

# Chapter 7

## Deimination in Skin and Regulation of Peptidylarginine Deiminase Expression in Keratinocytes

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**Keywords** Peptidylarginine deiminase • Keratinocyte • Immunohistochemistry • Localization • Gene regulation • Differentiation • Skin

### 7.1 Introduction

The existence of citrulline in proteins was first described in the skin. In a paper published in *Nature* in 1958, George Rogers reported citrulline in a protein of hair follicles (Rogers and Simmonds 1958). Twenty-eight years later, Rothnagel and Rogers purified and characterised the corresponding protein and called it trichohyalin (Rothnagel and Rogers 1986). Since then, deiminated proteins have been detected in almost all cells, tissues and organs. The enzymes responsible for this posttranslational modification, the peptidylarginine deiminases (PADs), also known as protein-arginine deiminases, are becoming increasingly well known. Five types of PADs have been identified in humans and other mammals, the PAD1, 2, 3, 4 (also known as PAD5), and 6 (Vossenaar et al. 2003; Chavanas et al. 2004; Balandraud et al. 2005). They are encoded by five paralogous genes clustered on chromosome 1p35-36 and named *PADI1*, 2, 3, 4 and 6 (Vossenaar et al. 2003; Chavanas et al. 2004). The importance of PADs in many cellular processes is now recognised (Klose and Zhang 2007; Li et al. 2010; Struyf et al. 2009; Esposito et al. 2007) and PADs have

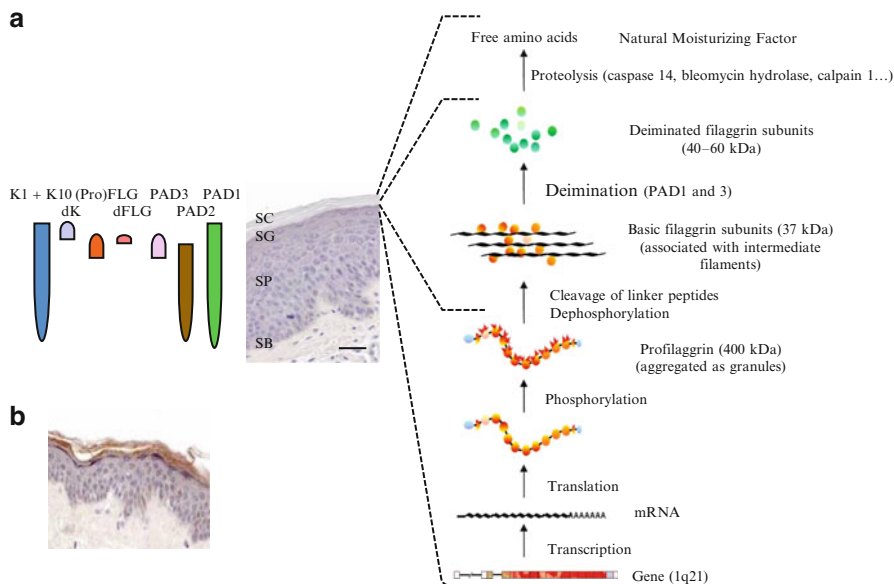
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**Fig. 7.1** Deiminated human epidermal proteins: involvement of PADs in the hydration of the *stratum corneum*. **(a)** The four epidermal keratinocyte layers are shown on a stained section of human skin (*center*): the *stratum corneum* (SC), *granulosum* (SG), *spinosum* (SP) and *basale* (SB). The immunodetection patterns of keratin (K) 1 and K10, profilaggrin and filaggrin ((pro) FLG), deiminated keratins (dK) and filaggrin (dFLG), and PADs in human epidermis are schematically indicated on the *left*. The complex metabolism of profilaggrin is schematically represented on the *right*: deimination of filaggrin, performed by PAD1 and PAD3, is essential for the degradation of the protein to free amino acids and the production of the natural moisturizing factor. **(b)** Immunochemical detection of deiminated proteins (in *brown*) in the *stratum corneum* of human epidermis. Scale bar = 40  $\mu$ m

been involved in the pathogenesis of autoimmune diseases, e.g. rheumatoid arthritis (Klareskog et al. 2008; Sebbag et al. 2004), multiple sclerosis (Harauz and Musse 2007; Kim et al. 2003) and cancer (Slack et al. 2011a), that are described in more detail in other chapters of this book. Here, we report on the location of PADs expressed in skin; the mechanisms involved in the regulation of their expression and activity in keratinocytes, their skin targets and physiological roles; and, finally, their possible contribution to skin diseases.

