Medical Coverage Policy

Array Comparative Genomic Hybridization (aCGH) for the Genetic Evaluation of Patients with Developmental Delay/Mental Retardation or Autism Spectrum Disorder - PREAUTH

Prospective review is recommended/required. Please check the member agreement for preauthorization guidelines.

Prospective review is not required.

Description:
Chromosomal microarray (CMA) testing has been proposed for detection of genetic imbalances in infants or children with characteristics of developmental delay/intellectual disability or autism spectrum disorder. G-banded karyotyping has for many years been the standard first-line test for this purpose. G-banded karyotyping allows visualization and analysis of chromosomes for chromosomal rearrangements including genomic gains and losses. CMA analysis performs a similar, although non-visual, analysis at a much higher resolution. As a result, CMA has the potential to increase the diagnostic yield in this population and change clinical interpretation in some cases.

Children with signs of neurodevelopmental delays or disorders in the first few years of life may eventually be diagnosed with intellectual disability or autism syndromes, serious and lifelong conditions that present significant challenges to families and to public health. Cases of developmental delay/intellectual disability (DD/ID) and of autism spectrum disorder (ASD) may be associated with genetic abnormalities. For children with clear, clinical symptoms and/or physiologic evidence of syndromic neurodevelopmental disorders, diagnoses are based primarily on clinical history and physical examination, and then may be confirmed with targeted genetic testing of specific genes associated with the diagnosed syndrome. However, for children who do not present with an obvious syndrome, who are too young for full expression of a suspected syndrome, or who may have an atypical presentation, genetic testing may be used as a basis for establishing a diagnosis.

Current guidelines for these patients, such as those published by the American Academy of Pediatrics (AAP) and the American Academy of Neurology (AAN), recommend cytogenetic evaluation to look for certain kinds of chromosomal abnormalities that may be causally related to their condition. The AAN guidelines note that only in occasional cases will an etiologic diagnosis lead to specific therapy that improves outcomes, but suggest the more immediate and general clinical benefits of achieving a specific genetic diagnosis from the clinical viewpoint, as follows:

- limit additional diagnostic testing;
- anticipate and manage associated medical and behavioral comorbidities;
- improve understanding of treatment and prognosis; and
allow counseling regarding risk of recurrence in future offspring and help with reproductive planning.

AAP and AAN guidelines also emphasize the importance of early diagnosis and intervention in an attempt to ameliorate or improve behavioral and cognitive outcomes over time.

Most commonly, genetic abnormalities associated with neurodevelopmental disorders are deletions and duplications of large segments of genomic material, which are called “copy number variants,” or CNVs. For many well-described syndromes, the type and location of the chromosomal abnormality has been established with the study of a large number of cases and constitutes a genetic diagnosis; for others, only a small number of patients with similar abnormalities may exist to support a genotype-phenotype correlation.

Finally, for some patients, cytogenetic analysis will discover entirely new chromosomal abnormalities that will require additional study to determine their clinical significance.

Conventional methods of cytogenetic analysis, including karyotyping (e.g., G-banded) and fluorescence in situ hybridization (FISH), have relatively low resolution and a low diagnostic yield (i.e., proportion of tested patients with clinically relevant genomic abnormalities), leaving the majority of cases without identification of a chromosomal abnormality associated with the child’s condition. CMA Analysis is a newer cytogenetic analysis method that increases the chromosomal resolution for detection of CNVs, and, as a result, increases the genomic detail beyond that of conventional methods and may increase the diagnostic yield. CMA results are clinically informative in the same way as results derived from conventional methods, and thus aCGH represents an extension of standard methods with increased resolution. Array CGH is often ordered when conventional results are negative, although some believe it will soon replace conventional technology.

CMA analysis to determine genetic etiology
CMA analysis detects CNVs by comparing a reference genomic sequence (“normal”) with the corresponding patient sequence. Each sample has a different fluorescent label so that they can be distinguished, and both are co-hybridized to a sample of a specific reference (also normal) DNA fragment of known genomic locus. If the patient sequence is missing part of the normal sequence (deletion) or has the normal sequence plus additional genomic material within that genomic location (e.g., a duplication of the same sequence), the sequence imbalance is detected as a difference in fluorescence intensity. For this reason, standard CMA (non-SNP, see following) cannot detect balanced CNVs (equal exchange of material between chromosomes) or sequence inversions (same sequence is present in reverse base pair order) because the fluorescence intensity would not change.

