

# Transglutaminase Function in Epidermis

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**Surface epithelial cells, such as the epidermal keratinocyte, undergo a process of terminal cell differentiation that results in the construction of a multilayered epithelium. This epithelium functions to protect the organism from the environment. Transglutaminases, enzymes that catalyze the formation of isopeptide protein-protein cross-links, are key enzymes involved in the construction of this structure. This brief review will focus on the role of these enzymes in constructing the epidermal surface.**

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A major function of the epidermis is protection of the organism from the environment. Construction of the epidermal surface begins with regulated cell proliferation in the innermost epidermal cell layer—the basal layer (Cotsarelis *et al*, 1989; Fuchs and Byrne, 1994). The daughter cells are then displaced outward towards the cell surface. As the cells move outward, they lose the ability to proliferate and initiate the differentiation program (Fuchs and Byrne, 1994; Eckert *et al*, 1997) (Fig 1). The second epidermal layer, the spinous layer, is characterized by cells containing a large number of desmosomal connections. The desmosomes contribute strength. Cells in the third layer, the granular layer, contain granule-enclosed proteins and lipids (Matoltsy, 1966; Lavker and Matoltsy, 1971; Holbrook and Odland, 1975; Lavker, 1976; Ishida Yamamoto *et al*, 1993). Some of these granules, for example, contain cornified envelope precursors (Steven *et al*, 1990) that are ultimately deposited onto the inner surface of the developing cornified envelope. The transition zone is a region of extensive remodeling that marks the transition between living and dead epidermis. In this zone, the intracellular organelles are destroyed by proteases and nucleases. Concomitant with this destruction is assembly of the cornified envelope and the stabilization of the keratin intermediate filament bundles. The result of this process is the construction of the outermost epidermal layer, which is comprised of terminally differentiated keratinocytes—called corneocytes. Corneocytes consist of two major structures—a network of disulfide bond-stabilized keratin filament bundles surrounded by an envelope of covalently cross-linked protein (Nemes and Steinert, 1999) and associated lipid (Segre, 2003). Millions of corneocytes are required to cover the body surface.

## The Cornified Envelope

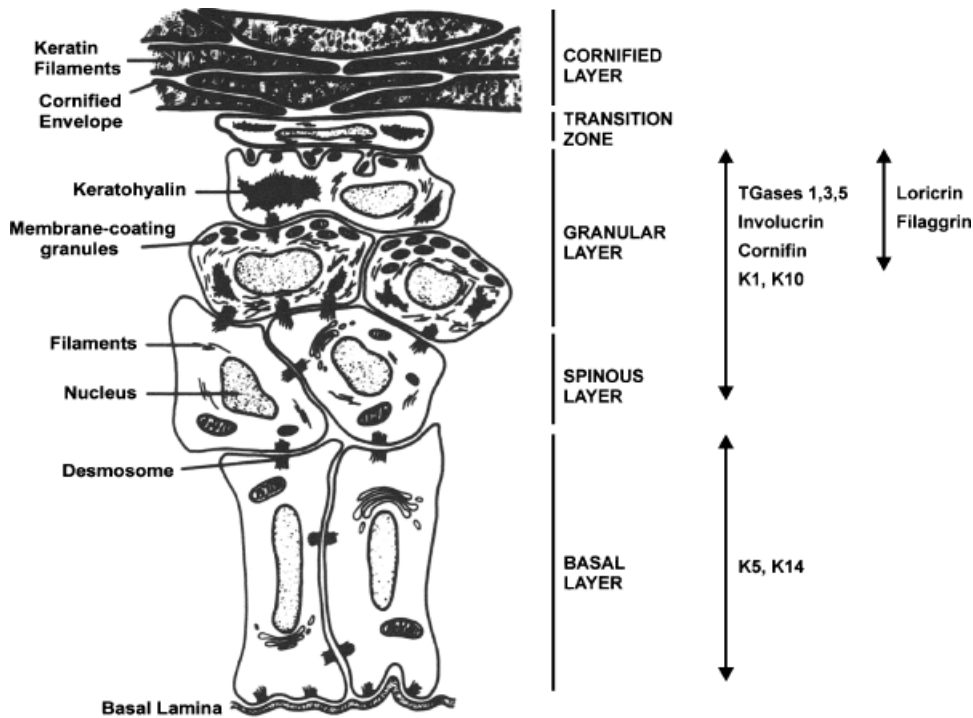
The cornified envelope is a covalently cross-linked structure that forms beneath the plasma membrane in differentiating

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Abbreviations: SPR, small proline-rich proteins; TGase, transglutaminase

keratinocytes (Matoltsy and Odland, 1955; Matoltsy, 1976; Steven and Steinert, 1994; Nemes and Steinert, 1999). The envelope includes two functional parts—an insoluble 15 nm thick structure consisting of covalently cross-linked protein (10 nm thick) that comprises the backbone of the envelope and covalently linked lipids (5 nm thick) that coat the exterior (Matoltsy and Matoltsy, 1966; Elias and Friend, 1975; Grayson and Elias, 1982; Wertz *et al*, 1989b; Robinson *et al*, 1997; Nemes and Steinert, 1999; Nemes *et al*, 1999a; Steinert and Marekov, 1999). Various proteins function as substrates and are incorporated into this structure (Table I). These include soluble (e.g., involucrin and small proline-rich proteins (SPR)) and insoluble (e.g., loricrin, periplakin, and envoplakin) proteins. Several soluble precursors are initially deposited to form a scaffold (Eckert *et al*, 1993; Nemes and Steinert, 1999; Kalinin *et al*, 2002). The insoluble precursors are subsequently deposited on the inner surface of the scaffolding. For example, loricrin is a major protein of the envelope that is cross-linked to the inner surface of the scaffolding (Mehrel *et al*, 1990; Hohl *et al*, 1991b; Nemes and Steinert, 1999).