The skin provides mechanical protection to the organism and is an important barrier for preventing the invasion of pathogens, the entry of exogenous substances including allergens and toxins, and the uncontrolled loss of body water and solutes. This so-called barrier function is performed by the epidermis (Madison 2003), a stratified squamous epithelium mainly composed of keratinocytes.

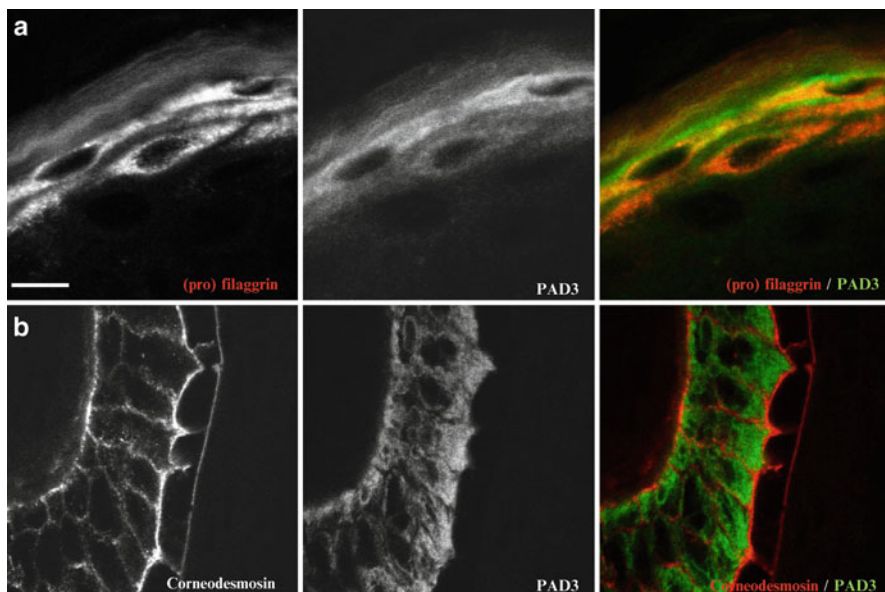
Terminal differentiation of keratinocytes is an oriented and complex program of gene expression from the proliferative basal layer of the epidermis to the upper horny layer, also named the *stratum corneum* (Fig. 7.1a). During their journey

through the spinous and granular layers, the cells sequentially turn specific genes on and off and undergo a series of structural and metabolic modifications. For instance, the expression of keratins KRT1 and KRT10 starts in the spinous layer, whereas filaggrin (FLG) is detected from the granular layer. Finally, the granular keratinocytes undergo a specialised form of programmed cell death called cornification. Cornification is characterised by (1) the elimination of all organelles and the nucleus; (2) the formation of a resistant and insoluble protein shell at the keratinocyte periphery, the cornified cell envelope; (3) the transformation of desmosomes, the intercellular junctional structures, into corneodesmosomes; and (4) the aggregation of the keratin intermediate filaments to form a macrofibrillar intracellular matrix. The resulting corneocytes are embedded in lipidic lamellae and form the thin, highly organised and resilient horny layer (Madison 2003; Candi et al. 2005). In order to maintain the thickness of the horny layer, the upper corneocytes detach from the skin surface during the strongly controlled process of desquamation and are replaced by newly differentiated cells. When human and rodent skin was probed with the anti-modified citrulline antibodies developed by Tatsuo Senshu (Yokohama, Japan), only the horny layer was stained (Senshu et al. 1996) (Fig. 7.1b).