CMA analysis uses thousands of cloned or synthesized DNA fragments of known genomic locus immobilized on a glass slide (microarray) to conduct thousands of comparative reactions at the same time. The prepared sample and control DNA are hybridized to the fragments on the slide, and CNVs are determined by computer analysis of the array patterns and intensities of the hybridization signals. Array resolution is limited only by the average size of the fragment used and by the chromosomal distance between loci represented by the reference DNA fragments on the slide.

There are some differences in CMA technology, most notably in the various types of microarrays. They can differ first by construction; earliest versions were used of DNA fragments cloned from bacterial artificial chromosomes (BAC). These have been largely replaced by oligonucleotide (oligos; short, synthesized DNA) arrays, which offer better reproducibility. Finally, arrays that detect hundreds of thousands of single nucleotide polymorphisms (SNP) across the genome have some advantages as well. Oligo/SNP hybrid arrays have been constructed to merge the advantages of each. Regardless of the array components used, all microarrays allow the deposition of many thousands of short, DNA probe sequences on a small, solid surface in an orderly fashion. The location of each known probe sequence allows the identification of the test sequence bound to it, and when compared to a control sequence, the identification of missing sequences or sequences with extra copies (i.e. copy number variants).
Microarrays may be prepared by the laboratory utilizing the technology, or, more commonly by commercial manufacturers, and sold to laboratories who must qualify and validate the product for use in their assay, in conjunction with computerized software for interpretation. The proliferation of in-house developed and commercially available platforms prompted the American College of Medical Genetics (ACMG) to publish guidelines for the design and performance expectations for clinical microarrays and associated software in the post-natal setting. (2)

Targeted CMA analysis provides high-resolution coverage of the genome primarily in areas containing known, clinically significant CNVs. The ACMG guideline for designing microarrays recommends probe enrichment in clinically significant areas of the genome to maximize detection of known abnormalities, but also recommends against the use of targeted arrays in the post-natal setting. Rather, a broad genomic screen is recommended to identify atypical, complex, or completely new rearrangements, and to accurately delineate breakpoints.

Whole-genome CMA analysis has allowed the characterization of several new genetic syndromes, with other potential candidates currently under study. However, the whole-genome arrays also have the disadvantage of potentially high numbers of apparent false-positive results, because benign CNVs are found in phenotypically normal populations; both benign and pathogenic CNVs are continuously cataloged and to some extent made available in public reference databases to aid in clinical interpretation. Additionally, some new CNVs are neither known to be benign nor causal; these CNVs may require detailed family history and family genetic testing to determine clinical significance, and/or may require confirmation by subsequent accumulation of similar cases and so, for a time, may be considered a CNV of undetermined significance (some may eventually be confirmed true positives or causal, others false positives or benign).

To determine clinical relevance (consistent association with a disease) of CNV findings, the following actions are taken:

- CNVs are confirmed by another method (e.g., FISH, MLPA, PCR).
- CNVs detected are checked against public databases and, if available, against private databases maintained by the laboratory. Known pathogenic CNVs associated with the same or similar phenotype as the patient are assumed to explain the etiology of the case; known benign CNVs are assumed to be nonpathogenic.
- A pathogenic etiology is additionally supported when a CNV includes a gene known to cause the phenotype when inactivated (microdeletion) or overexpressed (microduplication).
- The laboratory may establish a size cutoff; potentially pathogenic CNVs are likely to be larger than benign polymorphic CNVs; cutoffs for CNVs not previously reported typically range from 300 kb to 1 Mb.
- Parental studies are indicated when CNVs of appropriate size are detected and not found in available databases; CNVs inherited from a clinically normal parent are assumed to be benign polymorphisms whereas those appearing de novo are likely pathogenic; etiology may become more certain as other similar cases accrue.

