

Eosinophilic esophagitis: Immune mechanisms and therapeutic targets

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Abstract

Eosinophilic esophagitis (EoE) is an emerging chronic inflammatory disease of the oesophagus and is clinically characterized by upper gastrointestinal (GI) symptoms including dysphagia and esophageal food impaction. Histopathologic manifestations, which include intraepithelial eosinophilic inflammation and alterations of the esophageal squamous epithelium, such as basal zone hyperplasia (BZH) and dilated intercellular spaces (DIS), are thought to contribute to esophageal dysfunction and disease symptoms. Corroborative clinical and discovery science-based studies have established that EoE is characterized by an underlying allergic inflammatory response, in part, related to the IL-13/CCL26/eosinophil axis driving dysregulation of several key epithelial barrier and proliferative regulatory genes including kallikrein (KLK) serine proteases, calpain 14 (CAPN14) and anoctamin 1 (ANO1). The contribution of these inflammatory and proliferative processes to the clinical and histological manifestations of disease are not fully elucidated. Herein, we discuss the immune molecules and cells that are thought to underlie the clinical and pathologic manifestations of EoE and the emerging therapeutics targeting these processes for the treatment of EoE.

KEYWORDS

eosinophilic esophagitis, cytokines, mast cell, eosinophils, biologics

1 | INTRODUCTION

Eosinophilic esophagitis (EoE) is an emerging chronic inflammatory disease of the oesophagus characterized by upper gastrointestinal (GI) symptoms including dysphagia and esophageal food

impaction.^{1,2} The histopathological manifestations involve intraepithelial infiltration of eosinophils (≥ 15 Eos/HPF) and remodelling of the esophageal epithelium including basal zone hyperplasia (BZH) and dilated intercellular spaces (DIS), which can lead to strictures and narrow-caliber oesophagus.^{3,4}

Dilawar Khokhar and Sahiti Marella contributed equally to this study.

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Eosinophilic esophagitis is a complex disease characterized by heterogeneous clinical presentation (age of onset, symptomology, varying clinical manifestations and comorbidities, natural history, and responsiveness to therapy).⁵ Despite challenges in disease diagnosis and management, there is corroborative clinical and experimental evidence to suggest that EoE is driven by an underlying CD4⁺ T helper type 2 (Th2) allergic inflammatory response to dietary food allergens in the esophageal mucosa.^{6–10} Esophageal epithelial derived signals (e.g. thymic stromal lymphopoietin (TSLP) and interleukin (IL)-33) are thought to induce Type-2 allergic cytokines, including IL-5 and IL-13, which stimulate the recruitment and activation of the allergic effector cells, eosinophils and mast cells. Eosinophil and mast cell-derived mediators stimulate dysregulation of epithelial barrier regulatory and proliferative response genes within the esophageal epithelial compartment leading to esophageal epithelial remodelling and fibrosis. Compelling evidence supporting a role for allergic inflammatory cells (CD4⁺ Th2-type cells, eosinophils, and mast cells) and cytokines in EoE has led to using biologics that target these inflammatory cells and mediators as potential treatments for EoE. Herein, we summarize the current understanding of processes that underlie the esophageal inflammation and remodelling in EoE and discuss the mechanisms of action, specific indications, benefits and side-effects of biological therapies for EoE.

2 | PREVALENCE AND INCIDENCE

Over the last three decades, EoE has evolved from a rare, case-reportable diagnosis to an increasingly common encounter in a multitude of settings across healthcare systems throughout the world.¹¹ Current estimates of EoE incidence in Europe and in the United States range from 1.30 to 12.8 cases per 100,000.¹² Incidence rates have been increasing in paediatric and adult EoE, with incidence levels reported to have increased 131-fold in the Netherlands (1996–2010), 20-fold in Denmark (1997–2012) and 5.1-fold in Calgary, Canada (2004–2008).^{13–15} The prevalence of EoE is significantly higher in male patients than in female patients, in the adult population (18–65 years of age) and in Whites than in Asians and African Americans.¹⁶ The male predominance persists across demographic groups, regardless of age, geographic region, socio-economic status or race.^{17–19} While there are no observed gender differences in EoE severity, the clinical and histologic presentation of EoE can differ between the sexes in both paediatric and adult EoE.^{20,21} For example, paediatric male patients are more likely to present with food impaction and feeding refusal, whereas female patients report more abdominal pain.¹⁷

3 | RISK FACTORS OF EoE

3.1 | Genetic

The demonstration of increased risk of EoE in first-degree relatives (10- to 64-fold) compared with that of the general population has led to the concept of a genetic contribution to the disease.^{22,23}

Key messages

- Eosinophilic esophagitis (EoE) is a chronic inflammatory disease of the oesophagus characterized epithelial remodelling that drives esophageal dysfunction and disease symptoms.
- Dietary food antigens stimulate a pro-type 2 inflammatory response in the esophageal mucosa driving dysregulation of esophageal epithelial barrier and proliferative regulatory genes and epithelial remodelling.
- Biologics targeting key aspects of Type-2 immune signals (IL-4, IL-5, IL-5R α and IL-13) are emerging treatment modalities for the treatment of EoE.

