# Genomic Testing for Diagnosis of Genetic Disorders in Children: Chromosomal Microarray and Next–Generation Sequencing

**Dhanya Lakshmi Narayanan and Katta Mohan Girisha**

*From Department of Medical Genetics, Kasturba Medical College, Manipal, India.*

*Correspondence to: Dr Girisha KM, Professor, Department of Medical Genetics, Kasturba Medical College, Manipal Academy of Higher Education, Manipal 576 104, India. girish.katta@manipal.edu*

Chromosomal microarray and Next-generation sequencing are two widely used genomic tests that have improved the diagnosis of children with a genetic condition. Chromosomal microarray has become a first-tier test in evaluating children with intellectual disability, multiple malformations and autism due to its higher yield and resolution. Next generation sequencing, that includes targeted panel testing, exome sequencing and whole genome sequencing ends diagnostic odyssey in 25-30% of unselected children with rare monogenic syndromes, especially when the condition is genetically heterogeneous. This article provides a review of these genomic tests for pediatricians.

**Keywords:** *Chromosomal disorders, Exome sequencing, Whole genome sequencing.*

Genomic testing refers to the analysis of human DNA to detect disease-causing variations. These variations could be chromosomal abnormalities or single gene defects (monogenic or Mendelian disorders). Chromosomal abnormalities can be numerical (aneuploidy) or structural, which include loss or gain of a large part of one or more chromosomes, translocations, inversions and insertions. Loss or gain of smaller regions of a chromosome, known as copy number variations (CNV), usually involve more than one gene and are implicated in many human diseases [1]. While chromosomal aneuploidies are traditionally detected by karyotyping, chromosomal microarray analysis (CMA) is now widely used to detect chromosomal abnormalities. Next generation sequencing (NGS), which includes targeted panel testing, exome sequencing (ES) and whole genome sequencing (WGS), has emerged as the most powerful tool for diagnosis of monogenic disorders, which are mostly caused by sequence variations in the coding portion of the DNA. With technological advances, cost of these tests has decreased drastically and they have become widely available. This review discusses the techniques, clinical utility, advantages and limitations of CMA and NGS.

## CHROMOSOMAL MICROARRAY

CMA, otherwise known as genomic microarray, enables the study of chromosomes at a higher resolution as compared to traditional karyotyping. It has replaced karyotyping as the first-tier investigation of children with intellectual disability, multiple malformations and autism [2,3].

### Principle

CMA is based on complementary hybridization of nucleotides in the probe and target DNA. Probes are oligonucleotides, varying in length from 25 to 70 bp, which are immobilized on a glass slide or a chip (array) [4-7]. They are spread across the genome at regular intervals (form the 'backbone' and defines the resolution of CMA) and are usually enriched for regions of clinical interest. They are designed to detect CNVs or single nucleotide polymorphisms (SNPs) or both. A CNV is a segment of DNA, which is 1kb or more, and has a variable copy number (extra or less) compared to reference genome [8]. SNPs are the most common genetic variations found in a population across the human genome. Genotyping of millions of SNPs across the genome provides information on alleles and their copy numbers, in addition to mosaicism, uniparental disomy, triploidy and regions of homozygosity. The different types of oligo array platforms include comparative genomic hybridization arrays (array CGH) and SNP arrays (***Fig.*** **1a** and **1b**). Most commercially available platforms are hybrid arrays and contain oligonucleotide probes for detecting both CNVs and SNPs. Array design can be targeted (for specific regions of interest), whole genome (evaluates entire genome) or a combination of whole genome and targeted (most commercially available platforms).