The interprotein cross-links that hold together this multiprotein assembly (Hennings *et al*, 1981; Yaffe *et al*, 1993; Steven and Steinert, 1994; Steinert and Marekov, 1995; Robinson *et al*, 1996; Robinson *et al*, 1997; Steinert and Marekov, 1997; Steinert *et al*, 1998) are formed by transglutaminases (TGase). These enzymes catalyze interprotein bond formation by forming a thiolester acyl-enzyme intermediate and subsequently transferring the acyl residue to a primary amine (Folk and Finlayson, 1977; Folk, 1980). The amine acceptor is generally provided by the  $\epsilon$ -amino group of a protein-bound lysine and the ultimate link is an N<sup>6</sup>-( $\gamma$ -glutamyl)lysine isopeptide bond. Three TGase are known to be active in surface epithelia and are thought to participate to varying degrees in cross-link formation. These include TGase 1, TGase 3, and TGase 5 (Buxman and Wuepper, 1976; Goldsmith, 1983; Peterson and Wuepper, 1984; Rothnagel and Rogers, 1984; Thacher and Rice, 1985; Michel and Demarchez, 1988; Kim *et al*, 1991, 1993, 1995b; Polakowska *et al*, 1991; Hitomi *et al*, 1999, 2003). In



**Figure 1**  
**Keratinocyte differentiation.** Keratinocytes begin in the basal layer as undifferentiated cells that have proliferative potential and express keratins 5 and 14. As they exit the basal layer, the daughter cells lose proliferative ability and give rise to differentiated cells comprising the spinous, granular, and cornified layers. Cornified envelope assembly begins in the late spinous layer and continues as the cells progress into the granular layer. The approximate range of expression of each protein is shown by the arrows. Transglutaminase (TGase) 1, TGase 3, and TGase 5 are expressed in the spinous and granular layers along with the indicated envelope precursors (e.g., involucrin, cornifin), and keratins K1 and K10. The cornified envelope precursors, loricrin and filaggrin, are expressed later in differentiation. The rate of incorporation of envelope precursors and the deposition of covalent cross-links accelerates in the transition zone as the available level of free calcium increases and activates TGase. Cross-linking in the transition zone finishes production of the cornified layer that comprises the dead protective epidermal surface.

this brief review, we will describe some of the structural precursors involved in keratinocyte cornified envelope assembly, and the role of the various TGase in assembling the cornified structure.

### Structural Components of the Cornified Envelope

**Involucrin** As mentioned above, the cornified envelope consists of a host of proteins (Table I). Involucrin was the

first precursor discovered and cloned (Rice and Green, 1979; Eckert and Green, 1986). It is expressed throughout the suprabasal layers (Rice and Green, 1979; Banks-Schlegel and Green, 1981; Crish *et al*, 1993, 1998) in stratified epithelia, including the cervix, epidermis, esophagus, cornea, trachea, and conjunctiva (Banks-Schlegel and Green, 1981; Walts *et al*, 1985; Crish *et al*, 1993; Crish *et al*, 2002). Involucrin expression is controlled by AP1, Sp1, and C/EBP regulatory factors (Welter *et al*, 1995; Banks *et al*, 1998; Crish *et al*, 1998, 2002; Banks *et al*, 1999; Eckert *et al*,

**Table I. Cornified envelope precursors**

Protein	Size (kDa)	Chromosome location	Cornified envelope (%) <sup>b</sup>	Other names
Involucrin <sup>a</sup>	65	1q21	5	
Loricrin <sup>a</sup>	26	1q21	80	
SPR <sup>a</sup>	5–26	1q21(Gibbs <i>et al</i> , 1993)	3–5	Cornifins, pancornulins
Cystatin A	12	3cen–q21	2–5	Keratolinin
Proelafin	10	20q12–q13	< 1	Elastase-specific inhibitor, SKALP
Profilaggrin <sup>a</sup>	> 400	1q21	< 1	Filaggrin
Type II keratins	56–60	12q13	< 1	
Desmoplakin	330/250	6p21–ter	< 1	
Envoplakin	210	17q25	< 1	
Periplakin	195	16p13.3	< 1	
S100A10 and S100A11 <sup>a</sup>	12	1q21	< 1	Calpactin light chain and S100C/calgizzarin
Annexin I	36	9q12–q21.2	< 1	Lipocortin I
Cornifelin	12.5	19q13		

<sup>a</sup>Localized in the epidermal differentiation complex (Zhao and Elder, 1997; South *et al*, 1999).

<sup>b</sup>Nemes and Steinert (1999).  
 SPR, small proline-rich proteins.

2004), and the function of these factors is controlled by an nPKC, Ras, MEKK1, MEK3, p38 MAPK signaling cascade (Efimova *et al*, 1998; Efimova *et al*, 2003; Eckert *et al*, 2004). Involucrin contains thirty-seven 10 amino acid repeats, with each repeat containing three glutamine and two glutamate residues (Rice and Green, 1979; Simon and Green, 1985; Etoh *et al*, 1986; Simon and Green, 1988; Lambert *et al*, 2000). The entire protein is 15% glutamine and 20% glutamate (Eckert and Green, 1986). The predominant structure is  $\alpha$ -helical (Yaffe *et al*, 1992) but additional secondary structural features have been proposed (Lazo and Downing, 1999; Kajava, 2000). Although multiple glutamines on involucrin are TGase substrates (Etoh *et al*, 1986; LaCelle *et al*, 1998), TGase preferentially labels a single residue, glutamine496 (Simon and Green, 1988; Nemes *et al*, 1999b). Involucrin is one of the first precursors cross-linked during envelope assembly and is thought to form a scaffold for subsequent cross-linking of additional precursors (Nemes and Steinert, 1999).

