



Phenotypic diversity of 15q11.2 copy number variants: a case series and review of the literature

¹University of Health Sciences, Tepecik Training and Research Hospital, Department of Pediatric Neurology, Izmir, Türkiye, ²Izmir Katip Celebi University, Faculty of Medicine, Department of Pediatric Neurology, Izmir, Türkiye, ³University of Health Sciences, Tepecik Training and Research Hospital, Genetic Diagnosis Center, Izmir, Türkiye

The proximal region of the long arm of human chromosome 15 (15q) is relatively susceptible to the non-allelic homologous recombination of low copy repeat elements.¹ The clusters of low copy repeats are referred as breakpoint (BP) regions.² The six BP regions (BP1-BP6) on the proximal 15q mediate microdeletions and microduplications, which are collectively termed as copy-number variants (CNVs).^{2,3} The four highly conserved and nonimprinted genes (NIPA1, NIPA2, CYFIP1 and TUBGCP5) are located in the region between BP1 and BP2 which spans approximately 500 kb.⁴ NIPA1, NIPA2, and CYFIP1 are extensively expressed in the central nervous system, whereas TUBGCP5 is more specific to the subthalamic nuclei.⁵ These four highly conserved genes have several functions in neuronal connectivity and axonal growth.⁶

OBJECTIVES

Several reports have linked microdeletions and microduplications on the 15q11.2 BP1-BP2 region involving these four genes with behavioural disorder disorders, autism spectrum (ASD) developmental delay, learning disabilities and seizures.⁶⁻¹⁴ Moreover, heterogeneous phenotypes from severely affected individuals to healthy carriers suggest incomplete penetrance or variable expressivity of these genes.¹⁴ In the present study, first we report on the phenotypic features of 17 patients with 15q11.2 CNVs. Moreover, we conduct a review of the literature to compare the phenotypic diversity of 15q11.2 CNVs and contribute to the current knowledge from previous case series.

MATERIALS & METHODS

We performed a retrospective case series of the patients with 15q11.2 CNVs who were referred to the Genetic Diagnosis Center of our hospital between January 2015-January 2021. Patient demographics,

magnetic brain imaging, resonance electroencephalography, chromosomal microarray results and the clinical data were obtained from the PROBEL hospital information management system. For the interpretation of CNVs, variants were checked in the databases; DGV and DECIPHER, and the phenotypes were compared with the literature and databases such OMIM, ECARUCA, ORPHANET. For the review of the literature, we performed a PubMed search and included all studies reporting the 15q11.2 CNVs between 2007 and 2022 except overlapping studies. After the articles were assessed for eligibility, and data from 15 articles were included. The data were analyzed using the software Statistical Package for Social Science for Windows, version 22.

RESULTS

Of the 17 patients, 65% (n=11) had microduplication and 35% (n=6) had microdeletion in the 15q11.2 BP1-BP2 region. The mean size of the CNVs was 485±165 kb. Patients had a variety of phenotypic features including neurodevelopmental delay (59%), dysmorphic features (41%), epilepsy (41%), cognitive impairment (29%), behavioral problems/psychiatric symptoms (18%), hypotonicity/muscle weakness (18%), scoliosis (12%), neuropathy with liability to pressure palsies (6%), microcephaly (6%), and hydrocephalus (6%). No significant difference was detected between the phenotypic features of microduplication and microdeletion groups (all p>0.05). Results of the other studies reporting the phenotypic features of the patients with 15q11.2 CNVs are summarized in Table 1 and Table 2.

REFERENCES

- 2002;10(1):26-35.
- family and an unrelated boy. Mol Genet Genomic Med. 2020;8(4):e1109.
- dysmorphic features. J Genet Syndr Gene Ther. 2014;5(5):1
- Genet B Neuropsychiatr Genet. 2016:171(8):1088-98.

<u>Gunce Basarir¹, Irmak Erdogan¹, Nihal Olgac Dundar², Berk Özyilmaz³, Pinar Gencpinar²</u>

Table 1: Comparison of previously described 15q11.2 microduplication cases with the present study

	Present	Van der	Burnside	Abdelmoity	Picinelli	Mohan	Chu	% Total
	study	Zwaag	et al,	et al,	et al,	et al,	et al,	(present
		et al, 2010	2011	2012	2016	2018	2021	study and literature)
Hypotonicity	1/11 (9%)	0/3	7/49	N/A	1/5	N/A	N/A	9/68 (13.2%)
Neurodevelop- mental delay	7/11 (63%)	2/3	19/49	8/10	5/5	86/215	0/9	127/302 (42%)
Speech impairment	0/11 (0%)	1/3	22/44	N/A	5/5	N/A	0/9	27/72 (37.5%)
Cognitive impairment	3/11 (27%)	N/A	N/A	8/10	4/5	N/A	N/A	15/26 (57.6%)
Epilepsy	4/11 (36%)	0/3	6/49	3/10	0/5	18/215	N/A	31/293 (10.6%)
ADHD	0/11 (0%)	0/3	18/44	0/10	2/5	N/A	N/A	20/73 (27.3%)
Abnormal Brain MRI findings	1/8 (12.5%)	N/A	N/A	2/10	2/5	N/A	1/3	6/26 (23%)
Dysmorphic features	5/11 (45%)	0/3	22/49	4/10	0/5	25/215	1/9	57/302 (18.9%)
Behavioral/ psychiatric symptoms	2/11 (18%)	N/A	19/49	2/10	3/5	30/215	0/9	56/299 (18.7%)