## 7.2 PADs Expressed in Skin

### 7.2.1 *In the Epidermis*

The expression of only three *PADI* genes, i.e. *PADI1*, 2 and 3 (Guerrin et al. 2003; Nachat et al. 2005a), has been evidenced in human skin and epidermis by RT-PCR experiments. In cultured human primary keratinocytes, mRNAs encoding the same three PAD isotypes, but not PAD4 or PAD6, have also been detected (Méchin et al. 2010). In agreement with these findings, only PAD1, 2 and 3 have been immunodetected on skin sections with anti-peptide antibodies specific for each of the isoforms. PAD1 has been localised in the cytoplasm of keratinocytes throughout the whole human epidermis, with a higher expression in the granular cells and in the corneocyte intracellular matrix. In the granular cells, it is associated with keratohyalin granules and with keratin intermediate filaments. PAD2 has been detected in the cytoplasm of spinous keratinocytes and, with a more intense staining, at the periphery of granular keratinocytes. PAD3 is located in keratohyalin granules, in the cytoplasm of granular keratinocytes and in the matrix of the lower corneocytes (Figs. 7.1a and 7.2a). Immunoblotting experiments have confirmed these data. In particular, immunoblotting carried out on samples obtained from the superficial horny layer using adhesive tape stripping has evidenced that PAD1 is the only PAD isotype present in the upper corneocytes. The same pattern of PAD expression has been described in mouse



**Fig. 7.2** Immunodetection of PAD3 in the epidermis and inner root sheath of hair follicles. Cryosections of human skin were analysed by confocal microscopy with anti-PAD3 rabbit antibodies, with a monoclonal antibody directed against profilaggrin and filaggrin ((pro) filaggrin) and with a monoclonal antibody specific for corneodesmosin. **(a)** In the epidermis, PAD3 is co-located with profilaggrin in the cytoplasm of the upper granular keratinocytes and with filaggrin in the lower corneocytes. **(b)** In the hair follicles, PAD3 is detected in the cytoplasm of keratinocytes in the Huxley layer of the inner root sheath. Bar: 10  $\mu$ m

epidermis (Guerrin et al. 2003; Nachat et al. 2005a; Méchin et al. 2005; Coudane et al. 2011). In addition, the expression of PAD4 in rat epidermis has also been reported (Ishigami et al. 2001).

### 7.2.2 In Skin Appendages

PAD1 and PAD3 have been immunodetected in the concentric epithelial sheaths forming hair follicles at the anagen stage (Nachat et al. 2005b). PAD1 is expressed by differentiated keratinocytes, first those of the cuticle and Huxley's layer of the inner root sheath and second those of the companion layer between the inner and the outer root sheaths. PAD3 is expressed in cells of the inner root sheath (Fig. 7.2b) and the medulla. Both enzymes have been immunodetected in the keratinocyte cytoplasm.

PAD1 and PAD2 have also been observed in the secretory and myoepithelial cells of the sweat glands and in the arrector pili muscles (Nachat et al. 2005b). So far, no PADs have been detected in human sebaceous glands.

## 7.3 Regulation of PAD Expression in Keratinocytes

### 7.3.1 Minimal Promoters of PADI Genes and Bound Transcription Factors

Most of the genes expressed during the program of keratinocyte differentiation are regulated at the transcriptional level. This is probably also the case for the *PADI* genes. When differentiation of cultured human epidermal keratinocytes is induced by treatment with  $10^{-7}$  M of 1- $\alpha$ ,25-dihydroxy-vitamin D3 (VitD) for 24 h, higher amounts of mRNAs encoding PAD1 (~3-fold increase), PAD2 (~8-fold) and PAD3 (~10-fold) are detected (Méchin et al. 2010). Expression of *PADI1*, 2 and 3 mRNAs is also improved when the extracellular calcium concentration is increased (Méchin et al. 2010; Chavanas et al. 2008; Dong et al. 2005), another well-known way of inducing the differentiation of keratinocytes.

The minimal promoters of the *PADI1*, *PADI2* and *PADI3* genes have recently been delineated as short sequences of 195, 132 and 129 base pairs, respectively, upstream of the transcription initiation site (Dong et al. 2005, 2006, 2008). Electrophoretic mobility-shift assays, chromatin immunoprecipitation and small interfering RNA experiments have shown that binding of transcription factors of the ubiquitous stimulator protein (Sp) family, namely, Sp1 and Sp3, is crucial for the activity of these proximal promoters in keratinocytes (Dong et al. 2005, 2006, 2008). This is not surprising, since functional binding sites for Sp1 are frequently found in the promoter regions of genes expressed during the late steps of keratinocyte differentiation. These include the genes encoding keratin 1, transglutaminases 1 and 3, cornified cell envelope components and profilaggrin (Lee et al. 1996; Wong et al. 2005; Jang and Steinert 2002; Crish et al. 2006; Eckert et al. 2004; Markova et al. 2007).

