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IL-17 family cytokines: signaling mechanisms, biological activities and therapeutic implications

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Abstract

The cytokines of the IL-17 family play a central role in the control of infections, especially extracellular fungi. Conversely, if unrestrained, these inflammatory cytokines contribute to the pathology in numerous autoimmune and chronic inflammatory conditions. Recent advances have led to the approval of IL-17A-blocking biologics for the treatment of moderate to severe plaque psoriasis, but much remains to be understood about the biological functions, regulation and signaling pathways downstream of these factors. In this review, we outline the current knowledge on signal transduction and known physiological activities of IL-17 family cytokines. We will highlight in particular the current understanding of these cytokines in the context of skin manifestations of disease.

1. INTRODUCTION TO IL-17 LIGANDS AND RECEPTORS

IL-17A, the founding and most studied member of the IL-17 family, was cloned in 1993 and initially named CTLA-8. Its sequence and predicted structure were markedly different from other known cytokines, but interestingly was homologous to an open reading frame (ORF) in the T cell tropic *Herpesvirus saimiri* virus [1]. A decade later IL-17A took central stage with the discovery of Th17 cells as a T helper (Th) subset distinct from Th1 and Th2 cells [2, 3]. Five additional family members have been described, designated IL-17B, C, D, E, and F. Of these, IL-17F shares the greatest degree of conservation to IL-17A (55%) and is commonly produced by the same cell types. IL-17F was the first member of this family for which a crystallographic structure was elucidated. Interestingly, structural analysis revealed the formation of a cysteine-knot fold, similar to that adopted by neurotrophins such as NGF [4]. IL-17E, also known as IL-25, displays the lowest degree of sequence conservation (16%) [5]. In turn, other family members derive from different cellular sources and are associated with varying functions. IL-17A, IL-17F, IL-17C and IL-17E function in host defense against pathogens and play various but not fully understood roles in mediating inflammation in autoimmune, allergic and chronic inflammatory conditions. Given the central role of IL-17A in autoimmunity, much effort has focused on the development of

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neutralizing antibodies for therapeutic use. Indeed, IL-17A-blocking antibodies secukinumab and ixekizumab recently received FDA-approval for the treatment of psoriasis, ankylosing spondylitis (AS) and psoriatic arthritis (PsA) [6, 7]. Nonetheless, many aspects of IL-17A function, and especially of other cytokines in this family, remain poorly defined.

All known IL-17 family cytokines signal via a receptor family that is distinct from other known cytokine receptors [8]. The IL-17R family contains five members, IL-17RA-E, all of which are single-pass transmembrane receptors with conserved structural features [9]. Specifically, all family members encode two extracellular fibronectin II-like domains and an intracellular “SEFIR” domain; the name alludes to the presence of this domain in SEF/IL-17RD and other IL-17 Receptor proteins. The SEFIR is structurally related to the TIR domain found in the TLR/IL-1R family and is crucial for triggering downstream signaling events (see also section 3, “**IL-17 CYTOKINE SIGNALING AND REGULATION**”) [10]. The prevailing paradigm for most IL-17 cytokines is that signaling occurs through heterodimeric receptors composed of a common IL-17RA chain and a second chain that determines ligand or signaling specificity. The second receptor chains are as follows: IL-17RC for IL-17A and IL-17F [11], IL-17RB for IL-17E [12], and IL-17RE for IL-17C [13] (Figure 1). IL-17B is also reported to bind IL-17RB, albeit less strongly than IL-17E [14]. In addition, the requirement for IL-17RA in IL-17B signaling is still under debate, and the receptor for IL-17D remains undefined. Here, we review the current understanding of cellular sources of the IL-17 family of cytokines, signal transduction mechanisms that govern their function, and the cutaneous biological processes in which these cytokines participate.

2. CELLULAR SOURCES OF IL-17 FAMILY CYTOKINES

IL-17A and IL-17F

More than 30 years ago, the paradigm of T helper (Th) differentiation postulated that two discrete Th populations, Th1 and Th2 cells, acquired the ability to produce canonical thereby “tuned” to contain biologically dissimilar pathogens [15]. Although a useful model, there were numerous discrepancies that called this view into question [16]. Indeed, in 2005 a third Th cell subset was described that producing IL-17A, IL-17F, as well as IL-21, IL-22 and GM-CSF [3, 17–19], and hence came to be known as ‘Th17’. Like other Th subsets, naïve CD4⁺ T cells become committed to the Th17 lineage via cytokine cues received during antigen presentation in secondary lymphoid organs. For Th17 cells, this is a combination of IL-1b, IL-6, TGF-b and IL-21 for initial commitment [20–23], and IL-23 for full acquisition of their pathogenic capacity [24–26]. Like Th1 and Th2 cells, Th17 cells express a lineage-determining ‘master’ transcription factor, Rorgt, which directs the production of their hallmark cytokines [27].

More recently, it has become clear that additional populations of cells are also important sources of IL-17A and IL-17F. . These include CD8⁺ Tc cells [28, 29] and innate tissue-resident cells that are rapidly activated upon injury or pathogenic insult. Among these subsets are gd T cells (including Vg4⁺ and Vg6⁺ cells [30]) innate lymphoid cells (ILCs, specifically the ILC3 subset) [31], “natural” Th17 cells [32] and NKT cells [33]. These cells share a common dependence on IL-23 and on the transcription factor Rorgt for IL-17

production, and express the chemokine receptor CCR6 [30]. In addition, given their positioning at barrier sites and their fast responsiveness, these innate-like cells constitute important early sources of IL-17 during infection and tissue damage. Recent reports have also proposed the expression of IL-17A by myeloid cells, including macrophages, neutrophils and mast cells [30, 34, 35]. However, these findings remain controversial, especially given the low levels of IL-17 detected in these cells and their propensity for phagocytosis. Indeed, a recent article demonstrated that mast cells can take up IL-17A from the extracellular environment via receptor-mediated endocytosis and subsequently release it to promote inflammation [36]. Similarly, neutrophils and mast cells have been shown to release IL-17 via extracellular traps [37].

