



Review

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Biomarkers in oral immunotherapy

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Abstract: Food allergy (FA) is a global health problem that affects a large population, and thus effective treatment is highly desirable. Oral immunotherapy (OIT) has been showing reasonable efficacy and favorable safety in most FA subjects. Dependable biomarkers are needed for treatment assessment and outcome prediction during OIT. Several immunological indicators have been used as biomarkers in OIT, such as skin prick tests, basophil and mast cell reactivity, T cell and B cell responses, allergen-specific antibody levels, and cytokines. Other novel indicators also could be potential biomarkers. In this review, we discuss and assess the application of various immunological indicators as biomarkers for OIT.

Key words: Food allergy; Oral immunotherapy; Biomarker; Immune tolerance; Desensitization

1 Introduction

Food allergy (FA) has become a major public health problem, affecting nearly 5% of adults and 8% of children (Sicherer and Sampson, 2014; Lopes and Sicherer, 2020). The incidence is still increasing. Foods, such as hen's eggs, cow's milk, and peanuts, are the major culprits causing life-threatening allergic reactions (Bock et al., 2007; Anagnostou, 2018). Traditional management of FA includes food avoidance and prompt identification and treatment of acute anaphylactic reactions (e.g., rapid access to epinephrine) (Gernez and Nowak-Wegrzyn, 2017). However, accidental allergen exposure is difficult to avoid, and strict diet avoidance would significantly lower the quality of life and result in several adverse outcomes such as nutritional deficiencies and psychological disorders. Current pharmaceutical agents provide only instant relief from allergies without addressing their fundamental causes. Many individuals may experience relapses of allergic reactions. Therefore, there is a need

for effective and rational therapies for re-establishing tolerance to symptom-eliciting foods.

Currently, allergen-specific immunotherapy (AIT) is the only etiology-based treatment with the potential capacity for long term modification of allergic diseases (Krishna and Huissoon, 2011; Mousallem and Burks, 2012; Pajno et al., 2017). Emerging AIT strategies include subcutaneous immunotherapy (SCIT), epicutaneous immunotherapy (EPIT), sublingual immunotherapy (SLIT), and oral immunotherapy (OIT) (Nurmatov et al., 2017). Several studies have demonstrated that OIT could effectively induce short-term hyposensitization (an increased reaction threshold to food allergen during treatment) or desensitization in most enrolled subjects (with average desensitization rates of 80%–85%). Also, a minority of subjects have shown sustained unresponsiveness (SU, an absence of allergic symptoms upon allergen re-exposure weeks to years after treatment ends) (Leung et al., 2003; Akdis and Akdis, 2014; Jones et al., 2016; Nurmatov et al., 2017; Nachshon et al., 2018; Nagakura et al., 2018; The PALISADE Group of Clinical Investigators, 2018; Kim EH et al., 2020). The term SU is often regarded as a surrogate for permanent tolerance. In OIT, a dose of natural or processed food is orally administered in a gradually increasing manner to establish permanent tolerance. Protocols vary, but most include an initial rapid dose escalation phase, followed by a

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buildup phase, and then a maintenance phase. Several questions remain unsolved, such as the optimal dose of the offending food-allergen at each stage, the time course of the maintenance phase, and the sustainability of the desensitization process. The first controlled OIT trial for FA was reported by Patriarca et al. (1998). In the past decade, OIT has emerged as one of the most promising therapies for FA, with satisfactory therapeutic efficacy in advanced phase 3 trials (Nowak-Węgrzyn and Albin, 2015). Currently, the US Food and Drug Administration (FDA) has approved peanut allergen powder (Palforzia) for clinical application as an OIT remedy to gradually desensitize patients with a confirmed peanut allergy (The Medical Letter, 2020). Ideally, OIT aims to alleviate an allergic response by suppressing inflammatory effector cells and inducing the reinstatement of immune tolerance toward food allergens. A desensitization state is frequently induced by regular intake of the allergenic food following a schedule for conferring protection from allergic reactions. Oral tolerance is considered achieved if the food antigens can be ingested without inducing any allergic symptoms or adverse reactions despite a prolonged period of food avoidance. In general, oral food challenges (OFCs), especially double-blind placebo-controlled food challenges (DBPCFCs), are regarded as the gold standard for FA diagnosis and immune-status assessment (Bock et al., 1988; Rolinck-Werninghaus et al., 2005; Nowak-Węgrzyn and Albin, 2015). However, OFCs are time-consuming and expensive, and have a potential risk of causing anaphylactic reactions, making them unsuitable for large-scale clinical applications during OIT. Moreover, the processes of immune induction and tolerance reinstatement in OIT are complicated; OFCs are probably unable to fully reflect the immunologic status of the participants receiving OIT. Thus, biomarkers in OIT are needed for easier and more efficient clinical assessment. Ideally, biomarkers would be used to (1) accurately predict treatment response (limited remission, transient state of desensitization, or SU), (2) effectively identify risks of severe reaction, and (3) timely monitor therapeutic efficiency. To date, investigators are still searching for such ideal biomarkers.

2 Immune mechanisms involved in OIT

Oral tolerance is a state of local and systemic unresponsiveness to food proteins. After ingestion,

goblet cells, microfold cells (M cells), and intestinal resident macrophages sample luminal food antigens and deliver them to lamina propria (LP) conventional dendritic cells (cDCs). Typically, cDCs (CD11c⁺ CD11b⁺ MHCII⁺ cells) comprise two predominant subsets: (1) CD103⁺ CX3CR1⁻ DCs, which imprint gut homing on lymphocytes and induce development of regulatory T cells (Tregs), and (2) CX3CR1⁺ DCs (with macrophage features), which facilitate tumor necrosis factor- α (TNF- α) production, colitis, and T helper 17 (Th17) cell development. Oral tolerance is initiated by CD103⁺ DCs that capture antigens in the LP and subsequently migrate into the draining lymph nodes, where they foster differentiation of naive CD4⁺ T cells into Tregs (Fig. 1). In addition to Tregs, T cell anergy, regulatory B cells (Bregs), host-microbe homeostasis and the functional intestinal barrier contribute significantly to the development of oral tolerance.

Although the mechanisms of OIT are not well understood, some investigations have indicated shared pathways between oral tolerance and OIT (Burks et al., 2012; Burton et al., 2014b; Nozawa et al., 2014; Escudero et al., 2015; Smaldini et al., 2015; Perezábad et al., 2017; Thota et al., 2017; Nachshon et al., 2018; Dreskin et al., 2019; Luce et al., 2020). During the initial phase of OIT, repeated exposure to a low-dose food antigen has direct effects on mast cells (MCs) and basophils, including immunoglobulin E (IgE) endocytosis and actin rearrangement, rendering these effector cells hyporesponsive to the culprit allergen. At an early stage of this phase, increased levels of specific IgE (sIgE) are commonly observed after the first allergen exposure, probably reinforcing B-cell pathogenic activities and creating an inhibitory milieu that hampers early development of Tregs. Subsequent chronic stimulation of allergen-specific Th2 cells with increasing doses of food allergen results in a counter-regulatory immune response. This presents as decreased Th2 activity and clonal expansion, increased expansion of interleukin-10 (IL-10) producing CD4⁺ T cells, and elevated production of sIgG. Considering that allergen-specific Th2 cells are at the core of the allergic process in FA individuals, changes in the quantity and polarization of allergen-specific CD4⁺ cells seem to be a crucial contributor to the effectiveness of OIT. Generally, the anti-inflammatory cytokine IL-10 is considered an important factor for the induction and maintenance of peripheral tolerance to allergens.

