements where there is no net gain or loss of the chromosomal material (Fruhman and Van den Veyver, 2010; Bui et al., 2011).

Clinical Evidence

Use in Obstetrics

Routine chromosome analysis has been used historically to identify chromosome abnormalities during pregnancy when risk factors are present, such as advanced maternal age and chromosome abnormalities. Chromosome microarray analysis (CMA) does not require cell culture or dividing cells, so it provides an advantage in turn-around time for time sensitive analysis, as is often the case during pregnancy. In addition, CMA can identify smaller chromosomal abnormalities than a routine chromosome analysis and is able to identify chromosomal breakpoints that are unbalanced but may appear balanced on a conventional karyotype. CMA does have limitations; it cannot detect totally balanced chromosomal material or low-level mosaicism. Some arrays may not detect triploidy. Clinicians may use CMA as a first line test, or only when fetal abnormalities are identified [Society for Maternal-Fetal Medicine (SMFM), 2016].

To examine diagnostic yields of genomic disorders and syndromic pathogenic copy number variants (pCNVs) associated with pregnancy loss and to approximate the risk of spontaneous abortion (SAB) by comparing the incidence of genomic disorders and syndromic pCNVs between products of conception (POC) and infants, Peng et al. (2023) performed a systematic review and meta-analysis of seven case series where CMA was used to test POC. Based on the meta-analysis of 35,130 results of cytogenomic tests on POC, the estimated diagnostic yields for chromosomal abnormalities and pCNVs were 49.9% (n = 17,548) and 2.5% (n = 957), respectively. After further refinement of pCNV categories, diagnostic yield was found to be 0.8% (n = 296) for genomic disorders and syndromic pCNVs, accounting for approximately 31% of the pCNVs detected overall. Two of the studies were noted to have lower yields of chromosome abnormalities and a higher yield of pCNVs; the authors speculate that this may have been due to the classification of larger terminal and interstitial imbalances, derivative chromosomes, and complex rearrangements into pCNVs. The overall incidence of genomic disorders and syndromic pCNVs in POC was collectively calculated to be 1/150. Newborn incidence was estimated from population genetic studies and a case series of 32,587 children with developmental delay where pCNVs were identified in 2312 individuals (Girirajan et al., 2012). When compared, newborn occurrence of ten genomic disorders and two syndromic pCNVs were significantly lower than that found in POC ($p < 0.05$). An additional five genomic disorders and two syndromic pCNVs were also found to have lower incidence in newborns than in POC, but the differences were statistically insignificant. Altogether, newborn incidence of genomic disorders and syndromic pCNVs was 1/540; substantially less than the corresponding findings of 1/150 in POC ($p < 0.05$). The authors calculated the overall risk of SAB for major genomic disorders and syndromic pCNVs to be 38%; this is significantly lower than the overall risk of SAB for chromosomal abnormalities (94%). They suggest that their results may assist with evidence-based interpretation of genomic disorders and syndromic pCNVs detected via CMA in prenatal diagnosis and provide better understanding of the relationship between genomic disorders and pCNVs and pregnancy loss. Noted limitations include study heterogeneity and gender bias for certain disorders, as well as the potential for impact to newborn incidence from certain genomic anomalies in specific ethnic groups. Additional large, population genetic studies across varying ethnic groups to better refine the evaluation of genomic disorders and syndromic pCNVs in newborns is recommended.

To more accurately assess the risk of chromosome anomalies in fetuses diagnosed with congenital heart disease (CHD), Wang et al. (2023) performed a meta-analysis of 4 prospective and 41 retrospectives studies including 16,484 fetuses with CHD. A secondary objective was the quantification of the prevalence of various chromosome abnormalities in fetuses with CHD. Results of the meta-analysis revealed a pooled proportion of 23% for overall chromosome abnormalities, 19% for aneuploidies, 2% for 22q11 deletion, and 4% for other CNVs. Of note, the rate of 2% for 22q11 microdeletions was significantly lower than the 4.2-9.6% rate found in other published studies (Hou et al., 2020, Hureaux et al., 2019, Maran et al., 2020). However, many of the incorporated studies did not include comprehensive outcomes and differing detection methods were used across studies, a limitation which may have led to an underestimation of the rate of 22q11 deletion. Pooled proportion of overall chromosome abnormalities in isolated CHD was 16% (95% CI 13%-20%) and in non-isolated CHD was 37% (95% CI 29%-44%), suggesting that fetuses with CHD along with other structural anomalies are at a higher risk of chromosome abnormalities. In addition, incidence of chromosome abnormalities was higher in septal defects than in conotruncal or other defects [odds ratio (OR) 1.60 and 3.61, respectively]. The authors indicate that their findings add to the evidence demonstrating relationships between CHD subtypes and chromosome abnormalities which will lead to improvements in genetic counseling and clinical decision-making. They recommend CMA for CHD if karyotyping for FISH is normal, especially in cases of non-isolated CHD and septal defects, where the incidence of chromosome abnormalities is higher. The heterogeneity of included studies was high, however, and interpretation processes were not described in most included studies, which limits the application of this meta-analysis. In addition, all but four of the studies were retrospective in design. Further large, high-quality, prospective studies focused on the specific pathogenicity of CNVs and variants of uncertain significance (VUS) in fetuses with diagnoses of CHD are recommended. Publication by Sagi-Dain et al. (2018), previously discussed in evidence, was included in this meta-analysis.

