

厚生労働科学研究費補助金（難治性疾患克服研究事業）
分担研究報告書

遺伝性汎発性色素異常症の原因遺伝子同定

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研究要旨 遺伝性対側性色素異常症（DSH）は遺伝子診断により確定診断を行っているが、DSHの亜型と考えられていた遺伝性汎発性色素異常症（DUH）の原因遺伝子はいまだ不明である。DUHと考えられる皮疹を持つ患者の家系を集積し、次世代シーケンサーを用いた手法で本疾患の原因遺伝子の同定を目指す。

A. 研究目的

遺伝性対側性色素異常症（DSH）は遺伝子診断により確定診断を行っているが、DSHの亜型と考えられていた遺伝性汎発性色素異常症（DUH）の原因遺伝子はいまだ不明である。DUHと考えられる皮疹を持つ患者の家系を集積し、次世代シーケンサーを用いた手法で本疾患の原因遺伝子の同定を目指す。

行い、ゲノムDNAを抽出する。SureSelectエキソームキャプチャーキットを用いて、全エクソン領域を選択し、ABI SOLiDで全エクソン領域の塩基配列決定を行う。そのデータから、変異を持つ遺伝子を候補遺伝子としてあげる。家系内の患者および非罹患者についてそれらの変異を調べて、候補遺伝子を絞り込んでいく。皮膚での発現や機能によっても更に候補遺伝子を絞り込み、最終的に原因遺伝子を同定する。

B. 研究方法

臨床的にDUHと考えられる患者が見つかった際に、臨床症状の記録および家系調査を行う。孤発例ではなく、少なくとも患者の前後1世代ずつに患者が存在する家族例である症例が見つかった際に名古屋大学皮膚科学教室と連携し、患者および家族に文書を用いて説明をし、同意を得られれば、採血を

（倫理面への配慮）

本研究は名古屋大学医学部生命倫理委員会の承認申請中であり、承認が得られたのちに札幌医科大学医学部の生命倫理委員会の承認申請を行う予定である。承認後に研究を行うにあたって、患者の人権および利益の

保護を遵守するために以下の対策を講じることとする。

(1) 患者本人に疾患遺伝子解析の内容と必要性を十分に説明し、個人情報秘匿するための対応についても説明し、予め作成しておいた書面による同意を得てから検体を採取する。なお、未成年の患者の場合は保護者に同様の説明をした後に保護者に署名をしてもらう。

(2) 採取した検体は個人IDで管理し、個人IDで連結できる患者の情報は鍵をかけた書庫で管理し、個人情報の流出を出来るだけ防ぐ手段をとる。

C. 研究結果

現在、協力していただける家系を探索中であり、まだ遺伝子解析は行っていない。

F. 健康危険情報

特になし。

G. 研究発表

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H. 知的所有権の取得状況

1. 特許取得

特になし。

2. 実用新案登録

特になし。

3. その他

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IV. 研究成果の刊行に関する一覧表

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V. 研究成果の刊行物・別刷



Correspondence

Dyschromatosis symmetrica hereditaria by *adar1* mutations and viral encephalitis: a hidden link?

Dyschromatosis symmetrica hereditaria (DSH; MIM no. 127400) is an autosomal dominant skin disease caused by a heterozygous mutation of adenosine deaminase acting on RNA 1 gene (*ADAR1*, NM_001111.3), previously termed double-stranded RNA-specific adenosine deaminase gene (*DSRAD*).¹ DSH is characterized by a mixture of hyper- and hypopigmented macules on the dorsal aspects of the extremities. The skin manifestation usually develops during infancy without any known trigger.