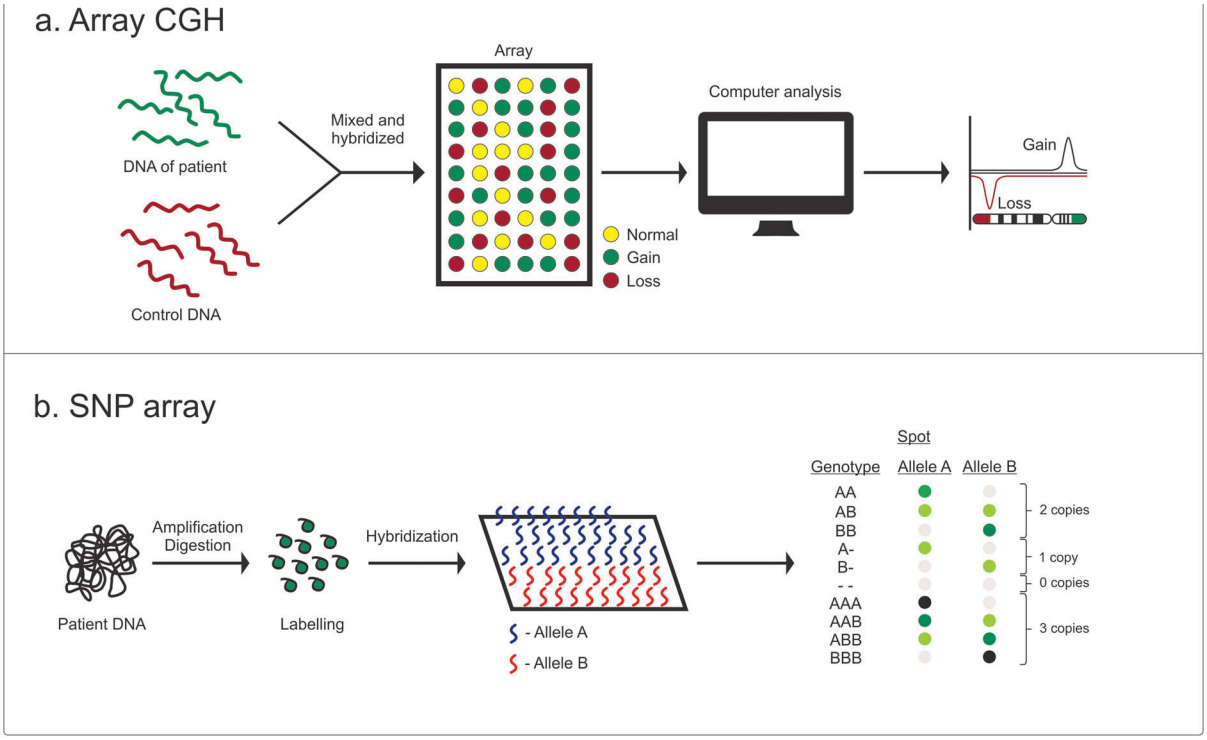



**Fig. 1** *(a) Comparative genomic hybridization array, and (b) Single nucleotide polymorphism array.*

## Interpretation

The variants identified are critically evaluated based on their size, gene content and published reports in literature [9,10]. Penetrance (how many of individuals with this variant have a phenotypic effect) and variable expressivity (varying severity of disease in individuals with a particular genotype) are considered. The databases used for CNV interpretation are given in ***Web Table* I**. The CNVs are classified into pathogenic, benign or variant of uncertain significance (VOUS) based on American College of Medical Genetics and Genomics (ACMG) criteria given in ***Table* I**. VOUS are variants, which are not directly linked to the patient's phenotype but have some evidence for causation. Usually laboratories using SNP arrays report variants above 50 to 100kb in size [11]. Testing of parents may be required to ascertain the significance of the variant.

CMA has the highest diagnostic yield for any single test in evaluating cognitive impairment, developmental delay, multiple malformations of unknown etiology or autistic spectrum disorder [2,12]. It is the first line investigation for antenatally detected structural abnormalities, stillbirth or intrauterine demise [13], and when a karyotype shows a marker chromosome or extra chromosome material of unknown origin. CMA can identify gain or loss of chromosomal material in up to 20% of individuals with an apparently balanced chromosome translocation [14,15]. ***Box* I** enumerates the advantages and disadvantages of CMA as compared to karyotyping.

One should know the design and resolution of the testing platform and the genomic regions covered. Most of the commercial platforms available have probes for known microdeletion/ duplication syndromes along with genome wide probes for other clinically significant CNVs. In a clinical setting, a low-resolution array, covering all well-delineated microdeletion and microduplication syndromes is usually sufficient. High-resolution arrays are more accurate in delineation of CNVs and SNPs, but result in a large number of variants, which are difficult to interpret. Its utility is limited to the research context. Both pretest counseling (for the yield, specific benefits and limitations) and post-test counseling are also essential.