**Loricrin** Loricrin is the major component of the cornified envelope in the epidermis (Steven and Steinert, 1994). Loricrin expression is induced by a variety of differentiating agents, including calcium (Hohl *et al*, 1991a; DiSepio *et al*, 1995), and is detected in granules in the granular layer (Steven *et al*, 1990; Ishida Yamamoto *et al*, 1993, 1996). It is likely that loricrin is sequestered in granules due to its low solubility. During terminal differentiation, in transition zone cells, loricrin is released from the granules and cross-linked to the inner surface of the nascent cornified envelope (Ishida-Yamamoto *et al*, 1999). Loricrin is also important in disease. Mutation of the glycine-rich domain of loricrin has been reported to result in the formation of arginine-rich nuclear localization sequences. The accumulation of mutated involucrin in the nucleus is thought to be the underlying cause of loricrin keratoderma (Ishida-Yamamoto, 2003).

**SPR** The SPR comprise a 14-member multigene family that contains three distinct subgroups—SPR1 (two members), SPR2 (11 members), and SPR3 (one member) (Tesfaigzi and Carlson, 1999). Expression of these genes is induced by calcium and other differentiating agents via activation of AP1, Sp1, and ets transcription factors (Gibbs *et al*, 1990; Fischer *et al*, 1996). The SPR structure includes eight or nine amino acid proline-rich repeats flanked by glutamine-, lysine-, and proline-rich ends (Gibbs *et al*, 1993). Glutamine and lysine residues, located at the amino and carboxy terminal ends of SPR proteins, participate in cross-link formation. These proteins have been proposed to function as bridges that link together other precursors (Steinert *et al*, 1998).

**Cystatin and elafin** Cystatin A, a cysteine protease inhibitor, is a minor component of the cornified envelope (Takahashi *et al*, 1994). Cystatin A expression is increased by treatment of keratinocytes with differentiating agents via an MAPK kinase cascade that includes Ras, MEKK1, MEK7, and JNK (Takahashi *et al*, 2001). A mutation in another cystatin family member, cystatin M/E, is thought to be an underlying cause of the disturbed epidermal cornification

observed in harlequin ichthyosis (Zeeuwen *et al*, 2002, 2004). Elafin, a potent inhibitor of elastase and proteinase 3, is translated as preproelafin, which is cleaved to release proelafin by removal of the 25 amino acid signal peptide. The proelafin protein is then cleaved to release elafin and cementoin. Cementoin is encoded by the pro-domain of elafin, and like elafin, can serve as a TGase substrate (Molhuizen *et al*, 1993; Nara *et al*, 1994; Steinert and Marekov, 1995). Members of the cystatin family and elafin may function to regulate protease activity that is required for envelope maturation. For example, cystatin M/E deficiency is associated with disturbed cornification, impaired barrier function, and dehydration (Zeeuwen *et al*, 2004). The function of cystatin M/E is to inhibit legumain, an asparaginyl endopeptidase. Thus, the increase in legumain activity resulting from cystatin M/E deficiency may be an underlying cause of harlequin ichthyosis (Zeeuwen *et al*, 2004).

**Filaggrin** Filaggrin is synthesized as profilaggrin, which consists of numerous filaggrin units flanked by amino- and carboxy-terminal domains (Presland *et al*, 1992, 1997; Pearton *et al*, 2002). Like several other envelope precursors (i.e., S100 proteins), profilaggrin contains two calcium-binding EF hand motifs (Presland *et al*, 1992; Markova *et al*, 1993). Filaggrin is a product of proteolytic cleavage of profilaggrin (Presland *et al*, 1997). In addition to its role in the cornified envelope, filaggrin also functions to bundle intermediate filaments (Dale *et al*, 1978; Mack *et al*, 1993). Filaggrin may also play a role in facilitating apoptotic responses due to its ability to alter keratin filament distribution (Presland *et al*, 2001).

**Desmoplakin, envoplakin, periplakin, and type II keratins** As mentioned above, the corneocyte consists of keratin intermediate filament bundles contained within an envelope of covalently cross-linked protein. Keratins are the most abundant proteins in the corneocyte and the assembled keratin intermediate filament bundles connect to the cell periphery at desmosomes (Green and Gaudry, 2000). Considering that cornified envelope assembly takes place at the plasma membrane, it is perhaps not surprising that both desmosomal components and keratin filaments are incorporated into the cornified envelope. The connection of the keratin filaments to the desmosome occurs through several proteins, including desmoplakin and envoplakin (Virata *et al*, 1992; Green and Gaudry, 2000). During terminal differentiation, the keratin filaments become covalently linked to the envelope via a specific lysine residue located at the amino terminus of type II keratins (Candi *et al*, 1998). Several other desmosomal proteins, including desmoplakin, desmoglein 3, desmocollins 3A/3B, plakoglobin, and plakophilin, are also incorporated into the cornified envelope (Robinson *et al*, 1997).

