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Kosaki R, Fujita H, Takada H, Okada M, Torii C, <u>Kosaki K</u>	Monozygotic twins of Rubinstein-Taybi syndrome discordant for glaucoma.	Am J Med Genet A	155A(5)	1189-91	2011
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資 料

2011.7.23 こすもす(ルビンシュタイン・テイビ症候群児・者 親の会) 交流会に参加

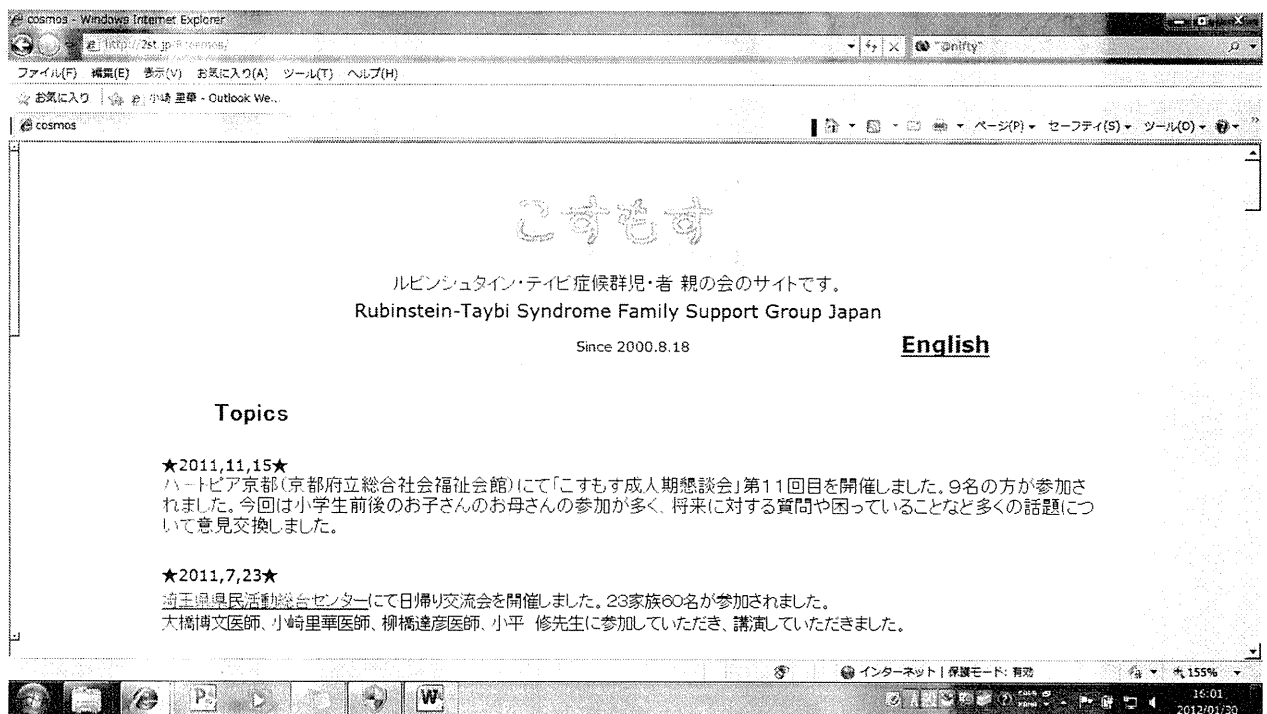
講演

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「Rubinstein-Taybi 症候群の臨床診断基準の策定と新基準にもとづく有病率の調査研究」班につ
いて」

柳橋達彦 慶應義塾大学医学部 小児科 (分担研究者)

「ルビンスタイン・テイビ症候群の行動とこころの問題～アンケート調査から～」



Monozygotic Twins of Rubinstein–Taybi Syndrome Discordant for Glaucoma

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TO THE EDITOR:

Rubinstein–Taybi syndrome (RTS) is characterized by broad thumbs and toes, downward slanted palpebral fissures, a prominent nose with the nasal septum extending below the alae nasi, a hypoplastic maxilla with a narrow plate, thick eyebrows, long eyelashes, a short stature, and moderate intellectual disability [Hennekam, 2006]; its incidence is estimated to be 1 in 100,000. Most cases are sporadic, and about half of all cases have a heterozygous mutation in the *CREBBP* gene; rare cases have a heterozygous *EP300* mutation. Both genes encode histone acetyltransferases (HAT), which are transcriptional co-activators that play critical roles in epigenetic regulation through histone acetylation [Roelfsema and Peters, 2007]. Among the more than 600 cases of RTS reported to date, at least 11 sets of monozygotic twins [Pfeifer, 1968; Gorlin et al., 1976; Schinzel et al., 1979; Kajii et al., 1981; Baraitser and Preece, 1983; Widd, 1983; Ghanem and Dawod, 1990; Hennekam et al., 1990; Robinson et al., 1993; Preis and Majewski, 1995] have been documented.

Here, we present monozygotic twins concordant for the RTS phenotype. The monozygosity and RTS diagnosis were both confirmed using molecular methods. Interestingly, the twins were concordant for facial and limb features but were discordant for body size and the presence of congenital glaucoma. The discordance in the former characteristic (i.e., the body size) was ascribed to a twin-to-twin transfusion between the twins, whereas the discordance in the latter characteristic (i.e., the glaucoma) could not be explained.

The male twins were born to a 24-year-old Japanese G1P1-2 woman with no previous medical problems. Consanguinity or a family history of mental retardation was not present. The placentation was diamniotic and monochorionic. The pregnancy was remarkable for the disproportionate growth of the twins. An ultrasonographic diagnosis of twin-to-twin transfusion syndrome was made, and the vascular connection on the placenta between the twins was successfully disconnected using laser ablation.

The twins were delivered at 30 weeks of gestation. At birth, the weight of Twin A was 1,174 g and his length was 36 cm whereas the birth weight of Twin B was 960 g and his length was 34.5 cm. The postnatal courses of the twins were similar. Developmental

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delays were apparent: the twins were able to hold their heads up at 10 months, to sit alone at around 18 months, to walk alone at 3–1/2 years, and to speak meaningful words at 7 years.

At the age of 16 months, the twins were referred to our genetic department because of developmental delays. Dysmorphic features (Fig. 1), which were all concordant between the twins, included broad thumbs and toe, downward slanting pleural fissures, a hypoplastic maxilla, a prominent nose with the nasal septum extending below the alae nasi, heavy eyebrows and long eyelashes, salmon patches, undescended testes, patent ductus arteriosus and a hearing impairment. However, only Twin A had bilateral congenital glaucoma and lens dislocations. A genotyping analysis using nine microsatellite markers (ALAS2, DXS1236, D7S527, D7S630, D9S1779, D9S15, D10S595, D10S2454, and D17S1705) confirmed the monozygosity of the twins. Chromosome analyses revealed normal karyotypes. Molecular screening of the *CREBBP* gene using denaturing high-performance liquid chromatography (DHPLC) was negative [Udaka et al., 2005].

Array comparative genomic hybridization using the Agilent 180K format CGH array designed by the International Standards for Cytogenomic Arrays Consortium (backbone resolution of 35 or 25 kb and 500 targeted regions including telomeres, centromeres, microdeletion/duplication regions, and X-linked mental retarda-

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FIG. 1. Facial features of monozygotic twins with Rubinstein-Taybi syndrome (left: Twin A and right: Twin B).

tion genes) revealed a loss in the copy number for the 16p13.3 region (Fig. 2). The size of the deletion was 210 kb, extending from 3,810,524 to 4,023,361 on 16p13.3 (hg18; NCBI Build 36.1). Genes within the deleted region included the 5' half of the *CREBBP* locus and its adjacent *ADCY9* locus. We further compared the genomic

