

Ⅲ. 研究成果の刊行に関する一覧表

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書籍

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Flamein F, Riffault L, Muselet-Charlier C, Pernelle J, Feldmann D, Jonald L, Durand-Schneider AM, Coulomb A, Maurice M, Nogee LM, <u>Inagaki N</u> , Amselem S, Dubus JC, Rigourd V, Brémont F, Marguet C, Brouard J, de Blic J, Clement A, Epaud R, Guillot L.	Molecular and cellular characteristics of ABCA3 mutation associated with diffuse parenchymal lung diseases in children.	<i>Hum. Mol. Genet.</i>	in press		2012
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Molecular and cellular characteristics of *ABCA3* mutations associated with diffuse parenchymal lung diseases in children

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ABCA3 (ATP-binding cassette subfamily A, member 3) is expressed in the lamellar bodies of alveolar type II cells and is crucial to pulmonary surfactant storage and homeostasis. *ABCA3* gene mutations have been associated with neonatal respiratory distress (NRD) and pediatric interstitial lung disease (ILD). The objective of this study was to look for *ABCA3* gene mutations in patients with severe NRD and/or ILD. The 30 *ABCA3* coding exons were screened in 47 patients with severe NRD and/or ILD. *ABCA3* mutations were identified in 10 out of 47 patients, including 2 homozygous, 5 compound heterozygous and 3 heterozygous patients. SP-B and SP-C expression patterns varied across patients. Among patients with *ABCA3* mutations, five died shortly after birth and five developed ILD (including one without NRD). Functional studies of p.D253H and p.T1173R mutations revealed that p.D253H and p.T1173R induced abnormal lamellar bodies. Additionally, p.T1173R increased IL-8 secretion *in vitro*. In conclusion, we identified new *ABCA3* mutations in patients with life-threatening NRD and/or ILD. Two mutations associated with ILD acted via different pathophysiological mechanisms despite similar clinical phenotypes.

INTRODUCTION

Pulmonary surfactant, a complex mixture of lipids and specific proteins located at the air–liquid interface, lowers alveolar surface tension, thereby preventing alveolar collapse at the

end of expiration. It is synthesized by alveolar type-II cells, stored in lamellar bodies and secreted by exocytosis. Phospholipids make up ~90% of pulmonary surfactant.

Recent studies indicate a role for several genes in diffuse lung diseases (1–3). Genes implicated to date include the

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Table 1. Genetic analysis results in the 10 children harboring homozygous and compound heterozygous (shaded) or heterozygous *ABCA3* mutations

Patient	NRD	Clinical outcome	<i>ABCA3</i> mutation cDNA level	Protein level	<i>ABCA3</i> SNPs dbSNPs rs# cluster id	<i>ABCA3</i> variants Missense variants in conserved amino acid
1	Yes	ILD	c.[3518C>G] + [3518C>G]	p.[T1173R] + [T1173R]	rs149532, rs13332514	
2	Yes	ILD	c.[757G>C] + [757G>C]	p.[D253H] + [D253H]		
3	Yes	Death	c.[1385T>G] + [2890G>A]	p.[L462R] + [G964S]	rs149532	
4	Yes	Death	c.[4747C>T] + c.[384delC]	p.[R1583W] + p.[S128Rfs]	rs149532	c.[450G>A] (het)
5	No	Death	c.[629G>T] + [3079G>C]	p.[G210V] + [A1027P]	rs149532	
6	Yes	ILD	c.[622C>T] + [4561C>T]	p.[R208W] + [R1521W]	rs149532, rs323043	
7	Yes	Death	c.[604G>C] + [907C>G]	p.[G202R] + [L303V]	rs149532, rs323043 (het), rs13332514	
8	Yes	Death	c.[2888A>G] + [?]	p.[Y963C] + [?]	rs149532 (het), rs323043 (het)	
9	Yes	ILD	c.[2125C>T] + [?]	p.[R709W] + [?]	rs149532	
10	Yes	ILD	c.[2614A>G] + [?]	p.[S872G] + [?]	rs149532 (het), rs323043, rs13332514 (het)	

het, heterozygous; NRD, neonatal respiratory distress; ILD, interstitial lung disease.

