

Immunohistochemical staining indicated that MBTPS2 is mainly expressed in the upper granular layer in normal skin, as previously shown (Aten et al., 2010); however, in OS skin, MBTPS2 was expressed throughout the epidermis (Figure 2c). There was no apparent difference in MBTPS2 localization in the skin of a KFSD patient with the p.N508S mutation (Aten et al., 2010). It is unclear why this is but it may be because of differences in processing of the mutants in the two diseases.

In summary, we demonstrate a novel association between an MBTPS2 mutation and an X-linked form of OS. This expands the number of disorders linked to MBTPS2 mutations and reveals clinical heterogeneity associated with different MBTPS2 mutations.

Written, informed consent was obtained from all family members or their legal guardians. This study was approved by the South East NHS Research Ethics Committee and was performed according to the Declaration of Helsinki Principles.

CONFLICT OF INTEREST

The authors state no conflict of interest.

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SUPPLEMENTARY MATERIAL

Supplementary material is linked to the online version of the paper at <http://www.nature.com/jid>

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Targeted Sequence Capture and High-Throughput Sequencing in the Molecular Diagnosis of Ichthyosis and Other Skin Diseases

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TO THE EDITOR

The inherited ichthyoses are a large and genetically heterogeneous group of

Mendelian disorders of cornification, characterized by scaling and/or hyperkeratosis over the majority of the

integument (Oji et al., 2010). The two main nonsyndromic ichthyosis groups are autosomal recessive congenital ichthyosis (ARCI), encompassing lamellar ichthyosis (LI), congenital ichthyosiform erythroderma (CIE), and harlequin ichthyosis (HI), in which patients are

Abbreviations: ARCI, autosomal recessive congenital ichthyosis; CIE, congenital ichthyosiform erythroderma; HI, harlequin ichthyosis; KPI, keratinopathic ichthyosis; LI, lamellar ichthyosis; NGS, next-generation sequencing; SPPK, striate palmoplantar keratoderma; SNP, single-nucleotide polymorphism

usually born as collodion babies; and keratinopathic ichthyoses (KPI), the two main groups of which are epidermolytic ichthyosis (EI) and superficial epidermolytic ichthyosis (SEI) (Oji *et al.*, 2010). KPI are linked to mutations in keratin genes. Mutations in *ABCA12* are associated with HI, the most devastating and frequently lethal form of ichthyosis (Akiyama *et al.*, 2005; Kelsell *et al.*, 2005). However, mutations in multiple genes (Table 1), including *ABCA12*, are linked to LI and CIE, which display clinical overlap (Akiyama *et al.*, 2003).

As mutations in multiple genes are linked to nonsyndromic and syndromic ichthyosis, undertaking genetic screening by PCR and Sanger sequencing in a gene-by-gene approach is labor-intensive and expensive. Screening known ichthyosis genes simultaneously in a patient (or multiple patients) could enable a swifter identification of gene mutations in patients and facilitate prenatal diagnosis and genetic counseling.

Next-generation sequencing (NGS) has proven effective in the discovery of mutations in novel disease-associated genes, for example, by exome sequencing (Ng *et al.*, 2009) or by targeted sequence capture of chromosomal regions previously linked to a condition (Blaydon *et al.*, 2011, 2012). For conditions associated with mutations in multiple known genes, targeted gene capture coupled with NGS has shown promise in the molecular diagnosis of disease (Berg *et al.*, 2011; Artuso *et al.*, 2012). Here, we designed a custom NimbleGen microarray for sequence capture and NGS of the *ABCA12* gene locus, as well as the exons of 23 other genes linked to nonsyndromic and syndromic forms of ichthyosis, acral peeling skin syndrome/peeling (APSS) skin syndrome (PSS) or striate palmoplantar keratoderma (SPPK; Table 1), on pooled DNA consisting of 14 genomic DNA samples (Supplementary Information and Supplementary Table S1 online).