In a systematic review, meta-analysis, and case series, Mastromoro et al. (2022a) studied diagnostic yields of genetic testing in cases where increased nuchal translucency (NT) was identified and compared these with results found in fetuses where cystic hygroma was detected, aiming to identify the differing chromosomal, genomic, and monogenic conditions present in this phenotypic spectrum. In addition, a case series including dicentric fetal findings where karyotyping, CMA and RASopathy panel was performed was gathered. A cohort of 96 fetuses was evaluated. Fetuses with isolated NT of at least 2.5 mm were found to have karyotype anomalies in 22.76% of cases and an incremental detection rate of 2.35% was identified when CMA was used. Those fetuses having isolated NT ≥ 3 mm resulted in an aneuploidy in 14.36% of cases and an incremental detection rate of 3.89% with CMA. When isolated NT was ≥ 3.5 mm, diagnostic yield of the karyotype was 34.35% with an incremental detection rate for CMA of 4.1%. In this group, the RASopathy panel yielded an incremental diagnostic rate of 1.44% and exome sequencing yielded a 2.44% incremental detection rate. The most frequent finding across the group was karyotype abnormalities regardless of size of NT. CMA resulted in a substantial diagnostic yield in fetuses where NT was found to be at least 3.5mm. The researchers recommend ongoing research to determine the diagnostic rate of CMA at all levels of increased NT with focus on analysis of monogenic conditions where NT measures between 2.5 and 2.9 mm or 2.5 and 3.4 mm in addition to studies which help define the best diagnostic algorithm which may include exome sequencing. Study by Egloff et al. (2018), previously discussed in this policy, was included in the systematic review and meta-analysis described above.

Mastromoro et al. (2022b) also performed a systematic review and meta-analysis focused on the incremental diagnostic yield of CMA in isolated cardiovascular abnormalities in fetuses and calculation of specific yield based on each category of heart disease. The end goal was to provide insight for genetic counseling for each subgroup of cardiovascular anomaly. Additionally, a comparison to the existing literature was performed with a group of fetuses (n = 59) who were found to have isolated cardiovascular malformations but a normal karyotype. After application of exclusion criteria, 18 articles were included in the analysis. The researchers found that in pooled cardiovascular anomalies, the diagnostic incremental yield of CMA was 5.79%; this is higher than the average for structural abnormalities, which verifies the importance of this type of testing. In conotruncal malformations, detection rate was highest at 15.93% and yields for ventricular septal defects and aberrant right subclavian artery were lowest at 2.64% and 0.66%, respectively. The majority of heart conditions evaluated yielded a detection rate in the rage of 4.42% to 6.67%, which did not vary greatly from the overall rate for cardiopathic disease. The highest detection rate (11.28%) was found in tetralogy of Fallot (TOF) which is likely due to the relationship with 22q11.2 deletion syndrome. In the group with cardiac anomalies and normal karyotypes, the diagnostic yield was consistent with the existing literature. The authors assert that CMA used to assess the cause of fetal cardiovascular anomalies in the prenatal setting is a helpful tool; information regarding unique risks associated with each type of cardiac malformation is highly valuable when customizing genetic counseling. Publications by Hureaux et al. (2019), Fu et al. (2017), and Shaffer et al. (2012), previously discussed in this policy, were included in this systematic review.

In addition to the studies above, Mastromoro et al. (2022c) performed another systematic review of the literature and meta-analysis, this time focused on examining the diagnostic yield and rates of VUS in a group of fetuses who had undergone non-targeted molecular diagnostic testing including CMA, whole exome sequencing (WES) or whole genome sequencing (WGS) related to findings on ultrasound evaluation. The researchers aimed to provide additional insights into the primary molecular testing modalities used in prenatal diagnostics and their use as part of a multidisciplinary evaluation. For CMA, the overall diagnostic yield for mixed anomalies was 5.72%. This included 2.15% for single soft markers (such as transient minor ultrasound findings), 3.44% for multiple soft markers, 3.66% for single structural anomalies and 8.57% for multiple structural anomalies. WES demonstrated a high incremental yield, with diagnostic rate of 19.47% including 27.47% for multiple structural abnormalities. Variability was seen related to the characteristics of participants, class of malformations and number of samples available. VUSs found for fetuses with structural abnormalities were 2.86% for CMA and 8.32% for WES. Existing data was not able to be used for meta-analysis in WGS. The authors assert that for structural anomalies in fetuses, CMA is considered a first-tier test and should be used in conjunction with parental segregation and karyotyping. They recommend considering findings of increased NT, short femur and mild ventriculomegaly to be similar to malformations, separate from other soft markers, and an indication for performing assessment with CMA. They further note that WES presents a very high incremental yield and a substantial VUS rate; as such the use of WES is recommended for selected cases. Further research focused on which findings should truly be considered “soft” markers is recommended in order to further refine testing recommendations. Publications by Song et al. (2020), Xia et al. (2020), Hureaux et. al. (2019), Egloff et al. (2018), Sagi-Dain (2018), Wang et al. (2018), Peng et al. (2017), Papoulidis et al. (2015) and Shaffer et al. (2012), previously discussed in this policy, were included in this systematic review.