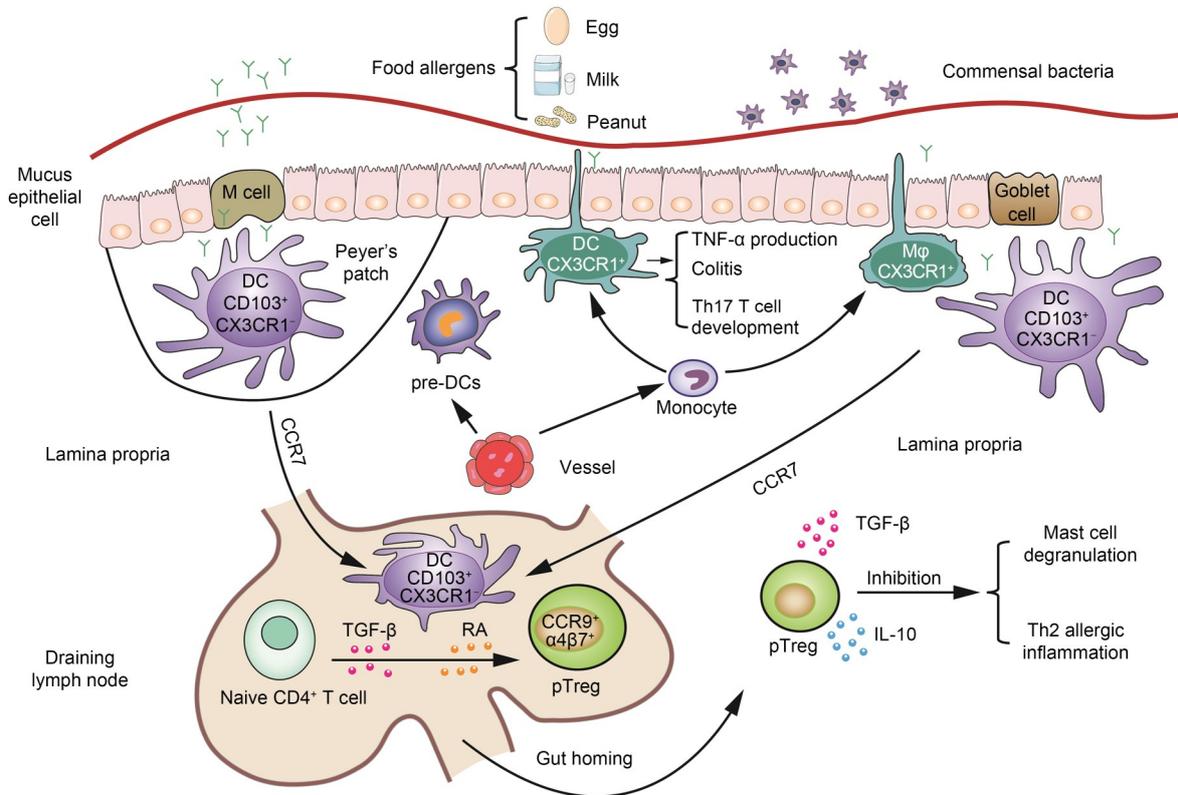


Fig. 1 Schematic diagram of immune tolerance to food antigens. Under physiological conditions, ingestion of a protein antigen can induce oral tolerance, which is mediated in part by a subset of intestinal dendritic cells (DCs) that promote the development of regulatory T cells (Tregs). Blood pre-DCs populate the lamina propria, Peyer’s patch, and draining lymph nodes, and differentiate into conventional/classical DCs (cDCs). The lamina propria contains a large population of cDCs (CD11c⁺ CD11b⁺ MHCII⁺ cells) comprising two predominant subsets: (1) CD103⁺ CX3CR1⁻ DCs, which imprint gut homing on lymphocytes and induce development of Tregs; and (2) CX3CR1⁺ DCs (with macrophage features), which facilitate tumor necrosis factor- α (TNF- α) production, colitis, and Th17 T cell development. During immunologic tolerance, several cell types are involved in antigen uptake: goblet cells, microfold cells (M cells), and intestinal epithelial cells, and CX3CR1⁺ macrophages (CX3CR1⁺ M ϕ). After being activated by the antigen, the cDCs (also called migratory DCs) migrate into the draining lymph nodes in a C-C chemokine receptor 7 (CCR7)-dependent manner, and then foster naive CD4⁺ T cell to differentiate into peripheral Tregs (pTregs) through epithelial cell-derived transforming growth factor- β (TGF- β) and retinoic acid (RA). The induction and development of Tregs can further prevent mast cell degranulation and Th2-dependent allergic inflammation. IL-10, interleukin-10.

Notably, the Bregs harboring immunosuppressive capacities also facilitate IL-10 production during tolerance induction (van de Veen et al., 2016). IL-10 is an important factor for IgG4 induction (Satoguina et al., 2005). During this phase, such immunologic changes are largely contingent upon continued OIT, otherwise the clinical benefits of OIT may be reduced or lost when dosing is interrupted. A possible reason is that a large population of allergen-specific CD4⁺ T cells still remain at this point. Successful immunotherapy may induce such CD4⁺ T cells to shift toward an “anergic” Th2 T-cell phenotype (Ryan et al., 2016). Besides, once a specific threshold of activation is achieved during chronic inflammation, IL-10- and cytotoxic

T-lymphocyte antigen-4 (CTLA-4)-producing Th2 inhibitory (Th2i) cells can develop directly from nonsuppressive Th2 effectors (Altin et al., 2012). The consolidation phase begins when threshold values of activation are reached, which probably induces a selective T-cell exhaustion response away from the pro-allergic Th2 response. Prolonged stimulation during the maintenance phase can enhance epigenetic modification of the forkhead box protein 3 (*FOXP3*) locus during Tregs differentiation (Syed et al., 2014), leading to direct consequences associated with SU. The inducible Treg is considered a central mediator in the pathogenesis of FA and the acquisition of oral tolerance to food antigens (Shreffler et al., 2009; Vonk

et al., 2017; de Quiros et al., 2018). SU achievement and maintenance also require the sustained suppression or deletion of pathogenic Th2 cells, as well as the longevity and immunomodulatory function of the induced B cell memory response. The relative importance of these mechanisms and their kinetics need to be further investigated.

In short, successful OIT has a wide range of effects on many components of the host immune system. The major outcomes include: (1) decreased basophil and MC reactivity; (2) changes in allergen-specific antibodies characterized by an initial increase followed by a decrease in sIgE and a gradual increase in sIgG; and (3) altered allergen-specific T- and B-cell responses (e.g., generation of inducible Tregs). In addition, local immunity in the gut needs to be investigated further, particularly with respect to several factors involved in antigen uptake, processing, and response at the site of administration during OIT. The associated influencing factors include epithelial cells, innate lymphoid cells (ILCs), DCs, intestinal flora, and metabolites. Together with existing advances, a better, unified understanding of the complex interplay among the molecular, cellular, and humoral changes throughout the whole OIT process will be beneficial in identifying more promising OIT biomarkers in the future.

3 Functional immunological tests

3.1 Skin prick test

The skin prick test (SPT) is the most common and popular method for allergic phenotype detection. Since the first publication on SPT by Ebruster (1959), it has become the first choice in the diagnostic workup for IgE-mediated allergic diseases (mainly type I hypersensitivity reactions). This detection method is convenient and reliable, and has low cost and minimal invasiveness (Uranüs et al., 1990; Frati et al., 2018). It usually has an excellent positive predictive value (PPV) ranging from 95% to 100% (Frati et al., 2018). SPT has additional advantages of enabling the testing of multiple allergens in a matter of minutes, offering a visual indication of sensitivity, and detecting some less common allergens (e.g., certain medications). SPT rarely triggers a severe allergic reaction; anaphylactic events are more likely to occur in subjects with a history of severe reactions.

SPT is conducted by pricking the skin, usually in the forearm, with a lancet (fine needle) for delivering a trace amount of allergen extract. In a sensitized host, the relevant allergen binds sIgE, thereby cross-linking high-affinity IgE receptors (FcεR1s) on MCs, leading to degranulation of mastocytes and then the release of histamine and other mediators which generate sizeable wheals. Generally, a positive SPT is recorded as a mean wheal diameter of >3 mm (Eigenmann and Sampson, 1998; Patel and Saltoun, 2019). However, in a large-scale study of children ($n=467$) who underwent OFCs, it was found that food-specific SPT wheal diameters of >8 mm (to cow's milk), >7 mm (to egg), and >8 mm (to peanut) were highly and correctly predictive of systemic responses (100% specificity) to each allergen (Sporik et al., 2000). The cut-offs may vary with the age of participants, the degree of cooking, and the type of allergens (commercial extract or raw food) (Komata et al., 2007; Nowak-Węgrzyn et al., 2008; Järvinen and Sicherer, 2012; Cuomo et al., 2017). Therefore, the relevance of such sensitivity to allergen extracts should be carefully interpreted in the light of the clinical history and situation, since many SPTs may yield false positives.

In an egg OIT study (Vickery et al., 2010), the wheal diameter of the OIT group decreased significantly from a median of 10 mm at baseline to 2.5 mm at the time of OFC. In contrast, there was no significant change in the placebo group. Similar SPT results have been reported in several OITs with different food allergens (Varshney et al., 2011; Nowak-Węgrzyn et al., 2019; Moraly et al., 2020). Overall, successful OIT is closely associated with reduced SPT reactivity after treatment, and a smaller SPT diameter at initiation of OIT may be predictive of better outcomes. It is considered that the SPT probably acts as an "in vivo" test for assessing the reactivity of sIgE-activated MCs and basophils. However, SPTs do not enable a valid distinction between sensitized but tolerant individuals and clinically allergic patients. SPT seems to be suitable for the general assessment of desensitization, but unsuitable for the accurate prediction of OIT directions and outcomes. SPT may be a useful marker for monitoring the immune response during therapy.

3.2 Basophil activation test

Basophils are the essential effector cells involved in initiating the innate immune response to allergen

exposure or parasite infection. They constitute about 1% or less of circulating leukocytes. Similar to MCs, basophils express FcεRI on cell surfaces. Cross-linking of FcεRI and food allergens triggers basophil activation, and initiates subsequent intracellular signaling events that lead to the production of granule contents (histamine, proteoglycans), lipid-derived mediators (leukotrienes), and cytokines (Sarfati et al., 2015). Several studies have demonstrated a good general agreement between the expression of basophil activation markers and the time course of clinical manifestations or the development of systemic reactions in allergic patients (Gober et al., 2007; Commins et al., 2014; Santos et al., 2014; Ruinemans-Koerts et al., 2019).

The basophil activation test (BAT), also called a flow-cytometric allergen stimulation test (FAST), is a functional assay in which the expression of activation biomarkers (e.g., CD63 and CD203c) is measured on the surface of basophils following allergen stimulation (Sanz et al., 2002). A BAT can be considered an *ex vivo* OFC in a test tube. Typically, basophil activation is assessed by plotting a response curve to increasing antigen doses. Based on the dose response, two indicators of basophil reactivity and basophil sensitivity (50% effective concentration (EC₅₀) or similar) have been extensively adopted and applied. In general, basophil reactivity refers to the proportion of basophils that express CD63 (percentage of CD63⁺ basophils) compared to the controls (Santos et al., 2015a, 2021). Basophil sensitivity is measured as the median effective dose (ED₅₀) or basophile allergen threshold sensitivity (CD-sens), expressed as the inverse of the EC₅₀ multiplied by 100 (CD-sens=1/EC₅₀×100) (Glauermann et al., 2012; Santos et al., 2015a; Santos and Lack, 2016).