This is further supported by the observed increased risk of EoE in second-degree relatives and first cousins who likely did not share a common environment.²⁴ However, genetic data indicate the EoE inheritance pattern is not clearly autosomal dominant or recessive or X-linked suggesting, a complex inheritance pattern.²³ Candidate and GWAS studies have identified 31 independent risk loci across the genome,²⁵ with four loci consistently demonstrating genome-wide significance (5q22 [TSLP/WDR36], 2p23 [CAPN14], 11q13 [LRR32/C11orf30] and 12q13 [STAT6]). The majority of the EoE genetic risk variants are positioned within either intergenic (36.7%) or within intronic genomic sequences (42.4%), with only 2.2% variants associated with amino acid substitutions.²⁵ These non-coding sequences include gene promoters, introns and genomic regulatory elements suggesting that these variants are likely to contribute to altered gene expression and function through transcriptional or epigenetic-dependent mechanisms.²⁵

3.2 | Environmental

While these studies suggest a genetic component, analyses of EoE concordance in a twins EoE cohort also suggest a greater environmental contribution to EoE risk.²³ This is best exemplified by the lack of significant difference in EoE concordance rates between monozygotic twins (~40%) and dizygotic twins (~30%).²³ Notably, genetics was found to contribute 14.5% and common environment 81.0% to the variation in EoE heritability. Consistent with this, antibiotic use in infancy, caesarean delivery, preterm birth, season of birth, birth-weight, and lack of breastfeeding have all been identified as factors that affect EoE risk.^{23,26} Future studies in larger patient cohorts are required to delineate the contribution of genetic versus environmental risk components to the predisposition to the development of EoE.

4 | EoE PHENOTYPES AND ENDOTYPES

Eosinophilic esophagitis is becoming increasingly recognized as a heterogeneous disease with different phenotypes.^{27,28} Patients

with EoE present at different ages, and with varying clinical, endoscopic, and histopathological manifestations, comorbidities, natural history, and are responsive to different treatments.^{16,29–32} For example, adults with EoE often experience symptoms of dysphagia, esophageal food impaction and upon endoscopic evaluation present with fibrostenotic phenotype with typical rings and strictures.^{4,33–36} In contrast, paediatric EoE presentation includes emesis, abdominal pain, gastroesophageal reflux, feeding difficulties and failure to thrive^{16,37} with an endoscopic phenotype characterized by mucosal findings of longitudinal furrows and exudates.^{34–36,38–40} Initial reports suggested that patients with EoE despite the disease heterogeneity possessed similar molecular signatures^{41,42} suggesting a common disease entity. However, recent reports in both adult and paediatric EoE suggest gender-related differences in the molecular signature and that these differences in transcriptional profiles may contribute to observed differences in clinical presentation EoE between male patients and female patients.^{43,44}

Clinical therapy trials have identified two distinct EoE treatment phenotypes (PPI-R EoE and PPI-UR EoE) based upon differential responsiveness to PPI.^{45,46} PPI-R EoE and PPI-UR EoE are clinically, endoscopically, and histologically indistinguishable at diagnosis.^{45,47–52} Furthermore, atopy status and molecular signature are also largely similar between the two phenotypes.^{5,53} PPI therapy in PPI-R EoE individuals induces clinicopathological remission with reports of 20%–80% of patients achieving symptom improvement^{47,54–56} with ~68% of patients achieving complete symptom-free remission with high-dose PPI.⁵⁷ Notably, there is not always concordance in clinical and histological response to PPI therapy with histologic remission achieved in only 33%–61% of individuals.⁵⁶ However, individuals who achieve complete histologic remission on PPI therapy often have improvement to complete symptom elimination.^{45,47,58} Recognition and characterization of the different EoE phenotypes will be critical in assisting clinicians with clinical care and likely to and favourable clinical outcome.

Allergic diseases including asthma and EoE are diseases of heterogeneous phenotypes with clinical differences including clinical symptoms, atopy history, responsiveness to therapy and anthropometrics are not predictive of treatment outcomes.^{31,59,60} To better understand disease heterogeneity and assist with management and treatment decisions, efforts have been made to stratify allergic diseases according to pathophysiologic mechanisms termed endotypes. These efforts have been greatly assisted by the advancement in molecular analysis and permitted classification of EoE patients based on molecular endotypes. For example, Shoda et al. recently performed a cross-sectional study across 10 CEGIR (Consortium of Eosinophilic Gastrointestinal Disorders) centres and analysed the association between histologic and endoscopic features of paediatric and adult EoE with the 96 gene eosinophilic esophagitis diagnostic panel molecular signature.⁵ The investigators identified 3 distinct EoE endotypes- EoEe1, EoEe2 and EoEe3. EoEe1 was associated with an endoscopically normal appearing oesophagus with mild histological changes and molecular signature that was distinguished by high expression of epithelial differentiation genes and

low expression of inflammatory and remodelling genes. EoEe2 was characterized by high degree of endoscopic and histological severity for the inflammatory component, high expression of inflammatory cytokine genes and refractoriness to steroids and EoEe3 was associated with adult-onset, fibrostenotic phenotype and a low expression of epithelial differentiation genes.⁵ The identification of EoE endotypes will provide a framework for precision medicine in future therapeutic prevention strategies for specific EoE populations. For example, the EoE endotype 2 which was characterized by type-2 immune responses and evidence of refractoriness to steroids may be more amendable to specific anti-type-2 immune biologic therapy such as anti-IL4Ra or anti-TSLP.⁵

5 | PATHOPHYSIOLOGY OF EoE

Histopathologic manifestations of EoE include intraepithelial eosinophilic inflammation and alterations of the esophageal squamous epithelium including BZH and DIS which are thought to contribute to esophageal dysfunction and disease symptoms. Recent studies have revealed an important role for Type-2 immune-induced expression and function of the ion transport proteins anoctamin 1 (ANO1) and sodium hydrogen exchange member 3 (NHE3) in the regulation of the esophageal epithelial proliferative response and DIS formation in EoE.^{61,62} Despite these advancements, the mechanism by which these ion transport proteins mediate BZH and DIS remains largely unclear and there is a paucity of data describing the interaction of these processes that drive esophageal epithelial remodelling in EoE.