Here we report a 4-year-old Hispanic girl who presented with classic DSH following an episode of viral encephalitis. She was healthy and had no skin manifestation until 11 months of age, when she had seizures and developmental delay following symptoms of viral infection, including exanthema over the whole body for several days. She was subsequently diagnosed as having postviral encephalitis. One month after the encephalitis episode, she started to develop the skin manifestations of DSH. At the age of 4, she developed hyper- and hypopigmented macules on the extremities and freckle-like macules on the face (Fig. 1). Mutation search using

gDNA eluted from peripheral blood leukocytes revealed that she was heterozygous for the novel mutation c.3102G>A (p.Met1034Ile) in *ADAR1* (Fig. 2).² This missense mutation considered to be pathogenic, because the altered amino-acid residue Met1034 is within the deaminase domain of *ADAR1* and conserved among diverse species, including zebrafish, frog, chicken, rat, mouse, cow, wolf, and chimpanzee. In addition, the mutation was not detected in the control genomic DNA samples from 102 unrelated, healthy Japanese volunteers.

Two isoforms of human *ADAR1* enzymes are known to exist. One is an interferon (IFN)-inducible full-length 150 kDa protein (the p150 isoform), and the other is a constitutively expressed, 110 kDa short isoform (the p110 isoform). Two mutations p.Gln102fs and p.His216fs, which we previously reported in patients with DSH,^{3,4} are located at the 5'-side upstream of codon 296 in exon 2, which is the translation initiation codon for *ADAR1-p110*. Therefore, normal *ADAR1-p110* isoform can be produced from the mutant alleles. Thus, DSH is thought to be caused by defects in the p150 isoform.² High IFN condition normally induces upregulated expression of *ADAR1-p150* isoform in individuals without *ADAR1* mutations. This IFN-inducible

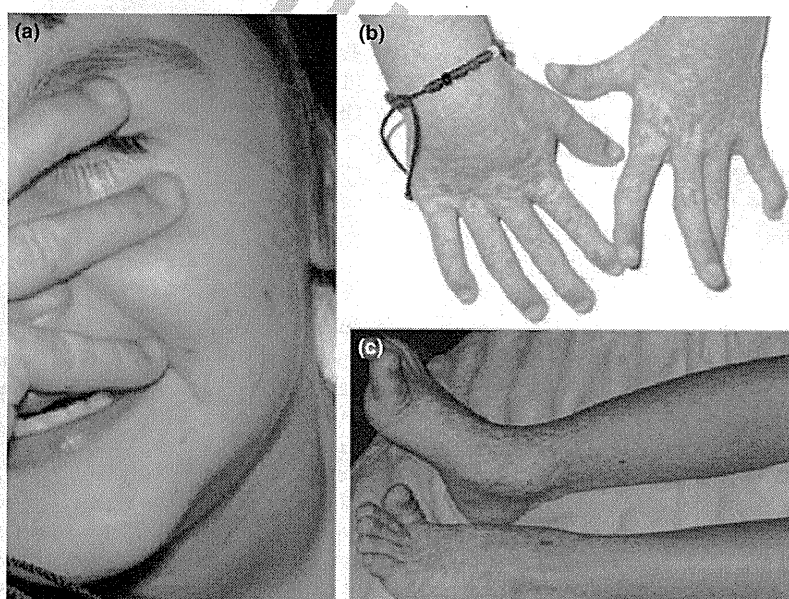


Figure 1 Clinical phenotype of the patient. Freckle-like macules on the face (a), and a mixture of hyper- and hypopigmented macules on the back of the hands (b) and legs (c) were observed

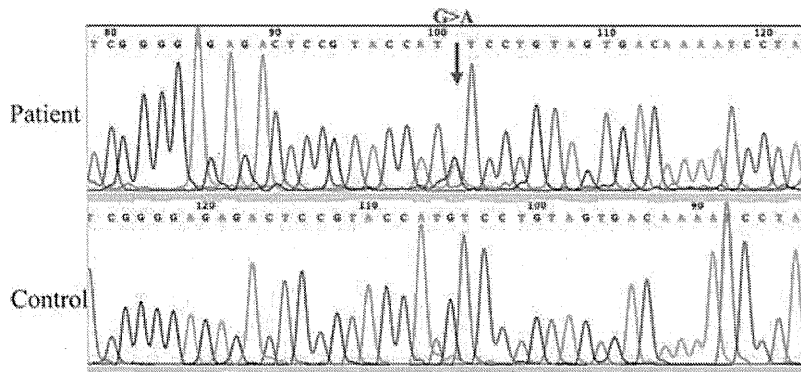


Figure 2 Sequence analysis of *ADAR1* genomic DNA from the patient. The chromatograph reveals c.3102G>A (p.Met1034Ile) in *ADAR1*

