Chromosomal Aberrations in Pediatric Patients with Developmental Delay/Intellectual Disability: A Single-Center Clinical Investigation

Ting Hu,1,2 Zhu Zhang,1,2 Jiamin Wang,1,2 Qinqin Li,1,2 Hongmei Zhu,1,2 Yi Lai,1,2 He Wang,1,2 and Shanling Liu,1,2

1Department of Obstetrics & Gynecology, West China Second University Hospital, Sichuan University, Chengdu, China
2Key Laboratory of Birth Defects and Related Diseases of Women and Children (Sichuan University), Ministry of Education, Chengdu, China

Correspondence should be addressed to Shanling Liu; sunny630@126.com

Received 17 July 2019; Revised 3 September 2019; Accepted 18 September 2019; Published 6 November 2019

Academic Editor: Siddharth Pratap

Copyright © 2019 Ting Hu et al. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Introduction. Chromosomal microarray analysis (CMA) has currently been considered as the first-tier genetic test for patients with developmental delay/intellectual disability (DD/ID) in many countries. In this study, we performed an extensive assessment of the value of CMA for the diagnosis of children with DD/ID in China. Methods. A total of 633 patients diagnosed with DD/ID in West China Second University Hospital, Sichuan University, were recruited from January 2014 to March 2019. The patients were classified into 4 subgroups: isolated DD/ID, DD/ID with multiple congenital anomalies (MCA), isolated autism spectrum disorders (ASDs), and DD/ID with epilepsy. CMA was performed on Affymetrix 750K platform. Results. Among the 633 patients, 127 cases were identified as having pathogenic copy number variations (pCNVs) with an overall positive rate of 20.06%. Of the 127 cases with abnormal results, 76 cases had 35 types of microdeletion/microduplication syndromes (59.84%) including 5 cases caused by uniparental disomy (UPD), and 18 cases had unbalanced rearrangements (14.17%) including 10 cases inherited from parental balanced translocations or pericentric inversions. The diagnostic yields of pCNVs for the subgroups of isolated DD/ID, DD/ID with MCA, isolated ASD, and DD/ID with epilepsy were 18.07% (60/332), 34.90% (52/149), 3.70% (3/81), and 16.90% (12/71), respectively. The diagnostic yield of pCNVs in DD/ID patients with MCA was significantly higher than that of the other three subgroups, and the diagnostic yield of pCNVs in isolated ASD patients was significantly lower than that of the other three subgroups (p < 0.05). Conclusion. Microdeletion/microduplication syndromes and unbalanced rearrangements are probably the main genetic etiological factors for DD/ID. DD/ID patients with MCA have a higher rate of chromosomal aberrations. Parents of DD/ID children with submicroscopic unbalance rearrangements are more likely to have chromosome balanced translocations or pericentric inversions, which might have been missed by karyotyping. CMA can significantly improve the diagnostic rate for patients with DD/ID, which is of great value for medical management and clinical guidance for genetic counseling.

1. Introduction

Developmental delay/intellectual disability (DD/ID) affects approximately 3% of the general population [1]. In China, 11,820,000 people were diagnosed with DD/ID, of whom 954,000 were younger than 6 years of age [2]. Taking care of a patient with DD/ID exerts a substantial financial and emotional burden on his/her family and society. Approximately more than half of DD/ID cases resulted from genetic etiologies, including chromosomal abnormalities, microduplication or microdeletion syndromes, and monogenic disorders [3]. Other etiologies include teratogenic exposures, perinatal asphyxia, infections, etc. [4].

Submicroscopic chromosomal aberrations (copy number variants, CNVs) play a significant role in the pathogenesis of DD/ID, and the diagnostic yield of chromosomal microarray analysis (CMA-) detected CNVs associated with these disorders ranges from 12% to 29% [5-8]. Currently,
the clinical utility of CMA has been recognized by several professional societies and has been recommended as the first-tier genetic test for patients with unexplained DD/ID, autism spectrum disorders (ASDs), and/or multiple congenital anomalies (MCAs) [9–12]. In this study, we investigated 633 Chinese children with unexplained DD/ID combined with other conditions by the Affymetrix® CytoScan™ 750K Array over a period of 5 years and extensively assessed the value of CMA for the diagnosis of children with DD/ID.

2. Methods

2.1. Patients. A total of 633 Chinese patients with varying degrees of DD/ID (359 males; 274 females), with ages from 3 months to 17 years, were recruited from the Department of Neurological Rehabilitation at West China Second University Hospital, Sichuan University, from January 2014 to March 2019. All patients were classified into 4 subgroups: isolated DD/ID (n = 332), DD/ID with MCA (n = 149), isolated ASD (n = 81), and DD/ID with epilepsy (n = 71).

The detailed evaluations of the patients included prenatal/birth history, family history, pedigree, physical examinations, and imageological examination. The inclusive criteria were as follows: DD/ID diagnosed according to the Diagnostic and Statistical Manual of Mental Disorders, Fifth Edition (DSM-5) with IQ/DQ < 70 assessed by the Gesell Development Scale, the Wechsler Preschool and Primary Scale Intelligence, or the Wechsler Intelligence Scale for Children. The exclusion criteria were as follows: (1) history of hypoxia, toxification, central nervous system infection, and cranial trauma; (2) evidence of recognizable inherited metabolic disorder; (3) typical clinical manifestation of Rett syndrome for female patients; (4) mutations in the FMR1 gene; (5) fetus or newborns with multiple malformations.

The peripheral blood samples of the patients were analyzed by CMA. Informed consent was obtained from their mentally healthy parents before detection. In addition, the peripheral blood samples of their parents underwent CMA to determine whether the CNVs of the patients were inherited or de novo to determine the clinical significance. The research was approved by the Medical Ethics Committee of West China Second University Hospital, Sichuan University.

2.2. Chromosomal Microarray Analysis. Whole genomic DNA was extracted from peripheral blood cells of each patient and his or her parents using QIAamp DNA Blood Mini Kit (Qiagen, Valencia, CA, USA) and subjected to CMA-single nucleotide polymorphism (SNP) array analysis by using the Affymetrix® CytoScan™ 750K Array (Affymetrix, Santa Clara, CA, USA). The procedure was described in our previous publication [13].

When the fragment size of absence of heterozygosity (AOH) was larger than one-third of the chromosome, analysis software UPD tool_0.2 was used to separate the AOH into uniparental disomy (UPD) or consanguinity by comparison with the parental results.

The detected CNVs were systematically evaluated for clinical significance. The procedure was also described in our previous publication [13].

2.3. Chromosomal Karyotyping. When a gain and a loss of more than 5 Mb were simultaneously detected at one end of two different chromosomes or at both ends of a single chromosome in one sample, peripheral blood samples of the normal parents were karyotyped to confirm whether the parents had chromosomal balanced translocations or inversions.

2.4. Statistical Analysis. Statistical analysis was performed by using SPSS software, version 24. The frequency of pCNVs was compared among subgroups of isolated DD/ID, DD/ID with MCA, DD/ID with ASD, and DD/ID with ASD by using the chi-square test. A value of p < 0.05 was considered to indicate statistical significance.

3. Results

3.1. Diagnostic Yields of pCNVs. We detected 149 pCNVs (including 5 UPDs) in 127 cases (65 males; 62 females), accounting for 20.06% of the series (Table 1). These pCNVs, including 100 deletions and 44 duplications, were highly variable in size, ranging from 223 kb to 102,400 kb (Table 2).

