

From the outside-in: Epidermal targeting as a paradigm for atopic disease therapy

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pathophysiology of AD includes cutaneous inflammation, disrupted epidermal barrier function, xerosis and propensity to secondary infections. AD had previously been thought to arise from the systemic atopic immune response and therapies are therefore directed towards ameliorating Th2-mediated inflammation. However in recent years the focus has shifted towards primary defects in the skin barrier as an initiating event in AD. Links between loss-of-function variants in the gene encoding filaggrin and disrupted activity of epidermal serine proteases and AD have been reported. Based on these observations, a mechanism has been described by which epidermal barrier dysfunction may lead to inflammation and allergic sensitization. Exogenous and endogenous stressors can further exacerbate inherited barrier abnormalities to promote disease activity. Pathways underlying progression of the atopic march remain unclear, but recent findings implicate thymic stromal lymphopoietin as a factor linking AD to subsequent airway inflammation in asthma. This new appreciation of the epidermis in the development of AD should lead to deployment of more specific strategies to restore barrier function in atopic patients and potentially halt the atopic march.

Key words: Atopic dermatitis; Eczema; Filaggrin; Skin barrier; Kallikrein; Thymic stromal lymphopoietin; Allergic sensitization; Atopic march

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Core tip: Atopic diseases [including atopic dermatitis (AD), allergic rhinitis and asthma] are characterised by Th2-type inflammation. Research over the past decade has highlighted a crucial role for primary skin barrier impairment in the pathogenesis of AD and associated atopic phenotypes. Notably, the epidermal protein, filaggrin, epidermal serine proteases, and the pro-Th2 cytokine thymic stromal lymphopoietin, have been implicated in disease development. We review the evidence upholding a role for epidermal defects in the

Abstract

Atopic dermatitis (AD) is a chronic inflammatory skin disorder which can precede asthma and allergic rhinitis in a disease trajectory known as the atopic march. The

initiation of skin inflammation in AD, allergic sensitization and pathogenesis of the “atopic march”, and discuss the clinical implications of these findings.

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INTRODUCTION

Atopic diseases are reaching epidemic proportions^[1-4], affecting up to 20%-30% of children in developed nations^[5-7]. Prominent among these disorders are atopic dermatitis (AD, synonymous with atopic eczema), atopic asthma and allergic rhinitis. Atopic diseases constitute a major source of physical and psychosocial distress^[8-10] and account for a large portion of general paediatric practice^[11]. Atopic diseases demonstrate complex inheritance patterns and extensive phenotypic variation, and as such their aetiology is poorly understood^[12]. However the disorders appear to be underpinned by some common features: they are often associated with elevated levels of total serum IgE and with “atopy” - a personal and/or familial tendency to become sensitized and produce specific IgE against environmental allergens^[13] - but this association is hotly debated^[14,15]. Atopic diseases are thus presumed to arise as a result of interplay between inherited disposition and environmental factors^[16,17].

Longitudinal studies have revealed that approximately half of patients with AD develop asthma later in life and two-thirds go on to exhibit allergic rhinitis^[18]. This phenomenon, dubbed the “atopic march” describes the tendency for AD (usually apparent within the first two years of life) to precede the development of food allergies, asthma and allergic rhinitis in a typical temporal sequence^[17,19,20]. As AD is now a recognised “gateway” to the atopic march, its diagnosis in infants often prompts parental enquiries about disease prognosis as regards the development of subsequent disorders^[17]. AD therefore represents an important focus for interventions which may modify the natural course of atopic disease in high-risk patients.

AD is a chronic, inflammatory skin disease affecting an estimated 10%-20% of children and 1%-3% of adults^[6]. The skin of AD patients shows widespread xerosis (dryness) and a disturbance of epidermal barrier function. AD lesions (Figure 1A and B) are additionally characterised by pruritus and a propensity to secondary infections (Figure 1C). Th2-deviated inflammation is widely accepted in the pathogenesis of atopic disease however inflammation in AD may be biphasic, with an initial Th2 response leading to a Th0/Th1 dominated phase in chronic lesions^[21]. Traditionally it has been presumed that epidermal barrier dysfunction in AD is

a downstream consequence of primary immunologic abnormality (the “inside-outside” hypothesis)^[22]. In recent years this view has been challenged, with new evidence shifting the focus towards an “outside-inside” model in which epidermal abnormality is not the result but rather the stimulus of inflammation^[23]. In light of this concept, this review will evaluate the evidence upholding a pivotal role for the epidermis in atopic disease pathogenesis, and consider the practical implications for therapy.

BARRIER DISRUPTION IN ATOPIC DERMATITIS

The skin forms an essential barrier between the interior of the body and the external environment. Multiple protective roles are fulfilled by the epidermis and many are mediated by its outermost layer (and end product of keratinocyte differentiation), the stratum corneum (SC; Figure 2)^[24,25].

The SC comprises layers of protein-rich anucleate corneocytes interconnected by corneodesmosomes and enclosed within a coat of cross-linked proteins and lipids which together form the cornified envelope (CE)^[26]. The CE replaces the plasma membrane during terminal differentiation of keratinocytes into corneocytes and is in turn surrounded by a matrix of intercellular lamellar sheets enriched by 50% ceramides, 25% cholesterol and 15% free fatty acids (FFAs)^[27]. This amalgam of highly hydrophobic lipids, together with the CE, provides selective permeability to the epidermis.

Intercellular lipids are secreted as precursors from a unique epidermal organelle, the lamellar body (LB), along with the hydrolytic enzymes required for precursor transformation^[24]. At the granular cell-to-corneocyte transition, LBs fuse with the plasma membrane and discharge their contents into the intercellular space by exocytosis. LB extrusion also delivers antimicrobial peptides (AMPs) and the proteases and inhibitors which together orchestrate corneodesmosome cleavage during desquamation. Beneath the SC, the stratum granulosum (SG) provides a second barrier to environmental stressors; keratinocytes in the outer SG layers are intimately connected by tight junctions (TJs) - multi-protein complexes which control paracellular transport.