ADHD, attention deficit hyperactivity disorder; MRI, magnetic resonance imaging; N/A, not applicable.

Table 2: Comparison of previously described 15q11.2 microdeletion cases with the present study

	Present study	Murthy	Doornbos et al, 2009	von der Lippe et al, 2011	Burnside et al, 2011	Sempere Pérez et al, 2011	Madr igal et al, 2012	Abdelmoity et al, 2012	Cafferkey et al, 2014	Vanlerberghe et al, 2015	Hashemi et al, 2015	Mohan et al, 2018	Han et al, 2021	Chu et al, 2021	% (pr stuc liter
		et al, 2007													
Microcephaly	1/6 (16%)	N/A	N/A	N/A	N/A	N/A	2/2	4/16	N/A	10/42	3/22	N/A	0/3	N/A	20 (2
Hypotonicity	2/6 (33%)	N/A	N/A	N/A	N/A	N/A	N/A	2/15	N/A	9/41	2/22	N/A	3/3	N/A	18 (20
Neurodevelop- mental delay	3/6 (50%)	1/1	8/9	3/7	20/56	1/1	2/2	N/A	65/77	18/41	19/22	91/262	3/3	5/10	239 (4
Speech impairment	1/6 (16%)	1/1	8/8	7/7	44/49	1/1	2/2	N/A	37/77	35/41	4/22	N/A	3/3	2/10	14 <u>!</u> (63
Cognitive impairment	2/6 (33%)	1/1	N/A	N/A	11/49	1/1	2/2	13/16	N/A	28/41	N/A	N/A	3/3	N/A	61 (5:
Epilepsy	3/6 (50%)	0/1	2/8	1/7	14/56	0/1	0/2	2/15	13/83	9/48	3/22	27/262	1/3	N/A	75 (1
ADHD	1/6 (16%)	1/1	2/8	1/7	16/49	1/1	0/2	7/12	N/A	20/41	6/22	N/A	0/3	N/A	55 (36
Abnormal Brain MRI findings	1/2 (50%)	0/1	1/4	1/2	N/A	N/A	N/A	N/A	N/A	12/31	6/16	N/A	0/3	1/5	22 (34
Dysmorphic features	2/6 (33%)	N/A	6/9	N/A	27/56	1/1	N/A	N/A	28/83	30/42	8/19	44/262	0/3	1/10	14) (3
Behavioral/ psychiatric symptoms	1/6 (16%)	0/1	0/9	1/7	N/A	0/1	N/A	N/A	35/73	0/40	4/22	25/262	0/3	0/10	66 (15

ADHD, attention deficit hyperactivity disorder; MRI, magnetic resonance imaging; N/A, not applicable.

8. Abdelmoity AT, LePichon JB, Nyp SS, et al. 15g11.2 proximal imbalances associated with a diverse array of neuropsychiatric disorders and mild dysmorphic

- features. J Dev Behav Pediatr. 2012;33(7):570-6 9. Doornbos M, Sikkema-Raddatz B, Ruijvenkamp CA, et al. Nine patients with a microdeletion 15q11.2 between breakpoints 1 and 2 of the Prader-Willi critical
- region, possibly associated with behavioural disturbances. Eur J Med Genet. 2009;52(2-3):108-15. 10. Murthy SK, Nygren AO, El Shakankiry HM, et al. Detection of a novel familial deletion of four genes between BP1 and BP2 of the Prader-Willi/Angelman syndrome
- critical region by oligo-array CGH in a child with neurological disorder and speech impairment. Cytogenet Genome Res. 2007;116(1-2):135-40.

11. van der Zwaag B, Staal WG, Hochstenbach R, et al. A co-segregating microduplication of chromosome 15q11.2 pinpoints two risk genes for autism spectrum disorder. Am J Med Genet B Neuropsychiatr Genet. 2010;153B(4):960-6.

12. Vanlerberghe C, Petit F, Malan V, et al. 15q11.2 microdeletion (BP1-BP2) and developmental delay, behaviour issues, epilepsy and congenital heart disease: a series of 52 patients. Eur J Med Genet. 2015;58(3):140-7.