**S100 proteins and annexin I** S100 proteins are calcium-regulated EF hand-containing proteins (Donato, 1999). The genes encoding many S100 proteins are clustered in the epidermal differentiation complex on chromosome 1q21 (Celis and Olsen, 1994). S100A10 and S100A11 are incorporated into the cornified envelope in normal human keratinocytes (Robinson *et al*, 1997). In addition, the cross-

linking sites have been identified on several S100 proteins at the amino- and carboxy-termini (Robinson and Eckert, 1998; Ruse *et al*, 2001). In response to increased calcium, S100A11 moves to the cell periphery via a tubulin filament-dependent mechanism indicating that tubulin filaments are required to position this envelope precursor in the vicinity of the plasma membrane (Broome and Eckert, 2004).

**S100A11 forms a complex with annexin I** The S100A11/annexin I complex is a heterotetramer consisting of two S100A11 and two annexin I proteins. Rety *et al* (2000) solved the structure of this complex, confirming a novel mode of interaction of S100A11 with annexin I, and suggesting a model whereby the calcium-regulated (annexin I/S100A11)<sub>2</sub> heterotetramer functions to organize membrane fusion events. In addition, almost all annexins, including annexin I and annexin II, display calcium channel activity in *in vitro* systems (Chen *et al*, 1993; Cohen *et al*, 1995; Benz *et al*, 1996; Burger *et al*, 1996; Gerke and Moss, 2002). This activity has not been demonstrated in cells under normal intracellular conditions, but such activity may be possible under oxidizing and reduced pH conditions (Gerke and Moss, 2002); thus, annexin-dependent channel activity may be possible in keratinocytes in the oxidizing, acidic environment observed during terminal keratinocyte differentiation and may contribute to calcium influx.

**Cornifelin** Cornifelin is a recently described protein that is encoded on chromosome 19q13 (Michibata *et al*, 2004). Cornifelin is expressed in the epidermal suprabasal layers (Michibata *et al*, 2004). Like several other cornified envelope precursor genes, including involucrin (Eckert and Green, 1986), the first exon of the cornifelin gene is non-coding. Robinson *et al* (1997) reported an amino acid sequence, ARELKIRE, obtained by CNBr digestion of highly purified cornified envelopes, that matches a segment of cornifelin sequence (Michibata *et al*, 2004), suggesting that cornifelin is a bona fide envelope precursor.

## TGase in Keratinocytes

TGase comprise a family of calcium-dependent enzymes that catalyze the formation of isopeptide bonds. Several members of this family have been characterized (Phillips *et al*, 1990; Kim *et al*, 1991; Aeschlimann *et al*, 1998; Grenard *et al*, 2001) (Table II). These include Factor XIIIa, which is involved in stabilization of fibrin clots and in wound healing (Siefing Jr *et al*, 1978; Lorand and Graham, 2003), TGase 4, which is involved in the cross-linking of seminal fluid (Dubbink *et al*, 1998), Band 4.2, an inactive TGase, which is a structural protein in erythroblasts and erythrocytes (Lorand *et al*, 1987), TGase 2, a ubiquitously expressed TGase with multiple functions (Fesus and Piacentini, 2002; Griffin *et al*, 2002), and the epidermal-specific TGase, TGase 1 (Phillips *et al*, 1990; Polakowska *et al*, 1991), TGase 3 (Kim *et al*, 1994a), and TGase 5 (Candi *et al*, 2001, 2002, 2004; Grenard *et al*, 2001). Four TGase family members are expressed in keratinocytes and/or in epidermal tissues—TGase 1, TGase 2, TGase 3, and TGase 5 (Table III). These enzymes are discussed below.

**TGase type 1** The TGase 1 protein is encoded by the TGM1 gene located on chromosome 14q11.2 (Yamanishi *et al*, 1992). As measured by *in situ* hybridization, TGase 1 expression is differentiation-dependent and initiates in the spinous layer (Michel *et al*, 1992). TGase 1 promoter activity in cultured keratinocytes appears to require two Sp1 sites and an AP1 site within the distal region of the gene (Floyd and Jetten, 1989; Liew and Yamanishi, 1992; Yamada *et al*, 1994; Mariniello *et al*, 1995; Medvedev *et al*, 1999; Jessen *et al*, 2000a, b, 2001; Phillips *et al*, 2004).

Most TGase 1 is anchored to the keratinocyte plasma membrane via fatty acyl linkages (myristate, palmitate) that are present at the TGase 1 amino terminus (Rice *et al*, 1990; Phillips *et al*, 1993; Steinert *et al*, 1996b). Treatment with the protein synthesis inhibitors suggests that the myristylation occurs co-translationally and that palmitate labeling occurs

**Table II. The transglutaminase (TGase) family**

TGase <sup>a</sup>	Synonyms	Chromosome location	Gene	Function	Size aa (kDa)	Location
Factor XIII	Fibrin stabilizing factor	6p24–25	F13A1	Blood clotting and wound healing	732 (83)	Cytosol, extracellular
Band 4.2	Erythrocyte membrane protein	15q15.2	EPB42	Structural protein in erythrocytes—no activity	690 (72)	Membrane
<b>TGase 1</b>	<b>Keratinocyte TGase</b>	14q11.2	TGM1	Cornified envelope assembly in surface epithelia	814 (90)	Cytosol, membrane
<b>TGase 2</b>	<b>Tissue TGase</b>	20q11–12	TGM2	Cell death/differentiation, adhesion, matrix assembly	686 (80)	Cytosol, nucleus, membrane, cell surface, extracellular
<b>TGase 3</b>	<b>Epidermal TGase</b>	20q11–12	TGM3	Cornified envelope assembly in surface epithelia	692 (77)	Cytosol
TGase 4	Prostate TGase	3q21–22	TGM4	Semen coagulation in rodents	683 (77)	Unknown
<b>TGase 5</b>	<b>TGase X</b>	15q15.2	TGM5	Epidermal differentiation	719 (81)	Nuclear matrix, cytoskeleton
TGase 6	TGase Y	20q11	TGM6	Unknown	Unknown	Unknown
TGase 7	TGase Z	15q15.2	TGM7	Unknown	710 (80)	Unknown

<sup>a</sup>Transglutaminase subtypes indicated in bold are expressed in epidermis.