Fifty-two pCNVs (34.90%, 52/149) were detected in patients with MCA. In the subgroup of MCA, several clinical manifestations were found, including facial dysmorphic features, growth disorders, micro/macrocephaly, cleft palate, ear deformity, abnormal hands or feet, abnormal heart morphology, and abnormal genital system. In addition, 60 pCNVs (18.07%, 60/332) were detected in patients with isolated DD/ID, 3 pCNVs (3.70%, 3/81) were detected in patients with isolated ASD, and 12 pCNVs (16.90%, 12/71) were detected in patients with epilepsy. The proportion of pCNVs detected in patients with MCA was significantly higher than that in patients with isolated DD/ID (p ≤ 0.001 (34.90% vs. 18.07%)) or patients with isolated ASD (p ≤ 0.001 (34.90% vs. 3.70%)) or patients with epilepsy (p = 0.004 (34.90% vs. 16.90%)). The proportion of pCNVs in patients with isolated ASD was significantly lower than that in patients with isolated DD/ID (p ≤ 0.001 (3.70% vs. 18.07%)) or patients with ASD (p = 0.007 (3.70% vs. 16.90%)).

3.2. Microdeletion/Microduplication Syndromes. Of the 127 cases with abnormal results, 76 cases had 35 types of microdeletion/microduplication syndromes (59.84%), including Williams–Beuren syndrome, Angelman syndrome, Prader–Willi syndrome, 22q11 deletion syndrome (velocardiofacial/DiGeorge syndrome), and Wolf–Hirschhorn syndrome. Twenty-nine microdeletion/microduplication syndromes were detected in patients with isolated DD/ID (8.73%, 29/332), 40 in patients with MCA (26.85%, 40/149),
3.3. Submicroscopic Unbalance Rearrangements. Of the 127 cases with abnormal results, 18 cases were detected with submicroscopic unbalance rearrangements (14.17%), including 10 cases inherited from parental balanced translocations or pericentric inversions (Figure 1(b)). Fifteen cases had subtelomeric aberrations at the end of two different chromosomes, of which 8 cases were inherited from normal parents with balanced translocations confirmed by karyotyping. Three cases had subtelomeric aberrations at both ends of the same chromosome, of which 2 cases were inherited from normal parents with pericentric inversions confirmed by karyotyping.

4. Discussion

The establishment of genetic etiological diagnoses for DD/ID children is usually challenging due to the high frequency of relatively nonspecific symptoms shared by numerous potential syndromes. We identified pCNVs in 20.06% of cases, which was comparable to other reported series [8, 14–17]. Interestingly, our study revealed some new findings with certain clinical significance.

4.1. More Deletions than Duplications in pCNVs. In our study, the proportion of deletions was extremely higher than duplications in pCNVs. This finding is consistent with the notion of Ruderfer et al. [18] that many duplications present in the human genome are benign, and most phenotypically normal individuals possess a higher number of duplications than deletions. The dosage-sensitive genes have the ability to cause phenotypes [9]. In our study, 32 genes were confirmed with “sufficient evidence for haploinsufficiency” in the pathogenic deletions, while only 2 genes were confirmed with “sufficient evidence for triplosensitivity” in the pathogenic duplications (https://www.clinicalgenome.org/), which influenced the phenotypes of these patients. Thus, deletions contributed more pathogenic interpretations than duplications.

4.2. Diagnostic Yields Associated with the Phenotypes. The diagnostic yield of pCNVs (including microdeletion/microduplication syndromes) in the MCA subgroup was significantly higher than that in the other 3 subgroups, which implied that severe and complex phenotypes, such as dysmorphology or congenital anomalies, tend to have a higher likelihood of identifying a genetic etiology [4]. Case 92 is a 13-year-old female who has mild ID, specifically a learning disability with a cleft palate. CMA revealed a 5242-kb duplication in the 15q11.2q13.3 (15q11-q13 duplication syndrome) inherited from her normal mother and a 748-kb deletion in 16p11.2 (16p11.2 recurrent microdeletion) inherited from her normal father. Evidence suggests that maternally derived 15q11.2q13.3 duplications are more frequently associated with abnormal phenotypes [19]. Weiss et al. [20] reported that the phenotype of 16p11.2 recurrent microdeletion is characterized by DD, ID, and/or ASD. It is rare that one patient suffers from two different microdeletion/microduplication syndromes. We hypothesized that both the duplication and deletion contributed to the phenotype of the patient. The probability of her parents having another baby with one of the pCNVs or for both is extremely as high as 75%. Wolfe et al. [21] identified that 16p11.2 deletions and 15q11.2q13.3 duplications had incomplete penetrance with high frequencies in neurodevelopmental disorders; however, they sometimes can be observed in healthy controls. So, the phenotype of the baby with pCNV(s) could not be confirmed before birth.

In the isolated DD/ID subgroup and DD/ID with epilepsy subgroup, the diagnostic yields of pCNVs were significantly lower than that of the MCA subgroup but significantly higher than those of the isolated ASD subgroup. The more phenotypes the patients had, such as epilepsy, the higher the likelihood of finding a genetic etiology [9]. However, the diagnostic yields of pCNVs between these two subgroups were not statistically significant. Next-generation sequencing (NGS) also contributes to the identification of epilepsy caused by monogenic mutations [22], which might be omitted by CMA.

The diagnostic yield of pCNVs was significantly lower in the patients with isolated ASD than in the other 3 subgroups, which was consistent with the results of Ho et al. [16]. We assumed that some other genetic etiologies, such as single-gene disorders, may contribute to the pathogenesis of ASD,
Table 2: Characteristics of pCNVs detected by CMA among the 127 patients.

