Loss of Corneodesmosin Leads to Severe Skin Barrier Defect, Pruritus, and Atopy: Unraveling the Peeling Skin Disease

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Generalized peeling skin disease is an autosomal-recessive ichthyosiform erythroderma characterized by lifelong patchy peeling of the skin. After genome-wide linkage analysis, we have identified a homozygous nonsense mutation in CDSN in a large consanguineous family with generalized peeling skin, pruritus, and food allergies, which leads to a complete loss of corneodesmosin. In contrast to atopic dermatitis, which is responsible for NS, 15 in patients with PSD. 9 Moreover, PSD has to be differentiated from the acral peeling skin syndrome (MIM 609796), which is due to autosomal-recessive mutations in the gene of transglutaminase 5 (TGMS, MIM 603805), 17 and from peeling skin syndrome type A, which is characterized by asymptomatic and noninflammatory peeling and often starts at 3 to 6 years of age. 5,18

We have studied a large consanguineous Roma family from Germany with four individuals with generalized superficial skin peeling since birth (Figure 1), severe pruritus, and atopic manifestations with seasonal variation. The study was approved by the institutional review board of the University Hospital of Münster, and all patients enrolled gave their informed consent. A detailed medical and dermatological history was obtained from all affected persons. The clinical features are summarized in Table 1. The initial clinical presentation was in the first week of life in all four patients. The disease presented as an unusual ichthyosiform erythroderma with white, superficial exfoliation (Figure 1A), with normal birth weight and growth, and without clinical signs for a syndromic form of ichthyosis. However, an initial mild failure to thrive and some periods of Staphylococcus aureus skin infections were noted in the first few years of life. Most strikingly, the affected individuals showed severe pruritus, especially in warm weather, food allergies to nuts and fish, and repeated episodes of angioedema, urticaria, and/or asthma. Overall IgE levels were highly elevated (Table 1). Two children had unusually fine hair in early infancy,
and it could be plucked easily (P2 and P3). Patients did not show any hair loss, and hair shaft analysis did not reveal trichorrhexis invaginata, which would have been diagnostic for NS. Punch biopsies (4 mm) for histopathology and immunofluorescence analysis were taken from all patients. In addition, biopsies for ultrastructural analysis and isolation of keratinocytes were taken from patient 3 (P3). Specimens for ultrastructural analysis were proceeded and examined as described previously.16 Similarly to NS, histological and ultrastructural analyses of the skin showed an enhanced detachment of corneocytes (Figure 1B).4,16 However, we have not identified mutations in the genes SPINK5 or TGM5.

We carried out a whole-genome linkage analysis via chip-based SNP analysis. Peripheral blood was collected in EDTA from all available family members, and DNA was extracted from leukocytes via standard procedures. DNA samples of three affected children and their parents, representing one family branch each (see Figure S1 available online), were genotyped via the Affymetrix GeneChip Human Mapping 250K Sty Array (Affymetrix). Genotypes were called by the GeneChip DNA Analysis Software (Affymetrix). Data were checked using the program Graphical Representation of Relationships.19 Parametric linkage analysis was done with the programs Allegro20 and MERLIN.21 All data handling was done via the graphical user interface ALOHOMORA.22 Linkage analysis identified a candidate region on chromosome 6p (Figure 2A). Refined mapping localized the gene to a 3.3 cM interval with a maximum LOD score of 5.4, corresponding to 5.7 Mb in length, assuming two separate pedigrees with two affected individuals each (Figure S1). Because an undefined connection exists between both branches of the family and because they originated from the same tribe, we then searched for identical homozygous intervals between all four patients by using SNPs and microsatellites in the linked region. The largest homozygous interval was 3.0 Mb in length and contained 195 genes. CDSN (MIM 602593), located in the minimal interval, was chosen as a functional candidate gene because it encodes a component of the corneodesmosomes in the epidermal stratum corneum, and it was analyzed for mutations. The coding region was sequenced in the patients and in their parents and siblings (NM_001264.3; Table S1). All four affected children showed the same homozygous nonsense mutation in CDSN, c.175A>T, resulting in a premature termination codon, p.Lys59X (Figures 2B and 2C). We observed full cosegregation of the mutation in the entire family (Figure S1) and did not detect the mutation among 220 chromosomes from ethnically matching control persons.