AD is characterised by widespread skin barrier dysfunction in both lesional and non-lesional skin^[28], as indicated by increases in transepidermal water loss (TEWL)^[29-31] and percutaneous penetration^[32]. This enhanced permeability has been attributed to abnormalities in the composition and architecture of extracellular lipid bilayers, reductions in total lipid and ceramide content^[33] and average ceramide chain length^[34], as well as an altered ceramide profile^[33,35]. The resultant barrier defect renders the skin of AD patients more permissive to the ingress of irritants, allergens and pathogens.

Atopic skin is more susceptible to bacterial and viral infections^[10], reflecting defects in the antimicrobial

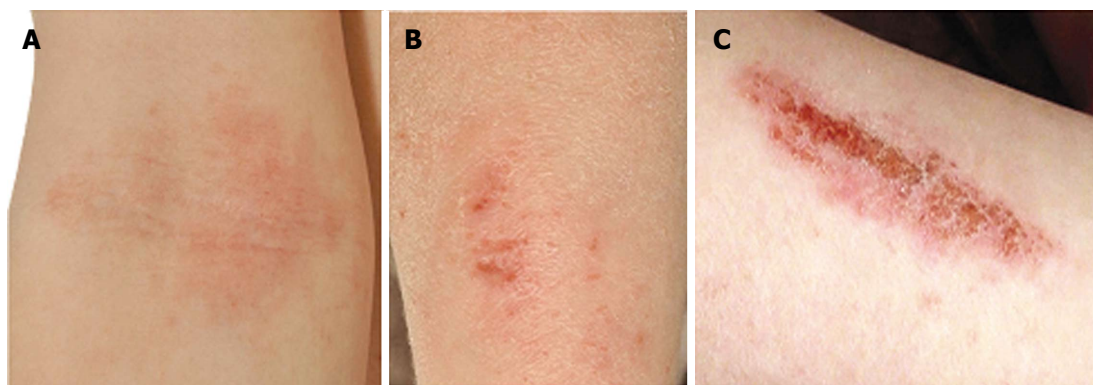


Figure 1 Clinical features of atopic dermatitis. A: Flexural eczema; B: Eczema and ichthyosis; C: Infected excoriation. Clinical photographs (University of Dundee Computing and Media Services, Ninewells Hospital and Medical School) reproduced with patient and/or parental consent.

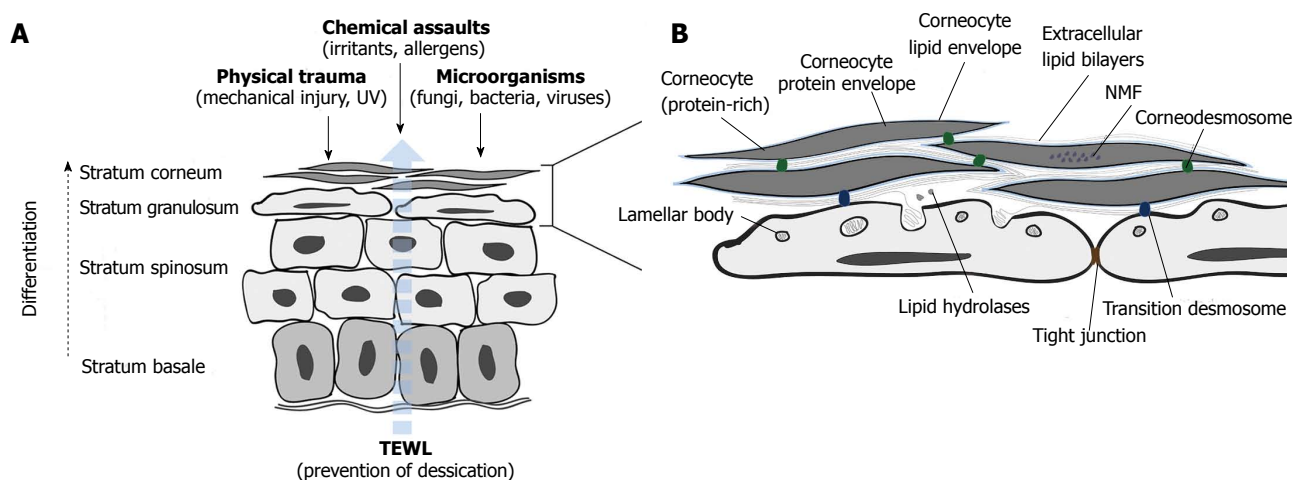


Figure 2 Outside-inside and inside-outside barrier functions of the epidermis. A: The epidermis forms a barrier against multiple external threats and prevents excessive transepidermal water loss (TEWL, indicated by the dashed blue arrow) from the interior of the body; B: Components of the stratum corneum (SC) and stratum granulosum (SG) barriers. During terminal differentiation of SG keratinocytes into corneocytes, lamellar bodies (LBs) fuse with the plasma membrane and their contents is extruded at the SG-SC interface. LB-derived lipids are processed and arranged into continuous bilayers parallel to the corneocyte surface using the covalently bound corneocyte lipid envelope (pale blue) as a scaffold. NMF: Natural moisturising factor.

barrier. 80%-100% of AD patients show colonisation by *Staphylococcus aureus* (*S. aureus*) compared with 5%-30% of non-atopic individuals^[36-38]. Flare-ups of AD are often associated with *S. aureus* infection, but whether infection represents a cause or consequence of inflammation remains unclear.