## NEXT-GENERATION SEQUENCING

NGS, also known as massively parallel sequencing or deep sequencing, is a high throughput sequencing technology which allows simultaneous sequencing of millions of DNA base pairs at a comparatively lower cost and higher speed. Exomes comprise only 1% of 6.2 billion base pairs in human DNA, which code for proteins [16].

**Table I Classification of Copy Number Variants (CNVs) Based on American College of Medical Genetics and Genomics criteria [9]**

| *Type of CNVs* | *Criteria* |
|---|---|
| *Pathogenic* | |
| | • CNVs associated with a known microdeletion/duplication syndrome |
| | • CNVs reported as clinically significant in peer-reviewed journals and public databases |
| | • CNVs that are more than 3-5Mb size and are cytogenetically visible |
| *Uncertain clinical significance* | |
| Likely pathogenic | |
| | • CNVs reported in a single case report, but with breakpoints and phenotype correlating to the patient's features |
| | • CNV interval has a gene whose function is relevant to the clinical features of the patient |
| No sub-classification | |
| | • CNVs described in multiple peer-reviewed journals with no conclusive evidence regarding clinical significance. |
| | • CNV interval has genes but it is not known whether the genes are dosage sensitive |
| Likely benign | |
| | • CNVs are seen in small number of people in databases of variations in normal individuals |
| | • No gene in the CNV interval; but it is included because of the size cut off set by the laboratory |
| *Benign* | |
| | • CNVs reported as benign variants in multiple peer- reviewed publications or curated databases |
| | • CNVs whose benign nature has been characterized |
| | • CNVs represents a common polymorphism and has a population frequency of more than 1% |

**Box I Advantages and Limitations of Chromosomal Microarray over Karyotyping**

Advantages

- CMA can be done from DNA isolated from any type of tissue unlike karyotyping which requires live, actively dividing cells.
- Higher resolution: CMA detects CNVs as small as 10 to 20 kb [9], unlike karyotype for which the resolution is 5 Mb.
- Objective result interpretation
- Can detect cryptic imbalances in chromosomes in apparently balanced karyotype.

Limitations

- Does not detect balanced translocations that do not alter the CNVs.
- Inability to detect point mutations, deletions or duplications at the single gene level.
- Does not detect low-level mosaicism and polyploidy.
- Missing of variations in regions that are not targeted by the probes in targeted arrays.
- Difficulty interpretation of VOUS.

*CNV* : *Copy number variant*; VOUS: *Variants of unknown significance*.

NGS can analyze the whole genome (whole genomic sequencing, WGS), exome (exome sequencing, ES) or a targeted region of interest in the human genome (targeted gene panel testing). The features of WGS, ES and targeted sequencing are summarized in ***Table* II.** The steps involved are illustrated in ***Web Fig.* I**. Depth of sequencing is the number of times a nucleotide is read during sequencing. A depth of 20x implies that a particular variant or nucleotide is sequenced 20 times. Coverage usually refers to the fraction of the target region of interest sequenced satisfactorily (usually at least 20 times or 20x).

**Interpretation**

The variants are sorted to narrow down to a single variant that is likely to explain the disease or phenotype. As monogenic diseases are rare, it is assumed that the disease-causing variant is usually not seen in genomes of healthy individuals in the population. Disease-causing variants are likely to result in a change in quantity or quality of the protein coded by the gene, thus affecting the function of the protein. They are also likely to be conserved across different species. Several computational tools are now available to predict the effect of a change in the nucleotide sequence of a gene. The sorting (also popularly called filtering) is also aided by published databases of normal variants and disease-causing variants (***Web Table* II**). If in-house databases with frequency of variants in a particular population are available, they can be very powerful tools for variant analysis as we expect unique genetic variations in different ethnicities. In 2015, ACMG published

