



신경모세포종을 동반한 *EZH2* 유전자 변이가 확인된 위버증후군의 국내 첫 증례 보고

First Korean Case of Weaver Syndrome Along with Neuroblastoma and Genetic Confirmation of *EZH2* Variant

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Weaver syndrome (WS) is a rare congenital disorder characterized by overgrowth and accelerated osseous maturation. This syndrome is caused by a variant in the enhancer of zeste homolog 2 (*EZH2*) gene. No genetically confirmed cases of WS have been reported in Korea. In this case report, we discuss a case in which a variant in *EZH2* was detected and confirmed as WS in a patient showing overgrowth syndrome accompanied by neuroblastoma. A 7-month-old female presented to the out-patient pediatrics clinic of Seoul National University Hospital because of multiple palpable masses. Pathological examination confirmed that the mass was neuroblastoma. The patient's height, head circumference, and weight were $\geq 97\%$ of those expected for her age. The c.2050C > T (p.Arg684Cys) variant of *EZH2* was confirmed through next-generation sequencing-based gene panel testing. Although overgrowth syndrome caused by variants in *EZH2* is rare, screening for this condition should be included in the gene panel to evaluate overgrowth syndrome. The possibility of WS should be considered in cases of overgrowth syndrome accompanied by neuroblastoma.

Key Words: Weaver syndrome, Neuroblastoma, Enhancer of zeste homolog 2, Congenital Disorder

INTRODUCTION

Weaver syndrome (WS; OMIM 277590), first reported in 1974, is a rare congenital disorder characterized by overgrowth, distinct facial features, and accelerated osseous maturation. According to a previous study, WS is caused by a variant in the enhancer of zeste homolog 2 (*EZH2*) gene [1]. *EZH2* variants were also identified in

48 patients with WS with the clinical phenotype described above [1]. Approximately 50% patients were *de novo* cases, whereas familial cases were inherited in an autosomal dominant pattern [2]. In Korea, although potential WS cases have been reported, an *EZH2* variant has not been confirmed [3]. In this case report, we discuss the first Korean case of WS along with genetic confirmation of an *EZH2* variant. The Institutional Review Board of Seoul National University Hospital (Seoul, Korea) approved the study (approval number: 2111-131-1275). Informed consent was obtained from the patient's legal guardians.

CASE

A 7-month-old female was presented to the out-patient pediatrics clinic of Seoul National University Hospital with multiple palpable masses on her back, left side of the head, and extremities. The masses were approximately 1-3 cm in size and moved upon touch, but were reportedly not painful. The patient did not have

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any perinatal problems and was delivered at full-term. However, her height, head circumference, and weight were $\geq 97\%$ of those expected for her age. The patient was tall in stature and exhibited macrocephaly. Physical examinations revealed doughy skin and umbilical hernia; however, camptodactyly, hoarse cry, and abnormal tone were absent. Her characteristic facial features included frontal bossing, round face, retrognathia, wide-spaced eyes, low-set ears, and cleft chin (Table 1). In the magnetic resonance imaging examination, a 7 cm mass was found on the left adrenal gland. Pathological examination of the mass revealed neuroblastoma on

the left adrenal gland, and bone marrow aspiration confirmed the presence of neuroblastoma cells in the bone marrow (Fig. 1A).

As the patient was suspected of having overgrowth syndrome, she underwent next-generation sequencing-based gene panel testing, which revealed a heterozygous missense variant in NM_004456.4 (*EZH2*):c.2050C>T (p.Arg684Cys) (Fig. 1B). This variant is absent from large population databases such as gnomAD (<https://gnomad.broadinstitute.org/>) and the Korean Reference Genome Database (<http://coda.nih.go.kr/coda/KRGDB/>). A previous functional study demonstrated that, in the presence of the c.2050C>T

Table 1. Comparison of clinical phenotype of our patient with those of previous cases of Weaver syndrome

	Current study	Case 1 [14]	Case 2 [22]	Case 3 [23]	n/N* (%) [24]	n/N* (%) [2]
Facial features [†]	+	+	+	+	3/3 (100)	31/48 (65)
Hypertonia	-	-	+	-	1/3 (33)	11/39 (28)
Hypotonia	-	-	-	-	2/3 (67)	18/41 (44)
Camptodactyly	-	-	-	+	2/3 (67)	17/38 (45)
Umbilical hernia	+	-	+	-	3/3 (100)	17/40 (43)
Doughy skin	+	-	-	-	2/3 (67)	17/35 (49)
Hoarse cry	-	-	-	-	3/3 (100)	10/27 (37)
Malignancy	NB	AML	-	-	0/3 (0)	2/48 (4) [‡]
<i>EZH2</i>						
AA change	R684C	P132L	E745K	H240R		

*n/N refers to the proportion of patients exhibiting the corresponding phenotype among the total number of patients included in the reference reports describing the presence of a specific phenotype. [†]Facial features characterizing WS, namely ocular hypertelorism, frontal bossing, round face, and retrognathia, [‡]Three types of cancer occurred in two patients with WS (lymphoma, NB and ALL).

