Original Article

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Effects of Copy Number Variations on Developmental Aspects of Children With Delayed Development

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Objective To determine effects of copy number variations (CNV) on developmental aspects of children suspected of having delayed development.

Methods A retrospective chart review was done for 65 children who underwent array-comparative genomic hybridization after visiting physical medicine & rehabilitation department of outpatient clinic with delayed development as chief complaints. Children were evaluated with Denver Developmental Screening Test II (DDST-II), Sequenced Language Scale for Infants (SELSI), or Preschool Receptive-Expressive Language Scale (PRES). A Mann-Whitney U test was conducted to determine statistical differences of developmental quotient (DQ), receptive language quotient (RLQ), and expressive language quotient (ELQ) between children with CNV (CNV(+) group, n=16) and children without CNV (CNV(–) group, n=37).

Results Of these subjects, the average age was 35.1 months (mean age, 35.1±24.2 months). Sixteen (30.2%) patients had copy number variations. In the CNV(+) group, 14 children underwent DDST-II. In the CNV(–) group, 29 children underwent DDST-II. Among variables, gross motor scale was significantly (p=0.038) lower in the CNV(+) group compared with the CNV(–) group. In the CNV(+) group, 5 children underwent either SELSI or PRES. In the CNV(–) group, 27 children underwent above language assessment examination. Both RLQ and ELQ were similar between the two groups.

Conclusion The gross motor domain in DQ was significantly lower in children with CNV compared to that in children without CNV. This result suggests that additional genetic factors contribute to this variability. Active detection of genomic imbalance could play a vital role when prominent gross motor delay is presented in children with delayed development.

Keywords Developmental disabilities, DNA copy number variations, Array-based comparative genomic hybridization, Motor skills, Hypotonia

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INTRODUCTION

Over the recent years, our knowledge of copy number variation (CNV) in the human genome has evolved rapidly. Applications of increasingly higher resolution array based techniques, particularly microarray-based comparative genomic hybridization (array-CGH), have been proven invaluable in discovering disease-causing CNV in a wide variety of disorders ranging from pediatric diseases (neurological and congenital birth defects) to adult-onset neuropsychiatric diseases such as Alzheimer disease [1-3].

CNVs represent the imbalance of genomic sequence compared with the reference genome. They may range in size from kilobases (kb) to megabases (Mb). CNV can occur due to structural changes within the genome, including duplications, deletions, insertions, and translocations. It can lead to either an increase or decrease of genomic segments [4-6].

CNV can be expressed in disease phenotype by various mechanisms. Alteration of coding regions in copy number of dosage-sensitive genes plays a primary role in pathogenesis [1,7]. Disruption of regulatory elements on non-coding region may also play some crucial roles [8]. Establishing pathogenicity of CNV is the major challenge in the interpretation of array results due to rarity of many individual CNV, difficulty of identifying exact dosage-sensitive genes, and considerable variations in expressivity [1,9]. The clinical significance of a CNV is usually determined by its mode of inheritance, size, type (deletion and duplication), gene content, and comparison with CNV databases [10-12].

Developmental delay refers to children who significantly lag in developmental features and skills in motor, language, social, and cognitive developmental domains at expected age [13]. The cause of developmental disabilities is diverse and often unknown. However, environmental factors, biological factors, and complications of pregnancy have been suggested as possible causes [14].

Early detection of pathogenic CNV plays a crucial role as it allows referrals for appropriate treatment, improves prognosis, and enables better genetic counseling for the family. Consequently, effort has been made to identify clinically relevant CNV that can facilitate the characterization of phenotypic consequences [7,14].

Although array-CGH has been adopted as a first-tier clinical diagnostic test in individuals with developmental disabilities, especially in economically developed countries [11], applying array-CGH to every individual presented with delayed development as a routine study is impractical due to limited accessibility to facilities offering comprehensive diagnostic testing and its high cost [14,15].

Patients with CNV may present with varying clinical features. It is highly probable that CNV plays a role in the manifestation of symptoms for those who have delayed development [1]. To the best of our knowledge, studies utilizing quantified measurements for development domains of children with delayed development have not been reported yet. Therefore, the objective of this study was to determine effects of CNV on developmental aspects of children suspected of having delayed development. Clinical development aspect of children suspected of having delayed development was compared between those who had CNV and those who did not have CNV.