ACMG has also published guidelines for the interpretation and reporting of CNVs in the post-natal setting, in order to promote consistency among laboratories and CMA results. (10) Three categories of clinical significance are recommended for reporting: pathogenic, benign, and uncertain clinical significance.

Definitions:

As defined by the American College of Medical Genetics Guideline, Evaluation of the Newborn with Single or Multiple Congenital Anomalies:

- A malformation refers to abnormal structural development.
- A major malformation is a structural defect that has a significant effect on function or social acceptability. Examples: ventricular septal defect or a cleft lip.
- A minor malformation is a structural abnormality that has minimal effect on function or societal acceptance. Examples: preauricular ear pit or partial syndactyly (fusion) of the second and third toes.
A syndrome is a recognizable pattern of multiple malformations. Syndrome diagnoses are often relatively straightforward and common enough to be clinically recognized without specialized testing. Examples include Down syndrome, neural tube defects and achondroplasia. However, in the very young, or in the case of syndromes with variable presentation, confident identification may be difficult without additional testing.

The following healthcare professionals may provide genetic counseling:

- certified genetic counselors;
- medical geneticists;
- pediatric neurologists; or
- developmental pediatricians.

In some cases of CMA analysis, the laboratory performing the test confirms all reported CNVs with an alternative technology such as fluorescence in situ hybridization (FISH) analysis.

**Medical Criteria:**

**Preauthorization is required for Blue CHiP for Medicare and recommended for all other BCBSRI products.**

Chromosomal microarray analysis may be considered medically necessary for diagnosing a genetic abnormality in children with apparent nonsyndromic cognitive developmental delay/intellectual disability (DD/ID) or autism spectrum disorder (ASD) according to accepted Diagnostic and Statistical Manual of Mental Disorders-IV criteria when all of the following conditions are met:

- Any indicated biochemical tests for metabolic disease have been performed, and results are non-diagnostic, and
- \textit{FMR1} gene analysis (for Fragile X), when clinically indicated, is negative, and
- In addition to a diagnosis of nonsyndromic DD/ID or ASD, the child has one or more of the following:
  - two or more major malformations, or
  - a single major malformation or multiple minor malformations, in an infant or child who is also small-for-dates, or
  - a single major malformation and multiple minor malformations, and
- The results for the genetic testing have the potential to impact the clinical management of the patient, and
- Testing is requested after the parent(s) have been engaged in face-to-face genetic counseling with a healthcare professional who has appropriate genetics training and experience.

CMA analysis is considered not medically necessary in all other cases of suspected genetic abnormality in children with developmental delay/intellectual disability or autism spectrum disorder.

In some cases of CMA analysis, the laboratory performing the test confirms all reported CNVs with an alternative technology such as fluorescence in situ hybridization (FISH) analysis. Chromosomal microarray analysis to confirm the diagnosis of a disorder or syndrome that is routinely diagnosed based on clinical evaluation alone is not medically necessary.

In recognition of the limitations and disadvantages of CMA in the prenatal setting, the American Congress of Obstetricians and Gynecologists published a Committee Opinion in November, 2009, recommending against CMA as a replacement for classic cytogenetics.\(^1\) CMA is considered not medically necessary for prenatal genetic testing as there is insufficient peer-reviewed scientific literature to demonstrate its efficacy.

**Policy:**

Chromosomal microarray analysis is considered medically necessary when the medical criteria above is met and is considered not medically necessary for all other indications.
Coverage:
Benefits may vary between groups/contracts. Please refer to the appropriate Evidence of Coverage, Subscriber Agreement, or Benefit Booklet for applicable benefits/coverage.

Coding:
The following test requires preauthorization:
S3870

NOTE: S3870 is the correct code for chromosomal microarray analysis and must be used. Use of a CPT code in it's place would be considered incorrect coding.

Also Known As:
Not applicable

Related Topics:
Not applicable

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References:


Schaefer GB, Mendelsohn NJ. Clinical genetics evaluation in identifying the etiology of autism spectrum disorders. American College of Medical Genetics;2008(4);10(4);301-305.


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