The additional binding of MZF1 and NF-Y transcription factors is necessary to regulate the expression of *PADI1* and *PADI3*, respectively (Dong et al. 2006, 2008). Also, the expression of both Sp1 and MZF1 is increased after calcium stimulation of keratinocyte differentiation (Dong et al. 2008; Wong et al. 2005). Interestingly, Sp1 and MZF1 are also involved in the regulation of the *BLMH* gene (Kamata et al. 2011). This gene encodes a neutral cysteine protease, bleomycin hydrolase, implicated downstream of PAD1 and PAD3 in the processing of FLG (see Sect. 5.2). This suggests a possible co-regulation of FLG processing-related enzymes. In addition, a proximal TATA-box is present in *PADI1* and *PADI3*, but not *PADI2*, genes (Dong et al. 2005, 2006, 2008).

Since binding sites for Sp1, MZF1 and NF-Y have been identified in silico upstream of the transcription start site of the mouse orthologous genes (*Padi1*, *Padi2* and *Padi3*) (Dong et al. 2005, 2006, 2008), the same transcription factors are probably involved in the regulation of both human and mouse PAD genes. As in humans, when wild-type, but not VitD receptor null, mouse keratinocytes are treated with an analogue of VitD (EB1089), *Padi3* is up-regulated. This twofold activation occurs through the binding of activated VitD receptor- $\beta$ -catenin complexes to two VitD response elements located ~3 kb upstream of the transcription initiation site (Pálmer et al. 2008).

### 7.3.2 Role of Non-coding Conserved Sequences

However, considered alone, Sp1 and NF-Y binding to its proximal promoter cannot explain the tight control of *PADI3* expression in the granular keratinocytes, since these transcription factors are also involved in the regulation of *PADI4* (Dong et al. 2007), the expression of which has not been detected in the keratinocytes. Therefore, other levels of *PADI3* control have been suspected, in particular the role of non-coding evolutionarily conserved sequences.

The first to be identified was an 8-kb region located between *PADI2* and *PADI1*, 42 kb upstream of *PADI2* and 37 kb upstream of *PADI1* (the two genes are in the opposite transcription orientation). This sequence groups together many potential transcription factor-binding sites and is in an open conformation state of the chromatin in differentiated keratinocytes. It is therefore likely to bind transcriptional activators (Chavanas et al. 2004, 2008). In addition, by the chromosome conformation capture technique, it has been shown to physically interact with the *PADI3* promoter in the nuclei of differentiating keratinocytes through a chromatin loop spanning 86 kb (Chavanas et al. 2008). Several long-range enhancers and bound activators have been experimentally recognised in this region. Two segments of 346 and 245 bp, 1 kb distant from each other, cooperate in calcium-differentiated epidermal keratinocytes to enhance the activity of the *PADI3* gene minimal promoter located 82 kb away (Adoue et al. 2008). They have no effect when tested independently but act in an orientation-independent and copy number-dependent manner. Their effect has not been observed in proliferative epidermal keratinocytes, in human fibroblasts or cervix adenocarcinoma HeLa cells or on the *PADI2* minimal promoter. This strongly suggests that these two segments, called PAD intergenic enhancer segment 1 (PIE-S1) and PIE-S2, form a real *PADI3* bipartite enhancer. PIE-S2 binds distinct transcription factors of the AP-1 family according to the differentiation state of keratinocytes, junD homodimer in proliferative cells and c-Jun homodimer in differentiated cells (Adoue et al. 2008). PIE-S1 contains an MIBP1/RFX1-binding site (Adoue et al. 2008), but binding of either of these two transcription factors has not yet been proved.

An additional non-coding conserved segment of 63 bp, called PIE, has also been shown to display strong enhancer activity on the *PADI3* gene minimal promoter in calcium-differentiated keratinocytes (Chavanas et al. 2008). The enhancer activity of PIE does not depend on its orientation; it is low in proliferative keratinocytes and insignificant in HaCaT and Hela cells. It is low on the *PADI2* minimal promoter and null on *PADI1* and *PADI4* promoter. To be active, PIE requires the binding of c-Jun and c-Fos, another transcription factor of the AP-1 family. In addition, PIE seems to interact functionally with the two CAAT boxes of the PADI promoter, probably through a direct interaction between c-Jun and NF-Y (Chavanas et al. 2008).