| No. | Clinical feature | Age  | Gender | CMA results | Sizes of CNVs (kb) | Copy number | Syndromes                      | OMIM gene     | Inherited or de novo |
|-----|-----------------|------|--------|-------------|-------------------|-------------|--------------------------------|---------------|---------------------|
| 1   | ID              | 17y  | F      | arr[GRCh37] | 12p12.1(21369190_25634175)x1 | 3995        | Loss                           | Lamb-Shaffer syndrome | SOX5     | de novo            |
| 2   | DD              | 3y   | F      | arr[GRCh37] | 4p16.3p16.1(68345_8066350)x1 | 7998        | Loss                           | Wolf–Hirschhorn syndrome | de novo |
| 3   | ID              | 5y   | M      | arr[GRCh37] | 7q11.23(72723370_74136633)x1 | 1413        | Loss                           | Williams-Beuren syndrome | ELN     | de novo            |
| 4   | DD              | 4y   | M      | arr[GRCh37] | Xq28(153118233_153878720)x2 | 760         | Gain                           | Xq28 (MECP2) duplication | MECP2   |                  |
| 5   | ID              | 5y   | M      | arr[GRCh37] | 15q11.2q26.3(22817870_102397317)hmz | 79,579      | LOH (paternal UPD15)       | Angelman syndrome | UBE3A   | de novo            |
| 6   | DD              | 4y   | M      | arr[GRCh37] | 7q11.23(72718123_74136633)x1 | 1419        | Loss                           | Williams-Beuren syndrome | ELN     | de novo            |
| 7   | DD              | 19m  | M      | arr[GRCh37] | 15q11.2q3.1(23632677_28704050)x1 | 5071        | Loss                           | Williams-Beuren syndrome | UBE3A   | de novo            |
| 8   | ID              | 16y  | F      | arr[GRCh37] | 7q11.23(72718123_74141494)x1 | 1423        | Loss                           | Williams-Beuren syndrome | ELN     | de novo            |
| 9   | DD              | 16m  | M      | arr[GRCh37] | 11p11.2(44506359_47897669)x1 | 3391        | Loss                           | Potocki–Shaffer syndrome | MYBPC3  | de novo            |
| 10  | ID              | 6y   | M      | arr[GRCh37] | 15q11.2q13.1(23290787_28526905)x1 | 5147        | Loss                           | Xq28 (MECP2) duplication | UBE3A   | de novo            |
| 11  | ID              | 7y   | M      | arr[GRCh37] | Xq28(153030708_155233098)x2 | 2202        | Gain                           | LOH (paternal UPD15)       | MECP2   | Inherited from normal mother |
| 12  | ID              | 16y  | F      | arr[GRCh37] | 15q11.2q26.3(22817870_102397317)hmz | 79,579      | Loss                           | Williams-Beuren syndrome | UBE3A   | de novo            |
| 13  | ID              | 6y   | M      | arr[GRCh37] | 7q11.23(7261954_75147402)x1 | 1745        | Loss                           | Williams-Beuren syndrome | ELN     | de novo            |
| 14  | ID              | 5y   | M      | arr[GRCh37] | 16p13.3(85880_2045435)x1 | 1960        | Loss                           | ATR-16 syndrome        | ELN     | de novo            |
| 15  | DD              | 17m  | F      | arr[GRCh37] | 7q11.23(72692112_74148740)x1 | 1496        | Loss                           | Williams-Beuren syndrome | ELN     | de novo            |
| 16  | ID              | 16y  | F      | arr[GRCh37] | 22q13.33(50974299_51197766)x1 | 223         | Loss                           | 22q13 deletion syndrome (Phelan–Mcdermid syndrome) | SHANK3  | de novo            |
| 17  | ID              | 9y   | F      | arr[GRCh37] | 17p11.2(16761814_20304118)x3 | 3542        | Gain                           | Potocki–Lupski syndrome (17p11.2 duplication syndrome) | ELN     | de novo            |
| 18  | DD              | 9m   | F      | arr[GRCh37] | 7q11.23(72723370_74136633)x1 | 1413        | Loss                           | Williams-Beuren syndrome | ELN     | de novo            |
| No. | Clinical feature | Age | Gender | CMA results | Sizes of CNVs (kb) | Copy number | Syndromes | OMIM gene | Inherited or de novo |
|-----|------------------|-----|--------|-------------|-------------------|-------------|-----------|-----------|---------------------|
| 19  | ID               | 6 y | F      | arr[GRCh37] | 22q13.31q13.33(482,348,411-511,977,766) x1 | 2963 | Loss | 22q13 deletion syndrome (Phelan–Mcdermid syndrome) | SHANK3 | de novo |
| 20  | DD               | 13 m| F      | arr[GRCh37] | 22q11.21(189,947,771-214,360,003)x3 | 2516 | Gain | 22q11 duplication syndrome | de novo |
| 21  | ID               | 9 y | M      | arr[GRCh37] | 7q11.23(727,233,700-741,366,333)x1 | 1413 | Loss | Williams-Beuren syndrome 16p13.11 recurrent microduplication (neurocognitive disorder susceptibility locus) | ELN | de novo |
| 22  | ID               | 12 y| M      | arr[GRCh37] | 16p13.11(148,929,750-165,385,964)x3 | 1646 | Gain | Inherited from normal mother |
| 23  | ID               | 5 y | F      | arr[GRCh37] | 15q11.2q13.1(227,704,211-285,606,664)x3 | 5790 | Gain | 15q11-q13 duplication syndrome | de novo |
| 24  | ID               | 17 y| F      | arr[GRCh37] | 15q11.2q13.1(227,704,211-285,269,053)x3 | 5756 | Gain | 15q11-q13 duplication syndrome | de novo |
| 25  | DD               | 13 m| F      | arr[GRCh37] | 15q11.2q13.1(129,023,365-139,475,046)x3 | 10,272 | Gain | de novo |
| 26  | ID               | 16 y| F      | arr[GRCh37] | 8p23.3p23.1(158,048,971-50,009)x1 | 9623 | Loss | 8p23.1 deletion syndrome | CSMD1 | de novo |
| 27  | ID               | 9 y | F      | arr[GRCh37] | 7q36.1q36.3(151,376,795-159,197,007)x1 | 7743 | Loss | 1q43-q44 deletion syndrome | SHH; KMT2C; DPP6; MNX1; CHRM3; AKT3; HNRNPU | de novo |
| 28  | DD               | 3 y | M      | arr[GRCh37] | 14q34.4(239,750,391-249,224,884)x1 | 9474 | Loss | 1q43-q44 deletion syndrome | de novo |
| 29  | ID               | 12 y| M      | arr[GRCh37] | 14q34.4(239,750,391-249,224,884)x1 | 9868 | Loss | ZIC1; ZIC4 | de novo |
| 30  | DD               | 4 y | F      | arr[GRCh37] | 18p11.22p11.21(136,227,073-123,421,941)x1 | 12,206 | Loss | TGIF1 | de novo |
| 31  | ID               | 16 y| F      | arr[GRCh37] | 11q24.2q25(124,419,906-134,937,416)x1 | 10,518 | Loss | de novo |
| 32  | ID               | 17 y| F      | arr[GRCh37] | 3p27.3q29(187,067,328-194,717,786)x1 | 7699 | Loss | TP63; FGF12 | de novo |
| 33  | DD               | 8 m | M      | arr[GRCh37] | 10q26.13q26.3(123,584,417-135,426,386)x1 | 11,842 | Loss | EBF3 | de novo |
| 34  | DD               | 3 y | M      | arr[GRCh37] | 11q14.1(77,492,774-853,128,284)x1 | 7820 | Loss | DLG2 | de novo |
| 35  | DD               | 4 y | M      | arr[GRCh37] | 15q14.24.1(350,024,775-797,290,909)x1.63 | 40,923 | Loss (Mosaic) | 15q24 recurrent microdeletion syndrome | de novo |
| No. | Clinical feature | Age | Gender | CMA results | Sizes of CNVs (kb) | Copy number | Syndromes | OMIM gene | Inherited or de novo |
|-----|-----------------|-----|--------|-------------|-------------------|-------------|-----------|-----------|---------------------|
| 36  | DD              | 4y  | M      | arr[GRCh37] 1q42.13q44(228801_122_249181_598)x3 | 20,380 | Gain | 4p16.3 terminal (Wolf-Hirschhorn syndrome) region | SOX7 | de novo |
| 37  | ID              | 6y  | M      | arr[GRCh37] 1q42.13q44(22991797_249222468)x3 | 19,307 | Gain | | | de novo |
| 38  | DD              | 3y  | F      | arr[GRCh37] 12p13.33q12(173786_40931729)x3 | 40,758 | Gain | Partial chromosome 12 trisomy | | de novo |
| 39  | ID              | 8y  | M      | arr[GRCh37] Xp21.3p11.23(27954516_48270449)x1 | 20,316 | Loss | Xp11.23 region (includes MAOA and MAOB) | | de novo |
| 40  | ID              | 10y | F      | arr[GRCh37] 18q21.3q23(5861060_78013728)x1 | 19,847 | Loss | | | de novo |
| 41  | ID              | 16y | F      | arr[GRCh37] 11q14.2q22.3(67455736_10977755)x1 | 22,322 | Loss | | | de novo |
| 42  | DD              | 4y  | F      | 4p16.3p15.31(290685_18118492)x3 | 17,828 | Gain | 4p16.3 terminal (Wolf-Hirschhorn syndrome) region | | de novo |
| 43  | DD              | 3y  | M      | arr[GRCh37] 4q34.1q35.2(176152080_190957460)x1 | 14,805 | Loss | 8p23.1 duplication syndrome | SOX7 | de novo |
| 44  | ID              | 8y  | M      | arr[GRCh37] 4p16.3p16.1(68345_9514461)x3 | 9446 | Gain | 4p16.3 terminal (Wolf-Hirschhorn syndrome) region | | de novo |
| 45  | ID              | 17y | F      | arr[GRCh37] 8p23.3p23.1(158048_10915395)x3 | 6886 | Loss | Paternal balanced translocation 46,XY,t(4;8) (p16q23) | CSMD1 | |
| 46  | ID              | 3y  | M      | arr[GRCh37] 6q27(169727875_170914297)x3 | 12,107 | Loss | Maternal balanced translocation 46,XX,t(11;18) (q25; q21.2) | CHAMP1; BSVD2 | |
| 47  | ID              | 17y | M      | arr[GRCh37] 11q25(13100110_134937416)x1 | 3936 | Loss | | | |
|     |                 |     |        | arr[GRCh37] 18q21.2q23(50912872_78013728)x3 | 27,101 | Gain | | | |
| No. | Clinical feature                  | Age | Gender | CMA results                                                                 | Sizes of CNVs (kb) | Copy number | Syndromes                  | OMIM gene | Inherited or de novo                  |
|-----|----------------------------------|-----|--------|-------------------------------------------------------------------------------|-------------------|-------------|-----------------------------|-----------|---------------------------------------|
| 48  | ID                               | 16y | F      | arr[GRCh37] 9p24.3p21.1(208454_30555044)x3                                  | 30,347            | Gain        | Paternal balanced translocation 46,XY,t(9;18) (p21; p11.3) |
|     |                                  |     |        |                                                                               |                   |             |                             |           |                                       |
| 49  | ID                               | 7y  | M      | arr[GRCh37] 18p11.32p11.31(136227_5485196)x1                              | 5349              | Loss        | TGIF1          | CNTN4; CNTN6; ITPR1         | de novo                             |
|     |                                  |     |        |                                                                               |                   |             |                             |           |                                       |
| 50  | DD                              | 3y  | F      | 7q33q36.3(134287922_159119707)x3                                          | 24,832            | Gain        | SHH             |                                    |                                    |
|     |                                  |     |        |                                                                               |                   |             |                             |           |                                       |
| 51  | ID                               | 16y | F      | 6q25.3q27(159131590_170914297)x3                                          | 11,783            | Gain        | TGIF1          |                                    |                                    |
|     |                                  |     |        |                                                                               |                   |             |                             |           |                                       |
| 52  | DD                              | 3y  | M      | arr[GRCh37] 10p15.3(100047_1947393)x1                                       | 1847              | Loss        | ZMYND11        |                                    |                                    |
|     |                                  |     |        |                                                                               |                   |             |                             |           |                                       |