In an attempt to identify possible miscarriage-associated submicroscopic CNVs, target regions of large CNVs and recognize miscarriage candidate genes, Wang et al. (2020) analyzed 5180 POC samples by quantitative fluorescent-polymerase chain reaction (QF-PCR)/CNV-sequencing and CMA. Significant submicroscopic CNVs were determined by comparing the frequency of recurrent submicroscopic CNVs between cases and a published control cohort. Genes found within critical regions of miscarriage associated CNVs were prioritized by integrating Residual Variance Intolerance Score

and the human gene expression data for identification of possible miscarriage candidate genes. A total of 2955/5033 (59.1%) showed clinically significant chromosomal abnormalities. Three areas of recurring CNVs (microdeletions of 22q11.21, 2q37.3 and 9p24.3p24.2) were detected and considered to be associated with miscarriage. Forty-four critical regions of large CNV were noted which included 14 deletions and 30 duplications. A total of 209 genes were identified as possible miscarriage candidate genes.

Geffen et al. (2020) examined the prevalence of pathogenic and likely-pathogenic variants detected by CMA in pregnancies with ultrasound findings of fetal short, long bones. The cohort included 66 cases of CMA performed nationwide with the indication of short, long bones; 6% (n = 4) cases had pathogenic/likely pathogenic results. Chromosome anomaly rates were significantly increased compared to the background risk for CNV in pregnancies with no ultrasound abnormalities ($p < 0.001$). The authors reported that the yield of CMA in their study was significantly higher for both isolated and non-isolated cases, for cases in which the lowest determined bone length percentile was over the 3rd percentile (below 5th percentile) and for cases diagnosed with short bones after 22 weeks but not after 24 weeks. It was concluded by the authors that CMA should be offered in pregnancies with fetal short, long bone diagnosis due to the significantly higher likelihood of CMA yield compared to background risk in pregnancies with no ultrasound findings.

The University of California-San Francisco performed a retrospective study of prenatally diagnosed non-immune hydrops fetalis (NIHF) from 2008-2018. Mardy et al. (2020) reported on 131 cases which revealed 43/44 cases had CMA performed and results were categorized as normal or likely benign. One case had a large, pathogenic duplication. The authors stated that these results demonstrated the low diagnostic utility of CMA for NIHF.

Pasternak et al. (2020) analyzed the diagnostic yield of CMA among pregnancies terminated for fetal malformations detected on ultrasound. CMA was performed for 71 pregnancies using fetal or placental DNA. The authors reported that "findings were abnormal in 17 cases (23.9%), 13 of which were detectable by karyotype. The incremental yield of CMA was 4/71 (5.6%); 1/32 (3.1%) for cases with an isolated anomaly and 3/39 (7.7%) for cases with non-isolated anomalies."

A systematic review and meta-analysis was performed by Srebniak et al. (2017). In the initial analysis, 10,614 fetal CMA results were reviewed from ten large studies; 1/119 (0.84%) of cases referred for advanced maternal age (AMA) and/or anxiety revealed a clinically significant CNV (95% CI). A analysis of a subset including 8 of the initial ten studies (10,314 fetuses) demonstrated CNVs associated with early onset syndromes in 1/270 (0.37%) of pregnancies (95% CI). A total of 1/909 (0.11%) revealed late onset diseases, and CNV susceptibility was found in 1/333 (0.3%). By combining the individual risk for CNVs with individual risk for chromosome abnormalities detectable by karyotype, the author reported an overall risk of greater than 1/180 for a significant cytogenetic abnormality. Because women less than 36 years of age have a higher risk for CNV than for Down syndrome, the authors surmised that all women should be advised of these overall individual risks and not just of individual trisomic risks. Studies by Papoulidis et al. (2015) and Shaffer et al. (2012), previously discussed in this policy, were included in the 2017 Srebniak publication.

In a large cohort study, Maya et al. (2018) evaluated the frequency of penetrance of CNVs in low and high risk prenatal and postnatal samples. The cohort was grouped according to CMA indication with group I including low-risk, prenatal women as the control group; group II including high risk prenatal women with fetuses that had congenital malformations; and group III including post-natal individuals with a variety of genetic based conditions. Within this cohort, 21,594 CMAs were performed and the frequency of high penetrance CNVs was 0.1% in group I, 0.9% in group II, and 2.6% in group III. CNV frequency of moderate penetrance was 0.3%, 0.6%, and 1.2%, respectively, and these differences were statistically significant. The frequency of low-penetrance CNVs was not significantly different among groups: 0.6%, 0.9%, and 1.0%, respectively. The study concluded that high penetrance CNVs may be a factor in heritability of various anomalies, however low penetrance CNVs do not seem to contribute.

Pauta et al. (2017) performed a systemic review of the literature and meta-analysis to determine the utility of CMA by either aCGH or SNP-microarray, when compared to traditional karyotyping in early pregnancy loss. In 23 studies, 5520 pregnancy losses up to 20 weeks gestational age were reviewed. CMA provided informative results on 95% of cases compared to 67% with karyotyping, and CMA provided a 2% greater yield of pCNVs. The authors concluded that CMA resulted in diagnostic information in early pregnancy loss in significantly more cases when compared to conventional chromosome analysis.

Clinical Practice Guidelines

American College of Medical Genetics and Genomics (ACMG)

The 2018 ACMG clinical practice report on genetic testing after CMA for the diagnosis of neurodevelopmental disability and congenital anomalies (Waggoner et al.) states that "chromosomal microarray (CMA) is recommended as the first-tier test in evaluation of individuals with neurodevelopmental disability and congenital anomalies. CMA may not detect

balanced cytogenomic abnormalities or uniparental disomy (UPD), and deletion/duplications and regions of homozygosity may require additional testing to clarify the mechanism and inform accurate counseling."