In healthy individuals, the desiccating surface, acidic pH and resident microflora of the skin cooperate with AMPs and lipids to provide protection against invading pathogens^[39]. In AD, a number of factors - including the defective epidermal barrier, attenuated innate immune response and increased bacterial adhesion - may promote skin colonisation by *S. aureus*^[40]. Among the human AMPs, levels of the cathelicidin, LL-37, and human beta-defensin-2 (hBD-2) are reduced in AD lesions^[41], and deficiency of sphingosine - a natural ceramide metabolite and potent anti-*S. aureus* agent - is also evident in the SC^[42]. Furthermore, *in vitro* studies have suggested that the Th2 inflammatory response in AD may feed back to the epidermis to promote bacterial colonisation^[41,43]. For

instance, IL-4, which is over-expressed in AD skin, has been reported to increase skin expression of fibronectin and fibrinogen - receptors which may facilitate attachment of *S. aureus* to the SC^[43].

Finally, it should be noted that several other protective functions of the skin barrier are impaired in AD. The skin of AD patients shows disrupted SC integrity (reflected by excess scale^[31]) and widespread xerosis, indicated by reduced SC water content^[30]. Additionally, pruritus - a prominent characteristic of AD^[44] - indirectly aggravates skin barrier impairment *via* the resultant scratching. The itch sensation is believed to result from cross-talk between the SC, keratinocytes, immune cells and nerve fibres^[45]. Excoriations directly disrupt the mechanical barrier of skin, creating additional portals of entry for pathogens. Moreover, it has been reported that a subset of AD patients develop serum IgE which is auto-reactive against a variety of keratinocyte proteins^[46]. Thus damage to the epidermis may itself intensify pruritus, driving the vicious "itch-scratch" cycle of AD^[45].

EPIDERMAL DIFFERENTIATION PROTEINS

Filaggrin-related barrier dysfunction

The outside-inside phenomenon of AD drew sharp attention from the research community when a significant link between loss-of-function variants in the gene encoding filaggrin (*FLG*) and AD was demonstrated in three European case collections^[47]. *FLG* mutations were originally identified as the cause of ichthyosis vulgaris (IV)^[48] and have since been demonstrated to be the strongest known risk factor for AD in European and Asian populations^[49-56]. Cases of AD associated with *FLG* mutations are more likely to be severe, persistent^[57-60], and complicated by secondary infections^[61,62] than non-*FLG*-related cases. Importantly, *FLG* mutations are now established as an independent risk factor at every step of the atopic march including allergic sensitization^[60,63-68], allergic rhinitis^[60,64,66-68], food allergies^[69,70] and the sub-phenotype of asthma associated with AD^[7,60,63,64,66-68].

Profilaggrin is a large precursor molecule (> 400 kDa) containing 10, 11 or 12 tandem repeats of the 37 kDa filaggrin peptide^[71]. Insoluble, heavily phosphorylated profilaggrin is the main constituent of keratohyalin granules in the SG. During terminal differentiation, profilaggrin is dephosphorylated and cleaved in a multistep process to release filaggrin monomers, which bind and aggregate keratin filaments, facilitating the collapse of the cytoskeleton and contributing to the flattening of keratinocytes to produce corneocytes^[72]. Filaggrin, along with several other cytosolic proteins, is cross-linked into the CE by transglutaminases. As corneocytes move outwards through the SC, filaggrin detaches from the CE and undergoes further degradation within the cytosol, ultimately generating a hygroscopic pool of amino acids and derivatives thereof [including pyrrolidone carboxylic acid (PCA) and trans-urocanic acid (UCA)], contributing to natural moisturising factor (NMF)^[73]. NMF appears to play a role in multiple aspects of epidermal homeostasis including SC hydration^[73,74], UV photo-protection^[75], immunosuppression^[76,77] and by acting as a natural acidifier, modulation of enzymatic activity^[78-80] and antimicrobial defence^[81].

Each of the reported null mutations in *FLG* has an equivalent biological effect, producing a truncated profilaggrin molecule^[82]. This precursor cannot be fully processed into filaggrin monomers thus individuals with two *FLG* null alleles (homozygous or compound heterozygous, *FLG*^{-/-}) exhibit an almost complete absence of functional filaggrin^[82]. Inherited filaggrin deficiency results in both intracellular and extracellular changes in keratinocyte architecture and altered epidermal physiology. Histological examination of skin from *FLG*-deficient AD and IV patients reveals increased SC thickness^[83] and a granular cell layer that is either strongly reduced or absent^[84]. At the ultrastructural level, reduction in filaggrin correlates with perinuclear retraction of granular cell keratin filaments, impaired corneocyte integrity and reduced corneodesmosome density, concomitant with reduced SC cohesion^[84]. The molecular mechanisms by which deficiency in filaggrin - an intracellular protein -

impairs the paracellular skin barrier in AD remains unclear. However it is plausible that the cytoskeletal abnormalities associated with filaggrin deficiency impede the granular cell-to-corneocyte transition and thus formation of the SC extracellular environment. Consistent with this hypothesis, impaired cargo loading into LBs, partially compromised LB secretion and disorganised lamellar bilayers are observed in the skin of AD and IV patients^[84,85]. Reduced expression of SG TJ proteins^[84] is also likely to further contribute to barrier impairment.

Alternatively or in addition, it may be the biochemical consequences of filaggrin deficiency that are important in AD pathogenesis. *FLG* null mutations effect a dose-dependent reduction in SC NMF levels^[86-89], which in turn correlate inversely with skin surface pH^[87,89] and TEWL^[89]. Additionally, *FLG* exhibits intragenic copy number variation, and a lower number of repeats correlates significantly with AD risk^[90], SC UCA levels^[90] and the presence of self-perceived “dry skin”^[91]. Thus enhanced TEWL in *FLG*-associated AD can be explained in part by reduced SC hydration; deficiency of hygroscopic NMF components would be expected to result in lower SC water content hence a steeper water gradient across the epidermis. In addition, altered skin pH is likely to perturb the natural balance of enzymatic activities in the SC. The elevated pH of AD patient skin would be predicted to favour the net activity of SC-resident serine proteases (SPs)^[78,80] whilst reducing that of key SC lipid biosynthesis enzymes. SP hyperactivity drives premature degradation of corneodesmosomes and lipid-processing enzymes^[80], likely contributing to defective lamellar bilayer formation. In line with the proposed mechanisms, it has been demonstrated that levels of filaggrin breakdown products correlate with aberrant SC lipid organisation and decreased barrier function in AD patients^[34,86,92]. A recent study using a reconstructed human epidermis model has suggested that filaggrin deficiency may also promote enhanced epidermal sensitivity to UVB^[93], but this connection remains to be demonstrated in patients.