**Table II Characteristics of NGS Based Tests**

| *NGS platform* | *Regions covered* | *Advantages* | *Disadvantages* |
|---|---|---|---|
| Targeted gene panel | Genes of interest (usually associated with the same phenotype/ disease) | Can cover the regions of interest with increased depth. When the genes of interest are less in number, targeted panel testing is less expensive than exome or genome testing. | Will not be able to identify new genes responsible for a phenotype. Gene panels get outdated as new genes are discovered for the same phenotype. |
| Exome sequencing (also called whole exome sequencing') | Exons and flanking intronic regions of all genes | Covers entire coding region (exome) New genes responsible for a phenotype may be identified | Coverage is less compared to targeted panel. Does not cover non-coding portions of genome well, unless specific modifications are done. Secondary findings (in other genes, not relevant for the disease in question) may be identified. |
| Whole genome sequencing | Entire coding and non-coding regions in human genome | Coverage of coding regions is better than exome sequencing as this technique avoids 'capture' step of exome sequencing. Covers non-coding regions of the genome | Expensive currently. Secondary findings may be identified. |

guidelines for interpretation of sequence variants and categorized them into five categories, i.e., pathogenic, likely pathogenic, benign, likely benign and VOUS [17]. The results are then correlated with clinical features and communicated to the patient. For efficient filtering and clinical interpretation of the variants, a patient should be referred to a trained clinical geneticist.

NGS testing generates a large number of variants in an individual's exome or genome. Clues from evaluation of pedigree, clinical examination and routine medical tests are vital to determine the effect of the variant on the phenotype. Often Human Phenotype Ontology [HPO] terms are used for this purpose. NGS should not be considered as an alternative for thorough clinical examination and ancillary laboratory tests.

**Clinical Indications**

- Targeted panel testing can be done when a particular phenotype is caused by variations in more than one gene (locus heterogeneity). For example, variations in about 20 different genes are implicated in osteogenesis imperfecta. A panel, which covers all the genes for osteogenesis imperfecta is more efficient than Sanger sequencing one gene after the other. Other examples are deafness, Noonan syndrome (RASopathies), congenital myopathy and pediatric epilepsy. Large genes like dystrophin can be tested by NGS either singly or in a panel for muscular dystrophy or myopathy when deletion and duplications are ruled out by multiplex ligation dependent probe amplification (MLPA) in a child with Duchenne muscular dystrophy.
- ES can be performed in patients with genetically heterogenous monogenic disorders when targeted panel testing fails.
- WGS may be considered when ES fails to identify a disease-causing variant. It detects variants in coding and non-coding regions of the genome and regions not well captured and sequenced in ES, CNVs and structural chromosomal abnormalities. It has the potential to become a single test replacing most of the current tests.
- NGS-based tests hold promise in area of carrier testing, pre-symptomatic testing, pharmacogenetic testing, and predictive testing, which are beyond the scope of this review.

Even though genome sequencing and exome sequencing are described as 'whole' genome or 'whole' exome sequencing, they do not evaluate all the genes in the human genome. The word 'whole' distinguishes these tests from panel testing and should not mislead clinicians and patients to believe that these tests would be 100%

sensitive to detect all the disease-causing variants. The coverage of known genes by these tests vary from 85%-92% [18]. 'Clinical exome' or 'focused exome' is a commercial panel test that uses a customized capture kit to interrogate only genes associated with a known clinical phenotype, usually listed in Online Mendelian Inheritance in Man (OMIM). Hence the term 'clinical exome' is better avoided. In strict sense, 'clinical' genome or exome sequencing implies sequencing of exome or genome for clinical applications [19]. Before ordering a test, it is essential to check the coverage of genes of interest. The decision whether to order a targeted panel test or ES or WGS will depend on the clinical features of a patient and the ability of a clinician to arrive at a diagnosis. An ideal targeted panel test should be able to diagnose disease-causing variants in the genes of interest of the suspected genetic disorder and should also include methods to detect deletion and duplications, which can cause a specific disease phenotype. Analyzing only selected regions or genes of interest may not qualify to be called a targeted panel, unless the laboratory fills the gaps in sequencing by alternate methods like Sanger sequencing and does a deletion/ duplication analysis. For example, in a child with leukodystrophy, before ordering a targeted panel test for leukodystrophy, it is essential to check whether all the genes of interest are covered. Krabbe disease is often caused by deletions in GALC gene and might be missed if an NGS test is ordered without asking for deletion/duplication analysis of GALC gene. If a specific genetic diagnosis cannot be made, ES or WGS may be considered. ES is cheaper and is often preferred to WGS as the first investigation for undiagnosed single gene diseases, which mostly result from variations in exons. A singleton or single exome means exome sequencing of a proband, whereas 'trio' exome means exome sequencing of the proband and parents.