To investigate CDSN expression, we isolated total RNA from primary keratinocytes cultured with 1.2 mM Ca2+. RNA was adjusted and quantified via one-step qRT-PCR (Table S1) with SYBR GreenER labeling (Invitrogen) on a LightCycler 480 system (Roche Applied Sciences). Normalization was done with ACTB, RPS18, and 18S RNA. Relative quantification showed a reduction of CDSN mRNA amounts by 75%, pointing to nonsense-mediated CDSN mRNA decay (Figure S2). Equal quantities of protein isolated from primary keratinocytes were separated by 10% SDS-PAGE under reducing conditions and transferred to polyvinylidene fluoride membrane (Millipore). The blots were probed with primary antibodies directed against corneodesmosin, transglutaminase 1, and actin. Immunoblot analysis demonstrated the absence of corneodesmosin in the patient, whereas differentiated...
keratinocytes of healthy controls showed a strong signal (Figure 2D). Transglutaminase 1 was detected as a late differentiation control in differentiated keratinocytes from both patients and unaffected persons.

Immunohistochemistry on skin biopsy samples was performed with antibodies against involucrin, filaggrin, loricrin, and keratins 2, 10, and 14. Direct immunofluorescence analysis was performed on cryosections for corneodesmosin, desmocollin 1, transglutaminase 1, LEKTI, desmoglein 1, transglutaminase 5, and elafin. Antigen mapping of corneodesmosin was negative for all skin biopsies of the patients (Figure 3A). In contrast, other

Table 1. Clinical Features of Patients P1–P4

<table>
<thead>
<tr>
<th>Disease Phenotype</th>
<th>P1 10 yrs (male)</th>
<th>P2 8 yrs (female)</th>
<th>P3 9 yrs (male)</th>
<th>P4 1 yr (male)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Onset and initial clinical presentation</td>
<td>Second day of life</td>
<td>Second day of life</td>
<td>Second day of life</td>
<td>Second day of life</td>
</tr>
<tr>
<td>Disease course</td>
<td>Erythematous patches that start scaling after few days, heal, and reoccur; severe exacerbations within the first 4 years of life</td>
<td>Erythematous patches that start scaling after few days, heal and reoccur; severe exacerbations within the first 4 years of life</td>
<td>Erythematous patches that start scaling after few days, heal and reoccur; severe exacerbations within the first 4 years of life</td>
<td>Erythematous patches that start scaling after few days, heal and reoccur; severe exacerbations within the first 4 years of life</td>
</tr>
<tr>
<td>Seasonal variation</td>
<td>Not specifically</td>
<td>Yes (severe scaling in winter, severe pruritus in summer)</td>
<td>Yes (severe pruritus in summer)</td>
<td>Yes</td>
</tr>
</tbody>
</table>