| 53  | ID                               | 7y  | F      | arr[GRCh37] 9p24.3p13.3(208454_33702198)x3                               | 33,494            | Gain        | ARID2          |                                    | de novo                             |
|     |                                  |     |        |                                                                               |                   |             |                             |           |                                       |
| 54  | DD                              | 4y  | M      | arr[GRCh37] 12q12(44719567_46210900)x1                                       | 1491              | Loss        | ZEB2           |                                    | de novo                             |
|     |                                  |     |        |                                                                               |                   |             |                             |           |                                       |
| 55  | ID                               | 16y | M      | arr[GRCh37] Xq28(154476199_155233098)x1                                     | 759               | Loss        | RAB39B         | Inherited from normal mother  | de novo                             |
|     |                                  |     |        |                                                                               |                   |             |                             |           |                                       |
| 56  | ID                               | 10y | M      | arr[GRCh37] 8p11.22(38344498_39172014)x3                                     | 8575              | Gain        | GNB1; GABRD    |                                    | de novo                             |
|     |                                  |     |        |                                                                               |                   |             |                             |           |                                       |
| 57  | ID                               | 10y | M      | 1p36.33p36.32(1156338_2468052)x1                                            | 1302              | Loss        | SPTAN1         |                                    | de novo                             |
|     |                                  |     |        |                                                                               |                   |             |                             |           |                                       |
| 58  | ID                               | 14y | F      | 9q34.11(113123815_132005416)x1                                             | 774               | Loss        | ERMARD; TBP    |                                    | de novo                             |
|     |                                  |     |        |                                                                               |                   |             |                             |           |                                       |
| 59  | ID                               | 17y | F      | 6q27(169471201_170914297)x1                                               | 1443              | Loss        | GNB1; GABRD    |                                    | de novo                             |
|     |                                  |     |        |                                                                               |                   |             |                             |           |                                       |
| 60  | ID                               | 12y | F      | 1p36.33p36.32(849466_2516031)x1                                            | 1667              | Loss        | HUWE1          | Inherited from normal mother  | de novo                             |
|     |                                  |     |        |                                                                               |                   |             |                             |           |                                       |
| 61  | DD + MCA (short status)         | 3y  | M      | Xp11.22(53359258_53647606)x2                                               | 288               | Gain        | Xp11.22-linked intellectual disability |                                    |                                    |
|     | (microtia, cleft palate, ventricular septal defect) | |        |                                                                               |                   |             |                             |           |                                       |
| 62  | DD + MCA (microtia, cleft palate, ventricular septal defect) | 8m  | F      | arr[GRCh37] 4p16.3(68345_3488721)x1                                         | 3420              | Loss        | Wolf–Hirschhorn syndrome        |                                    | de novo                             |
| No. | Clinical feature                                      | Age | Gender | CMA results | Sizes of CNVs (kb) | Copy number | Syndromes          | OMIM gene | Inherited or de novo |
|-----|------------------------------------------------------|-----|--------|-------------|---------------------|-------------|---------------------|------------|----------------------|
| 63  | DD + MCA (facial dysmorphism, supravalvar aortic stenosis (SVAS) and supravalvar pulmonary stenosis) | 11 m | M      | arr[GRCh37] 7q11.23(72718123_74136633)x1 | 1419 | Loss | Williams-Beuren syndrome | ELN | de novo |
| 64  | ID + MCA (facial dysmorphism, short status)          | 6 y | M      | arr[GRCh37] 17p11.2(16657318_20287758)x1 | 3630 | Loss | Smith–Magenis syndrome | RAI1; FLCN | de novo |
| 65  | DD + MCA (facial dysmorphism, short status)          | 9 m | M      | arr[GRCh37] 7q11.23(72697461_74136633)x1 | 1439 | Loss | Williams-Beuren syndrome | ELN | de novo |
| 66  | ID + MCA (facial dysmorphism, short status)          | 16 y | F      | arr[GRCh37] 17p11.2(16736261_20417235)x1 | 3681 | Loss | Smith–Magenis syndrome | RAI1; FLCN | de novo |
| 67  | ID + MCA (facial dysmorphism, cleft palate, short status) | 6 y | F      | arr[GRCh37] 7q11.23(2713282_74154209)x1 | 1441 | Loss | Williams-Beuren syndrome | ELN | de novo |
| 68  | DD + MCA (facial dysmorphism, muscular hypotonia)    | 2 y | F      | arr[GRCh37] 7p22.3p11.1(50943_58019983)hmz | 57,969 | Loss | Silver–Russell syndrome | (maternal UPD7) | de novo |
| 69  | ID + MCA (ventricular septal defect)                  | 5 y | F      | arr[GRCh37] 15q11.2q13.1(22770421_28704050)x1 | 5934 | Loss | Prader–Willi syndrome | UBE3A | de novo |
| 70  | DD + MCA (facial dysmorphism, short status)          | 16 m | M      | arr[GRCh37] 7q11.23(72697239_74136633)x1 | 1439 | Loss | Williams-Beuren syndrome | ELN | de novo |
| 71  | DD + MCA (facial dysmorphism, hypoplasia of the corpus callosum, ventricular septal defect, short status) | 9 m | M      | arr[GRCh37] 17p13.3(525_2780094)x1 | 2780 | Loss | Miller–Dicker syndrome | PAFAH1B1 | de novo |
| 72  | DD + MCA (facial dysmorphism, supravalvar aortic stenosis (SVAS), ventricular septal defect) | 9 m | M      | arr[GRCh37] 7q11.23(72713282_74136633)x1 | 1423 | Loss | Williams-Beuren syndrome | ELN | de novo |
| 73  | DD + MCA (muscular hypotonia, dysphagia, cryptorchidism) | 3 m | M      | arr[GRCh37] 15q11.2q13.1(23290787_28540345)x1 | 5250 | Loss | Prader–Willi syndrome | UBE3A | de novo |
| 74  | DD + MCA (triangular shaped face, short status, body asymmetry) | 13 m | F      | arr[GRCh37] 7p22.3p11.1(50943_58019983)hmz | 57,969 | Loss | Silver–Russell syndrome | (maternal UPD7) | de novo |
| No. | Clinical feature                                                                 | Age | Gender | CMA results                                                                 | Sizes of CNVs (kb) | Copy number | Syndromes                                      | OMIM gene | Inherited or de novo |
|-----|----------------------------------------------------------------------------------|-----|--------|--------------------------------------------------------------------------------|-------------------|-------------|------------------------------------------------|-----------|---------------------|
| 75  | DD + MCA (facial dysmorphism, cafe-au-lait spots, atrial septal defect)           | 18m | M      | arr[GRCh37] 17q11.2(29025996_30369402)x1                                      | 1343              | Loss        | NF1-microdeletion syndrome                      | NF1       | de novo             |
| 76  | ID + MCA (facial dysmorphism, short status)                                      | 13y | F      | arr[GRCh37] 5p15.3p15.31(113576_9756329)x1                                  | 9643              | Loss        | Cri du chat syndrome (5p deletion)             |           |                    |
| 77  | ID + MCA (facial dysmorphism, brachydactyly)                                     | 9y  | F      | arr[GRCh37] 2q37.3(239757969_242782258)x1                                  | 3026              | Loss        | 2q37 monosomy                                   |           | de novo             |
| 78  | DD + MCA (hypertelorism, overgrowth)                                             | 5m  | F      | arr[GRCh37] 15q24.3q26.3(78160033_102429040)x3                              | 24,269            | Gain        | 15q26 overgrowth syndrome                      |           |                    |
| 79  | ID + MCA (facial dysmorphism, esophageal atresia, external auditory canal atresia)| 7m  | M      | arr[GRCh37] 22q13.3q13.33(48283717_51197766)x1                            | 2914              | Loss        | 22q13 deletion syndrome (Phelan–Mcdermid syndrome) | SHANK3    | de novo             |
| 80  | ID + MCA (atrial septal defect, cleft palate, hearing impairment)                 | 5y  | M      | arr[GRCh37] 9q34.2q34.3(13624652_141018648)x3                            | 4774              | Gain        | Cat eye syndrome                               |           |                    |
| 81  | DD + MCA (polysyndactyly)                                                        | 7m  | M      | arr[GRCh37] 22q11.1q11.2(1688889_20716903)x3                             | 3828              | Gain        |                                               |           |                    |
| 82  | DD + MCA (triangular shaped face, short status, muscular hypotonia)              | 14m | F      | arr[GRCh37] 16p11.2(29351825_30176508)x1                                 | 825               | Loss        | 16p11.2 recurrent microdeletion                 |           | de novo             |
| 83  | ID + MCA (atrial septal defect, ventricular septal defect)                        | 9y  | M      | arr[GRCh37] 7p22.3p11.1(50943_58019983)hmz                              | 57,969            | Loss        | Silver–Russell syndrome                        |           | de novo             |
| 84  | DD + MCA (short status)                                                          | 3y  | M      | arr[GRCh37] 22q11.2(18648855_21804071)x1                                 | 3152              | Loss        | 22q11 deletion syndrome (velocardiofacial/ DiGeorge syndrome) | TBX1      | de novo             |
| 85  | ID + MCA (congenital heart disease, polysyndactyly)                              | 16y | F      | arr[GRCh37] 15q12.2q13.1(23290787_28927830)x1                            | 5658              | Loss        | Angelman syndrome                              | UBE3A     | de novo             |
| 86  | DD + MCA (facial dysmorphism)                                                     | 13m | M      | arr[GRCh37] 16p13.11(14913788_16282869)x3                               | 1369              | Gain        |                                               |           | de novo             |