### Consent and Counseling in NGS Tests

Informed consent is essential before NGS based testing. Pretest counseling is essential to explain the yield, utility and implications of a 'negative' or 'positive' report for family. Limitations of science in interpreting VOUS and identification of secondary variants are specific issues in NGS testing. Secondary variants in genes are associated with diseases unrelated to the proband's condition and are common in ES and WGS. Secondary findings in genes causing cancer and sudden cardiac death may have implications for the patient and family members. A genetic diagnosis may not have any direct impact on the treatment of the patient but may aid in long-term management, genetic counseling and prenatal diagnosis. Post-test counseling by a geneticist is thus needed. Sanger sequencing is done to validate the variant in the proband and for segregation analysis. Good quality NGS often obviates the need for Sanger confirmation. Segregation analysis determines segregation of the variants in the other affected or unaffected members in the family and is crucial for causal association in the proband. If a negative test result is obtained, the family should be counseled about the need to re-evaluate the data at a later date.

At present there are no regulations governing clinicians, laboratories and counselors in India. Direct marketing of these tests may result unregulated commercialization.

### Variables to Consider in NGS Report

The NGS report mentions the methodology, capture kit, depth and coverage of sequencing. Capture kits may be customized for different panel tests and ES. It is important to check for depth and coverage of sequencing before conveying the report to the patient.

Some clinical scenarios where CMA and NGS have aided in diagnosis are described in ***Web Table*** **III.**

## CONCLUSIONS

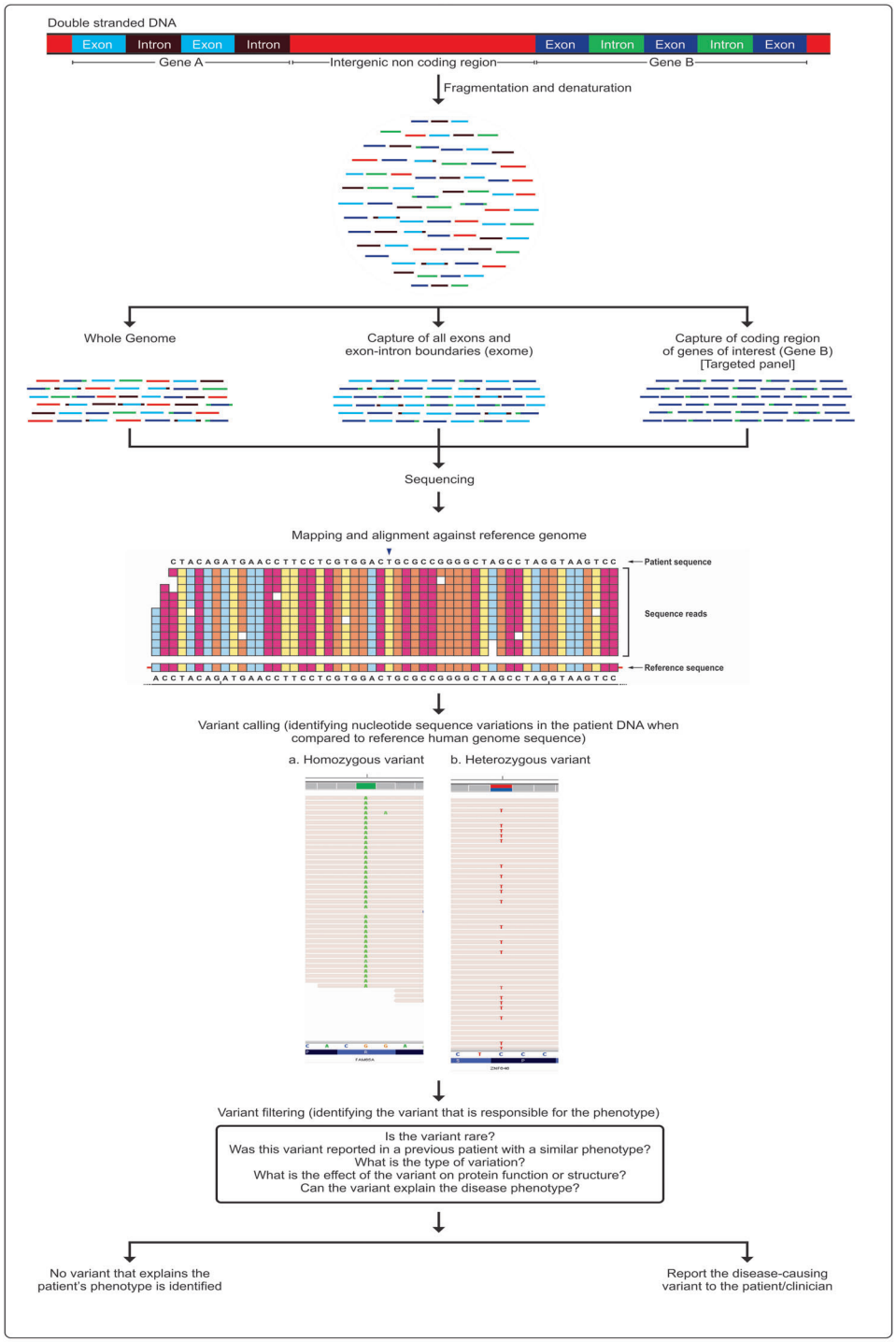
Chromosomal microarray, exome sequencing and whole genome sequencing using NGS techniques are powerful methods to investigate variations in human genome. It is essential for a pediatrician to know the strengths, limitations and advantages of these testing methods over traditional medical tests to apply optimally in clinical practice of pediatrics.