Table III. Transglutaminases (TGase) in surface epithelia

TGase	Epidermal expression	Cleavage modification	Subcellular distribution	Activity regulators
TGase 1	Expressed in spinous and granular layers	Phosphorylation, myristylation, palmitylation, cleavage to release 10, 33, and 68 kDa products	Plasma membrane	Calcium
TGase 2	Absent or minimal levels, expressed under specialized conditions		Cytosol	Calcium, GTP, GTPase cycle
TGase 3	Expressed in spinous and granular layers	Zymogen to active form transition involves protease cleavage at a site in the flexible loop surrounding Ser <sup>469</sup> (Ahvazi <i>et al</i> , 2002)	Cytosol	Calcium, GTP, GTPase cycle
TGase 5	Expressed in spinous and granular layers of epidermis, low level in basal layer (Candi <i>et al</i> , 2002)		Nuclear matrix and cytoskeleton (Candi <i>et al</i> , 2001)	Calcium, GTP

post-translationally (Steinert *et al*, 1996b). The target sites for myristate and palmitate addition are a cluster of five cysteine residues (Cys<sub>47</sub>, 48, 50, 51, and 53) within the sequence C<sub>47</sub>CGCCSC<sub>53</sub> at the TGase 1 amino terminus (Phillips *et al*, 1993). Deletion or mutation of the cysteines in this cluster reduces TGase 1 association with the keratinocytes plasma membrane. Although only a single cysteine need be present in this cluster for palmitate addition, more than one cysteine residue must be present to direct TG1 to the membrane. Expression of TGase 1 in 3T3 fibroblasts also results in a similar modification of TGase 1, indicating that this processing is not specific for keratinocytes (Phillips *et al*, 1993). Moreover, the membrane targeting domain can function in other contexts—a fusion protein containing the amino terminus of TGase 1 fused to involucrin protein directs involucrin to the plasma membrane (Phillips *et al*, 1993). The half-lives of the myristoyl and the palmitoyl adducts are less than that of the TGase 1 protein, suggesting that the rate of modification may influence TGase 1 membrane association.

A fraction of anchored TGase 1 undergoes proteolysis to yield fragments of 10, 33, and 68 kilodaltons (Steinert *et al*, 1996a). The level of these cleavage products increases with keratinocyte differentiation, suggesting that the process is regulated (Kim *et al*, 1995a, b; Steinert *et al*, 1996a, b). The 10 kDa subunit of processed TGase 1 contains the amino terminal region of TGase 1. *In vitro* studies suggest that this cleavage increases TGase 1 activity (Kim *et al*, 1994b, 1995a).

In addition to lipid acylation and proteolytic cleavage, TGase 1 is phosphorylated at amino-terminal serine residues—predominantly at Ser<sub>82</sub> (Chakravarty *et al*, 1990; Rice *et al*, 1996). Baseline phosphorylation is present in proliferating keratinocytes, and phorbol ester treatment produces a significant protein kinase c-dependent increase in TGase 1 phosphorylation at Ser<sub>82</sub> (Chakravarty *et al*, 1990; Rice *et al*, 1996). These phosphorylated serine residues reside in close proximity to the acylation/membrane anchoring sites at the TGase 1 amino terminus, suggesting that phosphorylation may influence membrane anchorage.

**TGase 1 in disease** Lamellar ichthyosis is a disorder of cornification that affects both the epidermis and hair. The phenotype includes large plate-like scales with underlying erythroderma, orthokeratotic hyperkeratosis, and mild-to-moderate acanthosis (Traupe *et al*, 1984). Mutations of the TGase 1 enzyme that reduces TGase 1 activity have been reported in lamellar ichthyosis patients (Huber *et al*, 1995a; Russell *et al*, 1995). These findings suggest that the TGase 1 mutation may be an underlying causative factor in the pathogenesis of this disease. The finding that mice lacking TGase 1 have an ichthyosis-like phenotype (Matsuki *et al*, 1998; Kuramoto *et al*, 2002) supports the idea that reduced TGase 1 activity can cause the disease. However, additional evidence suggests that a substantial percentage of ichthyosis patients have normal TGase 1 activity, indicating that the disease is genetically heterogeneous (Huber *et al*, 1995a, b).