Table 2: Continued.
| No. | Clinical feature | Age | Gender | CMA results | Sizes of CNVs (kb) | Copy number | Syndromes | OMIM gene | Inherited or de novo |
|-----|------------------|-----|--------|-------------|------------------|-------------|-----------|-----------|-------------------|
| 87  | DD + MCA (muscular hypotonia, ventricular septal defect, cryptorchidism) | 3m | M      | arr[GRCh37] 15q11.2q13.1(23290787_28540345)x1 | 5250 | Loss | Prader–Willi syndrome | UBE3A | de novo |
| 88  | DD + MCA (cleft palate) | 3y | M      | arr[GRCh37] 16p11.2(29428531_30176508)x1 | 748 | Loss | 16p11.2 recurrent microdeletion 17q21.31 recurrent microdeletion syndrome (Koolen–de Vries syndrome) | KANSL1 | de novo |
| 89  | ID + MCA (facial dysmorphism, cleft palate, polysyndactyly, short status) | 11y | M | arr[GRCh37] 17q21.31q22.32(43170339_4498790)x1 | 1818 | Loss | 22q11 deletion syndrome (velocardiofacial/ DiGeorge syndrome) 16p11.2 recurrent microduplication (neurocognitive disorder susceptibility locus) | TBX1 | de novo |
| 90  | ID + MCA (short status) | 9y | F      | arr[GRCh37] 22q11.21(18648855_21800471)x1 | 3169 | Loss | Cri du chat syndrome (5p deletion) | TRIO; CTNND2 | de novo |
| 91  | DD + MCA (cleft palate) | 3y | F      | arr[GRCh37] 16p13.11(1548174_16390970)x1 | 909 | Gain | Leri–Weill dyschondrosteosis (LWD): SHOX deletion | SHOX; ARSE | de novo |
| 92  | ID + MCA (cleft palate) | 13y | F | arr[GRCh37] 15q11.2q13.1(2328188_28526905)x3 | 5245 | Gain | Inherited from normal mother | Inherited from normal father |
| 93  | DD + MCA (facial dysmorphism, catlike cry, ventricular septal defect, short status) | 3m | M | arr[GRCh37] 15q11.2q13.1(2328188_28526905)x3 | 5245 | Gain | Leri–Weill dyschondrosteosis (LWD): SHOX deletion | SHOX; ARSE | de novo |
| 94  | DD + MCA (short status) | 11m | F | arr[GRCh37] Xp22.33p22.31(168551_8030262)x1 | 7862 | Loss | Inherited from normal father | Inherited from normal mother |
| 95  | ID + MCA (cleft palate) | 6y | F | arr[GRCh37] 7q11.23(7269212_74154209)x1 | 1462 | Loss | 8p23.1 deletion syndrome | CSMD1 | de novo |
| 96  | ID + MCA (micrognathia) | 16y | F | arr[GRCh37] 15q11.2q13.1(2328188_28526905)x3 | 5245 | Gain | Inherited from normal mother | Inherited from normal father |
| 97  | ID + MCA (atrial septal defect, microtia, polysyndactyly) | 7y | M | arr[GRCh37] 12p13.33p13.32(1737786_4264694)x1 | 4091 | Loss | 12p13.33 microdeletion syndrome | FBXW11 | Maternal balanced translocation 46,XX,t(5;12) (q34; p13.32) |
| 98  | DD + MCA (cryptorchidism, short status) | 19m | M | arr[GRCh37] 4q34.1q35.2(174352834_199587460)x3 | 16605 | Gain | de novo | 