ACMG (Cherry et al., 2017) published a practice resource guideline for laboratories for diagnostic testing following positive noninvasive prenatal screening (NIPS) recommending the following:

- CMA on CVS or amniocentesis may be used for confirmatory diagnosis for abnormal NIPS results or as a reflex to normal karyotype analysis.
- CMA testing should be utilized for follow-up when small copy number changes are reported as positive on NIPS.
- Testing of POC and/or fetus by karyotype or CMA should be considered on a case basis when prenatal diagnosis is not possible.
- For neonates with abnormal physical findings which are not suggestive of the trisomy suggested by original screening, CMA is recommended.
- CMA is recommended when NIPS sex determination is not concordant with physical examination or other clinical evidence reveals possible disorder of sexual differentiation.

American College of Obstetricians and Gynecologists (ACOG)/Society for Maternal Fetal Medicine (SMFM)

In a 2020 (reaffirmed 2021) Obstetric Care Consensus, ACOG and SMFM address microarray analysis as it relates to the management of stillbirth. Microarray analysis is noted to be the preferred method for evaluating stillbirth as it not only detects aneuploidy but correspondingly detects CNVs that are not measurable by karyotype. Microarray analysis is also more likely to offer a genetic diagnosis due to its success with nonviable tissue, making it particularly valuable in analysis of stillbirths with congenital anomalies or when karyotype outcomes cannot be obtained. The consensus document concludes that incorporating microarray analysis into stillbirth work up results in improvements in test success rates and detection of genetic anomalies compared with conventional testing with karyotype.

In a 2016 Committee Opinion on Microarrays and Next-Generation Sequencing Technology (ACOG, 2016a, reaffirmed 2023), ACOG and SMFM make the following recommendations for the use of chromosomal microarray analysis and newer genetic technologies in prenatal diagnosis:

- Most genetic changes identified by chromosomal microarray analysis that typically are not identified on standard karyotype are not associated with increasing maternal age; therefore, the use of this test can be considered for all women, regardless of age, who undergo prenatal diagnostic testing.
- Prenatal chromosomal microarray analysis is recommended for a patient with a fetus with one or more major structural abnormalities identified on ultrasonographic examination and who is undergoing invasive prenatal diagnosis. This test typically can replace the need for fetal karyotype.
- In a patient with a structurally normal fetus who is undergoing invasive prenatal diagnostic testing, either fetal karyotyping or a chromosomal microarray analysis can be performed.
- Chromosomal microarray analysis of fetal tissue (i.e., amniotic fluid, placenta, or POC) is recommended in the evaluation of intrauterine fetal death or stillbirth when further cytogenetic analysis is desired because of the test's increased likelihood of obtaining results and improved detection of causative abnormalities.
- Comprehensive patient pretest and posttest genetic counseling from an obstetrician-gynecologist or other health care provider with genetics expertise regarding the benefits, limitations, and results of chromosomal microarray analysis is essential. Chromosomal microarray analysis should not be ordered without informed consent, which should include discussion of the potential to identify findings of uncertain significance, non-paternity, consanguinity, and adult-onset disease.

In Practice Bulletin number 162 (ACOG, 2016b) which addresses prenatal diagnostic testing for genetic disorders, ACOG and SMFM recommend the following:

- CMA should be made available to any patient choosing to undergo invasive diagnostic testing (based on good/consistent scientific evidence: Level A).
- CMA should be the primary test (replacing conventional karyotype) for patients undergoing prenatal diagnosis for the indication of a fetal structural abnormality detected by ultrasound (based on good/consistent scientific evidence: Level A).
- Chromosomal microarray analysis may be used to confirm an abnormal FISH test (based on limited or inconsistent scientific evidence: Level B).

Society for Maternal-Fetal Medicine (SMFM)

SMFM Consult Series Number 52 (Martins, et al., 2020): Diagnosis and management of fetal growth restriction (FGR) recommends:

- Pregnant women should be offered fetal diagnostic testing, including CMA when FGR is detected and a fetal malformation, polyhydramnios, or both are present regardless of gestational age.
- Pregnant women should be offered prenatal diagnosis testing with CMA when unexplained isolated FGR is diagnosed < 32 weeks of gestation.

In an SMFM Consult Series publication (2016) on the use of CMA for prenatal diagnosis, SMFM makes the following recommendations:

- CMA should be offered when genetic analysis is performed in cases with fetal structural anomalies and/or stillbirth and replaces the need for fetal karyotype in these cases (GRADE 1A).
- Providers should discuss the benefits and limitations of CMA and conventional karyotype with patients who are considering amniocentesis and chorionic villus sampling (CVS) and that both options be available to women who choose to undergo diagnostic testing (GRADE 1B).
- The use of CMA is not recommended as a first-line test to evaluate first trimester pregnancy losses due to limited data (GRADE 1C).
- Pre- and post-test counseling should be performed by trained genetic counselors, geneticists, or other providers with expertise in the complexities of interpreting CMA results (Best practice).

Society of Obstetricians and Gynaecologists of Canada (SOGC)

In guideline number 442, the SOGC addressed the use of CMA in their recommendations regarding screening, diagnosis, and management of FGR in singleton pregnancies (Kingdom et al., 2023). The SOGC indicates that genetic consultation and amniocentesis with CMA of fetal DNA and molecular analysis for congenital infections should be offered to pregnant individuals with suspected early-onset FGR, especially if there is evidence of structural abnormalities, polyhydramnios, or multiple soft markers, when there is no indication of a placental basis for FGR. (Strong recommendation, high quality of evidence)

Society of Obstetricians and Gynaecologists of Canada (SOGC)/Canadian College of Medical Geneticists (CCMG)

A Joint Clinical Practice Guideline of the SOGC and CCMG recommended offering CMA in cases of multiple congenital anomalies revealed on ultrasound (II-1A) or fetal MRI. In addition, CMA was also recommended when single congenital defects in conjunction with other findings (e.g., IUGR, oligohydramnios) are detected. Prenatal CMA should be considered for certain malformations that have a high association with abnormal results. CMA is not recommended for pregnancies that are at low risk for a structural anomaly (Audibert et al., 2017).