*Contributors:* DLN: substantial contributions to design and draft of the work; GKM: substantial contributions to the conception and design of the work, drafting and revising it critically for important intellectual content. Both approve the final version to be published and agree to be accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved.
*Funding:* None; *Competing interest:* None stated.

## REFERENCES

1. Bernardini L, Alesi V, Loddo S, Novelli A, Bottillo I, Battaglia A, *et al.* High-resolution SNP arrays in mental retardation diagnostics: How much do we gain? Eur J Hum Genet. 2010;18:178-85.
2. Manning M, Hudgins L. Array-based technology and recommendations for utilization in medical genetics practice for detection of chromosomal abnormalities. Genet Med. 2010;12:742-5.
3. Miller DT, Adam MP, Aradhya S, Biesecker LG, Brothman AR, Carter NP, *et al*. Consensus Statement: Chromosomal Microarray is a First-tier Clinical diagnostic Test for Individuals With Developmental Disabilities or

Congenital Aanomalies. Am J Hum Genet. 2010;86: 749-64.
4. Snijders AM, Nowak N, Segraves R, Blackwood S, Brown N, Conroy J, *et al.* Assembly of microarrays for genome-wide measurement of DNA copy number. Nat Genet. 2001;29:263-4.
5. Beaudet AL. The utility of chromosomal microarray analysis in developmental and behavioral pediatrics. Child Dev. 2013;84:121-32.
6. Oostlander AE, Meijer GA, Ylstra B. Microarray-based comparative genomic hybridization and its applications in human genetics. Clin Genet. 2004;66:488-95.
7. LaFramboise T. Single nucleotide polymorphism arrays: A decade of biological, computational and technological advances. Nucleic Acids Res. 2009;37:4181-93.
8. Feuk L, Carson AR, Scherer SW. Structural variation in the human genome. Nat Rev Genet. 2006;7:85-97.
9. Kearney HM, Thorland EC, Brown KK, Quintero-Rivera F, South ST. American College of Medical Genetics Standards and Guidelines for Interpretation and Reporting of Postnatal Constitutional Copy Number Variants. Genet Med. 2011;13:680-5.
10. South ST, Lee C, Lamb AN, Higgins AW, Kearney HM. ACMG Standards and Guidelines for Constitutional Cytogenomic Microarray Analysis, Including Postnatal and Prenatal applications: Revision 2013. Genet Med. 2013;15:901-9.
11. Levy B, Wapner R. Prenatal diagnosis by chromosomal microarray analysis. Fertil Steril. 2018;109:201-12.
12. Rauch A, Hoyer J, Guth S, Zweier C, Kraus C, Becker C, *et al.* Diagnostic yield of various genetic approaches in patients with unexplained developmental delay or mental retardation. Am J Med Genet A. 2006;140:2063-74.
13. Karampetsou E, Morrogh D, Chitty L. Microarray technology for the diagnosis of fetal chromosomal aberrations: Which platform should we use? J Clin Med. 2014;3:663-78.
14. Edelmann L, Hirschhorn K. Clinical utility of array CGH for the detection of chromosomal imbalances associated with mental retardation and multiple congenital anomalies. Ann NY Acad Sci. 2009;1151:157-66.