6 | ESOPHAGEAL EPITHELIAL CELLS

The normal human esophageal epithelium consists of non-keratinized stratified squamous epithelium. The esophageal epithelium consists of the several layers including the stratum germinativum (basal layer) and stratum spinosum (suprabasal/prickle cell layer) and the stratum corneum (superficial/surface layer). The basal layer consists of proliferative cells and is not more than 3 cell layers thick or more than 15% of the total epithelial thickness. The suprabasal layer consists of transitional basal cells and the superficial layer consists of the simple and stratified squamous epithelial cells. In EoE, the esophageal epithelium and sub-epithelium undergo extensive remodelling manifested as BZH, DIS,^{3,63,64} fibrosis, angiogenesis and smooth muscle hyperplasia.^{65,66} This epithelial and subepithelial remodelling is thought to contribute to endoscopic (esophageal rings and stricture formation) and clinical (dysphagia and food impaction) manifestations typical of EoE.^{67–70}

6.1 | Basal zone hyperplasia

Esophageal epithelial BZ expansion in patients with EoE is defined as a basal cell layer exceeding 15% of total epithelial thickness.

The underlying pathways that induce esophageal epithelial BZH are poorly understood. Recently, we identified involvement of the calcium-activated chloride channel anoctamin 1 (ANO1) in the regulation of chloride transport and proliferation in esophageal epithelial cells.⁶¹ We demonstrated that biopsies from patients with EoE had increased mRNA expression of ANO1 and the level of ANO1 expression correlates with BZH.⁶¹ Immunofluorescence analyses localized ANO1 to esophageal basal cells suggesting a relationship between ANO1 expression and esophageal epithelial proliferation. In vitro studies revealed that ANO1 played an important role in esophageal epithelial chloride transport and that loss of ANO1-dependent chloride transport reduced esophageal epithelial proliferation.⁶¹ ANO1 was required for phosphorylation of cyclin-dependent kinase 2 (p-CDK2) and transition through G₁/S phase cell cycle check point to permit esophageal epithelial proliferation. Interestingly, a key requirement of G₁/S phase and G₂/M phase transition and cellular proliferation is increased cell volume, which is regulated in part by ion channel regulation of the membrane potential (V_{mem}).⁷¹⁻⁷⁷ The increased V_{mem} across the plasma membrane osmotically drives water influx from the extracellular to intracellular space leading to cell swelling.⁷⁸ The functional relevance of BZH and ANO1 expression and relationship to human EoE is unclear. Shoda et al. identified an EoE endotype (EoE Endotype 3)⁵⁵ that was associated with a fibrostenotic (rings, narrowing, strictures) phenotype and the highest degree of endoscopic and histological severity. Molecular analyses revealed that ANO1 was one of two discriminatory genes (ANO1 and UPK1A) to provide 98% PPV of EoE endotype 3 suggesting a link between ANO1 and the fibrostenotic and histologic phenotype.⁵ We speculate that ANO1's contribution to functional outcomes in EoE such as fibrostenosis is not through directly driving esophageal dysfunction but rather indirectly through chronicity of inflammation and subsequent development of secondary associated histopathologic manifestations such as BZH and DIS formation.

6.2 | Dilated intracellular spaces

Dilated intercellular spaces have been consistently described in the esophageal epithelium of both adult and paediatric patients with gastroesophageal reflux disease (GERD) and EoE.^{68,70,79-81} Histologically, DIS is significantly more intense in EoE than GERD.⁸² In EoE, the presence and magnitude of the DIS correlate with esophageal eosinophil numbers and disease severity.⁶⁹ Furthermore, decreased DIS is associated with symptom improvement with steroid therapy or elimination diet in EoE suggesting that DIS contributes to clinical signs and symptoms of disease.^{70,83,84} How DIS drives the clinical manifestations of EoE and the molecular basis underlying DIS formation are not fully elucidated. One proposed mechanism involves solute carrier family 9, subfamily A, member 3 (SLC9A3)-dependent acid extrusion by esophageal epithelial cells and acidification of the intercellular spaces.⁸⁵ The acidification of the intercellular spaces promotes the formation of

an electrochemical gradient and chloride (Cl⁻) diffusion, creating an osmotic force for water flux and intercellular space dilation.^{86,87} SLC9A3 encodes sodium hydrogen exchange member 3 (NHE3) and is specifically up-regulated in biopsy specimens from patients with EoE. Notably, the level of SLC9A3/NHE3 mRNA expression correlates with eosinophil count and the level of DIS.⁶² In an in vitro model of EoE, IL-13 stimulation of esophageal epithelial cells results in increased expression of SLC9A3/NHE3 and DIS formation.⁶² Pharmacological antagonism of NHE3 activity reduced DIS formation.⁶² In EoE, there is significant esophageal epithelial basal zone (BZ) expansion, and the basal cell layer can exceed 15% of the total epithelial thickness.⁸⁸ We speculate that the esophageal proliferative response and thickening of the epithelial basal zone leads to diminished capacity of the intercellular acid-protective mechanisms and leading to DIS. Consistent with the concept of esophageal epithelial intercellular acid as a primary driver for DIS in EoE, luminal acid has been shown to drive acidification of the intercellular spaces and DIS in non-erosive reflux disease.^{86,87,89,90} To further support this concept, a recent study reported a strong positive correlation between BZH and DIS ($r^2 \geq .67$) in both proximal and distal biopsy samples from paediatric patients with EoE.⁶⁹ Interestingly, the increased esophageal intercellular acid in non-erosive reflux disease is thought to activate afferent neurons (nociceptors) within the esophageal epithelium leading to the development of heartburn.⁹⁰ Although less common, EoE symptoms can include heartburn.⁴

