

## Mini Review

# Chromosomal Microarray Analysis in Prenatal Diagnosis Platform

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## Introduction

Genome copy number variation (CNV) (deletion/duplication) is widely distributed in the whole human genome [1]. It is closely connected with the emergence of new technologies, including high resolution methods of microarray and next-generation sequencing. Obviously, large-scale structural changes profoundly influence genetic variation. By various molecular mechanisms, including gene dosage, gene disruption, gene fusion, and position effects, CNVs can cause Mendelian or sporadic traits, or be associated with complex diseases [2, 3]. It is also clear that many gene copy number variations produce deleterious phenotypic consequences. Particularly, de novo gene copy number variation is one of the important causes of genetic and developmental disorders including severe mental disabilities, autism, schizophrenia and heart defects and is frequently found in cancer cells [2, 4-6].

## CNV Detection Method

In the past 40 years, chromosome analysis using G banding has been considered the gold standard for detection of chromosomal abnormalities. However, this method is time-consuming, requires cell culture, has limited resolution, and is not sufficient for the detection of less than 5 MB of chromosomal abnormalities. To further identify changes less than 5 MB in size, a combination of genetics and molecular biology methods was developed. FISH (fluorescence in situ hybridisation technique) and MLPA (multiplex ligation-dependent probe amplification) can detect chromosome imbalances smaller than 1 MB, but these techniques can only be used in the limited area of chromosomal abnormalities, and the pre-test must be expected for the detection of disease and targeted. In prenatal diagnosis, CMA (chromosomal microarray analysis) can detect genome level abnormalities, and no cell culture is required, thus shortening the time that patients await results that can be used for the detection of foetal death or stillbirth. Additionally, CMA is a standardised process that utilises computer analysis, whereas karyotyping requires

## Abstract

Genome copy number variation is an important cause of genetic and developmental disorders. In recent years, chromosomal microarray analysis technology to test for genomic copy number variation has been developed and gradually applied in prenatal diagnostics, offering high diagnostic ability. Here, we summarise the chromosomal microarray analysis testing platform established in clinical settings, as well as the significance and clinical application of the standard analyses. We also emphatically discuss the key problems in the establishment process of the platform in prenatal diagnostics in the clinic.

**Keywords:** Genome copy number variation; Chromosomal microarray analysis; Prenatal diagnosis; Detection platform

microscopic examination of chromosomes after staining. Karyotype analysis may be more subjective and prone to human error.

CMA technology, also known as molecular karyotype analysis technique (molecular karyotyping), is based on microarray genome copy number analysis technologies including comparative genomic hybridisation array (aCGH) technology and single nucleotide polymorphism microarray (SNP array) technology. CMA can detect unbalanced chromosome CNV at the whole genome level and can be used to identify chromosomal abnormalities, including those that are too small to detect by conventional karyotype analysis tiny chromosomal abnormalities. The probe design, the original data acquisition, the data analysis algorithms and other factors are the key causes to inconsistent results, and the CMA detection technology in clinical diagnostics using quality requirements are presented here along with the corresponding goals [7].

## CMA Clinical Application of the Status Quo

CMA is currently the most effective tool to evaluate copy number abnormalities, which are abnormalities due to large spanning length CNVs that can contain a part of a gene or genes and can span multiple genes [8, 9]. CMA can detect the total number of nucleotides in the genome more effectively than single nucleotide polymorphisms (SNP) [10-13]. CNV formation occurs by both recombination-based and replication-based mechanisms, and de novo locus-specific mutation rates are much higher for CNVs than for SNPs. The locus-specific mutation rates for CNVs have been observed to be ~100 to 10,000 times higher than those for nucleotide substitution rates [2, 14]. Additionally, postpartum data from multiple centres indicated that the overall risk of not diagnosing a micro deletion or micro duplication syndrome associated with a CNV is higher than for chromosomal or single gene disease, thus contributing to a relatively high risk of mental retardation and abnormal growth and development [12, 15-17].