15. Sismani C, Kitsiou-Tzeli S, Ioannides M, Christodoulou C, Anastasiadou V, Stylianidou G, *et al.* Cryptic genomic imbalances in patients with de novo or familial apparently balanced translocations and abnormal phenotype. Mol Cytogenet. 2008;1:15.
16. Thiffault I, Lantos J. The challenge of analyzing the results of next-generation sequencing in children. Pediatrics. 2016;137:S3-7.
17. Richards S, Aziz N, Bale S, Bick D, Das S, Gastier-Foster J, *et al.* Standards and Guidelines for the Interpretation of Sequence Variants: A Joint Consensus Recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. Genet Med. 2015;17:405-24.
18. Biesecker LG, Biesecker BB. An approach to pediatric exome and genome sequencing. Curr Opin Pediatr. 2014;26:639-45.
19. Biesecker LG, Green RC. Diagnostic clinical genome and exome sequencing. N Engl J Med. 2014;371:1170.
20. Schwarze K, Buchanan J, Taylor JC, Wordsworth S. Are whole-exome and whole-genome sequencing approaches cost-effective? A systematic review of the literature. Genet Med. 2018;20:1122-30.
21. Yang Y, Muzny DM, Reid JG, Bainbridge MN, Willis A, Ward PA, *et al.* Clinical whole-exome sequencing for the diagnosis of mendelian disorders. N Engl J Med. 2013;369:1502-11.




**Web Fig. I** *Steps in NGS: Double stranded DNA is fragmented into smaller segments and denatured. In whole genome sequencing, all these fragments (exons, introns, non-coding intergenic segments) are sequenced. In exome sequencing, capture kits that selectively capture the exome (all exons and flanking introns) are used and those fragments are sequenced. In a targeted panel, capture kits that selectively capture the coding portion of the genes of interest are used (in this example, capture kit for Gene B). Once sequencing is done, mapping and alignment of reads against a reference genome is done. The next step is variant calling, which detects variants in the subject against the reference sequence. A homozygous variant is seen as a change in almost all reads whereas a heterozygous change is seen in nearly half of the total number of reads. The final step is variant filtering, interpretation and reporting. From a list of variants, pathogenic and benign variants are identified by several filtering approaches.*

**Web Table I Popular Databases used in Interpretation of Copy Number Variants**

| *Database* | *Key features* |
|---|---|
| DECIPHER (DatabasE of genomiC varIation and Phenotype in Humans using Ensembl Resources) *https://decipher.sanger.ac.uk* | Interactive web based free browser where the patient's variant is displayed along with normal and pathogenic variants in that locus |
| DGV (Database of Genomic Variants) *http://dgv.tcag.ca/dgv/app/home* | Database of common structural variations in healthy individuals |
| ISCA (International Standards for Cytogenomic Arrays) *http://dbsearch.clinicalgenome.org/search/* | Database of pathogenic, likely pathogenic, uncertain, likely benign, and benign CNVs |

*Other databases include UCSC genome browser (University of California, Santa Cruz), ECARUCA (European Cytogeneticists Association Register of Unbalanced Chromosome Aberrations) and OMIM (Online Mendelian Inheritance in Man).*