IL-17E (IL-25)

IL-17E, also known as IL-25, was discovered through a bioinformatics search for proteins homologous to IL-17A [38]. At the protein level, IL-17E bears 16–20% sequence similarity to IL-17A, B and C. IL-17E derives from both hematopoietic and non-hematopoietic cells [38]. In mice, IL-17E is expressed by innate immune cells such as mast cells and alveolar macrophages in response to allergic stimuli [39]. This also seems to be true in humans, as blood eosinophils and basophils from normal and allergic subjects expressed IL-17E mRNA, which was further boosted upon IL-5 treatment [40]. In addition, tissue stromal cells can express IL-17E. Human lung epithelial cells and murine primary type II alveolar epithelial cells express IL-17E following challenge with *Aspergillus oryzae*, ragweed allergens, and allergen proteases [41, 42]. Concordantly, IL-17E was detected at higher levels via immunohistochemistry (IHC) in the bronchial mucosa of asthmatics [43]. The triggers for IL-17E production in many of these cells remains an active area of investigation.

IL-17E is a pleiotropic cytokine, acting on stromal, innate immune and adaptive immune cells to orchestrate Th2-type inflammation. Consistent with the association of dysregulated Th2 responses with the development of allergy, IL-17E production is linked to the severity of chronic allergic conditions [44]. Thus, IL-17E-induced inflammation can be distinguished from IL-17A- and IL-17F-induced inflammation through the nature of the immune infiltrate, which mostly consists of eosinophils for the former and neutrophils for the latter [39]. However, IL-17E expression can be advantageous in some situations, as IL-17E can inhibit Th17 development through the induction of IL-13 by DCs and by inhibiting macrophage-derived IL-23 production [45]. In addition, IL-17E delivery ameliorates autoimmune diabetes [46, 47]. IL-17E therefore seems to be an atypical IL-17 family member, both in terms of low sequence homology and different biological actions.

IL-17C

IL-17C was also identified during the search for IL-17A-related cytokines [48]. IL-17C is mainly expressed by epithelial cells following stimulation with TLR2 and TLR5 ligands or with the proinflammatory cytokines IL-1 β and TNF- α [13]. Its expression has also been reported to be induced in CD4⁺ T cells, dendritic cells and macrophages in inflamed tissues [48, 49]. IL-17C has been suggested to act via a heterodimeric receptor composed of IL-17RA and IL-17RE, mediating a seemingly overlapping function to that of IL-17A and IL-17F [13]. Indeed, intranasal delivery of IL-17C-expressing adenovirus triggers

neutrophilia and drives the expression of set of proinflammatory molecules that overlaps considerably with IL-17A-dependent target genes [50]. Its role in mediating inflammation in several inflammatory and infection settings is just beginning to be unraveled.

IL-17B and IL-17D

IL-17B and D were also found through a search for IL-17A homologs [48, 51]. IL-17B is expressed at the transcriptional level in many cell types, including chondrocytes, neurons, intestinal epithelial cells and breast cancer cells. Like IL-17E, IL-17B can bind to IL-17RB, albeit with a lower affinity [52]. However, its function in the context of these cells is still enigmatic. IL-17D mRNA is detected in various tissues, including brain, heart, lung, pancreas, skeletal muscle and adipose tissue [51]. In the immune system, expression seems to be restricted to naïve CD4⁺ T cells and B cells. IL-17D most closely resembles IL-17B, with which it shares 27% homology. Its C-terminal motif is absent in other IL-17 family members [51]. To date, its receptor remains unknown.

3. IL-17 CYTOKINE SIGNALING AND REGULATION

Most IL-17 family members characterized to date mediate signaling through heterodimeric receptors composed of IL-17RA and a subunit that confers ligand or signaling specificity. IL-17RA is widely expressed among cells of both hematopoietic and non-hematopoietic compartments [8, 53]. Other IL-17R family receptors generally exhibit expression more restricted to specific cell types, which helps explain the target cell specificity of different ligands. This situation is analogous to signaling by IL-6 or β c family cytokines, which use the common gp130 subunit or the common β subunit for signaling [54, 55]. The existence of conserved mechanisms of receptor binding in the IL-17 family is reinforced by crystallographic analyses of IL-17RA in complex with IL-17A and IL-17F. These analyses revealed the acquisition of a similar conformation by the receptor upon cytokine binding, and the requirement for the same amino acid residues for receptor-ligand interactions [56]. Stoichiometry of the receptor complex seems to be dimeric. The lack of further receptor chains may be explained by the induction of conformational changes in the receptors upon cytokine binding, which disfavor binding to a second homotypic receptor chain [56].

Signaling pathways downstream of IL-17 cytokine family members are beginning to be unraveled, with IL-17A-targeted signaling mechanisms having been most thoroughly studied. In this section, we will focus on current knowledge regarding the molecular actions downstream of IL-17A, and point out commonalities, divergences and gaps in our understanding of IL-17 family cytokines.