Clinical Features

Scaling

<table>
<thead>
<tr>
<th>Distribution</th>
<th>Generalized</th>
<th>Generalized</th>
<th>Generalized</th>
<th>Generalized</th>
</tr>
</thead>
<tbody>
<tr>
<td>Type</td>
<td>Exfoliative</td>
<td>Exfoliative</td>
<td>Exfoliative</td>
<td>Exfoliative</td>
</tr>
<tr>
<td>Color</td>
<td>White</td>
<td>White</td>
<td>White</td>
<td>White</td>
</tr>
<tr>
<td>Palmoplantar features</td>
<td>Episodically scaling, hyperhidrosis</td>
<td>Mostly uninvolved</td>
<td>Hyperhidrosis</td>
<td>Mostly uninvolved</td>
</tr>
<tr>
<td>Hair abnormalities</td>
<td>No trichorrhexis invaginata, normal hair growths, brittle hair in early infancy</td>
<td>No trichorrhexis invaginata, easy plugging of the hair, normal hair growths, brittle hair in early infancy</td>
<td>No trichorrhexis invaginata, easy plugging of the hair, normal hair growths</td>
<td>No trichorrhexis invaginata, normal hair growths</td>
</tr>
<tr>
<td>Nail abnormalities</td>
<td>Mild onychodystrophy, white nail changes</td>
<td>Recurrent onycholysis since sixth year of life</td>
<td>Not specifically, white nail changes</td>
<td>Not specifically, white nail changes</td>
</tr>
<tr>
<td>S. aureus superinfection</td>
<td>Frequent during the first 4 years of life</td>
<td>Frequent during the first 4 years of life</td>
<td>Frequent during the first 4 years of life</td>
<td>Present</td>
</tr>
<tr>
<td>Growth</td>
<td>Normal birth weight and size, mild failure to thrive during the first ~4 years of life</td>
<td>Normal birth weight and size, mild failure to thrive during the first ~4 years of life</td>
<td>Normal birth weight and size, mild failure to thrive during the first ~4 years of life</td>
<td>Normal</td>
</tr>
<tr>
<td>Height (present age)</td>
<td>At 50th percentile</td>
<td>At 50th percentile</td>
<td>At 50th percentile</td>
<td>At 50th percentile</td>
</tr>
<tr>
<td>Weight (present age)</td>
<td>At 10th percentile</td>
<td>At 10th percentile</td>
<td>At 10th percentile</td>
<td>At 10th percentile</td>
</tr>
</tbody>
</table>

Atopic Features

| Pruritus | Moderate to severe | Moderate to severe | Moderate to severe | Moderate |
| Total IgE level | 2076 IU/ml (<100)* | ND | >2000 IU/ml (<100)* | ND |
| Eosinophils | 0.7 × 10⁷/µl (<0.44)* | ND | 0.79 × 10⁷/µl (<0.60)* | ND |
| Food intolerances | Nuts, fish | Fish | Nuts, fish | Unknown |
| Others | – | History of urticaria with angioedema | History of asthma when in contact with fish | – |

ND, not determined.
* Normal values.
components of the desmosomes and corneodesmosomes, i.e., desmocollin 1 and desmoglein 1, showed an almost regular expression. LEKTI, missing in NS, presented a broadened signal zone in the upper epidermal layers of our patients, transglutaminase 5 was normal, and further late epidermal differentiation markers, e.g., filaggrin, involucrin, loricrin, transglutaminase 1, and keratin 2, likewise showed an enhanced immunohistochemical staining (Figure 3B; Figure S3). These proteins are important for the cornified cell envelope formation, and the changes probably reflect homeostatic responses to epidermal stress or inflammation.

To further study the lack of corneodesmosin in PSD that is supposed to lead to an increased desquamation of the corneocytes, we generated three-dimensional skin models by using organotypic tissue coculture systems. Primary human keratinocytes (NHEKs) were isolated from foreskin obtained after juvenile circumcision in an age-matched boy and from patient skin punch biopsy samples (P3) and cultivated in the presence of a feeder layer of irritated 3T3 mouse fibroblasts. Normal human dermal fibroblasts (NHDF) were isolated from neonatal foreskin and patient skin biopsy samples and were cultivated in DMEM with 10% fetal calf serum (FCS), 100 IU/ml penicillin, and 100 μg/ml streptomycin. Six-well plates with 3 μm inserts were used. For each well, a mixture of collagen I (bovine, Nutacon) and 10× HBSS was brought to neutral pH with NaOH, 2.5×10^5 NHDF in FCS was added, and the mixture was poured into the filter insert. The matrix was stored for 2–4 hr in a CO2-free incubator before keratinocyte growth medium was added. The system was transferred to an incubator with 5% CO2 and 95% humidity. After removing the medium from the top, 4.5×10^6 to 5.2×10^6 NHEK was seeded onto the matrices. On the next day, the medium was changed to defined cultivation medium. Models were cultivated for 8 days and then harvested with biopsy punches (5 to 8 mm). Either samples were processed and embedded in paraffin or RNA and protein were isolated.