13. von der Lippe C, Rustad C, Heimdal K, Rødningen OK. 15q11.2 microdeletion - seven new patients with delayed development and/or behavioural problems. Eur J Med Genet. 2011;54(3):357-60.

14. Benítez-Burraco A, Barcos-Martínez M, Espejo-Portero I, Jiménez-Romero S. Variable Penetrance of the 15q11.2 BP1-BP2 Microduplication in a Family with

Cognitive and Language Impairment. Mol Syndromol. 2017;8(3):139-47. 15. Pérez AS, Trives IM, Azorín IP, et al. Microdeleción 15q11. 2 (BP1-BP2). Un nuevo síndrome con expresividad variable. In Anales de Pediatría 2011 Jul 1 (Vol. 75, No. 1, pp. 58-62). Elsevier Doyma.



CONCLUSIONS

The 15q11.2 BP1-BP2 region has been suggested to be a "susceptibility" locus for neurodevelopmental and neuropsychiatric disorders since the phenotypic variability and low penetrance.¹⁴ The associated phenotypes of CNVs on BP1-BP2 region range from normal phenotypes to neurodevelopmental delay, behavioral problems, seizures, dyslexia, dyscalculia, mild dysmorphic features, anorexia, neuropsychiatric conditions such as schizophrenia, ASD, and attention deficit/hyperactivity disorder.⁷⁻²¹ We believe that greater understanding of the possible influences of the CNVs in this susceptibility locus will aid in our clinical approach in the future.

16. Madrigal I, Rodríguez-Revenga L, Xunclà M, Milà M. 15q11. 2 microdeletion and FMR1 premutation in a family with intellectual disabilities and autism. Gene. 2012;508(1):92-5.

17. Cafferkey M, Ahn JW, Flinter F, Ogilvie C. Phenotypic features in patients with 15q11.2(BP1-BP2) deletion: further delineation of an emerging syndrome. Am J Med Genet

A. 2014:164A(8):1916-22 18. Hashemi B, Bassett A, Chitayat D, et al. Deletion of 15q11.2(BP1-BP2) region: further evidence for lack of phenotypic specificity in a pediatric population. Am J Med Genet A. 2015:167A(9):2098-102.

19. Han JY, Park J. Phenotypic Diversity of 15q11.2 BP1-BP2 Deletion in Three Korean Families with Development Delay and/or Intellectual Disability: A Case Series and Literature Review. Diagnostics (Basel). 2021;11(4):722.

20. Chu FC, Shaw SW, Lee CH, et al. Adverse Perinatal and Early Life Outcomes following 15q11.2 CNV Diagnosis. Genes (Basel). 2021;12(10):1480. 1. Mohan KN, Cao Y, Pham J, et al. Phenotypic association of 15q11.2 CNVs of the region of breakpoints 1-2 (BP1-BP2) in a large cohort of samples referred for genetic

CONTACT

diagnosis. J Hum Genet. 2019;64(3):253-5.

. : +905059356330 Gunce Basarir, MD 📧 : <u>guncebasarir@gmail.com</u>.



% Total (present tudy and terature) 20/91 (22%) 18/87 (20.7%) 239/497 (48%) 145/227 (63.9%) 61/118 (51.7%) 75/514 (15%) 55/152 (36.2%) 22/63 (34.9%) 147/491 (30%) 66/434 (15.2%)

^{1.} Gillentine MA, Schaaf CP. The human clinical phenotypes of altered CHRNA7 copy number. Biochem Pharmacol. 2015;97(4):352-62 2. Pujana MA, Nadal M, Guitart M, et al. Human chromosome 15q11-q14 regions of rearrangements contain clusters of LCR15 duplicons. Eur J Hum Genet.

^{3.} Pavone P, Ruggieri M, Marino SD, et al. Chromosome 15q BP3 to BP5 deletion is a likely locus for speech delay and language impairment: Report on a four-member

^{4.} Chai JH, Locke DP, Greally JM, et al. Identification of four highly conserved genes between breakpoint hotspots BP1 and BP2 of the Prader-Willi/Angelman

syndromes deletion region that have undergone evolutionary transposition mediated by flanking duplicons. Am J Hum Genet. 2003;73(4):898-925. 5. Elert-Dobkowska E, Stepniak I, Rajkiewicz M, et al. Familial 15q11. 2 microdeletions are not fully penetrant in two cases with hereditary spastic paraplegia and 6. Picinelli C, Lintas C, Piras IS, et al. Recurrent 15q11.2 BP1-BP2 microdeletions and microduplications in the etiology of neurodevelopmental disorders. Am J Med

^{7.} Burnside RD, Pasion R, Mikhail FM, et al. Microdeletion/microduplication of proximal 15q11.2 between BP1 and BP2: a susceptibility region for neurological dysfunction including developmental and language delay. Hum Genet. 2011;130(4):517-28.