Table 2: Continued.
| No. | Clinical feature                              | Age | Gender | CMA results                                | Sizes of CNVs (kb) | Copy number | Syndromes                                      | OMIM gene     | Inherited or de novo |
|-----|-----------------------------------------------|-----|--------|--------------------------------------------|--------------------|-------------|-----------------------------------------------|---------------|----------------------|
| 99  | DD + MCA (gallbladder agenesis)               | 3y  | F      | arr[GRCh37] Xp22.33p22.31(168551_6455151)x0 | 6287               | Loss        | Leri–Weill dyschondrosteosis (LWD): SHOX deletion | SHOX; ARSE    | de novo               |
| 100 | ID + MCA (atrial septal defect, hypermyotonia)| 6y  | M      | arr[GRCh37] 8p23.3p23.1(158048_7044046)x1 | 6686               | Loss        | CSMD1                                          | de novo       |
| 101 | DD + MCA (hypoplasia of the corpus callosum) | 3m  | F      | arr[GRCh37] 8p23.1p12(1936000_33616234)x3  | 21,860             | Gain        | SPAST                                          | de novo       |
| 102 | DD + MCA (micrognathia, polysyndactyly)       | 14y | F      | arr[GRCh37] 13q33.2q34(106348324_115107733)x1 | 8759               | Loss        | CHAMP1; BSVD2                                 | de novo       |
| 103 | DD + MCA (hypermotonia, blepharophimosis)     | 3m  | M      | arr[GRCh37] 18p11.32q11.2(36227_20989843)x3 | 20,854             | Gain        | Maternal balanced translocation 46,XX,t(18;21) (q11.2; q21) |
| 104 | DD + MCA (facial dysmorphism)                 | 8m  | F      | arr[GRCh37] 10q26.3(134248768_135426386)x1 | 1178               | Loss        | Paternal inversion 46,XY,inv(10) (p12q26)      |
| 105 | DD + MCA (ventricular septal defect, aortic stenosis) | 21m | M      | arr[GRCh37] 3q22.1q23(132876177_139772196)x1 | 6896               | Loss        | FOXL2                                          | de novo       |
| 106 | DD + MCA (facial dysmorphism, cryptorchidism) | 3y  | M      | arr[GRCh37] 7p21.1p11.2(16641066_56373573)x3 | 39,733             | Gain        | de novo                                       |
| 107 | ID + MCA (facial dysmorphism)                 | 3y  | M      | arr[GRCh37] 4q13.1q13.2(6581383_68116457)x1 | 2298               | Loss        | FOXG1                                          | de novo       |
| 108 | DD + MCA (atrial septal defect)               | 14m | F      | arr[GRCh37] 14q12(28897081_31268243)x1 | 2371               | Loss        | Rett syndrome                                 | de novo       |
| 109 | DD + MCA (facial dysmorphism, overgrowth, body asymmetry) | 2y  | F      | arr[GRCh37] 20p13(61661_2150330)x1 | 2089               | Loss        | CSNK2A1; PDYN                                  | de novo       |
| 110 | DD + MCA (cryptorchidism, hypospadias)        | 3m  | M      | arr[GRCh37] Xq21.31q27.3(86577241_145860589)x3 | 59,283             | Gain        | Pelizaeus–Merzbacher disease (carrier)           | PLP1          | de novo               |
| No. | Clinical feature | Age | Gender | CMA results | Sizes of CNVs (kb) | Copy number | Syndromes | OMIM gene | Inherited or de novo |
|-----|-----------------|-----|--------|-------------|-----------------|-------------|-----------|-----------|---------------------|
| 111 | DD + MCA (facial dysmorphism, bilateral single transverse palmar creases) | 3 m | F | arr[GRCh37] 9p24.3q13(208454–2016577)x3 | 10,188 | Gain | Chromosome 9p trisomy | | de novo |
| 112 | ID + MCA (facial dysmorphism, webbed neck, low-set ears) | 5 y | F | arr[GRCh37] Xp22.33p11.22(168551–52706689)x1 | 52,538 | Loss | | | de novo |
| 113 | ID + ASD | 13y | F | arr[GRCh37] Xp11.22q28(52332230_155233098)x3 | 102,400 | Gain | Smith–Magenis syndrome | RA11; FLCN | de novo |
| 114 | DD + ASD | 3 y | M | arr[GRCh37] 17p11.2 (16745600_20417235)x3 | 3672 | Gain | Potocki–Lupski syndrome (17p11.2 duplication syndrome) | | de novo |
| 115 | ID + ASD | 10 y | M | 2q37.2q37.3(235790877–24278258)x1 | 6991 | Loss | 2q37 monosomy | HDAC4 | Paternal inversion 46,XY,inv(2) (p24q37.2) |
| 116 | ID + epilepsy (ichthyosis) | 12 y | M | arr[GRCh37] 2p25.3p24.3(12770–12658812)x3 | 1686 | Loss | Steroid sulphatase deficiency (STS) | STS | Inherited from normal mother |
| 117 | ID + epilepsy | 8 y | M | arr[GRCh37] Xp22.31(6455151–8141076)x0 | 5934 | Loss | Angelman syndrome | UBE3A | de novo |
| 118 | DD + epilepsy | 3 y | F | arr[GRCh37] 16q13.12p13.11(14777379–16533107) | 1756 | Loss | 16p11.2 recurrent microdeletion (neurocognitive disorder susceptibility locus) | | de novo |
| 119 | ID + epilepsy | 6 y | M | arr[GRCh37] 15q11.2q13.1(2362091_28526905)x1 | 4907 | Loss | Angelman syndrome | UBE3A | de novo |
| 120 | DD + epilepsy | 3 y | F | arr[GRCh37] 16p11.22(28557432–30176508)x1 | 1619 | Loss | 16p11.2 microduplication syndrome | SH2B1 | de novo |
| 121 | DD + epilepsy | 11 m | F | arr[GRCh37] 20q13.33(61485437_62790113)x1 | 1305 | Loss | | CHRNA4; KCNQ2; CHAMP1; BSVD2 | de novo |
| 122 | ID + epilepsy | 5 y | F | arr[GRCh37] 13q33.3q34(108237906–115107733)x1 | 6870 | Loss | | | |
| 123 | DD + epilepsy | 4 y | F | arr[GRCh37] Xq23q24(111170674–117964845)x1 | 6794 | Loss | | | |
| 124 | ID + epilepsy | 8 y | M | arr[GRCh37] Xp22.12p22.13(17125886_28993521)x2 | 11,868 | Gain | | | de novo |
| 125 | ID + epilepsy | 6 y | M | arr[GRCh37] 2p24.3p24.2(15850097_16790467)x1 | 940 | Loss | MYCN | | de novo |
| No. | Clinical feature | Age | Gender | CMA results | Sizes of CNVs (kb) | Copy number | Syndromes | OMIM gene | Inherited or de novo |
|-----|------------------|-----|--------|-------------|-------------------|-------------|-----------|------------|---------------------|
| 126 | ID+epilepsy      | 3 y | M      | arr[GRCh37] 2q24.3(164444391_168745074)x1 | 4301 | Loss | SCN1A; SCN2A; SCN9A | de novo |
| 127 | ID+epilepsy      | 6 y | M      | arr[GRCh37] 1p36.33(849466_2226509)x1 | 1377 | Loss | GNB1; GABRD | de novo |