Skin equivalents with patient fibroblasts and keratinocytes (Figure 4A) demonstrated formation of the basal keratinocyte layer and the dermal-epidermal junction zone and terminal keratinocyte differentiation in the epidermis models, as shown by hematoxylin and eosin (H & E)
staining (Figure 4A) and immunofluorescence staining of markers such as integrin β1, collagen IV, keratin 14, and keratin 10 (data not shown). Less well-organized epidermal structure and extended expression of late differentiation markers such as involucrin and filaggrin (Figure 4B) compared to skin equivalents with normal keratinocytes resembled our findings in patient skin. Consistent with the findings in patient skin biopsy specimens, we showed a complete loss of corneodesmosin (Figure 4B). We furthermore analyzed the presence of secreted serine proteases of the epidermis. Staining of kallikrein 5 was elevated in patient models and the expression was broadened in the epidermis, consistent with the results from a recent study.9 These results pointed to a disturbance of terminal epidermal differentiation upon loss of corneodesmosin and a deregulation of proteins playing a role for the cornified cell envelope and corneodesmosome degradation. The generation of three-dimensional models precisely replicating the epidermal skin enabled us to further analyze the epidermal barrier integrity. Test substances were the Organisation for Economic Cooperation and Development-proposed standard compounds for cutaneous absorption studies, caffeine and testosterone (Sigma-Aldrich). Experiments were performed according to a validated protocol,25 which was proved to be applicable to the use of reconstructed full-thickness skin.26 Briefly, stock solutions of testosterone (40 μg/ml) and caffeine (1000 μg/ml) were spiked with an appropriate amount of the radiolabeled agent to achieve a total radioactivity of 2 μCi/ml. Special inserts constructed for the EPISKIN model27 were used with an assayed surface area of 0.357 cm². Skin models were mounted into Franz cells (diameter 15 mm, volume 12 ml; PermeGear) with the stratum corneum facing the air. The system was allowed to equilibrate for 30 min before a sample of receptor fluid was collected. Subsequently, 110 μl of spiked caffeine and testosterone solutions was applied on the reconstructed skin model, resulting in a dose of 284.1 μg/cm² of caffeine and a dose of 11.36 μg/cm² of testosterone, respectively. Receptor fluid was sampled repeatedly every half hour and replaced by fresh PBS. Permeation tests were performed at least in quadruplicates except for the first experiment with patient cells, which was performed in duplicate. Two independent experiments were performed with control cells and patient cells. For each experiment, cumulative amounts of the permeated compounds in the receptor medium were plotted versus time (mean values ± standard deviation [SD]). The apparent permeability coefficient P app and lag time were calculated from a regression line based on mean values of the experiment.25 Normal skin models showed significantly lower permeation values (Figure 4C), though they slightly exceeded those obtained with a commercially available reconstructed skin model.26 The P app values with testosterone were 8.58 × 10⁻⁶ ± 1.47 × 10⁻⁶ cm/s and 5.29 × 10⁻⁶ ± 0.72 × 10⁻⁶ cm/s, respectively, in patient models compared to models with normal keratinocytes (mean values ± SD; p = 0.0039) and 13.79 × 10⁻⁶ ± 1.84 × 10⁻⁶ cm/s and 10.78 × 10⁻⁶ ± 0.82 × 10⁻⁶ cm/s, respectively, with caffeine (p = 0.017). Thus, we identified a severe barrier defect in patient models with the lack of corneodesmosin.