7 | IMMUNOLOGICAL PROCESSES

Corroborative clinical and experimental studies indicate that an underlying allergic sensitization to dietary food antigens and development of a CD4⁺ Th2 and ILC2 inflammatory response in the esophageal mucosa drive the eosinophilic inflammation and esophageal remodelling in EoE^{3,63,91,92} (Figure 1). Dietary modification (i.e. complete or targeted food antigen avoidance) and swallowed glucocorticoids alleviate much of the disease pathology,^{93,94} suggesting a food-induced CD4⁺ Type-2 allergic inflammatory response.^{6,95-99} Consistent with this, animal-based studies have revealed important roles for CD4⁺ Th2 cells, pro-allergic cytokines [IL-5 and IL-13] in the histopathologic manifestations of disease.^{9,100,101} These cytokines are thought to mobilize eosinophils and promote eosinophil survival, activation and degranulation and also dysregulate the expression of several key epithelial barrier regulatory genes driving the esophageal remodelling and clinical symptoms (Figure 1).¹⁰²⁻¹⁰⁴

7.1 | The eosinophil, eotaxin subfamily and IL-5

The eosinophil is a pleiotropic granulocytic leukocyte that is histologically characterized by a bilobed nucleus and cytoplasmic granules and arises from CD34⁺ progenitor cells within the bone marrow.¹⁰⁵ The eosinophil possesses homeostatic functions

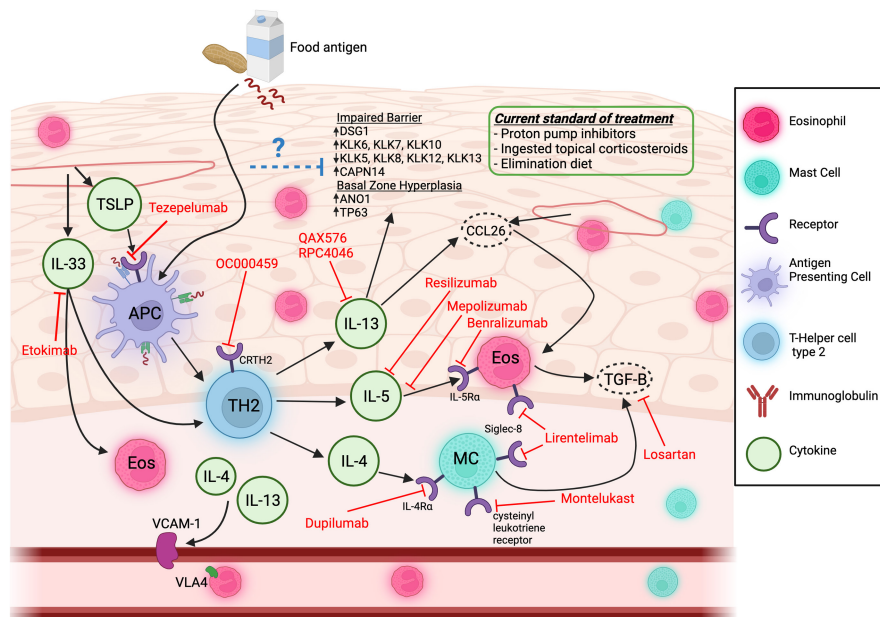


FIGURE 1 Pathophysiology and clinical management of eosinophilic esophagitis (EoE). EoE is a chronic inflammatory disease of the oesophagus driven by food allergen exposure which triggers esophageal eosinophilia and esophageal epithelial remodelling. Esophageal epithelial derived cytokines TSLP and IL-33 stimulate antigen presenting cells (APCs) presentation of food antigens to CD4⁺ T helper type 2 (TH2) cells and secretion of the cytokines IL-4, IL-5 and IL-13. IL-4 is responsible for driving mast-cell (MC) and vascular endothelial adhesion responses, IL-5 is responsible for eosinophil maturation, activation and survival, and IL-13 is responsible for inducing pro-inflammatory and pro-adhesion pathways and inducing expression of pro-proliferation, pro-inflammatory, and barrier regulatory genes within the esophageal epithelial compartment which contribute to the “EoE Transcriptome.” Current standards to manage EoE symptoms include proton-pump inhibitor (PPI) therapy, food elimination diet, and ingested topical corticosteroids. Several therapeutics and biologics, including monoclonal antibodies and small molecule inhibitors are under investigation which target various aspects of EoE pathophysiology. Created with [BioRender.com](https://www.biorender.com)

including tissue development, thymic T cell selection and innate host defense; however eosinophils also contribute to the initiation and propagation of inflammatory responses including parasitic helminth, bacterial and viral infections, tissue injury, tissue immunity and allergic diseases.^{106–109} Under homeostatic conditions, the eosinophil is found in all portions of the gastrointestinal (GI) tract apart from the oesophagus.¹¹⁰ The most characteristic histopathologic feature of EoE is esophageal intraepithelial eosinophilia (≥ 15 eosinophils/HPF). Eosinophil numbers can be significant with micro-abscesses and esophageal eosinophilia correlates with histopathologic features (including DIS and BZH) and disease severity.^{111,112} In a registry of EoE patients, O'shea *et al* compared patients with high-grade esophageal eosinophilia (>350 eosinophils per hpf) to patients with low-grade eosinophilia (15–24 eosinophils per hpf) and found statistically significant differences in histologic severity, endoscopic severity and gene expression but not symptoms.¹¹³