- An SOGC/CCMG Practice Guideline for the use of CMA for prenatal diagnosis and assessment of fetal loss in Canada (Armour et al., 2018) recommends the following: Offering CMA following normal aneuploidy screen results when multiple fetal malformations are detected (II-1A) or NT ≥ 3.5MM (II-2B).
- Genetic counseling should be provided to obtain informed consent; parental decisions for reporting of incidental findings (II-2A); and for post-test results reporting counseling (III-A).
- CMA resolution should be similar to postnatal CMA panels for the detection of small pathogenic variants.
- VUS smaller than 500 Kb deletion or 1 Mb duplication should not be reported in prenatal setting.
- VUS above such cut-offs should only be reported if there is significant evidence that deletion or duplication or the region may be pathogenic (III-B).
- Secondary findings associated with significant childhood onset conditions should be reported; variants associated with adult-onset conditions should only be reported if previously requested by parents or if disclosure could prevent harm to family members (III-A).

Use in Pediatrics

In 2023, Hayes published a Clinical Utility Evaluation addressing the use of genetic testing in individuals with clinically diagnosed autism spectrum disorder (ASD) and their first-degree relatives. The report addresses several types of genetic testing that may be used for the diagnosis of ASD including CMA, which is the most common first-tier test used to help diagnose ASD (Hyman et al., 2020). In terms of clinical utility, Hayes found limited evidence from low-quality studies suggesting that genetic testing in individuals diagnosed with ASD may assist with medical management in some individuals, but no studies were found that included outcomes based on long-term follow-up or compared the outcomes of individuals who underwent genetic testing with a group of affected individuals who did not have the testing. Hayes concluded that the existing evidence is therefore insufficient to support clinical utility for use in those affected with ASD and their relatives.

Landis et al. (2023) evaluated the association of CHD diagnoses with abnormal CMA findings in a study of 1363 children with CHD from nine pediatric cardiac centers in the U.S. Each participant had both CHD (per abnormal findings on echocardiogram) and at least one abnormal clinical finding on CMA. Cardiac phenotypes were described in detail and analytically grouped according to their relationship with abnormal CMA results. Overall, 28% of the 1363 participants had genomic disorders with a well-known CHD association, 67% had clinical results indicating CNVs with rare/no prior CHD association, and 5% had areas of homozygosity without evidence of CNV. Both expected categories of CHD in genomic disorders, as well as those that were unexpected, were identified. Of the CNVs with rare/no prior association with CHD, submicroscopic CNVs included more complex types of CHD when compared with large CNVs. Through their analysis, the researchers identified potential new cardiogenomic associations, expanded CHD phenotypes in genomic disorders, detected new candidate genes, and stratified phenotypes associated with CHD based on gene/CNV size. They conclude that these findings may help to fill current gaps in the interpretation of CMA results for individuals with CHD, which may in turn lead to better clinical management.

In a comprehensive 2022 systematic review and meta-analysis, Sheidley et al. evaluated the diagnostic yield of genetic tests commonly used for individuals with epilepsy as well as other, non-yield outcomes, including such items as changes in treatment or management, recurrence risk determination, prognostic information, and genetic counseling. One hundred fifty-four articles describing diagnostic yield for 39,094 individuals were included. Of those, 43 were used for assessment of outcomes other than yield. Overall, the diagnostic yield for all test types was 17%. Genome sequencing had the highest yield at 48%, followed by exome sequencing at 24%. Multigene panels had a yield of 19% and CMA had the lowest yield at 9%. Phenotypic factors that were significantly associated with increased yield included presence of developmental and epileptic encephalopathy and/or the presence of comorbid neurodevelopmental conditions. The authors call out the need for prospective evaluation of clinical utility of commonly used genetic tests for epilepsy to help to standardize reporting of patient characteristics and help support clinician decision making. (Publications by Coppola et al. (2019), Berg et al. (2017) and d'Orsi et al (2017), previously discussed in this policy were included in the Sheidley (2022) systematic review and meta-analysis.

Miclea et al. (2022) sought to identify clinically relevant CNVs in children with a diagnosis of GDD/ID using CMA. The study included 189 Romanian children (3-18 years of age) who had been diagnosed with GDD/ID. The average age of participants was 11.17 years. A complete clinical evaluation was performed which included examination for dysmorphic and internal malformations, neuropsychological and psychiatric assessment, metabolic evaluation, standard karyotyping, and genomic testing using CMA. Individuals determined to have trisomy 21 as confirmed by karyotype were excluded. Pathogenic findings, [which included pCNVs and uniparental disomy (UPD)] and VUSs were found in 28% of participants. pCNVs/UPD were seen in 18.5% of the participants. UPD for chromosome 15 was found in two individuals, one of whom showed a clinical phenotype consistent with Prader-Willi syndrome and the other with clinical phenotype of Angleman syndrome. Recurrent CNVs were observed in 60% of participants. The authors concluded the high percentage of pathogenic structural variations found via CMA in children with GDD/ID lends support to the use of CMA in individuals with a non-specific phenotype.