isoform is involved in anti-apoptotic pathways⁵ and appears to regulate cellular RNA interference (RNAi) efficacy.⁶ Thus, under high IFN condition, reduced or absent *ADAR1-p150* isoform function might fail to regulate those pathways and be involved in the development of DSH. Further accumulation of data on correlation between DSH and viral infection/high IFN condition will be needed to confirm this hypothesis.

There seems to be no apparent genotype/phenotype correlation in patients with DSH. Carriers with identical mutations can show different clinical features and severity, indicating the contribution of environmental or extrinsic factors on disease development.² Viral infection frequently induces increased levels of IFN in the peripheral blood and other tissues. In the present case, it is possible that the high IFN condition induced by systemic viral infection and encephalitis caused the patient's latent shortage of *ADAR1* enzymatic ability to become apparent, triggering the development of the DSH phenotype.

Notably, the IFN-inducible *p150* isoform of *ADAR1* was recently revealed to suppress the replication of paramyxoviruses and orthomyxoviruses.⁷ Thus, a loss-of-function mutation of the *ADAR1 p150* isoform might be a risk factor for severe infection by measles and other viruses. Further accumulation of cases and experimental data will be needed to elucidate the exact link between DSH with *ADAR1* mutations and viral infection.

Acknowledgments

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Conflict of interest: None.

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| 2 | AUTHOR: Please provide the qualification for author Amarilis Sanchez-Valle. | |
| 3 | AUTHOR: Sequence analysis of ADAR1 genomic DNA from the patient.—should this also read 'and control' at the end of this sentence? | |
| 4 | AUTHOR: Figure 2 has been saved at a low resolution of 273 dpi. Please resupply at 600 dpi. Check required artwork specifications at http://authorservices.wiley.com/submit_illust.asp?site=1 | |

LETTER TO THE EDITOR

Four novel *ADAR1* gene mutations in patients with dyschromatosis symmetrica hereditaria

Dear Editor,

Dyschromatosis symmetrica hereditaria (DSH; Mendelian Inheritance in Man no. 127400) is a highly penetrant autosomal dominant skin disease and is characterized by a mixture of hyper- and hypopigmented macules on the dorsal aspects of the hand and foot. This disorder commonly develops during infancy or early childhood.¹

Previous work has shown that a heterozygous mutation of the adenosine deaminase acting on RNA1 gene (*ADAR1* or *DSRAD*) caused DSH in four Japanese DSH families.² Subsequently, 115 mutations in the *ADAR1* gene (GenBank accession no. NM_001111.3, <http://www.ncbi.nlm.nih.gov/genbank/>) have been reported in Japanese, Taiwanese and Chinese patients with DSH. The *ADAR1* protein catalyzes the deamination of adenosine to inosine in double-stranded RNA.³ This creates alternative splice sites or alterations of the codon that lead to functional changes in the target substrate(s). However, the target gene(s) for *ADAR1* in the skin as well as the mechanisms by which mutations in *ADAR1* cause DSH remain unknown. In this study, we performed mutational analysis of the *ADAR1* gene in three Japanese and a Chinese Canadian with DSH.