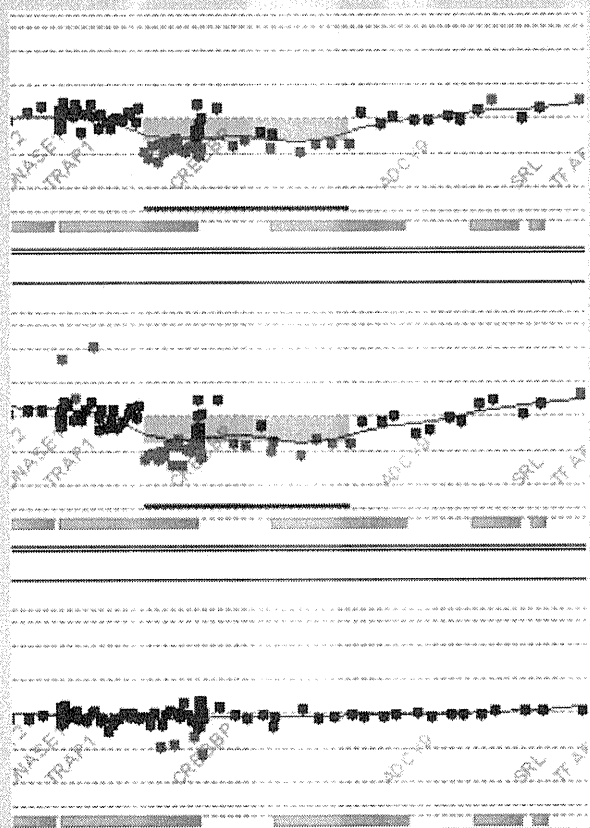


FIG. 2. Result of CGH array analysis (top: Twin A vs. control; middle: Twin B vs. control; bottom: Twin A vs. Twin B). The CGH array analysis revealed a 210 kb interstitial deletion of 16p13.3 involving *CREBBP* gene (top: gray area; middle: blue area).

DNA of Twin A and Twin B using the array, but no copy number differences were detected.

Here, we document a case of monozygotic twins concordant for the RTS phenotype. To our knowledge, this twin pair represents the first twins whose monozygosity and RTS diagnosis have been confirmed using molecular methods. The monozygosity and diagnosis of several twin pairs with genetically determined multiple congenital anomaly syndromes have been reported including those with Smith-Magenis syndrome [Kosaki et al., 2007], Crouzon syndrome, Alagille syndrome, Sotos syndrome, and 22q11.2 deletion syndrome. RTS can now be added to this list.

The twins had concordant facial and limb features but were discordant for the presence of congenital glaucoma. Three potential mechanisms are capable of explaining this discordance: first, the glaucoma phenotype may not be causally related to the deletion of the RTS locus and may have appeared by chance as a polygenetic trait [Libby et al., 2005]. However, the occasional documentation of glaucoma in other RTS cases [Hennekam, 2006] suggests that the glaucoma phenotype is likely to be associated with the RTS deletion. Second, only Twin A might have experienced a "second hit" in a genomic region(s) other than chromosome 16p. Indeed, array CGH genomic studies of monozygotic twin genomes have revealed occasional differences in copy numbers [Bruder et al., 2008]. However, we did not detect such differences in the presently reported twins (data not shown). Thirdly, the discordance in the severities of the twin pairs could be ascribed to chance-like variations in the pathogenetic actions of the mutated gene. Intriguingly, epigenetic regulation plays a critical role in the stochastic nature of embryonic development, and *CREBBP*, the causative gene in the presently reported twins, represents an epigenetic regulator of embryogenesis [Robinson et al., 1993]. Indeed, a previously reported difference in the neurodevelopment of twins with RTS may support such a notion [Pfeifer, 1968; Buchinger and Stroder, 1973; Preis and Majewski, 1995].

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