IL-17A, IL-17F and IL-17A/F

IL-17A and IL-17F signal through the IL-17RA/RC heterodimer, evidenced by a complete loss of responsiveness in *Il17ra*^{-/-} and *Il17rc*^{-/-} mice or cell lines derived from them [57]. Importantly, this receptor can bind to three different covalent cytokine dimers: IL-17A homodimers, IL-17F homodimers or IL-17A/F heterodimers, albeit with varying affinities [58]. IL-17RA has a 100-fold weaker affinity for IL-17F and an intermediate affinity for the IL-17A/F heterodimer and bears weaker affinity for IL-17B, C, D and E. Conversely,

IL-17RC has a higher affinity for IL-17F than for IL-17A [59]. Overall, IL-17A signaling induces stronger responses than IL-17F (10–30 times more potent, as assessed by downstream gene induction), which may explain its dominant role in driving autoimmunity [60]. Receptor expression patterns also differ between the two chains, with IL-17RA being expressed more highly in the immune compartment, and IL-17RC expression being largely restricted to non-immune cells [53, 59]. Whether varying expression patterns, coupled with the different affinity of each receptor chain for IL-17A or IL-17F underlies their diverging biological functions remains an open question.

Detailed sequence analysis of IL-17R family members revealed the presence of a conserved intracellular subdomain with homology to Toll-IL-1R (TIR) domains, which are essential for signaling downstream of the IL-1 receptor and TLRs. These motifs share sequence homology with boxes 1 and 2 of the TIR domain, but lack box 3. Interestingly, this motif was discovered in SEF proteins (an IL-17RD orthologue called “similar expression to fibroblast growth factor”) from zebrafish and chicken and hence became known as the SEF/IL-17R domain (SEFIR) [10]. Upon cytokine ligation, the IL-17 receptor complex is thought to undergo a conformational change enabling the establishment of homotypic interactions between the SEFIR domains of the receptor and the signaling adaptor Act1 [61]. Act1, also known as CIKS (connection to I κ B kinase and stress-activated protein kinases), is an adapter required for all known downstream IL-17A signaling pathways. The canonical pathway relies on the E3 ligase activity of Act1, which mediates Lys63-linked ubiquitylation of TRAF6 [62]. This event leads to activation of the canonical NF- κ B and MAPK pathways, which include ERK, p38 and JNK, as well as the CCAAT-enhancer-binding proteins (C/EBP) pathway [8, 63]. Together, these transcription factors drive transcriptional activation of IL-17A target genes, which play key roles in inflammation.

In contrast, a second, non-canonical pathway is elicited by IL-17A, which leads to the stabilization of mRNA transcripts, particularly those encoding for intrinsically unstable targets such as cytokines and chemokines. This mRNA stabilization pathway is dependent on I κ B kinase (IKKi) and TBK1-mediated phosphorylation of Act1 at residue 311 [64, 65]. TRAF2 and TRAF5 are thereby recruited to the receptor complex, which results in the recruitment of molecules that control mRNA turnover [66]. In particular, TRAF2 and TRAF5 can sequester the RNA destabilizing factor ASF/SF2 and recruit the mRNA stabilizing factor HuR, thereby enhancing the half-life of various mRNAs [66, 67]. In addition, Act1 is reported to interact with Hsp90 to activate IL-17 activity [68]. A psoriasis-associated genetic variant in Act1 carrying the D10N mutation abrogates this interaction [69–71]. Together, IL-17-mediated events at both the transcriptional and post-transcriptional levels enhance production of genes that underlie its functions, including cytokines and chemokines, antimicrobial peptides (AMPs), acute phase proteins and other inflammatory effectors [72]. IL-17RA/RC signaling is summarized in Figure 2.

IL-17E (IL-25)

IL-17E signals through a heterodimer of IL-17RA and IL-17RB [12], as summarized in Figure 3. Unlike the relatively stromal-restricted activity of IL-17A and IL-17F, IL-17E acts mainly on immune cells, including Th2, Th9 and NKT cells. IL-17E induces the production

of classical Type-2 cytokines, such as IL-4, IL-5, IL-9 and IL-13, in a GATA-3, c-MAF, and JunB-dependent fashion [40]. IL-17RB is also expressed on monocytes, certain populations of type 2 innate lymphocytes such as nuocytes, non-T/non-B cells, multipotent progenitor type 2 cells and innate type 2 helper cells [73–76]. In addition, stromal cells such as intestinal and pulmonary epithelial cells also respond to IL-17E. Similar to IL-17A/F signaling, IL-17RB interacts with Act1 via homotypic SEFIR interactions [77, 78]. Act1 recruits TRAF6, enabling NF- κ B activation [79]. However, the pathways diverge, in that IL-17RB can recruit TRAF4 via Act1, leading to the further recruitment of the E3 ligase SMURF2 [80]. This leads to the ubiquitylation and subsequent degradation of the IL-17RB inhibitor DAZAP2, consequently reinforcing IL-17E-mediated signaling [80]. Further, IL-17E is reported to activate STAT5 in an Act1-independent manner, which further potentiates a Th2 response [81]. The precise stoichiometry of the receptor required for signaling via IL-17E is currently unclear, as there are reports of IL-17E being unable to bind IL-17RA in vitro [4]. Whether the nature of the receptor varies depending on the cell type is another area of inquiry.