Long-range regulatory elements are important for the coordinated regulation of many clustered genes, at distances of up to 1 Mb from their cognate promoters and in several cell types (Li et al. 2002). Whether this is also a key mechanism in regulating genes essential for terminally differentiated keratinocytes is less certain.

However, a network of conserved non-coding sequences involved in the regulation of the numerous genes of the so-called epidermal differentiation complex in keratinocytes has been described recently (Martin et al. 2004; de Guzman Strong et al. 2010). The expression of the p63 gene is also controlled by a long-range keratinocyte-specific enhancer (Antonini et al. 2006).

When orthologous PADI genes from multiple mammalian species are aligned, a highly conserved 1 kb region is revealed in the *PADI1* first intron, suggestive of a biological role (Ying et al. 2010). A 267 bp fragment of this region has been shown to enhance the activity of the *PADI1* minimal promoter in an orientation-independent manner in both proliferative and calcium-differentiated human keratinocytes. Binding of p65 and p50 subunits of NF-kappaB transcription factor is necessary for this enhancer activity. A physical interaction between the *PADI1* minimal promoter and these intronic conserved non-coding sequences, located 2.2 kb apart, has been evidenced, indicating chromatin looping (Ying et al. 2010). NF-kappaB involvement in keratinocyte differentiation and senescence is well known, as is its transcriptional effect via direct binding to response elements located in gene introns, including c-Fos (Bernard et al. 2004; Bell et al. 2003; Charital et al. 2009).

As a whole, these data show that the transcription of *PADI* gene during keratinocyte differentiation is under the control of multiple and complex regulatory mechanisms, including chromatin structure remodelling (Fig. 7.3).

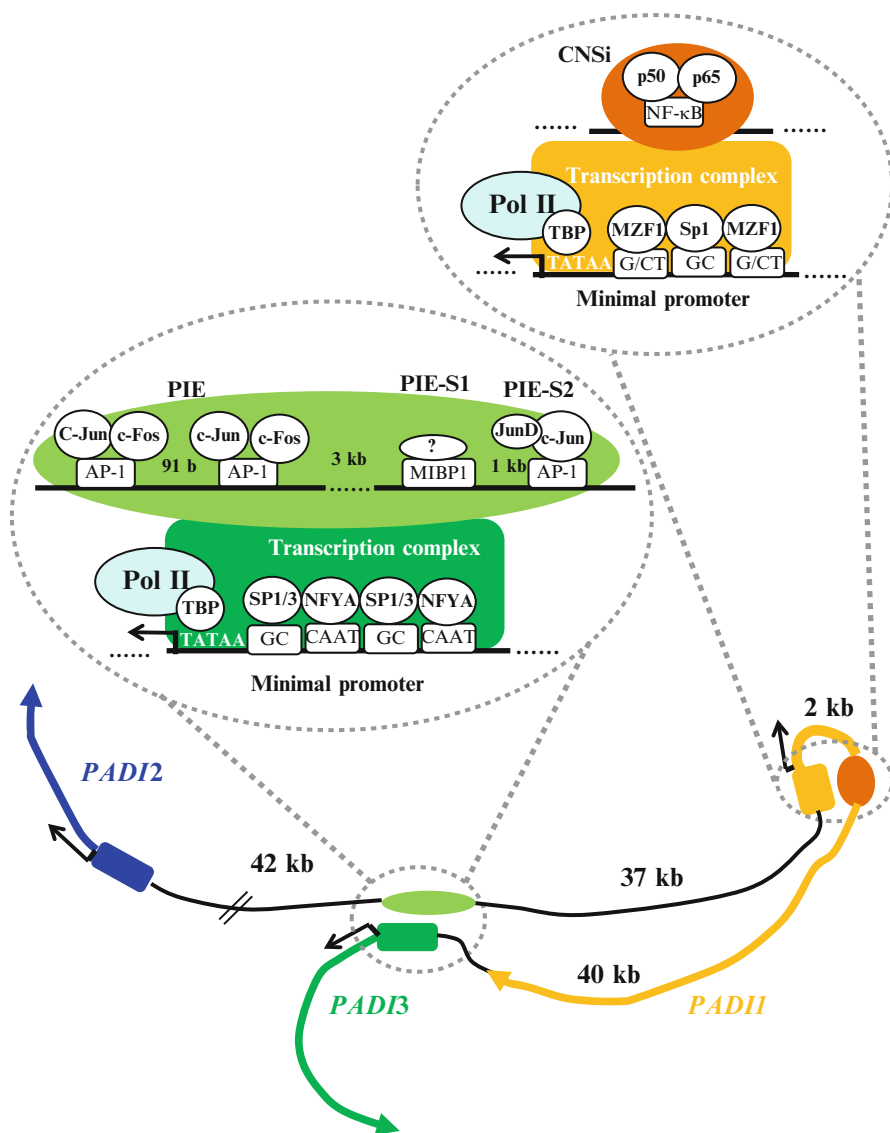
### 7.3.3 Regulation at the Translational Level