Abbreviations: AA, amino acid; NB, neuroblastoma; ALL, acute lymphoblastic leukemia; AML, acute myeloid leukemia; WS, Weaver syndrome.

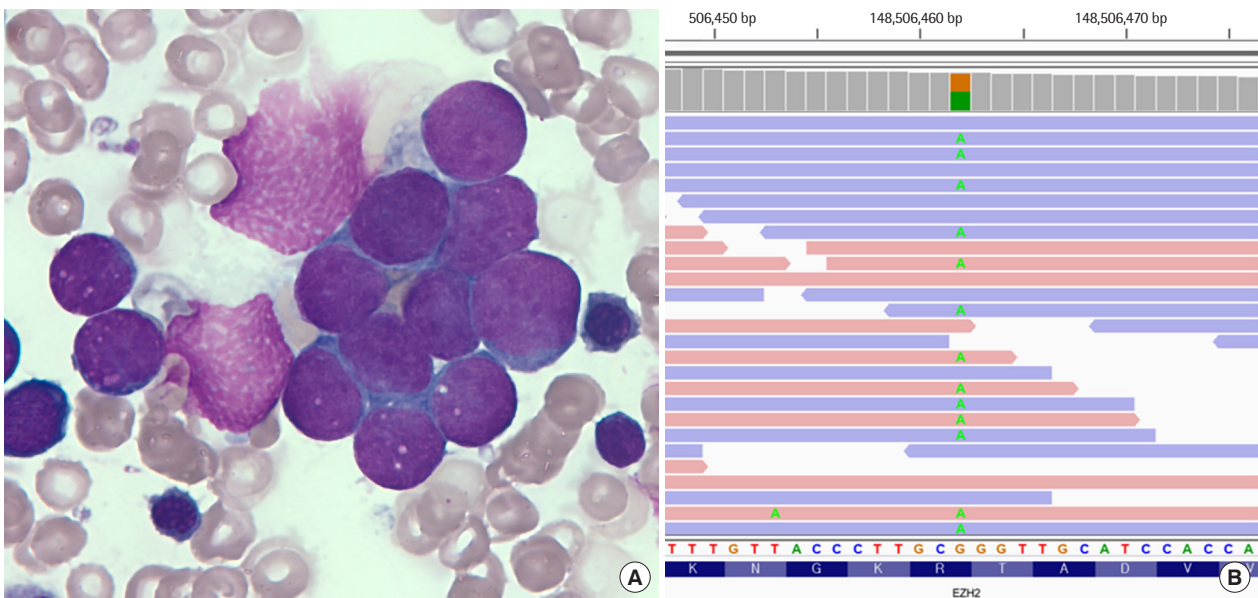


Fig. 1. Morphological characteristics of bone marrow aspirate and visualization of next-generation gene sequencing data of the patient. (A) Neuroblastoma cells cluster with fibrils (Wright-Giemsa stain, $\times 1,000$). (B) Sequence visualization of enhancer of zeste homolog 2 (*EZH2*) gene showing a missense variant, c.2050C>T.

(p.Arg684Cys) variant of *EZH2*, the histone methyltransferase activity of the polycomb repressive complex-2 (PRC2) protein was significantly decreased compared to that of the wild-type enzyme [4]. In addition, a different missense change in the same codon (p.Arg684His) has been reported as a pathogenic variant [2]. *In silico* analyses using SIFT, Polyphen-2, and Mutation Taster supported the finding that this variant has deleterious effects on the protein function. This variant was previously reported as pathogenic [2, 4, 5]; thus, we subsequently classified it as pathogenic (PS3, PM2, PM5, PP3, and PP5) based on the 2015 American College of Medical Genetics and Genomics and Association for Molecular Pathology guidelines [6]. Other genes in the panel, including *AKT3*, *BRWD3*, *DNMT3*, *EED*, *GPC3*, *HIST1H1E*, *MTOR*, *NFIX*, *NSD1*, *PIK3CA*, *PPP2R5D*, and *PTEN*, did not contain variants. Moreover, the *EZH2* variant was detected in the adrenal gland biopsy tissue, and as a result, the patient was diagnosed with WS. She was started on chemotherapy with etoposide and doxorubicin, and her neuroblastoma showed a partial response after 10 cycles of treatment.