Finally, filaggrin deficiency in AD has implications for the antimicrobial skin barrier. As described, the natural acidity of the SC in healthy individuals provides innate antimicrobial protection - a function which is likely to be diminished in NMF-deficient AD patients. Furthermore, recent data suggest that filaggrin may play a unique role in protection against *S. aureus* infection, by mediating keratinocyte secretion of sphingomyelinase - an enzyme which reduces the number of *S. aureus* α -toxin binding sites on the keratinocyte surface^[94]. These findings indicate a mechanism by which filaggrin-deficient skin may be preferentially targeted by *S. aureus*-induced cytotoxicity. Clinically, the consequences of *FLG* null mutations in AD manifest as a 7-fold increase in the risk of recurrent bacterial infections relative to wild-type *FLG* patients^[62].

Thus our understanding of the mechanisms by which *FLG* genotype translates to disease phenotype remains incomplete. Furthermore, recent findings indicate additional levels of complexity to the *FLG*-AD

relationship which are likely to influence the pathogenic mechanisms discussed above. For instance, preliminary data indicate that epigenetic, as well as genetic variation can influence disease outcome. Indeed, a recent study has shown that methylation of a specific CpG site adjacent to *FLG* can modify the influence of *FLG* null mutations on AD risk^[95]. Whether inherent variation in enzymes involved in profilaggrin biosynthesis and maturation can also affect atopic disease pathogenesis has yet to be ascertained. Future lines of investigation should clarify how individual variations in filaggrin biology at the DNA, RNA and protein levels interact to determine distinct atopic phenotypes.

Epidermal differentiation genes in addition to *FLG*

Whilst inherited variation in *FLG* undoubtedly contributes to skin barrier dysfunction in AD, *FLG* null variants are carried by less than one-third of European patients with AD^[66] and broad defects in epidermal differentiation are characteristic of the disease regardless of *FLG* genetic status^[96]. Taken together, these observations suggest that other factors must modify epidermal homeostasis. Genetic association studies have identified links between AD and gene variants distinct from *FLG* but also located on chromosome 1q21 within the Epidermal Differentiation Complex - a region comprising over sixty genes essential for epidermal structure and function^[97]. Of note, a single nucleotide polymorphism (SNP) 7 kb downstream of the gene encoding hornerin (*HRNR*) and an 8-amino acid insertion in the gene encoding small proline-rich protein 3 (*SPRR3*) have been identified as risk factors for AD^[98,99]. Additionally, a recent study by Margolis *et al.*^[100] using whole-exome sequencing and targeted analysis in an African American cohort has identified mutations in *FLG2* (encoding filaggrin-2) that show a significant association with persistent AD - the first established link between a skin barrier gene and AD in subjects of African descent. However, it should be noted that these risk variants lie within a block of linkage disequilibrium and it remains possible that they are tagging unidentified variants within *FLG*. Hornerin and filaggrin-2 are S100-fused type proteins, and thus share a structural organisation similar to filaggrin. Both proteins mirror the subcellular localisation of filaggrin in the differentiating epidermis are believed ultimately (along with *SPRR3*) to become incorporated into the CE^[97]. The precise contributions of these proteins to skin barrier function remain unknown, but available data indicate that filaggrin, hornerin and filaggrin-2 have overlapping or complementary functions in the epidermis^[97] and the expression of each may be down-regulated in AD skin^[96].

TJs comprise both cytoplasmic and transmembrane proteins, key among which are the claudins, representing the main determinants of barrier selectivity against macromolecules^[101]. Claudin-1 expression is down-regulated in non-lesional AD skin and inversely correlated with Th2 cytokines. Variants within the claudin-1 gene, *CLDN1*, have shown association with AD in two ethnically distinct North American populations^[102]. Interestingly, this

study also demonstrated links between *CLDN1* variants and AD severity, total serum IgE and asthma in subjects of African, but not European ancestry. Given that at present, *FLG* null mutations appear to be considerably less prevalent in African populations relative to European or Asian cohorts^[89], these findings (together with those of Margolis *et al.*^[100] regarding *FLG2*) indicate population specificity in the genetic mechanisms which dominate skin barrier dysfunction in AD.

Finally, protein regulators of lamellar bilayer formation have been implicated in the pathogenesis of AD. Mutations in the gene encoding fatty acid transporter 4 (*FATP4*)^[103] and *MATT* (encoding matrinin, a component of the LB secretory system in flaky tail (*maft*) mice^[104]) are associated with increased risk of AD^[105]. *Maft* mice harbour mutations in both *Flg* and *Matt* genes, and have been used for many years as an experimental model of AD. However, it has recently been shown that *ma/ma* mice, which carry mutations in *Matt* but not in *Flg*, exhibit enhanced TEWL and decreased SC hydration, and develop the spontaneous dermatitis and atopy exhibited by *maft* mice to a greater extent than the filaggrin-null (*Flg*^{-/-}) mice^[104-106]. *Matt* may therefore play a greater role than *Flg* in driving the dermatitis phenotype in *maft* mice, supporting a key role for SC lipid secretion in the development of AD.

Thus skin barrier genes may act alone or in combination with *FLG* to modify AD pathogenesis. Whether or not the same genes are also associated with subsequent steps of the atopic march remains to be elucidated.