As previously reported for other tissues or cells, including optic nerve cells (Bhattacharya et al. 2006) and monocytes (Vossenaar et al. 2004), PAD expression in keratinocytes seems to be also regulated at the translational level. For example, treatment of keratinocytes with VitD strongly increases the amount of PAD1, PAD2 and PAD3 mRNA but has no effect on the corresponding protein (Méchin et al. 2010).

## 7.4 Regulation of PAD Activity in Keratinocytes

The presence of one PAD in keratinocytes at a particular time does not necessarily mean that the deimination of proteins takes place at the same time. Although PADs are immunodetected in basal and suprabasal living epidermal keratinocytes, deiminated proteins are only immunostained in corneocytes. In addition, even though Hela and HaCaT cells express at least one PAD, we have not been able to detect deiminated proteins, even in cells cultured at a high extracellular calcium concentrations (Méchin et al. 2010). In the same way, no deiminated proteins have been detected in cells of sweat glands and arrector muscles, where PAD1 and PAD2 are expressed (Nachat et al. 2005b). We suspect that the local intracellular





**Fig. 7.3** Schematic model of the transcriptional regulation of *PADI1* and *PADI3* gene expression in human keratinocytes. Part of the *PADI* gene locus is located in shown: the 5' region of *PADI2*, the intergenic region including two long-distance enhancers (namely, PIE and PIES1/S2), the entire *PADI1* gene including the conserved non-coding sequence its first intron (CNSi) and the 5' region of *PADI3*. Minimal promoters are indicated by coloured rectangular boxes and the orientation of transcription by black arrows. Bound transcription factors are shown, as are their binding sites. To allow activation of the *PADI3* promoter by PIE and PIES1/S2 enhancers located 87 kb upstream, chromatin has to form a large loop to bring them into physical contact. Similarly, a chromatin loop allows the activation of *PADI1* transcription through an interaction between the transcription complex and p50/p65 NF-κB transcription factors bound 2 kb downstream on the CNSi. Transcription factors (MZF1, c-Jun, c-Fos, JunD, NFYA and Sp1/3), the TATA-box-binding protein (TBP) and RNA polymerase II complex (Pol II) are shown as open circles and the transcription factor-binding sites by open boxes. Note that the distances (in bases) are not drawn to scale



concentration of calcium plays a role in controlling PAD activity, this ion being required for their activity *in vitro*.

Auto-deimination of PADs may also be involved in the regulation of their activity. We have observed calcium-dependent auto-deimination of PAD1, 2 and 3 during *in vitro* incubations. This modification reduces, but does not suppress, their activity and changes PAD3 structure. In particular, the distances between the four major amino acids of the active site increase (Méchin et al. 2010). Considering the high sequence homologies between the three isotypes, this is probably true for PAD1 and PAD2 as well. Similarly, PAD4 is also auto-deiminated *in vitro* and *in vivo* in activated neutrophils. This posttranslational modification changes the structure of the enzyme and could either inactivate it or modulate its ability to interact with other histone-modifying enzymes (Slack et al. 2011b; Andrade et al. 2010).