The mechanisms by which eosinophils drive histopathologic features of EoE are not fully elucidated. Eosinophils possess granules that consist of cytotoxic proteins including eosinophil peroxidase (EPX), major basic protein (MBP), eosinophil cationic protein (ECP) and eosinophil-derived neurotoxin (EDN).¹¹⁴ Electron microscopy analysis of EoE esophageal biopsy specimens revealed evidence of esophageal eosinophil piecemeal degranulation or cytolysis.¹¹⁵ Consistent with this finding, esophageal biopsy specimens from

patients with EoE demonstrated increased EPX, MBP and EDN extracellular deposition.^{116,117} Notably, the presence of these proteins correlated with histologic features including intercellular oedema, BZH, lamina propria elongation and lamina propria fibrosis suggesting a pathogenic role for eosinophils in disease.^{116,118} Using an antigen-induced model of EoE, investigators demonstrated that depletion of eosinophils using neutralizing monoclonal antibody (anti-Siglec F antibody) led to decreased esophageal eosinophilia, angiogenesis, BZH and fibronectin deposition.¹¹⁹ Similarly, mice deficient in eosinophils have a decrease in allergen-induced esophageal BZH and esophageal lamina propria thickness and do not develop esophageal strictures.^{120–122} Notably, these mice still had evidence of esophageal motility dysfunction, suggesting the presence of eosinophil-independent processes in histopathological manifestations of disease.¹²²

Eosinophil development, maturation and survival is largely regulated by the cytokine IL-5. Patients with active EoE have increased levels of IL-5 as compared to inactive EoE patients and healthy controls.⁸ Overexpression of IL-5 in the esophageal squamous epithelia of mice that received oxazolone (OXA) sensitization and topical challenge of the oesophagus leads to increased level of esophageal eosinophilia. Conversely, neutralization of IL-5 reduces esophageal eosinophil numbers in an allergen-induced EoE model⁹ supporting a role for IL-5 in maintenance of esophageal eosinophilia in EoE.

Eosinophil trafficking is primarily regulated by the chemokine receptor CCR3 and eotaxin subfamily of chemokines (eotaxin-1/CCL11; eotaxin-2/CCL24 and eotaxin-3/CCL26).^{123,124} CCR3 is predominantly expressed on eosinophils and CCR3 gene deletion impairs eosinophil recruitment in models of allergic inflammation including allergen-induced esophageal eosinophilic inflammation.^{123,125,126} Transcriptional analysis of biopsy specimens from patients with EoE revealed significant up-regulation of CCL26 mRNA compared with healthy individuals.¹²⁵ Furthermore, CCL26 mRNA expression was shown to directly correlate with esophageal eosinophilia in EoE.¹²⁷ Notably, a single-nucleotide polymorphism (SNP) in the CCL26 gene has been associated with EoE disease susceptibility.¹²⁵ Collectively, these clinical and mouse-based analyses suggest that IL-5 regulates eosinophils maturation and survival in the oesophagus, whereas CCL26/eotaxin-3 likely regulates eosinophil recruitment into the oesophagus in EoE.

7.2 | Esophageal epithelial cells

Transcriptomics analysis has revealed altered gene expression in esophageal epithelial cells from EoE individuals.^{128,129} Esophageal epithelial cells from EoE individuals are enriched for genes involved in molecular functions including structural molecule activity (SPRR1 and 2 family members, Keratin family members), Serine-type peptidase activity (KLK6-8, KLK10-12), Serine-type endopeptidase inhibitor activity (SERPINB2-5, 7 and SPINK5) and IL1 receptor binding (IL33, IL36B, IL36A, IL36RN, IL1A, IL1RN).^{128,129} These molecular functions are involved in biological processes such as epidermis development, keratinocyte differentiation, epithelial cell development, desmosome organization and establishment of skin barrier which is consistent with the observed esophageal epithelial proliferative response, BZH and impaired barrier function.^{128,129}

SPRR proteins are 6-18kDa proteins encoded within the epidermal differentiation complex region (EDC). SPRR1 and SPRR2 proteins are predominantly expressed in the skin, oral mucosa and oesophagus and are thought to cross-link EDC proteins including loricrin and involucrin. EoE has been associated with decreased expression of epithelial barrier function genes including SPRR proteins as well as desmoglein 1 (DSG1) and structural epithelial genes including filaggrin (FLG), involucrin (IVL) which likely contributes to loss of esophageal barrier integrity. SPRR1a and SPRR2a have recently been shown to possess potent bactericidal activity which suggests a possible role for these proteins in the regulation of esophageal host defense.¹³⁰

Kallikreins (KLKs) are a subgroup of serine proteases that possess trypsin- or chymotrypsin-like activity.¹³¹ KLK6, KLK7 and KLK10 are significantly increased, whereas KLK5, KLK8, KLK12 and KLK13 are down-regulated in EoE.¹⁰² KLK5 is thought to regulate squamous epithelial barrier properties through processing of barrier proteins including DSG1.¹³²⁻¹³⁴ KLK5 is also known to stimulate pro-inflammatory signals via cleavage and activation of protease-activated receptor 2 (PAR2) and activate TSLP production.¹³⁵ Recent

studies indicate that KLK5 is a direct target of SPINK7.¹³⁶ The two most highly expressed SPINK genes in the human oesophagus are SPINK5 and SPINK7. In EoE, both SPINK5 (1.9-fold) and SPINK7 (16-fold) are significantly down-regulated as compared with control individuals.¹³⁷ Mechanistic analyses have revealed that reduced expression of SPINK7 in esophageal epithelial cells leads to increased barrier dysfunction, loss of cellular differentiation and increased pro-allergic signals including production of TSLP and urokinase plasminogen-type activator (uPA). TSLP is a key cytokine involved in the generation of CD4⁺ Th2 responses and genetic variants have been linked with increased EoE risk.^{25,138,139} UPA is a serine protease that has been shown to promote uPA receptor-dependent eosinophil activation.¹³⁷ The altered expression of an array of structural proteins, proteases and protease inhibitors within the esophageal epithelial layer during EoE suggests a complex interaction between regulatory and counter-regulatory processes likely in effort to promote esophageal epithelial proliferation and differentiation and sustain barrier integrity.