MATERIALS AND METHODS

Subjects

A retrospective chart review was done for 65 children who underwent array-CGH after visiting physical medicine & rehabilitation department of outpatient clinic with delayed development as chief complaints from January 2016 to November 2017. More than one test of Sequenced Language Scale for Infants (SELSI), Preschool Receptive-Expressive Language Scale (PRES), and Denver Developmental Screening Test II (DDST-II) was conducted for these children.

Inclusion criteria were: (1) interpreted as 'suspect' in DDST-II defined as those who scored two or more cautions and/or one or more delays [16], and (2) at least one of receptive or expressive language domains in SELSI or PRES fell below 2 standard deviations compared to children of the same age.

Methods

This study was carried out through retrospective chart review. It was approved by Institutional Review Board of Seoul St. Mary's Hospital (No. KC18RCSI0483). The requirement for informed consent from individual patients was omitted because of the retrospective design of this study. Thorough chart review was performed to distin-

guish factors that might affect general development of the patient, including prenatal, natal, postnatal risk factors and brain magnetic resonance imaging interpretation. Prenatal factors consisted of diagnosis of intrauterine growth restriction, eclampsia, hydramnios or oligoamnios, threatened abortion, and placenta previa. Natal factors included history of asphyxia, jaundice, meconium staining, premature birth, and low birth weight. Postnatal factors included neonatal convulsion and feeding difficulty.

Children were evaluated by DDST-II, SELSI, or PRES. DDST was first introduced in 1967 and revised in 1992. It targets infants and children aged between 0 and 6 years old. It is one of the most widely utilized tools for screening children with delayed development. DDST-II is assessed in four developmental domains: gross motor, fine motor-adaptive, language, and social-personal domains [17]. Although DDST-II is not intended to yield a developmental quotient (DQ) originally, recent study has suggested that DQ from DDST-II may correlate well with diagnosis of several pediatric developmental and behavioral disorders [18]. Thus, DQ has been utilized in number of studies [19-22]. In addition, several studies have compared DDST-II with various diagnostic tools for developmental delay, revealing some correlations. In one study, mental developmental index from the Bayley Scales of Infant Development II was significantly correlated with all four domains of DDST-II and psychomotor development index was significantly related with gross motor, fine motor-adaptive, and social-personal domains of DDST-II [23]. Therefore, in the current study, DQ was utilized to assess different domains of development between the two groups. Functional age of the patient was measured with the four developmental domains of DDST-II. DQ was calculated by dividing the developmental age by chronologic age. It is expressed in percentage [19]. For language assessment, we used SELSI and PRES depending on patient's age. Receptive language quotient (RLQ) and expressive language quotient (ELQ) were calculated by dividing receptive score and language score by chronologic age, respectively. They are expressed in percentage [24]. The first test from the date of referral was utilized if the patient was evaluated with serial tests.

Array-CGH analysis was performed with SurePrint G3 Human CGH Microarray 8×60K kit (Agilent Technologies, Santa Clara, CA, USA) which consisted of 62,976 oligonucleotide probes spaced at 41 kbp intervals (median probe spacing) according to the manufacturer's protocol. CNVs were detected using Aberration Detection Method 2 (ADM-2) algorithm. Genomic positions were defined according to human reference genome hg19/GRCh37.

Statistics

The statistical software SPSS version 24.0 for Windows (IBM, Armonk, NY, USA) was utilized for data processing. A Mann-Whitney U test was conducted to determine statistical differences of DQ, RLQ, and ELQ between children with CNV (CNV(+) group, n=16) and children without CNV (CNV(–) group, n=37). Statistical significance was set at $p<0.05$.

Table 1. General demographics of subjects included for this study

Variable	Patients with CNV (n=16)	Patients without CNV (n=37)	p-value
Age (mo)	27.6±21.6	39.4±24.3	0.072
Gender, male (%)	56.25	62.16	0.741
Intrauterine periods (wk)	38.18±1.53	37.47±3.67	0.915
Birth weight (g)	2,843±58.64	2,774±75.05	0.892
Prenatal risk factors (%)	18.8	16.2	0.831
Natal risk factors (%)	43.8	35.1	0.564
Postnatal risk factors (%)	18.8	10.8	0.464
Abnormal brain MRI (%)	31.3	24.3	0.551

Values are presented as mean±standard deviation.
CNV, copy number variation; MRI, magnetic resonance imaging.