## 7.5 Deiminated Proteins and Role of Deimination in Skin

### 7.5.1 *In the Appendages*

As already mentioned in the introduction (Sect. 1) to this chapter, the first protein shown to be deiminated was trichohyalin. Trichohyalin is a member of the S100 fused-type protein (SFTP) family (Henry et al. 2012). Like the other SFTPs, trichohyalin is a large protein (220 kDa in human) formed by three domains: an amino-terminal domain homologous to S100A proteins and containing two functional EF-hand calcium-binding sites (91 amino acids long), a highly charged central domain formed by a series of peptide repeats (1,581 amino acids long) and a short carboxy-terminal tail (50 amino acids long). Trichohyalin is preferentially expressed in the inner root sheath and medulla of hair follicles and in the granular layer of the epithelium of dorsal tongue papillae (Hamilton et al. 1991; O'Keefe et al. 1993). It initially accumulates as large cytoplasmic granules. Then it associates with keratin intermediate filaments. Later it becomes cross-linked to itself, to keratin head and tail domains and to several cornified cell envelope components through  $\epsilon$ -( $\gamma$ -glutamyl) lysine isodipeptide bonds catalysed by transglutaminases (O'Keefe et al. 1993). Trichohyalin serves as a strengthener of the envelopes and as an anchor between the envelope and the corneocyte cytoplasmic matrix. This forms a continuous hardened supramolecular structure conferring high mechanical strength on the inner root sheath (Steinert et al. 2003). Trichohyalin contains 435 arginine residues, many of them being citrullinated. Trichohyalin deimination modifies its  $\alpha$ -helical structure, resulting in unfolding; makes it more soluble, inducing granule solubilisation; and makes it a better substrate for transglutamine 3 (Tarcza et al. 1996, 1997). Because PAD3 and trichohyalin expression patterns are very similar, this isotype is certainly responsible for trichohyalin deimination. In addition, the tail of mouse inner root sheath-specific type-I keratin 27 (formerly K25irs3) and type-II keratin 71 (K6irs1) are also deiminated before the proteins are cross-linked by transglutaminase 3 (Steinert et al. 2003).

S100A3, a calcium- and zinc-binding protein, is another substrate of PAD3 in the hair follicles. S100A3 is located in the cuticle and the cortex of the hair shaft and is believed to be involved in hair shaft formation. In vitro deimination of S100A3 by PAD3 promotes the assembly of a homotetramer and increases its affinity for calcium ions (Kizawa et al. 2008). This is described in greater detail in Chap. 8.

As a whole, these data indicate that deimination in the hair follicles is important for the mechanical resistance of cells in the inner root sheath and hair shaft. No deiminated proteins have yet been identified in sweat gland or arrector muscle cells.

### 7.5.2 *In the Epidermis*

Several epidermal deiminated proteins have been characterized, and all of them are modified in the horny layer (Fig. 7.1a, b). The effect of deimination on their properties is starting to be unravelled and will be described below.

The major targets of PADs in the epidermis are two closely related SFTPs, i.e. FGL and FLG-2 (Henry et al. 2012). Their repetitive central domains show 45 % amino-acid sequence similarity and similar amino-acid compositions with particular high levels of serine, glycine, histidine, glutamine and arginine (70.4 and 74.2 %, respectively, of total amino acids). Both are specifically expressed in the granular layer of the epidermis in the form of large insoluble precursors (400 and 248 kDa) which accumulate in the cytoplasmic keratohyalin granules (Henry et al. 2012; Dale et al. 1990; Hsu et al. 2011). At the *stratum granulosum/stratum corneum* transition, they are proteolytically processed to smaller basic subunits that interact with and are believed to aggregate keratin intermediate filaments. In the lower *stratum corneum*, they are co-located in the corneocyte filamentous matrix (Henry et al. 2012; Dale et al. 1990; Hsu et al. 2011). In the upper *stratum corneum*, FLG and probably FLG-2 subunits are totally degraded by several proteases, including caspase-14, calpain-1 and bleomycin hydrolase (Hsu et al. 2011; Hoste et al. 2011; Kamata et al. 2009; Yamazaki et al. 1997). The resulting amino acids form part of the natural moisturizing factor, a mixture of osmotic molecules allowing water retention in the upper *stratum corneum* (Harding and Scott 1983; Rawlings and Matts 2005). Some of the amino acids are further modified. For example, trans-urocanic acid, involved in photoprotection since it absorbs part of ultraviolet radiation, is derived from histidine in a reaction catalysed by histidase (Barresi et al. 2011). In contrast, pyrrolidone carboxylic acid, the most hygroscopic amino acid, derives from glutamine (Rawlings and Matts 2005). With a pKa of 3.9, it also contributes to the acidification of the superficial *stratum corneum*. This acidic pH is crucial for the antimicrobial activity of the layer, for its waterproof nature through the control of lipase activities and for the regulation of desquamation (Rawlings and Matts 2005; Harding et al. 2000).