LOH: loss of heterozygosity; UPD: uniparental disomy.
which requires further investigation. We detected 3 microdeletion/microduplication syndromes in this subgroup, including Smith–Magenis syndrome, Potocki–Lupski syndrome, and 2q37 monosomy, which were reported in the previous studies [23, 24].

Thus, we believe that the correct genetic diagnosis confirmed by CMA is imperative to medical management and prognostic evaluation of patients with DD/ID.

4.3. Assessment of Recurrence Risks. In our study, microdeletion/microduplication syndromes were detected in 76 patients. As most of the syndromes are de novo (63/77), the recurrence risk of these sporadic syndromes is extremely low. However, the parents of the DD/ID patients with maternally derived 15q11-q13 duplication (Cases 23, 24, and 92) or some parentally derived recurrent CNVs such as 16p11.2 microdeletion (Case 92) or 16p13.11 microduplication/microdeletion (Cases 22 and 86) have a recurrence risk of 50%. In addition, the parents of male patients with maternally derived X-chromosomal aberrations including Xp22.31 deletion, Xq28 duplication, or Xp11.22 duplication have a recurrence risk of 25%. Hence, the CMA results of these parents are more vital to evaluate the recurrence risk in reproduction.

In the 127 cases with pCNVs, 18 cases (14.17%) were identified with submicroscopic subtelomeric aberrations, including 7 patients suffering from microdeletion/microduplication syndromes, which was consistent with the

| Syndromes Isolated DD/ID DD/ID with MCA DD/ID with ASD DD/ID with epilepsy Total |
|-----------------------------|-----------------|-----------------|-----------------|-----------------|-----------------|
| Williams-Beuren syndrome    | 7               | 6               | 0               | 0               | 13              |
| Angelman syndrome           | 4               | 1               | 0               | 2               | 7               |
| Silver–Russell syndrome     | 0               | 3               | 0               | 0               | 3               |
| 15q11-q13 duplication syndrome | 2             | 1               | 0               | 0               | 3               |
| 16p11.2 recurrent microdeletion | 0             | 3               | 0               | 0               | 3               |
| 16p13.11 recurrent microduplication (neurocognitive disorder susceptibility locus) | 1          | 2               | 0               | 0               | 3               |
| 22q11 deletion syndrome (velocardiofacial/ DiGeorge syndrome) | 0             | 3               | 0               | 0               | 3               |
| 8p23.1 deletion syndrome    | 2               | 1               | 0               | 0               | 3               |
| Prader–Willi syndrome       | 0               | 3               | 0               | 0               | 3               |
| Smith–Magenis syndrome      | 0               | 2               | 1               | 0               | 3               |
| 22q13 deletion syndrome (Phelan–Mcdermid syndrome) | 2           | 1               | 0               | 0               | 3               |
| 2q37 monosomy               | 0               | 1               | 1               | 0               | 2               |
| Cri du chat syndrome (5p deletion) | 0       | 2               | 0               | 0               | 2               |
| Leri–Well dyschondrosteosis (LWD): SHOX deletion | 0           | 2               | 0               | 0               | 2               |
| Potocki–Lupski syndrome (17p11.2 duplication syndrome) | 1           | 0               | 1               | 0               | 2               |
| Wolf–Hirschhorn syndrome    | 1               | 1               | 0               | 0               | 2               |
| Xq28 (MECP2) duplication    | 2               | 0               | 0               | 0               | 2               |
| Cat eye syndrome            | 0               | 1               | 0               | 0               | 1               |
| 12p13.33 microdeletion syndrome | 0           | 1               | 0               | 0               | 1               |
| 15q24 recurrent microdeletion syndrome | 1             | 0               | 0               | 0               | 1               |
| 15q26 overgrowth syndrome   | 0               | 1               | 0               | 0               | 1               |
| 16p11.2 microduplication syndrome | 0           | 0               | 0               | 1               | 1               |
| 16p13.11 recurrent microduplication (neurocognitive disorder susceptibility locus) | 0           | 0               | 0               | 1               | 1               |
| 17q21.31 recurrent microdeletion syndrome (Koolen–de Vries syndrome) | 0           | 1               | 0               | 0               | 1               |
| 1q43-q44 deletion syndrome  | 1               | 0               | 0               | 0               | 1               |
| 22q11 duplication syndrome  | 1               | 0               | 0               | 0               | 1               |
| ATR-16 syndrome             | 1               | 0               | 0               | 0               | 1               |
| Lamb–Shaffer syndrome       | 1               | 0               | 0               | 0               | 1               |
| Miller–Dieker syndrome      | 0               | 1               | 0               | 0               | 1               |
| NF1-microdeletion syndrome  | 1               | 0               | 0               | 0               | 1               |
| Pelizaeus–Merzbacher disease (carrier) | 0           | 1               | 0               | 0               | 1               |
| Potocki–Shaffer syndrome     | 1               | 0               | 0               | 0               | 1               |
| Rett syndrome               | 0               | 1               | 0               | 0               | 1               |
| Steroid sulphatase deficiency (STS) | 0             | 0               | 0               | 0               | 1               |
| Xp11.22-linked intellectual disability | 0         | 1               | 0               | 0               | 1               |
| Total                       | 29              | 40              | 3               | 5               | 77              |
results of Cheng et al. [25]. In the 18 cases, 8 families were confirmed with parental balanced translocations and 2 families were confirmed with pericentric inversions by karyotyping. These families have an extremely high risk of having another child with submicroscopic subtelomeric aberrations induced DD/ID (10/18). Conventional cytogenetics can only recognize chromosomal rearrangements with a limited resolution of 5–10 Mb [9]. There were still 8 cases diagnosed as de novo submicroscopic subtelomeric aberrations by comparing with the karyotypes of their parents. These parents should be further tested whether they have balanced translocations or pericentric inversions by locus specific FISH probes according to the results of CMA. Fortunately, all the 18 families may possibly have a healthy child if effective genetic counseling was given based on reasonable techniques of prenatal or preimplantational diagnosis.

4.4. Limitations of CMA. Parental study is usually indispensable because it not only helps with the interpretation of the clinical significance of CNVs but also contributes to genetic counseling and the evaluation of recurrence risk of genetic abnormalities [26]. However, even though the results of normal parents were compared with their children, there was still 1.11% VUS in our study. In general, the rate of VUS will decrease as more CMA results are obtained from the normal parents. The establishment of a normal individual CMA database might be helpful to address this issue.

CMA has been confirmed as a vital technology to offer extremely higher diagnostic yield compared with chromosomal karyotype analysis in DD/ID. However, the genetic etiology of approximately 80% of patients remains unknown. Development of NGS offers another option for the genetic diagnosis of DD/ID. Currently, with an increased number of pathogenic mutations of genes associated with DD/ID detected by NGS, the diagnostic yield could be further improved by 20–30% [27, 28]. A combination of CMA and NGS could be a comprehensive strategy, but the cost-effectiveness should be considered.

Data Availability

The CMA data used to support the findings of this study may be released upon application to Prenatal Diagnosis Center, West China Second University Hospital, Sichuan University, who can be contacted at e-mail of the director of Prenatal Diagnosis Center.

Conflicts of Interest

The authors declare that there are no conflicts of interest regarding the publication of this paper.

