Chromosomal Microarray

What is CMA?



Chromosomal Microarray (CMA) can detect the most known cytogenetic disease among the existing genetic tests. It can identify Chromosomal Abnormalities that cause developmental disabilities, mental retardation, autism, and multiple congenital malformations that could not be detected using previous techniques such as Karyotyping.



American Academy of Pediatrics

Several famous groups (ACMG, AAP)guideline recommend CMA as the first genetic test to order for a patient with autism, developmental delay, intellectual disabillity and/or multiple congenital anomalies.

 Accurate and comprehensive analysis of chromosomal abnormalities
 Can lead to direct diagnosis of chromosomal disease. Accurate location, size, and genetic information of chromosomal abnormalities · Genetic Counseling required by family members

According to ACMG guideline,

CMA is recommended as a 1st-tier test for developmental disorders, mental retardation, autism, multiple congenital malformations due to small size of DNA deletion/duplication which cannot be detected by conventional karyotyping test.

Manning, M., & Hudgins, L. (2010, November). Array-based technology and recommendations for utilization in medical genetics practice for detection of chromosomal abnormalities. Genetics in Medicine, 12(11), 742–745. https://doi.org/10.1097/gim.0b013e3181f8baad

What can we know from CMA?



Normal diploid genome

- Aneuploidy
- CNV (Copy Number Variation): Deletion, Duplication
- Unbalanced translocation
- LOH (Loss of Heterozygosity): LOH is only reported when the size is sufficiently suspicious for UPD (Uniparental Disomy).
- Mosaicism: Low level mosaicism may not be detected.

Chromosomal **Microarray**

How is it different from Karyotyping?

	Karyotyping	СМА
Resolution	Low (5~10Mb)	High (25~400kb)
Cell cultured	Required	Not required
Diagnosis rate	2~3%	15~20%
Target diseases	Down syndrome, Edward syndrome, Patau syndrome	Development disorders, Mental retardation, Autism, Multiple congenital anomalies etc.
Diagnosis example	Detect numerical or structural changes $\begin{array}{c} \begin{array}{c} \begin{array}{c} \begin{array}{c} \end{array}\\ \end{array}\\ \end{array}\\ \begin{array}{c} \end{array}\\ \end{array}\\ \begin{array}{c} \end{array}\\ \end{array}\\ \begin{array}{c} \end{array}\\ \end{array}\\ \begin{array}{c} \end{array}\\ \begin{array}{c} \end{array}\\ \end{array}\\ \begin{array}{c} \end{array}\\ \begin{array}{c} \end{array}\\ \end{array}\\ \begin{array}{c} \end{array}\\ \begin{array}{c} \end{array}\\ \begin{array}{c} \end{array}\\ \end{array}\\ \begin{array}{c} \end{array}\\ \end{array}$ \begin{array}{c} \end{array}\\ \begin{array}{c} \end{array}\\ \begin{array}{c} \end{array}\\ \end{array} \begin{array}{c} \end{array}\\ \begin{array}{c} \end{array} \begin{array}{c} \end{array}\\ \begin{array}{c} \end{array}\\ \end{array} \begin{array}{c} \end{array} \begin{array}{c} \end{array} \begin{array}{c} \end{array} \begin{array}{c} \end{array} \begin{array}{c} \end{array} \begin{array}{c} \end{array} \end{array} \begin{array}{c} \end{array} \end{array} \begin{array}{c} \end{array}	Observe the microscopic duplication or deletion of chromosomes at higher resolution
Analytical time	Long for cell culture	Fast

CMA can detect small-sized chromosomes that are difficult to identify through conventional karyotyping, allowing for the detection of microdeletion/duplication of the copy number variation (CNV).

It enables precise identification of the exact location of mutations, leading to more accurate predictions of the severity of genetic disorder using software for objective result analysis.

Service features				
Test	Chromosomal Microarray (CMA)	Code	OM001	
Specimen	EDTA WB 3 ml	ТАТ	9 days	
Method	Microarray	Sample Storage	Room temperature (Refrigerated is recommended.)	
Test description	This test can detect copy number variation (CNV) (deletion >25kb, duplication >50kb) and loss of heterozygosity (LOH) (>3Mb) across the entire genome. It reports all CNVs of >400kb and clinically significant CNVs of any size. Also, LOH is also considered to be reported when associated with clinically significant situations such as uniparental disomy (UPD) or consanguinity.			
Caution & Limitation	 Low levels of mosaicism, balanced translocation, inversion, and point mutations cannot be detected. If the LOH area is small or is a heterodisomic UPD, UPD may not be detected on the test principle. Undetectable CNV area: 13p, 14p, 15p, 21p, 22p, Yq11.23, Yq12 and pericentric heterochromatin regions of all chromosomes 			



GCGenome Cell Center Bldg 1F, 107, Ihyeon-ro 30beon-gil, Giheung-gu, Yongin-si, Gyeonggi-do, Republic of Korea (16924) Online : www.gc-genome.com | Contact : +82) 31-280-9910