Table 2. Array-CGH results and clinical features of 16 patients with CNV

Patient no.	Age (mo)	Gender	Array result	Size (Mb)	Inheritance	Clinical features
1	8	M	arr[hg19] 8q21.11q21.13 (76069471_81532974)x1	5.5	De novo	DD, DLD, facial dysmorphism, simian crease, abnormal patterns of toes, neonatal hypotonia
2	2.5	M	arr[hg19] 12p13.33p11.1 (450479_34345585)x3-4	33.9	Unknown	DD, dextroversion of the heart, ICH, hypotonia
3	0.9	F	arr[hg19] 4q35.1q35.2 (185274461_190469337) x1, 10p15.3p11.23 (148206_29975521)x3	5.2, 30	Unknown	DD, cardiomegaly, ASD secundum with septal aneurysm, severe hypotonia, congenital arachnoid cyst
4	42	M	arr[hg19] 13q12.3 (30656355_31905182)x3	1.2	Unknown	DD, DLD, hyperactivity, bronchomalacia, ID, ASD, facial dysmorphism, hypotonia
5	22	M	arr[hg19] 21q21.1 (20090,068_22116178)x1	2.0	Unknown	DD, congenital hypotonia, pes planus, ataxic gait
6	13	F	arr[hg19] 15q11.2q13.1 (23739358_29213461)x1	5.5	Unknown	DD, severe hypotonia, DDH
7	18	M	arr[hg19] 1q21.1q21.2 (146564743_149224043)x1	2.7	Unknown	DD, DLD, HIE, ataxic gait, planovalgus, hammer toe
8	60	F	arr[hg19] Xp22.33p22.2 (61091_10125133)x1	10	Unknown	DD, DLD, facial dysmorphism, moderate ID
9	48	F	arr[hg19] 17q12 (34817422_36168104)x3	1.4	Unknown	DD, DLD
10	17	F	arr[hg19] 9q33.2q33.3 (124628147_127176303)x1	2.5	De novo	DD, inguinal hernia, hypotonia
11	72	M	arr[hg19] 3q29 (195740357_197395697)x1	1.7	Unknown	DD, DLD, exotropia
12	16	M	arr[hg19] 16p12.3p11.2 (16899617_28574419)x3	11.7	De novo	DD, facial dysmorphism, hypertelorism, high arched palate, hypotonia, ID
13	10	F	arr[hg19] 17p11.2 (16822683_20193169)x1	3.4	Unknown	DD, CoA, PDA, hypotonia
14	9	F	arr[hg19] 12q23.1q23.3 (98731852_104856429)x1	6.1	Unknown	DD, cleft lip, hypotonia
15	48	M	arr[hg19] 15q13.1q13.3 (29213402_32914140)x1	3.7	Unknown	DD, DLD, ITP
16	19.2	M	arr[hg19] Xp22.31 (6552712_8115153)x2	1.6	Unknown	DD, facial dysmorphism, frontal boldness, hypotonia, high arched palate

CGH, comparative genomic hybridization; CNV, copy number variation; DD, delayed development; DLD, developmental language delay; ID, intellectual disability; DDH, developmental dysplasia of the hip; HIE, hypoxic-ischemic encephalopathy; ITP, idiopathic thrombocytopenic purpura; CoA, coarctation of aorta; PDA, patent ductus arteriosus.

RESULTS

General demographics

Of 65 children who underwent array-CGH after visiting physical medicine & rehabilitation department outpatient clinic with delayed development as chief complaints, 53 patients met the inclusion criteria. Forty-three patients undertook DDST-II and 32 patients took at least one of SELSI or PRES. Twenty-three patients received both DDST-II and at least one of SELSI or PRES. Nine patients were evaluated only with SELSI/PRES. They were not evaluated with DDST-II because they were either more than 6 years old or had prior test results from different clinics. Average age of all patients was 35.1 months (mean age, 35.1±24.2 months). There were 32 (60.4%) boys. The CNV(+) group consisted of 16 patients (9 males) aged between 1 month and 72 months (mean age, 27.6±21.6 months). The CNV(–) group consisted of 37 patients (23 males) aged between 1.5 months and 84 months (mean age, 39.4±24.3 months). There was no significant difference in age or gender between the two groups (Table 1).