IL-17B, C and D

Our current understanding of signaling downstream of IL-17 family members other than IL-17A, F and E remains very limited. IL-17B has been shown to induce proinflammatory cytokine secretion by the THP-1 acute monocytic leukemic cell line, and to enhance inflammation, survival and metastasis in breast and pancreatic cancer [82, 83]. IL-17RB engagement in these cells recruited the Act1-TRAF6-TAK1 complex to the receptor [83]. Interestingly, IL-17B and IL-17E seem to present antagonistic activities, despite reportedly binding to the same receptor [84]. IL-17C has been reported to signal via a heterodimeric IL-17RA/RE complex [13]. Expression of IL-17RE is restricted to epithelial cells, specialized epithelial cells like keratinocytes and Th17 cells (reviewed in [85]). In line with other proinflammatory cytokines in the family, IL-17C signaling activates the NF- κ B and MAPK pathways [86]. Similar to other cytokines in the family, IL-17C signaling also seems to be dependent on Act1, and Song et al have recently reported their unpublished findings that IL-17RE associates with Act1 [85]. As noted above, the action of IL-17D, its receptor and the signaling mechanisms it elicits, remain entirely obscure.

Regulation of IL-17 family cytokines

Given its central role in inflammation, numerous mechanisms have evolved to restrict the IL-17A signaling pathway, presumably to curtail bystander inflammation. For example, TRAF3 and TRAF4 interfere with early events in IL-17A signaling by competing with Act1 or TRAF6 for IL-17RA binding [87, 88]. The deubiquitinase A20 is induced downstream of IL-17A and dampens the activation of NF- κ B and MAPK pathways by removal of K63-linked ubiquitin chains on TRAF6 [89]. Thus, A20 serves as a feedback regulator of the IL-17 pathway, analogous to its effect for TNF α and IL-1 signaling as well [90–92]. Similarly, the deubiquitinase USP25 acts on TRAF5 and TRAF6, suppressing IL-17A signaling [93]. GSK-3 β -mediated phosphorylation of the transcription factor C/EBP β inhibits IL-17 target gene expression [94]. GWAS analysis of psoriasis has revealed genetic associations with known regulators of immune signaling, including *TNFAIP3* (A20), *TNIP1* (ABIN-1, NAF1) and *NFKB1A* (I κ B α) [95]. Importantly, ABIN-1 was recently shown to

regulate IL-17A signaling in keratinocytes. Correspondingly, *Tnfr1*-deficient mice develop cutaneous inflammation with psoriasiform characteristics, linking findings in this mouse model to the enhanced susceptibility to psoriasis of individuals with *TNIP1* SNPs [96]. Finally, the endoribonuclease MCPIP1 (also known as Regnase-1, encoded by *ZC3H12A*) limits IL-17 signaling through the degradation of IL-17-driven genes, including *Il6*, *Nfkbiz* and *Il17ra* and *Il17rc* [97–99]. To date, 11 non-synonymous SNPs have been described for the *ZC3H12A* gene, but so far none are associated with human disease [100].

With an emerging role in inflammatory diseases [93], IL-17C may similarly be subject to robust control mechanisms, although little is currently known about this issue. We recently demonstrated that the action of MCPIP1 can also curb IL-17C-mediated inflammation in murine keratinocytes both in vitro and in vivo, thereby limiting skin inflammation in the imiquimod-driven psoriasis model [101]. Given the high degree of conservation across signaling pathways in the IL-17 family of cytokines, it is tempting to speculate that other members of the IL-17 will share common regulatory mechanisms.

4. IL-17 family cytokines in host protection and inflammation

IL-17A, F and A/F in infection

IL-17A and IL-17F evolved to protect from infection, and it is now clear that they orchestrate protective responses against infections at mucosal and epithelial surfaces, demonstrated in the intestine, skin, lung, and oral cavity. Their central role in mediating protective immunity relies on the induction of molecules that stimulate epithelial barrier function. Signaling downstream of IL-17RA/RC elicits the expression of antimicrobial peptides (AMPs), including α -defensins, S100 proteins and Lipocalin-2 (Lcn2, also known as NGAL) [102]. Lcn2 competes with bacterial siderophores for acquisition of free iron and thus limits bacterial growth [103]. In addition, IL-17A and IL-17F induce a proinflammatory milieu with enhanced cytokine and chemokine, and matrix metalloproteinase (MMP) production. These factors mediate the activation and recruitment of immune cells to the site of infection, promoting a potent immune response to the invading pathogen. One of the hallmarks of IL-17A-driven inflammation is neutrophil accumulation. Indeed, induction of G-CSF production regulates neutrophil production, while chemokines such as CXCL1, CXCL5 and CCL2 stimulate neutrophil chemotaxis [104]. In addition, IL-17 induces CCL20, which recruits CCR6-expressing cells such as Th17 and ILC3s [105]. In this manner, IL-17A and to a lesser extent IL-17F regulate the coordinated action of stromal, innate and adaptive immune cells.

The central role of IL-17A and IL-17F in protective immunity against infections is highlighted by the increased susceptibility of IL-17A or IL-17F-deficient mice to pathogens. For example, IL-17A^{-/-} mice are unable to control lung infection with *Klebsiella pneumoniae* [106]. In addition, IL-17A stimulates macrophage-derived IL-12, which is required to promote protective Th1 responses against pulmonary infection with *Francisella tularensis* live vaccine strain [107]. Furthermore, IL-17 levels are elevated during acute lung infection with *Pseudomonas aeruginosa*, which contributes to neutrophil recruitment and bacterial containment [108, 109]. Similarly, a deficiency in IL-17 or the IL-17-promoting

cytokine IL-23 renders mice more susceptible to *Citrobacter rodentium* intestinal infection [23], as well as to a number of other bacterial pathogens (reviewed in [110, 111]).

Candida albicans is a commensal fungal organism in about 70% of healthy individuals, residing in the skin, mouth, gastrointestinal tract and vagina without causing disease. However, following loss of immune control mechanisms, *C. albicans* can become an opportunistic pathogen. Chronic mucocutaneous candidiasis (CMC) can ensue in individuals with primary and acquired immunodeficiencies, leading to oropharyngeal candidiasis (OPC or thrush), or to cutaneous lesions. Importantly, defects in the IL-17/IL-23 axis render the host exquisitely susceptible to CMC, highlighting the importance of this pathway in controlling *C. albicans* infections. Genetic variants in IL-12Rb1 and STAT3, which compromise IL-23 signaling, have also been associated with diminished Th17 responses in humans and accordingly to CMC [112].