Corneodesmosin is a phosphorylated basic keratinocyte adhesion glycoprotein located in the extracellular part of the desmosomes and corneodesmosomes at the transition from the stratum granulosum (SG) to the stratum corneum (SC) and in the inner root sheath of the hair follicles.29

Figure 3. Characterization of Patient Epidermis

(A) Immunofluorescence study revealed a pericellular corneodesmosin signal within the upper SG and lower SC. In contrast, epidermis of patients 1 and 3 showed no signal. Scale bars represent 20 μm.

(Ba–Bf) LEKTI, deficient in Netherton syndrome, showed a broad and strong expression in the skin of the PSD patients (Ba and Bd). Further desmosomal components, i.e., desmocollin 1 (Dsc1, Bb and Be) and desmoglein 1 (Dsg1, Bc and Bf), showed a strong presence in the skin of the patients (only P3 is shown). Scale bars represent 20 μm.
The 52–56 kDa precursor form is synthesized in the middle epidermis, transported via lamellar bodies, and secreted into the extracellular space, where it associates to the desmosome core and the cornified cell envelope. Two glycine- and serine-rich domains, from amino acids 65–175 and 375–450, are responsible for forming adhesive secondary structures similar to glycine loops. Functionally, corneodesmosin reinforces cell-cell cohesion within the upper epidermis and the stratum corneum. Kallikrein 5 (stratum corneum tryptic enzyme) and kallikrein 7 (stratum corneum chymotryptic enzyme) cooperate to progressively proteolyse corneodesmosin. Its degradation is necessary for desquamation.30,31

An uncommon human hair disease was described earlier that was caused by autosomal-dominant mutations in CDSN: heterozygous nonsense mutations, namely p.Gln200X, p.Gln215X, and p.Tyr239X, were shown in a specific type of hypotrichosis simplex (MIM 146520).32,33 Affected individuals have normal hair in early childhood but experience progressive loss of scalp hair beginning in the middle of the first decade of life and almost complete baldness by the third decade; they do not show any signs of skin disease. It was assumed that abnormal corneodesmosin aggregates could exert a toxic effect to the hair follicle cells, thereby contributing to permanent hair loss.32 Of note, the phenotype of hypotrichosis simplex does not include skin peeling or ichthyosis, which could be explained by the presence of a normal allele in these patients. In our families, heterozygous carriers of the recessive mutation p.Lys59X did not show any skin or hair phenotype. Hence, hypotrichosis simplex and PSD can be assumed to involve different pathomechanisms.

Inactivation of corneodesmosin in mouse skin resulted in early postnatal death because of a breakdown of the epidermal barrier shortly after birth, when mechanical stress of a normal postnatal environment was exerted onto the skin.34 The defect of the epidermal barrier was accompanied by a 10-fold increase in transepidermal water loss.35 Here we have shown the impaired epidermal barrier caused by corneodesmosin deficiency in humans, which is evident clinically, e.g., by failure to thrive in early...
infancy, by ultrastructure analysis, which showed an extremely reduced coherence of corneocytes (Figure 1B), and by increased permeability of reagents into the epidermis (Figure 4C). The less-developed barrier is well in accordance with the sensitivity for irritants in patients with atopic diseases. We assume that the compromised epidermal barrier of corneodesmosin-deficient skin may facilitate the increased penetration of allergens into the epidermis, which could explain the development of atopic manifestations. A similar example is filaggrin deficiency, which can give rise to ichthyosis vulgaris and lead to an increased susceptibility to atopic dermatitis.2,3,37–39 Interestingly, our patients also showed manifest food allergies, i.e., to fish and nuts.

We conclude that a nonsense mutation in CDSN, which leads to the complete loss of corneodesmosin, causes peeling skin disease. Corneodesmosin is vastly important for the epidermal barrier integrity, and its absence may give rise to a strong predisposition to atopic manifestations. Corneodesmosin deficiency may therefore function as a novel human model disorder for atopic diseases, as did Netherton syndrome and ichthyosis vulgaris in the recent past.

Supplemental Data

Supplemental Data include one table and three figures and can be found with this article online at http://www.cell.com/AJHG/.

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