Perinatal history

Prenatal problems were observed in 3 patients (18.8%) in the CNV(+) group and 6 patients (16.2%) in the CNV(–) group. Natal risk factors were observed in 7 patients (43.8%) in the CNV(+) group and 13 patients (35.1%) in the CNV(–) group. Postnatal problems were presented in 3 patients (18.8%) in the CNV(+) group and 4 patients (10.8%) in the CNV(–) group. Average gestational age was 38.18 weeks in the CNV(+) group and 37.48 weeks in the CNV(–) group. Average birth weights were 2,843 g and 2,774 g in CNV(+) and CNV(–) groups, respectively. Eleven patients in the CNV(+) group and 26 patients in the CNV(–) group had brain magnetic resonance imaging records. Abnormal brain image findings were presented in 5 patients (31.3%) in the CNV(+) group and 9 patients (24.3%) in the CNV(–) group. There were no significant differences in prenatal problems, natal risk factors, postnatal problems, gestational age, or abnormal findings in brain images between the two groups (Table 1).

Clinical presentations

Clinical features of the 16 children with copy number variations are shown in Table 2. Amongst these 16 children in the CNV(+) group, 11 children (68.8%) presented with hypotonia. Amongst 37 children in the CNV(–) group, 10 children (27.0%) presented with hypotonia at the time of the first visit. Of these 21 patients who presented with hypotonia, 11 (52.4%) were diagnosed with copy number variations. Of the 16 CNV(+) patients, average size of CNV was 8.01 Mb (mean, 8.01±10.80 Mb).

Comparison of DDST-II between CNV(+) and CNV(–) groups

In the CNV(+) group, 14 children underwent DDST-II. In the CNV(–) group, 29 children underwent DDST-

Table 3. Comparison between two patient groups classified by copy number variation

	Total	Patients with CNV	Patients without CNV	p-value
DDST-II (developmental quotient)				
Personal-social	63.6±20.4	67.5±17.4	61.7±21.7	0.468
Fine motor-adaptive	71.1±19.9	69.4±21.1	71.9±19.7	0.338
Gross motor	64.0±19.1	57.7±13.2	67.1±21.0	0.038*
Language	57.1±22.1	65.9±25.0	52.9±19.7	0.140
Number of patients	43	14	29	
SELSI or PRES				
Receptive language quotient	49.6±20.6	47.8±16.9	49.9±21.4	0.938
Expressive language quotient	47.9±17.2	51.9±20.6	47.1±16.9	0.243
Number of patients	32	5	27	

Values are presented as mean±standard deviation.
DDST-II, Denver Developmental Screening Test II; SELSI, Sequenced Language Scale for Infants; PRES, Preschool Receptive-Expressive Language Scale.
*p<0.05.

II. Among variables, gross motor scale was significantly (p=0.038) lower in the CNV(+) group than that in the CNV(–) group. There was no significant difference in personal-social, fine motor-adaptive, or language domain between the two groups (Table 3).

Comparison of SELSI or PRES between CNV(+) and CNV(–) groups

In the CNV(+) group, 5 children underwent either SELSI or PRES. In the CNV(–) group, 27 children underwent the above language assessment examination. Both receptive and expressive language scores were similar between the two groups.

DISCUSSION

Diagnostic yield of genetic testing of patients with unexplained developmental delay, autism spectrum disorders, or multiple congenital anomalies is generally thought to be 15%–20% [11]. Cooper et al. [1] have calculated that 25.7% of individuals with developmental delay or intellectual disability have CNV >400 kb in length and estimated that 14.2% are due to these large CNVs. In our study, 16 of 53 (30.2%) yielded positive results for CNV, showing slightly higher yield.

CNV can be inherited or sporadic. Rare and de novo CNVs are thought to play more prominent roles in neurologic disorders [7,9,25,26]. Studies have suggested that vast majority of benign CNVs are inherited and most of inherited CNVs are lesser than 500 kb in size [27]. Larger CNVs have higher probability than smaller CNVs to cause disease. They are associated with more severe developmental phenotypes [1,28]. In our study, among 16 CNV (+) patients, three patients were found to have de novo CNVs. However, whether CNVs were inherited were unknown for most patients since few patients underwent parental study. Average size of CNVs was 8.01 Mb (mean, 8.01±10.80 Mb). All patients had CNV size greater than 1 Mb which increased the likelihood of pathogenicity cause by CNV and decreased the likelihood of false positive rate.