7.3 | T cells and Th2 cytokines: IL-4 and IL-13

Clinical studies have demonstrated increased frequency of CD4⁺ Th2 cells in the peripheral blood and esophageal biopsy samples from EoE individuals.^{127,140,141} scRNAseq analyses of esophageal biopsy samples from EoE patients revealed a prominent tissue resident CD4⁺ T cell population that expressed IL-4, IL-5 and IL-13.¹⁴¹ Notably, the percentage of these CD4⁺ Th2 cells correlated with esophageal tissue eosinophilia.¹⁴¹ IL-4 mRNA expression is increased in EoE patients and levels have been shown to be decreased in patients with EoE following glucocorticoid therapy or dietary elimination therapy suggesting a role for IL-4 in disease.^{8,142} IL-4 has been shown to regulate multiple aspects of eosinophil trafficking and function including eotaxin subfamily and adhesion molecule expression.^{143,144} IL-13 appears to be the dominant Type-2 cytokine involved in orchestrating the eosinophil dominant inflammatory response and the histologic manifestations of EoE. Overexpression of IL-13 in mice is sufficient to promote esophageal eotaxin subfamily expression, esophageal eosinophilia, epithelial hyperplasia, angiogenesis and fibrosis.^{10,145} Furthermore, the genes differentially expressed by primary esophageal epithelial cells following IL-13 stimulation significantly overlap with the EoE transcriptome (22%, $p < .05$) and transcriptional changes observed in the oesophagus of mice engineered to overexpress IL-13.¹⁰ Furthermore, IL-13 stimulation of esophageal epithelial cells in the absence of eosinophils is sufficient to promote esophageal remodelling including BZH and DIS formation.⁶²

7.4 | Mast cells

Mucosal biopsies from patients with EoE also demonstrate increased frequency of mast cells and evidence of

degranulation.^{146,147} Not only do EoE patients have a greater number of mast cells in the oesophagus, but also have alterations in mast cell gene expression such as up-regulation of carboxypeptidase A3 (CPA3) and tryptase, but not chymase.^{146,148} Intriguingly, increased esophageal mast cell density has been observed in EoE patients with persistent symptoms and endoscopic abnormalities in the absence of an esophageal eosinophilia supporting a key role for mast cells in EoE pathogenesis.¹⁴⁹ A recent study examining esophagectomy specimens from patients with EoE identified tryptase-positive mast cells infiltrating all layers of the oesophagus including mucosa, muscularis mucosa, submucosa, muscularis propria and adventitia.⁶⁵ Employing mouse models of EoE, investigators have demonstrated that mast cells increase concurrently with eosinophils in the oesophagus in response to allergen challenge.¹⁵⁰ Notably, the mast cell infiltration into the muscular layers of the oesophagus was associated with muscular hyperplasia and hypertrophy and this phenotype was diminished in mast cell deficient mice.¹⁵⁰ Mast cells are also thought to dysregulate esophageal muscle contractility and relaxation responses.¹²⁰ Tryptase-positive mast cells within the muscularis mucosae of patients with EoE have increased expression of TGF- β 1.⁶⁵ TGF β 1 stimulation of human esophageal smooth muscle cells promotes smooth muscle contraction.⁶⁵ Collectively, these studies suggest that mast cells through release of cytokines such as TGF β 1 and autocrine mediators may stimulate esophageal smooth muscle hyperplasia and exert procontractile effects on esophageal smooth muscle in EoE.¹⁵¹ The presence of mast cells in EoE may define a specific subtype that lacks significant esophageal eosinophilia and is prone to extra-intestinal symptoms such as dysphagia.¹⁴⁹

7.5 | Immunoglobulin

Eosinophilic esophagitis is often associated with atopic comorbidities including food allergy, asthma, allergic rhinitis and atopic dermatitis suggesting IgE involvement.^{20,152} EoE individuals often have food- or environmental-specific or elevated total IgE.^{142,152-154} Furthermore, there is evidence of local immunoglobulin class switching and IgE production in the esophageal mucosa of paediatric EoE patients¹⁵⁵ which had led investigators to propose that eosinophilic esophagitis is a IgE-mediated disease.^{153,156} However, the contribution of IgE to the pathogenesis of EoE is inconclusive. Treatment of paediatric and adult EoE patients with the anti-IgE humanized monoclonal antibody (omalizumab) resulted in only a 33% improvement in histologic and clinical outcomes despite significant reduction in tissue IgE levels.¹⁵⁷ Furthermore, a prospective randomized double-blind placebo-controlled trial of adults with EoE administered omalizumab ($n = 16$) or placebo ($n = 14$) every 2 to 4 weeks for 16 weeks revealed that while omalizumab induced a significant decrease in serum IgE, no reduction in EoE symptoms or eosinophil histologic involvement was observed.¹⁵⁸ Collectively, these studies suggest that specific IgE may be associated with EoE; however, it is not causative in the pathogenesis of EoE.

There is increasing evidence of a role for IgG4 in EoE. Adult EoE individuals have increased total and food-specific serum IgG4 compared with controls.^{158,159} Furthermore, levels of IgG4 in esophageal tissue from EoE patients are 45-fold higher than that observed in controls and evidence of IgG₄ extracellular deposits has been observed in the esophageal wall of EoE individuals.¹⁵⁸ Similarly, increased serum food-specific IgG₄ and increased IgG₄⁺ plasma cells have been observed in paediatric EoE and tissue IgG₄ levels positively correlate with peak eosinophil count and histologic involvement, in particularly BZH.¹⁶⁰⁻¹⁶³ Wright et al. demonstrated that 50% of peanut-allergic individuals that underwent peanut oral immunotherapy developed a new esophageal eosinophilia that was consistent with the pathologic criteria for EoE. Interestingly, all these individuals demonstrated marked esophageal tissue deposition of IgG4.¹⁶⁴ Recent studies also support a pathogenic role for IgG₄ in EoE. Treatment of EoE patients with the topical steroid budesonide (1 mg BID) led to a reduction in both serum and esophageal IgG₄ levels and this was associated with reduced EoE symptoms.¹⁶⁵ Furthermore, EoE individuals who responded to six-food elimination diet consisting of removal of common dietary allergens were shown to have reduced total IgG₄ levels and esophageal food-specific IgG4.¹⁶⁶ Further studies are required to delineate whether or not IgG4 plays a pathogenic role in EoE or is simply reflective of chronic antigen exposure (e.g. OIT) and activation of memory CD4 Th2 response.