IL-17A is dominant in the requirement for control of *C. albicans* OPC infection in mice, although IL-17F and IL-17AF may also contribute to protection [113]. Notably, a mutation in the *IL17F* gene was recently reported in a family with CMC [114]. This point mutation at position 65 in the polypeptide chain leads to the production of a dominant negative variant, which abrogates IL-17F homodimer and IL-17A/IL-17F heterodimer signaling. Likewise, mutations in IL-17RA, IL-17RC and Act1 lead to CMC in humans. Mutations in the *AIRE* gene (autoimmune regulator) lead to the development of the multiorgan autoimmune disease APECED (autoimmune polyendocrinopathy candidiasis ectodermal dystrophy). One of the main manifestations of APECED is an enhanced susceptibility to CMC [112]. Interestingly, compromised negative selection in the thymus due to AIRE deficiency leads to the development of neutralizing autoantibodies against IL-17A, IL-17F and IL-22 [115]. Importantly, the dependence of the host on IL-17 for containment of *Candida* infections is dependent on colonization route and tissue. For instance, vulvovaginal candidiasis is associated with alterations in other host factors, such as pH and microbial flora composition. In turn, control of systemic candidiasis seems to be more reliant on Th1 and NK cell responses [116].

Staphylococcus aureus dermatitis has been reported in patients with *ACT1* or *IL17RA* null variants [114, 117]. In line with a role for IL-17 in *S. aureus* control, *Il17ra*-deficient mice exhibit an increased susceptibility to cutaneous *S. aureus* infection [118, 119]. Given the emergence in recent years of methicillin-resistant *S. aureus* (MRSA) strains, harnessing the IL-17 axis in vaccination strategies may be of prophylactic promise.

IL-17A, F and A/F in chronic skin inflammatory and autoimmune diseases

Upregulation of inflammatory and tissue-remodeling molecules can lead to tissue damage if IL-17 activity is left uncontrolled. Indeed, IL-17A and related cytokines are upregulated in numerous autoimmune conditions, including psoriasis, rheumatoid arthritis, multiple sclerosis, scleroderma and lupus, among others. Similarly, GWAS studies have associated SNPs in genes of the IL-17 pathway with autoimmunity. A number of reviews have recently addressed the role of IL-17 in other autoimmune conditions [85, 120]. We will focus here on the role of IL-17A and IL-17F in driving cutaneous inflammation.

Psoriasis is a chronic inflammatory skin condition characterized by epidermal hyperplasia, affecting 2–3% of the world's population. One of the hallmarks of disease is neutrophilic infiltration and formation of neutrophil microabscesses [121]. Elevated IL-17A and Th17-related cytokines such as IL-22 and IL-23 are found in human psoriasis skin lesions [93, 122, 123]. In addition, IL-17A can directly act on human keratinocytes stimulated to upregulate AMPs and neutrophil-attracting chemokines [19, 124]. Consistently, GWAS studies have identified psoriasis-associated variants in genes participating in Th17 differentiation and IL-17A signaling, such as *IL23R* and *TRAF3IP2* (encoding Act1) [70, 71, 125–127]. Mouse preclinical models of psoriasis have confirmed a role for IL-17 family cytokines in mediating disease. In the imiquimod-driven dermatitis model (driven by a TLR7 agonist), IL-17RA-deficient mice show dramatically diminished skin involvement [128]. Interestingly, IL-17 signaling plays a dual role during imiquimod-driven psoriasis depending on cell type. Mice deficient in IL-17 signaling in keratinocytes present dampened keratinocyte proliferation and neutrophilic microabscess formation. In turn, Act1 deficiency in skin fibroblasts limits the recruitment of IL-17-producing cells, thereby controlling the amplification of skin inflammation [129]. Interestingly, intradermal injection of IL-22 or IL-23 into mouse ear also elicits the development of psoriasis-like disease, indicating that other cytokines in the IL-23/IL-17 axis can initiate disease [85]. The importance of IL-17A-mediated inflammation in psoriasis has been more recently highlighted by the clinical success of biologic drugs, including IL-17A-blocking antibodies secukinumab and ixekizumab and the IL-17RA-targeting antibody brodalumab [7, 130–133].

Atopic dermatitis affects 10–20% of children and 1–3% of adults in the Western world [134], and is characterized by chronic skin inflammation due to exacerbated responses to environmental antigens. The IL-17 axis has been reported to participate in allergic skin reactions, including atopic dermatitis and contact dermatitis. Serum levels of IL-17A and F are increased in children with atopic dermatitis and positively correlated with disease severity [135]. Expression of IL-17A at the mRNA level is increased in the skin of patients with nickel allergy [136]. In addition, increased Th17 cell infiltration was detected in a mouse model of contact dermatitis, and IL-17A-deficient mice displayed reduced pathology [137]. Whether the enhancement of IL-17 responses is a driver of pathology or reflects the immune efforts to limit colonization of skin lesions by bacteria remains an open question.

Strikingly, IL-17 signaling has been associated with the promotion of skin cancer development during chemical carcinogenesis in mouse models. Indeed, IL-17 or IL-17RA-deficient mice show considerably diminished incidence of DMBA/TPA-induced skin tumors [138, 139]. This pro-tumorigenic effect of IL-17 is thought to occur via the promotion of epithelial proliferation and the anti-apoptotic effect of STAT-3, which may be downstream of IL-17-induced genes such as IL-6. Importantly, IL-17RA blocking in mice with established tumors blocked further tumor progression [139]. Thus, IL-17A blockade may be useful for controlling at least some cancers.