CD63 is a lysosomal-associated membrane protein (LAMP) located on the membrane of secretory lysosomes in resting basophils. When the granules fuse with the plasmatic membrane of basophils during degranulation, CD63 begins to express on the cell surface (Amano et al., 2001). CD63 expression is directly and strongly correlated with histamine release in the cell supernatant. CD203c, a surface marker unique to basophils and MCs, is already expressed on resting cells and can be up-regulated by IL-13 stimulation. After activation, CD203c is up-regulated slightly earlier than CD63. In general, CD107a and CD107b co-localize with CD63 in secretory lysosomes,

whereas CD164 and CD13 co-localize with CD203c in vesicles.

Compared with SPTs, BATs are better for distinguishing between allergic and tolerant individuals (Ocmant et al., 2009; Song et al., 2015). In the first large-scale study assessing tests for the diagnosis of peanut allergy (Santos et al., 2014), BAT optimal diagnostic cutoffs showed 98% sensitivity, 96% specificity, and 97% accuracy, and also allowed a reduction of about 66.6% in the number of OFCs required. Moreover, the use of BATs in a two-step sequential approach (a combination of a BAT with another test of SPT or sIgE) could further improve diagnostic accuracy in children with an equivocal SPT and sIgE to peanut and its components. In recent years, subsequent studies have extensively assessed the performance of BATs in the diagnosis of allergy to different foods, including cow's milk (Rubio et al., 2011; Ruinemans-Koerts et al., 2019; Kim YH et al., 2020; Nucera et al., 2021), egg (Kim YH et al., 2020; Nucera et al., 2021), fish (Imakiire et al., 2020), wheat (Chinuki et al., 2012), hazelnut (Cucu et al., 2012), and shrimp (Song et al., 2015; Wai et al., 2021). The BAT seems to be a reliable and cost-effective tool in the management of pediatric FA. With high diagnostic accuracy, the BAT shows advantages when SPT and sIgE are equivocal and is a necessity for OFCs. The high specificity of BAT confers a high degree of certainty and consistency in confirming FA diagnosis (Kim YH et al., 2020; Santos et al., 2020, 2021). More importantly, the BAT is a useful tool to determine whether an OFC can be safely undertaken. Using a large cohort of well-characterized patients, Santos et al. (2020) first analyzed the utility of different indicators, including BAT, SPT, peanut-sIgE, *Arachis hypogaea 2* (Ara h 2)-sIgE, and peanut-sIgG4, in relation to peanut allergy status, severity, and threshold dose of allergic reactions during OFC (Santos et al., 2020). The data confirmed that the BAT is a superior biomarker for peanut allergy with high specificity (98.7%). Also, the BAT was the best predictor for identifying life-threatening allergic reactions (with 97% specificity and 100% sensitivity) and the threshold dose of reactivity to peanut (with 91% specificity and 95% sensitivity) during OFC. The BAT results appear to be unaffected by a relatively long-term (about three months) intake of antiallergic drugs (antihistamines) in FA patients (Nucera et al., 2021).

Apart from investigating a patient's allergic status at a given time point, BATs can be used to monitor clinical response, to evaluate the natural resolution of FA and to assess immunologic changes during immunotherapy. Of note, decreased basophil reactivity and sensitivity related to desensitization have been observed in OITs with different culprit foods, such as peanut (Jones et al., 2009; Marrs et al., 2015; Patil et al., 2019; Tsai et al., 2020), egg (Kim EH et al., 2020), and milk (Frischmeyer-Guerrero et al., 2017; Vonk et al., 2019). Loss of basophil activation may appear as one of the earliest readouts observed at an immunological level during OIT. Significantly, suppression of CD63 and/or CD203c expression of basophils was observed during the initial phases of OIT (Gorelik et al., 2015). This is consistent with the early immunologic changes during OIT. In a peanut OIT trial (Patil et al., 2019), an early decrease in basophil sensitivity to Ara h 2 within the first three months was closely correlated with SU after treatment. However, after four weeks of peanut avoidance (cessation of OIT), the basophil reactivity rebounded in subjects with transient desensitization. A recent peanut OIT trial also demonstrated that combined assessments of BAT and sIgE might be helpful in predicting therapeutic outcomes and differentiating between transient desensitization and an SU state (Tsai et al., 2020). Therefore, the combination of BAT and other tests or biomarkers may be a useful, less-invasive, and safe strategy for monitoring OIT efficacy. Notably, for large-scale clinical applications of BAT, it still requires analytical and clinical validation, standardization of procedures, and quality assurance to ensure the reproducibility and reliability of results. Currently, efforts are being made to establish a platform that can be used by laboratories in Europe and the USA for quality assurance and certification.

3.3 Mast cell reactivity

MCs are located in skin and gastrointestinal and respiratory tracts, where the host immune system frequently interacts with the external environment. They serve as tissue resident cells and function as the first line of defense against invading pathogens (Crivellato et al., 2010; Kubo, 2018).

Similarly to basophils, MCs play important roles in allergic processing. All these cells express FcεRI receptors, which are crucial for allergen recognition and successive cell activation/degranulation. A study in an

FA mouse model indicated that mucosal MCs may amplify the allergic response to ingested peanut and suppress the induction of peanut-specific Tregs (Burton et al., 2014a). Strikingly, deletion of spleen tyrosine kinase (Syk, FcεRI signaling kinase) solely from MCs was sufficient to restore Tregs induction. Accumulation of MCs in the local mucosa of gastrointestinal tracts is often observed during food-antigen-induced allergic diarrhea in murine models (Kurashima et al., 2007). Furthermore, duodenal biopsies from FA patients have shown enhanced expression of MC-associated transcripts when compared with controls (Chen et al., 2015). All these findings indicate that activated and degranulated MCs are essential pathological elements for the development of allergic reactions. Recent data also demonstrated that MC progenitors could become activated by IgE cross-linking, and may contribute to the pathology associated with acute allergic airway inflammation via the production of IL-13 (Méndez-Enríquez et al., 2022). In contrast, some studies have indicated that the MCs may exert immunoregulatory functions during long-term stimulation, which is confirmed by the production of regulatory cytokines, such as IL-2 and IL-10 (Leveson-Gower et al., 2013; Morita et al., 2015). The most probable cause is that continuous stimulation by the antigen-IgE complex can modulate FcεRI signal transduction, resulting in a functional change in MCs (Ang et al., 2016; Salamon et al., 2017). By developing a clinically relevant OIT murine model, Takasato et al. (2021) further demonstrated this innovative mechanistic immunological process in the intestinal mucosa upon successful OIT. In their study, ovalbumin (OVA) OIT could effectively induce oral unresponsiveness against allergen-induced allergic diarrhea in mice by conversion of activated pathogenic MCs to desensitized regulatory MCs. That is, OIT prompted desensitized regulatory MCs to produce IL-2 for the expansion of Treg populations and IL-10 for suppression of allergic responses, whereas the production of pathogenic Th2 cytokine was inhibited. Also, the desensitization process may modulate the activation of MCs, leading directly to enhanced induction of Tregs and promotion of clinical allergic unresponsiveness (Takasato et al., 2021). These findings provide new insights into the pathogenic and beneficial aspects of MCs, which can be manipulated by an appropriate form of OIT to regulate allergic responses.

Although MC activation tests (Bahri et al., 2018; Santos et al., 2018) and serologic determination of activation products (e.g., MC protease-1) (Burton et al., 2014a) provide favorable diagnostic performance, these tests may not perfectly recapitulate MC actions in situ since cell responses to micro-environmental cues may change MC phenotype and function. On the other hand, the MCs may also contribute to immunological transition from allergic promoter to suppressor during the desensitization process. Current available tests seem not to accurately reflect activation and functional changes of MCs during FA and OIT processes. Traditionally, since basophils are more accessible than MCs for ex vivo studies, most researchers prefer to apply the BAT as an assessment of therapeutic efficacy during OIT. However, MCs, especially mucosal MCs (MMC) localized in the intestinal mucosa, play a central role in the development of FA. The MMCs are a distinctly different population from connective tissue MCs (Nakano and Kitaura, 2022), and are gradually emerging as an attractive target for therapeutic intervention in food-induced disorders. The functions of MMCs are still poorly understood. Recent evidence suggests orally desensitized MCs (regulatory MCs) seem to form a regulatory network with Tregs for allergy treatment, potentially providing a promising target or biomarker for successful OIT (Takasato et al., 2021). Moreover, transcriptome and proteome analyses suggest that human MCs are not so different from mouse MCs (Plum et al., 2020). Thus, a mouse model of OIT is an excellent alternative at present for the detailed and in-depth study of human MMC without excessive technical and ethical difficulties. Research focusing on MCs will further improve the treatment of FA. With advances in the characterization of MC subtypes, molecular and regulatory mechanisms of MC expansion, differentiation, and activation, as well as in vivo living cell imaging techniques and humanized models, it should be possible to introduce more promising clinical indicators for prediction of AIT outcomes. Such progress will be beneficial for identifying the exact roles of innate immune cells in the development of an allergic or oral tolerance response.