The analysis was performed as follows. Genomic DNA was extracted from peripheral blood with a QIAamp DNA blood maxi kit (QIAGEN, Valencia, CA, USA) and was used as a template for mutational screening with a polymerase chain reaction (PCR)-based single-strand conformation polymorphism (SSCP)/heteroduplex (HD) analysis.⁴ Standard PCR amplification procedures were employed with high fidelity polymerase, Platinum Taq DNA Polymerase (Invitrogen, Carlsbad, CA, USA) and an annealing temperature of 62°C for all primers.⁵ SSCP gel with glycerol concentrations of 7.5% was used. PCR products showing aberrant patterns on SSCP were re-amplified and sequenced directly to identify a mutation. In patients without any mutation detected by the SSCP/HD method, all of their PCR products were directly sequenced to identify mutations. Informed consent and blood samples of patients were

obtained under protocols approved by the Ethics Committee of Nagoya University School of Medicine. Three Japanese patients in this study were not related to each other.

We identified four novel heterozygous *ADAR1* mutations including one splice mutation (IVS9-1G>T) and three frame-shift mutations (p.Lys1167fsX1178, p.Asn398fsX401 and p.Asp1147fsX1152) (Table 1).

The three frame-shift mutations code a different amino acid sequence and eventually make a new stop codon. In a previous report,⁶ the *ADAR1* mutations p.Gln513X and p.Cys519fs, which lead to premature termination codon (PTC) and to nonsense-mediated mRNA decay (NMD), were reported to result in *ADAR1* haploinsufficiency. Generally, PTC could initiate NMD as long as the stop codons are located more than 50–55 nucleotides upstream of the 3'-most splice site.⁷ We speculate that p.Asn398fsX401 on exon 2 of 15 exons in the present patient would also lead to haploinsufficiency of *ADAR1* enzyme activity. The other two frame-shift mutations made PTC in exon 15. Thus, these mutations would not result in NMD, but made aberrant proteins.

On the other hand, the site of the novel splice mutation (IVS9-1G>T) was the conserved sequence on splice acceptor site on intron 9 (Fig. 1a). On the *ADAR1* gene of a DSH patient some splice mutations have been reported.⁸ So far, only one investigation on aberrant splicing of the *ADAR1* gene by the splice mutation has been reported.⁵ We investigated aberrant splicing of the mutation IVS9-1G>T. Total RNA was extracted from whole blood of patient 4 and a healthy control.

Reverse transcription PCR was done for amplification of the 172-bp fragment at the boundary between exon 9 and 10 on mRNA from whole blood of the patient. Extra and normal bands, 172 bp (normal product) and 160 bp (aberrantly splicing product), were confirmed in mRNA from the patient (Fig. 1b). These were separated by agarose gel extraction and subcloned each with a TOPO TA Cloning kit for Sequencing (Invitrogen). DNA sequencing of subcloned PCR products showed the truncation of the 12-bp nucleotides

Table 1. Four mutations of the *ADAR1* gene in the patient with dyschromatosis symmetrica hereditaria

| Patient no. | Patient | | | Mutation | | |
|-------------|------------------|-------------|-------------------------------|--------------------------------|--------------------|----------|
| | Race | Onset | Complication | Nucleotide change [†] | Amino acid change | Position |
| 1 | Japanese | 3 years old | Healthy | c.3499del A | p.Lys1167fsX1178 | Exon 15 |
| 2 | Japanese | 2 years old | Healthy | c.1192-3 del AA | p.Asn398fsX401 | Exon 2 |
| 3 | Chinese Canadian | At birth | Healthy | c.3440insG | p.Asp1147fsX1152 | Exon 14 |
| 4 | Japanese | 6 years old | Febrile seizure at 2 year-old | c.IVS9-1 G>T | p.Arg921_Tyr924del | IVS9 |

[†]GenBank accession no. NM_001111.3. Position 1 is A of the translation initiation codon.