DISCUSSION

EZH2 encodes a histone-lysine N-methyltransferase that is a component of PRC2, which is associated with epigenetic silencing in cells. PRC2 exhibits histone methyltransferase activity and methylates histone H3 on lysine 27; the *EZH2* variant causes a partial loss of this methyltransferase function [7]. Variants in other PRC2 elements or other histone methyltransferase-related genes are genetically distinct from WS; however, some cases exhibit an overgrowth phenotype [8]. Particularly, these mechanisms are similar to the impaired histone methyltransferase activity of the variant of nuclear receptor binding SET domain protein 1 (*NSD1*), which causes Sotos syndrome, a type of overgrowth syndrome [9]. Sotos syndrome shows a high level of phenotypic overlap with WS [10]; therefore, overgrowth is expected to occur in cases of impaired methylation regulation [11]. However, analysis of *EZH2* protein in patients with WS did not reveal a clear correlation between the severity of clinical symptoms and greatly decreased histone methyltransferase activity [4]. Therefore, phenotypic differences among patients with WS may be related to additional factors.

Both somatic gain-of-function and loss-of-function mutations of *EZH2* are associated with solid tumors, such as breast and pros-

tate cancer, or hematologic cancers [12]. In contrast, evidence for the increased risk of malignancy in patients with *EZH2* germline variants is not sufficient [13]. Previous studies reported that cancers such as neuroblastoma, acute myeloid leukemia, acute lymphoblastic leukemia, teratoma, ovarian tumor, and lymphoma occur at an early age in patients with WS [1, 2, 14]. Three cases of neuroblastoma have been reported in 3-, 8-, and 9-month-old patients with WS, whereas only one case has been reported for each of the other cancer types [2]. Our patient was 6 months old at the time of neuroblastoma onset (7 months old when she presented to the clinic), which is consistent with similar cases. This case supports the finding that germline variants in *EZH2* may be associated with cancer, specifically neuroblastoma [15].

Diagnosing overgrowth syndrome is important for providing genetic counseling for cancer surveillance and prognosis [16]. Particularly, patients with Beckwith-Wiedemann syndrome show an increased risk of Wilms' tumor [17]. The incidence of cancer is reportedly increased in patients with other overgrowth syndromes, and variants in genes such as DNA (cytosine-5)-methyltransferase 3A (*DNMT3A*) are associated with solid or hematologic cancer [18-20]. The regular cancer screening plan has been proposed for patients with these syndromes [21]. As neuroblastoma occurs increasingly in WS, we recommend that patients with WS should also undergo cancer surveillance.

This is the first Korean case of genetically confirmed WS, accompanied by the rare occurrence of early onset neuroblastoma. Although *EZH2* variant-induced overgrowth syndrome is rare, it should be included in the gene panel when evaluating overgrowth syndrome. Moreover, if overgrowth is accompanied by neuroblastoma, the probability of WS is high, and genetic testing for germline variants can help to confirm this diagnosis.

요 약

위버증후군은 과성장과 가속화된 골성숙을 특징으로 하는 드문 선천성 질환이다. 이 증후군은 *EZH2* 유전자의 변이에 의해 발병되는 것으로 알려져 있으며, 국내에서는 *EZH2* 유전자변이를 확인한 위버증후군은 보고된 증례가 없다. 본 증례에서는 신경모세포종이 동반된 과성장증후군 환자에서 *EZH2* 유전자의 변이가 검출되어 위버증후군으로 확인된 사례를 보고하고자 한다. 출생 후 7개월 된 환아가 신체에서 촉진되는 다발성의 종괴를 주소로 내원하였다. 종괴는 조직검사상 신경모세포종으로 확인되었으며, 환자

는 키, 머리둘레, 몸무게 모두 소아발육표준치에 비해 상위 97% 이상인 특징을 보였다. 과성장증후군과 관련된 자세대염기서열분석 유전자 패널 검사에 의해 *EZH2* 유전자의 c.2050C>T (p.Arg684Cys) 변이를 확인하였다. 이는 *EZH2* 유전자의 변이에 의한 과성장증후군이 드물지만 과성장증후군을 평가하기 위한 유전자 패널에 포함되어야 하며, 신경모세포종이 동반되는 과성장증후군의 경우 위버증후군의 가능성을 고려해야 함을 시사하였다.

Conflicts of Interest

None declared.