Epidermal proteases and protease inhibitors

Maintenance of epidermal physiology is dependent on the coordinated activities of skin-resident proteases and anti-proteases. Perturbation of this balance in favour of protease hyperactivity can result in pathogenic barrier disruption, as exemplified in Netherton syndrome (NS). NS is an autosomal recessive disorder featuring ichthyosis and atopic manifestations, which is caused by loss-of-function mutations in *SPINK5*^[107] - the gene encoding lympho-epithelial Kazal-type-related inhibitor (LEKTI)^[108]. In healthy skin, proteolytic LEKTI fragments specifically co-localise with and regulate the activity of multiple SPs, including members of the kallikrein (KLK) family. KLKs are central to desquamation^[109] and also indirectly promote profilaggrin proteolysis^[110]. In the skin of NS patients, residual LEKTI expression correlates inversely with enhanced KLK activity^[111] resulting in dramatic SC thinning and attenuation of the permeability barrier through unrestricted degradation of corneodesmosomes^[109] and lipid-processing enzymes^[111] respectively. Permeability barrier function may additionally be compromised through activation of protease-activated receptor 2 (PAR-2), which is expressed in nucleated epidermal layers and can be induced by specific SPs to down-regulate LB secretion^[112-114].

A number of association studies have identified SNPs in *SPINK5* which are associated with AD risk in different ethnicities^[115-119]. In particular, one such variant, LEKTI E420K, has also been linked to elevated serum IgE^[118], food allergies^[116], AD severity^[116] and AD-

associated asthma^[120]. *In vitro* analysis has shown protease hyperactivity resulting from the E420K mutation to result in increased corneodesmosomal destabilisation and premature profilaggrin proteolysis^[121], suggesting a functional pathway by which E420K may contribute to filaggrin deficiency and the development of AD. In addition to *SPINK5* polymorphisms, a mutant allele of the *CSTA* gene (which encodes the skin-resident cysteine protease inhibitor, cystatin A) has been reported to associate with AD in a small UK cohort^[122]. Fewer data exist for associations between AD and epidermal protease genes; an association between AD and a putative gain-of-function insertion in the 3' UTR of *KLK7* has been described in a British case-control study^[122] but failed to be confirmed in subsequent investigations^[123,124].

BASIS FOR BARRIER-INITIATED INFLAMMATION

The above pathways together may account for the skin barrier phenotype in AD, but the mechanisms linking epidermal disruption and concomitant allergic inflammation remain unclear. The *maft* and more recently generated *Flg*^{-/-} mouse models^[106,125] serve as useful systems in which to study the aetiology of the immune response in the context of inherited barrier impairment. Although showing differences in disease phenotype, both mice exhibit increased percutaneous allergen penetration and a reduced inflammatory threshold to skin irritants and allergens^[106,126]. Based on these observations, it is widely postulated that inflammation in AD is a secondary reaction to increased entry of allergens and irritants through the compromised skin barrier. Whilst this is yet to be confirmed in human subjects, it is worth noting that AD patients with *FLG* null mutations have a significantly increased risk of allergic sensitization^[60] and irritant contact dermatitis^[127], and display elevated numbers of allergen-specific CD4⁺ T cells compared with wild-type *FLG* patients^[128]. Furthermore, it seems likely that in addition to the inflammatory response to penetrating antigens, barrier impairment itself may intrinsically promote downstream inflammation. For instance, elevated SP activity (induced in AD along the pathways described above) not only promotes epidermal barrier breakdown but leads to increased release of active IL-1 α and IL-1 β ^[129,130] from the corneocyte cytoplasm, thereby initiating inflammation. Furthermore, SP hyperactivity may stimulate inflammation indirectly by accelerating the degradation of transition desmosomes, leading to secretion of IL-1 β , IL-8 and TNF- α from mechanically stressed keratinocytes^[131]. Finally, accumulated data indicate that following activation by SPs, PAR-2^[131], together with pro-inflammatory cytokines, induces NF- κ B-mediated over-expression of the pro-Th2 cytokine, thymic stromal lymphopoietin (TSLP)^[132], and IL-6^[133]. Evidence in support of the latter pathway has been observed in studies of *maft* mice and *FLG* knock-down keratinocytes *in vitro*^[134], suggesting that this immunologic cascade may operate downstream of a primary filaggrin deficiency.

Whilst these data are compelling, the same pathogenic

mechanisms have yet to be demonstrated in human AD. Nonetheless, the strength and number of independent associations between *FLG* and atopic disorders greatly surpass those of any other gene expressed in the skin to date^[123]. As such, filaggrin deficiency is widely regarded as a primary abnormality leading to skin inflammation in AD^[135-138]. Leading on from this, a putative pathogenic pathway has been described in which the reduction in filaggrin acts as a central stimulus for increased SP activity, which in turn triggers the inflammatory response^[139]. AD patients with *FLG* null mutations exhibit increased skin levels of IL-1 cytokines, in a manner inversely correlating with NMF levels^[87]. This observation has been attributed to pH-induced stimulation of SPs, which can promote inflammation by the mechanisms described above^[139]. However, no correlation between SC pH and levels of either IL-1 α or IL-1 β could be demonstrated in the same study, and recent findings have indicated that *FLG* status is not an essential determinant of SC pH^[79,93,106]. Thus whilst these data do not rule out a role for skin pH changes in initiation of inflammation in *FLG*-related AD, it is likely that protease activity and consequently IL-1 levels are modulated by additional factors. For instance, Kezic *et al*^[87] have proposed that increased SC calcium concentration (resulting from reduced SC hydration) may favour the activation of calcium-dependent SPs, but based on our current knowledge, this pathophysiological pathway remains entirely speculative.

INSIDE-OUTSIDE PATHOGENIC MECHANISMS

Despite the undisputed involvement of *FLG* null variants in the atopic march, it is important to note that filaggrin deficiency is observed in AD patients even in the absence of known *FLG* mutations^[96]. Whilst this may be explained in part by other forms of genetic regulation, it is apparent that a number of additional factors can reduce expression of functional filaggrin, resulting in barrier disruption. In particular, accumulating evidence points to components of the acquired immune response as key players in endogenous barrier impairment, prompting the proposition of a self-sustaining “outside-inside-outside” pathogenic loop in AD^[139].