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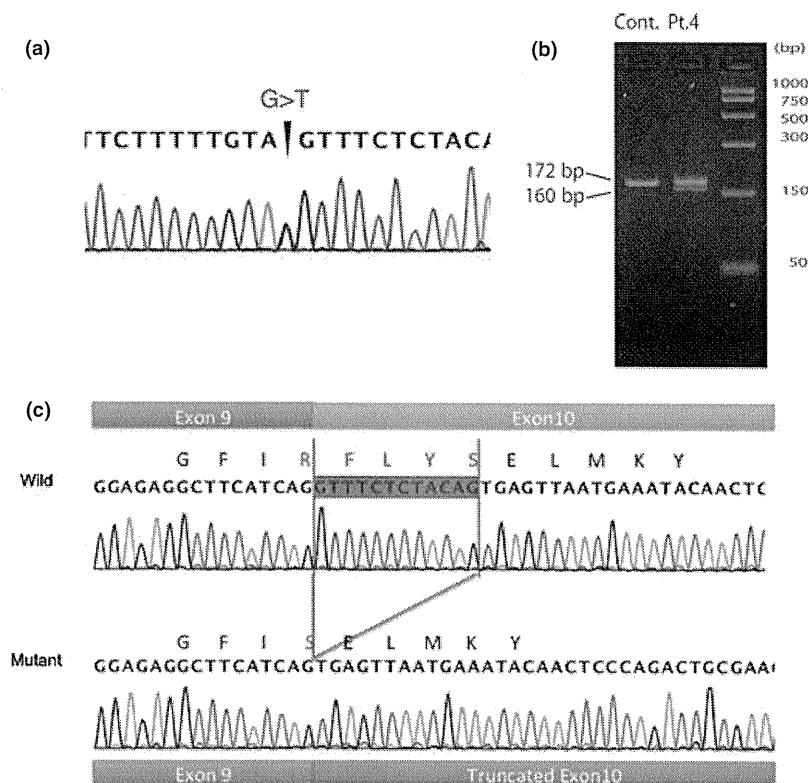


Figure 1. Molecular analysis of splicing mutation on *ADAR1* of patient 4. (a) Sequence analysis of boundary between exons 9 and 10 on *ADAR1* genomic DNA from patient 4 reveals G to T transversion, IVS9-1G>T. (b) Agarose gel electrophoresis of reverse transcription polymerase chain reaction (RT-PCR) products of boundary between exons 9 and 10 on *ADAR1* gene. The RT-PCR product from the patient 4 shows 172-bp (normally spliced fragment) and 160-bp (aberrantly spliced fragment) bands, although a control specimen exhibits only a 172-bp band. (c) Sequence analysis of boundary between exons 9 and 10 on *ADAR1* cDNA. In the mutant cDNA, the aberrant splicing results in 12-bp deletion.

on the 5'-side of exon 10 (Fig. 1c). Subsequently, the deletion of four amino acids (p.Arg921-Tyr924del) was in the deaminase domain and should produce the aberrant protein of ADAR1.

All patients phenotypically presented typical macules on the dorsal aspects of the hands and feet, lower arms and lower legs. No patients had complications but patient 4 had a febrile seizure at 2 years old. The mutations reported in the published work including the present report are scattered through the entire gene and there is no hotspot for the *ADAR1* gene mutations. However, in more than 100 mutations on *ADAR1*, all missense mutations except for p.Arg26Lys were in the adenosine-deaminase domain. Thus, this domain is thought to be essential for the biochemical function of ADAR1. There is no apparent genotype/phenotype correlation in *ADAR1* mutations. Even in one family, the identical mutation was reported to lead to different phenotypes.⁵ The reason why a low activity of ADAR1 induces the peculiar skin lesions localized on the extremities is still unknown. We speculate that, when melanoblasts migrate from the neural crest to the skin during development, insufficient ADAR1 enzyme activity might affect differentiation of melanoblasts to melanocytes and the melanoblasts located distant from the neural crest might be most seriously affected during migration.⁹

In conclusion, we reported four novel mutations in the *ADAR1* genes of DSH patients. The accumulation of the patients with genetic information may provide new insight into the pathogenesis of DSH.

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