CNV enrichment is known to differ depending on clinical phenotype. Patients with cardiac congenital anomalies and craniofacial abnormalities are known to have the most significant CNV burden [1]. In our study, significantly more patients in the CNV(+) group presented with either cardiac abnormality or facial dysmorphism compared to those in the CNV(–) group (50.0% vs. 13.5%, p=0.0434). Many CNVs of specific genes such as 17q21.31 microdeletion, 2q11.2 duplication, 2q13 deletion, and 1q21.1 deletions/duplications [7,29] are associated with hypotonia amongst many clinical phenotypes. In 17q21.31 microdeletion, two candidate genes (*CRHR1* and *MAPT*) have been proposed to be pathogenic [7]. In our study, it was apparent that more patients in the CNV(+) group had hypotonia than those in the CNV(–) group (68.8% vs. 28.3%, p=0.012). Similar to previous studies, patients in the CNV(+) group manifested with varying clinical features involving variable genes. However, no significant study has compared major genetic burden utilizing quantitative measurements of developmental domains. The current study revealed significant difference in gross motor domain in DDST-II between patients with or without CNV. This result suggests that gross motor skills might be affected the most severely when patients with delayed development show CNV, although CNV may present diverse clinical features.

Gialluisi et al. [30] have investigated effects of CNV on reading and language performance by measuring relationship between genomic burden and the first principal component score derived from reading and language traits. Their results suggested that CNV did not contribute a substantial proportion to variance in language and reading performance. In our study, both receptive and expressive language scores from SELSI/PRES and language domain from DDST-II were similar between the two groups.

High resolution array-CGH provides a way for detecting microdeletions and microduplications. It has replaced G-band karyotype analysis or fluorescent in situ hybridization. Array-CGH has effectively increased diagnostic yield in genomic disorders, leading to its application as the first tier of testing by many centers around the world for individuals with neurodevelopmental disorders and congenital abnormalities [11,31]. The benefit of early detection of specific genetic diagnosis in congenital disorders is paramount as it allows higher rate of recommendation for clinical action, especially for inborn errors of metabolism [14,32], surveillance for potential future involvement of other pathogenic conditions, and appropriate recurrence risk counseling for the family [1,11]. However, when presented with borderline symptoms of delayed

development or in places with scarce resources, it is impractical to apply array-CGH to every individual [15]. Our study could help us prioritize and decide whether to apply array-CGH to patients suspected with delayed development. Our results suggest that active detection of patients with prominent gross motor skill decline with hypotonia may increase the likelihood of CNV detection.

Our study had a few limitations. First, the sample size was limited to 53 patients. Especially, the number of patients with CNV who took SELSI/PRES was only 5. Second, our study incorporated developmental quotient in DDST-II. The use of psychometric characteristic scale is questioned. Future studies incorporating different diagnostic tools such as composite scales of the Bayley Scales of Infant Development II may yield additional results. Third, patients were selected only at a single tertiary medical institution which might contain selection bias. Fourth, patients selected were diverse in age, especially for the CNV(–) group. In addition, average age of selected patients was generally very young. Consequently, delay in motor function might be the most noticeable feature compared to cognitive or language domain. Grouping or narrowing down of age group with larger population may yield additional results. On the other hand, studying a younger age group may provide more valuable information as it is related to early detection and intervention. Lastly, detecting CNV through microarray studies does not completely exclude genetic causality since single-nucleotide variations and small insertion/deletions not detectable by array-CGH might have been the origin of pathogenicity. Additional next-generation sequencing techniques such as whole genome sequencing may increase the diagnostic yield. However, clinical implementation of whole genome sequencing remains limited, although it has been gaining popularity [15,33]. Similar experiment utilizing whole genome sequencing may yield additional results. Therefore, future large-scale prospective studies are warranted.

In conclusion, the role of CNV in human disease has become increasingly revealed as a result of advanced tools for genome analysis. In our study, the gross motor domain in DQ was significantly lower in children with CNV compared to that in children without CNV. This result suggests that additional genetic factors may contribute to this variability. Active detection of genomic imbalance could play some vital roles when children with delayed development show prominent gross motor delay.

CONFLICT OF INTEREST

No potential conflict of interest relevant to this article was reported.

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AUTHOR CONTRIBUTION

Conceptualization: Park KB, Cho AR, Park JH. Methodology: Park KB, Cho AR, Jang WR, Kim MS, Park JH. Formal analysis: Park KB, Park JH. Funding acquisition: Park JH. Project administration: Park JH. Visualization: Park KB, Nam KE, Park JH. Writing – original draft: Park KB. Writing – review and editing: Park KB, Nam KE, Jang WR, Kim MS, Park JH. Approval of final manuscript: all authors.

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