**Control of TGase 1-dependent cross-linking** The activity of TGase 1, which is known to require calcium as a cofactor, increases when cells are treated with calcium (Ogawa and Goldsmith, 1976; Hennings *et al*, 1981; Goldsmith, 1983). The increase in extracellular calcium is associated with an increase in intracellular calcium (Hennings *et al*, 1989). The observation that TGase 1 activity is calcium-dependent is physiologically important, as increased calcium levels have been reported in the suprabasal epidermal layers (Menon *et al*, 1985). Moreover, for cultured epidermal keratinocytes, a standard method of triggering increased TGase activity is shifting the cells from a low-calcium medium (0.09 mM calcium) to a culture medium containing >0.3 mM calcium (Green, 1980; Li *et al*, 1995a, b). This shift results in an increase in cornified envelope precursor protein expression, increased TGase level and activity (Eckert *et al*, 1997), and increased cornified envelope formation (Green, 1980; Hennings *et al*, 1989). Thus, calcium treatment increases TGase 1 protein level, TGase 1 activity, and the level of TGase 1 substrates (Hennings *et al*, 1981). Other agents, for example phorbol ester and retinoic acid, also influence TGase 1 level (Saunders *et al*, 1993; Medvedev *et al*, 1999).

Recently, a protein has been described that triggers TGase-associated cell death in the absence of increased extracellular calcium (Sturniolo *et al*, 2003). TIG3 is a member of a family of type II tumor suppressors (DiSepio *et al*, 1998; Deucher *et al*, 2000). TIG3 protein is expressed at very low levels, undetectable via immunoblot in cultured keratinocytes, but TIG3 mRNA is detected. TIG3 protein is detected in the suprabasal epidermal layers, in human epidermis (Duvic *et al*, 2000). Vector-mediated delivery of the TIG3 protein to keratinocytes results in substantial growth suppression and dramatic morphological changes to produce cells that resemble cornified envelopes (Sturniolo *et al*, 2003). TGase mRNA and protein levels are not changed by TIG3 expression, but TGase activity is increased. Detailed studies reveal that TIG3 co-localizes with TGase 1 and that TGase 1 activity is specifically increased at locations of co-localization (Sturniolo *et al*, 2003). Moreover, TIG3 activates TGase 1 in the absence of a level of extracellular calcium normally required to activate TGase 1. Recent studies indicate that TIG3 and TGase 1 co-precipitate, suggesting that these proteins interact as part of a complex (Sturniolo and Eckert, unpublished).

**Lipids and TGase 1** As noted above, TGase 1 is unique among TGase in that it is anchored to the plasma membrane via a specific linkage. This location suggests that TGase 1 activity and specificity could be influenced by the membrane environment. Simon and Green showed that involucrin is a TGase substrate when incubated with keratinocyte membranes, and that glutamine<sub>496</sub> is the preferred site of cross-link formation (Simon and Green, 1988). Parallel studies revealed that additional glutamine residues function as TGase substrate sites when the involucrin protein is fragmented. This finding suggests that the overall structure of the involucrin protein has a role in defining which glutamine residues are selected for cross-link formation (Simon and Green, 1988). Steinert and coworkers combined recombinant TGase 1 and involucrin in a lipid vesicle system (Nemes *et al*, 1999b). Under these conditions, both involucrin and TGase 1 bind to the vesicles. Vesicle association of TGase 1 sensitizes the enzyme to calcium—enzyme activity is optimal at 10  $\mu$ M calcium instead of at the 100  $\mu$ M calcium concentration that is required in a lipid-free system. When incubated with TGase 1 in solution, involucrin is labeled at multiple glutamine residues; however, in the presence of the vesicles, glutamine<sub>496</sub> of involucrin is the primary TGase-reactive residue (Nemes *et al*, 1999b). Thus, both involucrin structure and TGase 1/involucrin association with membranes may influence which substrate residues are selected for cross-linking.

A role for lipids as TGase 1 substrates has also been identified. The cornified envelope is composed of a layer of covalently cross-linked proteins and a layer of associated lipids (Wertz *et al*, 1989b; Elias and Feingold, 2001). It had been proposed that ceramide lipids may be covalently linked to the protein scaffolding (Wertz *et al*, 1989a). Ultimately, Steinert and coworkers demonstrated that TGase 1, when reconstituted with involucrin and a  $\omega$ -hydroxyceramide analog on phosphatidylserine vesicles, promotes lipid ester formation at Gln<sub>107</sub>, 118, 122, 133, and 496 of involucrin

(Nemes *et al*, 1999a). Three of these residues are sites of ceramide modification of involucrin *in vivo* (Marekov and Steinert, 1998). Thus, TGase 1 can also function to cross-link lipids to the envelope.

**TGase type 2** The TGM2 gene, which encodes TGase 2, is located on chromosome 20q11–12 (Wang *et al*, 1994). TGase 2 is only expressed in keratinocytes and other surface epithelial cells under specific conditions. Vitamin A treatment of cultured keratinocytes increases TGase activity (Yuspa *et al*, 1982). This is surprising since vitamin A treatment suppresses cornified envelope formation. It turns out, however, that the induced TGase activity in these experiments is TGase 2 (Lichti *et al*, 1985). It is not clear why TGase 2 is increased under these conditions, as vitamin A treatment of cultured ectocervical epithelial cells results in a suppression of TGase activity and a reduction in TGase 2 mRNA and protein level (Sizemore *et al*, 1993). TGase 2 can function as a calcium-activated cross-linking protein or as a guanine nucleotide-dependent signaling protein. Activation of the cross-linking function is associated with a reduction in its signaling activity and vice versa. Thus, TGase 2 has multiple roles (Nakaoka *et al*, 1994).