FLG and FLG-2 deimination are thought to be necessary for their dissociation from the matrix. They also promote their proteolysis by calpain-1 and are a requisite for their proteolysis by bleomycin hydrolase (Hsu et al. 2011; Kamata et al. 2009). As a consequence, deimination participates in, and presumably controls, the

hydration of the upper epidermis and the epidermal barrier functions. On the basis of their enzymatic properties and their diffuse location within the fibrous matrix of the lower corneocytes (Méchin et al. 2005), PAD1 and PAD3 are probably the isotypes responsible for the deimination of FLG and FLG-2.

In the upper cornified layer, the head and tail of keratin K1 and K10 are deiminated (Senshu et al. 1996; Méchin et al. 2005; Ishida-Yamamoto et al. 2002). The enzyme involved is probably PAD1, since it is the only PAD isoform detected in this location (Méchin et al. 2005). The effect of deimination on the properties of these keratins is not known; however, it is concomitant with the observed ultrastructural modifications of the intracorneocyte fibrous matrix. Similarly to inner root sheath keratins, we could suspect that deimination precedes the cross-linking of these proteins to the cornified cell envelopes.

FLG has been known for a long time. It came back under the spotlight when nonsense mutations of its gene were shown to be responsible for ichthyosis vulgaris (OMIM 146700) and to be a high-risk factor for atopic eczema (OMIM #605803) (Smith et al. 2006; Palmer et al. 2006; Irvine and McLean 2006; Sandilands et al. 2007).

## 7.6 Deimination and Skin Diseases

Despite the accumulating data obtained on PADs by using skin as a model and the importance of deimination in skin physiology, few data are available concerning PAD implication in skin diseases. Lower amounts of citrullinated keratins have been detected in the epidermis of patients with epidermolytic hyperkeratosis (OMIM #113800; also known as bullous congenital ichthyosiform erythroderma) and psoriasis (Ishida-Yamamoto et al. 2000) (in addition to our unpublished data). However, in one study, paclitaxel, a well-known drug used in cancer therapy, but also an *in vitro* inhibitor of PAD, has been reported to improve severe psoriasis (Ehrlich et al. 2004). No further data has been published about this topic.

PAD could also be involved in skin tumorigenesis. Differential expression of the four genes encoding PAD1 (*PADI1*), laminin- $\gamma$ 2 (*LAMC2*), collagen type IV  $\alpha$ 1 (*COL4A1*) and collagen type I  $\alpha$ 1 (*COL1A1*) has been claimed as a predictive biomarker of squamous cell carcinomas of the oral cavity and oropharynx (Chen et al. 2008). In a genome-wide study concerning 930 Icelanders with cutaneous basal cell carcinoma, which is the most common cancer among Europeans, a single-nucleotide polymorphism in intron 13 of the PAD6 gene has been identified as a strong genetic risk factor (Stacey et al. 2008). This association has been replicated in an additional population from Eastern Europe. The estimated risk of the mutation carriers is 2.68 times that of noncarriers (Stacey et al. 2008). Finally, expression of PAD4, the isotype involved in gene expression regulation through deimination of histones, has been observed in skin carcinomas and extramammary Paget's disease (OMIM #167300) (Chang et al. 2009; Urano et al. 1990). Since PAD4 inhibition results in cell cycle arrest and apoptosis (Li et al. 2008) and since PAD4 represses the p53

target genes (Yao et al. 2008), this observation could be of relevance for skin tumours. A more detailed discussion on the role of deimination in cancer is discussed in Chap. 17.

## 7.7 Conclusion

PADs are increasingly considered as crucial molecular actors in cell physiology and human diseases. The data reported here highlight their importance in skin, particularly in the epidermis and hair follicles. However, more work needs to be done to definitively prove their contribution to skin diseases. Detailed analysis of mechanisms involved in controlling PAD expression and activity during keratinocyte differentiation indicates multiple levels of regulation. This indicates that deimination is a crucial post-translational modification of proteins that require tight control.

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