Studies in *maft* mice have shown that following initial sensitization, further defects in barrier function occur, suggesting exacerbation of the primary barrier impairment by the induced inflammatory response^[126]. Consistent with this, the Th2 cytokines, IL-4, IL-13, IL-22 and IL-25, which are over-expressed in AD lesions, have been shown to inhibit expression of filaggrin^[136-138] and profilaggrin-processing enzymes^[140,141] *in vitro*. Inflammation in AD may also compromise skin barrier function by a number of filaggrin-independent mechanisms. The epidermal AMPs, LL-37, hBD-2 and hBD-3, are down-regulated in a Th2-dependent manner^[141,142-144] and roles for Th2 cytokines in disruption of SC lipid synthesis^[145-147], SC protease activity^[148,149] and multiple processes in epidermal

differentiation^[147,149-151] have been reported. Finally, whilst not endogenously perturbing the skin barrier *per se*, the cytokines TSLP and IL-31 induce itch^[152,153], thereby aggravating the itch-scratch cycle.

ENVIRONMENTAL STRESSORS PLAY UPON BARRIER DEFECTS TO EXACERBATE DISEASE ACTIVITY

The avoidance of exogenous irritants is an important part of atopic disease management. Diverse environmental factors are known to exacerbate atopic disorders, but several are now recognised as having detrimental effects on the skin barrier. For instance, prolonged exposure to reduced ambient humidity (as may occur in centrally heated homes) has been shown to accelerate TEWL and promote profilaggrin proteolysis^[73], potentially driving further depletion of cutaneous filaggrin^[139]. External modifiers of skin surface pH may also aggravate disease activity *via* enzyme-mediated pathways; use of neutral-to-alkaline soaps is known to induce SC thinning and precipitate flares of AD^[154]. Protease activity in the epidermis of AD patients may be further intensified by airborne proteins; proteolytic allergens produced by house dust mites and cockroaches have been shown to penetrate the skin and can exacerbate barrier dysfunction^[155,156] both directly, by degrading barrier components^[157,158] and indirectly, through activation of PAR-2^[159-161]. Staphylococcal infection also has a number of implications for skin barrier function. Essential *S. aureus* surface proteins confer resistance to the bactericidal action of human epidermal FFAs and AMPs^[162] and once established on the skin, coagulase-negative staphylococci can secrete peptidases and lipid hydrolases^[163] which may further erode the skin barrier. Indeed it has been shown that elevated levels of the enzyme ceramidase (which catalyses the degradation of ceramide to sphingosine and FFAs) are secreted by the bacterial flora of AD patient skin relative to healthy controls^[164]. Finally, psychological stress (PS) may precipitate atopic diseases^[165] by disturbing the permeability barrier^[166,167], SC integrity^[166] and antimicrobial defences^[168] in the skin of mouse models, *via* a mechanism thought to be mediated by increased production of endogenous glucocorticoids^[167-169].

ALLERGIC SENSITIZATION AND TSLP: THE ATOPIC MARCH

The mechanistic link between AD and subsequent phenotypes in the atopic march remains unclear and has been the subject of intensive research in recent years. Generally, current data favour a model in which the downstream systemic effects of allergen penetration through the impaired skin barrier cause immune cells to mount an exaggerated inflammatory response at any allergen-exposed epithelial surface^[136,154,170]. This theory fits with several observations: (1) AD is usually the first manifestation of atopy^[18]; (2) *FLG* is not expressed in

bronchial airways^[171] nor the oesophageal epithelium beyond the oro-pharyngeal mucosa^[172], suggesting that filaggrin does not directly influence permeability of these epithelia; and (3) allergic sensitization induced by epicutaneous exposure to peanut allergen inhibits subsequent oral tolerance in mice^[173].

Central to the uncertainty over the atopic march is the strength of the connection between early allergic sensitization in AD and the risk of allergic airway disease, with the epidemiological data being somewhat inconsistent^[14]. Functional studies on the atopic march have identified a prominent role for the cytokine TSLP as a promoter of the Th2 response in AD and a trigger linking epicutaneous sensitization to subsequent asthma^[174,175]. TSLP is expressed primarily in lung and skin epithelia^[176] where it is recognised as a “master switch” from epithelial barrier disruption to Th2 inflammation^[177,178]. Accordingly, TSLP expression is up-regulated in the SC of AD patients compared with healthy subjects^[179]. Notably, a recent study using mice in which TSLP is selectively and inducibly ablated in epidermal keratinocytes suggests that skin-derived TSLP is essential for skin allergic inflammation and epicutaneous sensitization, which in turn leads to allergic asthma^[180]. This study, in contrast to previous findings^[181,182], indicated that keratinocyte-derived TSLP acts as an essential “adjuvant” to the Th2 response induced by topical allergen treatment, but that skin expression of TSLP caused by barrier disruption alone (*i.e.*, without allergen) is not sufficient to promote the full inflammatory phenotype. It is also noteworthy that in this model sensitization was achieved through barrier-defective skin (as opposed to intraperitoneal or intradermal injection of allergen^[181,183]), followed by airway challenge, conditions representative of those in human AD. Airway inflammation appears to require an antigen-specific memory CD4⁺ T cell response^[180,183], but occurs independently of TSLP presence in the lung^[175,180,183] and circulating TSLP^[183], suggesting that skin-derived TSLP is both necessary and sufficient for manifestation of asthma symptoms.