Harris et al. (2020) reported on the diagnostic yield of genetic testing in toddlers with a Diagnostic and Statistical Manual of Mental Disorders, Fifth Edition diagnosis of ASD. A retrospective chart review including 500 toddlers with ASD was conducted; genetic testing results were divided into normal and negative results, VUS, and pathogenic. 59.8% (n = 299) of subjects completed genetic testing and 12.0% (n = 36) had pathogenic results. No significant differences in Bayley Scales of Infant Development cognitive (p = .112), language (p = .898), or motor scores (p = .488) among toddlers with negative or normal findings compared to a variant of unknown significance versus pathogenic findings were reported. Medical recommendations following the genetic findings were made in 72.2% of those with pathogenic results. The authors concluded that these results confirm the importance of genetic testing in toddlers diagnosed with ASD due to the 12% yield and lack of phenotypic differences between subjects with and without pathogenic findings.

Jang et al. (2019) studied the impact of CMA analysis on patient management by conducting a multicenter, prospective study in Korea on patients with DD/ID, ASD, and multiple congenital anomalies (MCA). G-banding karyotype and CMA were both performed simultaneously on 617 patients in an attempt to determine if results affect treatment recommendations. 122/617 (19.8%) had abnormal CMA findings; 65 were pathogenic and 57 were variants of possible significance. Thirty-five known disorders were detected with the most common being 16p11.2 microdeletion, followed by 15q11-q13 duplication, Down syndrome, and Duchenne muscular dystrophy. VUS were seen in 51 (8.3%) of patients. CMA test results influenced clinical management decisions including imaging studies, referrals to specialists, and laboratory testing recommendations in 71.4% of those tested. Clinical management was also impacted in 86%, 83.3%, 75% and 67.3% of patients that had variants of possible significance, pathogenic variants, VOUS, and benign variants, respectively. More than 1,500 new medical management protocols were recommended based on the CMA results with an average of 2.9 new recommendations per patient. The final conclusion by the authors was that CMA as a first-tier test improves diagnostic yields and the overall quality of clinical management in patients with DD/ID, ASD, and MCA.

A pediatric CMA study was performed to identify recurrent pCNVs in patients with idiopathic short stature (Homma et al., 2018). The study researchers selected 229 children that did not have a well-recognized syndrome but had short stature and dysmorphic features, DD, and/or ID. CMA was used for evaluation of the patients and the study targeted pCNVs that were associated with short stature. In the 229 patients, 32 pathogenic or likely pathogenic CNVs were identified. The study also reviewed the literature and selected additional cohorts of patients with short stature to create a larger cohort of 671 patients. In total, CNVs were identified in 87 (13%) of patients with seven recurrent CNVs (22q11.21, 15q26, 1p36.33, Xp22.33, 17p13.3, 1q21.1, 2q24.2) that were identified as responsible for 40% of all genomic imbalances in this population. The authors recommend additional investigation of the role of novel candidate genes identified by CMA testing that may be involved in growth disorders.

Sys et al. (2018) evaluated CMA as a diagnostic tool for patients with ASD with a variety of clinical characteristics. The researchers stated that this tool may be restricted to patients that had specific characteristics or comorbidities. A retrospective review of the files of 311 children diagnosed with ASD was performed and the following clinical characteristics were captured: ID, major congenital anomalies, epilepsy, prematurity, familial history of ASD, electroencephalography, and brain MRI findings. Next, the results of any genetic analyses were evaluated in conjunction with the clinical data. CMA had been performed in 79 patients and was normal in 55 (group 1) and abnormal in 23 (group 2). There was no significant difference between the two groups regarding the presence of clinical characteristics. Additionally, the researchers determined that the diagnostic yield of CMA (8.9%) was higher than karyotyping (1.6%) and other genetic tests (3.8%).

Hussein et al. (2018) studied the role of CMA for diagnosis of CHDs in neonates. The researchers investigated 94 patients with CHDs that were associated with DD or other malformations. They used a high-density array-CGH 2 x 400K for 41 patients and CGH/SNP microarray 2 x 400k for 53 patients. In certain cases, confirmation was performed using Fluorescent in situ hybridization or qPCR. In 21 of 94 patients (22%) using both conventional cytogenetics and CMA, abnormalities were detected in trisomy 18, 13, 21, microdeletions: del22q11.2, del7q11.23, del18 (p11.32; p11.21), tetrasomy 18p, trisomy 9p, del11q24-q25, add 15p, add (18) (q21.3), and der 9, 15 (q34.2; q11.2). In 15 of 73 cases (20.5%), cryptic chromosomal abnormalities and pathogenic variants were detected. CMA was able to detect loss of heterozygosity in chromosomes in 10 of 25 patients. Cryptic chromosomal anomalies and pathogenic variants were detected in 15/73 (20.5%) cases.

Fan et al. (2018) performed a retrospective review of CMA results from a Chinese population with DD/ID in order to determine genotypes, diagnostic yields, and phenotypes among a diverse group with varying manifestations. A total of 710 patients were evaluated and 247 CNV were reported in 201 patients (28%). The authors reported that the diagnostic yields were significantly higher with co-existing congenital heart defects (CHD 55%), facial dysmorphism (39%), microcephaly (34%) or hypotonia (35%). Co-existing skeletal malformations (26%), brain malformations (24%) or epilepsy (24%) did not affect the diagnostic yield. ID severity correlated positively with CMA (mild: 19%, moderate: 22, severe: 33%); however, the correlation was not statistically significant ($p = 0.08$). Coexistence of CHD was the strongest phenotype associated with CNV (OR 5.52). The presence of facial dysmorphism with CHD increased the diagnostic yield to 62% (OR 10.81). The results showed that diagnostic yields vary based on phenotypic presentation. CHD, microcephaly, hypotonia and facial dysmorphism co-existing with DD/ID are associated with an increased likelihood of CNVs.