REFERENCES

1. Tatton-Brown K, Hanks S, Ruark E, Zachariou A, Duarte Sdel V, Ramsay E, et al. Germline mutations in the oncogene *EZH2* cause Weaver syndrome and increased human height. *Oncotarget* 2011;2:1127-33.
2. Tatton-Brown K, Murray A, Hanks S, Douglas J, Armstrong R, Banka S, et al. Weaver syndrome and *EZH2* mutations: Clarifying the clinical phenotype. *Am J Med Genet A* 2013;161A:2972-80.
3. Byun JC, Kim CS, Lee SL, Kwon TC, Lee HJ. A case of Weaver syndrome. *Korean J Pediatr* 2004;47:1216-9.
4. Cohen AS, Yap DB, Lewis ME, Chijiwa C, Ramos-Arroyo MA, Tkachenko N, et al. Weaver syndrome-associated *EZH2* protein variants show impaired histone methyltransferase function *in vitro*. *Hum Mutat* 2016; 37:301-7.
5. Polonis K, Blackburn PR, Urrutia RA, Lomberg GA, Kruisselbrink T, Cousin MA, et al. Co-occurrence of a maternally inherited *DNMT3A* duplication and a paternally inherited pathogenic variant in *EZH2* in a child with growth retardation and severe short stature: atypical Weaver syndrome or evidence of a *DNMT3A* dosage effect? *Cold Spring Harb Mol Case Stud* 2018;4:a002899.
6. Richards S, Aziz N, Bale S, Bick D, Das S, Gastier-Foster J, et al. Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. *Genet Med* 2015;17:405-24.
7. Gan L, Yang Y, Li Q, Feng Y, Liu T, Guo W. Epigenetic regulation of cancer progression by *EZH2*: from biological insights to therapeutic potential. *Biomark Res* 2018;6:10.
8. Deevy O and Bracken AP. PRC2 functions in development and congenital disorders. *Development* 2019;146:dev181354.
9. Qiao Q, Li Y, Chen Z, Wang M, Reinberg D, Xu RM. The structure of *NSD1* reveals an autoregulatory mechanism underlying histone H3K36 methylation. *J Biol Chem* 2011;286:8361-8.
10. Tatton-Brown K and Rahman N. The *NSD1* and *EZH2* overgrowth genes, similarities and differences. *Am J Med Genet C Semin Med Genet* 2013;163C:86-91.
11. Jeffries AR, Maroofian R, Salter CG, Chioza BA, Cross HE, Patton MA, et al. Growth disrupting mutations in epigenetic regulatory molecules are associated with abnormalities of epigenetic aging. *Genome Res* 2019;29:1057-66.
12. Kim KH and Roberts CW. Targeting *EZH2* in cancer. *Nat Med* 2016; 22:128-34.
13. Neylon OM, Werther GA, Sabin MA. Overgrowth syndromes. *Curr Opin Pediatr* 2012;24:505-11.
14. Usemann J, Ernst T, Schäfer V, Lehmborg K, Seeger K. *EZH2* mutation in an adolescent with Weaver syndrome developing acute myeloid leukemia and secondary hemophagocytic lymphohistiocytosis. *Am J Med Genet A* 2016;170A:1274-7.
15. Coulter D, Powell CM, Gold S. Weaver syndrome and neuroblastoma. *J Pediatr Hematol Oncol* 2008;30:758-60.
16. Kamien B, Ronan A, Poke G, Sinnerbrink I, Baynam G, Ward M, et al. A clinical review of generalized overgrowth syndromes in the era of massively parallel sequencing. *Mol Syndromol* 2018;9:70-82.
17. Mussa A, Duffy KA, Carli D, Griff JR, Fagiano R, Kupa J, et al. The effectiveness of Wilms tumor screening in Beckwith-Wiedemann spectrum. *J Cancer Res Clin Oncol* 2019;145:3115-23.
18. Tatton-Brown K, Seal S, Ruark E, Harmer J, Ramsay E, Del Vecchio Duarte S, et al. Mutations in the DNA methyltransferase gene *DNMT3A* cause an overgrowth syndrome with intellectual disability. *Nat Genet* 2014;46:385-8.
19. Brunetti L, Gundry MC, Goodell MA. *DNMT3A* in leukemia. *Cold Spring Harb Perspect Med* 2017;7:a030320.
20. Kim MS, Kim YR, Yoo NJ, Lee SH. Mutational analysis of *DNMT3A* gene in acute leukemias and common solid cancers. *APMIS* 2013;121: 85-94.
21. Villani A, Greer MC, Kalish JM, Nakagawara A, Nathanson KL, Pajtlér KW, et al. Recommendations for cancer surveillance in individuals with RASopathies and other rare genetic conditions with increased cancer risk. *Clin Cancer Res* 2017;23:e83-90.
22. Al-Salem A, Alshammari MJ, Hassan H, Alazami AM, Alkuraya FS. Weaver syndrome and defective cortical development: a rare association. *Am J Med Genet A* 2013;161A:225-7.

23. Turkkahraman D, Sakarya ANP, Randa NC. A novel *EZH2* gene variant in a case of Weaver syndrome with postaxial polydactyly. Am J Med Genet A 2021;185:2234-7.
24. Gibson WT, Hood RL, Zhan SH, Bulman DE, Fejes AP, Moore R, et al. Mutations in *EZH2* cause Weaver syndrome. Am J Hum Genet 2012; 90:110-8.