The relative importance of TSLP in the human atopic march remains to be clarified. A recent study in an American paediatric AD cohort identified the *TSLP* variant rs1898671 (which produces attenuated TSLP) as protective against the development of persistent AD^[184] however no association with comorbid asthma was identified^[184]. It has further been demonstrated that risk of childhood asthma is influenced by epistasis between *SPINK5* and *TSLP*^[185]. The authors postulate that *TSLP* and *SPINK5* function in a common pathway in which LEKTI deficiency ultimately leads to TSLP production, an exaggerated Th2 response and allergic lung inflammation^[185]. Although the analysed cohort comprised both asthmatic patients with and without concomitant AD, these findings support the view that the systemic consequences of an epidermal pathway are sufficient to induce inflammation at remote epithelia in the human atopic march (Figure 3). Thus it will be interesting to see if evidence for a similar pathway in patients with AD-associated asthma emerges in the

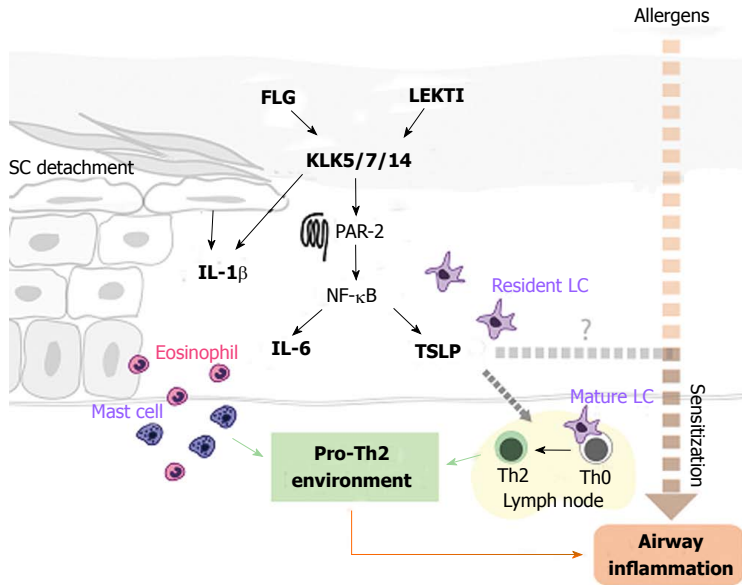


Figure 3 Hypothesised pathways from skin barrier impairment to inflammation and the atopic march. Deficiencies in FLG and LEKTI promote enhanced activity of KLKs, which induce over-expression of TSLP and IL-6 through the PAR-2-NF-κB pathway. KLK hyperactivity also degrades transition desmosomes, inducing the release of pro-inflammatory cytokines from mechanically stressed keratinocytes. The pro-inflammatory environment triggers eosinophil and mast cell recruitment and activation. TSLP activates LCs which promote the differentiation of naïve (Th0) T cells into Th2 cells in lymph nodes. Allergen ingress (dashed red arrow) promotes allergic sensitization and may, with TSLP, stimulate downstream airway inflammation. FLG: Filaggrin; LEKTI: Lympho-epithelial Kazal-type-related inhibitor; KLKs: Kallikrein proteases; TSLP: Thymic stromal lymphopoietin; IL-6: Interleukin-6; IL-1β: Interleukin-1β; LCs: Langerhans cells; SC: Stratum corneum; PAR-2: Protease-activated receptor-2; NF-κB: Nuclear factor kappa-light-chain-enhancer of activated B cells.

coming years. Together, the above findings reinforce the attractive idea that early and aggressive intervention directed towards the skin barrier may impede the progression from AD to subsequent airway inflammation in atopic patients.

CLINICAL IMPLICATIONS: A PARADIGM FOR THERAPY?

The pathogenic mechanisms described above create a strong case for prioritising protection and restoration of the skin barrier in atopic individuals. The current foundations of general AD management include the avoidance of triggering factors and optimal skin care^[165], with efforts to address epidermal barrier defects centred on the regular use of emollients. Emollients help to hydrate the skin and soothe pruritus^[186]; when applied liberally, they can provide a short-term artificial barrier to reduce TEWL and protect against the penetration of allergens and irritants. The benefits of emollient therapy in controlling the cutaneous symptoms of AD are accepted on the basis of clinical experience^[186]. A recent feasibility study of early emollient therapy for AD prevention has shown promising preliminary results^[187], but further trials are warranted before the efficacy of this approach can be confirmed. Thus far, emollient monotherapy has rarely proved sufficient for disease resolution in moderate-to-severe AD, in which the use of anti-inflammatory agents is often necessary for exacerbation management^[165].

However, corticosteroids and topical calcineurin inhibitors are associated with a spectrum of cutaneous and systemic side effects^[165,188] including the impairment of both permeability and antimicrobial barrier functions in AD skin^[189-191]. Interestingly, selected emollients have also been reported to disrupt the skin barrier. The majority of over-the-counter (OTC) moisturisers contain non-physiological ingredients (*e.g.*, petrolatum and lanolin) which function by undefined biological mechanisms and in certain cases have been found to compromise SC

integrity, permeability barrier function^[192] and epidermal differentiation^[193]. The above findings, together with recent advances in our understanding of skin pathophysiology, have shifted interest towards novel “barrier replacement strategies”. Such therapies aim to correct underlying biochemical abnormalities; they are based upon physiological components and may therefore minimise the likelihood of an unfavourable response^[194]. For instance, prescription barrier repair creams (BRCs) are based on SC lipids and differ from their non-physiological counterparts in that they are taken up by keratinocytes, packaged into LBs and ultimately secreted to form lamellar bilayers^[195]. In accordance with the lipid deficits in AD skin, a number of “designer” ceramide-dominant and triple-lipid-based barrier repair formulations have now been tested in AD patients^[196]. Trials of one ceramide-dominant BRC demonstrated significant reductions in disease severity^[197,198] and marked restoration of the epidermal barrier when used as adjunct to topical anti-inflammatories^[197]. Moreover, improvements in severity, pruritus and sleep were comparable to the effects of the TCS fluticasone^[198], suggesting that BRCs hold potential steroid-sparing effects. However small study size, variation in study design, commercial pressures and the possibility of publication bias make such data difficult to interpret. Furthermore, it is worth noting that the direct comparison of OTC emollients with BRCs has demonstrated equal efficacy for the treatment of mild-to-moderate AD^[199], with a notably significant cost disparity between the two treatments. Thus the prescription of BRCs over cheaper and simpler OTC alternatives remains contentious. Large-scale randomized control trials will be necessary to determine whether BRCs are indeed superior for long-term management of AD.