7.6 | TGF- β

Surgical resection specimens have revealed that the esophageal eosinophilic inflammation in EoE can extend throughout all layers of the oesophagus beyond the squamous epithelium. Notably, the subepithelial eosinophilic infiltrate is often associated with subepithelial fibrosis and endoscopic findings including esophageal furrowing or ridging and esophageal dysfunction (e.g. dysphagia and food impaction) which can progress to a fibrostenotic disease phenotype.^{4,118,167-169} Notably, the profibrotic cytokine TGF- β and downstream signalling molecules (phosphorylated SMAD2/3) has been found to be increased in esophageal biopsies from patients with EoE.⁶⁶ TGF- β promotes quiescent fibroblast to myofibroblast transdifferentiation and up-regulation of expression of extracellular matrix (ECM) proteins including Type I collagen.¹⁷⁰ TGF β is secreted by all cell types within the oesophagus, and fibroblasts when stimulated by TGF- β secrete extracellular matrix components such as collagens (COL1A1) and fibronectin.¹⁷¹ TGF- β is also thought to contribute smooth muscle dysfunction, collagen deposition, epithelial remodelling, barrier dysfunction and angiogenesis in EoE.¹⁷²

Genetic studies have previously linked a single-nucleotide polymorphism (SNP) in the promoter region of the TGF- β 1 gene (-509) with increased risk of asthma when exposed to traffic-related emissions.¹⁷³ Analyses of the TGF β 1 promoter C-509 genotypes CC, CT, and TT in EoE subjects revealed of 155 EoE subjects, 52% patients possessed the -509CT genotype, 35% -509CC genotype and

13% -509TT genotype. Notably, -509TT subjects possessed more esophageal TGF β 1⁺ cells and mast cells and higher esophageal epithelial remodelling scores than -509 CC and CT subjects. It is postulated that the TT genotype at -509 of the TGF β 1 gene leads to increased TGF β 1 gene transcription either through loss of AP1 suppressive signal or YY-1 positive transcriptional signal.¹⁷⁴ Consistent with this, fibroblasts with the TT genotype possessed significantly elevated baseline levels of TGF β 1 mRNA expression as well as TGF β 1 target genes including *collagen 1a1* and MMP2 compared with CC genotype fibroblasts. Functional assays have revealed that the TT genotype is also associated with increased TGF β 1-induced E-cadherin localization and epithelial barrier function suggesting that genotype at the TGF β 1 promoter SNP -509 is also associated with altered fibroblast function.¹⁷⁵ Recent *in vitro* studies suggest that TGF β 1 induction of *collagen 1a1* in esophageal fibroblasts involves Thrombospondin-1.¹⁷⁶ The frequency of -509TT genotype has not been shown to be significantly different between EoE and control populations indicating that this polymorphism is not likely a genetic risk factor for EoE but rather a disease modifying allele gene.¹⁷⁷

8 | DISEASE MONITORING AND EMERGING THERAPEUTICS

With the rising prevalence and incidence of EoE, and as diagnosis requires the identification of esophageal eosinophilia, an emerging challenge in management is disease monitoring.^{178,179} As symptoms of EoE are not consistently reliable in regard to correlation with disease activity, disease monitoring in EoE commonly requires repeated endoscopy with biopsies.¹⁸⁰ The development of minimally invasive monitoring tests for disease activity in EoE is an area of active investigation. Non-invasive tests such as the esophageal string test¹⁸¹ and Cytosponge¹⁸² are currently being evaluated. Furthermore, multiple biomarkers including plasma EDN, CCL26 and eosinophil progenitor levels are also under investigation for disease monitoring in EoE.^{183,184}

The focus of EoE treatment remains alleviation of symptoms and the prevention of complications of fibrostenotic remodeling. The current mainstays of effective treatment for EoE include proton-pump inhibitors (PPI), various elimination diets and topical corticosteroids such as swallowed fluticasone inhaler and oral viscous budesonide.^{48,185-188} Dietary and pharmacologic therapies are effective in inducing and maintaining disease remission, reducing the risk of esophageal food impactions, and improving quality of life.^{48,185-188} Recently, several corticosteroid formulations including fluticasone orodispersible tablet, budesonide oral solution and budesonide orodispersible tablet have been developed to specifically treat EoE.^{133,189} Some of these oesophagus-targeted formulations of topical steroids have demonstrated excellent response rates inducing clinical and histologic remission and improvement of QoL in patients with EoE.^{133,189,190} However, several patients do not respond to these standard therapies, histologic relapse in EoE is not uncommon and long-term efficacy remains unclear.¹⁹¹