McCormack et al. (2016) examined the utility of aCGH to replace karyotype in 5369 pre- and post-natal patients with an unexplained phenotype. In this cohort, 28% of those tested had a deletion or duplication. Ninety-seven percent of cases with a CNV that was less than five kilobases in size would not have been detected by routine chromosome analysis. Eight hundred forty-two (15.7%) had a variant of unknown significance. About 5% of the cohort met the criteria for a known syndrome. Using microarray as a primary analysis tool significantly increased the detection of CNV abnormalities, with one syndromic case identified per 20 referrals.

Clinical Practice Guidelines

American Academy of Pediatrics (AAP)

The AAP National Coordinating Center for Epilepsy (2022) states that “the genetic tests most commonly used in the evaluation of children with epilepsy include CMA, epilepsy gene panels and whole-exome sequencing.” Individual test type have specific benefits and limitations, and the utility of various tests may be different depending on individual circumstances. Decisions regarding testing may be influenced by factors including symptoms, turn-around time, insurance coverage, and cost. Due to the complex nature of genetic testing and potential implications it may have (e.g., impact on eligibility for life insurance, reproductive decisions, medical decisions), incorporating genetic counseling is encouraged.

A clinical report addressing the identification of infants/children with DD (Lipkin & Macias, 2020) recommends that children with suspected GDD or ID have genetic testing including chromosomal microarray and fragile-X testing. In addition, the preliminary genetic work-up of children with suspected ASD should also include chromosomal microarray and fragile-X testing.

In 2020, the AAP (Hyman et al.) published a clinical report addressing the identification, evaluation, and management of children with ASD. The report indicates that in the last ten years the development of CMA and other technologies has led to evolution and understanding of the multifaceted genetics of ASD. The identification of genetic etiology provides clinicians additional evidence for families about the prognosis and recurring risk which contributes to identifying, treating, and avoiding co-occurring medical situations. Additionally, the genetic etiology identification permits clinicians the information to guide patients and families to disorder specific resources and supports and avoid the collection of unnecessary tests. CMA recognizes CNVs, therefore it is the suggested testing if the etiology for developmental disability is unknown. The development of CMA and next-generation sequencing have given rise to identification of large-effect rare variants, including CNVs, that may be related to ASD.

In a 2014 clinical report, the Committee on Genetics for AAP stated that CMA is designated as a first-line test and replaces the standard karyotype and FISH subtelomere tests for the child with ID of unknown etiology. The authors recommend that CMA should be performed in all children with ID or GDDs (Moeschler and Shevell, 2014, reaffirmed 2019).

American Academy of Neurology (AAN)

In a model coverage policy for chromosomal microarray analysis for ID, the AAN recommends the following inclusion criteria for microarray testing:

- In children with DD/ID or ASD according to accepted Diagnostic and Statistical Manual of Mental Disorders-IV criteria.
- If warranted by the clinical situation, biochemical testing for metabolic diseases has been performed and is negative.
- Targeted genetic testing, (for example: FMR1 gene analysis for Fragile X), if or when indicated by the clinical and family history, is negative.
- The results for the testing have the potential to impact the clinical management of the patient.
- Face-to-face genetic counseling with an appropriately trained and experienced healthcare professional has been provided to the patient (or legal guardian(s) if a minor child). Patient or legal guardians have given their consent for testing. Cognitively competent adolescent patients have given their assent for testing as well.

The AAN model coverage policy states that the following circumstances limit the value of microarray testing:

- Absence of an appropriate and informed consent from the patient, a parent (in case of minors) or a guardian (in persons with cognitive impairment) is necessary prior to testing.
- Inadequacy of knowledge about the test and the actions required to address the results of the test.
- A lack of clear value for chromosomal microarray analysis in all instances other than those delineated above. Under these circumstances the test is considered investigational.
- Chromosomal microarray analysis would not be considered medically necessary when a diagnosis of a disorder or syndrome is readily apparent based on clinical evaluation alone.

The AAN model coverage policy further indicates the presence of major and minor congenital malformations and dysmorphic features should be considered evidence that microarray testing will be more likely to yield a diagnosis. However, dysmorphic and syndromic features are not required for testing (AAN, 2015).

American Academy of Child and Adolescent Psychiatry (AACAP)

In a 2020 Practice Parameter, the American Academy of Child and Adolescent Psychiatry (Siegel et al.) presented a diagnostic genetic testing algorithm for youth with developmental disorders including ASD, ID, or GDD, indicating that if there is a recognized genetic syndrome (e.g., Fragile X syndrome, PTEN hamartoma syndrome, Rett syndrome, tuberous sclerosis, Prader-Willi syndrome, Angelman syndrome, Down syndrome) after genetic counseling, specific and targeted testing for that syndrome is recommended first. If this testing does not yield a diagnosis, CMA and Fragile X testing are indicated. If findings remain unrevealing, additional testing including WES, karyotyping or mitochondrial DNA testing may be considered. The group states that “microarray is currently the genetic test with the highest diagnostic yield in children with unexplained ID/IDD, with an abnormal result reported in 7.8% of subjects with GDD/ID/IDD and in 10.6% of those with syndromic features, on average.”