The identification of filaggrin deficiency as a strong predisposing factor for atopic disorders has opened the prospect of filaggrin or NMF restoration as another barrier repair strategy. Topically applied recombinant filaggrin peptide has been shown to penetrate to the SG of reconstructed human epidermis, and is internalised and

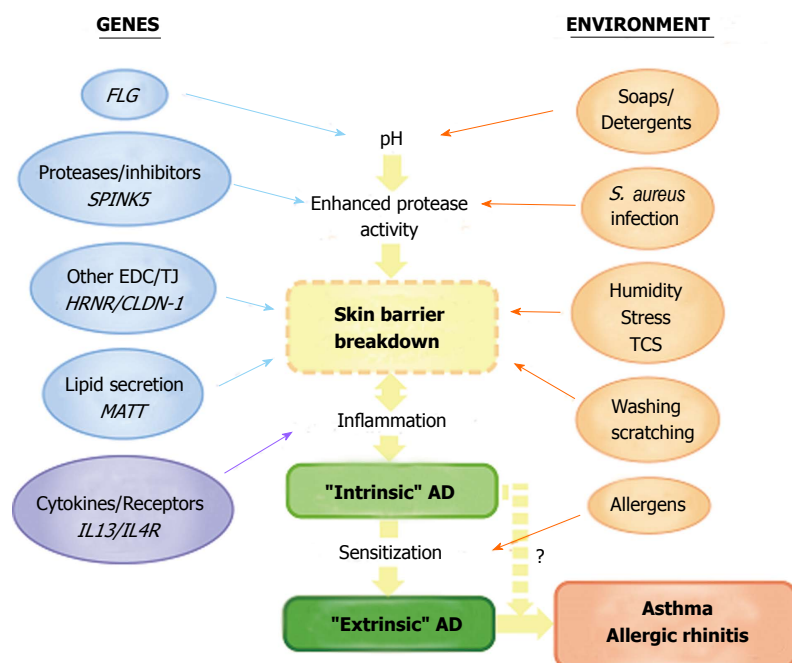


Figure 4 The combination of genetic and environmental factors in the natural history of atopic disease. Note that some allergens (e.g., house dust mite allergens) can also contribute to total protease activity in the skin. Stress: Psychological stress; TCS: topical corticosteroids; *S. aureus*: *Staphylococcus aureus*.

processed to restore epidermal structure in *maft* mice^[200]. Furthermore, a recent study has identified a candidate drug that promotes filaggrin mRNA and protein expression *in vitro*, and suppresses the development of skin inflammation when administered orally in the NC/Nga mouse model of AD^[201]. These findings, whilst preliminary, hold promise for filaggrin restoration as part of future AD therapy. Clarification of the relative importance of the functions of profilaggrin, filaggrin and filaggrin degradation products will be useful in directing research in this area^[202].

Thus the new appreciation of skin barrier pathophysiology should encourage greater clinical emphasis on the optimization of skin care and avoidance of barrier-breaching products in neonates and children. Yet a number of important questions remain. For instance, can restoration of the permeability barrier alone help to normalise epidermal gene expression? Will barrier-based interventions also protect against inflammation and the development of comorbid atopic disorders in patients with AD? Long-term follow-up studies with examination of treatment efficacy at the molecular level will be required. Finally, additional potential treatment avenues (e.g., selective inhibition of SPs and TSLP) have yet to be explored and it is expected that further elucidation of the mechanisms of skin barrier dysfunction in the coming years will identify practicable therapeutic targets.

CONCLUSION

The discovery of loss-of-function mutations in *FLG* has led to a new appreciation of skin barrier dysfunction as primary pathogenic mechanism in atopic disease. Undoubtedly one of the greatest challenges for future research is the dissection of the complex interactions between multiple genetic, environmental and immunologic factors which influence disease pathogenesis (Figure 4). Some interactions with *FLG* have already been identified.

Of note, the combined occurrence of mutations in *FLG*, an epidermal gene, and in the genes encoding IL-10 and IL-13, mediators of acquired immunity, have been shown to have a multiplicative effect on AD risk^[203] and inter-regulation by SC and SG skin barriers at the mRNA and protein levels has been reported^[101,204]. These interactions, whilst yet to be demonstrated in human patients, may present further difficulties in determining the relative importance of individual barrier components in AD pathogenesis. Progress in the molecular genetics of atopic disease has been accelerated by advances in next-generation sequencing techniques, but the additional complexity of multiple gene-gene and gene-environment interactions requires further development of bioinformatics analysis. The integration of genetic, transcriptomic and proteomic analyses is also computationally demanding. However, a recent transcriptomic analysis of AD skin used *FLG* genotype to stratify data and has offered insight into novel pathways and predicted functional networks^[205]. The expanding understanding of epigenetic variation is also predicted to contribute further novel mechanistic insights in the coming years.

Understanding the interplay between atopic genes and environmental factors will be vital to explaining (and perhaps controlling) the rising prevalence of atopic diseases. This will require long-term epidemiological studies in which early genetic profiling of *FLG* and other disease genes is coupled with careful monitoring of patient environment. Such studies may help to explain how specific gene variants act in the context of different external insults to induce a range of related yet distinct atopic phenotypes. Evaluation of *FLG* genetic status is not commonplace in pharmacogenetic studies or current clinical management of AD. However careful clinical examination can identify *FLG* null genotype^[206] and as the multiple influences of filaggrin on atopic disease trajectory are clarified, this will benefit clinical care and

prognostic predictions. More detailed knowledge of genotypes associated with atopic phenotypes could in the future help to direct the prescription of personalised therapeutic regimes, including focused instructions for disease prevention and targeted treatment. Thus early control of skin barrier function in high-risk patients may in future prevent allergic sensitization and what had previously been considered the inevitable path through the atopic march.

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