Acknowledgments

The authors wish to thank the patients and their families for their participation in this study. This study was supported by the National Key Research and Development Program of China (2018YFC1002200 to Jun Zhu) and Technology Research and Development Program of Science and Technology Department of Sichuan Province, China (2018SZ0127 to Shanling Liu and 2017SZ0125 to Ting Hu).
References

[1] A. Battaglia, V. Doccini, L. Bernardini et al., “Confirmation of chromosomal microarray as a first-tier clinical diagnostic test for individuals with developmental delay, intellectual disability, autism spectrum disorders and dysmorphic features,” European Journal of Paediatric Neurology, vol. 17, no. 6, pp. 589–599, 2013.

[2] Y. Wu, T. Y. Ji, J. M. Wang et al., “Submicroscopic subtelomeric aberrations in Chinese patients with unexplained developmental delay/mental retardation,” BMC Medical Genetics, vol. 11, no. 1, p. 70, 2010.

[3] S. Nambot, J. Thevenon, P. Kuentz et al., “Clinical whole-exome sequencing for the diagnosis of rare disorders with congenital anomalies and/or intellectual disability: substantial interest of prospective annual reanalysis,” Genetics in Medicine, vol. 20, no. 6, pp. 645–654, 2018.

[4] J. B. Moeschler, M. Shevell, and Committee on Genetics, “Array-based technology and

[5] G. S. Sagoo, A. S. Butterworth, S. Sanderson, C. Shaw-Smith, J. P. T. Higgins, and H. Burton, “Array CGH in patients with learning disability (mental retardation) and congenital anomalies: updated systematic review and meta-analysis of 19 studies and 13,926 subjects,” Genetics in Medicine, vol. 11, no. 3, pp. 139–146, 2009.

[6] E. B. Kaminsky, V. Kaul, J. Paschall et al., “An evidence-based approach to establish the functional and clinical significance of copy number variants in intellectual and developmental disabilities,” Genetics in Medicine, vol. 13, no. 1, pp. 1–47, 2011.

[7] G. M. Cooper, B. P. Coe, S. Girirajan et al., “A copy number variation morbidity map of developmental delay,” Nature Genetics, vol. 43, no. 9, pp. 838–846, 2011.

[8] M. Roselló, F. Martínez, S. Monfort, S. Mayo, O. Oltra, and C. Orellana, “Phenotype profiling of patients with intellectual disability and copy number variations,” European Journal of Paediatric Neurology, vol. 18, no. 5, pp. 558–566, 2014.

[9] D. T. Miller, M. P. Adam, S. Aradhya et al., “Consensus statement: chromosomal microarray is a first-tier clinical diagnostic test for individuals with developmental disabilities or congenital anomalies,” The American Journal of Human Genetics, vol. 86, no. 5, pp. 749–764, 2010.

[10] D. A. Regier, J. M. Friedman, and C. A. Marra, “Value for money? Array genomic hybridization for diagnostic testing for genetic causes of intellectual disability,” The American Journal of Human Genetics, vol. 86, no. 5, pp. 765–772, 2010.

[11] M. Manning and L. Hudgins, "Array-based technology and recommendations for utilization in medical genetics practice for detection of chromosomal abnormalities," Genetics in Medicine, vol. 12, no. 11, pp. 742–745, 2010.

[12] J. B. Moeschler, M. Shevell, and Committee on Genetics, “Comprehensive evaluation of the child with intellectual disability or global developmental delays,” Pediatrics, vol. 134, no. 3, pp. e903–e918, 2014.

[13] T. Hu, Z. Zhang, I. Wang et al., “Prenatal diagnosis of chromosomal aberrations by chromosomal microarray analysis in fetuses with ultrasound anomalies in the urinary system,” Prenatal Diagnosis, 2019.

[14] M. Bartnik, E. Szczepaniak, K. Derwińska et al., “Application of array comparative genomic hybridization in 102 patients with epilepsy and additional neurodevelopmental disorders,” American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, vol. 159B, no. 7, pp. 760–771, 2012.

[15] K. S. Ho, H. Twede, R. Vanzo et al., “Clinical performance of an ultrahigh resolution chromosomal microarray optimized for neurodevelopmental disorders,” BioMed Research International, vol. 2016, Article ID 3284534, 7 pages, 2016.

[16] K. S. Ho, E. R. Wassman, A. L. Baxter et al., “Chromosomal microarray analysis of consecutive individuals with autism spectrum disorders using an ultra-high resolution chromosomal microarray optimized for neurodevelopmental disorders,” International Journal of Molecular Sciences, vol. 17, no. 12, 2016.

[17] P. Sharma, N. Gupta, M. R. Chowdhury et al., “Application of chromosomal microarrays in the evaluation of intellectual disability/global developmental delay patients—a study from a tertiary care genetic centre in India,” Gene, vol. 590, no. 1, pp. 109–119, 2016.

[18] D. M. Ruderfer, T. Hamamsy, M. Lek et al., “Patterns of generic intolerance of rare copy number variation in 59,898 human exomes,” Nature Genetics, vol. 48, no. 10, pp. 1107–1111, 2016.

[19] A. Ingason, G. Kirov, I. Giegling et al., “Maternally derived microduplications at 15q11-q13: implication of imprinted genes in psychotic illness,” American Journal of Psychiatry, vol. 168, no. 4, pp. 408–417, 2011.

[20] L. A. Weiss, Y. Shen, J. M. Korn et al., “Association between microdeletion and microduplication at 16p11.2 and autism,” New England Journal of Medicine, vol. 358, no. 7, pp. 667–675, 2008.

[21] K. Wolfe, A. Strydom, D. Morrogh et al., “Chromosomal microarray testing in adults with intellectual disability presenting with comorbid psychiatric disorders,” European Journal of Human Genetics, vol. 25, no. 1, pp. 66–72, 2016.

[22] J. Wang, G. Gotway, J. M. Pascual, and J. Y. Park, “The Diagnostic yield of clinical next—generation sequencing panels for epilepsy,” JAMA Neurology, vol. 71, no. 5, pp. 650–651, 2014.

[23] V. Oikonomakis, K. Kosma, A. Mitarakos et al., “Recurrent copy number variations as risk factors for autism spectrum disorders: analysis of the clinical implications,” Clinical Genetics, vol. 89, no. 6, pp. 708–718, 2016.

[24] D. Pinto, E. Delaby, D. Merico et al., “Convergence of genes and cellular pathways dysregulated in autism spectrum disorders,” The American Journal of Human Genetics, vol. 94, no. 5, pp. 677–694, 2014.

[25] S. S. W. Cheng, K. Y. K. Chan, K. K. P. Leung et al., “Experience of chromosomal microarray applied in prenatal and postnatal settings in Hong Kong,” American Journal of Medical Genetics Part C: Seminars in Medical Genetics, vol. 181, no. 2, pp. 196–207, 2019.

[26] S. Shin, N. Yu, J. R. Choi, S. Jeong, and K.-A. Lee, “Routine chromosomal microarray analysis is necessary in Korean patients with unexplained developmental delay/mental retardation-autism spectrum disorder,” Annals of Laboratory Medicine, vol. 35, no. 5, pp. 510–518, 2015.

[27] F. Martínez, A. Caro-Llopis, M. Roselló et al., “High diagnostically instrument of syndromic intellectual disability by targeted next-generation sequencing,” Journal of Medical Genetics, vol. 54, no. 2, pp. 87–92, 2017.

[28] C. Gilsen, J. Y. Hehir-Kwa, D. T. Thung et al., “Genome sequencing identifies major causes of severe intellectual disability,” Nature, vol. 511, no. 7509, pp. 344–347, 2014.