4 B cell responses

B cells play an important role both in the development of allergen sensitization and induction of

allergen tolerance. The contribution of B cells to such processes is associated with antibody production, interplay with other cell types, secretion of various cytokines, and expression of surface molecules. In the sensitization of FA, B cells respond to allergic stimuli primarily by producing high-affinity specific antibodies which serve as hallmarks of an adaptive immune response (Calderon et al., 2010; Shakoor et al., 2016; Smeekens and Kulis, 2020). During OIT, major changes of humoral response are associated with increased food-specific IgG and IgA, as well as initially increased, but subsequently decreased, food-specific IgE. The involvement of B cells themselves in tolerance induction is not as well understood as that of T cells, but a few studies focused mainly on the Bregs have implicated the role of B cells in AIT.

4.1 Immunoglobulin quantification

4.1.1 Immunoglobulin E (IgE)

Testing for IgE sensitization is the cornerstone of diagnostic evaluation in suspected allergic conditions (Ansotegui et al., 2020). The level of sIgE may serve as a useful tool for estimating the probability of immune reaction to raw food, food extracts, or molecular components (Hao et al., 2016). However, a high sIgE level does not directly correlate with the severity of the reaction. The epitopes (regions on the allergen) to which IgE binds seem to have more clinical relevance to factors such as patient heterogeneity and clinical reactivity. IgE epitope mapping is usually conducted using a peptide microarray immunoassay. Determination of epitope recognition provides an additional tool in predicting the phenotype of milk allergy (Sackesen et al., 2019), as well as identifying symptomatic peanut allergy, especially in children with peanut sIgE below diagnostic decision levels (Beyer et al., 2003). A linear epitope analysis of sIgE in peanut-sensitized patients revealed not only variability in the number of bound epitopes (Shreffler et al., 2005), but also a positive association with reaction severity (Flinterman et al., 2008). Patients with greater epitope diversity (number of epitopes recognized) appear to be more sensitive than those with the lower diversity (Flinterman et al., 2008). The qualitative aspects of sIgE, such as clonality, epitope specificity and diversity, and post-translational modifications, may also play a decisive role in the allergic process. In a prospective cohort study of infants at high risk for allergy,

an algorithm combining epitope sIgE with peanut sIgE outperformed different clinically relevant IgE cutoffs, predicting allergy status on an “unseen” set of patients at the end point (Suprun et al., 2020).

Several studies have shown that food sIgE is up-regulated after the onset of OIT and decreases thereafter over the course of therapy (Varshney et al., 2011; Anagnostou et al., 2014; The PALISADE Group of Clinical Investigators, 2018; Hourihane et al., 2020). The level of component-specific IgE also seems to follow trends similar to those of food-specific IgE. In a pilot clinical trial of peanut OIT, the change over time in total peanut sIgE levels was paralleled by similar changes in IgE specific for Ara h 1 and Ara h 2 (Vickery et al., 2014). However, the levels of other component-sIgEs (specific for Ara h 3, Ara h 8, and Ara h 9) did not change at different time points, indicating that IgE binding to major allergen components is an important target during OIT. During peanut OIT, in subjects with peanut sIgE of ≥ 35 kIU/L, a combined model of IgE binding to epitopes 1, 5, and 6 (linear epitopes of Ara h 2) with peanut-sIgE was highly predictive of attainment of SU after OIT (Dreskin et al., 2019). In a cow’s milk study (Savilahti et al., 2014b), children who attained desensitization showed decreased epitope sIgE and increased epitope sIgG4 following therapy. However, in subjects with OIT discontinuation, the reduced quantity/affinity of epitope sIgE was reversed, and there was a broader diversity of IgE and IgG4 binding. Further study demonstrated that as a predictive model of SU, IgE-binding epitopes alone performed significantly better than models using standard serum component sIgE (Suárez-Fariñas et al., 2019). Therefore, measuring the epitope repertoire may be a reliable approach to predict the probability of SU and the threshold of clinical reactivity after OIT.

In addition, the ratio of sIgE to total IgE has been reported to be more predictive for OFC outcomes than sIgE alone (Gupta et al., 2014). The ratio has been investigated as another potential biomarker for OIT (Patil et al., 2020). However, such indicators were examined in a small cohort and need to be further verified with more trials involving larger sample sizes.

4.1.2 Immunoglobulin G (IgG)

Food sIgG antibody often rises in the setting of naturally resolving FAs, but in unsensitized individuals, IgG production to ingested foods is in the normal

range (Schwarz et al., 2016). This raises the possibility that IgG may serve as an indicator for allergy and tolerance evaluation. As OIT continues and higher doses of antigen are administered, the level of allergen sIgG, particularly IgG4, gradually increases in a dose-dependent manner within weeks to months (Jones et al., 2009; Burks et al., 2012; Vickery et al., 2014). In general, the IgG4 level increases more than 10-fold from the baseline value and remains elevated, even after several years of OIT. The phenomenon of an initial up-regulated sIgG4 level followed by a later plateau phase has been reported in several OIT trials with different foods including peanut, egg, and milk (Jones et al., 2009; Burks et al., 2012; Nozawa et al., 2014; Tang et al., 2015; Wright et al., 2016; Vickery et al., 2017; Nagakura et al., 2021). In the mouse model of FA, allergen sIgG can facilitate tolerance restoration and sustainability, favoring expansion of Foxp3⁺ Tregs along with suppression of existing Th2 and IgE responses (Burton et al., 2018). Other studies have also demonstrated the ability of IgG to suppress IL-4 secretion and shift the Tregs/Th2 balance (Burton et al., 2014b, 2018). Increases in sIgG4 antibody levels, with or without decreases in IgE levels, are directly associated with successful immunotherapy, and IgG blocking activity is correlated with SU.

After peanut OIT, increases in Ara h 2 sIgG4 and total IgG levels coincide with the increase in the frequency of memory B cells and plasma cells during the initiation phase of OIT. This suggests that these cells provide a clonal contribution to the functionally suppressive antibody. This viewpoint is further supported by the appearance of somatic hypermutation in allergen sIgG4 (Hoh et al., 2016) and the observation of global epitope-specific shifts from IgE to IgG (induction of new Ara h 2 sIgG4) (Vickery et al., 2013). The up-regulated secretion of IgG4 also may be related to IL-10 production by Tregs and Bregs (Satoguina et al., 2005; van de Veen et al., 2013). Typically, serum sIgG4 acts as a blocking antibody isotype to compete with sIgE for allergen binding, thereby suppressing allergen-IgE complex formation (namely allergen neutralization) and preventing MC and basophil degranulation. Also, IgG bound to the surface receptor FcγRIIb can trigger inhibitory signaling with IgE and IgG cross-linking (Cassard et al., 2012; Burton et al., 2014b, 2018). Coaggregation of FcεRI with FcγRIIb further suppresses the adaptive allergic responses by preventing

both degranulation and downstream cytokine synthesis (e.g., IL-4).

In recent peanut OITs, plasma from subjects with active OIT and peanut tolerance (peanut-sensitized, but tolerant) significantly inhibited basophil activation. Furthermore, depletion of IgG4 reversely restored the peanut-induced basophil/MC activation (Santos et al., 2015b; Orgel et al., 2019), suggesting that BATs may be useful for assessing functional changes in IgG blocking functionality during OIT. A comprehensive assessment of the magnitude and blocking-activity of sIgG4 may greatly improve the predictive values of this immunological parameter in relation to OIT response. During OIT, a rapid increase of IgG4-binding epitopes and a slow decrease in IgE amounts and/or binding epitopes have been often observed in participants who reached desensitization (Vickery et al., 2013; Savilahti et al., 2014b; Martínez-Botas et al., 2015). Therefore, the development of higher sIgG/IgE ratios may be more likely to predict lasting tolerance than the absolute quantity of IgG4 (Wright et al., 2016; Chinthrajah et al., 2019). The practicability of such ratios for predictive modeling application needs further assessment in more clinical trials.

Other subclasses of the IgG family, including IgG1, IgG2, and IgG3, have also been investigated and quantified in the course of AIT (Sugimoto et al., 2016; Heeringa et al., 2020). During OIT, serum levels of these IgGs change in a manner similar to that of IgG4 (Savilahti et al., 2014a; Sugimoto et al., 2016). Significant high-fold increases in egg sIgG1 have been observed in responders with sustained desensitization, rendering the characteristic changes of IgG1 level as a potential biomarker for the prediction of a positive clinical response to OIT (Sugimoto et al., 2016). However, there have been few such studies, and each included only a few patients, and the precise responses of such sIgG subclasses during OIT still remain to be clarified.

4.1.3 Immunoglobulin A (IgA)

IgA, as the major secretory immunoglobulin isotype found at mucosal surfaces, plays a key role in immune exclusion. Repeated mucosal allergen exposure in OIT has the potential to induce the production of allergen sIgA and secretory IgA. The secretory IgA has the ability to prevent allergens from accessing the systemic immune system and suppressing inflammatory

responses. Moreover, for maintenance of intestinal homeostasis, secretory IgA and Tregs regulate each other in a double negative-feedback loop, which can be transferred maternally through the entero-mammary axis (Tsuji et al., 2009; Feng et al., 2011; Ramanan et al., 2020).