**Web Table II Databases Used in Exome or Genome Data Analysis**

| *Name of database* | *Description* | *Website* |
|---|---|---|
| *Population database of variants* | | |
| Genome Aggregation Databases (gnomAD) | Disease specific or population specific exome and genome data from unrelated individuals | *https://gnomad.broadinstitute.org* |
| The International Genome Sample Resource (IGSR) (1000 Genomes Project) | Database of genetic variants with a frequency of more than 1% | *http://www.internationalgenome.org* |
| The Exome Aggregation Consortium (ExAC) | Exome sequencing data from disease specific and population genetic studies | *http://exac.broadinstitute.org* |
| *Databases of disease causing variants* | | |
| The Human Gene Mutation Database (HGMD) | All known published disease-causing variants | *http://www.hgmd.cf.ac.uk/ac/index.php* |
| ClinVar | Clinical description and variants | *https://www.ncbi.nlm.nih.gov/clinvar/* |
| Leiden Open Variation Database (LOVD) | Variant database | *http://www.lovd.nl* |
| Online Mendelian Inheritance in Man (OMIM) | Human diseases and variants | *https://www.omim.org* |

**Web Table III Clinical Scenarios where Genomic Testing is Useful**

**Scenario 1:** A non-consanguineous couple with a five-years-old girl with autism wanted to know the risk of recurrence of autism in subsequent pregnancies. Chromosomal microarray was opted as the first tier test in this child. No pathogenic copy number variant causing autism was identified. They were offered exome/genome sequencing as well, but did not opt for it in view of high cost and low yield. Only an empiric risk of recurrence of 10% was provided to the family. Since exact genetic etiology was not identified in the child, prenatal diagnosis could not be offered.

**Scenario 2:** A three-years-old boy born to third degree consanguineous parents had spastic diplegia and was being treated as cerebral palsy. There was no history of any adverse perinatal events. In the absence of a perinatal insult, exome sequencing done for this child, identified a biallelic pathogenic variant c.700G>C (p.Asp234His) in *ARG1* causing arginase deficiency (MIM#207800). Parents were heterozygous carriers for the same variant. The child was advised supportive care. The parents were counseled about the recurrence risk of 25% of this condition in every pregnancy and prenatal diagnosis was offered by chorionic villus sampling.

**Scenario 3:** A four-years-old girl had developmental delay, repetitive hand wringing movements and hyperventilation. DNA methylation analysis for Angelman syndrome and sequencing of *MECP2* gene for Rett syndrome were normal. Exome sequencing identified a de novo heterozygous disease-causing variant, c.1512insA (p.Ser505Glu*8) in TCF4 gene, causing Pitt Hopkins syndrome (MIM#610954). Since the parents did not have this variant, they were counseled about very low risk of recurrence (usually less than one percent) in subsequent pregnancies.

**Scenario 4:** Six-years-old girl, who was the first child of non-consanguineous parents, was evaluated for developmental delay and intellectual disability. Chromosomal microarray and fragile X mutation analysis did not reveal disease- causing variants. Exome sequencing of the child was performed. A heterozygous novel variant c.3817C>A, p.(His1273Asn) in HIVEP2 gene causing autosomal dominant mental retardation type 43(MIM#616977) was reported. The variant was interpreted as VUS (variant of unknown significance). It was noted that the parents were not tested for this variant. On testing them, the same variant was observed in heterozygous state in her father who had normal intellect. Hence this variant was re-classified as a benign variant in HIVEP2. Exome sequencing was performed in parents to complete the trio (parents-child) and a novel biallelic compound heterozygous variant in a novel gene in the proband was identified (suggesting the possibility of a hitherto unknown disease with intellectual disability and its genetic cause). Further validation of these findings by more patients with similar condition and experiments are awaited to provide definitive genetic counseling and prenatal diagnosis to the family.

**Scenario 5:** A 12-years-old girl with multiple fractures was diagnosed to have osteogenesis imperfecta (OI). She did not have blue sclera or dentinogenesis imperfecta. Her radiographs showed hyperplastic callus and calcified interosseus membrane in forearm. Since this pointed to a specific diagnosis of osteogenesis imperfecta type V (MIM#610967), instead of ordering a panel test covering all genes causing OI, Sanger sequencing of only the particular region of *IFITM5* was done. A de novo heterozygous pathogenic variant c.-14C>T was identified in this gene. This variant was not identified in her parents. Clinical and radiological examination is useful even in genomic era.