IL-17B

IL-17B is expressed by neutrophils in the synovial tissue of RA patients [140]. Treatment of human fibroblasts with IL-17B synergized with TNF- α to induce G-CSF and IL-6 [140].

Intriguingly, IL-17B is expressed in limb buds during mouse embryonic development, suggesting a role in chondrogenesis and osteogenesis that may be dysregulated in autoimmune processes affecting the joints [141]. IL-17B, like IL-17E (IL-25), has been shown to bind to IL-17RB. IL-17B can oppose IL-25-driven inflammation, and has been shown to play an antagonistic role. In a DSS-driven colitis mouse model, IL-25 administration exacerbated colonic damage [142]. In contrast, in a second report, IL-25-deficient mice exhibited reduced weight loss, inflammation and tissue damage [84], which may result from discrepancies in microbiome composition or animal housing between the two studies. Interestingly, IL-17B-deficient mice developed increased susceptibility to DSS colitis, with enhanced weight loss, proinflammatory cytokine production and colonic tissue destruction [84]. Similarly, IL-17B and IL-25 play opposing roles in the context of *Citrobacter rodentium* infection and OVA-induced lung inflammation [84]. In vitro, co-treatment of primary colonic epithelial cells with IL-17B diminished IL-25-, but not IL-17A-driven IL-6 production. IL-17B remains the most obscure of all IL-17 family members, with a role in skin immunity and pathology yet to be ascribed. The described antagonism to IL-25 function is interesting in this context, particularly given the association between IL-25 expression and skin atopy. The potential role of IL-17B in skin immunity and pathology should therefore be explored.

IL-17C

As noted above, IL-17C induces a similar pattern of gene expression to IL-17A, which poses the question of functional redundancy. However, despite the overlap in target gene induction, IL-17C-deficient mice do not exhibit a compromised ability to control oral, dermal or disseminated candidiasis, in contrast to IL-17RA deficient mice [143]. In addition, the IL-17RA-dependent gene signature associated with immunity against *C. albicans* was unchanged in IL-17C-deficient mice. Concordantly, IL-17RE deficiency did not lead to enhanced susceptibility to candidiasis. Interestingly, IL-17C can be induced in keratinocytes infected with *S. aureus* via a NOD2-dependent mechanism. Using this in vitro system, suppression of IL-17C expression rendered keratinocytes slightly more permissive to *S. aureus* survival [144]. Thus, IL-17C may contribute to the control of infections, potentially through the activation of common mechanisms with IL-17A and F.

A common feature for IL-17 family cytokines, or indeed, all inflammatory stimuli, is their propensity to promote protective immunity while simultaneously exacerbating tissue damage. IL-17C is the most highly expressed IL-17 family member in psoriatic lesions [93, 122, 123], and drives the expression of AMPs, proinflammatory cytokines and neutrophil-attracting chemokines in keratinocytes [19, 124]. Consistent with a role in mediating cutaneous pathology, intradermal delivery of recombinant IL-17C into mouse ears led to epidermal thickening and neutrophil recruitment, whereas IL-17C-deficient mice developed less skin inflammation upon imiquimod treatment [13]. In line with these findings, keratinocyte-specific IL-17C transgenic mice develop spontaneous psoriasiform dermatitis with epidermal hyperplasia, increased leukocytosis and overexpression of proinflammatory cytokines [93]. In concordance with manifestations in human psoriasis, these mice display an enhanced proclivity toward thrombotic arterial occlusion, indicating the potential systemic effects of a skin inflammatory process [145]. Therefore, IL-17C is clearly a driver

of psoriasis that could be a safer target for blockade since its role in immunity to infection, at least in mice, appears to be less central [143].

IL-17D

As mentioned, the orphan cytokine IL-17D is poorly understood, with recent reports showing that this cytokine can induce IL-6, IL-8 and GM-CSF expression in endothelial cells [51] and IL-6 and IL-8 in chicken fibroblasts [146]. Interestingly, the stress-sensing protein NRF2 induces IL-17D expression in cancer cells. IL-17D-deficient mice displayed increased tumor growth when compared to wild type mice [147]. Recent studies have also linked IL-17D to the recruitment of NK cells into the tumor microenvironment and subsequent activation [148, 149]. Indeed, IL-17D plays a dual role in promoting human NK cell cytotoxicity and inducing NK-recruiting MCP-1 by tumor endothelial cells, thus placing this cytokine in a central role in tumor surveillance [149]. The potential involvement of IL-17D in cutaneous surveillance mechanisms remains an open question.

IL-17E

IL-17E is an interesting example of an IL-17-family cytokine that possesses a divergent function to its founding member IL-17A. Like IL-17A, IL-17E can activate NF- κ B and induce the production of IL-8. In addition, transgenic mice overexpressing IL-17E develop common features of IL-17A-driven inflammation, including neutrophilia and elevated circulating G-CSF [150]. However, IL-17E functions mainly to stimulate Th2 responses, promoting Th2 cytokine secretion, class switch recombination to IgE, IgG1 and IgA, and the recruitment and activation of eosinophils, in both mice and humans. Concordantly, IL-17E transgenic mice present with eosinophilia, increased IgE and IgG1 and elevated serum IL-5 and IL-13 [150]. Given its role in promoting Th2-mediated immunity, IL-17E plays a central role in protection against helminth infection [151, 152]. In turn, *IL17E* mRNA expression is enhanced in the lungs of asthmatic patients [40] and IL-17E delivery promotes Th2 cytokine and IgE production, as well as eosinophil infiltration in a mouse model of asthma [153].