IgA deficiency may increase the risk of FA and other allergic manifestations (e.g., allergic rhinitis and atopic eczema) in childhood (Lúðvíksson et al., 2005; Janzi et al., 2009). During egg OIT, increased levels of serum egg-white sIgA and sIgA2 were associated with the clinical response to immunotherapy (Wright et al., 2016). Compared to sufferers with transient desensitization, subjects with SU showed higher levels of allergen sIgA. In contrast, a previous study suggested that serum sIgA appeared not to be associated with induced or natural tolerance, since it remained unchanged after egg OIT or avoidance (Vazquez-Ortiz et al., 2013). Interestingly, peanut sublingual immunotherapy demonstrated that salivary IgA might be useful in determining therapeutic efficacy and could serve as a potential biomarker to follow throughout therapy (Kulis et al., 2012). The precise role of IgA in FA development and tolerance induction is still poorly understood. For OIT studies, the existing findings are not sufficient to determine whether IgA is an efficient biomarker for predicting treatment response and SU. Note, however, the thorough elucidation of key pathways in oral tolerance at mucosal sites and emerging tools for IgA detection (e.g., high affinity recombinant IgA-binding peptide probes and enzyme immunoassays for salivary IgA) (Planchais and Mouquet, 2020; Costantini et al., 2022) will likely render IgA a complementary indicator for OIT efficacy.

4.2 B cells

In peanut allergic patients, allergen-specific B cells can be found in circulation at very low frequencies of 0.0097% (Ara h 1) or 0.029% (Ara h 2) of B cells at baseline (Hoh et al., 2016). Approximately three-fold increases in the frequencies of such circulating allergen-specific B cells were observed in response to OIT (Patil et al., 2015; Hoh et al., 2016). The allergen-specific B cells were primarily of the memory phenotype, and predominantly expressed somatically mutated antibodies of IgG and IgA which recognize a variety of conformational or linear epitopes (Hoh et al., 2016; Boonpiyathad et al., 2019).

Notably, during OIT, increasing somatic mutations of IgG4 members of a peanut-specific clone were detected, whereas IgE-expressing clone members showed no change in mutation. This indicates that the ongoing somatic mutation of IgG4-expressing B cells might improve OIT efficacy, possibly by enhancing IgG4 affinity for the allergen.

Bregs are a subset of IL-10-producing B cells involved in the maintenance of tolerance and the restoration of homeostasis following inflammation. IL-10 serves as an essential activator for inducing an immunoregulatory phenotype in B cells (Stanic et al., 2015). IL-10-overexpressing B cells regulate the responses in both innate and adaptive immunity via various pathways (Stanic et al., 2015), such as (1) suppressing DC maturation, T effector cell proliferation, and IgE production, (2) promoting production of anti-inflammatory factors, and (3) lowering production of pro-inflammatory cytokines. In addition to IL-10, secretion of transforming growth factor- β (TGF- β) and IL-35 may contribute to Breg-mediated immunosuppression. There is still a lack of distinctive phenotypic or lineage markers and specific cytokine profiles that can accurately characterize Bregs. One study indicated that human-inducible IL-10-secreting Bregs (CD73⁺CD25⁺CD71⁺ B cells, Br1 cells) take an active part in peripheral allergen tolerance in beekeepers (van de Veen et al., 2013). An increased frequency of Br1 cells was observed in bee venom allergic subjects receiving AIT. The inducible Br1 cells could potently suppress antigen-specific CD4⁺ T-cell proliferation and produce sIgG4 when they switched to plasma cells. Allergen sIgG4 is a crucial contributor for inducing and sustaining immune tolerance during OIT. A subsequent study further demonstrated a similar immunoregulatory role for such B cells (Br1 cells and sIgG4-switched memory B cells) in allergen tolerance in both AIT patients and naturally exposed beekeepers (Boonpiyathad et al., 2017). In a casein-induced allergy model in mice, IL-10-producing CD5⁺ B cells derived from mesenteric lymph nodes (MLNs) effectively inhibited the allergic response in a Foxp3⁺ Tregs-dependent manner. The underlying mechanism likely involves the paracrine action of Breg-derived IL-10 on Foxp3⁺CD25⁺ T cells within MLN, possibly providing a novel therapeutic regulator for FA treatment. A recent study suggested for the first time that pollen SCIT could lead to an increase in the number of IL-10-producing Bregs (CD19⁺CD5^{hi}CD1d1⁺

and CD19⁺CD24^{hi}CD38^{hi} B cells), which was associated with an increased IgG4 level and enhanced local IgE inhibitory activity in nasal fluid (Shamji et al., 2019). The nasal IgG4-associated inhibitory activity correlated closely with the clinical response of SCIT. The study indicates the potential role of Bregs in inducing immune tolerance against aeroallergens. These findings should be investigated in other AIT models to define the capacity of Bregs to serve as candidate biomarkers for a successful AIT response.

5 T cell responses

During an allergic response, T-cell activation drives the main effector phases of sensitization (Schmidt-Weber and Blaser, 2002; Tordesillas and Berin, 2018). T-cell differentiation and activation events take place primarily through a Th2-biased response pathway initiated by epithelium-derived cytokines (Th2-inducing cytokines), such as thymic stromal lymphopoietin (TSLP), IL-25, and IL-33 (Eiwegger et al., 2019; Hong et al., 2020; Nakajima et al., 2020). In contrast, immune tolerance to food antigens is mediated mainly by Tregs induction. Indeed, FA is induced by the loss of tolerance to food proteins, and is characterized by an altered balance of Treg cells and a shift to Th2-type cytokines in the intestinal lamina propria. Thus, Th2 cell activation and Tregs deficiency are vital features of allergy. The changes in the magnitude and polarization of allergen-specific T cells are likely to be key components of OIT effectiveness, emerging as biomarkers for predicting OIT outcomes.

5.1 Tregs

Tregs, as essential mediators of peripheral tolerance to self- and non-self-antigens, are critical to the induction and maintenance of oral tolerance. To a certain degree, Foxp3⁺ Tregs rather than T cell anergy or depletion confer functional oral tolerance. As demonstrated in patients with immune dysregulation, polyendocrinopathy, enteropathy, and X-linked (IPEX) syndrome, dysfunction of transcription factor Foxp3⁺, which drives the genetic programming of Treg cells, is closely related to an increased incidence of FA (Torgerson et al., 2007; Attias et al., 2019). In a mouse model of OVA-induced allergic diarrhea, Foxp3⁺ Tregs proliferated and accumulated in the intestinal

LP during tolerance induction, and depletion of Foxp3⁺ cells completely abolished established oral tolerance (Hadis et al., 2011). Similarly, in a model of contact hypersensitivity (CHS), transfer of CD4⁺CD25⁺ cells into invariant chain knock-out mice (deficient in CD4⁺ T cells) prevented the CHS response and skin infiltration mediated by CD8⁺ T cells (Dubois et al., 2003). In normal mice, in vivo depletion of CD4⁺CD25⁺ cells by antibody (clone PC61) treatment reversely impaired oral tolerance. In FA mice, intragastric administration of cow's milk proteins (OIT intervention) pre- or post-sensitization suppressed the Th2-immune response and simultaneously alleviated hypersensitivity symptoms, mainly through the elicitation of mucosal IL-10- and TGF- β -producing Tregs (Smaldini et al., 2015). Tregs are well known to be associated with the production of IL-10, TGF- β , and IL-35. IL-10 can significantly suppress sIgE production and induce sIgG4 production via Treg-B cell interaction (Jutel et al., 2003). Tregs also express suppressor molecules, such as CTLA-4 and programmed cell death-1 (PD-1), both of which contribute to immune tolerance as co-stimulation blockades. In a clinical trial (Syed et al., 2014), 23 participants underwent peanut OIT for 24 months. They were deemed to have clinical immune tolerance if they had no detectable allergic reactions to OFC after three months of treatment withdrawal. Compared to non-tolerant and control participants, immune tolerance participants showed higher numbers of antigen-induced Treg (ai-Treg) with greater suppressive function and higher levels of *FOXP3* hypomethylation. In contrast, the state of "resensitization" was correlated with increased methylation of cytosine-phosphate-guanosine (CpG) sites in the *FOXP3* locus.

Besides conventional Foxp3⁺ Tregs, another type of Tregs named Th3 cells, also contributes a crucial role in oral tolerance. Th3 cells do not express Foxp3 or CD25 molecular, but express latency-activated peptide (LAP) on their surface. These cells produce high amounts of TGF- β and moderate amounts of IL-10, and are usually identified as TGF- β -producing CD4⁺Foxp3⁻LAP⁺ T cells. In the absence of inflammation, TGF- β secretion can promote the expression of the *FOXP3* gene in activated T cells during T cell expansion, thereby inducing the differentiation of Tregs in the peripheral repertoire in the absence of thymic CD25⁺ Tregs (Carrier et al., 2007). Therefore, Th3 cells probably act as a central mediator of peripheral

immune tolerance both directly by TGF- β production and indirectly by Foxp3⁺ Tregs induction. EPIT generates gut-homing LAP⁺ Treg cells that can directly suppress systemic anaphylaxis without upstream modification of humoral or cellular immunity (Tordesillas et al., 2017). The mechanism of protection is considered a novel pathway of direct TGF- β -dependent Treg-cell suppression of MC activation.

All these data indicate that induction and expansion of Tregs might be available and crucial indicators for reflecting the state of immune tolerance during OIT. Epigenetic changes in the *FOXP3* locus appear to be the crucial factor directly regulating Treg plasticity and suppressive function. However, these findings are based on studies with small sample sizes and short follow-up periods. In future, with exploration of the precise relationships among different Treg subsets and identification of unique phenotypes, large-scale, long-term follow-up studies may further assess the clinical significance of Tregs for predicting OIT outcomes, particular SU.