TGase 2 plays an important role in wound healing. In fact, wound healing in surface epithelia requires the concerted action of several TGase. For example, Factor XIIIa is involved in control of blood loss (i.e., clotting) after traumatic injury, TGase 1, TGase 3, and TGase 5 are involved in stabilization of resident keratinocytes, and TGase 2 is involved in matrix repair and remodeling (Haroon *et al*, 1999; Griffin *et al*, 2002; Zhang *et al*, 2004). For example, in rat corneal epithelial wounds, TGase 2 mRNA and protein are detected in migrating epithelial cells and the activity co-localizes with high levels of extracellular matrix proteins, suggesting a role in the maintenance of corneal integrity and cell migration (Zhang *et al*, 2004). In addition, TGase 2 profoundly influences fibroblast function—both by regulating intracellular signaling pathways (Stephens *et al*, 2004) and by regulating extracellular matrix remodeling (Griffin *et al*, 2002). TGase 2 is released into and interacts with the matrix in specific ways (Gaudry *et al*, 1999; Griffin *et al*, 2002). Thus, TGase 2 appears to have intracellular functions in surface epithelial cells and in the underlying fibroblasts, and to also have a role in stabilizing the extracellular matrix (Griffin *et al*, 2002).

**TGase type 3** The TGM3 gene, encoding TGase 3, is located on chromosome 20q11–12 (Wang *et al*, 1994). TGase 3 expression is increased in calcium-treated keratinocytes by a mechanism that may involve interaction of ets and Sp1 transcription factors with binding sites in the TGM3 gene promoter (Lee *et al*, 1996; Kim *et al*, 2004). TGase 3 is expressed in the upper epidermal layers and is localized in the cytoplasm (Hitomi *et al*, 2003).

The TGase 3 zymogen consists of four folded domains that share a common structure with other TGase. An N-terminal  $\beta$ -sandwich domain, encompassing amino acids 1–134, contains nine  $\beta$ -sheets intermingled with three  $\alpha$ -helices. The catalytic core encompasses amino acids from

Asn<sub>135</sub> to Gly<sub>472</sub> and includes 15  $\beta$ -sheets interspersed with 15  $\alpha$ -helices. The longest of these helices encodes the active site Cys<sub>272</sub> residue (Ahvazi *et al*, 2002, 2004). Adjacent  $\beta$ -sheets encode the remaining two residues, His<sub>330</sub> and Asp<sub>353</sub>, which comprise the active site triad. The barrel 1 and 2 domains span amino acids 473–592 and 593–692, respectively. The active site is buried in a narrow cleft formed by two  $\beta$ -sheets of the catalytic core and the barrel 1 c-terminus (Ahvazi *et al*, 2002). Residues 462–471 comprise a flexible loop that joins the last  $\alpha$ -helix of the catalytic domain to the first  $\beta$ -strand of barrel 1. Cleavage at Ser<sub>469</sub>, within this loop, converts the zymogen form to a form that can be activated by calcium. The zymogen form of TGase 3 contains one calcium ion per protein monomer. This calcium ion is retained in the inactive and activated form and is thought to be required for stability. For activation, however, binding of two additional calcium ions is required. Binding of the second calcium ion produces a minimal change in protein-active site conformation. Binding of the third calcium ion, in contrast, produces a dramatic change in structure that results in the opening of a channel. (Ahvazi *et al*, 2003). The active channel forms a cone that extends inward toward the catalytic triad (Ahvazi *et al*, 2002, 2003). Once the zymogen is proteolytically cleaved in the 462–471 loop, magnesium (intracellular concentration = 2 mM) fills the third calcium binding site and the enzyme remains inactive. Only when intracellular calcium levels rise does calcium displace Mg<sup>2+</sup> at site three and activate the enzyme. Thus, TGase 3 activity requires the proteolytic cleavage of the zymogen and the binding of calcium at three locations. Once these requirements are met, cross-linking ensues (Ahvazi *et al*, 2003; Ahvazi and Steinert, 2003). In addition, TGase 3 activity is regulated by guanine nucleotides (Ahvazi *et al*, 2004). Binding of GTP is associated with substitution of Ca<sup>2+</sup> with Mg<sup>2+</sup> at the binding site three. This results in a conformation change that closes the active site channel. The channel remains closed as long as GTP is present; however, when this GTP is hydrolyzed to GDP the enzyme reverts to the active channel state. Both GTP and GDP bind to a pocket formed between the core domain and the  $\beta$ -barrel 1 domain (Ahvazi *et al*, 2004). The importance of the GTP-associated regulation is not well understood, although it may function in a manner similar to the GTPase function of TGase 2 (Iismaa *et al*, 1997, 2000).

TGase 3 is also an auto-antigen in skin disease. Gluten sensitivity typically presents as celiac disease, a common chronic small intestinal disorder (Reif and Lerner, 2004). In certain individuals, however, celiac disease is associated with dermatitis herpetiformis, a blistering skin disease characterized by granular IgA deposits in the papillary dermis. Antibodies produced by dermatitis herpetiformis patients show a high avidity for TGase 3 (Sardy *et al*, 2002). Moreover, the IgA precipitates that appear in the papillary dermis of patients with dermatitis herpetiformis contain TGase 3. These findings suggest that TGase 3 may serve as the auto-antigen involved in producing the skin phenotype.