American College of Medical Genetics and Genomics (ACMG)

In a 2021 revision to the technical standard of the ACMG, Shao et al. state that chromosomal microarray technologies are well accepted and used in evaluation of both constitutional and neoplastic disorders. For chromosomal imbalances related to multiple congenital anomalies, autism, and/or ID, CMA (including both array CGH and single nucleotide polymorphism array) is considered the first-tier test. In the case of individuals where ultrasound has identified major fetal structural abnormalities and invasive prenatal diagnostic testing will be performed, chromosome microarray is the recommended test. This is also true for further workup of intrauterine fetal demise or stillbirth when parents/providers make the decision to pursue potential genetic diagnosis.

The 2013 ACMG guideline for identifying the etiology of ASD lists chromosomal microarray testing (array CGH or SNP array) as a first-tier diagnostic test for the evaluation of ASDs. According to the ACMG, many recognizable syndromes (i.e., Fragile X syndrome, Rett syndrome) have a firmly documented association with ASDs. For these conditions, further investigation into the etiology of the ASD is unnecessary (Schaefer & Mendelsohn, 2013).

The ACMG published a resource that focused on when CGH should be used. The specific recommendations listed in the 2010 guideline are as follows (Manning and Hudgins, 2010, reaffirmed 2020):

- Cytogenetic microarray (CMA) testing for CNV is recommended as a first-line test in the initial postnatal evaluation of individuals with the following:
  - Multiple anomalies not specific to a well-delineated genetic syndrome
  - Apparently non-syndromic DD/ID
  - ASD
- Further determination of the use of CMA testing for the evaluation of the child with growth retardation, speech delay, and other less-well studied indications is recommended, particularly via prospective studies and aftermarket analysis.
- Appropriate follow up is recommended in cases of chromosome imbalance identified by CMA, to include cytogenetic/FISH studies of the patient, parental evaluation, and clinical genetic evaluation and counseling.

This guideline did not address testing for prenatal gene mutations. These guidelines also do not specify what type of microarray platform should be used (i.e., microarray based CGH versus SNP microarray), although they do state that any ordering physician should be aware of the information generated and the limitations of the particular test performed.

ACMG Practice Guidelines regarding the interpretation and reporting of microarray results in postnatal clinical settings were published in 2011 and include recommendations regarding how to define the various types of CNVs (pathogenic versus benign versus uncertain significance), the confirmation of abnormal results, the information that should be included in laboratory reports, and how to handle unanticipated or ambiguous results. Of importance, it is noted that if a CMA is identified that has unknown clinical significance, the parents of the proband should be tested to determine if the CNV is de novo or inherited, which may allow the clinician to determine the clinical significance of the result (Kearney et al., 2011).

Canadian College of Medical Genetics (CCMG)

In a 2023 position statement, the CCMG recommends CMA as a first-tier test for individuals with GDD, ID or ASD. Fragile X testing is advised when family history or clinical symptoms are suggestive of this disorder. Further recommendations include the use of WES or comprehensive gene panels as second-tier testing for individuals with GDD/ID. The CCMG does not recommend genetic tests for individuals with neurodevelopmental disorders when GDD, ID or ASD is not present, unless the phenotype is suggestive of a syndromic etiology or an inherited metabolic disease (Carter et al., 2023).

International Standards for Cytogenomic Array (ISCA) Consortium

The ISCA reviewed the literature and meta-analyses on the clinical indications and diagnostic utility of chromosomal microarray testing and issued a consensus statement recommending that CMA be the first-tier clinical diagnostic test for individuals with developmental disabilities or congenital anomalies, followed by specific gene testing for the suspected condition(s) if CMA results are negative (Miller et al., 2010).

U.S. Food and Drug Administration (FDA)

This section is to be used for informational purposes only. FDA approval alone is not a basis for coverage.

Genetic tests are regulated under the Clinical Laboratory Improvement Amendments (CLIA) of 1988. Refer to the following website for more information: http://www.fda.gov/MedicalDevices/DeviceRegulationandGuidance/IVDRegulatoryAssistance/ucm124105.htm. (Accessed February 7, 2024)

Refer to the following website for a list of nucleic acid-based tests/platforms that have been cleared or approved by the FDA's Center for Devices and Radiological Heath: https://www.fda.gov/medical-devices/in-vitro-diagnostics/nucleic-acid-based-tests. (Accessed March 20, 2024)

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Policy History/Revision Information

Date	Summary of Changes

12/01/2024	**Applicable Codes**
	• Updated list of applicable ICD-10 diagnosis codes to reflect annual edits:
	  ○ Added Q23.81, Q23.82, Q23.88, and Q87.86
	  ○ Removed Q23.8
	Supporting Information
	• Archived previous policy version CSNCT0559.06

Instructions for Use

This Medical Policy provides assistance in interpreting UnitedHealthcare standard benefit plans. When deciding coverage, the federal, state or contractual requirements for benefit plan coverage must be referenced as the terms of the federal, state or contractual requirements for benefit plan coverage may differ from the standard benefit plan. In the event of a conflict, the federal, state or contractual requirements for benefit plan coverage govern. Before using this policy, please check the federal, state or contractual requirements for benefit plan coverage. UnitedHealthcare reserves the right to modify its Policies and Guidelines as necessary. This Medical Policy is provided for informational purposes. It does not constitute medical advice.

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