5.2 Th2-type cytokines

Th2 cytokines, including IL-4, IL-5, IL-6, IL-9, IL-13, and IL-17E (IL-25), are all-important hormonal messengers responsible for several biological effects in the host immune system (Berger, 2000; Smart and Kemp, 2002; Akdis et al., 2016; Chinthrajah et al., 2016; Shik et al., 2017) (Table 1). For example, in allergic inflammation, IL-5 is associated with eosinophil recruitment. IL-4 and IL-13 are associated with induction of IgE class switch recombination, smooth muscle cell contraction, and mucus production. IL-25 is involved in mucosal immunity and inducing production of other Th2 cytokines IL-4, IL-5, and IL-13 (Chinthrajah et al., 2016). In sensitization, epithelial disruption allows increased antigen exposure and induces production/release of epithelial cytokines (e.g., IL-33, TSLP, and IL-25) which can up-regulate OX40 ligand (OX40L) on DCs. The activated DCs then promote differentiation of naive T cells into Th2 cells producing cytokines that recruit eosinophils (IL-5) and promote IgE class-switching in B cells (IL-4 and IL-13).

In OIT studies, measurements of secreted Th2 cytokines in vitro can be performed in serum or stimulated peripheral blood mononuclear cells (PBMCs). Various testing methods, including enzyme-linked immunosorbent assay (ELISA), enzyme-linked immunospot

Table 1 Th2 differentiation/secreted cytokine profiles

Cytokine	Cell source	Classification	Characteristics and functionality
IL-2	T cells (mainly Th1 cells)	Common γ -chain family (IL-2 family)	Required for differentiation to Th1 and Th2 subsets Promotes proliferation of T cells, B cells, and NK cells Involved in Tregs development Augments cytokine secretion and cytolytic activity
IL-4	T cells, NK cells, eosinophils, mast cells	IL-4/IL-13 family	Promotes Th2 cell differentiation Stimulates expansion of activated B cells, T cells, and mast cells Induces class switch of antibodies; promotes IgE production
IL-6	Th2 cells, monocytes, macrophages, BMSCs	IL-6 family	Keystone cytokine in health and disease Exhibits contrasting features of proinflammatory and anti-inflammatory profiles Induces differentiation of monocytes and Tfh cells Involved in B cell maturation; induces fever and APP synthesis Regulates naive CD4 ⁺ T cell differentiation Dysregulation is implicated in the onset/development of AICIDs (offering IL-6-targeted therapies, e.g., Satralizumab, Siltuximab, Tocilizumab, and Olamkicept)
IL-27	Monocytes, endothelial cells, DCs	IL-6 family	Dual immune-regulations depending on context Induces Th1 cell expansion Synergizes with IL-12 to promote production of IFN- γ by naive CD4 ⁺ T cells Promotes IL-10 production and specializes Treg response Candidate antitumor agent
IL-17E (IL-25)	Epithelial cells, macrophages, mast cells, Th2 cells, eosinophils, basophils	IL-17 family	Promotes cell expansion and Th2 cytokine production (IL-4, IL-5, IL-13, and TSLP), and sustains type 2 immunity A “barrier surface” cytokine, involved in mucosal immunity Therapeutic target for treatment of severe asthma exacerbation
IL-33	Endothelial cells (e.g., HEVECs), epithelial cells, fibroblast-like cells, myofibroblasts (e.g., pericryptal fibroblasts), mast cells, DCs (in inflammatory condition)	IL-1 family	Drives early immune response against allergens and other environmental insults, necessary for Th2 cytokine production Regulates DC functions, drives and influences development of Th2, Tfh, and Treg cells A central pathway in pathogenesis of allergic inflammation (IL-33-ST2-ILC2s axis), biomarkers for defining AAD subtypes Maintenance of tissue homeostasis, repair, and remodeling
IL-31	Th2 cells, mast cells, macrophages, DCs, eosinophils	Gp130/IL-6 family	Implicated in ASDs; offers candidate therapeutic approaches (e.g., Nemolizumab) Potential pathway of inflammation in allergic and autoimmune diseases (IL-31/IL-33 axis) Recruitment of PMNs, monocytes, and T cells to inflammatory sites (by inducing chemokine production) Dual role in immunomodulation (in murine asthma models, early proinflammation Th2 response \rightarrow later negative feedback response)
IL-3	T cells, NK cells, mast cells	HCs family	Supports growth and differentiation of hematopoietic cells Stimulates mast cell growth and histamine secretion
IL-5	Th2 cells, mast cells	HCs family	Stimulates B cell/eosinophil growth and differentiation Induces class switch to IgA Candidate therapeutic target for NPs, asthma, and other ADs (e.g., Mepolizumab, Reslizumab, and Benralizumab)

To be continued

Table 1 (continued)

Cytokine	Cell source	Classification	Characteristics and functionality
IL-10	T cells (mainly Th2 cells), macrophages, monocytes, DCs, neutrophils, mast cells, eosinophils, NK cells, epithelial cells, tumor cells	IL-10 family	Triggers a robust immune suppressive response (classic role) Enhances B cell survival, proliferation, and antibody production Limits damaging effects of neuroinflammation Involved in AT regulation; promotes epithelial wound healing Therapeutic manipulations in various pathologies (e.g., IBD, cancer, psoriasis, hepatitis C, RA, SLE, and asthma)
IL-13	Th2 cells (mainly), mast cell	IL-4/IL-13 family	Similar to IL-4 functions Potential pathways in allergic, autoimmune, fibrotic and neoplastic diseases (IL-4/IL-13 axes) Candidate therapeutic approaches (e.g., Dupilumab, Lebrikizumab, Anrukizumab, Tralokinumab, and AS1517499)

IL, interleukin; Th1, T helper type 1; Tregs, regulatory T cells; NK, natural killer; IgE, immunoglobulin E; BMSCs, bone marrow stromal cells; Tfh, T follicular helper; APP, acute-phase protein; AICIDs, autoimmune and chronic inflammatory diseases; DCs, dendritic cells; IFN- γ , interferon- γ ; TSLP, thymic stromal lymphopoietin; Gp130, glycoprotein 130; ILC2s, group 2 innate lymphoid cells; ST2, tumorigenicity 2 receptor (a receptor for IL-33); HEVECs, high endothelial venule endothelial cells; AAD, allergic airway disease; ASDs, autoimmune skin diseases; PMNs, polymorphonuclear leukocytes; HCs, hematopoietic cytokines; NPs, nasal polyps; ADs, allergic diseases; AT, adipose tissue; IBD, inflammatory bowel disease; RA, rheumatoid arthritis; SLE, systemic lupus erythematosus.

assay (ELISpot), co-culturing T cells with DCs, tetramer analysis, and intracellular staining, have been used to detect not only Th2 response (IL-4, IL-5, IL-9, and IL-13), but also Th1 (IFN γ) and Treg (IL-10 and TGF- β) responses during AIT. Generally, AIT intervention appears to act through down-regulation of allergen-specific Th2 response or increased Th1 response, or through the induction of Tregs. In an egg OIT study (Perezábad et al., 2015), at baseline, the egg-allergic patients presented a trend toward a higher production of Th2 cytokines (IL-5 and IL-13) and significantly lower levels of IL-10 ($P<0.01$) after PBMC stimulation with OVA. After completing egg OIT, these subjects showed cytokine profiles of decreased production of IL-5 and IL-13, as well as higher levels of OVA-specific IL-10 ($P<0.05$). Cytokine variation during OIT might be a feature of the transition from allergen-specific Th2 to Treg predominance.

Several studies have indicated that Th2 cytokines (IL-5 and IL-13) decline significantly during peanut OIT (Varshney et al., 2011; Kulis et al., 2019). One study involving 39 peanut-allergics demonstrated that subjects with clinical desensitization had higher secretion of IL-10, IFN- γ , and TNF- α from PBMCs over a period of 6 to 12 months (Jones et al., 2009). However, in another study, only a transient increase in TGF- β level was observed in peanut OIT subjects (Varshney et al., 2011), and no significant change was observed in IL-10 or IFN- γ (Varshney et al., 2011; Kulis et al., 2019). Similarly, transient increases were

seen in egg-induced IL-10 and TGF- β levels, and the ratio of Th2:Th1 cytokine production decreased (Vickery et al., 2010). In a study of cow's milk allergy, a marked decrease in IL-13, IL-5, and IL-10 production (statistically significant for IL-13 and IL-10) by PBMCs upon β -casein stimulation was observed in children after OIT treatment (Perezábad et al., 2017). Interestingly, IL-10 production from non-allergic donors was significantly higher ($P<0.01$) than that from allergic patients at the end of OIT, and Th1 cytokines of IFN- γ or TNF- α were not detected. Another study indicated that there were no significant changes in the cytokine profiles of IL-4, IL-5, IL-6, IL-10, or IL-12p70 during the cow's milk OIT process (Salmivesi et al., 2018). The possible reason is either that blood cytokine levels cannot completely reflect mucosal production or that mucosal and periphery Tregs have different functions. At present, cytokine detection serves as an available and relatively economic indicator for monitoring OIT effectiveness. In the future, more research should be conducted to explore the precise role and pattern of variation of these cytokines during OIT.

5.3 Th2 cells

As mentioned above, several studies have investigated the variation of cytokines secreted from Th2 cells during OIT. However, few studies have focused on the changes in Th2 cells themselves. Th2 cells are also important as mediators in initiating and orchestrating the allergic response, as well as in influencing

the course of AIT. At present, a major factor limiting the extensive use of such atopic disease-causing T cells as both therapeutic targets and clinical biomarkers is the lack of a suitable strategy to identify and distinguish these “bad” cells that involve allergic reactions from overall nonpathogenic Th2 cell types.