We discovered 12 sequence variants, which, to our knowledge, have not been reported previously (three deletions leading to frameshifts, seven missense, one nonsense, and one splice site), and four known disease-associated mutations (Table 2). The hetero-

Table 1. Genes implicated in ichthyosis and other skin diseases on the custom capture microarray

Gene	OMIM	Cytogenetic location (hg19)	Disease(s) with skin phenotype
<i>Exons captured</i>			
<i>ABHD5</i>	*604780	3p21.33	CDS
<i>AP1S1</i>	*603531	7q22.1	MEDNIK
<i>ALOXE3</i>	*607206	17p13.1	ARCI (CIE)
<i>ALOX12B</i>	*603741	17p13.1	ARCI (CIE)
<i>CDSN</i>	*602593	6p21.33	Hypotrichosis, PSS
<i>CSTA</i>	*184600	3q21.1	AREI
<i>CYP4F22</i>	*611495	19p13.12	ARCI (LI)
<i>DSG1</i>	*125670	18q12.1	SPPK1
<i>DSP</i>	*125647	6p24.3	DCWHK, LAEB, SFWHS, SPPK2
<i>GJB2</i>	*121011	13q12.11	BPS, HID, KID, PPK with deafness
<i>GJB3</i>	+603324	1p34.3	EKV
<i>GJB4</i>	*605425	1p34.3	EKV
<i>KRT1</i>	*139350	12q13.13	AEI, EI, EPPK, ICM, NEPPK, SPPK3
<i>KRT2</i>	*600194	12q13.13	SEI
<i>LOR</i>	*152445	1q21.3	LK
<i>NIPAL4</i>	*609383	5q33.3	ARCI (CIE)
<i>POMP</i>	*613386	13q12.3	KLICK
<i>SLC27A4</i>	*604194	9q34.11	IPS
<i>SLURP1</i>	*606119	8q24.3	MDM
<i>SPINK5</i>	*605010	5q32	Atopy, NS
<i>STS</i>	#308100	Xp22.31	XLI
<i>TGM1</i>	*190195	14q12	ARCI (CIE, LI)
<i>TGM5</i>	*603805	15q15.2	APSS
<i>Exons, introns</i>			
<i>ABCA12</i>	*607800	2q35	ARCI (CIE, LI, HI)

Abbreviations: AEI, annular epidermolytic ichthyosis; APSS, acral peeling skin syndrome; ARCI, autosomal recessive congenital ichthyosis; AREI, autosomal recessive exfoliative ichthyosis; BPS, Bart-Pumphrey syndrome; CDS, Chanarin-Dorfman syndrome; CIE, congenital ichthyosiform erythroderma; DCWHK, dilated cardiomyopathy with woolly hair and keratoderma; EI, epidermolytic ichthyosis; EKV, erythrokeratoderma variabilis; EPPK, epidermolytic palmoplantar keratoderma; HI, harlequin ichthyosis; HID, hystrix-like ichthyosis with deafness; ICM, ichthyosis hystrix, Curth-Macklin type; IPS, ichthyosis prematurity syndrome; KID, keratitis-ichthyosis-deafness syndrome; KLICK, keratosis linearis-ichthyosis congenital-keratoderma; LAEB, lethal acantholytic epidermolysis bullosa; LI, lamellar ichthyosis; LK, loricrin keratoderma; MDM, mal de Meleda; MEDNIK, mental retardation, enteropathy, deafness, peripheral neuropathy, ichthyosis, and keratoderma; NEPPK, nonepidermolytic palmoplantar keratoderma; NS, Netherton syndrome; PPK, palmoplantar keratoderma; PSS, peeling skin syndrome; SEI, superficial epidermolytic ichthyosis; SFWHS, skin fragility-woolly hair syndrome; SPPK, striate palmoplantar keratoderma; XLI, X-linked recessive ichthyosis.

zygous whole-exon 8 deletion previously discovered by multiplex and oligonucleotide array analysis (Thomas *et al.*, 2006) in Sample 11 was not detected, indicating that currently NGS may not be sensitive enough to detect all complex or large insertion/deletion mutations. However, a predicted intronic splice site mutation

was found, and this is likely to be the second disease-causing mutation in Sample 11. In contrast, a homozygous large 101 bp deletion (p.I1128EfsX38) within exon 24 of *ABCA12* was detected by this capture method. Known whole-exon deletions have been undetectable in other sequence capture investigations (Berg *et al.*, 2011). Other non-microarray

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