surfactant protein (SP)-B and SP-C genes (*SFTPB*, MIM 178640; and *SFTPC*, MIM 178620) and the ATP-binding cassette subfamily A member 3 gene (*ABCA3*, MIM 601615). SP-B deficiency has long been known to cause lethal neonatal respiratory distress (NRD) (4). More recently, *SFTPC* mutations were reported in newborns and infants with severe alveolar-interstitial syndrome (3,5). *ABCA3* is a 1704-amino acid protein expressed selectively—but not specifically—in the lung, where it is found in the limiting membrane of lamellar bodies (1,6,7). *ABCA3* is encoded by an 80 kb gene mapped to 16p13.3 in humans and is thought to regulate lipid transport and organization during lamellar body formation (8,9).

ABCA3 gene mutations are transmitted by autosomal recessive inheritance. As with SP-B deficiency, *ABCA3* deficiency should be suspected in full-term infants with severe NRD refractory to maximal conventional treatment (10,11). In addition, *ABCA3* gene mutations have been found in children and young adults with interstitial lung disease (ILD) (1,3,12). For instance, the heterozygous c.875A>T (p.Glu292Val, p.E292V) *ABCA3* mutation was identified in several older children and young adults with desquamative interstitial pneumonitis (1). The large size and marked allelic heterogeneity of the *ABCA3* gene create challenges in mutation identification.

The objectives of this study were to identify and characterize *ABCA3* variations in a large population of pediatric patients with NRD and/or ILD. We identified new *ABCA3* gene mutations and found that these mutations were not associated with a specific expression profile of SP-B and SP-C in bronchoalveolar lavage fluid (BALF). Functional analysis of two mutations associated with ILD showed different pathophysiological mechanisms, despite the similar clinical phenotype.

RESULTS

Study patients

Of the 47 children enrolled in the study (Supplementary Material, Supporting Information 1), 23 (49%) were male and 24 (51%) female. The patients were from Europe ($n = 27$), North Africa ($n = 12$), Reunion Island ($n = 6$), West Africa ($n = 1$) and Haiti ($n = 1$). Among them, 6 (13%) were born

prematurely (<36 weeks) and 31 (66%) had NRD. ILD developed in 31 (66%) patients, and 21 (36%) patients had both NRD and ILD. Nine (19%) patients died of respiratory failure.

Genetic analysis

Of the 47 patients, 10 had *ABCA3* mutations. We identified 15 mutations, including 13 that had not been described previously. The two mutations p.G210V and p.R208W have been already identified (13,14). There were 14 missense mutations and 1 heterozygous nonsense mutation (p.Ser128ArgfsX23, designated hereafter as p.S128Rfs) (Table 1).

Analysis of genomic DNA from the parents and kindred showed that the compound heterozygous p.R1583W/p.S128Rfs (Fig. 1A) and p.R208W/p.R1521W (Fig. 1B) mutations were inherited, as well as the homozygous mutations p.T1173R (Fig. 1C) and p.D253H (Fig. 1D). For the other mutations, genomic DNA samples from family members were not available.

None of these newly identified *ABCA3* mutations has been previously described as polymorphisms (<http://ncbi.nih.gov/SNP>). In addition, none of the new variants was detected in the 46 alleles from our 23 controls. Alignment of the human and other mammalian amino acid sequences (by Multiple Sequence Comparison using Log-Expectation, MUSCLE analysis) indicated that almost all the *ABCA3* mutations occurred in highly conserved residues (not illustrated). They were located across the protein in the extracellular domains (ECD1 and ECD2), as well as in internal domains (NBD1 and NBD2) (Fig. 2). Finally, complete *ABCA3* sequencing disclosed previously described single-nucleotide polymorphisms (SNPs) (Table 1), as well as a missense variant affecting a conserved amino acid in the patient harboring the c.[4747C>T]+[384delC] mutation.

In the 37 patients without *ABCA3* mutations, four SNPs were identified in the coding region of *ABCA3*. These SNPs were in exons 7, 9, 14 and 26, respectively, and did not induce amino acid variations. A missense variant in the conserved amino acid c.1059C>T was identified in nine children. We found these variants neither in the public polymorphism database nor in our controls.