Over the past 10 years, the efficiency of CMA has been widely recognised. CMA improves the detection level of known diseases as well as syndromes that are caused or associated with unknown chromosomal micro-deletions/duplications, promoting the diagnostic accuracy in clinical settings. When CMA was first implemented as a clinical application, many scholars suspected that CMA would likely replace the existing cytogenetic analysis method. However, CMA can only detect abnormal genome copy number changes relative to a reference genome, but does not enable the detection of balanced translocations, inversions, or inverted insertions, low levels of mosaicism, gene rearrangements or point mutations. Furthermore, CNVs in the human genome contribute to both Mendelian and complex traits, as well as to genomic plasticity in evolution, and especially to common and complex diseases [18]. Therefore, CMA, as well as other techniques, would be important in our clinical platform for the detection of various diseases caused by genomic rearrangement. In addition, a recent study showed that non-invasive prenatal testing (NIPT) using microarray analysis delivered a more accurate cell-free DNA (cfDNA) analysis than next-generation sequencing (NGS), and can be performed in less time [19].

## The Establishment of the CMA Testing Platform

Prenatal CMA requires professional genetic counselling before and after the test results are presented to the patients, so that the patients are aware of the benefits and limitations of the testing such that they can independently make choices regarding their pregnancy based on a full understanding of the benefits, limitations, and the results of CMA testing [10, 15, 20, 21]. Based on data from multiple prenatal diagnosis centres, it is apparent that variant of unknown significance (VOUS) is inevitably best as an antenatal examination, although it is not difficult to understand the status quo from the aspects of the complexity of human genome diversity and restructuring. However, this undoubtedly increases the complexity of clinical genetic counselling, and represents the main limitation of CMA in the clinical application of prenatal diagnosis [13, 22]. Through continuous accumulation of experience, test results can be increasingly clearly identified as benign or pathological. However, in prenatal diagnosis, due to the instability of expression and incomplete penetrance, many test results remain poorly understood [13]. The comparison between the large sample size case group and the control group can establish each CNV pathogenic spectrum, allowing for the minimisation of VOUS, it is only a matter of time before VOUS is mediated [23]. Furthermore, the satisfaction of patient genetic counselling is associated with the experience of genetic counsellors with CMA, the high enthusiasm genetic counsellors for CMA and additional CMA professional training [24, 25].

Assessing the clinical relevance of copy number variation, as a clinical test, should follow compliance-based medicine (Evidence-based medicine, EBM) rules; that is, that medical decisions should be based on the best scientific evidence attainable [17, 26]. The sources of evidence, including clinical case reports, case series, and case-control analyses, among others, should be added to and supplemented by a public database that can be shared, such as DECIPHER, DGVs, ISCA, OMIM et al [27-29]. However, these data should be used with caution and common sense: the quality of these databases, inconsistent

reference populations, poor annotation of genomic and phenotypic data, a lack of data curation, and inconsistent descriptions of the phenotype variation all may affect the effective application and clinical interpretation of the CMA results [30]. In addition to the testing results of different technical platforms for the inconsistencies in probe design, original data acquisition and data analysis algorithms can lead to inconsistent results, and use of CMA technology for clinical diagnostics requires corresponding quality requirements [7]. However, most of these problems will be solved in line with the development of concern regarding them [31-33].

In summary, CMA testing technology is of realistic significance in clinical practice and can be applied to large patient cohorts. The diagnostic implementation of NGS technologies creates new possibilities for the simultaneous testing of single nucleotide variations (SNVs), indels and CNVs [34]. Once CNV detection is combined with the detection of other types of genomic variation using whole exome and genome sequencing, these technologies will further improve. While identification of all genomic variation in a single experiment is on the horizon, effective and confident clinical interpretation of the extensive quantity and variety of data information will remain a considerable challenge.

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