Recently, there has been increasing focus on the utilization of biologic agents focussed on targeting specific aspects of eosinophil biology (IL-4, IL-5, IL-5R α , IL-13 and siglec-8) for the treatment of EoE¹⁸⁸ (Figure 1). There are currently three IL-5 directed agents (Mepolizumab, Reslizumab and Benralizumab) originally approved for treatment of asthma that have been examined for EoE treatment.¹⁹²⁻¹⁹⁴ Mepolizumab, a humanized anti-IL-5 monoclonal antibody which inhibits IL-5 binding to its receptor¹⁹³ was shown to significantly reduce esophageal eosinophilia in EoE patients, however, failed to show a reduction in symptoms.¹⁹⁵⁻¹⁹⁷ Reslizumab a fully humanized IgG4 antibody with high affinity and specificity for IL-5¹⁹⁸ also demonstrated a reduction in esophageal eosinophilia but failed to show a consistent symptomatic response.^{199,200} Benralizumab, a fully humanized, afucosylated anti-IL-5 receptor α antibody is currently in Phase 3 trial for EoE.²⁰¹

Sialic acid binding immunoglobulin-like lectin (Siglec) 8 is a surface receptor expressed on mature eosinophils, mast cells and basophils.²⁰² Cross-linking of Siglec-8 has been demonstrated to induce eosinophil apoptosis and thus it has been proposed as a therapeutic target for eosinophilic disorders.^{202,203} Lirentelimab is a humanized anti-Siglec 8 antibody and has been shown to elicit antibody-dependent cell-mediated cytotoxicity against human eosinophils and inhibit mast cell activity.²⁰⁴ Lirentelimab has recently been evaluated in a clinical trial with patients with either eosinophilic gastritis (EoG) or duodenitis (EoD).²⁰⁵ In this phase 2 multi-center clinical trial, lirentelimab reduced gastrointestinal eosinophil levels and disease symptoms.²⁰⁵ Notably, a subset of patients who had concomitant EoE was noted to have decreased esophageal eosinophilia after treatment.²⁰⁵

Biologics targeting the IL-4/IL-13 signalling pathway have also been examined in the context of EoE and individuals with esophageal eosinophilia.²⁰⁶ Treatment of adult patients with PPI resistant esophageal eosinophilia with QAX576, a fully human monoclonal antibody against IL-13, reduced esophageal eosinophil counts and improved expression of esophageal transcripts involved in EoE.²⁰⁶ However, significant improvement of clinical symptoms was not observed, and the study failed to meet its primary end-point.²⁰⁶ RPC4046, a recombinant humanized monoclonal antibody against IL-13, was examined in a multicenter double-blind placebo-controlled trial of adults with EoE.²⁰⁷ In a phase 2 16-week short-course treatment study, RPC4046 demonstrated statistically significant changes in histologic and endoscopic outcomes; however, limited improvement in symptomatic outcomes was observed.²⁰⁷ Patients who completed the 16-week, double-blind, induction portion of the phase 2 study of RPC4046 (180 mg or 360 mg/wk) that enrolled into the 52-week open-label, long-term extension (LTE) study receiving open-label RPC4046 360 mg/week demonstrated sustained endoscopic, histologic and clinical improvement.²⁰⁸

Dupilumab is a fully human IgG4 monoclonal antibody that binds the IL4R α chain, and is approved the treatment of multiple allergic conditions including atopic dermatitis, asthma, and chronic rhinosinusitis with nasal polyps.²⁰⁹ Through its ability to bind to the IL-4R α receptor subunit that is shared by both type 1 and type 2 IL-4 receptor, it can antagonize both IL-4 and IL-13 signalling.²¹⁰ In a phase

2 multi-center study, adults with active EoE who received weekly subcutaneous injections of dupilumab (300mg/dose) (loading dose, 600mg on Day 1) demonstrated reduced peak esophageal eosinophil count, decreased histologic and endoscopic severity scores, and increased esophageal distensibility.²¹¹ Preliminary data from a phase 3, randomized, 3-Part study to investigate the efficacy and safety of dupilumab in adult and adolescent patients with EoE shows that weekly dupilumab promotes similar improvements in histologic, symptomatic and endoscopic measures.²¹² These findings suggest that concurrent antagonism of IL-4 and IL-13 may be a viable treatment option for EoE.

Anti-IL-33 therapies have been investigated in murine models of atopic dermatitis as well as asthma and demonstrated anti-inflammatory effects.^{213,214} Data in humans are limited, but Etokimab (an IgG1 anti-IL-33 monoclonal antibody) has been examined in both atopic dermatitis and peanut allergy in humans.^{215,216} Initial results from these human trials suggest that antagonism of IL-33 results in several anti-inflammatory effects which may be clinically significant. Anti-IL33 therapy has yet to be examined in EoE but has the potential to become a viable therapeutic in this context. Given the prominent role TSLP in inducing Th2 responses, blockade of TSLP has been investigated for treatment of various allergic diseases.²¹⁷ Tezepelumab is a human monoclonal antibody that binds to TSLP and prevents its interaction with the TSLP receptor complex and has shown efficacy in the treatment of severe asthma,²¹⁸ but limited effect in atopic dermatitis.²¹⁹ Tezepelumab has not been studied in patients with EoE.

9 | CONCLUSION

Our understanding of EoE has rapidly evolved over the last two decades. There have been significant advancements in defining the complex interplay between the immune system, epithelial barrier and environmental exposures that lead to the development of EoE. EoE is now recognized as a Th2-mediated, food-antigen-driven disease that is characterized by impaired barrier function. The current challenges facing EoE include the development of novel therapeutics including biologic therapies and non-invasive testing for diagnosis and disease monitoring and defining distinct endotypes and phenotypes to tailor specific therapies for a given patient. The solution to such challenges requires further inquiry into the mechanisms of disease.

AUTHOR CONTRIBUTIONS

KD, MS and SPH drafted the manuscript; IG, JWC, CM and SPH reviewed and revised the manuscript. All authors approved the final version of the manuscript.

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DATA AVAILABILITY STATEMENT

Data sharing not applicable to this article as no datasets were generated or analysed during the current study.

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