Recently, Wambre et al. (2012, 2017) have described a subset of human memory Th2 cells confined to atopic subjects that includes all allergen-specific Th2 cells. This proinflammatory Th2 cell subpopulation (named the Th2a cell subset) comprises terminally differentiated CD4⁺ T cells characterized by stable co-expression of CRTh2, CD161, and CD49d, and low expression of CD45RB and CD27 (CD4⁺, CRTh2⁺, CD161⁺, CD49d⁺, CD27⁻, and CD45RB⁻). Th2a cells also exhibit numerous functional attributes distinct from those of conventional Th2 cells. Importantly, Th2a cells are specifically involved in the allergic response, but are virtually absent in non-allergic individuals. Moreover, food/component-specific Th2a cells are preferentially deleted after successful OIT, indicating that allergen-specific Th2a may represent a suitable therapeutic target and surrogate marker of clinical efficacy during AIT. In future, further detailed studies focusing on the Th2a subset may be of critical importance for understanding the mechanisms of action associated with the allergic process and successful AIT. They also may contribute greatly to response-monitoring and the design of appropriate immunomodulatory strategies (Wambre et al., 2017; Luce et al., 2020, 2021).

IL-4 is the quintessential Th2 cytokine produced by CD4⁺ T cells (e.g., T follicular helper cells) in response to sensitization. As the important linker between Th2 cells and B cells, it can promote Th2 differentiation and the IgG/IgE isotype-switched antibody response. A combination of assessment of Th2a cells and residual IL-4-producing T cells may be clinically useful for monitoring OIT response and predicting SU durability.

5.4 DCs

DCs play a central role in initiating immune responses to culprit allergens and subsequently driving T cell differentiation (Ruiter and Shreffler, 2012; Liu et al., 2021). DCs, along with monocyte-macrophages, dictate oral tolerance against allergy by shaping the T-cell and subsequent B-cell antibody response.

DCs from children with FA appear to generate more pro-inflammatory cytokines, and the CD4⁺ T cells of subjects can be spontaneously activated to produce Th2 cytokines in the presence of FcεRI-bearing DCs (Frischmeyer-Guerrerio et al., 2011). In the context of oral tolerance, after innocuous food ingestion, goblet cells and intestinal resident macrophages (CX3CR1⁺ macrophages) sample luminal food antigens and deliver them to LP CD103⁺ CX3CR1⁻ DCs (Bogunovic et al., 2009; Varol et al., 2009; Niess and Adler, 2010; McDole et al., 2012; Welty et al., 2013; Rivas et al., 2015; Esterhazy et al., 2016; Shiokawa et al., 2017; Kulkarni et al., 2020). After being activated by the antigen, these cDCs (also called migratory DCs) migrate via afferent lymphatics to the draining lymph nodes in a chemokine (C-C motif) receptor 7 (CCR7)-dependent manner. They then foster naive CD4⁺ T to differentiate into peripheral Treg (pTreg) cells through epithelial cell-derived TGF-β and retinoic acid. Induction of Tregs can inhibit Th2-dependent allergic inflammation and MC degranulation (Fig. 1).

In general, the subset of cDCs (namely CX3CR1⁺ DCs) are regarded as inflammatory, nonmigratory gut-resident T cells that have the capacity to promote production of TNF-α, induce Th17 cells, and activate Th1 cells. However, a recent study has suggested that CX3CR1⁺ DCs may contribute to pTreg expansion and oral tolerance (Esterházy et al., 2016). In a murine oral tolerance model for FA, administration of a large amount of food additives significantly inhibited the migration of CD103⁺ DCs into MLN and decreased the cell populations, thereby preventing the acquisition of oral tolerance (Yamashita et al., 2017). In the context of FA treatment, it was also shown that oral administration of probiotics could alleviate allergy symptoms and lead to an increase in Tregs induced by mucosal CD103⁺ DCs (Fu et al., 2017). OIT seems to have an impact on circulating DCs, since the peripheral blood DCs after peanut OIT suppress methylation of FOXP3 CpG sites in effector T cells (Syed et al., 2014). Besides, a pilot study had demonstrated for the first time in humans that both OIT and SLIT are associated with changes in the innate functions of DCs, which may inhibit allergic reaction and promote tolerance development (Frischmeyer-Guerrerio et al., 2014). The therapeutic efficacy may be associated with the reduced pro-inflammatory cytokine (IL-6) secretion and increased IL-10 production by myeloid

DCs (mDCs). Moreover, increased IFN- α secretion from plasmacytoid DCs (pDCs) was also observed in subjects undergoing OIT. As IFN- α can act on mDCs to augment autocrine secretion of IL-10, which contributes to suppression of the Fc ϵ RI-dependent allergic response, OIT seems to exert pro-tolerogenic changes in both pDC and mDC innate immunity.

Notably, data focusing on the role of DCs in relation to FA and oral tolerance are almost entirely derived from mouse models and immunophenotyping of circulating cells with no distinct DC subsets. Small sample sizes in clinical trials also render it impossible to make more definitive statements regarding the relationships between the obtained DC findings and clinical outcomes. So far, no biomarker has been identified that is applicable for clinical use in OIT. Nevertheless, a greater understanding of how DCs contribute to the effectiveness of AIT and influence adaptive immune responses may inform the development of novel therapeutic strategies, both in FA and autoimmunity and transplantation. The present challenges provide the impetus to examine the above questions in larger clinical trials.

6 Potential cell markers

6.1 Myeloid-derived suppressor cells (candidate contributors to oral tolerance)

Myeloid-derived suppressor cells (MDSCs) are a heterogeneous population of cells consisting of immature myeloid cells and myeloid progenitor cells. Besides playing an essential role in metastasis (Wang et al., 2019), such cells have the ability to suppress effector T-cell responses and activate Tregs by generating suppressive factors, including IL-10, TGF- β , and nitric oxide. Generally, MDSCs in mice are broadly identified on the basis of their coexpression of Gr1 and CD11b markers (Ji et al., 2016). The MDSCs can be further subdivided into two subsets: (1) polymorphonuclear MDSCs (PMN-MDSCs, CD11b⁺Ly6G⁺Ly6C^{int}), and (2) monocytic MDSCs (Mo-MDSCs, CD11b⁺Ly6G⁻Ly6C^{hi}). In the mouse models of OVA-induced FA and OIT, OIT induced systemic expansion of IL-10-producing CD4⁺ T cells and MDSCs, particularly the monocytic MDSC subpopulation (Yoneyama et al., 2021). Notch signaling was involved in these processes. Moreover, the contribution of MDSCs

to OIT-induced SU was confirmed by the prevention of establishment of SU after MDSC depletion with the anti-Gr1 antibody. Interestingly, repeated challenges with OVA reversely induced the development of severe allergic reactions in OVA-sensitized mice. Chronic and low-intensity stimulation or inflammation by OIT may contribute to the expansion of these suppressor cells, whereas excessive inflammation induced by the allergic process results in the activation/expansion of inflammatory cells, such as basophil and MC degranulation. A similar situation has also been observed in the immunological transition of MCs during FA and OIT processing. The frequencies of MDSCs and IL-10-producing CD4 T cells seem to be indicators of whether OIT can be successfully completed. For the moment, MDSCs may be regarded only as an indicator that reflects the immune status of subjects receiving immunotherapy. The practical application of MDSCs as a biomarker for predicting OIT outcomes remains to be confirmed with more supportive data.

6.2 Innate lymphoid cells (novel player in immune tolerance)

ILCs are new, intriguing lymphocytic populations that lack diversified antigen receptors expressed on T cells and B cells. They are largely tissue-resident cells and are involved with tissue development, remodeling, and inflammation (Vivier et al., 2018). ILCs can be categorized into subtypes including: (1) group 1 ILCs (ILC1s) and natural killer (NK) cells, (2) group 2 ILCs (ILC2s), and (3) group 3 ILCs (ILC3s) and lymphoid tissue inducer (LTi) cells, with comparable cytokine profiles to Th1, Th2, and Th17 subsets, respectively. ILC2s are heavily involved in allergic inflammation by amplifying the Th2 response. Also, they bear a resemblance to Th2 cells by sharing functional similarities. Usually, ILC2s reside in the skin, airway, and intestinal mucosa, and can respond to non-specific stimuli (such as IL-25, IL-33, and TSLP) after allergen exposure. Such cells appear to play a central role in allergic inflammation. Following resolution of inflammation, ILC2s may contribute to the re-establishment of epithelial barrier function and maintenance of tissue homeostasis through expression of the growth factor amphiregulin (Monticelli et al., 2015). Increasing evidence indicates that successful AIT is capable of leading to a significant reduction of

ILC2s in the peripheral blood of subjects (Lao-Araya et al., 2014; Fan et al., 2016; Mitthamsiri et al., 2018), suggesting that ILC2 detection may be an effective indicator for SCIT monitoring. Qualitative and quantitative measurements of ILC2s might also serve as promising biomarkers during FA-OIT processing. The precise impacts of these cells in the course of OIT and tolerance induction should further be investigated.