IL-17E expression has been reported in patients with several skin conditions. In particular, a SNP in the *IL17E* gene is positively correlated with severe forms of psoriasis in a Spanish cohort of patients [154]. However, the effect of this polymorphism on IL-17E expression and/or function remains unknown. Atopic dermatitis often presents in association with mutations in the gene encoding filaggrin [155–157]. IL-25 was overexpressed in the epidermis of atopic dermatitis patients and in corresponding mouse models [158, 159]. In cultured keratinocytes, IL-25 treatment inhibited the expression of filaggrin, which may account for the loss of skin barrier function associated with atopic dermatitis [158]. In addition, IL-25 can mediate the recruitment of “type 2” cytokine-producing ILC2 in atopic dermatitis [160]. Therefore, IL-25 plays a dual role in promoting atopic dermatitis via stimulation of type 2 responses and through its direct action on keratinocytes.

Concluding remarks

The IL-17 family of cytokines plays a central part in the induction of inflammation to limit numerous pathogenic insults. Here, we have reviewed the prominent role of IL-17A in

orchestrating protective responses against cutaneous bacterial and fungal infections, and the emerging roles of other IL-17 family members in boosting immunity. Given the recent development of novel therapies to block IL-17A and IL-17RA signals in chronic inflammatory diseases, the potential long-term consequences of such treatments vis-à-vis the exacerbation of fungal and extracellular bacterial infections should be examined. In that light, dissecting the commonalities and divergences in signaling pathways that drive protective versus tissue disruptive functions could provide alternative therapeutic strategies for at-risk populations. Given the pleiotropic roles of IL-17 family members, an in-depth analysis of individual cytokines' roles during infection and inflammation could provide insight into the advantages of the therapeutic alternatives that are currently under study, including IL-17A versus IL-17RA-blocking strategies.

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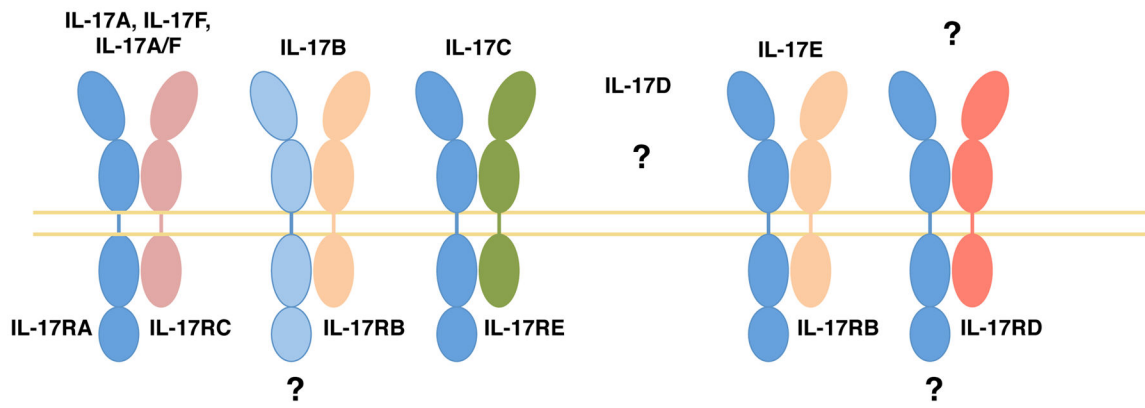


Figure 1. IL-17 family cytokines and their receptors

Most IL-17 family cytokines signal via a heterodimeric receptor composed of IL-17RA and a second chain that varies depending on ligand, as indicated. Despite advances in the characterization of receptor-ligand interactions, several questions remain. Namely, a role for IL-17RA in IL-17B signaling has not been fully demonstrated. In addition, the receptor for IL-17D, as well as the ligand for IL-17RD remain unknown.