**TGase type 5** The gene encoding TGase 5 is localized on chromosome 15q15.2 (Grenard *et al*, 2001). TGase 5 is expressed in the spinous and granular layers of human ep-

idermis (Candi *et al*, 2002), and TGase 5 expression in cultured keratinocytes is increased by treatment with the keratinocyte differentiating agent, calcium. Treatment of keratinocytes with elevated calcium resulted in a transient increase in TGase 5 mRNA, after 24 h of treatment, followed by a return to the level observed in untreated cells by 72 h. In contrast, the level of TGase 1 mRNA increases after 24 h and remains elevated. Thus, the kinetics of accumulation of the two TGase mRNA differs. RNA isolated from human keratinocytes reveals the presence of full-length TGase 5 mRNA and three alternate splice products—delta 3, delta 11, and delta 3/11—in which exons 3, 11, or 3 and 11 are absent (Candi *et al*, 2001). The splice products that lack exon 11 have a shift in frame that results in the translation of 25 new amino acids followed by a premature stop codon. Cell-free studies reveal that recombinant full-length and delta 11 spiced forms of TGase 5 are active, while spiced forms lacking the third exon (delta 3 and delta 3/11) are not active (Candi *et al*, 2001). The N-terminus of TGase 5 is also acetylated (Rufini *et al*, 2004).

Recombinant TGase 5 can utilize classical keratinocyte TGase substrates, including involucrin, loricrin, SPR1, and SPR2 (Candi *et al*, 1995). Moreover, the various TGase 5 forms have the expected reactivity - full-length and the delta 11 splice variant are fully active for all substrates, whereas the delta 3 and delta 3/11 splice variants are not active. TGase 5-dependent cross-linking of loricrin results in the formation of loricrin multimers, indicating that TGase 5 can utilize both glutamine and lysine residues from loricrin—both inter- and intra-protein cross-links are formed.

TGase 5 is half-maximally activated at 45  $\mu$ M calcium (Candi *et al*, 2004). Like TGase 2 (Nakaoka *et al*, 1994; Iismaa *et al*, 2000), TGase 5 is regulated by nucleotides (Candi *et al*, 2004). GTP and ATP inhibit the calcium-dependent cross-linking activity of recombinant TGase 5. In the presence of high calcium more GTP or ATP is required to inhibit calcium-dependent cross-linking. This response reflects the inverse relationship between TGase cross-linking activity and the nucleotide-dependent signaling activity, as previously reported for TGase 2 and TGase 3 (Iismaa *et al*, 2000; Ahvazi *et al*, 2004). TGase 5 is a relatively uncharacterized enzyme; thus, it is not known how its GTPase activity is involved in regulating cell function.

TGase 5 also displays an interesting *in situ* resistance to extraction with detergent, salt and reducing agent. Due to the low level of expression, TGase 5 has been studied in keratinocytes by overexpressing the protein. Expressed TGase 5 is not extracted from keratinocytes by non-ionic detergents, reducing agent, varied ionic strength, or pH. It is only extracted by treatment with SDS or urea—conditions required to extract insoluble proteins. Cell fractionation studies reveal that TGase 5 is associated with nuclear matrix and the cytoskeleton. Confocal analysis indicates that transfected TGase 5 is co-localized in a perinuclear location with vimentin, but not with keratin intermediate filaments (Candi *et al*, 2001). Thus, TGase 5 associates with insoluble filamentous structures. TGase 5 level is also increased in several epidermal diseases—it may contribute to the hyperkeratotic phenotype observed in ichthyosis (Candi *et al*, 2002).

## TGase—Progressive and Selective Roles in Cornified Envelope Assembly

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The experiments summarized in this review support several conclusions. First, the conservation of protein cross-linking sites, the morphological conservation of epidermal structure, and the ordered deposition of envelope precursors suggest that assembly of the envelope is a directed process (Eckert *et al*, 1993; Steinert, 1995). For example, membrane-associated proteins, including desmoplakin, envoplakin, and periplakin, are always present at the plasma membrane. Thus, it is not surprising that these proteins are envelope components. An involucrin-enriched scaffolding is constructed against this background of membrane-associated proteins (Eckert *et al*, 1993; Murthy *et al*, 1993; Steinert and Marekov, 1997; Jarnik *et al*, 1998). The involucrin scaffolding then provides deposition sites for the cross-linking of other envelope proteins, including cystatin A, proelafin, SPR, and loricrin (Nemes and Steinert, 1999). Second, in spite of the fact that the assembly is ordered, the system is also resilient, since altering the expression of specific precursors does not produce a visible phenotype (Yoneda and Steinert, 1993; Djian *et al*, 2000). This is in part due to the fact that when one precursor is eliminated, for example by gene ablation, the level of others is increased. Third, discovery of three major TGase types in the epidermis, each with a different localization, suggests different roles in assembly. Several studies suggest that TGase may differentially participate to produce the cornified envelope (Candi *et al*, 1995, 1999; Tarcsa *et al*, 1997, 1998). For example, TGase 3 utilizes SPR1 head domain A sequences as cross-linking substrates, whereas TGase 1 utilizes SPR1 head domain B sequences (Candi *et al*, 1999). Experiments with SPR1 in the presence of both TGase 1 and TGase 3 indicate that SPR1 will not polymerize in the absence of TGase 1. This information suggests that each TGase has a specific role in cross-link formation *in vivo*. TGase type-specific patterns of cross-link formation are also observed for cross-linking of loricrin (Candi *et al*, 1995). TGase 3 promotes the formation of intrachain cross-links at favored lysine and glutamine residues in loricrin, whereas TGase 1 catalyzes the formation of loricrin multimers using many glutamine and lysine residues. The loricrin residues selected for *in vitro* cross-link formation by the combined action of TGase 1 and TGase 3 mirror the residues utilized for cross-link formation *in vivo* (Candi *et al*, 1995). These findings, and the observation that TGase 1, TGase 3, and TGase 5 are differentially distributed at the subcellular level, suggest that each TGase has distinct and complementary roles in envelope assembly.

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