Human ILC3s are located mainly in the intestinal LP, and also contribute to the maintenance of mucosal immune tolerance. A recent study has suggested that activated CD40L⁺ ILC3s may provide innate B cell help and are involved in an innate immunoregulatory mechanism through induction of IL-10-secreting immature transitional Breg (itBreg) differentiation (Komlósi et al., 2018). A decreased ILC3 level contributes to insufficient Breg-mediated immune tolerance in patients with various allergic disorders. Moreover, ILC3 also supports the generation, maintenance, and function of Tregs by controlling the production of IL-2 in the small intestine. ILC3s seem to exert a crucial role in the regulation of immunologic homeostasis and oral tolerance to dietary antigens (Zhou et al., 2019). Recently, a novel subset of ILCs with IL-10 production was identified as regulatory ILCs (ILCregs) (Wang et al., 2017). ILCregs exist in the gut and harbor a unique gene identity that is distinct from other subsets of ILCs and Tregs. They exert their regulatory functions by inhibiting inflammation via IL-10 and TGF- β 1 production. All these ILC subsets appear to be important in orchestrating inflammation, immune tolerance, and tissue homeostasis, rendering them great potential indicators for FA-OIT assessment and SU predication. Uncovering the signaling circuits that manipulate the development and function of ILCs will help provide an integrated and comprehensive understanding of the regulation of tissue-specific immunity.

7 Omics-based tests

Emerging high-throughput “omics” technologies which provide molecular profiles for bio-specimens have been extensively used in experimental and clinical studies to reveal molecular subtypes and variation tendencies, elucidate the physico-pathological mechanisms of disease, develop mathematical models to predict clinical endpoints, and facilitate application of

precision medicine (Mcshane et al., 2013; Yee et al., 2018; Giudice and Petsalaki, 2019; Crestani et al., 2020; Do et al., 2020; Mersha et al., 2021) (Table 2). In short, omics refers to measurable differences or changes in biological molecules, such as genes, epigenomes, proteins, metabolites, microflora, RNA, and environmental factors (Baar et al., 2014; Azad et al., 2015; di Girolamo et al., 2015; Greenhawt, 2015; Hesselmar et al., 2015; Li et al., 2015; Perkin et al., 2016; Turcanu et al., 2017; Kiyotani et al., 2018; Krutz et al., 2019; Mondoulet et al., 2019; Alhamwe et al., 2020; Kostara et al., 2020; Spertini, 2020) (Table 2). In a multi-center intervention trial comparing the efficacy of baked egg or egg OIT for the treatment of egg allergy (CoFAR7, NCT01846208) (Kosoy et al., 2016), measurement of transcriptional profiling by microarray was conducted to analyze PBMCs obtained from children with egg allergy, children with egg tolerance (to baked egg), and non-allergic children (controls). In combination with multiplex cytokine detection, the data revealed that increased expression of genes associated with allergic inflammation (carcinoembryonic antigen-related cell adhesion molecule 1 (CEACAM1) and cytokine-inducible Src homology 2 (SH2)-containing protein (CISH)) was linked with increased secretion of the cytokines IL-5, IL-9, and TNF- α . Transcriptional profiling is considered a useful tool to uncover novel immunologic processes in allergy and tolerance induction. In a pilot study (Crestani et al., 2020), mass spectrometry-based untargeted metabolomic profiling was performed to identify unique metabolites (candidate biomarkers) in sera collected from children with FA, asthma, or both. Lower levels of sphingolipids and ceramides were observed in children with FA, indicating the interplay between altered microbiota and immune cell subsets in the gut. In a mouse model of peanut allergy, elevated levels of uric acid (UA) were detected in mice undergoing sensitization by liquid chromatography-mass spectrometry (LC-MS)-based metabolomics analysis (Kong et al., 2015). During sensitization, depletion of UA prevented the development of peanut-specific IgE and IgG1, as well as anaphylaxis, while exogenous delivery of UA crystals (monosodium urate) restored the allergic phenotype.

Gut microbes can shape the development of the host immune system, and in turn the host immune status can influence the composition of the microbiome.

Table 2 Overview of current omics technologies

Omics	Scope of application	Samples	Methods	Discoveries
Genomics	Gene/exome sequencing, SNPs, mutations	DNAs	DNA sequencing	Genetic associations/inherited phenotypes with FA; discovery of genes involved in immune cell function
Epigenomics	Histone modification, CpG methylations	DNAs	Methylation array; genome-wide DNA methylation analysis; RNA methylation; ChIP-seq; ATAC-seq	Potential FA/AIT response biomarkers
Transcriptomics	Transcriptional regulation, sequencing	RNAs	Low-input RNA library sequencing; targeted RNA sequencing	Gene expression in immune cells is associated with FA and tolerant subjects; further characterization of allergen proteins
Proteomics	Peptide/protein identification, allergens, post-translational modification	Proteins	NMR; GC-MS; LC-MS; LC-QTOF-MS	Contributing to the diagnosis/prognosis of FA; characterization and quality testing of allergen proteins or immunotherapy products
Metabolomics	Signaling molecules, hormones, metabolites	Proteins	Similar to proteomics	Identifying metabolic profiles/pathway activities from host system or microbiome-derived products which are associated with FA
Microbiomics	Microflora, probiotics, dietary supplements	DNAs, RNAs, proteins, environments	MS, 16S rRNA sequencing	Potential biomarkers for FA development or resolution; potential probiotic candidates for OIT therapy
Exposomics	Pathogens, environmental exposures, drugs, toxins	Environments	MS	Risk factors contributing to FA incidence/prevalence/severity; offering protection against FA epidemic (e.g., early allergic food introduction)

SNPs, single nucleotide polymorphisms; FA, food allergy; CpG, cytosine-phosphate-guanosine; ChIP-seq, chromatin immunoprecipitation-based sequencing; ATAC-seq, assay for transposase-accessible chromatin with high-throughput sequencing; AIT, allergen-specific immunotherapy; NMR, nuclear magnetic resonance; GC-MS, gas chromatography-mass spectrometry; LC-MS, liquid chromatography-mass spectrometry; LC-QTOF-MS, liquid chromatography quadrupole time-of-flight mass spectrometry; rRNA, ribosomal RNA; OIT, oral immunotherapy.

Manipulating the intestinal flora has been proposed as an adjunct to AIT for improving efficacy and safety (Rachid and Chatila, 2016; Aitoro et al., 2017; Canani et al., 2019). Bunyavanich et al. (2016) published the first study to define the relationship between the microbiome and FA resolution, based on 226 children with cow’s milk allergy. By using high-throughput sequencing and microbiological analysis, enriched taxa from the Clostridia class and Firmicutes phylum in the infant flora (3–6 months) were observed in subjects with milk resolution by eight years of age. Previous studies suggested that colonization of mice by a mix of *Clostridium* strains provided an environment rich in TGF-β, and affected the number and function Foxp3⁺ Tregs in the colon (Atarashi et al., 2011, 2013). As described above, Foxp3⁺ Tregs play a critical role in oral tolerance. In a recent study (He et al., 2021), alpha diversity of the gut microbiota increased significantly in most allergic participants after a long-term

(52-week) peanut OIT. Therefore, not only specific taxa of microflora can be studied as probiotic candidates for FA treatment, but also the changes of microflora during OIT can serve as biomarkers for efficacy prediction. Moreover, metabolites, such as short-chain fatty acids, are crucial metabolic products of gut microbiota responsible for protective effects against FA. These compounds are also involved in epigenetic regulation of the immune system. Considering the complicated mechanisms and comprehensive components related to allergy and immunotolerance, further exploration of omics analysis technology (e.g., single-cell omics approaches), as well as optimized combinations of testing indexes (e.g., combining genomics, epigenomics, and transcriptomics for functional characterization, and combining microbiomics, metabiomics, and proteomics for integrative analysis) may lead to the identification of new promising biomarkers and potential therapeutic targets (Table 2). In the next

decades, parallel advances in bioinformatics and computational techniques will better enable the integration, analysis, and interpretation of these exponentially growing datasets and eventually provide the possibility of personalized or/and precision medicine for FA and AIT.

8 Conclusions

Typically, OIT exerts therapeutic effects by affecting many components of the host immune system. OIT-induced immune changes primarily include an early decrease in MC and basophil activation, up-regulated generation of allergen-specific Tregs and Bregs with decreased Th2 production, and changes in allergen-specific antibodies usually characterized by a temporary increase followed by a decrease in sIgE and a gradual increase in sIgG4. Nevertheless, the precise mechanisms underlying these changes and the precise sequence of immune events in the re-establishment of oral tolerance are still poorly understood. Ideal biomarkers with the capacity to accurately predict desensitization and/or tolerance development are needed to implement OIT. At least for safety, this is essential to inform allergic subjects about treatment duration and risk behavior if AIT is conducted. Several indicators such as DCs, B cell, macrophages, regulatory MCs, and ILC subsets have not been well studied in the context of predicting AIT outcomes. Currently available biomarkers in clinics (such as SPTs, BATs, cytokines, specific antibody levels and ratios, and Treg detection) appear to be insufficient to reliably distinguish subjects who have achieved desensitization or SU, and inadequately reflect the subtle immune status and regulatory processes occurring during FA and AIT. Continuing efforts are needed to greatly expand the repertoire of available biomarkers and to discover novel biomarkers for providing personalized and precise approaches to OIT.

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Author contributions

Haitao ZHU conceived the central idea and completed the manuscript. Kaifa TANG and Guoqiang CHEN contributed to manuscript review. Zhongwei LIU finalized the manuscript. All authors have read and approved the final manuscript.

Compliance with ethics guidelines

Haitao ZHU, Kaifa TANG, Guoqiang CHEN, and Zhongwei LIU declare that they have no conflict of interest.

This review does not contain any studies with human or animal subjects performed by any of the authors.

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