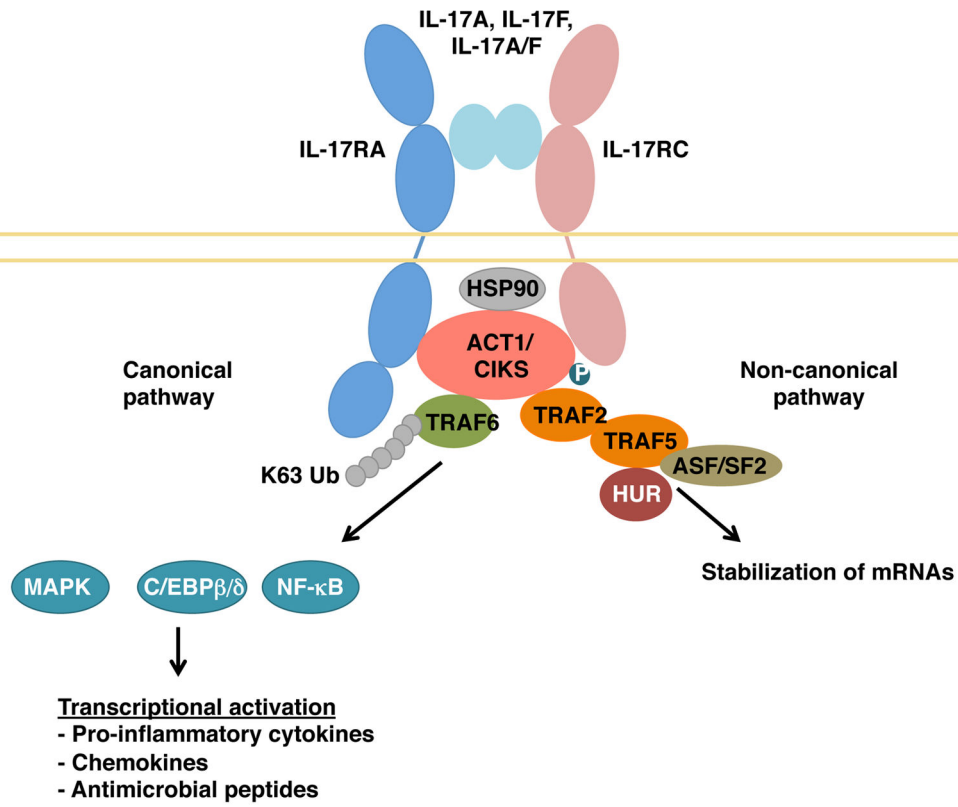


Figure 2. IL-17RA/RC signaling pathways

IL-17A/IL-17F/IL-17A/F binding to the receptor complex enables homotypic interactions between the SEFIR domains in the receptor and in the adapter Act1/CIKS. The canonical IL-17 signaling pathway initiates signaling through Act1- induced K63-linked ubiquitylation of TRAF6, thereby activating the MAPK, C/EBPβ and NF-κB pathways. This triggers transcriptional activation of downstream target genes, including pro-inflammatory cytokines, chemokines and antimicrobial peptides. In turn, non-canonical signaling relies on Act1 phosphorylation at amino acid 311. This recruits TRAF2 and TRAF5, which sequesters the mRNA destabilizing factor ASF/SF2 and recruits the mRNA stabilizing factor HuR. Together, these two pathways mediate the pro-inflammatory functions of IL-17A, IL-17F and IL-17A/F.

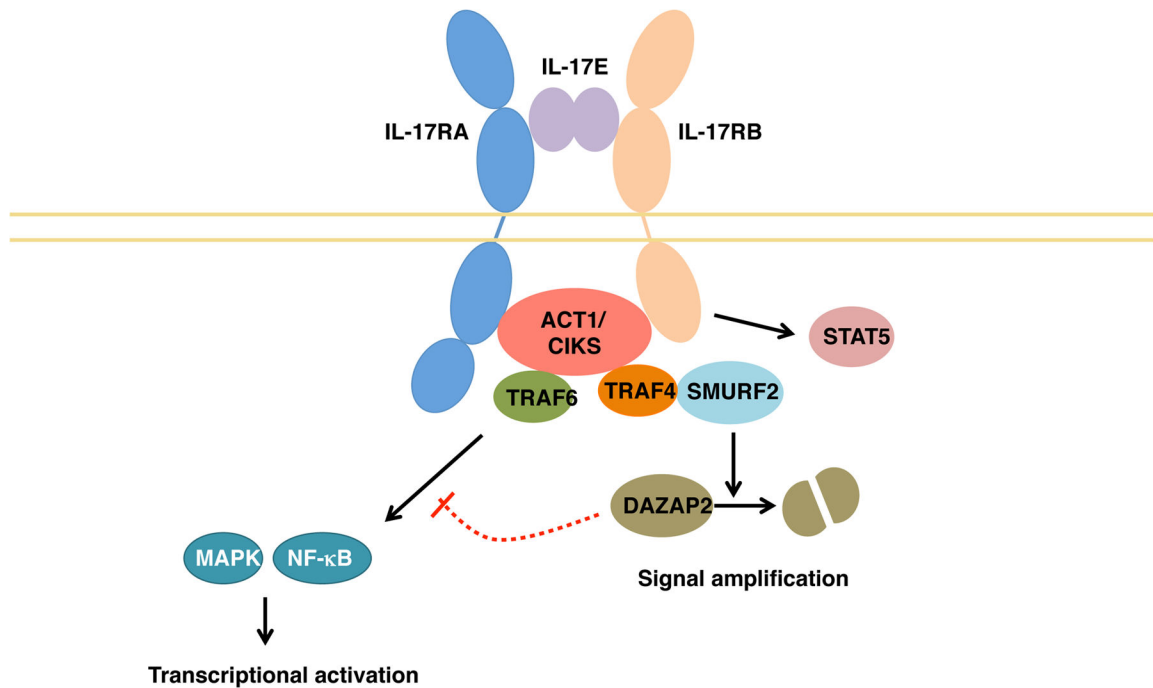


Figure 3. IL-17RA/RB signaling

Upon IL-17E binding to its receptor, homotypic interactions between the SEFIR domains in the receptor and in the adapter Act1/CIKS are established. This leads to the recruitment of TRAF6, activating the MAPK and NF- κ B signaling pathways. In turn, Act1 can recruit TRAF4, which activates the E3 ligase SMURF2. This leads to the ubiquitylation and subsequent degradation of the inhibitor DAZAP2, amplifying IL-17E-mediated signaling. In addition, IL-17RB can elicit STAT5 activation in an Act1-independent manner.

Table 1

Cytokines and receptors driving cutaneous inflammation

Cytokine	Receptor	Infection	Skin inflammatory phenotype(s)
IL-17A and IL-17F	IL-17RA/RC	<i>C. albicans</i> , <i>S. aureus</i>	Psoriasis, atopic dermatitis, skin cancer
IL-17B	IL-17RB/?	Undefined	Undefined
IL-17C	IL-17RA/RE	<i>S. aureus</i>	Psoriasis
IL-17D	Undefined	Undefined	Undefined
IL-17E (IL-25)	IL-17RA/RB	Undefined	Psoriasis, atopic dermatitis

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